

Validation documentation
HCK - nutritional supplements (Hepart)

HiperScan GmbH

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Introduction

The unequivocal proof of the identity of pharmaceutical raw materials based on a monograph or traditional alternative methods is work-intensive, time-intensive and economically often no longer makes sense. Near-infrared spectroscopy (NIR) provides a new means here. It enables relatively easy, fast and nonetheless safe identity testing via the preparation and evaluation of spectra.

The analysis system *Apo-Ident* was developed specially for pharmacy use. Pharmacists have the duty to check the identity of all raw materials for extemporaneous products in their pharmacies. This normally takes place based on the monographs for the respective substances in the European Pharmacopoeia. But also NIR spectroscopy is described in the European Pharmacopoeia as an identification method which, as opposed to the methods incorporated in the respective monographs, is approved for testing [1] (quotation translated)

with the prerequisite that the same results (“namely the determination of the identity” [2]), (quotation translated) are achieved as with the described methods and instruments.

The *Apo-Ident* analysis system serves to identify raw materials for prescriptions in the defined manner according to *ApBetrO* [Pharmacies Rules and Regulations] §§ 6 and 11 at pharmacies (NIR spectroscopy as an alternative testing method). *Apo-Ident* consists of three components:

- An *NIR spectrometer*, which records the spectra of non-preprocessed raw materials in a measuring glass in diffuse reflection or transfection.
- The *QuickStep* spectroscopy software controls the instrument and records the spectra and user inputs via a pharmacy-specific software plug-in. It also generates the test protocol for documentation of the testing and storage of the printout to be signed in the pharmacy.
- The software module *IdentModule* incorporates *reference databases*. The spectra from the *QuickStep* software are presented to it for evaluation.

NIR spectroscopy is a very powerful analytical method. It is also able to establish the identity of several chemical compounds and mixes in as far as an appropriate database (technically correct: a [chemometric model](#)) was created. Identity testing with *Apo-Ident* is a very safe, very fast and easy to operate analytical method for testing a large number of raw materials.

Context of this document

The suitability of the instrument, method and database is proven as follows:

- *NIR spectroscopy as a method for identity testing*: The *Ph. Eur.* [3] describes NIR spectroscopy in *Section 2.2.40* as an analytical method which is also suitable for the identification of raw materials. Therefore, validation of the method as such is not necessary.
- *Performance of the instrument*: The *Ph. Eur.* [3] furthermore describes the apparatus and the testing of its performance in *Section 2.2.40*. The document *Erfüllung von 2.2.40 Ph. Eur. durch Apo-Ident* [4] compares the implementation by *Apo-Ident* with this monograph in order to prove that *Apo-Ident* meets the specifications of the Pharmacopoeia. Each individual instrument delivered to a pharmacy is qualified in accordance with the tests described in “*Control of Instrument Performance*”. In this test, the unit consisting of analysis instrument hardware and the *QuickStep* spectroscopy software is assessed. The result is documented in a test protocol which is kept at the pharmacy.
- *Validation of the database* is documented separately for each substance class. The report at hand documents the substance class *HCK - nutritional supplements (Hepart)*.

The *Arbeitsgemeinschaft der Pharmazieräte Deutschlands (APD)* [Working Group of German Pharmacy Inspectors] has clarified the following in its resolution dated October 16, 2013 ([5], quotation translated):

NIR is a testing method incorporated in the Pharmacopoeia. The testing quality depends on the quality of the database stored. The APD views the use of NIR instruments in case of ensured validation of the databases used in conjunction with it as one of several options for identity testing.

The APD defined more precisely ([6], quotation translated) on October 1, 2014:

The use of near-infrared is a recognised testing method according to Ph. Eur. 8. For the use of NIR instruments in pharmacies for testing the identity of raw materials, sufficient and verifiable validation of the instrument used is required. The quality of the database stored by the instrument manufacturer is decisive for quality. Batch-specific differences with the same original substances must be taken into account if present.

So NIR is basically suitable. The validity of the reference database is proven with the existing validation documentation.

Criteria for the inclusion of substances

This validation documentation describes the results of the validation of the reference database for the substance class *HCK - nutritional supplements (Hepart)*. Validation documentation is created for each published version of the reference database for all substance classes incorporated.

The reference database is incorporated in the software module *IdentModule*. During identification testing with *Apo-Ident*, spectra which are used for evaluation purposes are presented to it by the *QuickStep* software. In the same manner, the *IdentModule* is presented all validation spectra successively during the validation runs for evaluation purposes. The *IdentModule* responds respectively (without taking the initial assumption into account) with the identified substance or rejects it as unknown. The correctness of this response is checked for each possible initial assumption and counted.

The results are summarised for each substance and reproduced in this document. The core statement of this validation report is that the following criteria must be fulfilled for each database entry, so that *Apo-Ident* offers verification of identity by means of NIR for the relevant substance/substance group:

- The database is exclusively generated from spectra which have been recorded by *HiperScan GmbH* on traceable samples in pharmaceutical quality.
 - The samples are procured via typical pharmacy sources (*DAC III.2.: Bezugsquellennachweis für Rezepturbestandteile [reference source for prescription components]* [7]).
 - A valid manufacturer's certificate exists (content, purity and identity of the batch).
 - The identity was confirmed by a certified test laboratory or *HiperScan GmbH*.
- Each version of the reference database (every update) is validated in-full.
 - Calibration spectra (*Type A*), other spectra recorded under the control of *HiperScan GmbH* (*Type B*), and spectra from the field (*Type C*) are presented to the *IdentModule* for evaluation in three separately evaluated validation runs.
 - Here, no single *false positive* result may arise.
 - Here, the various substance classes are also tested for reciprocal rejection, where this is objectively justified (see *Summary* section).
- In the validation with spectra recorded under the control of *HiperScan GmbH*, spectra of at least one independent sample must be considered, i.e. spectra from a batch whose spectra have not been used for the generation of the database. In addition, the set of *Type A* and *Type B* spectra must originate from at least three different batches.
- Spectra of additional substances may be used for the generation of the database even though they will not be offered for identification by this database. The purpose is the reliable distinction from these substances.

- Any positive result of *Apo-Ident* confirms the identity of the substance/substance group and distinguishes it from all other substances of the database. In the case of substance groups, the result is ambiguous: Distinction from all substances not belonging to the group is proven. The substance is identified as a member of this group. However, within the substance group, it is not possible to reliably classify which substance has been tested.
- The criteria for clear identifiability are a [specificity](#) of 100 % ([true negative rate](#)) and a minimum distance in the distance matrix. See 2. d) under [Model creation procedure and validation runs](#).

Validation concept

[Chemometrics](#) is a statistical technique for the extraction of relevant chemical information from spectra. In mathematics, this method is described as *multivariate data analysis*. Chemometrics proceeds here as follows:

1. Collection of spectra for the *calibration sample*. The results (identities) of the calibration sample must be known. The calibration samples must be representative for the samples which are to be evaluated later. Therefore, they must take the various possible (physical) compositions into account. (Therefore, sourcing calibration samples for NIR from the specialist trade is superior to the use of CRS reference substances.)
2. The first mathematical step is *calibration*. Here, the [chemometric model](#) is calculated from the *calibration sample spectra* ([reference spectra](#)) and limits as well as some parameters are stipulated. The chemometric model is used later to calculate the analysis result (*prediction*).
3. Collection of further spectra for the *validation sample* which should be independent of the *calibration sample*. The results (identities) of the *validation sample* must also be known. The textbook suggests a random sample with a normal scope of 25 % to 50 % of the *calibration sample* [8].
4. The second technical data step is *validation*. Here, the [chemometric model](#) created is evaluated based on the spectra of the *validation samples*. As validation parameters for the identification, the *Ph. Eur. Section 2.2.40* [3] specifies the [specificity](#) and [robustness](#).

The validation step according to the textbook has the target of estimating the performance capability of the model created based on a random sample. In order to achieve the best possible precision, attention is paid to the calibration sample. In the field of pharmaceuticals, the safety of the method has priority. In order to be able to [validate](#) the model within the regulatory scope, the validation step must include probative force. For this purpose, the validation sample must be *representative and complete* in order to enable the testing of all cases.

A *sufficient number of batches* must be secured for validation because validation finally proves whether the number of batches in calibration suffices.

Each substance is validated individually. The validation results are documented per substance in this document. Moreover, the documents show how many and which batches have been used for creating the model or model validation.

At least one certificate is taken in for each substance from an accredited test laboratory for the independent testing of identity of the sample. The identification number of the corresponding test certificate is listed in the report, enabling traceability of a substance tested according to the monographs in the Pharmacopoeia.

Model creation procedure and validation runs

The safety of the [chemometric models](#) is guaranteed by several measures during model creation, of which the validation step is the final one. Normally, the procedure is as follows. It is in particular valid for the active pharmaceutical ingredients (APIs) *solid API excipients*, *liquid/semi-solid API excipients* (*with a test certificate*) and *narcotics - solid medicinal substances*. If, for individual substance classes, variations are required, they are depicted in the section [Particularities of individual substance classes](#).

1. Collecting the reference spectra (calibration sample)

- a) Procurement of the samples from the same sources from which pharmacies source their raw material for compounding (Caelo, Fagron, Euro-OTC, . . . , see also *DAC III.2. Bezugsquellen-nachweis für Rezepturbestandteile* [Sources of supply for compounding] [7]).
- b) Testing the suitability according to *ApBetrO* [Pharmacies Rules and Regulations] §§ 6, 11, that is to say the availability of a valid manufacturer certificates via identity, purity and contents of the batch.
- c) Recording standard 40 spectra of the sample in different positions, as a standard on four instruments. Here, handling and presentation of the samples as later in the pharmacy.
- d) Visual checking for anomalies in the spectra. In case of indications of measurement errors, measurement must be repeated. If a signature is missing in the spectrum, the substance may be excluded from the start as not promising (the spectra are nonetheless entered in the database validation as independent *Type B* spectra).
- e) Testing identity. For each substance, a certificate of correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the respective following substance page of this validation documentation the *Mahalanobis distance* to this reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance. Such samples underline the statistical spread of the original reference substance, but cannot add any new characteristics of the substance.

HiperScan GmbH cooperates with some suppliers as follows: the raw materials supplier takes a sufficiently large sample in his incoming goods area so that part of it can be used for recording the NIR spectra. The remainder of the sample goes to analytics for market approval. The manufacturer's batch certificate emerges from these identity, contents and purity tests, which consequently also prove the correct identity of the NIR reference sample. Therefore, the NIR spectra are suitable for structuring the database (*Type A*) and can also optionally be used for validation (*Type B*). The samples which this applies to are marked in the validation report with a footnote.

- f) If the identity of the new sample is proven, it is declared as a reference sample and the spectra are approved for structuring the database.

2. Generating the chemometric models (calibration)

- a) Determination of the transformation matrix from the reference spectra using variance maximisation [8, 9]. (*All* reference spectra are always included, even if only a few spectra are added for an update.) All reference spectra receive the same data pre-treatment, which is also later applied to all measurement spectra in the field (in the pharmacies).
- b) Checking that the number of principal components used is still sufficient.
- c) Calculating the limits for each substance from the spread of the reference spectra. The calculation regulation is identical for each substance in a substance class.
- d) Checking the distances between the limits of the separable substances: The distance matrix contains the *Mahalanobis distances* from each substance to each other. The values in a bidirectional manner are different in each case because the spread of the initial substance is included. If a distance is smaller than the minimal distance, the substances are not considered to be reliably separable. The minimal distance is set at 9. The developer of the model may specify a larger minimal distance (one value for the entire *chemometric model*), to increase the selectivity.
- e) Verification of the model using the reference spectra. No *false-positive* results are permitted.
- f) If one of the criteria is violated (d) *Minimum distance between two substances undershot* or (e) *One substance is identified as another*, the database developers decide which of the following options to apply:

- They remove both substances from the database. (The spectra remain in the validation and may also be included when generating the model. However, they are not offered for testing.)
 - They form a substance group of several substances which cannot be reliably separated. The result is then ambiguous: The chemometric model determines that the sample is one of the substances in the group and not another substance. However, it cannot determine which of the group members it is. In order to determine the clear identity, the user must carry out a suitable additional analysis.
 - They create another *chemometric model* with a smaller scope, in which at least all substances of the non-separable substance group are included (second-stage model). Second-stage models are only called up if the first stage has established that only one of the substances included in the second-stage model can be involved.
- g) If *chemometric models* that fulfil both criteria (distance matrix and no *false positives*), are available for all substance classes, they are combined with the evaluation algorithms to form an *IdentModule* and encoded. This unit can no longer be changed. Its overall function is checked by the validation.

3. Set of validation spectra (validation samples)

The following is provided for validation:

- a) *Type A*: The reference spectra = calibration spectra from which the database was generated. These also include spectra from substances which the *chemometric model* should not identify, but were also recorded during generation in order to increase selectivity. (As a result, the model “learns” to differentiate from other substances which are actually unknown to it.)
- b) *Type B*: Spectra recorded under the control of *HiperScan GmbH* and not used for the generation of the database. These also include reference spectra of other substance classes, and spectra that are not used as reference spectra. Samples are considered to be independent, if they originate from a batch, of which no spectra have been used for the generation of the database. (Up to *IdentModule 2018-01*, samples were still considered independent if the sampling was done independently, i.e. if they originate from another sales container.)
- c) *Type C*: Spectra from the field, which have not been recorded under the control of *HiperScan GmbH* and have not been used for the generation of the database. The spectra include not only substances of the substance class to be tested, but also substances from other classes.

All manufacturers’ batches from which spectra are used for the validation are listed by substance in this document: for substances included in the substance class *HCK - nutritional supplements (Hepart)* in the respective validation reports; otherwise in attachments *A*, *B* and *C*.

Furthermore remains valid: validation spectra may only be removed if an error in the spectrum can be proven. Here, the spectra are not deleted, but instead placed on a *blacklist* incorporating the reason, date and initials in the commentary.

The section *Particularities of individual substance classes* treats the other substance classes from which *Type B* and *Type C* spectra are cited for validation purposes.

4. Validation runs and approval

- a) Validation spectra are transferred holistically to the *IdentModule* for evaluation in the same way as the spectroscopy software *QuickStep* transfers measured spectra.
- b) Following the provision of each spectrum, the *IdentModule* responds as to whether it has recognised a substance and which substance was recognised.
- c) The correctness of this response is checked for each possible initial assumption (each measurable substance with the substance class) and counted according to *true negative*, *false negative*, *true positive* and *false positive*. These figures are provided for each substance and additionally in the section *Summary*, separated according to types *A*, *B* and *C*.

- d) No *false positive* results whatsoever are permissible.
- e) If the criterion is also met for all substance classes, the *IdentModule* is approved.

Particularities of individual substance classes

Basically, *HiperScan GmbH* procures and tests the manufacturer's certificate for the batch, commissions external testing of the identity of the sample or carries it out independently and stores the certificates. As described, this process is established for the Pharmacopoeia substances, that is to say for substance classes **APIs & excipients, solid**, **APIs & excipients, liquid/semi-solid (with analysis certificate)** and **Narcotic substances, liquid/semi-solid**. Therefore, *HiperScan GmbH* is able to furnish proof of the identity of the reference samples. In case of manufacturer-specific substance classes and others, individual steps are organised differently in-part:

The substance class **APIs & excipients, liquid/semi-solid (other)** (often described as cosmetics) incorporates substances for which no specification of the requirements of the pharmaceutical quality is determined, neither in a Pharmacopoeia monograph, a DAC/NRF monograph nor via a manufacturer's specification. Consequently, neither the identity nor contents can be tested independently. No certificates whatsoever exist for the reference samples. So here, merely the matching of the sample with former samples of this product is established and confusion with the other substances is ruled-out. (If the manufacturer of such a substance prepares a specification, determines testing methods and provides manufacturer's certificates in accordance with *ApBetrO* [Pharmacies Rules and Regulations] §§ 6, 11, *HiperScan GmbH* can assign the substance to the substance class *APIs & excipients, liquid/semi-solid (with analysis certificate)* again in the future).

Substance class **HCK – nutritional supplements (Hepart)** contains the HCK micro-nutrients from the Swiss company *Hepart AG*. *HiperScan GmbH* receives the reference samples directly from the manufacturer. For each reference sample, *HiperScan GmbH* also receives manufacturer's certificates and keeps these. New checking of the identity of the reference sample is not carried out by *HiperScan GmbH*. The identity of the reference samples is therefore documented by *Hepart AG*. The spectra of all batches provided by *Hepart AG* are recorded by *HiperScan GmbH* and entered in the database.

All the manufacturer's batches are used for the generation and validation of the substance class *HCK*. The expected variation is also represented in the generation and validation if there are less than three batches.

Significance of testing with *Apo-Ident*

The analysis result is determined using sophisticated statistical methods according to state-of-the-art science and technology. Chemical and pharmaceutical knowledge is applied for the selection of the samples from which the calibration spectra and validation spectra are recorded. Otherwise it does not influence the further steps of model creation.

Verbally, the statement of the analysis result can be expressed as follows. Here "*the spectra match*" means that the criteria *Mahalanobis distance*, *outlier analysis* and *correlation* are met as shown in *Erfüllung von 2.2.40 Ph. Eur. durch Apo-Ident* [4]. "The spectra do not match", on the other hand, means that at least the criterion *Mahalanobis distance* is not met.

The positive analysis result "*was identified as ...*" is very meaningful because both the quantity of substances to be taken into account and the number of underlying samples is very comprehensive.

1. The spectrum of the sample measured matches spectra of the defined substance.
2. The spectrum of the sample measured does not match any spectrum of any other substance in this substance class. Therefore, all other substances can be clearly ruled-out.
3. As the spectra from other substance classes were used for validation, it is proven that no spectrum of one of these other substances matches the defined substance. (All substance classes with which a spectrum comparison is possible and makes sense are used for validation. This is documented for each substance class in the section *Summary*.)
4. If the defined substance belongs to a *substance group* which in itself is not clearly separable with *Apo-Ident*, matching with the spectra of one or several substances in this group is confirmed.

Which of these substances it actually is cannot be determined clearly. All other substances are excluded analogous to [2](#) and [3](#).

On the other hand, a negative analysis result “*was not identified as ...*” means:

1. The substance offered could not be recognised based on the spectrum of this sample.
2. The identity of this sample is not confirmed.
3. Testing must be repeated in accordance with the specifications of the Pharmacopoeia.

Conclusion

NIR spectroscopy is a testing method incorporated in the Pharmacopoeia. In case of successful database validation, it is a possible method for identity testing [\[5\]](#). *Apo-Ident* meets the criteria of the *European Pharmacopoeia* as a near-infrared spectrometer and proves the validity of the reference database with the existing validation documentation. This means that *Apo-Ident* can be used as an alternative testing method for testing raw materials at pharmacies.

Explanation of terminology

The following section serves to explain or define specialist terminology which is required in order to understand this document. If necessary, definitions for the analysis system *Apo-Ident* are defined more precisely.

The term database is used in this document exactly as in the *Ph. Eur. Section 2.2.40* [3] synonymous with [chemometric model](#). In order to differentiate the databases which are relatively independent of each other, *HiperScan GmbH* frequently also uses the term [substance class](#) (primarily in the plural). On the other hand, the spectra used to structure the database are termed spectrum collection and not database.

Substance classes are units of the organisational structure of the *IdentModule*. The substance classes are substance [databases](#) which are also broadly independently subscribable. On the one hand, the liquid and semi-solid substances are separated from the solid powders because they are measured against different references and therefore the spectra cannot be compared. On the other hand, for example the Pharmacopoeia substances are kept separated from the manufacturer-specific database HCK micro-nutrients from the Swiss company *Hepart AG*.

The individual substance classes need only be limited against each other in-part. Often, no risk of confusion exists because they can only be procured from different sources. On the other hand, in several cases we handle substances which need not be distinguished. For example, *Angelica root oil* of the substance class *APIs & excipients, liquid/semi-solid (with analysis certificate)* neither needs to be delimited from *Angelica root oil* of the substance class *APIs & excipients, liquid/semi-solid (other)* nor is matching required. Respectively one single [chemometric model](#) is behind a substance class. (Even if several reciprocally secured chemometric models would be permissible.) The terms *substance class*, *chemometric model* and *databases* are mostly used here as synonyms.

A substance group respectively summarises all the substances within a [substance class](#) which cannot safely be distinguished from one another based on their NIR spectra. However, all the other substances in the database can be excluded.

The formation of subgroups is mentioned in the *Ph. Eur. Section 2.2.40* [3]. In this manner, technical restrictions in case of extensive databases can be avoided and it is possible to prepare individual subgroups with different spectrum pre-treatment. Validation of the subgroups against each other is required. *HiperScan GmbH* has solved these technical restrictions and doesn't use any subgroups within a substance class any longer.

Principal component analysis (PCA) [8, 9] is a multivariate statistics process or multivariate data analysis. It serves to structure, simplify and illustrate comprehensive data records by describing a large number of statistical variables by describing a lower number of linear combinations (the *principal components*) which are as significant as possible. In the *Apo-Ident IdentModule*, *PCA* is used to evaluate the recorded spectrum data (corresponding with *Ph. Eur. 2.2.40* [3]).

The term validation is defined in both relevant contexts here with different (even if related) meanings.

Within the sense of the expert discipline of *chemometrics*, validation is a process step when creating a [chemometric model](#): after a transformation matrix, limits and various parameters have been calculated or determined from a set of reference spectra during the course of the calibration step [8, 9], the validation step determines the performance capability of the model (selectivity, precision, ...) based on the validation spectra. Normally, random sampling is planned here. In order for the validation to gain strength of proof, the validation spectrum set must be selected with an appropriately wide scope (*representative* and *complete*). The terms *validation run* and *validation step* always actually mean the process step in this sense.

In the regulatory sense (of pharmaceutical production), validation is the documented proof that a process or system meets the previously specified requirements reproducibly when applied practi-

cally. In this sense, the *Apo-Ident* databases only become validated databases with the validation documentation, which this document is part of.

The *European Pharmacopeia* uses the term validation in *Section 2.2.40* within the sense of the specialist discipline of *chemometrics* [3].

The robustness of a process is the property of only being influenced by environmental fluctuations (e.g. temperature or humidity) a little. A method is robust if the environmental conditions do not or hardly falsify the final result.

The specificity of a classification (of a [chemometric model](#)) is the [true negative rate](#).

The recognition rate (also sensitivity) is the [true positive rate](#). It defines in how many percent of cases a correctly set up substance is actually confirmed.

The true negative rate describes the share of spectra correctly classified as non-identity during validation. This is equivalent to correct classification. It means that a substance *A* within identity checking as substance *B* is judged as “*not identified*”. The *true negative rate* is equivalent to the conditional frequency

$$h(\text{rejected}|\text{genuinely no identity}) = \frac{r_n}{r_n + f_p}$$

with r_n as the total number of *true negative* classifications and f_p as the total number of *false positive* classifications. For successful validation of an *IdentModule*, all spectra presented belonging to this category must be classified as *not in accordance*.

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of this number. The weight of each spectrum of a substance/substance group *i* therefore results as

$$w_i = \frac{1}{n_i}$$

with n_i number of spectra in this substance/substance group. This weighting ensures that the overall result cannot be enhanced by adding especially large numbers of spectra from easily separable substances.

The true positive rate describes the share of spectra correctly classified as identity during validation. This is equivalent to correct classification. It means that a substance *A* within identity checking as substance *A* is judged as “*identified*”. The *true positive rate* is equivalent to the conditional frequency

$$h(\text{identified}|\text{genuine identity}) = \frac{r_p}{r_p + f_n}$$

with r_p as the total number of *true positive* classifications and f_n as the total number of *false negative* classifications. The *true positive rate* is a measure for the recognition rate of the validated *Apo-Ident IdentModule*.

In order to ensure that each substance is received with the same weight, the spectra are weighted as described for the [true negative rate](#).

The true negative result describes a spectrum correctly classified as non-identity during validation. It is equivalent to correct classification. It means that a substance *A* within identity checking as substance *B* is judged as “*not identified*”.

The false positive result describes a spectrum falsely classified as non-identity during validation. This is the most critical type of possible false classification. It means that a substance *A* within identity checking as substance *B* is judged as “*identified*”. For successful validation of an *IdentModule*, a number of false positive events of zero are demanded for all spectra entering the validation.

The true positive result describes a spectrum correctly classified as identity during validation. It is equivalent to correct classification. It means that a substance *A* within identity checking as substance *A* is judged as “*identified*”.

The false negative result describes a spectrum falsely classified as non-identity during validation. It is equivalent to false classification. It means that a substance *A* within identity checking as substance *A* is judged as “*not identified*”.

The ‘Rule of Three’ says that with a probability of 95 % the next random sample of the same size no more than three false results are to be expected if no false result existed in the existing random sample [10, 11].

The *specificity* and *recognition rate* are determined both globally and from the validation runs for all substances. The information is supplemented with the hypothetical value if there had been three false results more. The percent information is provided in parentheses with the “greater than” symbol ‘>’, e.g. *specificity* 100.000 % (>99.983 %) if 17 567 false spectra have been presented without one single *false positive* result. The larger the statistical basis, the lower the influence of the hypothetical false results.

The Mahalanobis distance is a distance measure between two points in *n*-dimensional vector space. Here, the respective direction component of the distance to *standard deviation* [12] of an *n*-dimensional distribution is standardised. In case of the *principal component analysis* [8, 9] this standardisation relates to the distribution of the respective calibration data set for a classification (substance/substance group) in the *principal component space* [8]. The *Mahalanobis distance* of a point (mapping of a spectrum) $\vec{y}$ in the *n*-dimensional principal component space to the expected value of an *n*-dimensional distribution $\mathbf{X}$ then results as

$$d(\mathbf{X}, \vec{y}) = \sqrt{(\bar{\mathbf{X}} - \vec{y})^T \mathbf{S}^{-1} (\bar{\mathbf{X}} - \vec{y})} \quad \text{with} \quad \mathbf{X} \in \mathbb{R}^{m \times n}, \vec{y} \in \mathbb{R}^m$$

[13]. Here, *m* is equivalent to the number of principal components used (dimension of the principal component space) and *n* the number of measurements existing in the calibration data set (spectra). $\bar{\mathbf{X}}$ is the expected value of the resulting distribution for the calibration data set (the average value of *n* measurements received). $\mathbf{S}^{-1}$ is the inverse covariance matrix [12] for distribution $\mathbf{X}$.

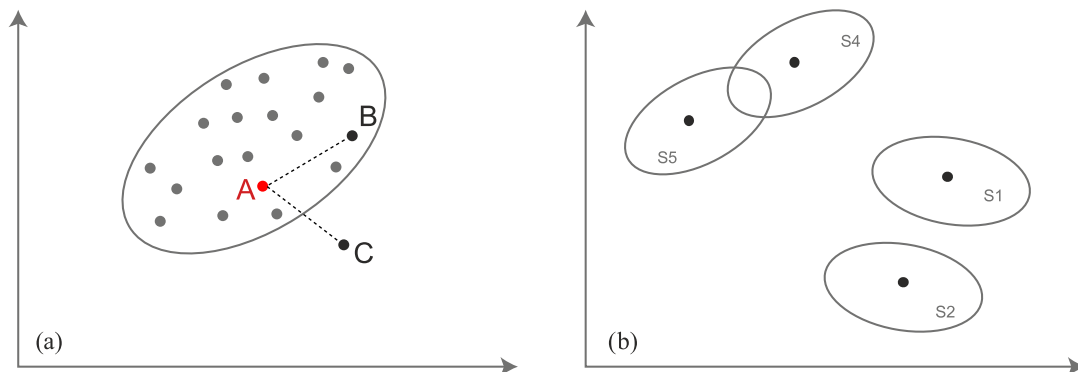


Figure 1: (a) The *Mahalanobis distance* from *A* to *B* is less than from *A* to *C*. However, the Euclidean distances are identical. (b) The *Mahalanobis distance* between the two measurement series *S4* and *S5* is smaller than between *S1* and *S2*. However, the Euclidean distances are identical.

The *Mahalanobis distance* offers advantages compared to the *Euclidean distance*: For the calculation of the distance it takes the statistical properties of a data point distribution (measurement series), i.e. average value, variance and covariance of the data points [14] into account. The *Mahalanobis distance* is applied while creating the reference database for evaluating the spectra from different samples of a substance.

A chemometric model is a classifier based on statistical methods [8, 9]. Through the respective algorithm used (e.g. *Principal Component Analysis*, *Cluster Analysis*), a maximum of chemical information is extracted from measurement data. Here, systematical or physical disturbances are eliminated using appropriate data pre-processing [15, 16].

At several places in this document, in order to simplify understanding, the term **database** is used instead of *chemometric model* – in the same manner as in the *Ph. Eur. Section 2.2.40* [3].

A sample (with its own sample ID) refers to substance in a sales container. Repeated sampling from the same sales container is listed under the same sample ID. (The suffix “SI” is not part of the sample ID.) Several samples may originate from the same batch. Samples are called “independent”, if they originate from a batch, of which no spectra have been used for the generation of the database. (Up to *IdentModule 2018-01*, samples from different sales packages were considered to be independent.) The information above the list of validation spectra now includes also the number of batches that deliver independent samples for the validation (for both *Type B* and *Type C*).

In case a supplier takes a sample for testing from its incoming goods and splits it to multiple laboratory containers, the substance in all laboratory containers will still be ascribed to the same sample. *HiperScan GmbH* only uses one of the subsamples.

Reference samples are used to structure the database. The *reference spectra* originate from these samples. In chemometric technical jargon you would normally say: For *calibration*, a **chemometric model** is generated from the *calibration spectra* recorded from the *calibration samples*, whose quality is subsequently assessed in **validation**.

Reference samples are procured via typical pharmacy sources. Their identity is tested. The *reference spectra* are recorded by *HiperScan GmbH*. The documentation also includes the manufacturer’s name and batch number.

Reference samples are clearly identified by a sample ID. Samples without sample ID may not be used as *reference samples*.

Summary

A total of 54 445 spectra from 2281 different batches for a total of 136 substances were used to validate the substance class *HCK - nutritional supplements (Hepart)*.

Validation samples

The validation samples can be categorised as follows:

Type A Calibration spectra. These are the spectra used to generate the chemometric model. They were recorded by *HiperScan GmbH*. Detailed information regarding the batches or samples can be found in the following validation reports under *calibration samples* and under *Type A*. Further information is listed in [Appendix A](#).

Substance class	Substances	Batches	Spectra
HCK - nutritional supplements (Hepart)	131	580	28 476

From category *A* a total of 28 476 spectra from 580 batches for a total of 131 substances were taken into account for validation.

Type B Spectra from independent samples which are not included in database generation. These spectra were recorded by *HiperScan GmbH*. Detailed information regarding the batches or samples can be found in the following validation reports in the section *Type B* or in [Appendix B](#).

Substance class	Substances	Batches	Spectra
HCK - nutritional supplements (Hepart)	78	504	22 999

From category *B* a total of 22 999 spectra from 504 batches for a total of 78 substances were taken into account for validation.

Type C Spectra from independent samples which are not included in database generation. *Apo-Ident* customers carried out the measurements. Detailed information regarding the batches or samples can be found in the following validation reports in the section *Type C* or in [Appendix C](#).

Substance class	Substances	Batches	Spectra
HCK - nutritional supplements (Hepart)	63	1468	2970

From category *C* a total of 2970 spectra from 1468 batches for a total of 63 substances were taken into account for validation.

Validation results

The validation runs checked whether all substances/substance groups in the substance class *HCK - nutritional supplements (Hepart)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, the matching of all relevant spectra of various substances with the substances/substance groups in the substance class *HCK - nutritional supplements (Hepart)* was checked and the correctness of the results was evaluated. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	28 476	0	2 306 556
Type B	0	22 300	259	1 863 161
Type C	0	2706	255	240 579

All substances/substance groups in the substance class *HCK - nutritional supplements (Hepart)* can be clearly distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.000 00 % (> 99.999 12 %)	100.000 00 % (> 99.929 02 %)
Type B	100.000 00 % (> 99.998 38 %)	96.692 50 % (> 96.622 64 %)
Type C	100.000 00 % (> 99.986 12 %)	87.125 42 % (> 86.632 00 %)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Acerola (H1516)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 10006322-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Acerola (H1516)

Special notes

When selecting the *Acerola (H1516)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Acerola (H1516)	1	0	0

Second-stage model

For differentiation of the substance/substance group *Acerola (H1516)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Acerola (H1516)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
ginkgo extract (H1024)	15.78	—
Flavour orange (H1405)	16.48	—
Rhodiola (H1064)	18.68	—
PET basis (H1503)	19.16	—
Antioxidants NAT complex (H1004)	20.35	—
Calcium L-(+) -lactate complex (H1008)	23.08	—
Vitamin C (H1104)	24.44	—
PET well-aging (H1500)	30.65	—
Vitamin B1 (H1101)	31.70	—
Arginine (L-) (H1036)	38.89	—
Green coffee extract (H1433)	39.91	—
Seabuckthorn (H1523)	42.09	—
Catechin extract (H1010)	43.00	—
PET joints (H1501)	44.38	—
Bioflavonoid complex (H1006)	47.29	—
Pathogene complex (H1803)	47.92	—
Potassium (H1030)	48.18	—
Carnitine (L-) (H1038)	48.40	—
Walnut leaf (H1114)	48.77	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Acerola (H1516)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Acerola (H1516)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Acerola (H1516)	23002135	81526	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 40 spectra of 1 reference samples from the substance/substance group *Acerola (H1516)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 1 different batches.
- 28 436 spectra from a total of 577 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 0 spectra of 0 reference samples from the substance/substance group *Acerola (H1516)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.
- 22 999 spectra from a total of 504 batches from further 78 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *Acerola (H1516)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Acerola (H1516)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Acerola (H1516)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	40	0	28 436
Type B	0	0	0	22 999
Type C	0	0	0	2970

The substance/substance group *Acerola (H1516)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9295 %)	100.0000 % (> 85.0000 %)
Type B	100.0000 % (> 99.8687 %)	n/a (n/a)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
81526	81526	0.00	16.59

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **a-Lipoic acid (H1000)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80022-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

a-Lipoic acid (H1000)

Special notes

When selecting the *a-Lipoic acid (H1000)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
a-Lipoic acid (H1000)	10	6	23

Second-stage model

For differentiation of the substance/substance group *a-Lipoic acid (H1000)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *a-Lipoic acid (H1000)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Vitamin E NAT (H1107)	26.57	—
Coenzyme Q10 (H1013)	36.36	—
Aminomix NAC (H1002)	39.16	—
Antibiosis forte complex (H1115)	52.31	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *a-Lipoic acid (H1000)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *a-Lipoic acid (H1000)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	a-Lipoic acid (H1000)	054301	80321	58	from supplier
Hepart	a-Lipoic acid (H1000)	14001420	80482	60	from supplier
Hepart	a-Lipoic acid (H1000)	14001726	80491	60	from supplier
Hepart	a-Lipoic acid (H1000)	15001526(B1.2)	80681	60	from supplier
Hepart	a-Lipoic acid (H1000)	14000497	80682	60	from supplier
Hepart	a-Lipoic acid (H1000)	20001859	81281	40	from supplier
Hepart	a-Lipoic acid (H1000)	20002669	81309	40	from supplier
Hepart	a-Lipoic acid (H1000)	22000274	81424	40	from supplier
Hepart	a-Lipoic acid (H1000)	22001329	81445	40	from supplier
Hepart	a-Lipoic acid (H1000)	22001766	81464	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 498 spectra of 10 reference samples from the substance/substance group *a-Lipoic acid (H1000)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 10 different batches.
- 27 978 spectra from a total of 568 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a †. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 320 spectra of 6 reference samples from the substance/substance group *a-Lipoic acid (H1000)*.
- Among them are spectra of independent samples from 6 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	a-Lipoic acid (H1000)	066601	80369	40
Hepart	a-Lipoic acid (H1000)	15001526(B1.1)	80680	60
Hepart	a-Lipoic acid (H1000)	14000497(F1)	80683	60
Hepart	a-Lipoic acid (H1000)	14000497(F2)	80684	60
Hepart	a-Lipoic acid (H1000)	15001526(MM)	80685	60
Hepart	a-Lipoic acid (H1000)	18000250	81017	40

- 22 679 spectra from a total of 498 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 52 spectra from 18 *Apo-Ident* customers from 26 batches from the substance/substance group *a-Lipoic acid (H1000)*.
- Among them are spectra of independent samples from 23 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
HCK	a-Lipoic acid (H1000)	14000497/0	1
HCK	a-Lipoic acid (H1000)	14000497-2	1
Hepart / Unisan	a-Lipoic acid (H1000)	150015262	1

continued on the next page

continued from previous page

Supplier	Substance	Batch	Spectra
Hepart ag/Unisan	a-Lipoic acid (H1000)	20001859	1
Hepart AG/Unisan	a-Lipoic acid (H1000)	20001859/1	1
Hepart AG	a-Lipoic acid (H1000)	1313025701	2
Hepart AG	a-Lipoic acid (H1000)	14000497/1	1
Hepart AG	a-Lipoic acid (H1000)	150001526/2	1
Hepart AG	a-Lipoic acid (H1000)	15001526/2	3
Hepart AG	a-Lipoic acid (H1000)	18000250/1	1
Hepart AG	a-Lipoic acid (H1000)	25701	1
Hepart AG	a-Lipoic acid (H1000)	54301	1
Hepart	a-Lipoic acid (H1000)	15001526/3	1
Hepart	a-Lipoic acid (H1000)	15001526-2	2
Hepart	a-Lipoic acid (H1000)	18000250	2
Hepart	a-Lipoic acid (H1000)	18000250/0	5
Hepart	a-Lipoic acid (H1000)	18000250/1	2
Hepart	a-Lipoic acid (H1000)	18000250/2	1
Hepart	a-Lipoic acid (H1000)	18000250/3	1
Hepart	a-Lipoic acid (H1000)	20001859/0	1
Hepart	a-Lipoic acid (H1000)	66601	2
Th. Geyer	a-Lipoic acid (H1000)	15001526/0	1
Unisan Gmbh, 78465 K...	a-Lipoic acid (H1000)	25701	2
Unisan/Hepart AG	a-Lipoic acid (H1000)	25701	1
Unisan/Hepart AG	a-Lipoic acid (H1000)	54301	1
Unisan	a-Lipoic acid (H1000)	1312993101	1
Unisan	a-Lipoic acid (H1000)	14000497	1
UNISAN	a-Lipoic acid (H1000)	14001726	2
Unisan	a-Lipoic acid (H1000)	25701	6
unisan	a-Lipoic acid (H1000)	66601	1
Unisan	a-Lipoic acid (H1000)	66601	1
Unisan	a-Lipoic acid (H1000)	993101	2
unisan	a-Lipoic acid (H1000)	H100031	1

- 2918 spectra from 26 *Apo-Ident* customers from a total of 1434 batches from a further 62 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *a-Lipoic acid (H1000)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *a-Lipoic acid (H1000)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	498	0	27 978
Type B	0	320	0	22 679
Type C	0	52	0	2918

The substance/substance group *a-Lipoic acid (H1000)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9274 %)	100.0000 % (> 98.7952 %)
Type B	100.0000 % (> 99.8644 %)	100.0000 % (> 98.1250 %)
Type C	100.0000 % (> 98.8280 %)	100.0000 % (> 88.4615 %)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80321	80321	0.00	60.00
80482	80482	0.00	80.44
80491	80491	0.00	60.06
80681	80681	0.00	61.31
80682	80682	0.00	60.86
81281	81281	0.00	54.46
81309	81309	0.00	53.56
81424	81424	0.00	35.50
81445	81445	0.00	51.81
81464	81464	0.00	67.79

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Aminomix NAC (H1002)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80003-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Aminomix NAC (H1002)

Special notes

When selecting the *Aminomix NAC (H1002)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Aminomix NAC (H1002)	10	16	33

Second-stage model

For differentiation of the substance/substance group *Aminomix NAC (H1002)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Aminomix NAC (H1002)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Pumpkin seed protein (H1509)	20.95	—
Isoflavone (H1025)	23.08	—
Coenzyme Q10 (H1013)	24.84	—
Amino V complex (H1400)	26.44	—
Antibiosis forte complex (H1115)	30.21	—
Glutamine (L-) (H1043)	30.97	—
Oat bran beta-glucan (H1529)	32.27	—
Lupin protein complex (H1510)	33.15	—
PET skin and hair (H1504)	34.05	—
Glutathione (H1020)	34.25	—
Vitamin E NAT (H1107)	36.24	—
Calcium L-(+) -lactate complex (H1008)	37.50	—
Antioxidants NAT complex (H1004)	37.81	—
Hemp protein (H1406)	38.81	—
α -Lipoic acid (H1000)	39.15	—
Collagen peptides-MTC (H1125)	40.59	—
Vitamin B1 (H1101)	40.73	—
Carnitine (L-) (H1038)	44.06	—
PET basis (H1503)	44.94	—
Flavour orange (H1405)	49.19	—
PET joints (H1501)	50.22	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Aminomix NAC (H1002)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Aminomix NAC (H1002)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Aminomix NAC (H1002)	041401	80312	40	from supplier
Hepart	Aminomix NAC (H1002)	041402	80314	60	from supplier

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Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Aminomix NAC (H1002)	14000258	80407	40	from supplier
Hepart	Aminomix NAC (H1002)	14000258	80444	40	from supplier
Hepart	Aminomix NAC (H1002)	14000259	80447	40	from supplier
Hepart	Aminomix NAC (H1002)	15000295 (B1)	80538	60	from supplier
Hepart	Aminomix NAC (H1002)	15000297 (F2)	80544	60	from supplier
Hepart	Aminomix NAC (H1002)	15000320	80545	60	from supplier
Hepart	Aminomix NAC (H1002)	15000321	80546	60	from supplier
Hepart	Aminomix NAC (H1002)	15000319 (F2)	80549	60	from supplier
Hepart	Aminomix NAC (H1002)	210008-03-02	81348	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 560 spectra of 11 reference samples from the substance/substance group *Aminomix NAC (H1002)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 10 different batches.
- 27 916 spectra from a total of 568 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a †. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 880 spectra of 18 reference samples from the substance/substance group *Aminomix NAC (H1002)*.
- Among them are spectra of independent samples from 16 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Aminomix NAC (H1002)	15000295	80537	60
Hepart	Aminomix NAC (H1002)	15000295 (F2)	80539	60
Hepart	Aminomix NAC (H1002)	15000298 (F2)	80540	60
Hepart	Aminomix NAC (H1002)	15000298	80541	60
Hepart	Aminomix NAC (H1002)	15000297	80542	60
Hepart	Aminomix NAC (H1002)	15000297 (B1)	80543	60
Hepart	Aminomix NAC (H1002)	15000321 (B1)	80547	60
Hepart	Aminomix NAC (H1002)	15000319	80548	60
Hepart	Aminomix NAC (H1002)	17000771	80937	40

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Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Aminomix NAC (H1002)	17000770	80947	40
Hepart	Aminomix NAC (H1002)	17000769	80948	40
Hepart	Aminomix NAC (H1002)	17000768	80949	40
Hepart	Aminomix NAC (H1002)	17000767	80950	40
Hepart	Aminomix NAC (H1002)	17000766	80951	40
Hepart	Aminomix NAC (H1002)	19002356	81214	40
Hepart	Aminomix NAC (H1002)	20001550	81285	40
Hepart	Aminomix NAC (H1002)	14000259	80408	40
Hepart	Aminomix NAC (H1002)	041401	80457	40

- 22 119 spectra from a total of 486 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 72 spectra from 18 *Apo-Ident* customers from 37 batches from the substance/substance group *Aminomix NAC (H1002)*.
- Among them are spectra of independent samples from 33 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
Euro OTC	Aminomix NAC (H1002)	16001017/0	1
HCK	Aminomix NAC (H1002)	15000297/0	1
HCK	Aminomix NAC (H1002)	15000320-0	1
HCK	Aminomix NAC (H1002)	16001453	1
Hepart / Unisan	Aminomix NAC (H1002)	19000543/0	1
Hepart / Unisan	Aminomix NAC (H1002)	19002356/0	1
Hepart AG, CH-8280 K...	Aminomix NAC (H1002)	1054019101	1
Hepart ag/Unisan	Aminomix NAC (H1002)	19002356/0	1
Hepart AG/Unisan	Aminomix NAC (H1002)	20000735/0	1
Hepart AG/Unisan	Aminomix NAC (H1002)	20001550/0	1
Hepart AG	Aminomix NAC (H1002)	1054019101	2
Hepart AG	Aminomix NAC (H1002)	15000320	1
Hepart AG	Aminomix NAC (H1002)	16001452	1
Hepart AG	Aminomix NAC (H1002)	16001552/0	1
Hepart AG	Aminomix NAC (H1002)	17000766	1
Hepart AG	Aminomix NAC (H1002)	17000766/0	1
Hepart AG	Aminomix NAC (H1002)	19000543/0	1
Hepart AG	Aminomix NAC (H1002)	41401	2
Hepart AG	Aminomix NAC (H1002)	41402	2
Hepart	Aminomix NAC (H1002)	16001452	1
Hepart	Aminomix NAC (H1002)	16001452-0	1
Hepart	Aminomix NAC (H1002)	16001453/0	1
Hepart	Aminomix NAC (H1002)	16001453-1	1
Hepart	Aminomix NAC (H1002)	17000766	2
Hepart	Aminomix NAC (H1002)	17000766/0	2
Hepart	Aminomix NAC (H1002)	18001998	1
Hepart	Aminomix NAC (H1002)	18001998/0	3
Hepart	Aminomix NAC (H1002)	19000543/0	2
Hepart	Aminomix NAC (H1002)	19000543/3	1

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Supplier	Substance	Batch	Spectra
Hepart	Aminomix NAC (H1002)	19002356/0	2
Hepart	Aminomix NAC (H1002)	20000735/0	1
Hepart	Aminomix NAC (H1002)	21000802/0	1
Hepart	Aminomix NAC (H1002)	21000803	1
Hepart	Aminomix NAC (H1002)	21000803/0	1
Hepart	Aminomix NAC (H1002)	21002331	1
Unisan 02.04.2016	Aminomix NAC (H1002)	15000320/0	1
Unisan/Hepart AG	Aminomix NAC (H1002)	41402	1
unisan	Aminomix NAC (H1002)		1
Unisan	Aminomix NAC (H1002)	140000259	1
Unisan	Aminomix NAC (H1002)	14000258	3
Unisan	Aminomix NAC (H1002)	14000259	1
Unisan	Aminomix NAC (H1002)	15000295/0	3
unisan	Aminomix NAC (H1002)	15000297	1
Unisan	Aminomix NAC (H1002)	15000298/0	1
Unisan	Aminomix NAC (H1002)	15000320	1
Unisan	Aminomix NAC (H1002)	15000320/0	2
Unisan	Aminomix NAC (H1002)	16001017/0	1
Unisan	Aminomix NAC (H1002)	16001453/0	1
Unisan	Aminomix NAC (H1002)	165001017/0	1
Unisan	Aminomix NAC (H1002)	17000766	2
Unisan	Aminomix NAC (H1002)	19101	1
Unisan	Aminomix NAC (H1002)	41401	1
Unisan	Aminomix NAC (H1002)	41402	4
Unisan	Aminomix NAC (H1002)	971701	1

- 2898 spectra from 26 *Apo-Ident* customers from a total of 1424 batches from a further 62 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Aminomix NAC (H1002)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Aminomix NAC (H1002)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	560	0	27 916
Type B	0	880	0	22 119
Type C	0	69	3	2898

The substance/substance group *Aminomix NAC (H1002)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9274 %)	100.0000 % (> 98.9286 %)
Type B	100.0000 % (> 99.8640 %)	100.0000 % (> 99.3182 %)
Type C	100.0000 % (> 98.8260 %)	95.8333 % (> 91.6667 %)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several

new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80312	80312	0.00	35.83
80314	80314	0.00	32.85
80407	80407	0.00	32.71
80444	80444	0.00	26.44
80447	80447	0.00	27.45
80538	80538	0.00	33.34
80544	80544	0.00	33.15
80545	80545	0.00	32.42
80546	80546	0.00	33.62
80549	80549	0.00	32.36
81348	81348	0.00	23.08

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group	Antibiosis forte complex (H1115) / Antibiose mite complex (H1113) / Pathogene complex (H1803)
Substance class	HCK - nutritional supplements (Hepat)
Report date	07/03/2025
Report number	80675-2025-03-07
Executing company	HiperScan GmbH Weißeritzstraße 3 01067 Dresden Germany

Relevant substance names

Antibiosis forte complex (H1115) / Antibiose mite complex (H1113) / Pathogene complex (H1803);
Antibiosis forte complex (H1115); Antibiosis mite complex (H1113); Pathogene complex (H1803)

Special notes

When selecting the *Antibiosis forte complex (H1115) / Antibiose mite complex (H1113) / Pathogene complex (H1803)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Antibiosis forte complex (H1115) / Antibiose mite complex (H1113) / Pathogene complex (H1803)	5	6	0

Second-stage model

For differentiation of the substance/substance group *Antibiosis forte complex (H1115) / Antibiose mite complex (H1113) / Pathogene complex (H1803)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Antibiosis forte complex (H1115) / Antibiose mite complex (H1113) / Pathogene complex (H1803)* in the substance class *HCK - nutritional supplements (Hepat)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Garcinia cambogia (H1017)	16.77	—
Copper (H1032)	20.37	—
Walnut leaf (H1114)	20.48	—
Chaga (H1011)	25.82	—
Histamine block complex (H1117)	25.87	—
Antioxidants NAT complex (H1004)	29.74	—
ginkgo extract (H1024)	31.85	—
Flavour orange (H1405)	31.86	—
Potassium (H1030)	33.95	—
Calcium L-(+) -lactate complex (H1008)	34.19	—
Artemisia annua extract (H1118)	34.39	—
PET basis (H1503)	35.20	—
Iron (H1015)	36.94	—
Trace elements SE complex (H1082)	37.73	—
PET joints (H1501)	41.26	—
Rhodiola (H1064)	47.48	—
Vitamin C (H1104)	48.21	—
Magnesium (H1060)	48.81	—
Amino V complex (H1400)	78.18	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Antibiosis forte complex (H1115) / Antibiose mite complex (H1113) / Pathogene complex (H1803)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Antibiosis forte complex (H1115) / Antibiose mite complex (H1113) / Pathogene complex (H1803)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Antibiosis forte complex ...	15001169	80675	60	from supplier
Hepart	Antibiosis forte complex ...	17001137	80912	40	from supplier
Hepart	Antibiosis mite complex (...)	16001074	80900	40	from supplier
Hepart	Antibiosis mite complex (...)	16001073	80903	40	from supplier
Hepart	Pathogene complex (H1803)	18000637	81038	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 220 spectra of 5 reference samples from the substance/substance group *Antibiosis forte complex (H1115) / Antibiose mite complex (H1113) / Pathogene complex (H1803)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 5 different batches.
- 28 256 spectra from a total of 573 batches from further 128 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a †. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 240 spectra of 6 reference samples from the substance/substance group *Antibiosis forte complex (H1115) / Antibiose mite complex (H1113) / Pathogene complex (H1803)*.
- Among them are spectra of independent samples from 6 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Antibiosis forte complex ...	17001151	81019	40
Hepart	Antibiosis forte complex ...	19000078	81152	40
Hepart	Antibiosis mite complex (...)	16001073 (B2)	80898	40
Hepart	Antibiosis mite complex (...)	16001074 (B2)	80899	40
Hepart	Antibiosis mite complex (...)	16001074 (B1)	80901	40
Hepart	Antibiosis mite complex (...)	16001073 (B1)	80902	40

- 22 759 spectra from a total of 498 batches from further 76 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B*

section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *Antibiosis forte complex (H1115)* / *Antibiose mite complex (H1113)* / *Pathogene complex (H1803)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Antibiosis forte complex (H1115)* / *Antibiose mite complex (H1113)* / *Pathogene complex (H1803)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Antibiosis forte complex (H1115)* / *Antibiose mite complex (H1113)* / *Pathogene complex (H1803)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	220	0	28 256
Type B	0	199	41	22 759
Type C	0	0	0	2970

The substance/substance group *Antibiosis forte complex (H1115)* / *Antibiose mite complex (H1113)* / *Pathogene complex (H1803)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9277 %)	100.0000 % (> 97.2727 %)
Type B	100.0000 % (> 99.8646 %)	82.9167 % (> 81.6667 %)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra ([Rule of Three](#) [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the [Mahalanobis distance](#) to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80675	80675	0.00	110.92
80900	80900	0.00	20.48
80903	80903	0.00	29.76
80912	80912	0.00	78.18
81038	81038	0.00	22.44

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Argentum (H1116)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80674-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Argentum (H1116)

Special notes

When selecting the *Argentum (H1116)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Argentum (H1116)	2	0	0

Second-stage model

For differentiation of the substance/substance group *Argentum (H1116)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Argentum (H1116)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Iron (H1015)	11.30	—
Copper (H1032)	20.18	—
Trace elements SE complex (H1082)	51.86	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Argentum (H1116)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Argentum (H1116)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Argentum (H1116)	15001151	80674	60	from supplier
Hepart	Argentum (H1116)	16001077	80890	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 100 spectra of 2 reference samples from the substance/substance group *Argentum (H1116)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 2 different batches.
- 28 376 spectra from a total of 576 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples

are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 0 spectra of 0 reference samples from the substance/substance group *Argentum (H1116)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.
- 22 999 spectra from a total of 504 batches from further 78 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *Argentum (H1116)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Argentum (H1116)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Argentum (H1116)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	100	0	28 376
Type B	0	0	0	22 999
Type C	0	0	0	2970

The substance/substance group *Argentum (H1116)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9282 %)	100.0000 % (> 94.0000 %)
Type B	100.0000 % (> 99.8687 %)	n/a (n/a)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80674	80674	0.00	11.30
80890	80890	0.00	15.84

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Arginine (L-) (H1036)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80026-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Arginine (L-) (H1036)

Special notes

When selecting the *Arginine (L-) (H1036)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Arginine (L-) (H1036)	5	9	24

Second-stage model

For differentiation of the substance/substance group *Arginine (L-) (H1036)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Arginine (L-) (H1036)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Iron (H1015)	39.71	—
Calcium L-(+) -lactate complex (H1008)	44.12	—
Aminomix NAC (H1002)	44.92	—
Vitamin B1 (H1101)	46.97	—
Orthocolon complex (H1800)	49.94	—
Coenzyme Q10 (H1013)	51.89	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Arginine (L-) (H1036)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Arginine (L-) (H1036)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Arginine (L-) (H1036)	066501	80373	40	from supplier
Hepart	Arginine (L-) (H1036)	16000949	80807	40	from supplier
Hepart	Arginine (L-) (H1036)	16000949	80867	40	from supplier
Hepart	Arginine (L-) (H1036)	16000950	80876	40	from supplier
Hepart	Arginine (L-) (H1036)	18001388	81113	40	from supplier
Hepart	Arginine (L-) (H1036)	210015-71-72	81371	50	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 250 spectra of 6 reference samples from the substance/substance group *Arginine (L-) (H1036)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 5 different batches.
- 28 226 spectra from a total of 573 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a †. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 400 spectra of 10 reference samples from the substance/substance group *Arginine (L-) (H1036)*.
- Among them are spectra of independent samples from 9 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Arginine (L-) (H1036)	052401	80330	60
Hepart	Arginine (L-) (H1036)	14000563	80446	20
Hepart	Arginine (L-) (H1036)	14000564	80448	40
Hepart	Arginine (L-) (H1036)	17000878	80928	40
Hepart	Arginine (L-) (H1036)	17000877	80929	40
Hepart	Arginine (L-) (H1036)	18001443	81114	40
Hepart	Arginine (L-) (H1036)	19000626	81188	40
Hepart	Arginine (L-) (H1036)	19000689	81189	40
Hepart	Arginine (L-) (H1036)	22002215	81457	40
Hepart	Arginine (L-) (H1036)	16000950	80808	40

- 22 599 spectra from a total of 494 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 68 spectra from 17 *Apo-Ident* customers from 24 batches from the substance/substance group *Arginine (L-) (H1036)*.
- Among them are spectra of independent samples from 24 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
Fagron	Arginine (L-) (H1036)	1324044301	1
HCK	Arginine (L-) (H1036)	14000563/2	1
HCK	Arginine (L-) (H1036)	14000564	1
Hepart AG/Unisan	Arginine (L-) (H1036)	19000626	1
Hepart AG/Unisan	Arginine (L-) (H1036)	19000626/0	1
Hepart AG	Arginine (L-) (H1036)	14000563/2	1
Hepart AG	Arginine (L-) (H1036)	17000877/0	1
Hepart AG	Arginine (L-) (H1036)	17000878/0	9
Hepart AG	Arginine (L-) (H1036)	66501	1
Hepart	Arginine (L-) (H1036)	16000950/0	1
Hepart	Arginine (L-) (H1036)	17000877	1
Hepart	Arginine (L-) (H1036)	17000877/0	2
Hepart	Arginine (L-) (H1036)	17000877-0	2
Hepart	Arginine (L-) (H1036)	17000878	4
Hepart	Arginine (L-) (H1036)	17000878/0	4
Hepart	Arginine (L-) (H1036)	17000878/1	2
Hepart	Arginine (L-) (H1036)	17000878-0	1
Hepart	Arginine (L-) (H1036)	18001443/0	3
Hepart	Arginine (L-) (H1036)	19000626	2
Hepart	Arginine (L-) (H1036)	19000626/0	4
Hepart	Arginine (L-) (H1036)	19000689/0	2
Unisan GmbH, 78465 K...	Arginine (L-) (H1036)	52401	2
Unisan/Hepart AG	Arginine (L-) (H1036)	1324044301	1
Unisan	Arginine (L-) (H1036)	1324950601	1
Unisan	Arginine (L-) (H1036)	14000563	1
Unisan	Arginine (L-) (H1036)	14000564/0	1
Unisan	Arginine (L-) (H1036)	14000564/2	1
Unisan	Arginine (L-) (H1036)	16000949/0	2
Unisan	Arginine (L-) (H1036)	17000877	3
Unisan	Arginine (L-) (H1036)	27802	1
Unisan	Arginine (L-) (H1036)	44301	2
unisan	Arginine (L-) (H1036)	52401	1
Unisan	Arginine (L-) (H1036)	52401	1
Unisan	Arginine (L-) (H1036)	66501	5
UNISAN	Arginine (L-) (H1036)	66501	1

- 2902 spectra from 26 *Apo-Ident* customers from a total of 1436 batches from a further 62 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Arginine (L-) (H1036)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Arginine (L-) (H1036)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	250	0	28 226
Type B	0	400	0	22 599
Type C	0	67	1	2902

The substance/substance group *Arginine (L-) (H1036)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9276 %)	100.0000 % (> 97.6000 %)
Type B	100.0000 % (> 99.8643 %)	100.0000 % (> 98.5000 %)
Type C	100.0000 % (> 98.8263 %)	98.5294 % (> 94.1176 %)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80373	80373	0.00	52.61
80807	80807	0.00	46.46
80867	80867	0.00	40.26
80876	80876	0.00	42.09
81113	81113	0.00	41.24
81371	81371	0.00	50.64

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Artemisia annua extract (H1118)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80665-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Artemisia annua extract (H1118)

Special notes

When selecting the *Artemisia annua extract (H1118)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Artemisia annua extract (H1118)	3	1	0

Second-stage model

For differentiation of the substance/substance group *Artemisia annua extract (H1118)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Artemisia annua extract (H1118)* in the substance class *HCK - nutritional supplements (Hepat)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Garcinia cambogia (H1017)	12.85	—
Silicium (H1070)	18.37	—
Ginseng (H1018)	18.78	—
Juniper (H1112)	19.20	—
Marshmallow extract (H1439)	20.95	—
Artichoke extract (H1440)	21.56	—
Saffron flowers (H1435)	21.70	—
Copper (H1032)	22.92	—
Saffron style (H1434)	23.90	—
Coenzyme Q10 (H1013)	33.43	—
Vitamin K2 (75µg Mono) (H1108)	34.46	—
Ashwagandha (H1132)	36.84	—
Pathogene complex (H1803)	37.65	—
Walnut leaf (H1114)	37.92	—
Vitamin B1 (H1101)	38.02	—
Vitamin B12 (H1102)	38.04	—
Magnesium (H1060)	38.22	—
Lycopene (H1058)	38.50	—
Detox complex (H1111)	38.58	—
Vitamin E NAT (H1107)	38.62	—
Gentian extract (H1438)	38.73	—
Iron (H1015)	40.17	—
Leaky gut complex (H1802)	40.25	—
Ginger extract (H1437)	41.01	—
Zinc (H1110)	41.43	—
Calcium L-(+)-lactate complex (H1008)	41.82	—
Flavour orange (H1405)	42.44	—
Biotin (H1007)	44.07	—
Antioxidants NAT complex (H1004)	44.61	—
Rhodiola (H1064)	46.36	—
Glutathione (H1020)	47.11	—
Aminomix NAC (H1002)	47.91	—
Trace elements SE complex (H1082)	50.91	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Artemisia annua extract (H1118)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Artemisia annua extract (H1118)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Artemisia annua extract (...)	15001134	80665	60	from supplier
Hepart	Artemisia annua extract (...)	19002655	81291	40	from supplier
Hepart	Artemisia annua extract (...)	21000173	81332	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 140 spectra of 3 reference samples from the substance/substance group *Artemisia annua extract (H1118)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 3 different batches.
- 28 336 spectra from a total of 575 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 40 spectra of 1 reference samples from the substance/substance group *Artemisia annua extract (H1118)*.
- Among them are spectra of independent samples from 1 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Artemisia annua extract (...)	20000169	81292	40

- 22 959 spectra from a total of 503 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *Artemisia annua extract (H1118)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Artemisia annua extract (H1118)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Artemisia annua extract (H1118)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	140	0	28 336
Type B	0	40	0	22 959
Type C	0	0	0	2970

The substance/substance group *Artemisia annua extract (H1118)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9279 %)	100.0000 % (> 95.7143 %)
Type B	100.0000 % (> 99.8691 %)	100.0000 % (> 85.0000 %)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra ([Rule of Three](#) [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the [Mahalanobis distance](#) to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80665	80665	0.00	21.70
81291	81291	0.00	19.20
81332	81332	0.00	21.38

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group	Artichoke extract (H1440)
Substance class	HCK - nutritional supplements (Hepart)
Report date	07/03/2025
Report number	81088-2025-03-07
Executing company	HiperScan GmbH Weißeritzstraße 3 01067 Dresden Germany

Relevant substance names

Artichoke extract (H1440)

Special notes

When selecting the *Artichoke extract (H1440)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Artichoke extract (H1440)	5	1	0

Second-stage model

For differentiation of the substance/substance group *Artichoke extract (H1440)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Artichoke extract (H1440)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Marshmallow extract (H1439)	12.73	—
Juniper (H1112)	15.70	—
Gentian extract (H1438)	16.04	—
Selenium yeast (H1068)	17.28	—
Detox complex (H1111)	18.21	—
Saffron style (H1434)	19.05	—
Silicium (H1070)	21.54	—
Rhodiola (H1064)	22.26	—
Boron (H1005)	22.27	—
Garcinia cambogia (H1017)	22.66	—
Artemisia annua extract (H1118)	24.05	—
Ginseng (H1018)	24.10	—
Leaky gut complex (H1802)	25.97	—
Isoflavone (H1025)	26.47	—
Lycopene (H1058)	27.86	—
Psyllium husks (H1527)	29.16	—
Ginger extract (H1437)	30.06	—
Baobab (H1410)	30.45	—
Biotin (H1007)	31.66	—
Green coffee extract (H1433)	32.52	—
Magnesium (H1060)	32.93	—
Coenzyme Q10 (H1013)	33.52	—
Glutathione (H1020)	33.88	—
Vitamin B1 (H1101)	34.66	—
Ashwagandha (H1132)	34.74	—
Zinc (H1110)	35.16	—
Orthocolon complex (H1800)	35.46	—
Arginine (L-) (H1036)	35.96	—
Flavour orange (H1405)	36.47	—
Vitamins BAG complex (H1091)	36.58	—
Vitamin K2 (75µg Mono) (H1108)	36.69	—
Copper (H1032)	37.15	—
Vitamin B12 (H1102)	38.40	—
Calcium L-(+) -lactate complex (H1008)	39.99	—
Selenium (H1067)	40.79	—
Carrot (H1513)	41.30	—
Saffron flowers (H1435)	41.74	—
Orthovimin Neutral Complex (H1404)	43.99	—

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Substanz	Distance in main model	Distance in second-stage model
PET coenzyme Q10 (H1505)	44.57	—
Chromium (H1012)	45.53	—
Iron (H1015)	46.03	—
Vitamin D3 (H1105)	50.63	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Artichoke extract (H1440)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Artichoke extract (H1440)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Artichoke extract (H1440)	18001094	81088	40	from supplier
Hepart	Artichoke extract (H1440)	20001312	81278	40	from supplier
Hepart	Artichoke extract (H1440)	21001670	81372	50	from supplier
Hepart	Artichoke extract (H1440)	22002406	81466	40	from supplier
Hepart	Artichoke extract (H1440)	24001301	81550	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 210 spectra of 5 reference samples from the substance/substance group *Artichoke extract (H1440)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 5 different batches.
- 28 266 spectra from a total of 573 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a †. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 40 spectra of 1 reference samples from the substance/substance group *Artichoke extract (H1440)*.

- Among them are spectra of independent samples from 1 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Artichoke extract (H1440)	20000368	81234	40

- 22 959 spectra from a total of 503 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *Artichoke extract (H1440)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Artichoke extract (H1440)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Artichoke extract (H1440)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	210	0	28 266
Type B	0	40	0	22 959
Type C	0	0	0	2970

The substance/substance group *Artichoke extract (H1440)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9277 %)	100.0000 % (> 97.1429 %)
Type B	100.0000 % (> 99.8691 %)	100.0000 % (> 85.0000 %)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to

exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
81088	81088	0.00	17.62
81278	81278	0.00	24.73
81372	81372	0.00	22.70
81466	81466	0.00	15.70
81550	81550	0.00	15.46

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Ashwagandha (H1132)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 10006006-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Ashwagandha (H1132)

Special notes

When selecting the *Ashwagandha (H1132)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Ashwagandha (H1132)	3	0	0

Second-stage model

For differentiation of the substance/substance group *Ashwagandha* (H1132) the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Ashwagandha* (H1132) in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Detox complex (H1111)	13.09	—
Ginseng (H1018)	13.36	—
Marshmallow extract (H1439)	14.38	—
Saffron style (H1434)	17.26	—
Boron (H1005)	19.53	—
Vitamin K2 (75µg Mono) (H1108)	20.19	—
Gentian extract (H1438)	20.88	—
Juniper (H1112)	21.36	—
Silicium (H1070)	22.77	—
Baobab (H1410)	23.41	—
Green coffee extract (H1433)	25.29	—
Artemisia annua extract (H1118)	25.37	—
Artichoke extract (H1440)	25.39	—
Selenium yeast (H1068)	25.96	—
Leaky gut complex (H1802)	26.43	—
Ginger extract (H1437)	26.93	—
Biotin (H1007)	27.11	—
Zinc (H1110)	29.69	—
Garcinia cambogia (H1017)	32.67	—
Vitamin E NAT (H1107)	32.70	—
PET coenzyme Q10 (H1505)	33.36	—
Selenium (H1067)	33.42	—
Coenzyme Q10 (H1013)	34.06	—
Chromium (H1012)	34.39	—
Vitamin B12 (H1102)	34.42	—
Saffron flowers (H1435)	36.65	—
Lycopene (H1058)	37.27	—
Flavour orange (H1405)	38.24	—
Rhodiola (H1064)	38.36	—
Magnesium (H1060)	38.55	—
Glutathione (H1020)	38.57	—
Vitamin B1 (H1101)	39.69	—
Isoflavone (H1025)	42.68	—
Acacia gum (H1526)	42.77	—
Psyllium husks (H1527)	43.55	—
Chondroitin sulfate (H1065)	45.95	—
Vitamins BAG complex (H1091)	46.37	—
Aminomix NAC (H1002)	48.88	—

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Substanz	Distance in main model	Distance in second-stage model
Konjak Glucomannan (H1530)	49.06	—
Arginine (L-) (H1036)	49.19	—
Calcium L-(+) -lactate complex (H1008)	50.85	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Ashwagandha (H1132)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Ashwagandha (H1132)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Ashwagandha (H1132)	22000710	81441	40	from supplier
Hepart	Ashwagandha (H1132)	23001779	81513	40	from supplier
Hepart	Ashwagandha (H1132)	24001335	81551	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 120 spectra of 3 reference samples from the substance/substance group *Ashwagandha (H1132)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 3 different batches.
- 28 356 spectra from a total of 575 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 0 spectra of 0 reference samples from the substance/substance group *Ashwagandha (H1132)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

- 22 999 spectra from a total of 504 batches from further 78 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *Ashwagandha (H1132)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Ashwagandha (H1132)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Ashwagandha (H1132)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	120	0	28 356
Type B	0	0	0	22 999
Type C	0	0	0	2970

The substance/substance group *Ashwagandha (H1132)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9280 %)	100.0000 % (> 95.0000 %)
Type B	100.0000 % (> 99.8687 %)	n/a (n/a)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
81441	81441	0.00	17.26
81513	81513	0.00	13.36
81551	81551	0.00	13.09

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Betaine hydrochloride (H1119)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80926-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Betaine hydrochloride (H1119)

Special notes

When selecting the *Betaine hydrochloride (H1119)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Betaine hydrochloride (H1119)	4	2	0

Second-stage model

For differentiation of the substance/substance group *Betaine hydrochloride (H1119)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Betaine hydrochloride (H1119)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Calcium L-(+)-lactate complex (H1008)	20.93	—
Arginine (L-) (H1036)	22.78	—
Silymarin (H1071)	24.97	—
Vitamin B1 (H1101)	26.26	—
Coenzyme Q10 (H1013)	29.96	—
OPC Proanthocyanidins (Pine Bark) (...)	30.81	—
Carnitine (L-) (H1038)	31.05	—
Flavour orange (H1405)	34.96	—
Rhodiola (H1064)	36.64	—
Bioflavonoid complex (H1006)	39.04	—
Glutathione (H1020)	39.72	—
Orthoclon complex (H1800)	40.64	—
Antioxidants NAT complex (H1004)	42.10	—
Garcinia cambogia (H1017)	43.25	—
Orthovimin Neutral Complex (H1404)	47.15	—
Artichoke extract (H1440)	50.48	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Betaine hydrochloride (H1119)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Betaine hydrochloride (H1119)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Betaine hydrochloride (H1119)	17000829	80926	40	from supplier
Hepart	Betaine hydrochloride (H1119)	19000533	81169	40	from supplier
Hepart	Betaine hydrochloride (H1119)	21002227/1	81440	40	from supplier
Hepart	Betaine hydrochloride (H1119)	23002237	81518	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 160 spectra of 4 reference samples from the substance/substance group *Betaine hydrochloride (H1119)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 4 different batches.
- 28 316 spectra from a total of 574 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 80 spectra of 2 reference samples from the substance/substance group *Betaine hydrochloride (H1119)*.
- Among them are spectra of independent samples from 2 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Betaine hydrochloride (H1119)	19001723	81203	40
Hepart	Betaine hydrochloride (H1119)	22002247	81458	40

- 22 919 spectra from a total of 502 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *Betaine hydrochloride (H1119)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented

within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Betaine hydrochloride (H1119)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Betaine hydrochloride (H1119)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	160	0	28 316
Type B	0	80	0	22 919
Type C	0	0	0	2970

The substance/substance group *Betaine hydrochloride (H1119)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9278 %)	100.0000 % (> 96.2500 %)
Type B	100.0000 % (> 99.8664 %)	100.0000 % (> 92.5000 %)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra ([Rule of Three](#) [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the [Mahalanobis distance](#) to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80926	80926	0.00	51.93
81169	81169	0.00	46.43
81440	81440	0.00	24.97
81518	81518	0.00	26.91

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Broccoli (H1512)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 10006321-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Broccoli (H1512)

Special notes

When selecting the *Broccoli (H1512)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Broccoli (H1512)	1	0	0

Second-stage model

For differentiation of the substance/substance group *Broccoli (H1512)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Broccoli (H1512)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Flavour orange (H1405)	14.01	—
Calcium L-(+)-lactate complex (H1008)	17.66	—
Kale (H1126)	19.67	—
Rhodiola (H1064)	21.21	—
Antioxidants NAT complex (H1004)	25.51	—
Arginine (L-) (H1036)	26.35	—
Vitamin B1 (H1101)	28.96	—
Carrot (H1513)	29.53	—
PET basis (H1503)	35.72	—
Orthocolon complex (H1800)	36.08	—
Glutathione (H1020)	38.94	—
Seabuckthorn (H1523)	39.00	—
Cabbage mix (H1514)	39.15	—
Vitamin C (H1104)	39.53	—
Beetroot (H1515)	45.60	—
Catechin extract (H1010)	46.67	—
Carnitine (L-) (H1038)	46.83	—
PET joints (H1501)	48.66	—
Coenzyme Q10 (H1013)	48.69	—
PET well-aging (H1500)	48.82	—
Cranberry (H1519)	49.17	—
Bioflavonoid complex (H1006)	49.64	—
Garcinia cambogia (H1017)	50.31	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Broccoli (H1512)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Broccoli (H1512)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Broccoli (H1512)	23002194	81525	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 40 spectra of 1 reference samples from the substance/substance group *Broccoli (H1512)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 1 different batches.
- 28 436 spectra from a total of 577 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 0 spectra of 0 reference samples from the substance/substance group *Broccoli (H1512)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.
- 22 999 spectra from a total of 504 batches from further 78 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *Broccoli (H1512)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Broccoli (H1512)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Broccoli (H1512)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	40	0	28 436
Type B	0	0	0	22 999
Type C	0	0	0	2970

The substance/substance group *Broccoli (H1512)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9295 %)	100.0000 % (> 85.0000 %)
Type B	100.0000 % (> 99.8687 %)	n/a (n/a)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
81525	81525	0.00	19.67

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Caffeine guarana extract (H1425)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 10002191-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Caffeine guarana extract (H1425)

Special notes

When selecting the *Caffeine guarana extract (H1425)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Caffeine guarana extract (H1425)	2	0	0

Second-stage model

For differentiation of the substance/substance group *Caffeine guarana extract (H1425)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Caffeine guarana extract (H1425)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Carnitine (L-) (H1038)	15.04	—
Calcium L-(+) -lactate complex (H1008)	24.06	—
Coenzyme Q10 (H1013)	25.59	—
OPC Proanthocyanidins (Pine Bark) (...)	26.43	—
Vitamin complex (H1100)	29.51	—
Arginine (L-) (H1036)	34.50	—
Silymarin (H1071)	40.32	—
Glutathione (H1020)	41.43	—
Bioflavonoid complex (H1006)	45.65	—
Vitamin B1 (H1101)	45.70	—
Leaky gut complex (H1802)	47.78	—
Flavour orange (H1405)	49.55	—
Griffonia (H1035)	49.76	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Caffeine guarana extract (H1425)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Caffeine guarana extract (H1425)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Caffeine guarana extract ...	19000247/0	81212	40	from supplier
Hepart	Caffeine guarana extract ...	24001401	81553	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 80 spectra of 2 reference samples from the substance/substance group *Caffeine guarana extract (H1425)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 2 different batches.
- 28 396 spectra from a total of 576 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a †. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 0 spectra of 0 reference samples from the substance/substance group *Caffeine guarana extract (H1425)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.
- 22 999 spectra from a total of 504 batches from further 78 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *Caffeine guarana extract (H1425)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Caffeine guarana extract (H1425)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Caffeine guarana extract (H1425)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	80	0	28 396
Type B	0	0	0	22 999
Type C	0	0	0	2970

The substance/substance group *Caffeine guarana extract (H1425)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate* (*specificity*) and the weighted *true positive rate* (*recognition rate*) are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9284 %)	100.0000 % (> 92.5000 %)
Type B	100.0000 % (> 99.8687 %)	n/a (n/a)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
81212	81212	0.00	28.90
81553	81553	0.00	29.87

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Carnitine (L-) (H1038)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80013-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Carnitine (L-) (H1038)

Special notes

When selecting the *Carnitine (L-) (H1038)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Carnitine (L-) (H1038)	10	10	39

Second-stage model

For differentiation of the substance/substance group *Carnitine (L-) (H1038)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Carnitine (L-) (H1038)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Calcium L-(+) -lactate complex (H1008)	17.87	—
ginkgo extract (H1024)	23.90	—
Coenzyme Q10 (H1013)	24.03	—
Caffeine guarana extract (H1425)	24.04	—
Vitamin B1 (H1101)	26.40	—
Orthocolon complex (H1800)	27.06	—
Silymarin (H1071)	27.66	—
Antioxidants NAT complex (H1004)	28.85	—
Antibiosis forte complex (H1115)	33.12	—
Arginine (L-) (H1036)	33.78	—
Sunflower seed protein (H1511)	34.05	—
Flavour orange (H1405)	37.34	—
Vitamin complex (H1100)	38.84	—
Aminomix NAC (H1002)	39.21	—
Glutathione (H1020)	43.20	—
OPC Proanthocyanidins (Pine Bark) (...)	43.94	—
Leaky gut complex (H1802)	45.35	—
Rhodiola (H1064)	46.65	—
Pumpkin seed protein (H1509)	48.04	—
Isoflavone (H1025)	48.30	—
Betaine hydrochloride (H1119)	49.51	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Carnitine (L-) (H1038)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Carnitine (L-) (H1038)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Carnitine (L-) (H1038)	026010	80344	40	from supplier
Hepart	Carnitine (L-) (H1038)	130605300	80371	40	from supplier

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Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Carnitine (L-) (H1038)	130605302	80483	60	from supplier
Hepart	Carnitine (L-) (H1038)	15000052	80557	60	from supplier
Hepart	Carnitine (L-) (H1038)	15000054	80559	60	from supplier
Hepart	Carnitine (L-) (H1038)	16000453	80787	40	from supplier
Hepart	Carnitine (L-) (H1038)	18000538	81045	40	from supplier
Hepart	Carnitine (L-) (H1038)	21000309	81350	40	from supplier
Hepart	Carnitine (L-) (H1038)	23000597	81472	40	from supplier
Hepart	Carnitine (L-) (H1038)	23000596	81487	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 460 spectra of 10 reference samples from the substance/substance group *Carnitine (L-) (H1038)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 10 different batches.
- 28 016 spectra from a total of 568 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 440 spectra of 10 reference samples from the substance/substance group *Carnitine (L-) (H1038)*.
- Among them are spectra of independent samples from 10 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Carnitine (L-) (H1038)	15000053	80558	60
Hepart	Carnitine (L-) (H1038)	15000055	80560	60
Hepart	Carnitine (L-) (H1038)	16000450	80788	40
Hepart	Carnitine (L-) (H1038)	16000451	80817	40
Hepart	Carnitine (L-) (H1038)	16000454	80818	40
Hepart	Carnitine (L-) (H1038)	18000539	81046	40
Hepart	Carnitine (L-) (H1038)	18000418	81047	40
Hepart	Carnitine (L-) (H1038)	20001491	81289	40
Hepart	Carnitine (L-) (H1038)	19001233	81290	40
Hepart	Carnitine (L-) (H1038)	20001492	81293	40

- 22 559 spectra from a total of 494 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 101 spectra from 18 *Apo-Ident* customers from 45 batches from the substance/substance group *Carnitine (L-) (H1038)*.
- Among them are spectra of independent samples from 39 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
HCK	Carnitine (L-) (H1038)	1500003-0	1
HCK	Carnitine (L-) (H1038)	15000053-2	2
HCK	Carnitine (L-) (H1038)	15000054-0	4
Hepart AG, CH-8280 K...	Carnitine (L-) (H1038)	1184965901	1
Hepart AG, CH-8280 K...	Carnitine (L-) (H1038)	26010	1
Hepart AG, CH-8280 K...	Carnitine (L-) (H1038)	26020	2
Hepart AG/Unisan	Carnitine (L-) (H1038)	18000538/0	1
Hepart AG/Unisan	Carnitine (L-) (H1038)	18000539/0	1
Hepart AG/Unisan	Carnitine (L-) (H1038)	20001491/0	1
Hepart AG/Unisan	Carnitine (L-) (H1038)	20001492/0	1
Hepart AG	Carnitine (L-) (H1038)	1184026001	1
Hepart AG	Carnitine (L-) (H1038)	130605300	1
Hepart AG	Carnitine (L-) (H1038)	130605301	2
Hepart AG	Carnitine (L-) (H1038)	16000453/1	2
Hepart AG	Carnitine (L-) (H1038)	16000454/0	5
Hepart AG	Carnitine (L-) (H1038)	18000538/0	2
Hepart AG	Carnitine (L-) (H1038)	26001	1
Hepart AG	Carnitine (L-) (H1038)	26010	3
Hepart AG	Carnitine (L-) (H1038)	480g	1
Hepart/Unisan	Carnitine (L-) (H1038)	20001491/0	1
Hepart	Carnitine (L-) (H1038)	15000052	1
Hepart	Carnitine (L-) (H1038)	15000054/1	2
Hepart	Carnitine (L-) (H1038)	160000453	1
Hepart	Carnitine (L-) (H1038)	16000450-1	1
Hepart	Carnitine (L-) (H1038)	16000451/0	1
Hepart	Carnitine (L-) (H1038)	16000453	1
Hepart	Carnitine (L-) (H1038)	16000453/0	3
Hepart	Carnitine (L-) (H1038)	16000453-0	2
Hepart	Carnitine (L-) (H1038)	160004531	3
Hepart	Carnitine (L-) (H1038)	16000454	2
Hepart	Carnitine (L-) (H1038)	16000454/0	5
Hepart	Carnitine (L-) (H1038)	18000538/0	2
Hepart	Carnitine (L-) (H1038)	20001491	1
Hepart	Carnitine (L-) (H1038)	20001491/0	1
Hepart	Carnitine (L-) (H1038)	20001560/0	2
Hepart	Carnitine (L-) (H1038)	20001691/0	1
Unisan 2.10.2015	Carnitine (L-) (H1038)	15000052/0	2
Unisan	Carnitine (L-) (H1038)		2
Unisan	Carnitine (L-) (H1038)	1184026020	3
Unisan	Carnitine (L-) (H1038)	1184965901	1
Unisan	Carnitine (L-) (H1038)	130326002	1

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Supplier	Substance	Batch	Spectra
Unisan	Carnitine (L-) (H1038)	130605300	4
UNISAN	Carnitine (L-) (H1038)	130605300	3
Unisan	Carnitine (L-) (H1038)	130605300/3	1
Unisan	Carnitine (L-) (H1038)	130605301	1
Unisan	Carnitine (L-) (H1038)	130605302	2
UNISAN	Carnitine (L-) (H1038)	130605302	1
Unisan	Carnitine (L-) (H1038)	15000052	1
Unisan	Carnitine (L-) (H1038)	15000053	1
Unisan	Carnitine (L-) (H1038)	15000053/0	2
Unisan	Carnitine (L-) (H1038)	15000053/3	1
Unisan	Carnitine (L-) (H1038)	15000054	1
Unisan	Carnitine (L-) (H1038)	15000054/0	1
Unisan	Carnitine (L-) (H1038)	150000540	1
Unisan	Carnitine (L-) (H1038)	16000450	1
Unisan	Carnitine (L-) (H1038)	16000451	2
Unisan	Carnitine (L-) (H1038)	18000539/0	1
unisan	Carnitine (L-) (H1038)	26010	1
Unisan	Carnitine (L-) (H1038)	26010	2
Unisan	Carnitine (L-) (H1038)	965901	1
Unsan	Carnitine (L-) (H1038)	16000450	1

- 2869 spectra from 26 *Apo-Ident* customers from a total of 1416 batches from a further 62 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Carnitine (L-) (H1038)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Carnitine (L-) (H1038)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	460	0	28 016
Type B	0	440	0	22 559
Type C	0	97	4	2869

The substance/substance group *Carnitine (L-) (H1038)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9275 %)	100.0000 % (> 98.6957 %)
Type B	100.0000 % (> 99.8642 %)	100.0000 % (> 98.6364 %)
Type C	100.0000 % (> 98.8245 %)	96.0396 % (> 93.0693 %)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80344	80344	0.00	24.04
80371	80371	0.00	39.04
80483	80483	0.00	32.96
80557	80557	0.00	33.37
80559	80559	0.00	34.43
80787	80787	0.00	35.21
81045	81045	0.00	33.12
81350	81350	0.00	34.74
81472	81472	0.00	31.80
81487	81487	0.00	23.15

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Carnosine (L-) (H1014)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80153-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Carnosine (L-) (H1014)

Special notes

When selecting the *Carnosine (L-) (H1014)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Carnosine (L-) (H1014)	2	1	9

Second-stage model

For differentiation of the substance/substance group *Carnosine (L-) (H1014)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Carnosine (L-) (H1014)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Glycine (H1021)	45.40	–

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Carnosine (L-) (H1014)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Carnosine (L-) (H1014)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Carnosine (L-) (H1014)	074801	80393	40	from supplier
Hepart	Carnosine (L-) (H1014)	045901	80452	40	from supplier
Hepart	Carnosine (L-) (H1014)	074801	80655	60	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 140 spectra of 3 reference samples from the substance/substance group *Carnosine (L-) (H1014)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 2 different batches.
- 28 336 spectra from a total of 576 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with

the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 40 spectra of 1 reference samples from the substance/substance group *Carnosine (L-) (H1014)*.
- Among them are spectra of independent samples from 1 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Carnosine (L-) (H1014)	18001109	81071	40

- 22959 spectra from a total of 503 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 12 spectra from 7 *Apo-Ident* customers from 9 batches from the substance/substance group *Carnosine (L-) (H1014)*.
- Among them are spectra of independent samples from 9 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
HCK	Carnosine (L-) (H1014)	1813979202	1
HCK	Carnosine (L-) (H1014)	74801/4	1
HCK	Carnosine (L-) (H1014)	74801-4	1
Hepart AG, CH-8280 K...	Carnosine (L-) (H1014)	1812045901	1
Hepart AG	Carnosine (L-) (H1014)	1812045901	1
Hepart AG	Carnosine (L-) (H1014)	1812979202	1
Hepart AG	Carnosine (L-) (H1014)	45901	1
Hepart	Carnosine (L-) (H1014)	18001109/0	1
Hepart	Carnosine (L-) (H1014)	74801-8	1
Purren Apotheke	Carnosine (L-) (H1014)	1813979202	1
Unisan/Hepart AG	Carnosine (L-) (H1014)	45901	1
UNISAN	Carnosine (L-) (H1014)	74801	1

- 2958 spectra from 26 *Apo-Ident* customers from a total of 1451 batches from a further 62 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented

within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Carnosine (L-) (H1014)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Carnosine (L-) (H1014)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	140	0	28 336
Type B	0	40	0	22 959
Type C	0	12	0	2958

The substance/substance group *Carnosine (L-) (H1014)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9279 %)	100.0000 % (> 95.7143 %)
Type B	100.0000 % (> 99.8691 %)	100.0000 % (> 85.0000 %)
Type C	100.0000 % (> 98.8521 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra ([Rule of Three](#) [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the [Mahalanobis distance](#) to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80393	80393	0.00	86.69
80452	80452	0.00	80.63
80655	80655	0.00	84.58

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Carrot (H1513)/Beetroot(H1515)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 10006064-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Carrot (H1513)/Beetroot(H1515); Beetroot (H1515); Carrot (H1513)

Special notes

When selecting the *Carrot (H1513)/Beetroot(H1515)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Carrot (H1513)/Beetroot(H1515)	5	0	0

Second-stage model

For differentiation of the substance/substance group *Carrot (H1513)/Beetroot(H1515)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Carrot (H1513)/Beetroot(H1515)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Flavour orange (H1405)	11.34	—
Kale (H1126)	21.47	—
Glutathione (H1020)	21.88	—
Cabbage mix (H1514)	27.34	—
Orthocolon complex (H1800)	27.35	—
Marshmallow extract (H1439)	27.57	—
Arginine (L-) (H1036)	28.03	—
Calcium L-(+) -lactate complex (H1008)	28.79	—
Artichoke extract (H1440)	29.55	—
Vitamin B1 (H1101)	30.41	—
Rhodiola (H1064)	31.58	—
Broccoli (H1512)	31.62	—
Leaky gut complex (H1802)	33.45	—
Baobab (H1410)	35.61	—
Pomegranate (H1520)	36.17	—
Antioxidants NAT complex (H1004)	37.45	—
Detox complex (H1111)	38.40	—
Juniper (H1112)	39.01	—
Coenzyme Q10 (H1013)	39.70	—
Cranberry (H1519)	40.18	—
Ginseng (H1018)	45.24	—
Iron (H1015)	48.60	—
Potassium (H1030)	48.64	—
PET basis (H1503)	50.15	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Carrot (H1513)/Beetroot(H1515)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Carrot (H1513)/Beetroot(H1515)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Beetroot (H1515)	23000557	81475	40	from supplier
Hepart	Beetroot (H1515)	24000573	81538	40	from supplier
Hepart	Carrot (H1513)	21002986	81455	40	from supplier
Hepart	Carrot (H1513)	23001855	81499	40	from supplier
Hepart	Carrot (H1513)	23002234	81521	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 200 spectra of 5 reference samples from the substance/substance group *Carrot (H1513)/Beetroot(H1515)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 5 different batches.
- 28 276 spectra from a total of 573 batches from further 129 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 0 spectra of 0 reference samples from the substance/substance group *Carrot (H1513)/Beetroot(H1515)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.
- 22 999 spectra from a total of 504 batches from further 78 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *Carrot (H1513)/Beetroot(H1515)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Carrot (H1513)/Beetroot(H1515)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Carrot (H1513)/Beetroot(H1515)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	200	0	28 276
Type B	0	0	0	22 999
Type C	0	0	0	2970

The substance/substance group *Carrot (H1513)/Beetroot(H1515)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate* (*specificity*) and the weighted *true positive rate* (*recognition rate*) are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9277 %)	100.0000 % (> 97.0000 %)
Type B	100.0000 % (> 99.8687 %)	n/a (n/a)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra ([Rule of Three](#) [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the [Mahalanobis distance](#) to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
81455	81455	0.00	29.52
81475	81475	0.00	21.47
81499	81499	0.00	27.92
81521	81521	0.00	25.83
81538	81538	0.00	27.36

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances,

thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group	Catechin extract (H1010)
Substance class	HCK - nutritional supplements (Hepart)
Report date	07/03/2025
Report number	80031-2025-03-07
Executing company	HiperScan GmbH Weißeritzstraße 3 01067 Dresden Germany

Relevant substance names

Catechin extract (H1010)

Special notes

When selecting the *Catechin extract (H1010)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Catechin extract (H1010)	9	0	18

Second-stage model

For differentiation of the substance/substance group *Catechin extract (H1010)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Catechin extract (H1010)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Calcium L-(+)-lactate complex (H1008)	11.37	—
Carnitine (L-) (H1038)	15.01	—
Rhodiola (H1064)	16.58	—
Griffonia (H1035)	18.97	—
ginkgo extract (H1024)	18.99	—
Green coffee extract (H1433)	20.79	—
Bioflavonoid complex (H1006)	21.08	—
Vitamin complex (H1100)	24.11	—
OPC Proanthocyanidins (Pine Bark) (...)	24.94	—
Silymarin (H1071)	35.96	—
PET immune system (H1502)	36.36	—
Coenzyme Q10 (H1013)	39.52	—
Antibiosis forte complex (H1115)	39.88	—
Flavour orange (H1405)	39.92	—
Vitamin B1 (H1101)	41.60	—
Vitamin B6 (Pyridoxal 5'-phosphate)...	41.90	—
Arginine (L-) (H1036)	42.83	—
PET basis (H1503)	44.84	—
Betaine hydrochloride (H1119)	45.68	—
Antioxidants NAT complex (H1004)	46.90	—
Vitamin C (H1104)	49.28	—
Creatine (H1031)	50.11	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Catechin extract (H1010)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Catechin extract (H1010)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Catechin extract (H1010)	062901	80338	40	from supplier
Hepart	Catechin extract (H1010)	062701	80339	40	from supplier
Hepart	Catechin extract (H1010)	062801	80340	40	from supplier
Hepart	Catechin extract (H1010)	15000206	80555	60	from supplier
Hepart	Catechin extract (H1010)	15000206/4	80849	40	from supplier
Hepart	Catechin extract (H1010)	17000409/0	80880	40	from supplier
Hepart	Catechin extract (H1010)	18001420	81144	40	from supplier
Hepart	Catechin extract (H1010)	22000151	81404	40	from supplier
Hepart	Catechin extract (H1010)	22000851	81427	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 380 spectra of 9 reference samples from the substance/substance group *Catechin extract (H1010)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 9 different batches.
- 28 096 spectra from a total of 569 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 40 spectra of 1 reference samples from the substance/substance group *Catechin extract (H1010)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Catechin extract (H1010)	15000206	80872	40

- 22 959 spectra from a total of 503 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 37 spectra from 15 *Apo-Ident* customers from 19 batches from the substance/substance group *Catechin extract (H1010)*.
- Among them are spectra of independent samples from 18 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
HCK	Catechin extract (H1010)	62901	1
Heaprt AG	Catechin extract (H1010)	17000409/2	1
Hepart / Unisan	Catechin extract (H1010)	170004092	1
Hepart AG, CH-8280 K...	Catechin extract (H1010)	1571025702	1
Hepart AG, CH-8280 K...	Catechin extract (H1010)	18601	1
Hepart AG, CH-8280 K...	Catechin extract (H1010)	62901	1
Hepart AG/Unisan	Catechin extract (H1010)	18001420/0	1
Hepart AG/Unisan	Catechin extract (H1010)	18001420/1	1
Hepart AG	Catechin extract (H1010)	130208020	1
Hepart AG	Catechin extract (H1010)	15000206/2	1
Hepart AG	Catechin extract (H1010)	1574018601	1
Hepart AG	Catechin extract (H1010)	17000409/2	1
Hepart AG	Catechin extract (H1010)	18601	2
Hepart	Catechin extract (H1010)	115000206/5	1
Hepart	Catechin extract (H1010)	17000409	1
Hepart	Catechin extract (H1010)	17000409/0	1
Hepart	Catechin extract (H1010)	17000409/2	3
Hepart	Catechin extract (H1010)	17000409/3	5
Hepart	Catechin extract (H1010)	17000409/4	1
Hepart	Catechin extract (H1010)	18001420/0	1
Unisan/Hepart AG	Catechin extract (H1010)	18601	1
Unisan	Catechin extract (H1010)	130208020	1
Unisan	Catechin extract (H1010)	15000206/2	1
Unisan	Catechin extract (H1010)	1571025702	1
Unisan	Catechin extract (H1010)	1571681501	1
Unisan	Catechin extract (H1010)	17000409	1
Unisan	Catechin extract (H1010)	25702	1
Unisan	Catechin extract (H1010)	62801	1
Unisan	Catechin extract (H1010)	62901	1
Unisan	Catechin extract (H1010)	681501	1

- 2933 spectra from 26 *Apo-Ident* customers from a total of 1441 batches from a further 62 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Catechin extract (H1010)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Catechin extract (H1010)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	380	0	28 096
Type B	0	40	0	22 959
Type C	0	24	13	2933

The substance/substance group *Catechin extract (H1010)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9275 %)	100.0000 % (> 98.4211 %)
Type B	100.0000 % (> 99.8691 %)	100.0000 % (> 85.0000 %)
Type C	100.0000 % (> 98.8309 %)	64.8649 % (> 56.7568 %)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80338	80338	0.00	31.75
80339	80339	0.00	43.85
80340	80340	0.00	20.79
80555	80555	0.00	32.16
80849	80849	0.00	29.95
80880	80880	0.00	26.52
81144	81144	0.00	43.73
81404	81404	0.00	18.80
81427	81427	0.00	33.36

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Chaga (H1011)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80032-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Chaga (H1011)

Special notes

When selecting the *Chaga (H1011)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Chaga (H1011)	6	1	7

Second-stage model

For differentiation of the substance/substance group *Chaga (H1011)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Chaga (H1011)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Copper (H1032)	15.18	—
Garcinia cambogia (H1017)	16.52	—
Trace elements SE complex (H1082)	17.49	—
Walnut leaf (H1114)	24.40	—
Iron (H1015)	32.62	—
Magnesium (H1060)	38.16	—
Artemisia annua extract (H1118)	38.21	—
Argentum (H1116)	40.75	—
Antibiosis mite complex (H1113)	41.73	—
Potassium (H1030)	42.22	—
Pathogene complex (H1803)	46.68	—
PET basis (H1503)	49.34	—
PET immune system (H1502)	91.32	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Chaga (H1011)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Chaga (H1011)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Chaga (H1011)	14000951	80466	40	from supplier
Hepart	Chaga (H1011)	14001688	80493	60	from supplier
Hepart	Chaga (H1011)	16000976	80825	40	from supplier
Hepart	Chaga (H1011)	17001560	80952	40	from supplier
Hepart	Chaga (H1011)	21002785/0	81423	40	from supplier
Hepart	Chaga (H1011)	23000051	81465	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 260 spectra of 6 reference samples from the substance/substance group *Chaga (H1011)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 6 different batches.
- 28 216 spectra from a total of 572 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 60 spectra of 1 reference samples from the substance/substance group *Chaga (H1011)*.
- Among them are spectra of independent samples from 1 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Chaga (H1011)	16000235	80763	60

- 22 939 spectra from a total of 503 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 11 spectra from 4 *Apo-Ident* customers from 8 batches from the substance/substance group *Chaga (H1011)*.
- Among them are spectra of independent samples from 7 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
HCK	Chaga (H1011)	14001688/5	1
Hepart	Chaga (H1011)	16000235-1	3
Hepart	Chaga (H1011)	17001560/1	1
Purren Apotheke	Chaga (H1011)	1514675601	1
Unisan/Hepart AG	Chaga (H1011)	46701	1
Unisan	Chaga (H1011)	14001688	1
Unisan	Chaga (H1011)	16000235	1
Unisan	Chaga (H1011)	64001	2

- 2959 spectra from 26 *Apo-Ident* customers from a total of 1452 batches from a further 62 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Chaga (H1011)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Chaga (H1011)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	260	0	28 216
Type B	0	60	0	22 939
Type C	0	11	0	2959

The substance/substance group *Chaga (H1011)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9276 %)	100.0000 % (> 97.6923 %)
Type B	100.0000 % (> 99.8673 %)	100.0000 % (> 90.0000 %)
Type C	100.0000 % (> 98.8549 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra ([Rule of Three](#) [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the [Mahalanobis distance](#) to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80466	80466	0.00	72.57
80493	80493	0.00	40.66
80825	80825	0.00	32.76
80952	80952	0.00	32.05
81423	81423	0.00	25.09
81465	81465	0.00	33.76

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Chia seeds protein (H1506)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 10006319-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Chia seeds protein (H1506)

Special notes

When selecting the *Chia seeds protein (H1506)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Chia seeds protein (H1506)	1	0	0

Second-stage model

For differentiation of the substance/substance group *Chia seeds protein (H1506)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Chia seeds protein (H1506)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
PET immune system (H1502)	24.82	—
Cocoa (H1521)	42.11	—
ginkgo extract (H1024)	50.89	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Chia seeds protein (H1506)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Chia seeds protein (H1506)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Chia seeds protein (H1506)	23002137	81522	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 40 spectra of 1 reference samples from the substance/substance group *Chia seeds protein (H1506)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 1 different batches.
- 28 436 spectra from a total of 577 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with

the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a †. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 0 spectra of 0 reference samples from the substance/substance group *Chia seeds protein (H1506)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.
- 22 999 spectra from a total of 504 batches from further 78 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *Chia seeds protein (H1506)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Chia seeds protein (H1506)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Chia seeds protein (H1506)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	40	0	28 436
Type B	0	0	0	22 999
Type C	0	0	0	2970

The substance/substance group *Chia seeds protein (H1506)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9295 %)	100.0000 % (> 85.0000 %)
Type B	100.0000 % (> 99.8687 %)	n/a (n/a)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
81522	81522	0.00	24.82

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Chondroitin sulfate (H1065)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 10005853-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Chondroitin sulfate (H1065)

Special notes

When selecting the *Chondroitin sulfate (H1065)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Chondroitin sulfate (H1065)	6	3	14

Second-stage model

For differentiation of the substance/substance group *Chondroitin sulfate (H1065)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Chondroitin sulfate (H1065)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Coenzyme Q10 (H1013)	19.85	—
Vitamin E NAT (H1107)	38.90	—
Silicium (H1070)	40.45	—
PET coenzyme Q10 (H1505)	42.09	—
Ginseng (H1018)	45.52	—
Magnesium (H1060)	54.62	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Chondroitin sulfate (H1065)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Chondroitin sulfate (H1065)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Chondroitin sulfate (H1065)	14001991	80533	60	from supplier
Hepart	Chondroitin sulfate (H1065)	031801	80584	60	from supplier
Hepart	Chondroitin sulfate (H1065)	14001985/2	80779	60	from supplier
Hepart	Chondroitin sulfate (H1065)	17000211	80871	40	from supplier
Hepart	Chondroitin sulfate (H1065)	20002086/0	81393	50	from supplier
Hepart	Chondroitin sulfate (H1065)	21002683	81462	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 310 spectra of 6 reference samples from the substance/substance group *Chondroitin sulfate (H1065)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 6 different batches.
- 28 166 spectra from a total of 572 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a †. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 140 spectra of 3 reference samples from the substance/substance group *Chondroitin sulfate (H1065)*.
- Among them are spectra of independent samples from 3 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Chondroitin sulfate (H1065)	14001985	80532	60
Hepart	Chondroitin sulfate (H1065)	19000780	81180	40
Hepart	Chondroitin sulfate (H1065)	23000663	81490	40

- 22 859 spectra from a total of 501 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 40 spectra from 15 *Apo-Ident* customers from 16 batches from the substance/substance group *Chondroitin sulfate (H1065)*.
- Among them are spectra of independent samples from 14 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
Fagron	Chondroitin sulfate (H1065)	1821031801	1
Hepart AG, CH-8280 K...	Chondroitin sulfate (H1065)	1820031801	1
Hepart AG, CH-8280 K...	Chondroitin sulfate (H1065)	31801	1
Hepart AG	Chondroitin sulfate (H1065)	17000211/1	1
Hepart AG	Chondroitin sulfate (H1065)	19000780/0	1

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Supplier	Substance	Batch	Spectra
hepart ag	Chondroitin sulfate (H1065)	31801	1
Hepart AG	Chondroitin sulfate (H1065)	31801	1
Hepart AG	Chondroitin sulfate (H1065)	31801/1	1
Hepart/Unisan	Chondroitin sulfate (H1065)	19000780/1	1
Hepart	Chondroitin sulfate (H1065)		1
Hepart	Chondroitin sulfate (H1065)	14001985/5	1
Hepart	Chondroitin sulfate (H1065)	14001985-7	5
Hepart	Chondroitin sulfate (H1065)	17000211	1
Hepart	Chondroitin sulfate (H1065)	17000211/0	1
Hepart	Chondroitin sulfate (H1065)	17000211/1	1
Hepart	Chondroitin sulfate (H1065)	19000780	1
Hepart	Chondroitin sulfate (H1065)	19000780/0	6
Hepart	Chondroitin sulfate (H1065)	19000780/1	2
Purren Apotheke	Chondroitin sulfate (H1065)	1821964101	1
Unisan/Hepart AG	Chondroitin sulfate (H1065)	31801	2
Unisan	Chondroitin sulfate (H1065)	1801	2
Unisan	Chondroitin sulfate (H1065)	1820001801	2
Unisan	Chondroitin sulfate (H1065)	1821964101	1
Unisan	Chondroitin sulfate (H1065)	31801	4

- 2930 spectra from 26 *Apo-Ident* customers from a total of 1444 batches from a further 62 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Chondroitin sulfate (H1065)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Chondroitin sulfate (H1065)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	310	0	28 166
Type B	0	140	0	22 859
Type C	0	33	7	2930

The substance/substance group *Chondroitin sulfate (H1065)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9275 %)	100.0000 % (> 98.0645 %)
Type B	100.0000 % (> 99.8652 %)	100.0000 % (> 95.7143 %)
Type C	100.0000 % (> 98.8302 %)	82.5000 % (> 75.0000 %)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra ([Rule of Three](#) [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80533	80533	0.00	48.19
80584	80584	0.00	65.68
80779	80779	0.00	53.82
80871	80871	0.00	64.98
81393	81393	0.00	65.81
81462	81462	0.00	42.09

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Cocoa (H1521)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 10006306-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Cocoa (H1521)

Special notes

When selecting the *Cocoa (H1521)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Cocoa (H1521)	3	0	0

Second-stage model

For differentiation of the substance/substance group *Cocoa (H1521)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Cocoa (H1521)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Moringa (H1131)	25.22	—
PET immune system (H1502)	28.09	—
PET basis (H1503)	33.13	—
ginkgo extract (H1024)	44.07	—
Vitamin C (H1104)	46.55	—
Copper (H1032)	46.97	—
PET skin and hair (H1504)	50.58	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Cocoa (H1521)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Cocoa (H1521)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Cocoa (H1521)	23001438	81502	40	from supplier
Hepart	Cocoa (H1521)	24000472	81548	30	from supplier
Hepart	Cocoa (H1521)	24001271	81549	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 110 spectra of 3 reference samples from the substance/substance group *Cocoa (H1521)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 3 different batches.

- 28 366 spectra from a total of 575 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 0 spectra of 0 reference samples from the substance/substance group *Cocoa (H1521)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.
- 22 999 spectra from a total of 504 batches from further 78 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *Cocoa (H1521)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Cocoa (H1521)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Cocoa (H1521)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	110	0	28 366
Type B	0	0	0	22 999
Type C	0	0	0	2970

The substance/substance group *Cocoa (H1521)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9281 %)	100.0000 % (> 94.5455 %)
Type B	100.0000 % (> 99.8687 %)	n/a (n/a)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
81502	81502	0.00	25.22
81548	81548	0.00	25.55
81549	81549	0.00	28.09

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Coconut (H1522)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 10006010-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Coconut (H1522)

Special notes

When selecting the *Coconut (H1522)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Coconut (H1522)	2	0	0

Second-stage model

For differentiation of the substance/substance group *Coconut (H1522)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Coconut (H1522)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Glutathione (H1020)	13.70	—
Vitamin E NAT (H1107)	15.26	—
Coenzyme Q10 (H1013)	19.64	—
Oat bran beta-glucan (H1529)	22.14	—
Aminomix NAC (H1002)	26.39	—
Flavour orange (H1405)	30.61	—
Lutein-Zeaxanthin-Astaxanthin (H1129)	37.12	—
Calcium L-(+)-lactate complex (H1008)	38.63	—
Isoflavone (H1025)	40.98	—
Garcinia cambogia (H1017)	43.51	—
Ginseng (H1018)	44.29	—
Antioxidants NAT complex (H1004)	44.64	—
Antibiosis forte complex (H1115)	46.16	—
Leaky gut complex (H1802)	46.29	—
Ginger extract (H1437)	49.67	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Coconut (H1522)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Coconut (H1522)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Coconut (H1522)	21002574	81448	40	from supplier
Hepart	Coconut (H1522)	23000228	81463	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 80 spectra of 2 reference samples from the substance/substance group *Coconut (H1522)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 2 different batches.
- 28 396 spectra from a total of 576 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 0 spectra of 0 reference samples from the substance/substance group *Coconut (H1522)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.
- 22 999 spectra from a total of 504 batches from further 78 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *Coconut (H1522)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Coconut (H1522)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Coconut (H1522)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	80	0	28 396
Type B	0	0	0	22 999
Type C	0	0	0	2970

The substance/substance group *Coconut (H1522)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9284 %)	100.0000 % (> 92.5000 %)
Type B	100.0000 % (> 99.8687 %)	n/a (n/a)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
81448	81448	0.00	24.10
81463	81463	0.00	25.87

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group	Coenzyme Q10 (H1013)
Substance class	HCK - nutritional supplements (Hepart)
Report date	07/03/2025
Report number	80015-2025-03-07
Executing company	HiperScan GmbH Weißeritzstraße 3 01067 Dresden Germany

Relevant substance names

Coenzyme Q10 (H1013)

Special notes

When selecting the *Coenzyme Q10 (H1013)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Coenzyme Q10 (H1013)	10	4	40

Second-stage model

For differentiation of the substance/substance group *Coenzyme Q10 (H1013)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Coenzyme Q10 (H1013)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Vitamin E NAT (H1107)	16.98	—
Ginseng (H1018)	25.60	—
Aminomix NAC (H1002)	38.10	—
PET coenzyme Q10 (H1505)	40.81	—
α -Lipoic acid (H1000)	43.94	—
Glutathione (H1020)	44.02	—
Vitamin B1 (H1101)	44.41	—
Vitamin K2 (75 μ g Mono) (H1108)	45.21	—
Glutamine (L-) (H1043)	45.26	—
Antibiosis forte complex (H1115)	46.43	—
Chondroitin sulfate (H1065)	47.61	—
Ginger extract (H1437)	47.68	—
Oat bran beta-glucan (H1529)	54.67	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Coenzyme Q10 (H1013)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Coenzyme Q10 (H1013)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Coenzyme Q10 (H1013)	130521-300	80354	40	from supplier
Hepart	Coenzyme Q10 (H1013)	14001546	80484	60	from supplier
Hepart	Coenzyme Q10 (H1013)	14001546	80587	60	from supplier
Hepart	Coenzyme Q10 (H1013)	16000402/0	80794	40	from supplier
Hepart	Coenzyme Q10 (H1013)	16000402/0	80850	40	from supplier
Hepart	Coenzyme Q10 (H1013)	16001598/4	80854	40	from supplier
Hepart	Coenzyme Q10 (H1013)	16001598	80881	40	from supplier
Hepart	Coenzyme Q10 (H1013)	18000792/0	81048	40	from supplier
Hepart	Coenzyme Q10 (H1013)	18000806	81049	40	from supplier
Hepart	Coenzyme Q10 (H1013)	19002493/4	81213	40	from supplier

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Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Coenzyme Q10 (H1013)	20002171	81308	40	from supplier
Hepart	Coenzyme Q10 (H1013)	20002839	81346	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 520 spectra of 12 reference samples from the substance/substance group *Coenzyme Q10 (H1013)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 10 different batches.
- 27 956 spectra from a total of 569 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 170 spectra of 4 reference samples from the substance/substance group *Coenzyme Q10 (H1013)*.
- Among them are spectra of independent samples from 4 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Coenzyme Q10 (H1013)	16000402/4	80795	40
Hepart	Coenzyme Q10 (H1013)	16000402	80882	40
Hepart	Coenzyme Q10 (H1013)	20000802	81257	40
Hepart	Coenzyme Q10 (H1013)	210015-36-37	81373	50

- 22 829 spectra from a total of 500 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 107 spectra from 22 *Apo-Ident* customers from 47 batches from the substance/substance group *Coenzyme Q10 (H1013)*.
- Among them are spectra of independent samples from 40 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
HCK	Coenzyme Q10 (H1013)	14001546/4	2
HCK	Coenzyme Q10 (H1013)	14001546-2	1
HCK	Coenzyme Q10 (H1013)	16001598/1	1
Hepart / Unisan	Coenzyme Q10 (H1013)	160015991	1
Hepart AG, CH-8280 K...	Coenzyme Q10 (H1013)	1194015601	1
Hepart AG, CH-8280 K...	Coenzyme Q10 (H1013)	15601	1
Hepart AG/Unisan	Coenzyme Q10 (H1013)	200002171/0	1
Hepart AG/Unisan	Coenzyme Q10 (H1013)	200002171/1	1
Hepart ag/Unisan	Coenzyme Q10 (H1013)	2000080	1
Hepart AG/Unisan	Coenzyme Q10 (H1013)	20000802/0	3
Hepart ag/Unisan	Coenzyme Q10 (H1013)	20002171	1
Hepart AG/Unisan	Coenzyme Q10 (H1013)	20002839/1	1
Hepart AG	Coenzyme Q10 (H1013)	1194015601	2
Hepart AG	Coenzyme Q10 (H1013)	130521-300	5
Hepart AG	Coenzyme Q10 (H1013)	15601	4
Hepart AG	Coenzyme Q10 (H1013)	16000402/0	1
Hepart AG	Coenzyme Q10 (H1013)	16001598/1	1
Hepart AG	Coenzyme Q10 (H1013)	16001599/1	2
Hepart AG	Coenzyme Q10 (H1013)	16001599/2	12
Hepart AG	Coenzyme Q10 (H1013)	18000792/1	1
Hepart AG	Coenzyme Q10 (H1013)	19002493/1	1
Hepart	Coenzyme Q10 (H1013)	14001546	1
Hepart	Coenzyme Q10 (H1013)	16000402/1	1
Hepart	Coenzyme Q10 (H1013)	16000402-2	1
Hepart	Coenzyme Q10 (H1013)	16000402-3	1
Hepart	Coenzyme Q10 (H1013)	16000402-4	1
Hepart	Coenzyme Q10 (H1013)	16001598	1
Hepart	Coenzyme Q10 (H1013)	16001598/0	2
Hepart	Coenzyme Q10 (H1013)	16001598/1	2
Hepart	Coenzyme Q10 (H1013)	16001598/2	5
Hepart	Coenzyme Q10 (H1013)	16001598/3	3
Hepart	Coenzyme Q10 (H1013)	16001598-2	2
Hepart	Coenzyme Q10 (H1013)	16001599	1
Hepart	Coenzyme Q10 (H1013)	18000792/0	1
Hepart	Coenzyme Q10 (H1013)	18000792/2	1
Hepart	Coenzyme Q10 (H1013)	18001598	1
Hepart	Coenzyme Q10 (H1013)	19002492	1
Hepart	Coenzyme Q10 (H1013)	19002493/0	1
Hepart	Coenzyme Q10 (H1013)	20000802/0	2
Hepart	Coenzyme Q10 (H1013)	20002839	2
Hepart	Coenzyme Q10 (H1013)	20002839/0	1
Hepart	Coenzyme Q10 (H1013)	20002839/2	1
Hepart	Coenzyme Q10 (H1013)	21001536	1
Hepart	Coenzyme Q10 (H1013)	21001536/0	1
Hepart	Coenzyme Q10 (H1013)	21001537	1
Hepart	Coenzyme Q10 (H1013)	21001537/1	1
Unisan 02.04.2016	Coenzyme Q10 (H1013)	14001546/3	1
Unisan 2.10.2015	Coenzyme Q10 (H1013)	14001546/2	1
Unisan	Coenzyme Q10 (H1013)	1194015601	2
Unisan	Coenzyme Q10 (H1013)	130521-300	4
UNISAN	Coenzyme Q10 (H1013)	130521-300	2
Unisan	Coenzyme Q10 (H1013)	14001546	2
UNISAN	Coenzyme Q10 (H1013)	14001546	2
Unisan	Coenzyme Q10 (H1013)	14001546/1	2

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Supplier	Substance	Batch	Spectra
Unisan	Coenzyme Q10 (H1013)	15601	4
Unisan	Coenzyme Q10 (H1013)	16000402	1
Unisan	Coenzyme Q10 (H1013)	16000402/0	2
Unisan	Coenzyme Q10 (H1013)	16001598	1
Unisan	Coenzyme Q10 (H1013)	16001599	1
Unisan	Coenzyme Q10 (H1013)	992501	1
Unisan	Coenzyme Q10 (H1013)	H101311	1

- 2863 spectra from 26 *Apo-Ident* customers from a total of 1413 batches from a further 62 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Coenzyme Q10 (H1013)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Coenzyme Q10 (H1013)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	520	0	27 956
Type B	0	170	0	22 829
Type C	0	91	16	2863

The substance/substance group *Coenzyme Q10 (H1013)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9274 %)	100.0000 % (> 98.8462 %)
Type B	100.0000 % (> 99.8650 %)	100.0000 % (> 96.4706 %)
Type C	100.0000 % (> 98.8243 %)	85.0467 % (> 82.2430 %)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80354	80354	0.00	31.64
80484	80484	0.00	26.73
80587	80587	0.00	46.43
80794	80794	0.00	27.87
80850	80850	0.00	25.35
80854	80854	0.00	24.47
80881	80881	0.00	36.99
81048	81048	0.00	30.96
81049	81049	0.00	40.81
81213	81213	0.00	37.36
81308	81308	0.00	36.31
81346	81346	0.00	42.47

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group	Collagen peptides-MTC (H1125)
Substance class	HCK - nutritional supplements (Hepart)
Report date	07/03/2025
Report number	10006002-2025-03-07
Executing company	HiperScan GmbH Weißeritzstraße 3 01067 Dresden Germany

Relevant substance names

Collagen peptides-MTC (H1125)

Special notes

When selecting the *Collagen peptides-MTC (H1125)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Collagen peptides-MTC (H1125)	3	1	0

Second-stage model

For differentiation of the substance/substance group *Collagen peptides-MTC (H1125)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Collagen peptides-MTC (H1125)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Coenzyme Q10 (H1013)	25.94	—
Antibiosis forte complex (H1115)	30.77	—
Aminomix NAC (H1002)	36.83	—
PET skin and hair (H1504)	42.14	—
Glutamine (L-) (H1043)	49.26	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Collagen peptides-MTC (H1125)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Collagen peptides-MTC (H1125)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Collagen peptides-MTC (H1125)	21001193	81432	40	from supplier
Hepart	Collagen peptides-MTC (H1125)	22002703	81496	40	from supplier
Hepart	Collagen peptides-MTC (H1125)	23002071	81510	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 120 spectra of 3 reference samples from the substance/substance group *Collagen peptides-MTC (H1125)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 3 different batches.

- 28 356 spectra from a total of 575 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 40 spectra of 1 reference samples from the substance/substance group *Collagen peptides-MTC (H1125)*.
- Among them are spectra of independent samples from 1 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Collagen peptides-MTC (H1125)	24001329/0	81552	40

- 22 959 spectra from a total of 503 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *Collagen peptides-MTC (H1125)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Collagen peptides-MTC (H1125)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Collagen peptides-MTC (H1125)* and it was evaluated how many matches (positive) and rejections (negative) were

correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	120	0	28 356
Type B	0	40	0	22 959
Type C	0	0	0	2970

The substance/substance group *Collagen peptides-MTC (H1125)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate* (*specificity*) and the weighted *true positive rate* (*recognition rate*) are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9280 %)	100.0000 % (> 95.0000 %)
Type B	100.0000 % (> 99.8691 %)	100.0000 % (> 85.0000 %)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
81432	81432	0.00	31.67
81496	81496	0.00	31.82
81510	81510	0.00	30.77

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Creatine (H1031)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80149-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Creatine (H1031)

Special notes

When selecting the *Creatine (H1031)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Creatine (H1031)	6	3	7

Second-stage model

For differentiation of the substance/substance group *Creatine (H1031)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Creatine (H1031)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Vitamin complex (H1100)	29.40	—
Flavour orange (H1405)	44.15	—
Carnitine (L-) (H1038)	50.31	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Creatine (H1031)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Creatine (H1031)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Creatine (H1031)	025003	80440	40	from supplier
Hepart	Creatine (H1031)	025004	80441	40	from supplier
Hepart	Creatine (H1031)	15000749	80627	60	from supplier
Hepart	Creatine (H1031)	15000750	80628	60	from supplier
Hepart	Creatine (H1031)	20002161	81295	40	from supplier
Hepart	Creatine (H1031)	24000700	81543	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 280 spectra of 6 reference samples from the substance/substance group *Creatine (H1031)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 6 different batches.

- 28 196 spectra from a total of 572 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 120 spectra of 3 reference samples from the substance/substance group *Creatine (H1031)*.
- Among them are spectra of independent samples from 3 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Creatine (H1031)	17001177	80918	40
Hepart	Creatine (H1031)	18001411	81115	40
Hepart	Creatine (H1031)	24001358	81554	40

- 22 879 spectra from a total of 501 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 11 spectra from 5 *Apo-Ident* customers from 9 batches from the substance/substance group *Creatine (H1031)*.
- Among them are spectra of independent samples from 7 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
HCK	Creatine (H1031)	15000749/1	1
HCK	Creatine (H1031)	15000749-2	1
HCK	Creatine (H1031)	17001177	2
Hepart AG	Creatine (H1031)	15000749	1
Purren Apotheke	Creatine (H1031)	965201	1
Unisan Gmbh, 78465 K...	Creatine (H1031)	1830025003	1
Unisan	Creatine (H1031)	15000750	1
Unisan	Creatine (H1031)	15000750/0	1
Unisan	Creatine (H1031)	25003	2

- 2959 spectra from 26 *Apo-Ident* customers from a total of 1451 batches from a further 62 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Creatine (H1031)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Creatine (H1031)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	280	0	28 196
Type B	0	120	0	22 879
Type C	0	11	0	2959

The substance/substance group *Creatine (H1031)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9276 %)	100.0000 % (> 97.8571 %)
Type B	100.0000 % (> 99.8655 %)	100.0000 % (> 95.0000 %)
Type C	100.0000 % (> 98.8549 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra ([Rule of Three](#) [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the [Mahalanobis distance](#) to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80440	80440	0.00	47.09
80441	80441	0.00	54.68
80627	80627	0.00	44.17
80628	80628	0.00	49.87
81295	81295	0.00	52.65
81543	81543	0.00	51.82

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at

least 50% greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Curcumin and piperine (H1014)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 10005865-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Curcumin and piperine (H1014)

Special notes

When selecting the *Curcumin and piperine (H1014)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Curcumin and piperine (H1014)	6	2	11

Second-stage model

For differentiation of the substance/substance group *Curcumin and piperine (H1014)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Curcumin and piperine (H1014)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Antibiosis forte complex (H1115)	37.23	—
Betaine hydrochloride (H1119)	72.34	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Curcumin and piperine (H1014)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Curcumin and piperine (H1014)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Curcumin and piperine (H1014)	14001017	80475	40	from supplier
Hepart	Curcumin and piperine (H1014)	15001589	80705	60	from supplier
Hepart	Curcumin and piperine (H1014)	16000369	80796	40	from supplier
Hepart	Curcumin and piperine (H1014)	17000258	80883	40	from supplier
Hepart	Curcumin and piperine (H1014)	21000433	81336	40	from supplier
Hepart	Curcumin and piperine (H1014)	21000433	81406	40	from supplier
Hepart	Curcumin and piperine (H1014)	22000029	81416	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 300 spectra of 7 reference samples from the substance/substance group *Curcumin and piperine (H1014)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 6 different batches.

- 28 176 spectra from a total of 572 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 80 spectra of 2 reference samples from the substance/substance group *Curcumin and piperine (H1014)*.
- Among them are spectra of independent samples from 2 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Curcumin and piperine (H1014)	18001688	81128	40
Hepart	Curcumin and piperine (H1014)	18001687	81129	40

- 22 919 spectra from a total of 502 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 25 spectra from 10 *Apo-Ident* customers from 14 batches from the substance/substance group *Curcumin and piperine (H1014)*.
- Among them are spectra of independent samples from 11 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
HCK	Curcumin and piperine (H1014)	14001017/6	1
HCK	Curcumin and piperine (H1014)	16001002-1	1
Hepart AG, CH-8280 K...	Curcumin and piperine (H1014)	13901	1
Hepart AG	Curcumin and piperine (H1014)	13901	3
Hepart AG	Curcumin and piperine (H1014)	15001589	1
Hepart AG	Curcumin and piperine (H1014)	1534002201	1
Hepart AG	Curcumin and piperine (H1014)	18001687/1	1
Hepart AG	Curcumin and piperine (H1014)	72001	2
Hepart	Curcumin and piperine (H1014)	1017	1
Hepart	Curcumin and piperine (H1014)	17000258	2

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Supplier	Substance	Batch	Spectra
Hepart	Curcumin and piperine (H1014)	17000258-0	1
Hepart	Curcumin and piperine (H1014)	17000259/0	1
Hepart	Curcumin and piperine (H1014)	180016870	1
Unisan	Curcumin and piperine (H1014)	13901	1
Unisan	Curcumin and piperine (H1014)	14001017	1
Unisan	Curcumin and piperine (H1014)	14001017/6	1
Unisan	Curcumin and piperine (H1014)	17000259	1
Unisan	Curcumin and piperine (H1014)	72001	4

- 2945 spectra from 26 *Apo-Ident* customers from a total of 1446 batches from a further 62 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Curcumin and piperine (H1014)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Curcumin and piperine (H1014)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	300	0	28 176
Type B	0	80	0	22 919
Type C	0	23	2	2945

The substance/substance group *Curcumin and piperine (H1014)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9276 %)	100.0000 % (> 98.0000 %)
Type B	100.0000 % (> 99.8664 %)	100.0000 % (> 92.5000 %)
Type C	100.0000 % (> 98.8358 %)	92.0000 % (> 80.0000 %)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra ([Rule of Three \[10, 11\]](#)). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the [Mahalanobis distance](#) to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80475	80475	0.00	38.93
80705	80705	0.00	38.82
80796	80796	0.00	43.19
80883	80883	0.00	37.23
81336	81336	0.00	41.90
81406	81406	0.00	42.24
81416	81416	0.00	45.79

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Glucosamine sulfate (H1019)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80094-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Glucosamine sulfate (H1019); Glucosamine sulphate (H1019)

Special notes

When selecting the *Glucosamine sulfate (H1019)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Glucosamine sulfate (H1019)	3	7	15

Second-stage model

For differentiation of the substance/substance group *Glucosamine sulfate (H1019)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Glucosamine sulfate (H1019)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Flavour orange (H1405)	28.12	—
Creatine (H1031)	55.50	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Glucosamine sulfate (H1019)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Glucosamine sulfate (H1019)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Glucosamine sulfate (H1019)	038001	80319	60	from supplier
Hepart	Glucosamine sulfate (H1019)	038001	80362	40	from supplier
Hepart	Glucosamine sulfate (H1019)	075401	80402	40	from supplier
Hepart	Glucosamine sulfate (H1019)	16000948	80812	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 180 spectra of 4 reference samples from the substance/substance group *Glucosamine sulfate (H1019)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 3 different batches.
- 28 296 spectra from a total of 575 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A*

section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 280 spectra of 7 reference samples from the substance/substance group *Glucosamine sulfate (H1019)*.
- Among them are spectra of independent samples from 7 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Glucosamine sulfate (H1019)	034001	80454	40
Hepart	Glucosamine sulfate (H1019)	17000073	80877	40
Hepart	Glucosamine sulfate (H1019)	17001387	80954	40
Hepart	Glucosamine sulfate (H1019)	17001245	80955	40
Hepart	Glucosamine sulfate (H1019)	19000775	81181	40
Hepart	Glucosamine sulfate (H1019)	20000494	81261	40
Hepart	Glucosamine sulfate (H1019)	20002248/0	81317	40

- 22719 spectra from a total of 497 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 33 spectra from 12 *Apo-Ident* customers from 16 batches from the substance/substance group *Glucosamine sulfate (H1019)*.
- Among them are spectra of independent samples from 15 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
Hepart AG	Glucosamine sulfate (H1019)	1822038001	1
Hepart AG	Glucosamine sulfate (H1019)	38001	2
Hepart/Unisan	Glucosamine sulfate (H1019)	20000494/0	1
Hepart	Glucosamine sulfate (H1019)	17000073	1
Hepart	Glucosamine sulfate (H1019)	17000073-0	1
Hepart	Glucosamine sulfate (H1019)	17000073-1	1
Hepart	Glucosamine sulfate (H1019)	17001245	2
Hepart	Glucosamine sulfate (H1019)	17001387/0	9

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Supplier	Substance	Batch	Spectra
Hepart	Glucosamine sulfate (H1019)	19000775	1
Hepart	Glucosamine sulfate (H1019)	19000775/0	1
Hepart	Glucosamine sulfate (H1019)	20000494	1
Hepart	Glucosamine sulfate (H1019)	20000494/0	1
Hepart	Glucosamine sulfate (H1019)	34001	1
Unisan GmbH, 78465 K...	Glucosamine sulfate (H1019)	38001	1
Unisan/Hepart AG	Glucosamine sulfate (H1019)	38001	1
Unisan	Glucosamine sulfate (H1019)	16000948	1
Unisan	Glucosamine sulfate (H1019)	17000073/0	1
Unisan	Glucosamine sulfate (H1019)	1823954901	2
UNISAN	Glucosamine sulfate (H1019)	34001	1
Unisan	Glucosamine sulfate (H1019)	38001	2
Unisan	Glucosamine sulfate (H1019)	75401	1

- 2937 spectra from 26 *Apo-Ident* customers from a total of 1444 batches from a further 62 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Glucosamine sulfate (H1019)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Glucosamine sulfate (H1019)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	180	0	28 296
Type B	0	240	40	22 719
Type C	0	22	11	2937

The substance/substance group *Glucosamine sulfate (H1019)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9278 %)	100.0000 % (> 96.6667 %)
Type B	100.0000 % (> 99.8645 %)	85.7143 % (> 84.6429 %)
Type C	100.0000 % (> 98.8322 %)	66.6667 % (> 57.5758 %)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra ([Rule of Three](#) [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested

reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80319	80319	0.00	98.03
80362	80362	0.00	93.31
80402	80402	0.00	59.42
80812	80812	0.00	73.02

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Glutamine (L-) (H1043)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80089-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Glutamine (L-) (H1043)

Special notes

When selecting the *Glutamine (L-) (H1043)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Glutamine (L-) (H1043)	7	8	25

Second-stage model

For differentiation of the substance/substance group *Glutamine (L-) (H1043)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Glutamine (L-) (H1043)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Leaky gut complex (H1802)	36.07	—
PET skin and hair (H1504)	38.37	—
Aminomix NAC (H1002)	40.57	—
Antibiosis forte complex (H1115)	41.18	—
Coenzyme Q10 (H1013)	41.85	—
PET joints (H1501)	43.08	—
Vitamin E NAT (H1107)	43.53	—
Pumpkin seed protein (H1509)	51.24	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Glutamine (L-) (H1043)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Glutamine (L-) (H1043)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Glutamine (L-) (H1043)	061501	80336	40	from supplier
Hepart	Glutamine (L-) (H1043)	15000017	80551	60	from supplier
Hepart	Glutamine (L-) (H1043)	15000018	80552	60	from supplier
Hepart	Glutamine (L-) (H1043)	16000940	80802	40	from supplier
Hepart	Glutamine (L-) (H1043)	20001001	81263	40	from supplier
Hepart	Glutamine (L-) (H1043)	20001021	81264	40	from supplier
Hepart	Glutamine (L-) (H1043)	22000156-157-158	81410	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 320 spectra of 7 reference samples from the substance/substance group *Glutamine (L-) (H1043)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 7 different batches.
- 28 156 spectra from a total of 571 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 330 spectra of 8 reference samples from the substance/substance group *Glutamine (L-) (H1043)*.
- Among them are spectra of independent samples from 8 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Glutamine (L-) (H1043)	16000941	80803	40
Hepart	Glutamine (L-) (H1043)	16000942	80804	40
Hepart	Glutamine (L-) (H1043)	17000902	80930	40
Hepart	Glutamine (L-) (H1043)	17000901	80931	40
Hepart	Glutamine (L-) (H1043)	19000531	81190	40
Hepart	Glutamine (L-) (H1043)	19000650/0	81191	40
Hepart	Glutamine (L-) (H1043)	21000248	81351	40
Hepart	Glutamine (L-) (H1043)	21001702	81363	50

- 22 669 spectra from a total of 496 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 61 spectra from 16 *Apo-Ident* customers from 30 batches from the substance/substance group *Glutamine (L-) (H1043)*.
- Among them are spectra of independent samples from 25 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
HCK	Glutamine (L-) (H1043)	15000017/1	1
HCK	Glutamine (L-) (H1043)	16000941	2
Hepart / Unisan	Glutamine (L-) (H1043)	16000942	1
Hepart ag/Unisan	Glutamine (L-) (H1043)	20001001	1
Hepart AG	Glutamine (L-) (H1043)	15000017/1	1
Hepart AG	Glutamine (L-) (H1043)	160009420	1
Hepart AG	Glutamine (L-) (H1043)	17000901/0	2
Hepart, 27.03.19	Glutamine (L-) (H1043)	17000901/0	1
Hepart	Glutamine (L-) (H1043)	15000018-2	1
Hepart	Glutamine (L-) (H1043)	16000940/1	1
Hepart	Glutamine (L-) (H1043)	16000942/0	3
Hepart	Glutamine (L-) (H1043)	16000942-0	2
Hepart	Glutamine (L-) (H1043)	16001349/0	1
Hepart	Glutamine (L-) (H1043)	17000901	1
Hepart	Glutamine (L-) (H1043)	17000901/1	1
Hepart	Glutamine (L-) (H1043)	19000531	1
Hepart	Glutamine (L-) (H1043)	19000531/0	2
Hepart	Glutamine (L-) (H1043)	20001001	1
Hepart	Glutamine (L-) (H1043)	20001001/0	1
Hepart	Glutamine (L-) (H1043)	200010011	1
Unisan Gmbh, 78465 K...	Glutamine (L-) (H1043)	26904	1
Unisan/Hepart AG	Glutamine (L-) (H1043)	26901	1
Unisan	Glutamine (L-) (H1043)		1
Unisan	Glutamine (L-) (H1043)	15000017	1
Unisan	Glutamine (L-) (H1043)	15000017/0	1
UNISAN	Glutamine (L-) (H1043)	15000017/0	1
Unisan	Glutamine (L-) (H1043)	15000018	1
Unisan	Glutamine (L-) (H1043)	15000018/0	1
Unisan	Glutamine (L-) (H1043)	16000940	1
Unisan	Glutamine (L-) (H1043)	16000940/0	3
Unisan	Glutamine (L-) (H1043)	16000941	1
Unisan	Glutamine (L-) (H1043)	16000942	3
Unisan	Glutamine (L-) (H1043)	1814026901	5
Unisan	Glutamine (L-) (H1043)	26903	2
Unisan	Glutamine (L-) (H1043)	26904	1
Unisan	Glutamine (L-) (H1043)	61501	8
UNISAN	Glutamine (L-) (H1043)	61501	2
Unisan	Glutamine (L-) (H1043)	61501/4	1

- 2909 spectra from 26 *Apo-Ident* customers from a total of 1432 batches from a further 62 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Glutamine (L-) (H1043)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Glutamine (L-) (H1043)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	320	0	28 156
Type B	0	330	0	22 669
Type C	0	57	4	2909

The substance/substance group *Glutamine (L-) (H1043)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9275 %)	100.0000 % (> 98.1250 %)
Type B	100.0000 % (> 99.8644 %)	100.0000 % (> 98.1818 %)
Type C	100.0000 % (> 98.8270 %)	93.4426 % (> 88.5246 %)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80336	80336	0.00	36.07
80551	80551	0.00	40.20
80552	80552	0.00	38.37
80802	80802	0.00	44.61
81263	81263	0.00	45.88
81264	81264	0.00	43.76
81410	81410	0.00	44.87

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Glycine (H1021)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80168-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Glycine (H1021)

Special notes

When selecting the *Glycine (H1021)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Glycine (H1021)	11	7	11

Second-stage model

For differentiation of the substance/substance group *Glycine (H1021)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Glycine (H1021)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Lysine (L-) (H1047)	51.41	–

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Glycine (H1021)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Glycine (H1021)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Glycine (H1021)	061801	80348	40	from supplier
Hepart	Glycine (H1021)	075501	80436	40	from supplier
Hepart	Glycine (H1021)	14001730	80494	60	from supplier
Hepart	Glycine (H1021)	16000239	80764	60	from supplier
Hepart	Glycine (H1021)	16000238	80765	60	from supplier
Hepart	Glycine (H1021)	16000933	80805	40	from supplier
Hepart	Glycine (H1021)	18000449	81027	40	from supplier
Hepart	Glycine (H1021)	20002705	81319	40	from supplier
Hepart	Glycine (H1021)	22000003	81411	40	from supplier
Hepart	Glycine (H1021)	22001472/1	81478	40	from supplier
Hepart	Glycine (H1021)	23001649	81497	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 500 spectra of 11 reference samples from the substance/substance group *Glycine (H1021)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 11 different batches.
- 27 976 spectra from a total of 567 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a †. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 300 spectra of 7 reference samples from the substance/substance group *Glycine (H1021)*.
- Among them are spectra of independent samples from 7 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Glycine (H1021)	14001731	80495	60
Hepart	Glycine (H1021)	16000934	80806	40
Hepart	Glycine (H1021)	17001658	80981	40
Hepart	Glycine (H1021)	17001660	80982	40
Hepart	Glycine (H1021)	18000451/0	81028	40
Hepart	Glycine (H1021)	19001877	81216	40
Hepart	Glycine (H1021)	19001237	81217	40

- 22 699 spectra from a total of 497 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 23 spectra from 12 *Apo-Ident* customers from 14 batches from the substance/substance group *Glycine (H1021)*.
- Among them are spectra of independent samples from 10 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
Euro OTC	Glycine (H1021)	16000239/0	1
HCK	Glycine (H1021)		1

continued on the next page

continued from previous page

Supplier	Substance	Batch	Spectra
Hepart AG, CH-8280 K...	Glycine (H1021)	28101	1
Hepart AG	Glycine (H1021)	14001730/2	1
Hepart AG	Glycine (H1021)	16000239/0	1
Hepart AG	Glycine (H1021)	17001660/1	2
Hepart AG	Glycine (H1021)	18000449/0	1
Hepart AG	Glycine (H1021)	1803028101	1
Hepart AG	Glycine (H1021)	28101	3
Hepart AG	Glycine (H1021)	75501	1
Hepart	Glycine (H1021)	16000934	1
Hepart	Glycine (H1021)	17001660/0	1
Hepart	Glycine (H1021)	19001237	1
Hepart	Glycine (H1021)	20002705	1
Unisan/Hepart AG	Glycine (H1021)	28101	1
Unisan	Glycine (H1021)	14001730	1
Unisan	Glycine (H1021)	16000933	2
Unisan	Glycine (H1021)	28101	2

- 2947 spectra from 26 *Apo-Ident* customers from a total of 1446 batches from a further 62 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Glycine (H1021)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Glycine (H1021)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	500	0	27 976
Type B	0	300	0	22 699
Type C	0	23	0	2947

The substance/substance group *Glycine (H1021)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9274 %)	100.0000 % (> 98.8000 %)
Type B	100.0000 % (> 99.8644 %)	100.0000 % (> 98.0000 %)
Type C	100.0000 % (> 98.8371 %)	100.0000 % (> 73.9130 %)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra ([Rule of Three](#) [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80348	80348	0.00	91.64
80436	80436	0.00	95.05
80494	80494	0.00	82.22
80764	80764	0.00	95.19
80765	80765	0.00	88.23
80805	80805	0.00	87.77
81027	81027	0.00	90.03
81319	81319	0.00	84.72
81411	81411	0.00	85.25
81478	81478	0.00	86.42
81497	81497	0.00	82.13

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Green coffee extract (H1433)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 81037-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Green coffee extract (H1433)

Special notes

When selecting the *Green coffee extract (H1433)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Green coffee extract (H1433)	4	0	0

Second-stage model

For differentiation of the substance/substance group *Green coffee extract (H1433)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Green coffee extract (H1433)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Detox complex (H1111)	14.64	—
Rhodiola (H1064)	17.26	—
Baobab (H1410)	17.56	—
Artichoke extract (H1440)	18.89	—
Calcium L-(+)-lactate complex (H1008)	19.02	—
Silicium (H1070)	19.68	—
ginkgo extract (H1024)	19.81	—
Juniper (H1112)	19.96	—
Garcinia cambogia (H1017)	21.32	—
Leaky gut complex (H1802)	24.02	—
Marshmallow extract (H1439)	24.24	—
Antioxidants NAT complex (H1004)	24.94	—
Carnitine (L-) (H1038)	25.33	—
Flavour orange (H1405)	27.64	—
Glutathione (H1020)	28.22	—
Ginseng (H1018)	28.85	—
PET basis (H1503)	29.21	—
Orthocolon complex (H1800)	30.59	—
Saffron style (H1434)	30.66	—
Boron (H1005)	31.90	—
Coenzyme Q10 (H1013)	32.12	—
Catechin extract (H1010)	32.91	—
PET immune system (H1502)	33.55	—
Betaine hydrochloride (H1119)	35.28	—
Vitamin C (H1104)	35.49	—
Ashwagandha (H1132)	36.33	—
Vitamin B1 (H1101)	37.27	—
Vitamin B6 (Pyridoxal 5'-phosphate)...	37.54	—
Antibiosis forte complex (H1115)	38.11	—
PET well-aging (H1500)	39.84	—
Lycopene (H1058)	40.09	—
Magnesium (H1060)	40.19	—
Bioflavonoid complex (H1006)	41.75	—
Aminomix NAC (H1002)	41.77	—
Silymarin (H1071)	42.86	—
Oat bran beta-glucan (H1529)	44.43	—
Arginine (L-) (H1036)	44.73	—
Vitamin E NAT (H1107)	44.90	—

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Substanz	Distance in main model	Distance in second-stage model
PET joints (H1501)	45.91	—
Seabuckthorn (H1523)	48.19	—
Isoflavone (H1025)	49.82	—
Vitamins BAG complex (H1091)	49.89	—
Artemisia annua extract (H1118)	49.95	—
Zinc (H1110)	49.96	—
Gentian extract (H1438)	50.72	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Green coffee extract (H1433)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Green coffee extract (H1433)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Green coffee extract (H1433)	18000368	81037	40	from supplier
Hepart	Green coffee extract (H1433)	20002440	81323	40	from supplier
Hepart	Green coffee extract (H1433)	21000805	81331	40	from supplier
Hepart	Green coffee extract (H1433)	23002216	81519	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 160 spectra of 4 reference samples from the substance/substance group *Green coffee extract (H1433)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 4 different batches.
- 28 316 spectra from a total of 574 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 0 spectra of 0 reference samples from the substance/substance group *Green coffee extract (H1433)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.
- 22 999 spectra from a total of 504 batches from further 78 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *Green coffee extract (H1433)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Green coffee extract (H1433)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Green coffee extract (H1433)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	160	0	28 316
Type B	0	0	0	22 999
Type C	0	0	0	2970

The substance/substance group *Green coffee extract (H1433)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9278 %)	100.0000 % (> 96.2500 %)
Type B	100.0000 % (> 99.8687 %)	n/a (n/a)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra ([Rule of Three](#) [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
81037	81037	0.00	25.13
81323	81323	0.00	32.23
81331	81331	0.00	14.64
81519	81519	0.00	21.47

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Griffonia (H1035)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 10005948-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Griffonia (H1035)

Special notes

When selecting the *Griffonia (H1035)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Griffonia (H1035)	3	1	13

Second-stage model

For differentiation of the substance/substance group *Griffonia (H1035)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Griffonia (H1035)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Calcium L-(+)-lactate complex (H1008)	12.78	—
Vitamin complex (H1100)	20.70	—
OPC Proanthocyanidins (Pine Bark) (...)	27.87	—
Carnitine (L-) (H1038)	28.87	—
Creatine (H1031)	30.59	—
Silymarin (H1071)	36.04	—
Coenzyme Q10 (H1013)	41.97	—
Arginine (L-) (H1036)	44.48	—
Bioflavonoid complex (H1006)	45.23	—
Rhodiola (H1064)	46.82	—
Antibiosis forte complex (H1115)	48.80	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Griffonia (H1035)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Griffonia (H1035)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Griffonia (H1035)	16000441	80797	40	from supplier
Hepart	Griffonia (H1035)	21002732	81403	40	from supplier
Hepart	Griffonia (H1035)	23002380	81520	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 120 spectra of 3 reference samples from the substance/substance group *Griffonia (H1035)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 3 different batches.
- 28 356 spectra from a total of 575 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a †. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 40 spectra of 1 reference samples from the substance/substance group *Griffonia (H1035)*.
- Among them are spectra of independent samples from 1 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Griffonia (H1035)	16000441/0	80851	40

- 22 959 spectra from a total of 503 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 19 spectra from 7 *Apo-Ident* customers from 14 batches from the substance/substance group *Griffonia (H1035)*.
- Among them are spectra of independent samples from 13 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
HCK	Griffonia (H1035)	15001503/0	1
HCK	Griffonia (H1035)	15001503-5	1
HCK	Griffonia (H1035)	16000441	1
Hepart AG	Griffonia (H1035)	15001503	1
Hepart AG	Griffonia (H1035)	15001503/2	3
Hepart AG	Griffonia (H1035)	16000441/0	1
Hepart AG	Griffonia (H1035)	1837999801	1
Hepart	Griffonia (H1035)	16000441/2	1

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Supplier	Substance	Batch	Spectra
Hepart	Griffonia (H1035)	16000441-3	1
Hepart	Griffonia (H1035)	18000913	1
Unisan	Griffonia (H1035)	15001503/5	2
Unisan	Griffonia (H1035)	25006	3
Unisan	Griffonia (H1035)	25006/12	1
Unisan	Griffonia (H1035)	26102	1

- 2951 spectra from 26 *Apo-Ident* customers from a total of 1446 batches from a further 62 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Griffonia (H1035)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Griffonia (H1035)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	120	0	28 356
Type B	0	40	0	22 959
Type C	0	5	14	2951

The substance/substance group *Griffonia (H1035)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9280 %)	100.0000 % (> 95.0000 %)
Type B	100.0000 % (> 99.8691 %)	100.0000 % (> 85.0000 %)
Type C	100.0000 % (> 98.8405 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra ([Rule of Three](#) [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the [Mahalanobis distance](#) to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80797	80797	0.00	29.68
81403	81403	0.00	32.97
81520	81520	0.00	36.88

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group	HCK classification I
Substance class	HCK - nutritional supplements (Hepart)
Report date	07/03/2025
Report number	80331-2025-03-07
Executing company	HiperScan GmbH Weißeritzstraße 3 01067 Dresden Germany

Relevant substance names

HCK classification I; Acacia gum (H1526); Baobab (H1410); Biotin (H1007); Boron (H1005); Chromium (H1012); Detox complex (H1111); Gentian extract (H1438); Ginger extract (H1437); Ginseng (H1018); Guar (H1023); Iodine (H1044); Juniper (H1112); Levomefolic acid (L-5-MTHF) (H1128); Lycopene (H1058); Marshmallow extract (H1439); Saffron flowers (H1435); Saffron style (H1434); Selenium (H1067); Selenium yeast (H1068); Silicium (H1070); Vitamin B12 (H1102); Vitamin D3 (H1105); Vitamin K2 (75µg Mono) (H1108)

Special notes

When selecting the *HCK classification I* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
HCK classification I	74	35	170

Second-stage model

For differentiation of the substance/substance group *HCK classification I* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *HCK classification I* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
PET coenzyme Q10 (H1505)	11.90	—
Artichoke extract (H1440)	13.23	—
Leaky gut complex (H1802)	13.63	—
Artemisia annua extract (H1118)	14.53	—
Flavour orange (H1405)	14.73	—
Psyllium husks (H1527)	17.27	—
Vitamin E NAT (H1107)	17.47	—
Garcinia cambogia (H1017)	17.56	—
Green coffee extract (H1433)	18.74	—
Zinc (H1110)	19.85	—
Glutathione (H1020)	20.73	—
Vitamin B1 (H1101)	21.75	—
Coenzyme Q10 (H1013)	21.90	—
Ashwagandha (H1132)	22.54	—
Chondroitin sulfate (H1065)	25.01	—
Konjak Glucomannan (H1530)	28.49	—
Oat bran beta-glucan (H1529)	29.67	—
Vitamins BAG complex (H1091)	30.29	—
Rhodiola (H1064)	30.74	—
Orthocolon complex (H1800)	32.22	—
Trace elements BAG (H1078)	32.51	—
Isoflavone (H1025)	33.66	—
Magnesium (H1060)	34.57	—
Aminomix NAC (H1002)	34.76	—
Arginine (L-) (H1036)	34.76	—
Copper (H1032)	35.15	—
Calcium L-(+)-lactate complex (H1008)	36.83	—
Iron (H1015)	37.31	—
Lutein-Zeaxanthin-Astaxanthin (H1129)	38.97	—
Antioxidants NAT complex (H1004)	39.09	—
ginkgo extract (H1024)	43.33	—
Orthovimin Neutral Complex (H1404)	43.71	—
Betaine hydrochloride (H1119)	46.90	—

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Substanz	Distance in main model	Distance in second-stage model
Trace elements JK (H1080)	47.93	—
Carnitine (L-) (H1038)	49.57	—
Silymarin (H1071)	50.30	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *HCK classification I* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *HCK classification I*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Acacia gum (H1526)	23000659	81493	40	from supplier
Hepart	Baobab (H1410)	16001158	80921	40	from supplier
Hepart	Baobab (H1410)	18000501/0	81158	40	from supplier
Hepart	Biotin (H1007)	029601	80365	40	from supplier
Hepart	Biotin (H1007)	029601	80385	40	from supplier
Hepart	Biotin (H1007)	15000735	80586	60	from supplier
Hepart	Biotin (H1007)	16001396	80855	40	from supplier
Hepart	Boron (H1005)	17000827/1	81119	40	from supplier
Hepart	Boron (H1005)	23002123	81515	40	from supplier
Hepart	Chromium (H1012)	16000520/0	80791	40	from supplier
Hepart	Chromium (H1012)	16000520/4	80792	40	from supplier
Hepart	Chromium (H1012)	23000555	81470	40	from supplier
Hepart	Detox complex (H1111)	16001075(MM)	80894	40	from supplier
Hepart	Detox complex (H1111)	16001076	80895	40	from supplier
Hepart	Gentian extract (H1438)	18001096	81092	40	from supplier
Hepart	Gentian extract (H1438)	21001723	81368	50	from supplier
Hepart	Ginger extract (H1437)	18001115	81089	40	from supplier
Hepart	Ginger extract (H1437)	21001131	81377	50	from supplier
Hepart	Ginseng (H1018)	018502	80455	40	from supplier
Hepart	Ginseng (H1018)	067801	80456	40	from supplier
Hepart	Ginseng (H1018)	038802	80478	40	from supplier
Hepart	Ginseng (H1018)	14002047	80534	60	from supplier
Hepart	Ginseng (H1018)	15001047	80663	60	from supplier
Hepart	Ginseng (H1018)	15001047	80780	60	from supplier
Hepart	Ginseng (H1018)	22002234/0	81480	40	from supplier
Hepart	Ginseng (H1018)	23001439	81500	40	from supplier
Hepart	Guar (H1023)	20002454	81310	40	from supplier
Hepart	Guar (H1023)	24000935	81547	30	from supplier
Hepart	Iodine (H1044)	22002410	81509	40	from supplier
Hepart	Juniper (H1112)	15001004	80702	60	from supplier
Hepart	Juniper (H1112)	16000683	80891	40	from supplier
Hepart	Levomefolic acid (L-5-MTH...	22000772	81447	40	from supplier
Hepart	Lycopene (H1058)	053501	80335	40	from supplier
Hepart	Lycopene (H1058)	17000619	80913	40	from supplier
Hepart	Lycopene (H1058)	17000619/0	81024	40	from supplier
Hepart	Marshmallow extract (H1439)	18001095	81091	40	from supplier
Hepart	Marshmallow extract (H1439)	21003061/0	81422	40	from supplier
Hepart	Saffron flowers (H1435)	18000806	81056	40	from supplier
Hepart	Saffron flowers (H1435)	19000801	81204	40	from supplier
Hepart	Saffron style (H1434)	18001093	81090	40	from supplier
Hepart	Saffron style (H1434)	21001804	81370	50	from supplier

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Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Saffron style (H1434)	23001375/3	81546	30	from supplier
Hepart	Selenium (H1067)	065601	80361	40	from supplier
Hepart	Selenium (H1067)	065501	80364	40	from supplier
Hepart	Selenium (H1067)	065701	80366	40	from supplier
Hepart	Selenium (H1067)	15000157	80530	60	from supplier
Hepart	Selenium (H1067)	15000158	80531	60	from supplier
Hepart	Selenium (H1067)	15000159	80535	60	from supplier
Hepart	Selenium (H1067)	065501	80706	60	from supplier
Hepart	Selenium (H1067)	16001349	80822	40	from supplier
Hepart	Selenium (H1067)	18000578	81025	40	from supplier
Hepart	Selenium yeast (H1068)	16001450/1	81014	40	from supplier
Hepart	Silicium (H1070)	17000817	80914	40	from supplier
Hepart	Silicium (H1070)	18000448	81022	30	from supplier
Hepart	Silicium (H1070)	18001681	81127	40	from supplier
Hepart	Silicium (H1070)	19001317	81205	40	from supplier
Hepart	Silicium (H1070)	20002801	81306	40	from supplier
Hepart	Silicium (H1070)	210021-29-30	81400	50	from supplier
Hepart	Silicium (H1070)	23000181	81471	40	from supplier
Hepart	Silicium (H1070)	23000336	81473	40	from supplier
Hepart	Silicium (H1070)	23000337/1	81507	40	from supplier
Hepart	Silicium (H1070)	24002157	81560	40	from supplier
Hepart	Vitamin B12 (H1102)	025017	80353	40	from supplier
Hepart	Vitamin B12 (H1102)	15000993	80603	60	from supplier
Hepart	Vitamin B12 (H1102)	15000993(B1)	80604	60	from supplier
Hepart	Vitamin B12 (H1102)	17000277	80910	40	from supplier
Hepart	Vitamin B12 (H1102)	19001114	81201	40	from supplier
Hepart	Vitamin B12 (H1102)	23000507	81489	40	from supplier
Hepart	Vitamin D3 (H1105)	15000490	80580	60	from supplier
Hepart	Vitamin D3 (H1105)	16000952	80816	40	from supplier
Hepart	Vitamin D3 (H1105)	16001212	80863	40	from supplier
Hepart	Vitamin D3 (H1105)	18001951	81130	40	from supplier
Hepart	Vitamin D3 (H1105)	19001097	81206	40	from supplier
Hepart	Vitamin K2 (75µg Mono) (H1108)	16001559	80874	40	from supplier
Hepart	Vitamin K2 (75µg Mono) (H1108)	18001656	81126	60	from supplier
Hepart	Vitamin K2 (75µg Mono) (H1108)	20000422	81282	40	from supplier
Hepart	Vitamin K2 (75µg Mono) (H1108)	21000562	81328	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 3350 spectra of 77 reference samples from the substance/substance group *HCK classification I*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 74 different batches.
- 25 126 spectra from a total of 505 batches from further 108 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 1530 spectra of 38 reference samples from the substance/substance group *HCK classification I*.
- Among them are spectra of independent samples from 35 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Baobab (H1410)	17001785/0	81003	40
Hepart	Baobab (H1410)	20001258	81280	40
Hepart	Baobab (H1410)	21002191	81402	50
Hepart	Biotin (H1007)	20002313	81324	40
Hepart	Biotin (H1007)	21000967	81385	50
Hepart	Biotin (H1007)	22001540	81437	40
Hepart	Chromium (H1012)	977201	80033	15
Hepart	Chromium (H1012)	16000520/2	80793	40
Hepart	Chromium (H1012)	18002076	81148	40
Hepart	Detox complex (H1111)	16001075(Nr. 5-7)	80892	40
Hepart	Detox complex (H1111)	16001075(Nr. 1-4)	80893	40
Hepart	Ginseng (H1018)	17000285	80873	40
Hepart	Selenium (H1067)	16001350	80823	40
Hepart	Selenium (H1067)	16001351	80824	40
Hepart	Selenium (H1067)	18000422	81026	40
Hepart	Selenium (H1067)	18001021	81078	40
Hepart	Selenium (H1067)	18001022	81079	40
Hepart	Selenium (H1067)	21001836	81365	50
Hepart	Selenium (H1067)	21001761	81383	50
Hepart	Selenium (H1067)	22000058	81409	40
Hepart	Selenium (H1067)	23000482	81479	40
Hepart	Silicium (H1070)	17000326	80906	40
Hepart	Silicium (H1070)	19000534	81184	40
Hepart	Silicium (H1070)	20001082	81265	40
Hepart	Vitamin B12 (H1102)	15000993(F2)	80605	60
Hepart	Vitamin B12 (H1102)	17000276	80911	40
Hepart	Vitamin B12 (H1102)	21000708	81335	40
Hepart	Vitamin D3 (H1105)	17000874	80959	40
Hepart	Vitamin D3 (H1105)	19001583	81224	40
Hepart	Vitamin D3 (H1105)	20000338	81266	40
Hepart	Vitamin D3 (H1105)	20001988	81311	40
Hepart	Vitamin D3 (H1105)	20001952	81312	40
Hepart	Vitamin D3 (H1105)	21000024	81349	40
Hepart	Vitamin D3 (H1105)	210012-40-41	81389	45
Hepart	Vitamin D3 (H1105)	23001560	81503	40
Hepart	Ginseng (H1018)	067801	80403	40
Hepart	Ginseng (H1018)	17000285	81103	40
Hepart	Silicium (H1070)	18000448	81022 [†]	10

- 21 469 spectra from a total of 467 batches from further 69 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B*

section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 513 spectra from 22 *Apo-Ident* customers from 221 batches from the substance/substance group *HCK classification I*.
- Among them are spectra of independent samples from 198 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
Bombastus	Selenium (H1067)	1144010201	1
Euro OTC	Ginseng (H1018)	15001047/0	1
Fagron	Vitamin D3 (H1105)	63701	1
Falcento	Chromium (H1012)	16000520	4
Flaigg Ag CH-4147 Ae...	Vitamin K2 (75µg Mono) (H1108)	18001656/5	1
HCK	Vitamin B12 (H1102)	1000993-0	1
HCK	Chromium (H1012)	14000429	1
HCK	Chromium (H1012)	14000429/7	1
HCK	Ginseng (H1018)	14002047	1
HCK	Selenium (H1067)	15000157/1	1
HCK	Selenium (H1067)	15000157-1	1
HCK	Selenium (H1067)	15000157-2	1
HCK	Selenium (H1067)	15000158-0	1
HCK	Vitamin D3 (H1105)	15000490/1	1
HCK	Vitamin D3 (H1105)	15000490-4	1
HCK	Vitamin D3 (H1105)	15000490-5	1
HCK	Biotin (H1007)	15000735/2	2
HCK	Biotin (H1007)	15000735-2	1
HCK	Biotin (H1007)	15000735-5	3
HCK	Vitamin B12 (H1102)	15000993	1
HCK	Vitamin B12 (H1102)	15000993/0	1
HCK	Chromium (H1012)	16000520-0	2
HCK	Lycopene (H1058)	17000619	1
HCK	Lycopene (H1058)	17000619/0	1
HCK	Lycopene (H1058)	53501-8	2
HCK	Selenium (H1067)	65501/2	1
HCK	Selenium yeast (H1068)	71901	1
HCK	Vitamin B12 (H1102)	75301/4	1
HCK	Vitamin D3 (H1105)	8101	1
Hedinger	Selenium (H1067)	10201	9
Hepart AG, CH-8280 K...	Selenium (H1067)	10201	1
Hepart AG, CH-8280 K...	Vitamin B12 (H1102)	1064026401	1
Hepart AG, CH-8280 K...	Selenium (H1067)	1144010201	1
Hepart AG, CH-8280 K...	Vitamin D3 (H1105)	1336008101	2
Hepart AG, CH-8280 K...	Biotin (H1007)	1592029603	1
Hepart AG, CH-8280 K...	Vitamin D3 (H1105)	64801	1
Hepart AG, CH-8280 K...	Chromium (H1012)	977201	2
Hepart ag/ Unisan	Vitamin D3 (H1105)	20001952/0	1
Hepart AG/Unisan	Vitamin B12 (H1102)	17000276/2	1
Hepart ag/Unisan	Vitamin B12 (H1102)	17000277	1
Hepart AG/Unisan	Vitamin B12 (H1102)	17000277/0	1
Hepart AG/Unisan	Vitamin B12 (H1102)	17000277/2	2
Hepart ag/Unisan	Selenium (H1067)	18000578/1	1

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[†]These spectra were recorded from material of the same package as the corresponding calibration spectra (*Type A*). Hence, these spectra are not independent and are not of *Type B*.

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Supplier	Substance	Batch	Spectra
Hepart ag/Unisan	Selenium (H1067)	18001021	1
Hepart AG/Unisan	Vitamin D3 (H1105)	19001097	1
Hepart AG/Unisan	Vitamin D3 (H1105)	20000338/2	1
Hepart AG	Vitamin B12 (H1102)	1064025017	1
Hepart AG	Vitamin B12 (H1102)	1064026401	1
Hepart AG	Selenium (H1067)	1144010201	3
Hepart AG	Vitamin D3 (H1105)	1335008101	1
Hepart AG	Chromium (H1012)	14000429/4	1
Hepart AG	Selenium (H1067)	15000157/1	1
Hepart AG	Selenium (H1067)	15000158/0	1
Hepart AG	Vitamin D3 (H1105)	15000490/2	1
Hepart AG	Vitamin B12 (H1102)	15000993/0	1
Hepart AG	Ginseng (H1018)	15001047	1
Hepart AG	Chromium (H1012)	1582977201	3
Hepart AG	Biotin (H1007)	1592029603	3
Hepart AG	Chromium (H1012)	16000520/7	5
Hepart AG	Vitamin D3 (H1105)	16000952/1	1
Hepart AG	Selenium (H1067)	16001349/0	2
Hepart AG	Selenium (H1067)	16001350/0	16
Hepart AG	Biotin (H1007)	16001396/5	1
Hepart AG	Vitamin B12 (H1102)	17000276/0	1
Hepart AG	Vitamin B12 (H1102)	170002796/0	1
Hepart AG	Ginseng (H1018)	17000285/0	1
Hepart AG	Lycopene (H1058)	17000619/1	1
Hepart AG	Boron (H1005)	17000827/3	1
Hepart AG	Selenium (H1067)	18000422/2	1
Hepart AG	Vitamin B12 (H1102)	25017	4
Hepart AG	Biotin (H1007)	29601	2
Hepart AG	Biotin (H1007)	29603	3
Hepart AG	Ginseng (H1018)	38802	1
Hepart AG	Lycopene (H1058)	47301	1
Hepart AG	Lycopene (H1058)	53501	1
Hepart AG	Vitamin D3 (H1105)	63701	3
Hepart AG	Vitamin D3 (H1105)	64801	4
Hepart AG	Selenium (H1067)	65701	1
Hepart AG	Vitamin D3 (H1105)	8101	1
Hepart AG	Selenium (H1067)	933301	1
Hepart AG	Chromium (H1012)	977201	5
Hepart AG	Chromium (H1012)	H101221	1
Hepart/Unisan	Selenium (H1067)	18001021/0	1
Hepart	Biotin (H1007)	14000862/4	2
Hepart	Selenium (H1067)	15000157	1
Hepart	Selenium (H1067)	15000158	1
Hepart	Selenium (H1067)	15000158/1	1
Hepart	Selenium (H1067)	15000158-1	2
Hepart	Selenium (H1067)	15000159-0	1
Hepart	Selenium (H1067)	15000159-1	2
Hepart	Vitamin B12 (H1102)	15000993/2	1
Hepart	Vitamin B12 (H1102)	15000993-1	1
Hepart	Chromium (H1012)	16000520	1
Hepart	Chromium (H1012)	16000520/3	4
Hepart	Chromium (H1012)	16000520/4	1
Hepart	Chromium (H1012)	16000520/8	5
Hepart	Chromium (H1012)	16000520-1	3
Hepart	Chromium (H1012)	16000520-2	2
Hepart	Chromium (H1012)	160005203	1
Hepart	Vitamin D3 (H1105)	16000952	3
Hepart	Vitamin D3 (H1105)	16000952-0	1
Hepart	Vitamin D3 (H1105)	16000952-1	2
Hepart	Vitamin D3 (H1105)	16001212/0	1

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Supplier	Substance	Batch	Spectra
Hepart	Vitamin D3 (H1105)	16001212-0	1
Hepart	Vitamin D3 (H1105)	16001212-1	2
Hepart	Selenium (H1067)	16001349/0	2
Hepart	Selenium (H1067)	16001349-0	1
Hepart	Selenium (H1067)	160013497/0	1
Hepart	Selenium (H1067)	16001350	1
Hepart	Selenium (H1067)	16001350/0	3
Hepart	Selenium (H1067)	16001351/0	2
Hepart	Biotin (H1007)	16001396/0	1
Hepart	Biotin (H1007)	16001396/1	1
Hepart	Biotin (H1007)	16001396/4	2
Hepart	Biotin (H1007)	16001396-1	1
Hepart	Biotin (H1007)	16001396-2	2
Hepart	Vitamin B12 (H1102)	17000276	1
Hepart	Vitamin B12 (H1102)	17000276/0	1
Hepart	Vitamin B12 (H1102)	17000276/1	1
Hepart	Vitamin B12 (H1102)	17000276/2	1
Hepart	Vitamin B12 (H1102)	17000276-0	1
Hepart	Vitamin B12 (H1102)	17000277/0	4
Hepart	Vitamin B12 (H1102)	17000277/1	1
Hepart	Ginseng (H1018)	17000285	1
Hepart	Lycopene (H1058)	17000619	1
Hepart	Boron (H1005)	17000827/4	1
Hepart	Vitamin D3 (H1105)	17000874	2
Hepart	Vitamin D3 (H1105)	17000874/1	6
Hepart	Vitamin D3 (H1105)	17000874-0	4
Hepart	Silicium (H1070)	1700817/1	1
Hepart	Selenium (H1067)	18000422/0	1
Hepart	Selenium (H1067)	18000422/1	4
Hepart	Selenium (H1067)	18000422/2	2
Hepart	Selenium (H1067)	18000578	2
Hepart	Selenium (H1067)	18000578/0	2
Hepart	Selenium (H1067)	18000578/1	4
Hepart	Ginseng (H1018)	18000794/0	1
Hepart	Selenium (H1067)	18001021/0	4
Hepart	Selenium (H1067)	18001021/1	1
Hepart	Selenium (H1067)	18001022/0	4
Hepart	Selenium (H1067)	18001022/1	3
Hepart	Selenium (H1067)	18001022/2	1
Hepart	Vitamin K2 (75µg Mono) (H1108)	18001656	1
Hepart	Vitamin K2 (75µg Mono) (H1108)	18001656/13	1
Hepart	Vitamin K2 (75µg Mono) (H1108)	18001656/17	1
Hepart	Vitamin K2 (75µg Mono) (H1108)	18001656/171	1
Hepart	Vitamin K2 (75µg Mono) (H1108)	18001656/5	1
Hepart	Vitamin K2 (75µg Mono) (H1108)	18001656/7	1
Hepart	Vitamin D3 (H1105)	18001771/0	3
Hepart	Vitamin D3 (H1105)	18001951/0	3
Hepart	Vitamin D3 (H1105)	18001951/1	2
Hepart	Vitamin D3 (H1105)	18001951/2	2
Hepart	Vitamin D3 (H1105)	18001951/4	1
Hepart	Chromium (H1012)	18002076	1
Hepart	Chromium (H1012)	18002076/0	1
Hepart	Chromium (H1012)	18002076/1	1
Hepart	Chromium (H1012)	18002076/2	1
Hepart	Chromium (H1012)	18002076/6	1
Hepart	Chromium (H1012)	18002076/7	4
Hepart	Biotin (H1007)	19000754/0	1
Hepart	Biotin (H1007)	19000754/1	2
Hepart	Ginseng (H1018)	19000824/0	1
Hepart	Ginseng (H1018)	19000824/1	2

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Supplier	Substance	Batch	Spectra
Hepart	Ginseng (H1018)	19000824/2	1
Hepart	Ginseng (H1018)	19000824/5	1
Hepart	Vitamin D3 (H1105)	19001097/0	2
Hepart	Silicium (H1070)	19001317/0	2
Hepart	Vitamin D3 (H1105)	19001583/0	2
Hepart	Biotin (H1007)	20000178	1
Hepart	Biotin (H1007)	20000178/0	3
Hepart	Vitamin D3 (H1105)	20000338/0	1
Hepart	Vitamin D3 (H1105)	20000338/1	1
Hepart	Vitamin K2 (75µg Mono) (H1108)	20000422	1
Hepart	Vitamin K2 (75µg Mono) (H1108)	20000422/0	1
Hepart	Vitamin K2 (75µg Mono) (H1108)	20000422/1	1
Hepart	Vitamin K2 (75µg Mono) (H1108)	20000422/2	3
Hepart	Lycopene (H1058)	20001766/0	1
Hepart	Vitamin D3 (H1105)	20001952/0	4
Hepart	Vitamin D3 (H1105)	20001988/0	1
Hepart	Biotin (H1007)	20002313	1
Hepart	Biotin (H1007)	20002313/1	2
Hepart	Biotin (H1007)	20002313/2	1
Hepart	Vitamin D3 (H1105)	21000024	1
Hepart	Vitamin D3 (H1105)	21000024/0	4
Hepart	Vitamin K2 (75µg Mono) (H1108)	21000562	1
Hepart	Vitamin K2 (75µg Mono) (H1108)	210005627/3	1
Hepart	Boron (H1005)	21000564/1	1
Hepart	Boron (H1005)	21000564/2	2
Hepart	Boron (H1005)	21000564/3	1
Hepart	Vitamin D3 (H1105)	21001240/0	1
Hepart	Vitamin B12 (H1102)	21001674	1
Hepart	Selenium (H1067)	21001761/0	1
Hepart	Selenium (H1067)	21001836/0	2
Hepart	Vitamin B12 (H1102)	21002290/0	2
Hepart	Vitamin K2 (75µg Mono) (H1108)	21002794	1
Hepart	Chromium (H1012)	21003059/0	1
Hepart	Silicium (H1070)	2101442/0	1
Hepart	Selenium (H1067)	22000057/0	1
Hepart	Vitamin D3 (H1105)	22000391	1
Hepart	Vitamin D3 (H1105)	22000391/0	3
Hepart	Selenium yeast (H1068)	71901	2
Hepart	Vitamin B12 (H1102)	75301	1
Ichthyol Gesellschaft...	Biotin (H1007)	1591983601	1
Unisan GmbH, 78465 K...	Vitamin D3 (H1105)	63701	1
Unisan/Hepart AG	Ginseng (H1018)	38802	1
Unisan/Hepart AG	Lycopene (H1058)	47301	1
Unisan/Hepart	Vitamin D3 (H1105)	15000490/5	1
unisan	Chromium (H1012)		2
Unisan	Selenium (H1067)	10201	10
Unisan	Vitamin B12 (H1102)	1061025017	1
Unisan	Vitamin B12 (H1102)	1064025017	3
Unisan	Selenium (H1067)	1144010201	1
Unisan	Selenium (H1067)	1144933301	1
Unisan	Vitamin D3 (H1105)	1335008101	2
Unisan	Vitamin D3 (H1105)	1335008108	1
Unisan	Vitamin D3 (H1105)	1335959601	1
Unisan	Chromium (H1012)	14000429	2
UNISAN	Chromium (H1012)	14000429	4
Unisan	Vitamin D3 (H1105)	14000481	1
UNISAN	Vitamin D3 (H1105)	14000481	3
Unisan	Vitamin D3 (H1105)	14000481/2	3
Unisan	Lycopene (H1058)	14000803	1
Unisan	Biotin (H1007)	14000862	2

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Supplier	Substance	Batch	Spectra
Unisan	Biotin (H1007)	14000862/2	2
Unisan	Ginseng (H1018)	14002047/1	1
Unisan	Ginseng (H1018)	14002047/2	1
Unisan	Selenium (H1067)	15000157	3
Unisan	Selenium (H1067)	15000158	1
Unisan	Selenium (H1067)	15000158/0	3
Unisan	Selenium (H1067)	15000159	1
Unisan	Vitamin D3 (H1105)	15000490	4
Unisan	Vitamin D3 (H1105)	15000490/0	2
Unisan	Vitamin D3 (H1105)	15000490/5	1
Unisan	Biotin (H1007)	15000735	2
Unisan	Biotin (H1007)	15000735/0	1
Unisan	Biotin (H1007)	15000735/5	1
Unisan	Vitamin B12 (H1102)	15000993	4
Unisan	Vitamin B12 (H1102)	15000993/3	1
Unisan	Chromium (H1012)	1581977201	1
Unisan	Chromium (H1012)	1582977201	1
Unisan	Biotin (H1007)	1591983601	1
Unisan	Chromium (H1012)	16000520/0	1
Unisan	Vitamin D3 (H1105)	16000952	2
Unisan	Vitamin D3 (H1105)	16001212	3
Unisan	Vitamin D3 (H1105)	16001212/1	1
Unisan	Selenium (H1067)	16001349	1
Unisan	Biotin (H1007)	16001396	3
Unisan	Biotin (H1007)	16001396/0	1
Unisan	Selenium yeast (H1068)	16001450/0	1
Unisan	Vitamin B12 (H1102)	17000276	2
Unisan	Ginseng (H1018)	17000285	2
Unisan	Lycopene (H1058)	17000619/0	1
Unisan	Vitamin B12 (H1102)	25017	5
Unisan	Selenium yeast (H1068)	25709	1
Unisan	Vitamin B12 (H1102)	26401	1
Unisan	Biotin (H1007)	29601	2
Unisan	Biotin (H1007)	29603	3
Unisan	Vitamin B12 (H1102)	3441377	1
Unisan	Ginseng (H1018)	38802	2
Unisan	Lycopene (H1058)	4501	4
Unisan	Lycopene (H1058)	47301	2
Unisan	Lycopene (H1058)	53501	7
Unisan	Lycopene (H1058)	53501/7	1
UNISAN	Vitamin D3 (H1105)	63601	1
Unisan	Vitamin D3 (H1105)	63701	4
Unisan	Vitamin D3 (H1105)	64801	5
Unisan	Selenium (H1067)	65501	1
UNISAN	Selenium (H1067)	65501	1
Unisan	Selenium (H1067)	65501/2	1
Unisan	Selenium (H1067)	65601	6
Unisan	Selenium (H1067)	65601/1	1
Unisan	Selenium (H1067)	65601/2	1
Unisan	Selenium (H1067)	65701	4
Unisan	Ginseng (H1018)	67801	2
UNISAN	Ginseng (H1018)	67801	1
Unisan	Vitamin B12 (H1102)	75301	5
Unisan	Vitamin B12 (H1102)	75301/2	1
Unisan	Vitamin D3 (H1105)	8101	7
Unisan	Selenium yeast (H1068)	9001	1
Unisan	Chromium (H1012)	977201	3
Unisan	Biotin (H1007)	983601	1
Unisan	Lycopene (H1058)	H105811	1

- 2457 spectra from 26 *Apo-Ident* customers from a total of 1241 batches from a further 52 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *HCK classification I* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *HCK classification I* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	3350	0	25 126
Type B	0	1490	40	21 463
Type C	0	484	29	2457

The substance/substance group *HCK classification I* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9273 %)	100.0000 % (> 99.8209 %)
Type B	100.0000 % (> 99.8634 %)	97.3856 % (> 97.1895 %)
Type C	100.0000 % (> 98.8215 %)	94.3470 % (> 93.7622 %)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80335	80335	0.00	33.16
80353	80353	0.00	24.65
80361	80361	0.00	44.57
80364	80364	0.00	43.52
80365	80365	0.00	30.64
80366	80366	0.00	44.40
80385	80385	0.00	27.14
80455	80455	0.00	16.84
80456	80456	0.00	20.53
80478	80478	0.00	28.49

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Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80530	80530	0.00	29.76
80531	80531	0.00	30.74
80534	80534	0.00	11.95
80535	80535	0.00	27.02
80580	80580	0.00	35.00
80586	80586	0.00	27.36
80603	80603	0.00	26.05
80604	80604	0.00	25.97
80663	80663	0.00	24.92
80702	80702	0.00	26.94
80706	80706	0.00	35.95
80780	80780	0.00	21.18
80791	80791	0.00	30.72
80792	80792	0.00	33.81
80816	80816	0.00	32.75
80822	80822	0.00	23.44
80855	80855	0.00	27.78
80863	80863	0.00	28.60
80874	80874	0.00	23.30
80891	80891	0.00	26.46
80894	80894	0.00	18.74
80895	80895	0.00	19.48
80910	80910	0.00	25.68
80913	80913	0.00	17.27
80914	80914	0.00	27.03
80921	80921	0.00	24.44
81014	81014	0.00	20.13
81022	81022	0.00	30.52
81024	81024	0.00	21.72
81025	81025	0.00	26.51
81056	81056	0.00	14.53
81089	81089	0.00	25.51
81090	81090	0.00	27.56
81091	81091	0.00	28.93
81092	81092	0.00	23.56
81119	81119	0.00	24.63
81126	81126	0.00	24.66
81127	81127	0.00	27.62
81130	81130	0.00	29.44
81158	81158	0.00	22.13
81201	81201	0.00	30.83
81204	81204	0.00	24.61
81205	81205	0.00	19.61
81206	81206	0.00	29.89
81282	81282	0.00	27.08
81306	81306	0.00	25.27
81310	81310	0.00	40.49
81328	81328	0.00	23.25
81368	81368	0.00	31.91
81370	81370	0.00	29.08
81377	81377	0.00	11.90

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Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
81400	81400	0.00	19.33
81422	81422	0.00	17.44
81447	81447	0.00	30.56
81470	81470	0.00	25.58
81471	81471	0.00	20.53
81473	81473	0.00	20.64
81480	81480	0.00	30.34
81489	81489	0.00	47.30
81493	81493	0.00	36.98
81500	81500	0.00	24.38
81507	81507	0.00	33.46
81509	81509	0.00	40.98
81515	81515	0.00	30.88
81546	81546	0.00	28.33
81547	81547	0.00	30.67
81560	81560	0.00	28.77

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group	HCK classification II
Substance class	HCK - nutritional supplements (Hepart)
Report date	07/03/2025
Report number	80311-2025-03-07
Executing company	HiperScan GmbH Weißeritzstraße 3 01067 Dresden Germany

Relevant substance names

HCK classification II; Antioxidants NAT complex (H1004); Bioflavonoid complex (H1006); Cabbage mix (H1514); Calcium L-(+) -lactate complex (H1008); Camu Camu (H1518); Cranberry (H1519); Flavour orange (H1405); Garcinia cambogia (H1017); ginkgo extract (H1024); Glutathione (H1020); Isoflavone (H1025); Kale (H1126); OPC Proanthocyanidins (Pine Bark) (H1066); Orthocolon complex (H1800); PET basis (H1503); Rhodiola (H1064); Seabuckthorn (H1523); Vitamin B1 (H1101); Vitamin complex (H1100); Wild berry (H1524)

Special notes

When selecting the *HCK classification II* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
HCK classification II	150	169	349

Second-stage model

For differentiation of the substance/substance group *HCK classification II* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *HCK classification II* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Silymarin (H1071)	13.28	—
Griffonia (H1035)	13.46	—
Leaky gut complex (H1802)	13.72	—
Boron (H1005)	15.52	—
Silicium (H1070)	16.94	—
Carrot (H1513)	17.08	—
Green coffee extract (H1433)	17.53	—
Coenzyme Q10 (H1013)	17.76	—
Carnitine (L-) (H1038)	17.94	—
Arginine (L-) (H1036)	18.32	—
Vitamins BAG complex (H1091)	18.69	—
Oat bran beta-glucan (H1529)	19.22	—
Baobab (H1410)	19.44	—
Pathogene complex (H1803)	20.09	—
Aminomix NAC (H1002)	20.15	—
PET joints (H1501)	20.19	—
Catechin extract (H1010)	21.14	—
Beetroot (H1515)	21.23	—
Copper (H1032)	22.47	—
Betaine hydrochloride (H1119)	22.49	—
Broccoli (H1512)	23.62	—
Artichoke extract (H1440)	23.76	—
Vitamin E NAT (H1107)	23.84	—
Orthovimin Neutral Complex (H1404)	23.96	—
Pomegranate (H1520)	25.06	—
PET well-aging (H1500)	25.42	—
Zinc (H1110)	26.13	—
Juniper (H1112)	26.54	—
Detox complex (H1111)	28.92	—
PET immune system (H1502)	29.47	—
Marshmallow extract (H1439)	29.53	—
Magnesium (H1060)	29.60	—
Sunflower seed protein (H1511)	30.34	—

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Substanz	Distance in main model	Distance in second-stage model
Coconut (H1522)	30.44	—
Artemisia annua extract (H1118)	30.95	—
Vitamin B6 (Pyridoxal 5'-phosphate)...	31.27	—
Antibiosis forte complex (H1115)	31.74	—
Iron (H1015)	31.99	—
Ginseng (H1018)	32.07	—
Creatine (H1031)	32.24	—
Vitamin C (H1104)	32.92	—
Saffron style (H1434)	33.76	—
Saffron flowers (H1435)	33.82	—
Curcumin and piperine (H1014)	37.69	—
Psyllium husks (H1527)	39.01	—
Histamine block complex (H1117)	40.35	—
Konjak Glucomannan (H1530)	41.50	—
Chaga (H1011)	42.54	—
Yeast organic (H1525)	42.74	—
Potassium (H1030)	42.97	—
Acerola (H1516)	43.01	—
Trace elements SE complex (H1082)	43.42	—
Caffeine guarana extract (H1425)	43.50	—
Chondroitin sulfate (H1065)	45.08	—
Gentian extract (H1438)	46.77	—
Ginger extract (H1437)	47.44	—
Pumpkin seed protein (H1509)	47.48	—
Trace elements JK (H1080)	47.82	—
PET coenzyme Q10 (H1505)	47.98	—
α -Lipoic acid (H1000)	49.02	—
Selenium yeast (H1068)	49.22	—
Glutamine (L-) (H1043)	49.55	—
Selenium (H1067)	49.65	—
Argentum (H1116)	50.09	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *HCK classification II* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *HCK classification II*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Antioxidants NAT complex ...	051901	80311	60	from supplier
Hepart	Antioxidants NAT complex ...	052001	80313	60	from supplier
Hepart	Antioxidants NAT complex ...	052201	80315	50	from supplier
Hepart	Antioxidants NAT complex ...	052101	80317	50	from supplier
Hepart	Antioxidants NAT complex ...	051902	80318	60	from supplier
Hepart	Antioxidants NAT complex ...	067301	80404	40	from supplier
Hepart	Antioxidants NAT complex ...	067201	80405	40	from supplier
Hepart	Antioxidants NAT complex ...	14000044	80419	40	from supplier
Hepart	Antioxidants NAT complex ...	14000965	80469	40	from supplier
Hepart	Antioxidants NAT complex ...	14000964	80473	40	from supplier
Hepart	Antioxidants NAT complex ...	14001849	80504	60	from supplier
Hepart	Antioxidants NAT complex ...	14001850	80505	60	from supplier
Hepart	Antioxidants NAT complex ...	14001851	80506	60	from supplier

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Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Antioxidants NAT complex ...	14001846	80507	60	from supplier
Hepart	Antioxidants NAT complex ...	14001848	80508	60	from supplier
Hepart	Antioxidants NAT complex ...	14001847	80509	60	from supplier
Hepart	Antioxidants NAT complex ...	15000875(B1)	80607	60	from supplier
Hepart	Antioxidants NAT complex ...	15000880	80609	60	from supplier
Hepart	Antioxidants NAT complex ...	15000877(B1)	80613	60	from supplier
Hepart	Antioxidants NAT complex ...	15000878(B1)	80616	60	from supplier
Hepart	Antioxidants NAT complex ...	15000874	80618	60	from supplier
Hepart	Antioxidants NAT complex ...	15000874(B1)	80619	60	from supplier
Hepart	Antioxidants NAT complex ...	15000879	80621	60	from supplier
Hepart	Antioxidants NAT complex ...	15000876	80624	60	from supplier
Hepart	Antioxidants NAT complex ...	16000378	80783	40	from supplier
Hepart	Antioxidants NAT complex ...	17000260	80946	40	from supplier
Hepart	Antioxidants NAT complex ...	17000261	80986	40	from supplier
Hepart	Antioxidants NAT complex ...	17001756	80987	40	from supplier
Hepart	Antioxidants NAT complex ...	21000112	81329	40	from supplier
Hepart	Antioxidants NAT complex ...	21000123	81345	40	from supplier
Hepart	Antioxidants NAT complex ...	21001616-1748-1747-1652	81388	50	from supplier
Hepart	Antioxidants NAT complex ...	24000111/0	81533	40	from supplier
Hepart	Antioxidants NAT complex ...	24000540/0	81535	40	from supplier
Hepart	Antioxidants NAT complex ...	24002275	81570	40	from supplier
Hepart	Antioxidants NAT complex ...	24002278	81571	40	from supplier
Hepart	Antioxidants NAT complex ...	24002280	81572	40	from supplier
Hepart	Bioflavonoid complex (H1006)	068101	80342	40	from supplier
Hepart	Bioflavonoid complex (H1006)	14001675	80492	60	from supplier
Hepart	Bioflavonoid complex (H1006)	17000256	80878	40	from supplier
Hepart	Bioflavonoid complex (H1006)	20002413	81315	40	from supplier
Hepart	Bioflavonoid complex (H1006)	21002660	81412	40	from supplier
Hepart	Bioflavonoid complex (H1006)	22001793	81460	40	from supplier
Hepart	Cabbage mix (H1514)	23001164	81488	40	from supplier
Hepart	Calcium L-(+) -lactate co...	055201	80322	60	from supplier
Hepart	Calcium L-(+) -lactate co...	055001	80323	60	from supplier
Hepart	Calcium L-(+) -lactate co...	055101	80327	60	from supplier
Hepart	Calcium L-(+) -lactate co...	055601	80329	50	from supplier
Hepart	Calcium L-(+) -lactate co...	14000106	80422	40	from supplier
Hepart	Calcium L-(+) -lactate co...	14001933	80521	60	from supplier
Hepart	Calcium L-(+) -lactate co...	14001934	80522	60	from supplier
Hepart	Calcium L-(+) -lactate co...	14001937	80525	60	from supplier
Hepart	Calcium L-(+) -lactate co...	14001938	80526	60	from supplier
Hepart	Calcium L-(+) -lactate co...	14001939	80527	60	from supplier
Hepart	Calcium L-(+) -lactate co...	15001669	80707	60	from supplier
Hepart	Calcium L-(+) -lactate co...	15001672(B1)	80709	60	from supplier
Hepart	Calcium L-(+) -lactate co...	15001671	80711	60	from supplier
Hepart	Calcium L-(+) -lactate co...	15001673(MM)	80712	60	from supplier
Hepart	Calcium L-(+) -lactate co...	15001668(B1)	80715	60	from supplier
Hepart	Calcium L-(+) -lactate co...	15001667(MM)	80719	60	from supplier
Hepart	Calcium L-(+) -lactate co...	15001666(MM)	80722	60	from supplier
Hepart	Calcium L-(+) -lactate co...	15001665(B1)	80724	60	from supplier
Hepart	Calcium L-(+) -lactate co...	15001670(B2)	80729	60	from supplier
Hepart	Calcium L-(+) -lactate co...	15001675(B2)	80732	60	from supplier
Hepart	Calcium L-(+) -lactate co...	15001676(MM)	80734	60	from supplier
Hepart	Calcium L-(+) -lactate co...	15001677(B1)	80740	60	from supplier
Hepart	Calcium L-(+) -lactate co...	15001674(B2)	80741	60	from supplier
Hepart	Calcium L-(+) -lactate co...	21000180-80-81-82-83-84	81338	40	from supplier
Hepart	Calcium L-(+) -lactate co...	20020-12-13-14-16-18	81399	50	from supplier
Hepart	Calcium L-(+) -lactate co...	22001301-03	81439	40	from supplier
Hepart	Calcium L-(+) -lactate co...	24002388	81576	40	from supplier
Hepart	Camu Camu (H1518)	23000543	81476	40	from supplier
Hepart	Cranberry (H1519)	23000480	81482	40	from supplier
Hepart	Cranberry (H1519)	23002136	81512	40	from supplier

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Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Flavour orange (H1405)	16000262	80768	60	from supplier
Hepart	Flavour orange (H1405)	17000491/0	81016	40	from supplier
Hepart	Flavour orange (H1405)	19000149	81151	40	from supplier
Hepart	Flavour orange (H1405)	19000607/0	81170	40	from supplier
Hepart	Flavour orange (H1405)	21000861	81334	40	from supplier
Hepart	Garcinia cambogia (H1017)	056601	80346	40	from supplier
Hepart	Garcinia cambogia (H1017)	056601	80477	40	from supplier
Hepart	Garcinia cambogia (H1017)	14001687	80490	60	from supplier
Hepart	Garcinia cambogia (H1017)	15001048(F2)	80660	60	from supplier
Hepart	Garcinia cambogia (H1017)	17000873	80956	40	from supplier
Hepart	Garcinia cambogia (H1017)	18001849	81150	40	from supplier
Hepart	Garcinia cambogia (H1017)	21001144	81378	50	from supplier
Hepart	ginkgo extract (H1024)	067901	80391	80	from supplier
Hepart	ginkgo extract (H1024)	067901	80476	40	from supplier
Hepart	ginkgo extract (H1024)	15001039	80656	60	from supplier
Hepart	ginkgo extract (H1024)	15001038(F3)	80657	60	from supplier
Hepart	ginkgo extract (H1024)	15001038	80658	60	from supplier
Hepart	ginkgo extract (H1024)	17001832	81005	40	from supplier
Hepart	ginkgo extract (H1024)	18001386	81133	40	from supplier
Hepart	ginkgo extract (H1024)	19002623	81215	40	from supplier
Hepart	ginkgo extract (H1024)	21002839	81435	40	from supplier
Hepart	ginkgo extract (H1024)	23001413/0	81529	40	from supplier
Hepart	Glutathione (H1020)	074901	80430	40	from supplier
Hepart	Glutathione (H1020)	15000478	80583	60	from supplier
Hepart	Glutathione (H1020)	18000508/0	81316	40	from supplier
Hepart	Glutathione (H1020)	23002184	81541	40	from supplier
Hepart	Isoflavone (H1025)	056701	80345	40	from supplier
Hepart	Isoflavone (H1025)	15000205/2	80815	40	from supplier
Hepart	Isoflavone (H1025)	16001644/0	80853	40	from supplier
Hepart	Isoflavone (H1025)	24001858	81555	40	from supplier
Hepart	Kale (H1126)	22000777	81450	40	from supplier
Hepart	Kale (H1126)	23000479	81481	40	from supplier
Hepart	OPC Proanthocyanidins (Pi...	130208-77	80337	40	from supplier
Hepart	OPC Proanthocyanidins (Pi...	068301	80352	40	from supplier
Hepart	OPC Proanthocyanidins (Pi...	070401	80380	40	from supplier
Hepart	OPC Proanthocyanidins (Pi...	070401	80398	40	from supplier
Hepart	OPC Proanthocyanidins (Pi...	16001439	80864	40	from supplier
Hepart	OPC Proanthocyanidins (Pi...	17001805	81001	40	from supplier
Hepart	OPC Proanthocyanidins (Pi...	21001640	81390	40	from supplier
Hepart	OPC Proanthocyanidins (Pi...	22000705	81451	40	from supplier
Hepart	Orthocolon complex (H1800)	18000636	81041	40	from supplier
Hepart	Orthocolon complex (H1800)	18000641	81042	40	from supplier
Hepart	Orthocolon complex (H1800)	19000177	81202	40	from supplier
Hepart	PET basis (H1503)	15000402	80566	60	from supplier
Hepart	PET basis (H1503)	15000402	80636	60	from supplier
Hepart	Rhodiola (H1064)	070501	80390	40	from supplier
Hepart	Rhodiola (H1064)	070501	80632	60	from supplier
Hepart	Rhodiola (H1064)	15001045	80672	60	from supplier
Hepart	Rhodiola (H1064)	18000413	81136	40	from supplier
Hepart	Rhodiola (H1064)	21001642	81375	50	from supplier
Hepart	Rhodiola (H1064)	22001550	81461	40	from supplier
Hepart	Seabuckthorn (H1523)	24000627	81534	40	from supplier
Hepart	Vitamin B1 (H1101)	053301	80316	60	from supplier
Hepart	Vitamin B1 (H1101)	075001	80392	40	from supplier
Hepart	Vitamin B1 (H1101)	075001	80479	40	from supplier
Hepart	Vitamin B1 (H1101)	075001	80529	60	from supplier
Hepart	Vitamin B1 (H1101)	17000914	80953	40	from supplier
Hepart	Vitamin B1 (H1101)	17001075	80980	40	from supplier
Hepart	Vitamin B1 (H1101)	19000685	81183	40	from supplier
Hepart	Vitamin complex (H1100)	049201	80349	40	from supplier

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Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Vitamin complex (H1100)	077201	80411	40	from supplier
Hepart	Vitamin complex (H1100)	077001	80431	40	from supplier
Hepart	Vitamin complex (H1100)	077101	80432	40	from supplier
Hepart	Vitamin complex (H1100)	14001590	80485	60	from supplier
Hepart	Vitamin complex (H1100)	14001589	80486	60	from supplier
Hepart	Vitamin complex (H1100)	14001591	80487	60	from supplier
Hepart	Vitamin complex (H1100)	15001276 (B1)	80637	60	from supplier
Hepart	Vitamin complex (H1100)	15001277 (F2)	80638	60	from supplier
Hepart	Vitamin complex (H1100)	15001274 (B1)	80640	60	from supplier
Hepart	Vitamin complex (H1100)	15001275 (F2)	80642	60	from supplier
Hepart	Vitamin complex (H1100)	15001277	80643	60	from supplier
Hepart	Vitamin complex (H1100)	15001276 (F2)	80646	60	from supplier
Hepart	Vitamin complex (H1100)	15001274	80647	60	from supplier
Hepart	Vitamin complex (H1100)	15001275	80648	60	from supplier
Hepart	Vitamin complex (H1100)	16000957	80827	40	from supplier
Hepart	Vitamin complex (H1100)	17001751/0	80990	40	from supplier
Hepart	Vitamin complex (H1100)	19001423/0	81171	40	from supplier
Hepart	Vitamin complex (H1100)	19001424/0	81172	40	from supplier
Hepart	Vitamin complex (H1100)	19001023	81251	40	from supplier
Hepart	Vitamin complex (H1100)	20001890	81271	40	from supplier
Hepart	Vitamin complex (H1100)	2100-1518-1264	81357	50	from supplier
Hepart	Vitamin complex (H1100)	22000230-231	81415	40	from supplier
Hepart	Vitamin complex (H1100)	24000871	81539	40	from supplier
Hepart	Wild berry (H1524)	21002226	81449	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 7660 spectra of 157 reference samples from the substance/substance group *HCK classification II*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 150 different batches.
- 20 816 spectra from a total of 428 batches from further 111 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 7789 spectra of 170 reference samples from the substance/substance group *HCK classification II*.

- Among them are spectra of independent samples from 169 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Antioxidants NAT complex ...	14000043	80424	40
Hepart	Antioxidants NAT complex ...	14000042	80428	40
Hepart	Antioxidants NAT complex ...	14000961	80470	40
Hepart	Antioxidants NAT complex ...	14000962	80471	39
Hepart	Antioxidants NAT complex ...	14000963	80472	40
Hepart	Antioxidants NAT complex ...	14000966	80474	40
Hepart	Antioxidants NAT complex ...	15000875	80606	60
Hepart	Antioxidants NAT complex ...	15000875 (F2)	80608	60
Hepart	Antioxidants NAT complex ...	15000880 (B1)	80610	60
Hepart	Antioxidants NAT complex ...	15000880 (F2)	80611	60
Hepart	Antioxidants NAT complex ...	15000877	80612	60
Hepart	Antioxidants NAT complex ...	15000877 (F2)	80614	60
Hepart	Antioxidants NAT complex ...	15000878	80615	60
Hepart	Antioxidants NAT complex ...	15000878 (F2)	80617	60
Hepart	Antioxidants NAT complex ...	15000874 (F2)	80620	60
Hepart	Antioxidants NAT complex ...	15000879 (B1)	80622	60
Hepart	Antioxidants NAT complex ...	15000879 (F2)	80623	60
Hepart	Antioxidants NAT complex ...	15000876 (B1)	80625	60
Hepart	Antioxidants NAT complex ...	15000876 (F2)	80626	60
Hepart	Antioxidants NAT complex ...	16000380	80784	40
Hepart	Antioxidants NAT complex ...	16000376	80785	40
Hepart	Antioxidants NAT complex ...	16000377	80786	40
Hepart	Antioxidants NAT complex ...	16000965	80834	40
Hepart	Antioxidants NAT complex ...	16000966	80835	40
Hepart	Antioxidants NAT complex ...	16000967	80836	40
Hepart	Antioxidants NAT complex ...	16000968	80837	40
Hepart	Antioxidants NAT complex ...	16000969	80838	40
Hepart	Antioxidants NAT complex ...	16000970	80839	40
Hepart	Antioxidants NAT complex ...	16000971	80840	40
Hepart	Antioxidants NAT complex ...	16000972	80841	40
Hepart	Antioxidants NAT complex ...	16000973	80842	40
Hepart	Antioxidants NAT complex ...	16000974	80843	40
Hepart	Antioxidants NAT complex ...	17000268	80938	40
Hepart	Antioxidants NAT complex ...	17000269	80939	40
Hepart	Antioxidants NAT complex ...	17000267	80940	40
Hepart	Antioxidants NAT complex ...	17000266	80941	40
Hepart	Antioxidants NAT complex ...	17000264	80942	40
Hepart	Antioxidants NAT complex ...	17000263	80943	40
Hepart	Antioxidants NAT complex ...	17000262	80944	40
Hepart	Antioxidants NAT complex ...	17001754/0	80988	40
Hepart	Antioxidants NAT complex ...	17001757	80989	40
Hepart	Antioxidants NAT complex ...	17001758	81002	40
Hepart	Antioxidants NAT complex ...	17001755	81021	40
Hepart	Antioxidants NAT complex ...	18001181	81084	40
Hepart	Antioxidants NAT complex ...	18001182	81085	40
Hepart	Antioxidants NAT complex ...	18001812	81138	40
Hepart	Antioxidants NAT complex ...	18001814	81139	40
Hepart	Antioxidants NAT complex ...	18001815	81140	40
Hepart	Antioxidants NAT complex ...	18001816	81141	40
Hepart	Antioxidants NAT complex ...	18001817	81142	40
Hepart	Antioxidants NAT complex ...	18001818	81143	40
Hepart	Antioxidants NAT complex ...	19000449	81192	40
Hepart	Antioxidants NAT complex ...	19000603	81193	40
Hepart	Antioxidants NAT complex ...	19002532	81221	40
Hepart	Antioxidants NAT complex ...	20000224	81232	40
Hepart	Antioxidants NAT complex ...	20000225	81233	40

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Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Antioxidants NAT complex ...	20000805	81244	40
Hepart	Antioxidants NAT complex ...	20000806	81245	40
Hepart	Antioxidants NAT complex ...	20000720	81246	40
Hepart	Antioxidants NAT complex ...	20000722	81247	40
Hepart	Antioxidants NAT complex ...	20002053	81298	40
Hepart	Antioxidants NAT complex ...	20002054	81299	40
Hepart	Antioxidants NAT complex ...	20002055	81300	40
Hepart	Antioxidants NAT complex ...	21000122	81330	40
Hepart	Antioxidants NAT complex ...	21002561	81419	40
Hepart	Antioxidants NAT complex ...	24000541/0	81536	40
Hepart	Antioxidants NAT complex ...	24001952	81557	40
Hepart	Antioxidants NAT complex ...	24002267	81568	40
Hepart	Antioxidants NAT complex ...	24002268	81569	40
Hepart	Bioflavonoid complex (H1006)	17000257	80879	40
Hepart	Calcium L-(+) -lactate co...	055301	80324	60
Hepart	Calcium L-(+) -lactate co...	055401	80325	60
Hepart	Calcium L-(+) -lactate co...	055501	80326	60
Hepart	Calcium L-(+) -lactate co...	14000110	80406	40
Hepart	Calcium L-(+) -lactate co...	14000107	80412	40
Hepart	Calcium L-(+) -lactate co...	14000111	80414	40
Hepart	Calcium L-(+) -lactate co...	14000108	80415	40
Hepart	Calcium L-(+) -lactate co...	14000109	80417	30
Hepart	Calcium L-(+) -lactate co...	14001935	80523	60
Hepart	Calcium L-(+) -lactate co...	14001936	80524	60
Hepart	Calcium L-(+) -lactate co...	15001672(B2)	80708	60
Hepart	Calcium L-(+) -lactate co...	15001672(MM)	80710	60
Hepart	Calcium L-(+) -lactate co...	15001673(B2)	80713	60
Hepart	Calcium L-(+) -lactate co...	15001673(B1)	80714	60
Hepart	Calcium L-(+) -lactate co...	15001668(MM)	80716	60
Hepart	Calcium L-(+) -lactate co...	15001667(F2)	80717	60
Hepart	Calcium L-(+) -lactate co...	15001667(B1)	80718	60
Hepart	Calcium L-(+) -lactate co...	15001666(B1)	80720	60
Hepart	Calcium L-(+) -lactate co...	15001666(F2)	80721	60
Hepart	Calcium L-(+) -lactate co...	15001670(B1)	80723	60
Hepart	Calcium L-(+) -lactate co...	15001670(MM)	80725	60
Hepart	Calcium L-(+) -lactate co...	15001665(F2)	80726	60
Hepart	Calcium L-(+) -lactate co...	15001665(MM)	80727	60
Hepart	Calcium L-(+) -lactate co...	15001668(F2)	80728	60
Hepart	Calcium L-(+) -lactate co...	15001675(MM)	80730	60
Hepart	Calcium L-(+) -lactate co...	15001675(B1)	80731	60
Hepart	Calcium L-(+) -lactate co...	15001675/4	80733	60
Hepart	Calcium L-(+) -lactate co...	15001676(B2)	80735	60
Hepart	Calcium L-(+) -lactate co...	15001676/4	80736	60
Hepart	Calcium L-(+) -lactate co...	15001676(B1)	80737	60
Hepart	Calcium L-(+) -lactate co...	15001677(MM)	80738	60
Hepart	Calcium L-(+) -lactate co...	15001677/4	80739	60
Hepart	Calcium L-(+) -lactate co...	15001674(B1)	80742	60
Hepart	Calcium L-(+) -lactate co...	15001674(MM)	80743	60
Hepart	Calcium L-(+) -lactate co...	17000249MM	80971	40
Hepart	Calcium L-(+) -lactate co...	17000250	80972	40
Hepart	Calcium L-(+) -lactate co...	17000201MM	80973	40
Hepart	Calcium L-(+) -lactate co...	17000202MM	80974	40
Hepart	Calcium L-(+) -lactate co...	17000203	80975	40
Hepart	Calcium L-(+) -lactate co...	17000204MM	80976	40
Hepart	Calcium L-(+) -lactate co...	17000205	80977	40
Hepart	Calcium L-(+) -lactate co...	17000206	80978	40
Hepart	Calcium L-(+) -lactate co...	18001413	81105	40
Hepart	Calcium L-(+) -lactate co...	18001414/0	81106	40
Hepart	Calcium L-(+) -lactate co...	18001415/0	81107	40
Hepart	Calcium L-(+) -lactate co...	18001416/0	81108	40

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Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Calcium L-(+) -lactate co...	18001417/0	81109	40
Hepart	Calcium L-(+) -lactate co...	18001418	81110	40
Hepart	Calcium L-(+) -lactate co...	19001637	81238	40
Hepart	Calcium L-(+) -lactate co...	19001638	81239	40
Hepart	Calcium L-(+) -lactate co...	19001639	81240	40
Hepart	Calcium L-(+) -lactate co...	19001640	81241	40
Hepart	Calcium L-(+) -lactate co...	19001641	81242	40
Hepart	Calcium L-(+) -lactate co...	19001167	81243	40
Hepart	Calcium L-(+) -lactate co...	24002316	81575	40
Hepart	Flavour orange (H1405)	18000770	81064	40
Hepart	Flavour orange (H1405)	18001327	81095	40
Hepart	Flavour orange (H1405)	18001422/0	81096	40
Hepart	Garcinia cambogia (H1017)	15001048	80661	60
Hepart	Garcinia cambogia (H1017)	15001048(B1)	80662	60
Hepart	Garcinia cambogia (H1017)	22000028	81408	40
Hepart	ginkgo extract (H1024)	15001038(F1)	80659	60
Hepart	ginkgo extract (H1024)	18001110	81072	40
Hepart	Glutathione (H1020)	16000938	80813	40
Hepart	Isoflavone (H1025)	15000205	80556	60
Hepart	OPC Proanthocyanidins (Pi...	16001439(B1)	80865	40
Hepart	OPC Proanthocyanidins (Pi...	16001439(F1)	80866	40
Hepart	OPC Proanthocyanidins (Pi...	20002632/0	81307	40
Hepart	OPC Proanthocyanidins (Pi...	23000867	81508	40
Hepart	Orthocolon complex (H1800)	18000640	81043	40
Hepart	Orthocolon complex (H1800)	19000937	81185	40
Hepart	Rhodiola (H1064)	17000278	80915	40
Hepart	Rhodiola (H1064)	20000088	81235	40
Hepart	Rhodiola (H1064)	20002070	81318	40
Hepart	Vitamin B1 (H1101)	14001112	80480	40
Hepart	Vitamin B1 (H1101)	14001113	80481	40
Hepart	Vitamin complex (H1100)	15001275(B1)	80639	60
Hepart	Vitamin complex (H1100)	15001277(B1)	80641	60
Hepart	Vitamin complex (H1100)	15001274(F2)	80644	60
Hepart	Vitamin complex (H1100)	15001276	80645	60
Hepart	Vitamin complex (H1100)	16000958	80828	40
Hepart	Vitamin complex (H1100)	16000959	80829	40
Hepart	Vitamin complex (H1100)	16000960	80830	40
Hepart	Vitamin complex (H1100)	16000961	80831	40
Hepart	Vitamin complex (H1100)	16000962	80832	40
Hepart	Vitamin complex (H1100)	17001654	80984	40
Hepart	Vitamin complex (H1100)	17001752/0	80991	40
Hepart	Vitamin complex (H1100)	17000880/0	80992	40
Hepart	Vitamin complex (H1100)	17001753/0	80993	40
Hepart	Vitamin complex (H1100)	17001750/0	80994	40
Hepart	Vitamin complex (H1100)	19000433	81173	40
Hepart	Vitamin complex (H1100)	19000544	81174	40
Hepart	Vitamin complex (H1100)	19002512	81218	40
Hepart	Vitamin complex (H1100)	20000144/0	81226	40
Hepart	Vitamin complex (H1100)	20000836	81248	40
Hepart	Vitamin complex (H1100)	19001582	81249	40
Hepart	Vitamin complex (H1100)	19002234	81250	40
Hepart	Vitamin complex (H1100)	19001581	81252	40
Hepart	Vitamin complex (H1100)	24000857	81542	40
Hepart	Antioxidants NAT complex ...	17000261	80945	40

- 15 210 spectra from a total of 334 batches from further 65 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B*

section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 678 spectra from 26 *Apo-Ident* customers from 374 batches from the substance/substance group *HCK classification II*.
- Among them are spectra of independent samples from 347 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
Euro OTC	Antioxidants NAT complex ...	16000970	1
Flaigg Ag CH-4147 Ae...	OPC Proanthocyanidins (Pi...	1700185	1
Flaigg Ag CH-4147 Ae...	ginkgo extract (H1024)	18001386	1
Flaigg Ag CH-4147 Ae...	ginkgo extract (H1024)	18001386/1	1
HCK	Vitamin B1 (H1101)	14001112/0	1
HCK	Garcinia cambogia (H1017)	14001687/2	1
HCK	Calcium L-(+) -lactate co...	14001938/1	1
HCK	Calcium L-(+) -lactate co...	14001938-1	1
HCK	Glutathione (H1020)	15000478	1
HCK	Antioxidants NAT complex ...	15000876/0	1
HCK	Antioxidants NAT complex ...	15000878-0	1
HCK	Rhodiola (H1064)	1500104-3	1
HCK	Rhodiola (H1064)	15001045-3	2
HCK	Rhodiola (H1064)	15001045-4	3
HCK	Rhodiola (H1064)	15001045-5	3
HCK	Vitamin complex (H1100)	15001275/0	1
HCK	Vitamin complex (H1100)	15001275/1	2
HCK	Vitamin complex (H1100)	15001275-1	1
HCK	Vitamin complex (H1100)	15001276-0	3
HCK	Vitamin B1 (H1101)	15001620	1
HCK	Vitamin B1 (H1101)	15001622-0	1
HCK	Vitamin B1 (H1101)	15001622-1	2
HCK	Calcium L-(+) -lactate co...	15001667-0	1
HCK	Calcium L-(+) -lactate co...	15001672	2
HCK	Bioflavonoid complex (H1006)	17000256	1
HCK	Isoflavone (H1025)	56701	1
HCK	ginkgo extract (H1024)	67901-11	1
HCK	Rhodiola (H1064)	70501/7	1
HCK	Glutathione (H1020)	74901	1
Hedinger	Antioxidants NAT complex ...	51901	1
Hepart / Unisan	Calcium L-(+) -lactate co...	17000250	1
Hepart / Unisan	Antioxidants NAT complex ...	17000257	1
Hepart / Unisan	Antioxidants NAT complex ...	19000421/0	1
Hepart / Unisan	Antioxidants NAT complex ...	19000421/1	1
Hepart / Unisan	Vitamin complex (H1100)	19000544/1	1
Hepart / Unisan	Antioxidants NAT complex ...	20000720/0	1
Hepart AG, CH-8280 K...	Vitamin complex (H1100)	1014025101	1
Hepart AG, CH-8280 K...	Antioxidants NAT complex ...	1034019901	1
Hepart AG, CH-8280 K...	Antioxidants NAT complex ...	1034030901	1
Hepart AG, CH-8280 K...	Calcium L-(+) -lactate co...	1104008901	4
Hepart AG, CH-8280 K...	Glutathione (H1020)	1251019703	1
Hepart AG, CH-8280 K...	Glutathione (H1020)	1251025703	1
Hepart AG, CH-8280 K...	OPC Proanthocyanidins (Pi...	130208	1
Hepart AG, CH-8280 K...	Glutathione (H1020)	40201	1
Hepart AG, CH-8280 K...	Vitamin complex (H1100)	49301	5
Hepart AG, CH-8280 K...	Antioxidants NAT complex ...	52101	1
Hepart AG, CH-8280 K...	Vitamin B1 (H1101)	53301	1

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Supplier	Substance	Batch	Spectra
Hepart AG, CH-8280 K...	Calcium L-(+) -lactate co...	55501	2
Hepart AG, CH-8280 K...	Bioflavonoid complex (H1006)	56001	1
Hepart AG, Unisan GmbH	Vitamin B1 (H1101)	15001622/0	1
Hepart ag/ Unisan	Vitamin complex (H1100)	19001023/0	1
Hepart AG/Unisan	Vitamin complex (H1100)	19000544/1	1
Hepart AG/Unisan	Vitamin complex (H1100)	19001581/0	1
Hepart ag/Unisan	Calcium L-(+) -lactate co...	19001637	1
Hepart AG/Unisan	Vitamin complex (H1100)	20000144/0	1
Hepart AG/Unisan	Antioxidants NAT complex ...	20000224/0	1
Hepart AG/Unisan	Antioxidants NAT complex ...	20000806/1	2
Hepart AG/Unisan	Vitamin complex (H1100)	20000835/0	1
Hepart ag/Unisan	Vitamin complex (H1100)	20000836	1
Hepart AG/Unisan	Vitamin complex (H1100)	20001899/0	1
Hepart AG/Unisan	Antioxidants NAT complex ...	21000121/0	1
Hepart AG	Vitamin complex (H1100)	1014025101	1
Hepart AG	Vitamin complex (H1100)	1014025301	1
hepart ag	Vitamin complex (H1100)	1015954801	1
hepart ag	Vitamin complex (H1100)	10159548011	1
Hepart AG	Antioxidants NAT complex ...	1034019901	1
Hepart AG	Antioxidants NAT complex ...	1034030901	1
Hepart AG	Antioxidants NAT complex ...	1034030902	1
Hepart AG	Antioxidants NAT complex ...	1034030904	1
Hepart AG	Antioxidants NAT complex ...	1037030904	1
Hepart AG	Calcium L-(+) -lactate co...	1104008901	6
Hepart AG	Garcinia cambogia (H1017)	1221007401	1
Hepart AG	Glutathione (H1020)	1254025703	1
Hepart AG	Glutathione (H1020)	1254040201	1
Hepart AG	Bioflavonoid complex (H1006)	1284019001	1
Hepart AG	Bioflavonoid complex (H1006)	1284042501	1
Hepart AG	Isoflavone (H1025)	1314025704	1
Hepart AG	Isoflavone (H1025)	1314038801	1
Hepart AG	Antioxidants NAT complex ...	14000963	3
Hepart AG	Vitamin B1 (H1101)	14001112	1
Hepart AG	Vitamin complex (H1100)	14001589	2
Hepart AG	Bioflavonoid complex (H1006)	14001675/1	1
Hepart AG	Calcium L-(+) -lactate co...	14001933	1
Hepart AG	Antioxidants NAT complex ...	15000878/0	2
Hepart AG	ginkgo extract (H1024)	15001038	1
Hepart AG	ginkgo extract (H1024)	15001039/1	1
Hepart AG	Rhodiola (H1064)	15001045/4	1
Hepart AG	Vitamin complex (H1100)	15001275/1	1
Hepart AG	Vitamin complex (H1100)	15001277	1
Hepart AG	Vitamin B1 (H1101)	15001622/0	1
Hepart AG	Calcium L-(+) -lactate co...	15001668/0	2
Hepart AG	OPC Proanthocyanidins (Pi...	1504018401	2
Hepart AG	Antioxidants NAT complex ...	16000376	1
Hepart AG	Antioxidants NAT complex ...	16000378	1
Hepart AG	OPC Proanthocyanidins (Pi...	16000637	1
Hepart AG	Vitamin B1 (H1101)	16000698/0	1
Hepart AG	Glutathione (H1020)	16000938/1	1
Hepart AG	Glutathione (H1020)	16000938/2	1
Hepart AG	Vitamin complex (H1100)	16000957/0	1
Hepart AG	Antioxidants NAT complex ...	16000970/0	1
Hepart AG	Isoflavone (H1025)	16001644/2	1
Hepart AG	Isoflavone (H1025)	16001644/3	2
Hepart AG	Vitamin B1 (H1101)	1621030202	1
Hepart AG	Vitamin B1 (H1101)	1622030202	2
Hepart AG	Calcium L-(+) -lactate co...	17000203/0	2
Hepart AG	Calcium L-(+) -lactate co...	17000205/0	2
Hepart AG	Calcium L-(+) -lactate co...	17000206/0	1

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Supplier	Substance	Batch	Spectra
Hepart AG	Calcium L-(+) -lactate co...	17000252/0	1
Hepart AG	Calcium L-(+) -lactate co...	17000253/0	2
Hepart AG	Antioxidants NAT complex ...	17000264/0	1
Hepart AG	Antioxidants NAT complex ...	17000266/0	1
Hepart AG	Vitamin complex (H1100)	17000880/0	4
Hepart AG	Vitamin B1 (H1101)	17000914/1	1
Hepart AG	Vitamin complex (H1100)	17001750/0	2
Hepart AG	Vitamin complex (H1100)	17001751/0	2
Hepart AG	Antioxidants NAT complex ...	17001754/0	1
Hepart AG	Antioxidants NAT complex ...	18001182/0	2
Hepart AG	Antioxidants NAT complex ...	18001182/1	2
Hepart AG	Calcium L-(+) -lactate co...	18001414	1
Hepart AG	Calcium L-(+) -lactate co...	18001416/0	1
Hepart AG	Antioxidants NAT complex ...	18001815/0	2
Hepart AG	Garcinia cambogia (H1017)	18001849/0	2
Hepart AG	OPC Proanthocyanidins (Pi...	18401	1
Hepart AG	Vitamin complex (H1100)	19000364/0	1
Hepart AG	Vitamin complex (H1100)	19000433/0	2
hepart ag	Antioxidants NAT complex ...	19901	1
Hepart AG	Vitamin complex (H1100)	20000144/0	1
Hepart AG	Isoflavone (H1025)	38801	1
Hepart AG	Bioflavonoid complex (H1006)	42501	1
Hepart AG	Vitamin complex (H1100)	49201	4
Hepart AG	Vitamin complex (H1100)	49202	5
Hepart AG	Vitamin complex (H1100)	49301	7
Hepart AG	Antioxidants NAT complex ...	51902	1
Hepart AG	Antioxidants NAT complex ...	52101	3
Hepart AG	Antioxidants NAT complex ...	52201	2
Hepart AG	Vitamin B1 (H1101)	53301	2
Hepart AG	Calcium L-(+) -lactate co...	55001	1
Hepart AG	Calcium L-(+) -lactate co...	55201	1
Hepart AG	Calcium L-(+) -lactate co...	55301	2
Hepart AG	Calcium L-(+) -lactate co...	55401	4
Hepart AG	Calcium L-(+) -lactate co...	55501	5
Hepart AG	Bioflavonoid complex (H1006)	56001	2
Hepart AG	Isoflavone (H1025)	56701	1
Hepart AG	Antioxidants NAT complex ...	67201	1
Hepart AG	Antioxidants NAT complex ...	67301	2
Hepart AG	Antioxidants NAT complex ...	67501	1
Hepart AG	Bioflavonoid complex (H1006)	68101	1
Hepart AG	OPC Proanthocyanidins (Pi...	70401	2
Hepart AG	Rhodiola (H1064)	70501	1
Hepart AG	Garcinia cambogia (H1017)	7401	2
Hepart AG	Vitamin complex (H1100)	77201	3
Hepart AG	Calcium L-(+) -lactate co...	8901	2
Hepart AG	Vitamin complex (H1100)	H110031	1
Hepart/ unisan	OPC Proanthocyanidins (Pi...	20000179	1
Hepart/Hepart	Vitamin complex (H1100)	17000880/0	1
Hepart/Unisan	Calcium L-(+) -lactate co...	14001938/1	1
Hepart/Unisan	Antioxidants NAT complex ...	15000877/1	1
Hepart/Unisan	Vitamin complex (H1100)	15001275/0	1
Hepart/Unisan	Antioxidants NAT complex ...	16000376/0	1
Hepart/Unisan	Antioxidants NAT complex ...	16000967	1
Hepart/Unisan	Bioflavonoid complex (H1006)	17000256/3	2
Hepart/Unisan	Calcium L-(+) -lactate co...	19001639/0	1
Hepart/Unisan	Antioxidants NAT complex ...	20000805	1
Hepart/Unisan	Vitamin complex (H1100)	20000836	1
Hepart	Bioflavonoid complex (H1006)	14001675/5	1
Hepart	Bioflavonoid complex (H1006)	14001675-4	2
Hepart	Calcium L-(+) -lactate co...	14001937	1

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Supplier	Substance	Batch	Spectra
Hepart	Glutathione (H1020)	15000478	1
Hepart	Rhodiola (H1064)	150010145-6	1
Hepart	ginkgo extract (H1024)	15001038-2	2
Hepart	ginkgo extract (H1024)	150010391	1
Hepart	Rhodiola (H1064)	15001045	1
Hepart	Rhodiola (H1064)	15001045-6	2
Hepart	Calcium L-(+) -lactate co...	15001667/0	1
Hepart	Calcium L-(+) -lactate co...	150016740	1
Hepart	OPC Proanthocyanidins (Pi...	16000637-2	1
Hepart	Vitamin B1 (H1101)	16000698-0	1
Hepart	Glutathione (H1020)	16000938/0	4
Hepart	Vitamin complex (H1100)	16000957	1
Hepart	Vitamin complex (H1100)	16000957-0	1
Hepart	Vitamin complex (H1100)	16000958	1
Hepart	Vitamin complex (H1100)	16000959-0	1
Hepart	Vitamin complex (H1100)	16000960-0	1
Hepart	Antioxidants NAT complex ...	16000965-0	1
Hepart	Antioxidants NAT complex ...	16000968	2
Hepart	Antioxidants NAT complex ...	16000970	1
Hepart	Antioxidants NAT complex ...	16000970/0	3
Hepart	Antioxidants NAT complex ...	16000970-0	1
Hepart	Garcinia cambogia (H1017)	16001252	1
Hepart	Garcinia cambogia (H1017)	16001252/1	1
Hepart	OPC Proanthocyanidins (Pi...	16001439	1
Hepart	OPC Proanthocyanidins (Pi...	16001439-0	1
Hepart	Isoflavone (H1025)	16001644	1
Hepart	Isoflavone (H1025)	16001644/0	1
Hepart	Isoflavone (H1025)	16001644/1	3
Hepart	Isoflavone (H1025)	16001644/3	5
Hepart	Isoflavone (H1025)	16001644/4	3
Hepart	Calcium L-(+) -lactate co...	17000202/0	1
Hepart	Calcium L-(+) -lactate co...	17000204	1
Hepart	Calcium L-(+) -lactate co...	170002040	1
Hepart	Calcium L-(+) -lactate co...	17000205	1
Hepart	Calcium L-(+) -lactate co...	17000206	1
Hepart	Calcium L-(+) -lactate co...	17000206/0	1
Hepart	Calcium L-(+) -lactate co...	17000208/0	1
Hepart	Calcium L-(+) -lactate co...	17000250/0	4
Hepart	Calcium L-(+) -lactate co...	17000251/0	1
Hepart	Calcium L-(+) -lactate co...	17000253	1
Hepart	Calcium L-(+) -lactate co...	17000253/0	2
Hepart	Calcium L-(+) -lactate co...	17000254/0	1
Hepart	Bioflavonoid complex (H1006)	17000256	1
Hepart	Bioflavonoid complex (H1006)	17000256/2	7
Hepart	Bioflavonoid complex (H1006)	17000256/3	1
Hepart	Bioflavonoid complex (H1006)	17000257	3
Hepart	Bioflavonoid complex (H1006)	17000257/0	1
Hepart	Bioflavonoid complex (H1006)	17000257/1	2
Hepart	Antioxidants NAT complex ...	17000260	1
Hepart	Antioxidants NAT complex ...	17000264	2
Hepart	Antioxidants NAT complex ...	17000264-0	1
Hepart	Antioxidants NAT complex ...	17000265	1
Hepart	Rhodiola (H1064)	17000278	1
Hepart	Rhodiola (H1064)	17000278/0	1
Hepart	Rhodiola (H1064)	17000278/2	1
Hepart	Rhodiola (H1064)	17000278/4	3
Hepart	Rhodiola (H1064)	17000278-0	1
Hepart	Rhodiola (H1064)	17000278-1	2
Hepart	Rhodiola (H1064)	17000278-2	1
Hepart	Vitamin complex (H1100)	17000880	1

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Supplier	Substance	Batch	Spectra
Hepart	Vitamin complex (H1100)	17000880/0	2
Hepart	Vitamin complex (H1100)	17000880-0	1
Hepart	Vitamin B1 (H1101)	17000914	1
Hepart	Vitamin B1 (H1101)	17001075/0	1
Hepart	Vitamin B1 (H1101)	17001075-0	2
Hepart	Vitamin complex (H1100)	17001654	1
Hepart	Vitamin complex (H1100)	17001654/0	2
Hepart	Vitamin complex (H1100)	17001750	1
Hepart	Vitamin complex (H1100)	17001750/0	2
Hepart	Vitamin complex (H1100)	17001751	1
Hepart	Vitamin complex (H1100)	17001751/0	2
Hepart	Antioxidants NAT complex ...	17001754	1
Hepart	Antioxidants NAT complex ...	17001755/0	2
Hepart	Antioxidants NAT complex ...	17001756/0	1
Hepart	OPC Proanthocyanidins (Pi...	17001805	2
Hepart	OPC Proanthocyanidins (Pi...	17001805/0	1
Hepart	OPC Proanthocyanidins (Pi...	17001805/1	2
Hepart	OPC Proanthocyanidins (Pi...	17001805/2	2
Hepart	OPC Proanthocyanidins (Pi...	17001805/3	1
Hepart	OPC Proanthocyanidins (Pi...	17001805/4	1
Hepart	ginkgo extract (H1024)	17001832	1
Hepart	ginkgo extract (H1024)	17001832/0	2
Hepart	Bioflavonoid complex (H1006)	1700257/1	2
Hepart	ginkgo extract (H1024)	18001110	1
Hepart	ginkgo extract (H1024)	18001110/0	5
Hepart	Antioxidants NAT complex ...	18001181/0	1
Hepart	Antioxidants NAT complex ...	18001182	1
Hepart	ginkgo extract (H1024)	18001386/1	2
Hepart	ginkgo extract (H1024)	18001386/2	1
Hepart	Calcium L-(+) -lactate co...	18001413	1
Hepart	Calcium L-(+) -lactate co...	18001414/0	1
Hepart	Calcium L-(+) -lactate co...	18001415/0	1
Hepart	Calcium L-(+) -lactate co...	18001417/0	1
Hepart	Calcium L-(+) -lactate co...	18001418/0	1
Hepart	Antioxidants NAT complex ...	18001814/0	1
Hepart	Antioxidants NAT complex ...	18001816/0	1
Hepart	Antioxidants NAT complex ...	18001817/0	2
Hepart	Antioxidants NAT complex ...	18001818/0	1
Hepart	Vitamin B1 (H1101)	19000216/1	1
Hepart	OPC Proanthocyanidins (Pi...	19000258	1
Hepart	OPC Proanthocyanidins (Pi...	19000258/1	2
Hepart	Vitamin complex (H1100)	19000364/0	3
Hepart	Antioxidants NAT complex ...	19000420/0	1
Hepart	Vitamin complex (H1100)	19000433/0	2
Hepart	Vitamin complex (H1100)	19000544/0	1
Hepart	Antioxidants NAT complex ...	19000603	2
Hepart	Vitamin B1 (H1101)	19000685/0	1
Hepart	Vitamin B1 (H1101)	19000685/1	1
Hepart	Vitamin complex (H1100)	19001023/0	2
Hepart	Vitamin complex (H1100)	19001581	1
Hepart	Vitamin complex (H1100)	19001581/0	1
Hepart	Calcium L-(+) -lactate co...	19001638/0	1
Hepart	Calcium L-(+) -lactate co...	19001639/0	1
Hepart	Calcium L-(+) -lactate co...	19001640/0	1
Hepart	Calcium L-(+) -lactate co...	19001641	1
Hepart	Calcium L-(+) -lactate co...	19001641/0	1
Hepart	ginkgo extract (H1024)	19002623	2
Hepart	ginkgo extract (H1024)	19002623/0	5
Hepart	ginkgo extract (H1024)	19002623/1	1
Hepart	ginkgo extract (H1024)	19002623/2	1

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Supplier	Substance	Batch	Spectra
Hepart	Vitamin complex (H1100)	20000144	1
Hepart	Vitamin complex (H1100)	20000144/0	1
Hepart	OPC Proanthocyanidins (Pi...	20000179/0	1
Hepart	Antioxidants NAT complex ...	20000225/0	1
Hepart	Antioxidants NAT complex ...	20000805/0	2
Hepart	Vitamin complex (H1100)	20000835/0	1
Hepart	Vitamin complex (H1100)	20000836/0	1
Hepart	Vitamin B1 (H1101)	20001639	1
Hepart	Vitamin B1 (H1101)	20001639/0	3
Hepart	Vitamin complex (H1100)	20001890/0	1
Hepart	Vitamin complex (H1100)	20001899/0	2
Hepart	Antioxidants NAT complex ...	20002055/0	1
Hepart	Glutathione (H1020)	20002265	1
Hepart	Glutathione (H1020)	20002265/0	2
Hepart	Glutathione (H1020)	20002265/1	1
Hepart	Bioflavonoid complex (H1006)	20002413	1
Hepart	Bioflavonoid complex (H1006)	20002413/0	3
Hepart	Bioflavonoid complex (H1006)	20002413/1	6
Hepart	Vitamin B1 (H1101)	20002435/0	1
Hepart	OPC Proanthocyanidins (Pi...	20002632	2
Hepart	OPC Proanthocyanidins (Pi...	20002632/4	1
Hepart	Antioxidants NAT complex ...	21000112/0	2
Hepart	Calcium L-(+) -lactate co...	21000181	1
Hepart	Calcium L-(+) -lactate co...	21000181/0	1
Hepart	Calcium L-(+) -lactate co...	21000182/0	1
Hepart	Calcium L-(+) -lactate co...	21000183	1
Hepart	Calcium L-(+) -lactate co...	21000183/0	2
Hepart	Isoflavone (H1025)	21000565	1
Hepart	Isoflavone (H1025)	21000565/1	2
Hepart	Vitamin complex (H1100)	21001518	1
Hepart	Antioxidants NAT complex ...	21001652	1
Hepart	Antioxidants NAT complex ...	21001652/0	2
Hepart	Antioxidants NAT complex ...	21001747	1
Hepart	Antioxidants NAT complex ...	21001747/0	1
Hepart	Calcium L-(+) -lactate co...	21002012	1
Hepart	Calcium L-(+) -lactate co...	21002012/0	1
Hepart	Calcium L-(+) -lactate co...	21002013/0	1
Hepart	Calcium L-(+) -lactate co...	21002014	1
Hepart	Calcium L-(+) -lactate co...	21002014/0	1
Hepart	Calcium L-(+) -lactate co...	21002016	1
Hepart	Vitamin complex (H1100)	21002294/0	1
Hepart	Vitamin complex (H1100)	21002821/0	1
Hepart	Vitamin complex (H1100)	21002978	1
Hepart	Vitamin complex (H1100)	21002980	1
Hepart	Antioxidants NAT complex ...	21003089/0	1
Hepart	Vitamin complex (H1100)	22001108/0	1
Phönix	Antioxidants NAT complex ...	16000376	1
Purren Apotheke	Glutathione (H1020)	1254955501	1
Purren Apotheke	Isoflavone (H1025)	1314955701	1
Unisan 02.04.2016	Bioflavonoid complex (H1006)	14001675/2	1
Unisan 02.04.2016	Isoflavone (H1025)	15000205/1	1
Unisan 02.04.2016	Antioxidants NAT complex ...	15000874/0	2
Unisan 2.10.2015	Bioflavonoid complex (H1006)	14001675/1	1
Unisan 2.10.2015	Isoflavone (H1025)	15000205/0	3
Unisan Gmbh, 78465 K...	Antioxidants NAT complex ...	52201	1
Unisan Gmbh, 78465 K...	Calcium L-(+) -lactate co...	55401	1
Unisan Gmbh, 78465 K...	Antioxidants NAT complex ...	67301	1
Unisan/Hepart AG	Isoflavone (H1025)	38801	1
Unisan/Hepart AG	Vitamin complex (H1100)	48301	1
Unisan/Hepart AG	Vitamin complex (H1100)	49201	1

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Supplier	Substance	Batch	Spectra
Unisan/Hepart AG	Vitamin B1 (H1101)	53301	1
Unisan/Hepart AG	Calcium L-(+) -lactate co...	8901	1
Unisan	Antioxidants NAT complex ...		3
Unisan	Vitamin complex (H1100)	1014009901	1
Unisan	Vitamin complex (H1100)	1014025401	1
Unisan	Antioxidants NAT complex ...	1034030904	1
Unisan	Antioxidants NAT complex ...	11001	1
Unisan	Calcium L-(+) -lactate co...	1105008901	1
Unisan	Garcinia cambogia (H1017)	1221007401	1
Unisan	Glutathione (H1020)	1251019703	1
Unisan	Glutathione (H1020)	1254025703	1
Unisan	Bioflavonoid complex (H1006)	1281683901	1
Unisan	Bioflavonoid complex (H1006)	1284019001	1
Unisan	Bioflavonoid complex (H1006)	1284042501	1
Unisan	Bioflavonoid complex (H1006)	1284648802	1
UNISAN	Antioxidants NAT complex ...	14000042	1
Unisan	Antioxidants NAT complex ...	14000044	1
Unisan	Calcium L-(+) -lactate co...	14000108	1
Unisan	Calcium L-(+) -lactate co...	14000110	1
UNISAN	Calcium L-(+) -lactate co...	14000110	1
Unisan	Antioxidants NAT complex ...	1400042	1
Unisan	Antioxidants NAT complex ...	14000961	1
UNISAN	Antioxidants NAT complex ...	14000961	1
Unisan	Antioxidants NAT complex ...	14000963	2
Unisan	Vitamin B1 (H1101)	14001112/0	1
Unisan	Vitamin complex (H1100)	14001589	1
Unisan	Vitamin complex (H1100)	1400159/0	1
Unisan	Vitamin complex (H1100)	14001590/0	1
Unisan	Vitamin complex (H1100)	14001590/1	1
Unisan	Bioflavonoid complex (H1006)	14001675	2
Unisan	Bioflavonoid complex (H1006)	14001675/4	1
Unisan	Antioxidants NAT complex ...	14001847/0	2
Unisan	Antioxidants NAT complex ...	14001847/1	1
Unisan	Antioxidants NAT complex ...	14001848/0	1
Unisan	Antioxidants NAT complex ...	14001851/0	1
Unisan	Calcium L-(+) -lactate co...	14001934/0	1
Unisan	Calcium L-(+) -lactate co...	14001938/0	1
Unisan	Isoflavone (H1025)	15000205	1
Unisan	Isoflavone (H1025)	15000205/3	1
unisan	Antioxidants NAT complex ...	15000877	2
Unisan	Antioxidants NAT complex ...	15000877/0	1
Unisan	Antioxidants NAT complex ...	15000880	1
Unisan	ginkgo extract (H1024)	15001039/1	1
Unisan	Rhodiola (H1064)	15001045/8	1
Unisan	Vitamin complex (H1100)	15001275/0	1
Unisan	Vitamin complex (H1100)	15001276/0	1
Unisan	Vitamin complex (H1100)	15001277/0	1
Unisan	Vitamin B1 (H1101)	15001620/0	1
Unisan	Vitamin B1 (H1101)	15001622	1
Unisan	Vitamin B1 (H1101)	15001622/0	1
Unisan	Calcium L-(+) -lactate co...	15001666	1
Unisan	Calcium L-(+) -lactate co...	15001666/0	1
Unisan	Calcium L-(+) -lactate co...	15001667	2
Unisan	Calcium L-(+) -lactate co...	15001672	1
Unisan	Calcium L-(+) -lactate co...	15001672/0	1
Unisan	Antioxidants NAT complex ...	16000376	1
Unisan	Antioxidants NAT complex ...	16000378	1
Unisan	OPC Proanthocyanidins (Pi...	16000637	1
Unisan	Vitamin B1 (H1101)	16000698	1
Unisan	Glutathione (H1020)	16000938	1

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Supplier	Substance	Batch	Spectra
Unisan	Vitamin complex (H1100)	16000958/0	2
Unisan	Vitamin complex (H1100)	16000962	2
Unisan	Antioxidants NAT complex ...	16000966	1
Unisan	Antioxidants NAT complex ...	16000966/0	2
Unisan	Antioxidants NAT complex ...	16000968/0	1
Unisan	Antioxidants NAT complex ...	16000970	1
Unisan	Garcinia cambogia (H1017)	16001252/0	1
Unisan	OPC Proanthocyanidins (Pi...	16001439	2
Unisan	OPC Proanthocyanidins (Pi...	16001439/0	1
Unisan	Vitamin B1 (H1101)	1622977301	1
Unisan	Calcium L-(+) -lactate co...	17000201	1
Unisan	Bioflavonoid complex (H1006)	17000256	1
Unisan	Antioxidants NAT complex ...	17000260	2
Unisan	Antioxidants NAT complex ...	17000264	1
Unisan	Garcinia cambogia (H1017)	17000873	1
Unisan	Vitamin B1 (H1101)	17001075	1
Unisan	Vitamin complex (H1100)	17001750	1
Unisan	OPC Proanthocyanidins (Pi...	18401	1
Unisan	Antioxidants NAT complex ...	1851	1
Unisan	Antioxidants NAT complex ...	19901	2
Unisan	Vitamin complex (H1100)	25101	1
Unisan	Vitamin complex (H1100)	25201	1
Unisan	Glutathione (H1020)	25703	1
Unisan	Vitamin B1 (H1101)	30202	2
Unisan	Antioxidants NAT complex ...	30903	3
Unisan	Antioxidants NAT complex ...	30904	1
Unisan	Glutathione (H1020)	40201	3
Unisan	Bioflavonoid complex (H1006)	42501	1
Unisan	Vitamin complex (H1100)	49202	1
Unisan	Vitamin complex (H1100)	49301	2
unisan	Vitamin complex (H1100)	49302	1
Unisan	Vitamin complex (H1100)	49302	2
Unisan	Antioxidants NAT complex ...	51901	2
Unisan	Antioxidants NAT complex ...	51902	1
Unisan	Antioxidants NAT complex ...	52001	2
unisan	Calcium L-(+) -lactate co...	55001	1
Unisan	Calcium L-(+) -lactate co...	55001	1
Unisan	Calcium L-(+) -lactate co...	55101	3
Unisan	Calcium L-(+) -lactate co...	55301	1
Unisan	Calcium L-(+) -lactate co...	55401	1
Unisan	Calcium L-(+) -lactate co...	55501	1
Unisan	Calcium L-(+) -lactate co...	55601	2
Unisan	Garcinia cambogia (H1017)	56601	1
Unisan	Isoflavone (H1025)	56701	2
Unisan	Antioxidants NAT complex ...	67201	4
Unisan	Antioxidants NAT complex ...	67501	1
Unisan	Antioxidants NAT complex ...	67601	2
Unisan	Bioflavonoid complex (H1006)	68101	1
Unisan	Antioxidants NAT complex ...	68201	4
Unisan	OPC Proanthocyanidins (Pi...	68301	4
Unisan	OPC Proanthocyanidins (Pi...	70401	2
UNISAN	OPC Proanthocyanidins (Pi...	70401	1
Unisan	Vitamin complex (H1100)	74101	1
Unisan	Glutathione (H1020)	74901	3
UNISAN	Glutathione (H1020)	74901	1
UNISAN	Vitamin B1 (H1101)	75001	1
Unisan	Vitamin complex (H1100)	77001	2
Unisan	Vitamin complex (H1100)	77201	3
Unisan	Calcium L-(+) -lactate co...	8901	5
Unisan	Vitamin complex (H1100)	904006	1

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Supplier	Substance	Batch	Spectra
Unisan	Calcium L-(+) -lactate co...	956001	1
Unisan	Vitamin B1 (H1101)	977301	2
Unisan	Vitamin complex (H1100)	H110031	2

- 2292 spectra from 24 *Apo-Ident* customers from a total of 1087 batches from a further 52 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *HCK classification II* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *HCK classification II* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	7660	0	20 816
Type B	0	7732	57	15 018
Type C	0	639	39	2292

The substance/substance group *HCK classification II* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9273 %)	100.0000 % (> 99.9217 %)
Type B	100.0000 % (> 99.8620 %)	99.2682 % (> 99.2297 %)
Type C	100.0000 % (> 98.8214 %)	94.2478 % (> 93.8053 %)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra ([Rule of Three](#) [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the [Mahalanobis distance](#) to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80311	80311	0.00	37.77
80313	80313	0.00	32.69
80315	80315	0.00	39.51

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Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80316	80316	0.00	33.77
80317	80317	0.00	40.84
80318	80318	0.00	34.72
80322	80322	0.00	40.01
80323	80323	0.00	43.80
80327	80327	0.00	44.44
80329	80329	0.00	34.86
80337	80337	0.00	38.64
80342	80342	0.00	23.12
80345	80345	0.00	42.55
80346	80346	0.00	47.67
80349	80349	0.00	45.73
80352	80352	0.00	13.28
80380	80380	0.00	18.17
80390	80390	0.00	31.62
80391	80391	0.00	30.53
80392	80392	0.00	33.93
80398	80398	0.00	18.99
80404	80404	0.00	32.81
80405	80405	0.00	33.83
80411	80411	0.00	41.81
80419	80419	0.00	34.53
80422	80422	0.00	42.32
80430	80430	0.00	24.17
80431	80431	0.00	43.09
80432	80432	0.00	40.78
80469	80469	0.00	32.68
80473	80473	0.00	31.66
80476	80476	0.00	27.34
80477	80477	0.00	44.56
80479	80479	0.00	38.56
80485	80485	0.00	42.97
80486	80486	0.00	46.29
80487	80487	0.00	45.11
80490	80490	0.00	20.09
80492	80492	0.00	27.78
80504	80504	0.00	32.43
80505	80505	0.00	38.02
80506	80506	0.00	33.84
80507	80507	0.00	38.54
80508	80508	0.00	33.85
80509	80509	0.00	35.25
80521	80521	0.00	42.74
80522	80522	0.00	38.60
80525	80525	0.00	45.15
80526	80526	0.00	43.10
80527	80527	0.00	44.44
80529	80529	0.00	35.80
80566	80566	0.00	27.52
80583	80583	0.00	21.31
80607	80607	0.00	31.89

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Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80609	80609	0.00	31.63
80613	80613	0.00	32.22
80616	80616	0.00	32.96
80618	80618	0.00	34.70
80619	80619	0.00	35.50
80621	80621	0.00	31.63
80624	80624	0.00	31.70
80632	80632	0.00	30.74
80636	80636	0.00	20.19
80637	80637	0.00	46.26
80638	80638	0.00	47.41
80640	80640	0.00	47.02
80642	80642	0.00	45.72
80643	80643	0.00	45.92
80646	80646	0.00	45.76
80647	80647	0.00	47.19
80648	80648	0.00	45.56
80656	80656	0.00	30.70
80657	80657	0.00	30.03
80658	80658	0.00	29.47
80660	80660	0.00	23.59
80672	80672	0.00	31.76
80707	80707	0.00	49.22
80709	80709	0.00	46.56
80711	80711	0.00	44.96
80712	80712	0.00	46.55
80715	80715	0.00	45.11
80719	80719	0.00	40.70
80722	80722	0.00	45.27
80724	80724	0.00	45.84
80729	80729	0.00	47.65
80732	80732	0.00	45.27
80734	80734	0.00	46.01
80740	80740	0.00	44.64
80741	80741	0.00	47.52
80768	80768	0.00	38.46
80783	80783	0.00	35.92
80815	80815	0.00	39.01
80827	80827	0.00	47.25
80853	80853	0.00	28.76
80864	80864	0.00	18.19
80878	80878	0.00	34.62
80946	80946	0.00	25.14
80953	80953	0.00	39.32
80956	80956	0.00	16.94
80980	80980	0.00	43.37
80986	80986	0.00	28.14
80987	80987	0.00	27.14
80990	80990	0.00	42.12
81001	81001	0.00	18.63
81005	81005	0.00	31.61

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Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
81016	81016	0.00	41.19
81041	81041	0.00	29.73
81042	81042	0.00	29.09
81133	81133	0.00	17.94
81136	81136	0.00	30.77
81150	81150	0.00	29.03
81151	81151	0.00	77.22
81170	81170	0.00	75.79
81171	81171	0.00	43.50
81172	81172	0.00	50.75
81183	81183	0.00	42.27
81202	81202	0.00	33.21
81215	81215	0.00	20.84
81251	81251	0.00	31.74
81271	81271	0.00	43.42
81315	81315	0.00	26.12
81316	81316	0.00	22.39
81329	81329	0.00	36.03
81334	81334	0.00	66.25
81338	81338	0.00	42.88
81345	81345	0.00	35.69
81357	81357	0.00	30.35
81375	81375	0.00	33.00
81378	81378	0.00	25.28
81388	81388	0.00	33.09
81390	81390	0.00	16.80
81399	81399	0.00	40.14
81412	81412	0.00	21.14
81415	81415	0.00	41.78
81435	81435	0.00	26.30
81439	81439	0.00	34.37
81449	81449	0.00	25.06
81450	81450	0.00	21.23
81451	81451	0.00	15.52
81460	81460	0.00	23.09
81461	81461	0.00	28.92
81476	81476	0.00	28.43
81481	81481	0.00	23.62
81482	81482	0.00	37.42
81488	81488	0.00	29.22
81512	81512	0.00	38.00
81529	81529	0.00	24.09
81533	81533	0.00	36.58
81534	81534	0.00	29.24
81535	81535	0.00	35.58
81539	81539	0.00	36.33
81541	81541	0.00	25.68
81555	81555	0.00	31.43
81570	81570	0.00	40.28
81571	81571	0.00	39.51
81572	81572	0.00	39.95

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Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
81576	81576	0.00	38.15

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Hemp protein (H1406)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 81099-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Hemp protein (H1406)

Special notes

When selecting the *Hemp protein (H1406)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Hemp protein (H1406)	2	1	0

Second-stage model

For differentiation of the substance/substance group *Hemp protein (H1406)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Hemp protein (H1406)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Antibiosis forte complex (H1115)	31.73	—
PET skin and hair (H1504)	39.84	—
Aminomix NAC (H1002)	42.47	—
Amino V complex (H1400)	42.59	—
Coenzyme Q10 (H1013)	45.66	—
a-Lipoic acid (H1000)	51.97	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Hemp protein (H1406)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Hemp protein (H1406)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Hemp protein (H1406)	18001330	81099	40	from supplier
Hepart	Hemp protein (H1406)	18001679	81134	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 80 spectra of 2 reference samples from the substance/substance group *Hemp protein (H1406)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 2 different batches.

- 28 396 spectra from a total of 576 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 40 spectra of 1 reference samples from the substance/substance group *Hemp protein (H1406)*.
- Among them are spectra of independent samples from 1 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Hemp protein (H1406)	20000392	81256	40

- 22 959 spectra from a total of 503 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *Hemp protein (H1406)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Hemp protein (H1406)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Hemp protein (H1406)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	80	0	28 396
Type B	0	40	0	22 959
Type C	0	0	0	2970

The substance/substance group *Hemp protein (H1406)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9284 %)	100.0000 % (> 92.5000 %)
Type B	100.0000 % (> 99.8691 %)	100.0000 % (> 85.0000 %)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
81099	81099	0.00	31.73
81134	81134	0.00	33.71

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Histamine block complex (H1117)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80896-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Histamine block complex (H1117)

Special notes

When selecting the *Histamine block complex (H1117)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Histamine block complex (H1117)	1	1	0

Second-stage model

For differentiation of the substance/substance group *Histamine block complex (H1117)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Histamine block complex (H1117)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Garcinia cambogia (H1017)	19.49	—
Pathogene complex (H1803)	21.02	—
Copper (H1032)	22.09	—
Chaga (H1011)	30.51	—
Antibiosis mite complex (H1113)	30.73	—
PET basis (H1503)	35.61	—
ginkgo extract (H1024)	36.85	—
Antioxidants NAT complex (H1004)	37.90	—
PET joints (H1501)	40.00	—
Trace elements SE complex (H1082)	41.44	—
Flavour orange (H1405)	46.30	—
Iron (H1015)	46.96	—
Walnut leaf (H1114)	47.37	—
Magnesium (H1060)	50.10	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Histamine block complex (H1117)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Histamine block complex (H1117)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Histamine block complex (...)	16001078	80896	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 40 spectra of 1 reference samples from the substance/substance group *Histamine block complex (H1117)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 1 different batches.
- 28 436 spectra from a total of 577 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 40 spectra of 1 reference samples from the substance/substance group *Histamine block complex (H1117)*.
- Among them are spectra of independent samples from 1 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Histamine block complex (...)	16001079	80897	40

- 22 959 spectra from a total of 503 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *Histamine block complex (H1117)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Histamine block complex (H1117)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Histamine block complex (H1117)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	40	0	28 436
Type B	0	40	0	22 959
Type C	0	0	0	2970

The substance/substance group *Histamine block complex (H1117)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9295 %)	100.0000 % (> 85.0000 %)
Type B	100.0000 % (> 99.8691 %)	100.0000 % (> 85.0000 %)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80896	80896	0.00	21.02

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Iron (H1015) / Copper (H1032)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80341-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Iron (H1015) / Copper (H1032); Copper (H1032); Iron (H1015)

Special notes

When selecting the *Iron (H1015) / Copper (H1032)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Iron (H1015) / Copper (H1032)	14	11	50

Second-stage model

For differentiation of the substance/substance group *Iron (H1015) / Copper (H1032)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Iron (H1015) / Copper (H1032)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Argentum (H1116)	10.01	—
Trace elements SE complex (H1082)	19.35	—
Chaga (H1011)	37.47	—
Magnesium (H1060)	46.45	—
Garcinia cambogia (H1017)	46.61	—
Potassium (H1030)	49.50	—
Walnut leaf (H1114)	62.78	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Iron (H1015) / Copper (H1032)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Iron (H1015) / Copper (H1032)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Copper (H1032)	130415	80341	40	from supplier
Hepart	Copper (H1032)	15000211	80536	60	from supplier
Hepart	Copper (H1032)	19001347	81222	40	from supplier
Hepart	Copper (H1032)	20002434	81297	40	from supplier
Hepart	Copper (H1032)	21000943	81356	50	from supplier
Hepart	Iron (H1015)	14000285	80510	60	from supplier
Hepart	Iron (H1015)	040901	80511	60	from supplier
Hepart	Iron (H1015)	040901	80568	60	from supplier
Hepart	Iron (H1015)	14000285	80569	60	from supplier
Hepart	Iron (H1015)	15001258	80650	60	from supplier
Hepart	Iron (H1015)	15001259(B1)	80651	60	from supplier
Hepart	Iron (H1015)	15001259	80653	60	from supplier
Hepart	Iron (H1015)	20002186	81305	40	from supplier
Hepart	Iron (H1015)	21000845	81367	50	from supplier
Hepart	Iron (H1015)	23000509	81474	40	from supplier
Hepart	Iron (H1015)	24000872	81540	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 820 spectra of 16 reference samples from the substance/substance group *Iron (H1015) / Copper (H1032)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 14 different batches.
- 27 656 spectra from a total of 564 batches from further 129 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a †. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 560 spectra of 12 reference samples from the substance/substance group *Iron (H1015) / Copper (H1032)*.
- Among them are spectra of independent samples from 11 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Copper (H1032)	15000211/5	80875	40
Hepart	Copper (H1032)	23001418	81495	40
Hepart	Iron (H1015)	15001259(F2)	80649	60
Hepart	Iron (H1015)	15001258(F2)	80652	60
Hepart	Iron (H1015)	15001258(B1)	80654	60
Hepart	Iron (H1015)	17000279	80917	40
Hepart	Iron (H1015)	20000399	81254	40
Hepart	Iron (H1015)	20000089/0	81255	40
Hepart	Iron (H1015)	20002902	81347	40
Hepart	Iron (H1015)	21001399	81381	50
Hepart	Iron (H1015)	21001967	81394	50
Hepart	Iron (H1015)	14000285	80413	40

- 22 439 spectra from a total of 492 batches from further 76 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 128 spectra from 20 *Apo-Ident* customers from 57 batches from the substance/substance group *Iron (H1015) / Copper (H1032)*.
- Among them are spectra of independent samples from 50 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
Caelo	Copper (H1032)	933901	1
Flaigg Ag CH-4147 Ae...	Iron (H1015)	15001259/2	2
HCK	Iron (H1015)	1259	1
HCK	Iron (H1015)	15001258/1	1
HCK	Iron (H1015)	15001258-0	1
HCK	Iron (H1015)	15001258-1	1
HCK	Iron (H1015)	15001259-0	2
Hepart / Unisan	Iron (H1015)	17000279/1	1
Hepart AG, CH-8280 K...	Iron (H1015)	1114998701	1
Hepart ag/Unisan	Iron (H1015)	20000399/0	1
Hepart ag/Unisan	Iron (H1015)	20002186	1
Hepart AG	Iron (H1015)	1114040901	2
Hepart AG	Iron (H1015)	1114998701	1
Hepart AG	Copper (H1032)	13041501	1
Hepart AG	Copper (H1032)	130415-K1	1
Hepart AG	Copper (H1032)	15000211/4	2
Hepart AG	Iron (H1015)	15001258/0	1
Hepart AG	Copper (H1032)	1544007901	1
Hepart AG	Copper (H1032)	1544046401	1
Hepart AG	Iron (H1015)	40901	3
Hepart AG	Copper (H1032)	46401	1
Hepart/Unisan	Iron (H1015)	15001258/1	1
Hepart/Unisan	Iron (H1015)	20000399/0	1
Hepart	Copper (H1032)		1
Hepart	Copper (H1032)	15000211	1
Hepart	Copper (H1032)	15000211/5	1
Hepart	Copper (H1032)	15000211/8	2
Hepart	Copper (H1032)	150002117	1
Hepart	Iron (H1015)	15001258	3
Hepart	Iron (H1015)	15001258-4	1
Hepart	Iron (H1015)	15001259/1	4
Hepart	Iron (H1015)	15001259/2	3
Hepart	Iron (H1015)	17000279	1
Hepart	Iron (H1015)	17000279/0	3
Hepart	Iron (H1015)	17000279/1	2
Hepart	Iron (H1015)	17000279/2	1
Hepart	Copper (H1032)	19001221/0	1
Hepart	Copper (H1032)	19001347	1
Hepart	Copper (H1032)	19001347/0	6
Hepart	Copper (H1032)	19001347/1	2
Hepart	Copper (H1032)	19001347/2	1
Hepart	Iron (H1015)	20000399/0	1
Hepart	Iron (H1015)	20002186	1
Hepart	Iron (H1015)	20002186/0	3
Hepart	Iron (H1015)	20002186/1	1
Hepart	Iron (H1015)	20002902	1
Hepart	Iron (H1015)	2002186	1
Hepart	Copper (H1032)	21000943/0	2
Hepart	Copper (H1032)	21000943/3	1
Hepart	Iron (H1015)	21001399/0	1

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Supplier	Substance	Batch	Spectra
Hepart	Iron (H1015)	21001967/0	2
Unisan 02.04.2016	Iron (H1015)	15001258/0	1
Unisan 11.08.2105	Iron (H1015)	14000285/2	1
Unisan 2.10.2015	Iron (H1015)	14000285/3	2
Unisan/Hepart AG	Copper (H1032)	13041501	1
Unisan/Hepart AG	Iron (H1015)	40901	1
Unisan/Hepart	Iron (H1015)	15001259/0	1
Unisan	Iron (H1015)	1114040901	2
Unisan	Iron (H1015)	1114603206	1
Unisan	Iron (H1015)	1114998701	3
Unisan	Copper (H1032)	13041501	5
Unisan	Iron (H1015)	14000285	1
UNISAN	Iron (H1015)	14000285	1
Unisan	Iron (H1015)	14000285/1	2
Unisan	Iron (H1015)	14000285/5	1
Unisan	Copper (H1032)	15000211	1
Unisan	Copper (H1032)	15000211/0	1
Unisan	Iron (H1015)	15001258/0	1
Unisan	Iron (H1015)	15001258/2	2
Unisan	Iron (H1015)	15001259	2
Unisan	Copper (H1032)	1542933901	1
Unisan	Iron (H1015)	40901	9
Unisan	Copper (H1032)	46401	2
Unisan	Copper (H1032)	7901	1
Unisan	Copper (H1032)	933901	1
Unisan	Iron (H1015)	998701	6

- 2842 spectra from 26 *Apo-Ident* customers from a total of 1403 batches from a further 61 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Iron (H1015) / Copper (H1032)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Iron (H1015) / Copper (H1032)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	820	0	27 656
Type B	0	560	0	22 439
Type C	0	128	0	2842

The substance/substance group *Iron (H1015) / Copper (H1032)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9274 %)	100.0000 % (> 99.2683 %)
Type B	100.0000 % (> 99.8641 %)	100.0000 % (> 98.9286 %)
Type C	100.0000 % (> 98.8237 %)	100.0000 % (> 95.3125 %)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several

new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80341	80341	0.00	26.93
80510	80510	0.00	19.89
80511	80511	0.00	20.74
80536	80536	0.00	38.58
80568	80568	0.00	18.20
80569	80569	0.00	20.21
80650	80650	0.00	12.46
80651	80651	0.00	12.00
80653	80653	0.00	12.23
81222	81222	0.00	24.46
81297	81297	0.00	21.35
81305	81305	0.00	10.01
81356	81356	0.00	26.81
81367	81367	0.00	17.46
81474	81474	0.00	103.65
81540	81540	0.00	139.32

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Isoleucine (L-) (H1045)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80134-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Isoleucine (L-) (H1045)

Special notes

When selecting the *Isoleucine (L-) (H1045)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Isoleucine (L-) (H1045)	5	2	12

Second-stage model

For differentiation of the substance/substance group *Isoleucine (L-) (H1045)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Isoleucine (L-) (H1045)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Leucine (L-) (H1046)	18.89	—
Valine (L-) (H1056)	21.47	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Isoleucine (L-) (H1045)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Isoleucine (L-) (H1045)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Isoleucine (L-) (H1045)	066301	80368	40	from supplier
Hepart	Isoleucine (L-) (H1045)	14001772	80498	60	from supplier
Hepart	Isoleucine (L-) (H1045)	15001641	80678	60	from supplier
Hepart	Isoleucine (L-) (H1045)	15001640	80679	60	from supplier
Hepart	Isoleucine (L-) (H1045)	23000368	81485	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 260 spectra of 5 reference samples from the substance/substance group *Isoleucine (L-) (H1045)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 5 different batches.
- 28 216 spectra from a total of 573 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the

substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 80 spectra of 2 reference samples from the substance/substance group *Isoleucine (L-) (H1045)*.
- Among them are spectra of independent samples from 2 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Isoleucine (L-) (H1045)	17000900	80909	40
Hepart	Isoleucine (L-) (H1045)	18001412	81111	40

- 22919 spectra from a total of 502 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 24 spectra from 9 *Apo-Ident* customers from 14 batches from the substance/substance group *Isoleucine (L-) (H1045)*.
- Among them are spectra of independent samples from 12 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
Fritz Schiele	Isoleucine (L-) (H1045)	1805027701	1
HCK	Isoleucine (L-) (H1045)	14001772/3	1
HCK	Isoleucine (L-) (H1045)	15001641	2
Hepart AG, CH-8280 K...	Isoleucine (L-) (H1045)	1804968701	1
Hepart AG, CH-8280 K...	Isoleucine (L-) (H1045)	66301	1
Hepart AG	Isoleucine (L-) (H1045)	15001640/2	1
Hepart AG	Isoleucine (L-) (H1045)	15001641	1
Hepart AG	Isoleucine (L-) (H1045)	1805027701	2
Hepart AG	Isoleucine (L-) (H1045)	66301	1
Hepart	Isoleucine (L-) (H1045)	150001640-2	1
Hepart	Isoleucine (L-) (H1045)	15001640-2	2
Hepart	Isoleucine (L-) (H1045)	15001641-0	2
Hepart	Isoleucine (L-) (H1045)	17000900	1

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Supplier	Substance	Batch	Spectra
Hepart	Isoleucine (L-) (H1045)	17000900/0	2
Unisan	Isoleucine (L-) (H1045)	15001640	1
Unisan	Isoleucine (L-) (H1045)	1805968701	1
Unisan	Isoleucine (L-) (H1045)	27701	1
Unisan	Isoleucine (L-) (H1045)	66301	2

- 2946 spectra from 26 *Apo-Ident* customers from a total of 1446 batches from a further 62 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Isoleucine (L-) (H1045)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Isoleucine (L-) (H1045)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	260	0	28 216
Type B	0	80	0	22 919
Type C	0	18	6	2946

The substance/substance group *Isoleucine (L-) (H1045)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9276 %)	100.0000 % (> 97.6923 %)
Type B	100.0000 % (> 99.8664 %)	100.0000 % (> 92.5000 %)
Type C	100.0000 % (> 98.8364 %)	75.0000 % (> 62.5000 %)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra ([Rule of Three](#) [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the [Mahalanobis distance](#) to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80368	80368	0.00	32.37
80498	80498	0.00	32.56
80678	80678	0.00	32.76
80679	80679	0.00	28.99
81485	81485	0.00	43.72

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Konjak Glucomannan (H1530)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 10006305-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Konjak Glucomannan (H1530)

Special notes

When selecting the *Konjak Glucomannan (H1530)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Konjak Glucomannan (H1530)	1	0	0

Second-stage model

For differentiation of the substance/substance group *Konjak Glucomannan (H1530)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Konjak Glucomannan (H1530)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Ginseng (H1018)	10.16	—
Saffron style (H1434)	19.46	—
Lycopene (H1058)	19.98	—
Vitamins BAG complex (H1091)	21.59	—
Selenium yeast (H1068)	25.13	—
Gentian extract (H1438)	25.81	—
Zinc (H1110)	27.67	—
Vitamin B12 (H1102)	28.58	—
Selenium (H1067)	29.30	—
Guar (H1023)	32.16	—
Psyllium husks (H1527)	32.72	—
Marshmallow extract (H1439)	32.81	—
Arginine (L-) (H1036)	33.46	—
Vitamin B1 (H1101)	34.14	—
Ashwagandha (H1132)	35.06	—
Vitamin D3 (H1105)	36.15	—
Silicium (H1070)	36.48	—
Orthovimin Neutral Complex (H1404)	37.49	—
Coenzyme Q10 (H1013)	38.40	—
Artichoke extract (H1440)	38.56	—
Rhodiola (H1064)	39.36	—
Boron (H1005)	40.36	—
Biotin (H1007)	41.72	—
Artemisia annua extract (H1118)	42.72	—
Baobab (H1410)	42.86	—
Calcium L-(+)-lactate complex (H1008)	44.16	—
Chromium (H1012)	44.17	—
OPC Proanthocyanidins (Pine Bark) (...)	45.02	—
Magnesium (H1060)	45.27	—
Isoflavone (H1025)	45.86	—
Vitamin K2 (75µg Mono) (H1108)	46.88	—
Leaky gut complex (H1802)	50.25	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Konjak Glucomannan (H1530)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Konjak Glucomannan (H1530)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Konjak Glucomannan (H1530)	23001630	81501	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 40 spectra of 1 reference samples from the substance/substance group *Konjak Glucomannan (H1530)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 1 different batches.
- 28 436 spectra from a total of 577 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a †. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 0 spectra of 0 reference samples from the substance/substance group *Konjak Glucomannan (H1530)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.
- 22 999 spectra from a total of 504 batches from further 78 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *Konjak Glucomannan (H1530)*.

- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Konjak Glucomannan (H1530)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Konjak Glucomannan (H1530)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	40	0	28 436
Type B	0	0	0	22 999
Type C	0	0	0	2970

The substance/substance group *Konjak Glucomannan (H1530)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9295 %)	100.0000 % (> 85.0000 %)
Type B	100.0000 % (> 99.8687 %)	n/a (n/a)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra ([Rule of Three](#) [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the [Mahalanobis distance](#) to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
81501	81501	0.00	10.16

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical

variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Leaky gut complex (H1802)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 81039-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Leaky gut complex (H1802)

Special notes

When selecting the *Leaky gut complex (H1802)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Leaky gut complex (H1802)	3	1	0

Second-stage model

For differentiation of the substance/substance group *Leaky gut complex (H1802)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Leaky gut complex (H1802)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Ginseng (H1018)	10.79	—
Coenzyme Q10 (H1013)	16.47	—
Flavour orange (H1405)	16.80	—
Oat bran beta-glucan (H1529)	17.82	—
Glutathione (H1020)	19.60	—
Vitamin E NAT (H1107)	23.26	—
Aminomix NAC (H1002)	25.57	—
PET coenzyme Q10 (H1505)	27.45	—
Antioxidants NAT complex (H1004)	28.91	—
Ginger extract (H1437)	30.58	—
PET joints (H1501)	31.57	—
Glutamine (L-) (H1043)	35.90	—
Juniper (H1112)	39.07	—
Vitamin B1 (H1101)	39.08	—
Calcium L-(+) -lactate complex (H1008)	39.23	—
Baobab (H1410)	40.23	—
Lutein-Zeaxanthin-Astaxanthin (H1129)	40.70	—
Detox complex (H1111)	40.74	—
Silicium (H1070)	43.24	—
Boron (H1005)	44.63	—
Garcinia cambogia (H1017)	44.76	—
Isoflavone (H1025)	47.12	—
Saffron style (H1434)	47.22	—
Artemisia annua extract (H1118)	47.99	—
Lycopene (H1058)	48.59	—
Vitamin K2 (75µg Mono) (H1108)	48.83	—
Arginine (L-) (H1036)	49.58	—
Orthocolon complex (H1800)	50.17	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Leaky gut complex (H1802)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the

substance/substance group *Leaky gut complex (H1802)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Leaky gut complex (H1802)	18000638	81039	40	from supplier
Hepart	Leaky gut complex (H1802)	20001259/0	81270	40	from supplier
Hepart	Leaky gut complex (H1802)	22000099	81417	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 120 spectra of 3 reference samples from the substance/substance group *Leaky gut complex (H1802)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 3 different batches.
- 28 356 spectra from a total of 575 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 40 spectra of 1 reference samples from the substance/substance group *Leaky gut complex (H1802)*.
- Among them are spectra of independent samples from 1 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Leaky gut complex (H1802)	18000639	81040	40

- 22 959 spectra from a total of 503 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information

provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *Leaky gut complex (H1802)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Leaky gut complex (H1802)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Leaky gut complex (H1802)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	120	0	28 356
Type B	0	40	0	22 959
Type C	0	0	0	2970

The substance/substance group *Leaky gut complex (H1802)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9280 %)	100.0000 % (> 95.0000 %)
Type B	100.0000 % (> 99.8691 %)	100.0000 % (> 85.0000 %)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra ([Rule of Three](#) [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the [Mahalanobis distance](#) to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
81039	81039	0.00	28.91
81270	81270	0.00	18.96
81417	81417	0.00	19.36

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Leucine (L-) (H1046)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80150-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Leucine (L-) (H1046)

Special notes

When selecting the *Leucine (L-) (H1046)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Leucine (L-) (H1046)	4	3	9

Second-stage model

For differentiation of the substance/substance group *Leucine (L-) (H1046)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Leucine (L-) (H1046)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Isoleucine (L-) (H1045)	38.04	—
Valine (L-) (H1056)	45.81	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Leucine (L-) (H1046)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Leucine (L-) (H1046)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Leucine (L-) (H1046)	965101	80333	60	from supplier
Hepart	Leucine (L-) (H1046)	074301	80410	40	from supplier
Hepart	Leucine (L-) (H1046)	21001145	81362	50	from supplier
Hepart	Leucine (L-) (H1046)	22001194	81428	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 190 spectra of 4 reference samples from the substance/substance group *Leucine (L-) (H1046)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 4 different batches.
- 28 286 spectra from a total of 574 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A*

section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 140 spectra of 3 reference samples from the substance/substance group *Leucine (L-) (H1046)*.
- Among them are spectra of independent samples from 3 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Leucine (L-) (H1046)	15000283	80570	60
Hepart	Leucine (L-) (H1046)	18001305	81074	40
Hepart	Leucine (L-) (H1046)	20001576	81286	40

- 22 859 spectra from a total of 501 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 17 spectra from 10 *Apo-Ident* customers from 10 batches from the substance/substance group *Leucine (L-) (H1046)*.
- Among them are spectra of independent samples from 9 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
HCK	Leucine (L-) (H1046)	74301/3	1
HCK	Leucine (L-) (H1046)	965101	1
Hepart AG, CH-8280 K...	Leucine (L-) (H1046)	52601	2
Hepart AG	Leucine (L-) (H1046)	15000283/1	1
Hepart AG	Leucine (L-) (H1046)	18001305/0	2
Hepart AG	Leucine (L-) (H1046)	1809994101	1
Hepart	Leucine (L-) (H1046)	15000283	1
Hepart	Leucine (L-) (H1046)	18001305	1
Purren Apotheke	Leucine (L-) (H1046)	1809965101	1
Unisan/Hepart AG	Leucine (L-) (H1046)	52601	1
Unisan	Leucine (L-) (H1046)	15000283	1
Unisan	Leucine (L-) (H1046)	15000283/0	1
Unisan	Leucine (L-) (H1046)	15000283/1	1
Unisan	Leucine (L-) (H1046)	1809965101	1
Unisan	Leucine (L-) (H1046)	52601	1

- 2953 spectra from 26 *Apo-Ident* customers from a total of 1450 batches from a further 62 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Leucine (L-) (H1046)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Leucine (L-) (H1046)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	190	0	28 286
Type B	0	140	0	22 859
Type C	0	14	3	2953

The substance/substance group *Leucine (L-) (H1046)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9277 %)	100.0000 % (> 96.8421 %)
Type B	100.0000 % (> 99.8652 %)	100.0000 % (> 95.7143 %)
Type C	100.0000 % (> 98.8429 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra ([Rule of Three](#) [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the [Mahalanobis distance](#) to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80333	80333	0.00	43.77
80410	80410	0.00	50.54
81362	81362	0.00	49.74
81428	81428	0.00	57.30

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all

substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Liver kidney complex (H1801)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 81036-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Liver kidney complex (H1801)

Special notes

When selecting the *Liver kidney complex (H1801)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Liver kidney complex (H1801)	1	0	0

Second-stage model

For differentiation of the substance/substance group *Liver kidney complex (H1801)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Liver kidney complex (H1801)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Antibiosis forte complex (H1115)	30.51	—
Taurine (H1084)	74.07	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Liver kidney complex (H1801)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Liver kidney complex (H1801)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Liver kidney complex (H1801)	18000635	81036	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 40 spectra of 1 reference samples from the substance/substance group *Liver kidney complex (H1801)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 1 different batches.
- 28 436 spectra from a total of 577 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with

the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a †. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 0 spectra of 0 reference samples from the substance/substance group *Liver kidney complex (H1801)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.
- 22 999 spectra from a total of 504 batches from further 78 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *Liver kidney complex (H1801)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Liver kidney complex (H1801)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Liver kidney complex (H1801)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	40	0	28 436
Type B	0	0	0	22 999
Type C	0	0	0	2970

The substance/substance group *Liver kidney complex (H1801)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9295 %)	100.0000 % (> 85.0000 %)
Type B	100.0000 % (> 99.8687 %)	n/a (n/a)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
81036	81036	0.00	30.51

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Lupin protein complex (H1510)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 10006135-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Lupin protein complex (H1510)

Special notes

When selecting the *Lupin protein complex (H1510)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Lupin protein complex (H1510)	1	0	0

Second-stage model

For differentiation of the substance/substance group *Lupin protein complex (H1510)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Lupin protein complex (H1510)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Coenzyme Q10 (H1013)	21.17	—
Amino V complex (H1400)	22.81	—
Aminomix NAC (H1002)	23.08	—
Antibiosis forte complex (H1115)	27.35	—
Glutamine (L-) (H1043)	42.55	—
Pea protein BCAA complex (H1507)	50.12	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Lupin protein complex (H1510)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Lupin protein complex (H1510)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Lupin protein complex (H1510)	23000731	81484	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 40 spectra of 1 reference samples from the substance/substance group *Lupin protein complex (H1510)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 1 different batches.
- 28 436 spectra from a total of 577 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the

substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a †. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 0 spectra of 0 reference samples from the substance/substance group *Lupin protein complex (H1510)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.
- 22 999 spectra from a total of 504 batches from further 78 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *Lupin protein complex (H1510)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Lupin protein complex (H1510)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Lupin protein complex (H1510)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	40	0	28 436
Type B	0	0	0	22 999
Type C	0	0	0	2970

The substance/substance group *Lupin protein complex (H1510)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate* (*specificity*) and the weighted *true positive rate* (*recognition rate*) are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9295 %)	100.0000 % (> 85.0000 %)
Type B	100.0000 % (> 99.8687 %)	n/a (n/a)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
81484	81484	0.00	24.18

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Lysine (L-) (H1047)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80151-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Lysine (L-) (H1047)

Special notes

When selecting the *Lysine (L-) (H1047)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Lysine (L-) (H1047)	8	4	24

Second-stage model

For differentiation of the substance/substance group *Lysine (L-) (H1047)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Lysine (L-) (H1047)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Antibiosis forte complex (H1115)	47.88	—
Carnosine (L-) (H1014)	48.13	—
Glycine (H1021)	52.91	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Lysine (L-) (H1047)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Lysine (L-) (H1047)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Lysine (L-) (H1047)	065401	80343	40	from supplier
Hepart	Lysine (L-) (H1047)	028801	80360	40	from supplier
Hepart	Lysine (L-) (H1047)	065401	80453	40	from supplier
Hepart	Lysine (L-) (H1047)	028801	80458	40	from supplier
Hepart	Lysine (L-) (H1047)	14000944	80468	40	from supplier
Hepart	Lysine (L-) (H1047)	15000372	80562	60	from supplier
Hepart	Lysine (L-) (H1047)	16001395/0	80847	40	from supplier
Hepart	Lysine (L-) (H1047)	18001389	81131	40	from supplier
Hepart	Lysine (L-) (H1047)	21001735	81376	50	not required
Hepart	Lysine (L-) (H1047)	22000055	81413	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 430 spectra of 10 reference samples from the substance/substance group *Lysine (L-) (H1047)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 8 different batches.
- 28 046 spectra from a total of 570 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a †. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 160 spectra of 4 reference samples from the substance/substance group *Lysine (L-) (H1047)*.
- Among them are spectra of independent samples from 4 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Lysine (L-) (H1047)	16001503/0	80848	40
Hepart	Lysine (L-) (H1047)	19001154	81208	40
Hepart	Lysine (L-) (H1047)	20000950	81268	40
Hepart	Lysine (L-) (H1047)	23000775	81491	40

- 22 839 spectra from a total of 500 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 47 spectra from 14 *Apo-Ident* customers from 28 batches from the substance/substance group *Lysine (L-) (H1047)*.
- Among them are spectra of independent samples from 24 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
Flaigg Ag CH-4147 Ae...	Lysine (L-) (H1047)	18001389	1
Flaigg Ag CH-4147 Ae...	Lysine (L-) (H1047)	18001389/2	1
HCK	Lysine (L-) (H1047)	14000944/1	1
HCK	Lysine (L-) (H1047)	15000372	1
HCK	Lysine (L-) (H1047)	15000372/0	2

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Supplier	Substance	Batch	Spectra
Hepart AG, CH-8280 K...	Lysine (L-) (H1047)	1800955002	1
Hepart ag/Unisan	Lysine (L-) (H1047)	19001154	2
Hepart AG	Lysine (L-) (H1047)	15000372/2	1
Hepart AG	Lysine (L-) (H1047)	16001395/1	3
Hepart AG	Lysine (L-) (H1047)	16001503/0	2
Hepart AG	Lysine (L-) (H1047)	16001503/1	1
Hepart AG	Lysine (L-) (H1047)	65401	1
Hepart	Lysine (L-) (H1047)		1
Hepart	Lysine (L-) (H1047)	15000372-1	2
Hepart	Lysine (L-) (H1047)	16001395	4
Hepart	Lysine (L-) (H1047)	16001395/1	1
Hepart	Lysine (L-) (H1047)	16001503	2
Hepart	Lysine (L-) (H1047)	16001503/0	2
Hepart	Lysine (L-) (H1047)	18001389/0	1
Hepart	Lysine (L-) (H1047)	19001154	1
Hepart	Lysine (L-) (H1047)	19001154/0	4
Hepart	Lysine (L-) (H1047)	19001154/1	1
Hepart	Lysine (L-) (H1047)	1900154/1	1
Hepart	Lysine (L-) (H1047)	20000950	1
Hepart	Lysine (L-) (H1047)	20000950/0	1
Hepart	Lysine (L-) (H1047)	20000950/2	1
Hepart	Lysine (L-) (H1047)	21001735/0	1
Unisan/Hepart AG	Lysine (L-) (H1047)	65401	1
Unisan	Lysine (L-) (H1047)	14000944	1
Unisan	Lysine (L-) (H1047)	15000372/0	1
Unisan	Lysine (L-) (H1047)	1800017302	1
Unisan	Lysine (L-) (H1047)	1801028801	1
Unisan	Lysine (L-) (H1047)	65401/4	1

- 2923 spectra from 26 *Apo-Ident* customers from a total of 1432 batches from a further 62 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Lysine (L-) (H1047)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Lysine (L-) (H1047)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	430	0	28 046
Type B	0	160	0	22 839
Type C	0	45	2	2923

The substance/substance group *Lysine (L-) (H1047)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9275 %)	100.0000 % (> 98.6047 %)
Type B	100.0000 % (> 99.8651 %)	100.0000 % (> 96.2500 %)
Type C	100.0000 % (> 98.8288 %)	95.7447 % (> 89.3617 %)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80343	80343	0.00	49.56
80360	80360	0.00	60.11
80453	80453	0.00	51.46
80458	80458	0.00	51.09
80468	80468	0.00	61.37
80562	80562	0.00	58.85
80847	80847	0.00	70.07
81131	81131	0.00	65.33
81376	81376	0.00	47.88
81413	81413	0.00	68.86

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Magnesium (H1060) / Trace elements JK complex (H1080)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80061-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Magnesium (H1060) / Trace elements JK complex (H1080); Magnesium (H1060); Trace elements JK (H1080); Trace elements JK complex (H1080)

Special notes

When selecting the *Magnesium (H1060) / Trace elements JK complex (H1080)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Magnesium (H1060) / Trace elements JK complex (H1080)	14	42	85

Second-stage model

For differentiation of the substance/substance group *Magnesium (H1060) / Trace elements JK complex (H1080)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Magnesium (H1060) / Trace elements JK complex (H1080)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Trace elements BAG (H1078)	29.82	—
Garcinia cambogia (H1017)	39.93	—
Coenzyme Q10 (H1013)	54.18	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Magnesium (H1060) / Trace elements JK complex (H1080)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Magnesium (H1060) / Trace elements JK complex (H1080)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Magnesium (H1060)	069601	80378	40	from supplier
Hepart	Magnesium (H1060)	14001893	80515	60	from supplier
Hepart	Magnesium (H1060)	16000264	80767	60	from supplier
Hepart	Magnesium (H1060)	16000269	80770	60	from supplier
Hepart	Magnesium (H1060)	16001702	80856	40	from supplier
Hepart	Magnesium (H1060)	18000949	81058	40	from supplier
Hepart	Magnesium (H1060)	21000494-495-493	81327	40	from supplier
Hepart	Magnesium (H1060)	24002348	81577	40	from supplier
Hepart	Magnesium (H1060)	24002319	81579	40	from supplier
Hepart	Trace elements JK (H1080)	072701	80387	40	from supplier
Hepart	Trace elements JK (H1080)	072901	80388	40	from supplier
Hepart	Trace elements JK (H1080)	072801	80389	40	from supplier
Hepart	Trace elements JK (H1080)	072901	80701	60	from supplier
Hepart	Trace elements JK (H1080)	15000526	80766	60	from supplier
Hepart	Trace elements JK (H1080)	18000455	81029	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 700 spectra of 15 reference samples from the substance/substance group *Magnesium (H1060) / Trace elements JK complex (H1080)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 14 different batches.
- 27 776 spectra from a total of 564 batches from further 129 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 1930 spectra of 42 reference samples from the substance/substance group *Magnesium (H1060) / Trace elements JK complex (H1080)*.
- Among them are spectra of independent samples from 42 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Magnesium (H1060)	043601	80351	40
Hepart	Magnesium (H1060)	070001	80423	40
Hepart	Magnesium (H1060)	069801	80427	40
Hepart	Magnesium (H1060)	069901	80429	40
Hepart	Magnesium (H1060)	069701	80437	40
Hepart	Magnesium (H1060)	14001895	80516	60
Hepart	Magnesium (H1060)	14001889	80517	60
Hepart	Magnesium (H1060)	14001891	80518	60
Hepart	Magnesium (H1060)	14001894	80519	60
Hepart	Magnesium (H1060)	16000270	80769	60
Hepart	Magnesium (H1060)	16000267	80771	60
Hepart	Magnesium (H1060)	16000271	80772	60
Hepart	Magnesium (H1060)	16000268	80773	60
Hepart	Magnesium (H1060)	16000265	80774	60
Hepart	Magnesium (H1060)	16000272	80775	60
Hepart	Magnesium (H1060)	16000266	80776	60
Hepart	Magnesium (H1060)	16001703	80857	40
Hepart	Magnesium (H1060)	16001704	80858	40
Hepart	Magnesium (H1060)	16001705	80859	40
Hepart	Magnesium (H1060)	16001706	80860	40
Hepart	Magnesium (H1060)	18000420	81057	40
Hepart	Magnesium (H1060)	18000950	81059	40
Hepart	Magnesium (H1060)	18000951	81060	40

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Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Magnesium (H1060)	18000952	81061	40
Hepart	Magnesium (H1060)	18000953	81062	40
Hepart	Magnesium (H1060)	19001559/0	81175	40
Hepart	Magnesium (H1060)	19001153	81176	40
Hepart	Magnesium (H1060)	19001558	81177	40
Hepart	Magnesium (H1060)	19001560	81178	40
Hepart	Magnesium (H1060)	19001561	81179	40
Hepart	Magnesium (H1060)	210020-27-28-29-30	81397	50
Hepart	Magnesium (H1060)	24002317	81578	40
Hepart	Magnesium (H1060)	24002372	81580	40
Hepart	Magnesium (H1060)	24002373	81581	40
Hepart	Trace elements JK (H1080)	15000525	80673	60
Hepart	Trace elements JK (H1080)	17000870	80932	40
Hepart	Trace elements JK (H1080)	17000871	80933	40
Hepart	Trace elements JK (H1080)	17000869	80934	40
Hepart	Trace elements JK (H1080)	18000456	81030	40
Hepart	Trace elements JK (H1080)	18000457	81031	40
Hepart	Trace elements JK (H1080)	18000484	81032	40
Hepart	Trace elements JK (H1080)	21000245-376	81352	40

- 21 069 spectra from a total of 462 batches from further 76 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 193 spectra from 21 *Apo-Ident* customers from 88 batches from the substance/substance group *Magnesium (H1060) / Trace elements JK complex (H1080)*.
- Among them are spectra of independent samples from 85 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
Euro OTC	Trace elements JK (H1080)	15000526/0	1
HCK	Magnesium (H1060)	14001893/0	2
HCK	Trace elements JK (H1080)	15000526-1	1
HCK	Trace elements JK (H1080)	15000527-0	1
HCK	Magnesium (H1060)	16000265-0	2
HCK	Magnesium (H1060)	16000272	1
Hepart / Unisan	Magnesium (H1060)	19001560	1
Hepart AG, CH-8280 K...	Magnesium (H1060)	1134043601	1
Hepart AG, CH-8280 K...	Magnesium (H1060)	1134973501	2
Hepart AG, CH-8280 K...	Magnesium (H1060)	43602	1
Hepart AG/Unisan	Trace elements JK (H1080)	18000484/0	1
Hepart AG/Unisan	Trace elements JK (H1080)	18000484/1	1
Hepart AG/Unisan	Magnesium (H1060)	18000951/0	1
Hepart AG/Unisan	Magnesium (H1060)	19001558/0	1
Hepart AG/Unisan	Magnesium (H1060)	19001561/0	2
Hepart AG	Trace elements JK (H1080)	1026011701	2
Hepart AG	Magnesium (H1060)	1134973501	5
Hepart AG	Trace elements JK (H1080)	11701	8
Hepart AG	Magnesium (H1060)	14001894/0	1

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Supplier	Substance	Batch	Spectra
Hepart AG	Magnesium (H1060)	14001895/2	1
Hepart AG	Trace elements JK (H1080)	15000525	1
Hepart AG	Trace elements JK (H1080)	15000528/0	2
Hepart AG	Magnesium (H1060)	16000269	1
Hepart AG	Magnesium (H1060)	16000272/0	2
Hepart AG	Magnesium (H1060)	16001703/0	1
Hepart AG	Magnesium (H1060)	16001704/0	2
Hepart AG	Magnesium (H1060)	16001705	1
Hepart AG	Magnesium (H1060)	16001705/0	2
Hepart AG	Trace elements JK (H1080)	17000869	1
Hepart AG	Trace elements JK (H1080)	17000869/0	1
Hepart AG	Trace elements JK (H1080)	17000870/0	3
Hepart AG	Trace elements JK (H1080)	18000456/0	1
Hepart AG	Magnesium (H1060)	18000950/0	1
Hepart AG	Magnesium (H1060)	18000952/0	1
Hepart AG	Magnesium (H1060)	43501	1
Hepart AG	Magnesium (H1060)	43601	2
Hepart AG	Magnesium (H1060)	43602	4
Hepart AG	Magnesium (H1060)	43701	1
Hepart AG	Magnesium (H1060)	69901	3
Hepart AG	Trace elements JK (H1080)	72701	1
Hepart/Unisan	Magnesium (H1060)	16000267/0	1
Hepart	Magnesium (H1060)	14001893	1
Hepart	Magnesium (H1060)	14001893/0	1
Hepart	Trace elements JK (H1080)	15000525	1
Hepart	Trace elements JK (H1080)	15000527-1	1
Hepart	Trace elements JK (H1080)	15000529/0	1
Hepart	Magnesium (H1060)	16000269	1
Hepart	Magnesium (H1060)	16000269/0	1
Hepart	Magnesium (H1060)	16000272	1
Hepart	Magnesium (H1060)	16000272/0	2
Hepart	Magnesium (H1060)	16001702/0	1
Hepart	Magnesium (H1060)	16001704	1
Hepart	Magnesium (H1060)	16001704/0	1
Hepart	Magnesium (H1060)	16001706/0	3
Hepart	Trace elements JK (H1080)	17000869	1
Hepart	Trace elements JK (H1080)	17000869/0	2
Hepart	Trace elements JK (H1080)	17000870-0	1
Hepart	Trace elements JK (H1080)	17000871/0	1
Hepart	Trace elements JK (H1080)	17000896/0	1
Hepart	Magnesium (H1060)	18000420/0	1
Hepart	Trace elements JK (H1080)	18000455/0	1
Hepart	Trace elements JK (H1080)	18000456/0	2
Hepart	Trace elements JK (H1080)	18000457	1
Hepart	Trace elements JK (H1080)	18000457/0	2
Hepart	Trace elements JK (H1080)	18000484/0	2
Hepart	Trace elements JK (H1080)	18000484/1	1
Hepart	Magnesium (H1060)	18000949/0	1
Hepart	Magnesium (H1060)	18000950/0	1
Hepart	Magnesium (H1060)	18000951/0	3
Hepart	Magnesium (H1060)	18000952/0	1
Hepart	Magnesium (H1060)	18000953	1
Hepart	Magnesium (H1060)	18000953/0	1
Hepart	Magnesium (H1060)	1900	1
Hepart	Magnesium (H1060)	19001153/0	4
Hepart	Magnesium (H1060)	19001558	1
Hepart	Magnesium (H1060)	19001558/0	2
Hepart	Magnesium (H1060)	19001559/0	2
Hepart	Magnesium (H1060)	19001561/0	2
Hepart	Trace elements JK (H1080)	21000245/0	2

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Supplier	Substance	Batch	Spectra
Hepart	Trace elements JK (H1080)	21000376	1
Hepart	Trace elements JK (H1080)	21000376/0	1
Hepart	Magnesium (H1060)	21000493/0	1
Hepart	Magnesium (H1060)	21000494	1
Hepart	Magnesium (H1060)	21000494/0	3
Hepart	Magnesium (H1060)	21000495	1
Hepart	Magnesium (H1060)	21002028	1
Hepart	Magnesium (H1060)	21002028/0	1
Hepart	Magnesium (H1060)	21002029/0	2
Hepart	Trace elements JK (H1080)	22000100/0	1
Unisan Gmbh, 78465 K...	Trace elements JK (H1080)	1026011701	1
Unisan Gmbh, 78465 K...	Magnesium (H1060)	43702	1
Unisan/Hepart AG	Trace elements JK (H1080)	11701	3
Unisan/Hepart AG	Magnesium (H1060)	43601	1
Unisan/Hepart AG	Magnesium (H1060)	973501	1
Unisan	Trace elements JK (H1080)	1026011701	1
Unisan	Trace elements JK (H1080)	1026956901	1
Unisan	Trace elements JK (H1080)	1028956901	1
Unisan	Magnesium (H1060)	1134973501	2
Unisan	Trace elements JK (H1080)	11701	3
Unisan	Magnesium (H1060)	14001893	1
unisan	Magnesium (H1060)	14001895	2
Unisan	Magnesium (H1060)	14001895	4
Unisan	Trace elements JK (H1080)	15000525/0	1
Unisan	Trace elements JK (H1080)	15000526	1
Unisan	Magnesium (H1060)	16000265	1
Unisan	Magnesium (H1060)	16000265/0	1
Unisan	Magnesium (H1060)	16000265/1	3
Unisan	Magnesium (H1060)	16000272	1
Unisan	Trace elements JK (H1080)	17000870	2
Unisan	Magnesium (H1060)	43501	2
Unisan	Magnesium (H1060)	43601	1
Unisan	Magnesium (H1060)	43701	3
unisan	Magnesium (H1060)	43702	1
Unisan	Magnesium (H1060)	69601	1
Unisan	Magnesium (H1060)	69701	3
UNISAN	Magnesium (H1060)	69701	3
Unisan	Magnesium (H1060)	69801	4
Unisan	Magnesium (H1060)	69801/2	1
Unisan	Trace elements JK (H1080)	72701	1
UNISAN	Trace elements JK (H1080)	72701	1
Unisan	Trace elements JK (H1080)	72901	1
Unisan	Magnesium (H1060)	973501	2
Unisan	Magnesium (H1060)	H106021	1

- 2777 spectra from 26 *Apo-Ident* customers from a total of 1372 batches from a further 61 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Magnesium (H1060) / Trace elements JK complex (H1080)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Magnesium (H1060) / Trace elements JK complex (H1080)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following

table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	700	0	27 776
Type B	0	1930	0	21 069
Type C	0	173	20	2777

The substance/substance group *Magnesium (H1060)* / *Trace elements JK complex (H1080)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9274 %)	100.0000 % (> 99.1429 %)
Type B	100.0000 % (> 99.8638 %)	100.0000 % (> 99.6891 %)
Type C	100.0000 % (> 98.8228 %)	89.6373 % (> 88.0829 %)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80378	80378	0.00	83.05
80387	80387	0.00	36.54
80388	80388	0.00	36.03
80389	80389	0.00	37.45
80515	80515	0.00	80.67
80701	80701	0.00	39.77
80766	80766	0.00	51.35
80767	80767	0.00	60.59
80770	80770	0.00	55.07
80856	80856	0.00	61.77
81029	81029	0.00	29.82
81058	81058	0.00	63.40
81327	81327	0.00	44.79
81577	81577	0.00	77.48
81579	81579	0.00	79.83

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances,

thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Methylsulfonylmethane (MSM) (H1062)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80102-2025-03-07
Executing company HiperScan GmbH
 Weißeritzstraße 3
 01067 Dresden
 Germany

Relevant substance names

Methylsulfonylmethane (MSM) (H1062)

Special notes

When selecting the *Methylsulfonylmethane (MSM) (H1062)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Methylsulfonylmethane (MSM) (H1062)	8	1	14

Second-stage model

For differentiation of the substance/substance group *Methylsulfonylmethane (MSM) (H1062)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Methylsulfonylmethane (MSM) (H1062)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Antibiosis forte complex (H1115)	48.20	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Methylsulfonylmethane (MSM) (H1062)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Methylsulfonylmethane (MSM) (H1062)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Methylsulfonylmethane (MS...	056201	80332	60	from supplier
Hepart	Methylsulfonylmethane (MS...	14000921	80467	40	from supplier
Hepart	Methylsulfonylmethane (MS...	15001371	80703	120	from supplier
Hepart	Methylsulfonylmethane (MS...	17001247	80957	40	from supplier
Hepart	Methylsulfonylmethane (MS...	18001387	81117	40	from supplier
Hepart	Methylsulfonylmethane (MS...	20000221	81262	40	from supplier
Hepart	Methylsulfonylmethane (MS...	21000404	81333	40	from supplier
Hepart	Methylsulfonylmethane (MS...	21001430	81386	50	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 430 spectra of 8 reference samples from the substance/substance group *Methylsulfonylmethane (MSM) (H1062)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 8 different batches.

- 28 046 spectra from a total of 570 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 40 spectra of 1 reference samples from the substance/substance group *Methylsulfonylmethane (MSM) (H1062)*.
- Among them are spectra of independent samples from 1 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Methylsulfonylmethane (MS...	16000449/0	80782	40

- 22 959 spectra from a total of 503 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 25 spectra from 8 *Apo-Ident* customers from 19 batches from the substance/substance group *Methylsulfonylmethane (MSM) (H1062)*.
- Among them are spectra of independent samples from 14 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
HCK	Methylsulfonylmethane (MS...	1400921/1	1
Hepart AG	Methylsulfonylmethane (MS...	15001371	1
Hepart	Methylsulfonylmethane (MS...	16000449/4	2
Hepart	Methylsulfonylmethane (MS...	16000449-3	1
Hepart	Methylsulfonylmethane (MS...	17001247	1
Hepart	Methylsulfonylmethane (MS...	18001387	1
Hepart	Methylsulfonylmethane (MS...	18001387/0	1
Hepart	Methylsulfonylmethane (MS...	18001387/1	3
Hepart	Methylsulfonylmethane (MS...	20000221	1
Hepart	Methylsulfonylmethane (MS...	20000221/0	1
Hepart	Methylsulfonylmethane (MS...	210000404/0	1

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Supplier	Substance	Batch	Spectra
Hepart	Methylsulfonylmethane (MS...	21000404	1
Hepart	Methylsulfonylmethane (MS...	21000404/1	1
Unisan/Hepart AG	Methylsulfonylmethane (MS...	1819025013	1
Unisan	Methylsulfonylmethane (MS...	15001371	1
Unisan	Methylsulfonylmethane (MS...	16000449/1	1
Unisan	Methylsulfonylmethane (MS...	25013	2
Unisan	Methylsulfonylmethane (MS...	26101	1
Unisan	Methylsulfonylmethane (MS...	56201	2
Unisan	Methylsulfonylmethane (MS...	979401	1

- 2945 spectra from 26 *Apo-Ident* customers from a total of 1441 batches from a further 62 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Methylsulfonylmethane (MSM) (H1062)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Methylsulfonylmethane (MSM) (H1062)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	430	0	28 046
Type B	0	40	0	22 959
Type C	0	21	4	2945

The substance/substance group *Methylsulfonylmethane (MSM) (H1062)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9275 %)	100.0000 % (> 98.6047 %)
Type B	100.0000 % (> 99.8691 %)	100.0000 % (> 85.0000 %)
Type C	100.0000 % (> 98.8358 %)	84.0000 % (> 72.0000 %)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra ([Rule of Three](#) [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the [Mahalanobis distance](#) to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80332	80332	0.00	68.35
80467	80467	0.00	77.50
80703	80703	0.00	72.25
80957	80957	0.00	57.23
81117	81117	0.00	57.12
81262	81262	0.00	57.81
81333	81333	0.00	48.20
81386	81386	0.00	57.60

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Moringa (H1131)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 10006003-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Moringa (H1131)

Special notes

When selecting the *Moringa (H1131)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Moringa (H1131)	2	0	0

Second-stage model

For differentiation of the substance/substance group *Moringa (H1131)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Moringa (H1131)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
PET basis (H1503)	21.64	—
Cocoa (H1521)	27.21	—
ginkgo extract (H1024)	34.15	—
PET immune system (H1502)	37.22	—
PET well-aging (H1500)	40.38	—
Copper (H1032)	45.98	—
Iron (H1015)	55.83	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Moringa (H1131)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Moringa (H1131)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Moringa (H1131)	22001058	81434	40	from supplier
Hepart	Moringa (H1131)	23002138	81514	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 80 spectra of 2 reference samples from the substance/substance group *Moringa (H1131)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 2 different batches.

- 28 396 spectra from a total of 576 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 0 spectra of 0 reference samples from the substance/substance group *Moringa (H1131)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.
- 22 999 spectra from a total of 504 batches from further 78 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *Moringa (H1131)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Moringa (H1131)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Moringa (H1131)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	80	0	28 396
Type B	0	0	0	22 999
Type C	0	0	0	2970

The substance/substance group *Moringa (H1131)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9284 %)	100.0000 % (> 92.5000 %)
Type B	100.0000 % (> 99.8687 %)	n/a (n/a)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
81434	81434	0.00	21.64
81514	81514	0.00	34.21

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Niacin (Inositol hexanicotinate) (H1022)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80087-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Niacin (Inositol hexanicotinate) (H1022)

Special notes

When selecting the *Niacin (Inositol hexanicotinate) (H1022)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Niacin (Inositol hexanicotinate) (H1022)	6	4	18

Second-stage model

For differentiation of the substance/substance group *Niacin (Inositol hexanicotinate) (H1022)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Niacin (Inositol hexanicotinate) (H1022)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Antibiosis forte complex (H1115)	58.64	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Niacin (Inositol hexanicotinate) (H1022)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Niacin (Inositol hexanicotinate) (H1022)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Niacin (Inositol hexanico...	046001	80320	60	from supplier
Hepart	Niacin (Inositol hexanico...	14000920	80465	40	from supplier
Hepart	Niacin (Inositol hexanico...	15000013	80554	60	from supplier
Hepart	Niacin (Inositol hexanico...	18001390/0	81116	40	from supplier
Hepart	Niacin (Inositol hexanico...	22002214	81459	40	from supplier
Hepart	Niacin (Inositol hexanico...	21002810/1	81544	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 280 spectra of 6 reference samples from the substance/substance group *Niacin (Inositol hexanicotinate) (H1022)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 6 different batches.
- 28 196 spectra from a total of 572 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the

substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 160 spectra of 4 reference samples from the substance/substance group *Niacin (Inositol hexanicotinate)* (H1022).
- Among them are spectra of independent samples from 4 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Niacin (Inositol hexanico...	16000750	80814	40
Hepart	Niacin (Inositol hexanico...	20000182	81231	40
Hepart	Niacin (Inositol hexanico...	20001828	81314	40
Hepart	Niacin (Inositol hexanico...	23000655/0	81545	40

- 22 839 spectra from a total of 500 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 25 spectra from 8 *Apo-Ident* customers from 20 batches from the substance/substance group *Niacin (Inositol hexanicotinate)* (H1022).
- Among them are spectra of independent samples from 18 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
Fagron	Niacin (Inositol hexanico...	1811046001	1
Flaigg Ag CH-4147 Ae...	Niacin (Inositol hexanico...	16000750/13	1
Flaigg Ag CH-4147 Ae...	Niacin (Inositol hexanico...	18001390/3	1
HCK	Niacin (Inositol hexanico...	15000013/3	1
HCK	Niacin (Inositol hexanico...	19000750/4	1
Hepart AG	Niacin (Inositol hexanico...	15000013	1
Hepart AG	Niacin (Inositol hexanico...	16000750/4	1
Hepart AG	Niacin (Inositol hexanico...	1811979201	1
Hepart	Niacin (Inositol hexanico...	16000750	1
Hepart	Niacin (Inositol hexanico...	16000750/12	1

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Supplier	Substance	Batch	Spectra
Hepart	Niacin (Inositol hexanico...	16000750/2	1
Hepart	Niacin (Inositol hexanico...	18001390/3	1
Hepart	Niacin (Inositol hexanico...	18001390/4	2
Hepart	Niacin (Inositol hexanico...	20000182/0	1
Hepart	Niacin (Inositol hexanico...	20001828/0	1
Hepart	Niacin (Inositol hexanico...	20001828/1	1
Hepart	Niacin (Inositol hexanico...	20001828/2	1
Hepart	Niacin (Inositol hexanico...	20001828/3	1
Hepart	Niacin (Inositol hexanico...	20001828/4	1
Purren Apotheke	Niacin (Inositol hexanico...	1811979201	1
Unisan/Hepart AG	Niacin (Inositol hexanico...	46001	1
Unisan	Niacin (Inositol hexanico...	14000920	1
unisan	Niacin (Inositol hexanico...	15000013	1
Unisan	Niacin (Inositol hexanico...	46001	1

- 2945 spectra from 26 *Apo-Ident* customers from a total of 1440 batches from a further 62 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Niacin (Inositol hexanicotinate) (H1022)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Niacin (Inositol hexanicotinate) (H1022)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	280	0	28 196
Type B	0	160	0	22 839
Type C	0	25	0	2945

The substance/substance group *Niacin (Inositol hexanicotinate) (H1022)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9276 %)	100.0000 % (> 97.8571 %)
Type B	100.0000 % (> 99.8651 %)	100.0000 % (> 96.2500 %)
Type C	100.0000 % (> 98.8358 %)	100.0000 % (> 76.0000 %)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra ([Rule of Three](#) [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80320	80320	0.00	85.75
80465	80465	0.00	87.09
80554	80554	0.00	86.12
81116	81116	0.00	58.64
81459	81459	0.00	75.03
81544	81544	0.00	75.12

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Niacin (Nicotinamide) (H1133)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 10006004-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Niacin (Nicotinamide) (H1133)

Special notes

When selecting the *Niacin (Nicotinamide) (H1133)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Niacin (Nicotinamide) (H1133)	2	0	0

Second-stage model

For differentiation of the substance/substance group *Niacin (Nicotinamide) (H1133)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Niacin (Nicotinamide) (H1133)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Curcumin and piperine (H1014)	52.80	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Niacin (Nicotinamide) (H1133)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Niacin (Nicotinamide) (H1133)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Niacin (Nicotinamide) (H1133)	22000701	81436	40	from supplier
Hepart	Niacin (Nicotinamide) (H1133)	23002220	81527	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 80 spectra of 2 reference samples from the substance/substance group *Niacin (Nicotinamide) (H1133)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 2 different batches.
- 28 396 spectra from a total of 576 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with

the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a †. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 0 spectra of 0 reference samples from the substance/substance group *Niacin (Nicotinamide) (H1133)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.
- 22 999 spectra from a total of 504 batches from further 78 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *Niacin (Nicotinamide) (H1133)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Niacin (Nicotinamide) (H1133)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Niacin (Nicotinamide) (H1133)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	80	0	28 396
Type B	0	0	0	22 999
Type C	0	0	0	2970

The substance/substance group *Niacin (Nicotinamide) (H1133)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9284 %)	100.0000 % (> 92.5000 %)
Type B	100.0000 % (> 99.8687 %)	n/a (n/a)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
81436	81436	0.00	61.76
81527	81527	0.00	58.08

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Oat bran beta-glucan (H1529)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 10006062-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Oat bran beta-glucan (H1529)

Special notes

When selecting the *Oat bran beta-glucan (H1529)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Oat bran beta-glucan (H1529)	2	1	0

Second-stage model

For differentiation of the substance/substance group *Oat bran beta-glucan (H1529)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Oat bran beta-glucan (H1529)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Leaky gut complex (H1802)	11.67	—
Glutathione (H1020)	18.76	—
Aminomix NAC (H1002)	19.78	—
Coenzyme Q10 (H1013)	20.74	—
Flavour orange (H1405)	21.27	—
Vitamin E NAT (H1107)	21.35	—
Ginseng (H1018)	27.22	—
Calcium L-(+)-lactate complex (H1008)	28.77	—
Antioxidants NAT complex (H1004)	32.51	—
Isoflavone (H1025)	33.14	—
Vitamin B1 (H1101)	34.94	—
Orthocolon complex (H1800)	38.87	—
ginkgo extract (H1024)	39.86	—
Camu Camu (H1518)	40.58	—
Garcinia cambogia (H1017)	42.67	—
Sunflower seed protein (H1511)	43.51	—
Baobab (H1410)	43.81	—
PET coenzyme Q10 (H1505)	43.86	—
Ginger extract (H1437)	45.50	—
Coconut (H1522)	45.66	—
Arginine (L-) (H1036)	45.74	—
Chondroitin sulfate (H1065)	48.31	—
Lutein-Zeaxanthin-Astaxanthin (H1129)	49.19	—
Boron (H1005)	49.86	—
Detox complex (H1111)	50.38	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Oat bran beta-glucan (H1529)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Oat bran beta-glucan (H1529)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Oat bran beta-glucan (H1529)	22001850	81452	40	from supplier
Hepart	Oat bran beta-glucan (H1529)	23002222	81516	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 80 spectra of 2 reference samples from the substance/substance group *Oat bran beta-glucan (H1529)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 2 different batches.
- 28 396 spectra from a total of 576 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 40 spectra of 1 reference samples from the substance/substance group *Oat bran beta-glucan (H1529)*.
- Among them are spectra of independent samples from 1 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Oat bran beta-glucan (H1529)	23002723/0	81531	40

- 22 959 spectra from a total of 503 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *Oat bran beta-glucan (H1529)*.

- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Oat bran beta-glucan (H1529)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Oat bran beta-glucan (H1529)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	80	0	28 396
Type B	0	40	0	22 959
Type C	0	0	0	2970

The substance/substance group *Oat bran beta-glucan (H1529)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9284 %)	100.0000 % (> 92.5000 %)
Type B	100.0000 % (> 99.8691 %)	100.0000 % (> 85.0000 %)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra ([Rule of Three](#) [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the [Mahalanobis distance](#) to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
81452	81452	0.00	23.33
81516	81516	0.00	32.55

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances,

thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Ornithine (L-) (H1048)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80175-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Ornithine (L-) (H1048)

Special notes

When selecting the *Ornithine (L-) (H1048)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Ornithine (L-) (H1048)	6	2	12

Second-stage model

For differentiation of the substance/substance group *Ornithine (L-) (H1048)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Ornithine (L-) (H1048)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Lysine (L-) (H1047)	26.35	—
Tyrosine (L-) (H1054)	47.12	—
Glycine (H1021)	63.52	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Ornithine (L-) (H1048)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Ornithine (L-) (H1048)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Ornithine (L-) (H1048)	15000004	80629	60	from supplier
Hepart	Ornithine (L-) (H1048)	15001364	80667	60	from supplier
Hepart	Ornithine (L-) (H1048)	15001364(F1)	80669	60	from supplier
Hepart	Ornithine (L-) (H1048)	16000935	80811	40	from supplier
Hepart	Ornithine (L-) (H1048)	20002205	81321	40	from supplier
Hepart	Ornithine (L-) (H1048)	21001080	81366	50	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 310 spectra of 6 reference samples from the substance/substance group *Ornithine (L-) (H1048)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 6 different batches.

- 28 166 spectra from a total of 572 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 100 spectra of 2 reference samples from the substance/substance group *Ornithine (L-) (H1048)*.
- Among them are spectra of independent samples from 2 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Ornithine (L-) (H1048)	15001364(F2)	80668	60
Hepart	Ornithine (L-) (H1048)	23001728	81505	40

- 22 899 spectra from a total of 502 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 22 spectra from 10 *Apo-Ident* customers from 13 batches from the substance/substance group *Ornithine (L-) (H1048)*.
- Among them are spectra of independent samples from 12 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
HCK	Ornithine (L-) (H1048)	15000004-3	1
Hepart / Unisan	Ornithine (L-) (H1048)	15000004	2
Hepart AG	Ornithine (L-) (H1048)	16000935/1	1
Hepart	Ornithine (L-) (H1048)	16000935/0	2
Hepart	Ornithine (L-) (H1048)	16000935/1	1
Hepart	Ornithine (L-) (H1048)	16000935/2	1
Hepart	Ornithine (L-) (H1048)	16000935/3	2
Hepart	Ornithine (L-) (H1048)	16000935/4	1
Hepart	Ornithine (L-) (H1048)	16000935-0	2
Hepart	Ornithine (L-) (H1048)	16000935-2	2
Purren Apotheke	Ornithine (L-) (H1048)	1817979301	1

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Supplier	Substance	Batch	Spectra
Unisan/Hepart AG	Ornithine (L-) (H1048)	27001	2
Unisan	Ornithine (L-) (H1048)	16000935/0	1
Unisan	Ornithine (L-) (H1048)	1816979301	1
Unisan	Ornithine (L-) (H1048)	979301	2

- 2948 spectra from 26 *Apo-Ident* customers from a total of 1447 batches from a further 62 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Ornithine (L-) (H1048)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Ornithine (L-) (H1048)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	310	0	28 166
Type B	0	100	0	22 899
Type C	0	16	6	2948

The substance/substance group *Ornithine (L-) (H1048)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9275 %)	100.0000 % (> 98.0645 %)
Type B	100.0000 % (> 99.8659 %)	100.0000 % (> 94.0000 %)
Type C	100.0000 % (> 98.8379 %)	72.7273 % (> 59.0909 %)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra ([Rule of Three](#) [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the [Mahalanobis distance](#) to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80629	80629	0.00	77.67
80667	80667	0.00	74.58

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Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80669	80669	0.00	79.06
80811	80811	0.00	66.54
81321	81321	0.00	72.39
81366	81366	0.00	63.85

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Orthovimin Neutral Complex (H1404)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 10006664-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Orthovimin Neutral Complex (H1404)

Special notes

When selecting the *Orthovimin Neutral Complex (H1404)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Orthovimin Neutral Complex (H1404)	1	0	0

Second-stage model

For differentiation of the substance/substance group *Orthovimin Neutral Complex (H1404)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Orthovimin Neutral Complex (H1404)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Garcinia cambogia (H1017)	21.32	—
Magnesium (H1060)	26.05	—
Orthocolon complex (H1800)	30.40	—
Rhodiola (H1064)	33.77	—
Saffron style (H1434)	35.15	—
Zinc (H1110)	36.33	—
Calcium L-(+)-lactate complex (H1008)	36.97	—
Green coffee extract (H1433)	37.58	—
Juniper (H1112)	37.61	—
Artichoke extract (H1440)	39.02	—
Coenzyme Q10 (H1013)	39.25	—
Vitamins BAG complex (H1091)	39.49	—
Detox complex (H1111)	40.03	—
Vitamin B1 (H1101)	40.12	—
Boron (H1005)	40.21	—
Marshmallow extract (H1439)	40.37	—
Silymarin (H1071)	42.17	—
Trace elements JK (H1080)	42.64	—
Baobab (H1410)	42.72	—
Silicium (H1070)	43.01	—
Aminomix NAC (H1002)	43.42	—
Arginine (L-) (H1036)	43.58	—
Konjak Glucomannan (H1530)	45.70	—
Betaine hydrochloride (H1119)	48.55	—
Gentian extract (H1438)	48.56	—
Glutathione (H1020)	48.87	—
Artemisia annua extract (H1118)	48.99	—
Antioxidants NAT complex (H1004)	49.01	—
Leaky gut complex (H1802)	49.26	—
Trace elements BAG (H1078)	49.30	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Orthovimin Neutral Complex (H1404)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Orthovimin Neutral Complex (H1404)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Orthovimin Neutral Comple...	24002259	81573	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 40 spectra of 1 reference samples from the substance/substance group *Orthovimin Neutral Complex (H1404)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 1 different batches.
- 28 436 spectra from a total of 577 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 0 spectra of 0 reference samples from the substance/substance group *Orthovimin Neutral Complex (H1404)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.
- 22 999 spectra from a total of 504 batches from further 78 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *Orthovimin Neutral Complex (H1404)*.

- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Orthovimin Neutral Complex (H1404)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Orthovimin Neutral Complex (H1404)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	40	0	28 436
Type B	0	0	0	22 999
Type C	0	0	0	2970

The substance/substance group *Orthovimin Neutral Complex (H1404)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9295 %)	100.0000 % (> 85.0000 %)
Type B	100.0000 % (> 99.8687 %)	n/a (n/a)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra ([Rule of Three](#) [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the [Mahalanobis distance](#) to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
81573	81573	0.00	22.57

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical

variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group	Pea protein complex (H1428) / Amino V complex (H1400)
Substance class	HCK - nutritional supplements (Hepart)
Report date	07/03/2025
Report number	80749-2025-03-07
Executing company	HiperScan GmbH Weißeritzstraße 3 01067 Dresden Germany

Relevant substance names

Pea protein complex (H1428) / Amino V complex (H1400); Amino V complex (H1400); Pea protein BCAA complex (H1507)

Special notes

When selecting the *Pea protein complex (H1428) / Amino V complex (H1400)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Pea protein complex (H1428) / Amino V complex (H1400)	11	20	1

Second-stage model

For differentiation of the substance/substance group *Pea protein complex (H1428) / Amino V complex (H1400)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Pea protein complex (H1428) / Amino V complex (H1400)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Antibiosis forte complex (H1115)	19.69	—
Coenzyme Q10 (H1013)	32.54	—
Collagen peptides-MTC (H1125)	38.28	—
Aminomix NAC (H1002)	45.81	—
Lupin protein complex (H1510)	48.49	—
Glutamine (L-) (H1043)	49.46	—
Carnitine (L-) (H1038)	50.54	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Pea protein complex (H1428) / Amino V complex (H1400)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Pea protein complex (H1428) / Amino V complex (H1400)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Amino V complex (H1400)	15001365(MM)	80749	60	from supplier
Hepart	Amino V complex (H1400)	15001366(B1)	80750	60	from supplier
Hepart	Amino V complex (H1400)	16001268	80820	40	from supplier
Hepart	Amino V complex (H1400)	16001229	80821	40	from supplier
Hepart	Amino V complex (H1400)	15001365	80862	40	from supplier
Hepart	Amino V complex (H1400)	17000382	80885	40	from supplier
Hepart	Amino V complex (H1400)	18000194	80995	40	from supplier
Hepart	Amino V complex (H1400)	18000803	81051	40	from supplier
Hepart	Amino V complex (H1400)	23001198	81486	40	from supplier
Hepart	Pea protein BCAA complex ...	21001594	81446	40	from supplier
Hepart	Pea protein BCAA complex ...	23000263	81483	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 480 spectra of 11 reference samples from the substance/substance group *Pea protein complex (H1428) / Amino V complex (H1400)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 11 different batches.
- 27 996 spectra from a total of 567 batches from further 129 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 960 spectra of 20 reference samples from the substance/substance group *Pea protein complex (H1428) / Amino V complex (H1400)*.
- Among them are spectra of independent samples from 20 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Amino V complex (H1400)	15001365(F2)	80745	60
Hepart	Amino V complex (H1400)	15001365(B1)	80746	60
Hepart	Amino V complex (H1400)	15001366(MM)	80747	60
Hepart	Amino V complex (H1400)	15001366(F2)	80748	60
Hepart	Amino V complex (H1400)	15001366	80884	40
Hepart	Amino V complex (H1400)	18000192	80996	40
Hepart	Amino V complex (H1400)	17001819	80997	40
Hepart	Amino V complex (H1400)	18000195	80998	40
Hepart	Amino V complex (H1400)	18000193	80999	40
Hepart	Amino V complex (H1400)	18000822	81052	40
Hepart	Amino V complex (H1400)	18000823	81053	40
Hepart	Amino V complex (H1400)	18000824	81054	40
Hepart	Amino V complex (H1400)	18000825	81066	40
Hepart	Amino V complex (H1400)	18000826	81067	40
Hepart	Amino V complex (H1400)	18001324	81100	40
Hepart	Amino V complex (H1400)	18001328	81101	40
Hepart	Amino V complex (H1400)	18001675	81122	60
Hepart	Amino V complex (H1400)	18001674	81123	60
Hepart	Amino V complex (H1400)	18001575	81124	60
Hepart	Amino V complex (H1400)	18001676	81125	60

- 22 039 spectra from a total of 484 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 1 spectra from 1 *Apo-Ident* customers from 1 batches from the substance/substance group *Pea protein complex (H1428) / Amino V complex (H1400)*.
- Among them are spectra of independent samples from 1 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
Hepart	Amino V complex (H1400)	16001229-0	1

- 2969 spectra from 26 *Apo-Ident* customers from a total of 1459 batches from a further 62 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Pea protein complex (H1428) / Amino V complex (H1400)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Pea protein complex (H1428) / Amino V complex (H1400)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	480	0	27 996
Type B	0	959	1	22 039
Type C	0	1	0	2969

The substance/substance group *Pea protein complex (H1428) / Amino V complex (H1400)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9274 %)	100.0000 % (> 98.7500 %)
Type B	100.0000 % (> 99.8639 %)	99.8958 % (> 99.5833 %)
Type C	100.0000 % (> 99.1958 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra ([Rule of Three](#) [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80749	80749	0.00	22.29
80750	80750	0.00	22.22
80820	80820	0.00	22.69
80821	80821	0.00	23.10
80862	80862	0.00	21.12
80885	80885	0.00	21.69
80995	80995	0.00	21.70
81051	81051	0.00	21.84
81446	81446	0.00	20.00
81483	81483	0.00	19.69
81486	81486	0.00	22.71

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **PET coenzyme Q10 (H1505)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80561-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

PET coenzyme Q10 (H1505)

Special notes

When selecting the *PET coenzyme Q10 (H1505)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
PET coenzyme Q10 (H1505)	1	0	0

Second-stage model

For differentiation of the substance/substance group *PET coenzyme Q10 (H1505)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *PET coenzyme Q10 (H1505)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Vitamin E NAT (H1107)	12.46	—
Ginseng (H1018)	13.83	—
Coenzyme Q10 (H1013)	23.60	—
Ginger extract (H1437)	24.68	—
Flavour orange (H1405)	29.24	—
Chondroitin sulfate (H1065)	35.64	—
Boron (H1005)	38.94	—
Oat bran beta-glucan (H1529)	40.89	—
Vitamin K2 (75µg Mono) (H1108)	42.02	—
Aminomix NAC (H1002)	45.08	—
Garcinia cambogia (H1017)	50.69	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *PET coenzyme Q10 (H1505)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *PET coenzyme Q10 (H1505)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	PET coenzyme Q10 (H1505)	15000401	80561	60	from supplier
Hepart	PET coenzyme Q10 (H1505)	15000401	80635	60	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 120 spectra of 2 reference samples from the substance/substance group *PET coenzyme Q10 (H1505)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 1 different batches.
- 28 356 spectra from a total of 578 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 0 spectra of 0 reference samples from the substance/substance group *PET coenzyme Q10 (H1505)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.
- 22 999 spectra from a total of 504 batches from further 78 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *PET coenzyme Q10 (H1505)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *PET coenzyme Q10 (H1505)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *PET coenzyme Q10 (H1505)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	120	0	28 356
Type B	0	0	0	22 999
Type C	0	0	0	2970

The substance/substance group *PET coenzyme Q10 (H1505)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9280 %)	100.0000 % (> 95.0000 %)
Type B	100.0000 % (> 99.8687 %)	n/a (n/a)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80561	80561	0.00	23.42
80635	80635	0.00	21.16

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **PET immune system (H1502)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80564-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

PET immune system (H1502)

Special notes

When selecting the *PET immune system (H1502)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
PET immune system (H1502)	1	0	0

Second-stage model

For differentiation of the substance/substance group *PET immune system (H1502)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *PET immune system (H1502)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
PET basis (H1503)	24.59	—
ginkgo extract (H1024)	29.66	—
PET well-aging (H1500)	34.79	—
Chia seeds protein (H1506)	39.56	—
Cocoa (H1521)	44.25	—
Antibiosis forte complex (H1115)	44.82	—
Vitamin C (H1104)	57.08	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *PET immune system (H1502)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *PET immune system (H1502)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	PET immune system (H1502)	15000405	80564	60	from supplier
Hepart	PET immune system (H1502)	15000405	80634	60	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 120 spectra of 2 reference samples from the substance/substance group *PET immune system (H1502)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 1 different batches.

- 28 356 spectra from a total of 577 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 0 spectra of 0 reference samples from the substance/substance group *PET immune system (H1502)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.
- 22 999 spectra from a total of 504 batches from further 78 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *PET immune system (H1502)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *PET immune system (H1502)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *PET immune system (H1502)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	120	0	28 356
Type B	0	0	0	22 999
Type C	0	0	0	2970

The substance/substance group *PET immune system (H1502)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate* (*specificity*) and the weighted *true positive rate* (*recognition rate*) are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9280 %)	100.0000 % (> 95.0000 %)
Type B	100.0000 % (> 99.8687 %)	n/a (n/a)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80564	80564	0.00	26.35
80634	80634	0.00	24.59

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **PET joints (H1501)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80567-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

PET joints (H1501)

Special notes

When selecting the *PET joints (H1501)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
PET joints (H1501)	1	0	0

Second-stage model

For differentiation of the substance/substance group *PET joints (H1501)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *PET joints (H1501)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
PET basis (H1503)	17.63	—
Coenzyme Q10 (H1013)	27.94	—
Rhodiola (H1064)	34.11	—
Aminomix NAC (H1002)	35.53	—
Antioxidants NAT complex (H1004)	36.62	—
Calcium L-(+)-lactate complex (H1008)	40.64	—
Flavour orange (H1405)	40.79	—
Glutathione (H1020)	41.79	—
PET well-aging (H1500)	43.86	—
Glutamine (L-) (H1043)	47.79	—
Antibiosis forte complex (H1115)	48.83	—
Vitamin B1 (H1101)	49.14	—
Garcinia cambogia (H1017)	49.45	—
Arginine (L-) (H1036)	49.99	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *PET joints (H1501)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *PET joints (H1501)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	PET joints (H1501)	15000404	80567	60	from supplier
Hepart	PET joints (H1501)	15000404	80630	60	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 120 spectra of 2 reference samples from the substance/substance group *PET joints (H1501)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 1 different batches.
- 28 356 spectra from a total of 577 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 0 spectra of 0 reference samples from the substance/substance group *PET joints (H1501)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.
- 22 999 spectra from a total of 504 batches from further 78 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *PET joints (H1501)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *PET joints (H1501)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *PET joints (H1501)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	120	0	28 356
Type B	0	0	0	22 999
Type C	0	0	0	2970

The substance/substance group *PET joints (H1501)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9280 %)	100.0000 % (> 95.0000 %)
Type B	100.0000 % (> 99.8687 %)	n/a (n/a)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80567	80567	0.00	17.63
80630	80630	0.00	19.93

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **PET skin and hair (H1504)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80565-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

PET skin and hair (H1504)

Special notes

When selecting the *PET skin and hair (H1504)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
PET skin and hair (H1504)	1	0	0

Second-stage model

For differentiation of the substance/substance group *PET skin and hair (H1504)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *PET skin and hair (H1504)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Antibiosis forte complex (H1115)	50.10	–

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *PET skin and hair (H1504)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *PET skin and hair (H1504)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	PET skin and hair (H1504)	15000403	80565	60	from supplier
Hepart	PET skin and hair (H1504)	15000403	80633	60	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 120 spectra of 2 reference samples from the substance/substance group *PET skin and hair (H1504)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 1 different batches.
- 28 356 spectra from a total of 577 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with

the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 0 spectra of 0 reference samples from the substance/substance group *PET skin and hair (H1504)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.
- 22 999 spectra from a total of 504 batches from further 78 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *PET skin and hair (H1504)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *PET skin and hair (H1504)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *PET skin and hair (H1504)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	120	0	28 356
Type B	0	0	0	22 999
Type C	0	0	0	2970

The substance/substance group *PET skin and hair (H1504)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9280 %)	100.0000 % (> 95.0000 %)
Type B	100.0000 % (> 99.8687 %)	n/a (n/a)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80565	80565	0.00	51.04
80633	80633	0.00	50.10

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **PET well-aging (H1500)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80563-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

PET well-aging (H1500)

Special notes

When selecting the *PET well-aging (H1500)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
PET well-aging (H1500)	2	0	0

Second-stage model

For differentiation of the substance/substance group *PET well-aging (H1500)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *PET well-aging (H1500)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
PET basis (H1503)	14.43	—
Vitamin B1 (H1101)	28.36	—
PET joints (H1501)	29.17	—
Rhodiola (H1064)	29.47	—
Flavour orange (H1405)	34.06	—
ginkgo extract (H1024)	35.11	—
PET immune system (H1502)	36.15	—
Green coffee extract (H1433)	41.89	—
Carnitine (L-) (H1038)	42.09	—
Arginine (L-) (H1036)	45.36	—
Antibiosis forte complex (H1115)	46.69	—
Calcium L-(+) -lactate complex (H1008)	48.42	—
Antioxidants NAT complex (H1004)	53.58	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *PET well-aging (H1500)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *PET well-aging (H1500)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	PET well-aging (H1500)	15000401	80563	60	from supplier
Hepart	PET well-aging (H1500)	15000406	80631	60	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 120 spectra of 2 reference samples from the substance/substance group *PET well-aging (H1500)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 2 different batches.
- 28356 spectra from a total of 577 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 0 spectra of 0 reference samples from the substance/substance group *PET well-aging (H1500)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.
- 22999 spectra from a total of 504 batches from further 78 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *PET well-aging (H1500)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *PET well-aging (H1500)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *PET well-aging (H1500)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	120	0	28 356
Type B	0	0	0	22 999
Type C	0	0	0	2970

The substance/substance group *PET well-aging (H1500)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9280 %)	100.0000 % (> 95.0000 %)
Type B	100.0000 % (> 99.8687 %)	n/a (n/a)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80563	80563	0.00	15.77
80631	80631	0.00	14.43

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Phenylalanine (L-) (H1049)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80090-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Phenylalanine (L-) (H1049)

Special notes

When selecting the *Phenylalanine (L-) (H1049)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Phenylalanine (L-) (H1049)	4	1	10

Second-stage model

For differentiation of the substance/substance group *Phenylalanine (L-) (H1049)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Phenylalanine (L-) (H1049)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Tryptophan (L-) (H1053)	25.76	–

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Phenylalanine (L-) (H1049)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Phenylalanine (L-) (H1049)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Phenylalanine (L-) (H1049)	074401	80400	40	from supplier
Hepart	Phenylalanine (L-) (H1049)	16001096	80852	40	from supplier
Hepart	Phenylalanine (L-) (H1049)	19000779	81167	40	from supplier
Hepart	Phenylalanine (L-) (H1049)	21001354	81359	50	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 170 spectra of 4 reference samples from the substance/substance group *Phenylalanine (L-) (H1049)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 4 different batches.
- 28 306 spectra from a total of 574 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples

are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 40 spectra of 1 reference samples from the substance/substance group *Phenylalanine (L-)* (*H1049*).
- Among them are spectra of independent samples from 1 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Phenylalanine (L-) (H1049)	17000876	80916	40

- 22959 spectra from a total of 503 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 27 spectra from 9 *Apo-Ident* customers from 12 batches from the substance/substance group *Phenylalanine (L-)* (*H1049*).
- Among them are spectra of independent samples from 10 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
HCK	Phenylalanine (L-) (H1049)	74401/1	2
HCK	Phenylalanine (L-) (H1049)	74401/2	1
Hepart AG	Phenylalanine (L-) (H1049)	17000876/0	1
Hepart AG	Phenylalanine (L-) (H1049)	17000876/1	1
Hepart AG	Phenylalanine (L-) (H1049)	74401/1	1
Hepart	Phenylalanine (L-) (H1049)	16001096	1
Hepart	Phenylalanine (L-) (H1049)	16001096-1	1
Hepart	Phenylalanine (L-) (H1049)	17000876	1
Hepart	Phenylalanine (L-) (H1049)	17000876/1	3
Hepart	Phenylalanine (L-) (H1049)	170008760	3
Hepart	Phenylalanine (L-) (H1049)	19000779	1
Unisan/Hepart AG	Phenylalanine (L-) (H1049)	1828025009	1
Unisan	Phenylalanine (L-) (H1049)	16001096	2
Unisan	Phenylalanine (L-) (H1049)	25009	7
Unisan	Phenylalanine (L-) (H1049)	74401/0	1

- 2943 spectra from 26 *Apo-Ident* customers from a total of 1448 batches from a further 62 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Phenylalanine (L-) (H1049)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Phenylalanine (L-) (H1049)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	170	0	28 306
Type B	0	40	0	22 959
Type C	0	18	9	2943

The substance/substance group *Phenylalanine (L-) (H1049)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9278 %)	100.0000 % (> 96.4706 %)
Type B	100.0000 % (> 99.8691 %)	100.0000 % (> 85.0000 %)
Type C	100.0000 % (> 98.8347 %)	66.6667 % (> 55.5556 %)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra ([Rule of Three](#) [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the [Mahalanobis distance](#) to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80400	80400	0.00	41.49
80852	80852	0.00	41.14
81167	81167	0.00	41.08
81359	81359	0.00	48.03

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all

substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Pomegranate (H1520)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 10006506-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Pomegranate (H1520)

Special notes

When selecting the *Pomegranate (H1520)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Pomegranate (H1520)	1	0	0

Second-stage model

For differentiation of the substance/substance group *Pomegranate (H1520)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Pomegranate (H1520)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Vitamin B1 (H1101)	16.40	—
Carrot (H1513)	18.45	—
Calcium L-(+)-lactate complex (H1008)	20.91	—
Flavour orange (H1405)	20.97	—
Glutathione (H1020)	21.03	—
Cabbage mix (H1514)	21.84	—
Arginine (L-) (H1036)	22.33	—
Rhodiola (H1064)	22.48	—
Isoflavone (H1025)	24.11	—
Leaky gut complex (H1802)	25.53	—
Baobab (H1410)	26.45	—
Artichoke extract (H1440)	26.57	—
Orthocolon complex (H1800)	27.00	—
Wild berry (H1524)	28.57	—
Marshmallow extract (H1439)	33.09	—
Coenzyme Q10 (H1013)	34.17	—
OPC Proanthocyanidins (Pine Bark) (...)	39.38	—
Silymarin (H1071)	39.46	—
Beetroot (H1515)	40.60	—
Detox complex (H1111)	42.17	—
Antioxidants NAT complex (H1004)	42.45	—
Ginseng (H1018)	44.38	—
Vitamins BAG complex (H1091)	45.33	—
Vitamin complex (H1100)	47.34	—
Lycopene (H1058)	47.36	—
Juniper (H1112)	47.52	—
Carnitine (L-) (H1038)	47.63	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Pomegranate (H1520)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Pomegranate (H1520)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Pomegranate (H1520)	24001853	81556	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 40 spectra of 1 reference samples from the substance/substance group *Pomegranate (H1520)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 1 different batches.
- 28 436 spectra from a total of 577 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 0 spectra of 0 reference samples from the substance/substance group *Pomegranate (H1520)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.
- 22 999 spectra from a total of 504 batches from further 78 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *Pomegranate (H1520)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Pomegranate (H1520)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Pomegranate (H1520)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	40	0	28 436
Type B	0	0	0	22 999
Type C	0	0	0	2970

The substance/substance group *Pomegranate (H1520)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9295 %)	100.0000 % (> 85.0000 %)
Type B	100.0000 % (> 99.8687 %)	n/a (n/a)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
81556	81556	0.00	17.80

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Potassium (H1030)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80043-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Potassium (H1030)

Special notes

When selecting the *Potassium (H1030)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Potassium (H1030)	11	19	34

Second-stage model

For differentiation of the substance/substance group *Potassium (H1030)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Potassium (H1030)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Iron (H1015)	41.79	—
Calcium L-(+)-lactate complex (H1008)	48.39	—
Vitamin C (H1104)	51.32	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Potassium (H1030)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Potassium (H1030)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Potassium (H1030)	039302	80372	40	from supplier
Hepart	Potassium (H1030)	15000597	80571	60	from supplier
Hepart	Potassium (H1030)	15000598(B1)	80574	60	from supplier
Hepart	Potassium (H1030)	15000599	80576	60	from supplier
Hepart	Potassium (H1030)	15000600	80578	60	from supplier
Hepart	Potassium (H1030)	16001645	80868	40	from supplier
Hepart	Potassium (H1030)	19000026	81154	40	from supplier
Hepart	Potassium (H1030)	21002001	81396	50	from supplier
Hepart	Potassium (H1030)	24002232	81563	40	from supplier
Hepart	Potassium (H1030)	24002225	81566	40	from supplier
Hepart	Potassium (H1030)	24002230	81567	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 530 spectra of 11 reference samples from the substance/substance group *Potassium (H1030)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 11 different batches.
- 27946 spectra from a total of 567 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a †. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 860 spectra of 19 reference samples from the substance/substance group *Potassium (H1030)*.
- Among them are spectra of independent samples from 19 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Potassium (H1030)	130328001	80347	40
Hepart	Potassium (H1030)	069201	80376	30
Hepart	Potassium (H1030)	15000597 (B1)	80572	60
Hepart	Potassium (H1030)	15000598	80573	60
Hepart	Potassium (H1030)	15000598 (F2)	80575	60
Hepart	Potassium (H1030)	15000599 (F2)	80577	60
Hepart	Potassium (H1030)	15000600 (B1)	80579	60
Hepart	Potassium (H1030)	16001646	80869	40
Hepart	Potassium (H1030)	16001647	80870	40
Hepart	Potassium (H1030)	19000027	81155	40
Hepart	Potassium (H1030)	19000028	81156	40
Hepart	Potassium (H1030)	20001174	81283	40
Hepart	Potassium (H1030)	20001173	81287	40
Hepart	Potassium (H1030)	2100-1999-2000	81398	50
Hepart	Potassium (H1030)	23000438-439	81477	40
Hepart	Potassium (H1030)	24001742	81558	40
Hepart	Potassium (H1030)	24002229	81562	40
Hepart	Potassium (H1030)	24002231	81564	40
Hepart	Potassium (H1030)	24002207	81565	40

- 22139 spectra from a total of 485 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 88 spectra from 18 *Apo-Ident* customers from 37 batches from the substance/substance group *Potassium (H1030)*.
- Among them are spectra of independent samples from 34 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
Fagron	Potassium (H1030)	39301	1
HCK	Potassium (H1030)	15000597-1	1
HCK	Potassium (H1030)	15000599	1
Hepart / Unisan	Potassium (H1030)	160016460	1
Hepart AG	Potassium (H1030)	1124028903	1
Hepart AG	Potassium (H1030)	1124944201	1
Hepart AG	Potassium (H1030)	15000597/0	1
Hepart AG	Potassium (H1030)	16001645/0	4
Hepart AG	Potassium (H1030)	16001646/0	6
Hepart AG	Potassium (H1030)	16001647/0	1
Hepart AG	Potassium (H1030)	39301	1
Hepart AG	Potassium (H1030)	39302	1
Hepart	Potassium (H1030)	15000598	1
Hepart	Potassium (H1030)	15000598-3	1
Hepart	Potassium (H1030)	15000599/1	1
Hepart	Potassium (H1030)	16001645	1
Hepart	Potassium (H1030)	16001645/0	2
Hepart	Potassium (H1030)	16001646	1
Hepart	Potassium (H1030)	16001647	1
Hepart	Potassium (H1030)	16001647/0	2
Hepart	Potassium (H1030)	19000026/0	3
Hepart	Potassium (H1030)	19000027	1
Hepart	Potassium (H1030)	19000027/0	7
Hepart	Potassium (H1030)	19000028	1
Hepart	Potassium (H1030)	19000028/0	6
Hepart	Potassium (H1030)	20001173	1
Hepart	Potassium (H1030)	20001173/0	2
Hepart	Potassium (H1030)	20001174/0	1
Hepart	Potassium (H1030)	21001999/0	1
Unisan/Hepart AG	Potassium (H1030)	39302	1
Unisan	Potassium (H1030)	1124944201	1
Unisan	Potassium (H1030)	130328001	3
Unisan	Potassium (H1030)	15000597/0	1
Unisan	Potassium (H1030)	15000597/1	1
Unisan	Potassium (H1030)	15000598	1
Unisan	Potassium (H1030)	15000599	1
Unisan	Potassium (H1030)	15000599/0	1
Unisan	Potassium (H1030)	15000600	2
Unisan	Potassium (H1030)	288903	1
Unisan	Potassium (H1030)	28903	1
Unisan	Potassium (H1030)	39301	8
Unisan	Potassium (H1030)	39302	1
Unisan	Potassium (H1030)	69201	3
UNISAN	Potassium (H1030)	69201	1
Unisan	Potassium (H1030)	69301	3
Unisan	Potassium (H1030)	69401	1
Unisan	Potassium (H1030)	69401/0	1
Unisan	Potassium (H1030)	944201	3

- 2882 spectra from 26 *Apo-Ident* customers from a total of 1423 batches from a further 62 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the

samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Potassium (H1030)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Potassium (H1030)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	530	0	27 946
Type B	0	860	0	22 139
Type C	0	85	3	2882

The substance/substance group *Potassium (H1030)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9274 %)	100.0000 % (> 98.8679 %)
Type B	100.0000 % (> 99.8640 %)	100.0000 % (> 99.3023 %)
Type C	100.0000 % (> 98.8251 %)	96.5909 % (> 93.1818 %)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80372	80372	0.00	38.58
80571	80571	0.00	47.14
80574	80574	0.00	48.09
80576	80576	0.00	48.98
80578	80578	0.00	48.26
80868	80868	0.00	49.18
81154	81154	0.00	43.47
81396	81396	0.00	48.94
81563	81563	0.00	43.25
81566	81566	0.00	49.10
81567	81567	0.00	52.24

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at

least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Proline (-L) NF (H1050)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80905-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Proline (-L) NF (H1050); L-proline NF (H1050)

Special notes

When selecting the *Proline (-L) NF (H1050)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Proline (-L) NF (H1050)	3	0	1

Second-stage model

For differentiation of the substance/substance group *Proline (-L) NF (H1050)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Proline (-L) NF (H1050)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Antibiosis forte complex (H1115)	23.72	—
Carnitine (L-) (H1038)	53.01	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Proline (-L) NF (H1050)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Proline (-L) NF (H1050)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Proline (-L) NF (H1050)	16000951	80905	40	from supplier
Hepart	Proline (-L) NF (H1050)	17000952	80935	40	from supplier
Hepart	Proline (-L) NF (H1050)	18000403	81023	40	from supplier
Hepart	Proline (-L) NF (H1050)	16000951	81146	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 160 spectra of 4 reference samples from the substance/substance group *Proline (-L) NF (H1050)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 3 different batches.
- 28 316 spectra from a total of 575 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A*

section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 40 spectra of 1 reference samples from the substance/substance group *Proline (-L) NF (H1050)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Proline (-L) NF (H1050)	16000951	80936	40

- 22959 spectra from a total of 503 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 3 spectra from 2 *Apo-Ident* customers from 2 batches from the substance/substance group *Proline (-L) NF (H1050)*.
- Among them are spectra of independent samples from 1 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
Hepart	Proline (-L) NF (H1050)	17000952	2
Hepart	Proline (-L) NF (H1050)	17000952/0	1

- 2967 spectra from 26 *Apo-Ident* customers from a total of 1458 batches from a further 62 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Proline (-L) NF (H1050)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this

purpose, all relevant spectra of the various substances were compared with *Proline (-L) NF (H1050)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	160	0	28 316
Type B	0	35	5	22 959
Type C	0	3	0	2967

The substance/substance group *Proline (-L) NF (H1050)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9278 %)	100.0000 % (> 96.2500 %)
Type B	100.0000 % (> 99.8691 %)	87.5000 % (> 80.0000 %)
Type C	100.0000 % (> 98.9458 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80905	80905	0.00	26.88
80935	80935	0.00	26.24
81023	81023	0.00	29.00
81146	81146	0.00	23.72

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Psyllium husks (H1527)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 10006097-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Psyllium husks (H1527)

Special notes

When selecting the *Psyllium husks (H1527)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Psyllium husks (H1527)	1	0	0

Second-stage model

For differentiation of the substance/substance group *Psyllium husks (H1527)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Psyllium husks (H1527)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Saffron style (H1434)	19.87	—
Marshmallow extract (H1439)	23.76	—
Vitamin B1 (H1101)	24.84	—
Gentian extract (H1438)	26.91	—
Lycopene (H1058)	28.54	—
Coenzyme Q10 (H1013)	30.15	—
Silicium (H1070)	30.85	—
Selenium yeast (H1068)	33.69	—
Ginseng (H1018)	33.99	—
Zinc (H1110)	39.07	—
Juniper (H1112)	40.20	—
Baobab (H1410)	40.50	—
Arginine (L-) (H1036)	40.96	—
Magnesium (H1060)	41.21	—
Boron (H1005)	41.56	—
Artichoke extract (H1440)	41.64	—
Detox complex (H1111)	45.30	—
Saffron flowers (H1435)	46.62	—
Vitamin K2 (75µg Mono) (H1108)	47.67	—
Leaky gut complex (H1802)	48.05	—
Calcium L-(+) -lactate complex (H1008)	48.20	—
Garcinia cambogia (H1017)	48.36	—
Artemisia annua extract (H1118)	48.57	—
Glutathione (H1020)	48.64	—
Orthovimin Neutral Complex (H1404)	49.10	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Psyllium husks (H1527)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Psyllium husks (H1527)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Psyllium husks (H1527)	23000150	81468	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 40 spectra of 1 reference samples from the substance/substance group *Psyllium husks (H1527)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 1 different batches.
- 28 436 spectra from a total of 577 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 0 spectra of 0 reference samples from the substance/substance group *Psyllium husks (H1527)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.
- 22 999 spectra from a total of 504 batches from further 78 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *Psyllium husks (H1527)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Psyllium husks (H1527)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Psyllium husks (H1527)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	40	0	28 436
Type B	0	0	0	22 999
Type C	0	0	0	2970

The substance/substance group *Psyllium husks (H1527)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9295 %)	100.0000 % (> 85.0000 %)
Type B	100.0000 % (> 99.8687 %)	n/a (n/a)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
81468	81468	0.00	20.90

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Pumpkin seed protein (H1509)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 10006065-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Pumpkin seed protein (H1509)

Special notes

When selecting the *Pumpkin seed protein (H1509)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Pumpkin seed protein (H1509)	2	0	0

Second-stage model

For differentiation of the substance/substance group *Pumpkin seed protein (H1509)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Pumpkin seed protein (H1509)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Aminomix NAC (H1002)	15.11	—
Glutamine (L-) (H1043)	27.68	—
Antibiosis forte complex (H1115)	29.28	—
Carnitine (L-) (H1038)	29.61	—
Coenzyme Q10 (H1013)	32.24	—
Isoflavone (H1025)	39.17	—
Vitamin B1 (H1101)	40.51	—
Lupin protein complex (H1510)	46.07	—
Amino V complex (H1400)	47.26	—
Glutathione (H1020)	49.34	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Pumpkin seed protein (H1509)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Pumpkin seed protein (H1509)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Pumpkin seed protein (H1509)	22002186	81456	40	from supplier
Hepart	Pumpkin seed protein (H1509)	23002724	81532	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 80 spectra of 2 reference samples from the substance/substance group *Pumpkin seed protein (H1509)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 2 different batches.
- 28 396 spectra from a total of 576 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 0 spectra of 0 reference samples from the substance/substance group *Pumpkin seed protein (H1509)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.
- 22 999 spectra from a total of 504 batches from further 78 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *Pumpkin seed protein (H1509)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Pumpkin seed protein (H1509)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Pumpkin seed protein (H1509)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	80	0	28 396
Type B	0	0	0	22 999
Type C	0	0	0	2970

The substance/substance group *Pumpkin seed protein (H1509)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate* (*specificity*) and the weighted *true positive rate* (*recognition rate*) are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9284 %)	100.0000 % (> 92.5000 %)
Type B	100.0000 % (> 99.8687 %)	n/a (n/a)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
81456	81456	0.00	21.90
81532	81532	0.00	34.06

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Quercetin dihydrate (H1130)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 10006007-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Quercetin dihydrate (H1130)

Special notes

When selecting the *Quercetin dihydrate (H1130)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Quercetin dihydrate (H1130)	2	0	0

Second-stage model

For differentiation of the substance/substance group *Quercetin dihydrate (H1130)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Quercetin dihydrate (H1130)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Iron (H1015)	32.80	—
Calcium L-(+)-lactate complex (H1008)	48.65	—
Griffonia (H1035)	50.90	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Quercetin dihydrate (H1130)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Quercetin dihydrate (H1130)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Quercetin dihydrate (H1130)	22000700	81442	40	from supplier
Hepart	Quercetin dihydrate (H1130)	24000012	81530	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 80 spectra of 2 reference samples from the substance/substance group *Quercetin dihydrate (H1130)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 2 different batches.
- 28 396 spectra from a total of 576 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples

are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a †. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 0 spectra of 0 reference samples from the substance/substance group *Quercetin dihydrate (H1130)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.
- 22 999 spectra from a total of 504 batches from further 78 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *Quercetin dihydrate (H1130)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Quercetin dihydrate (H1130)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Quercetin dihydrate (H1130)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	80	0	28 396
Type B	0	0	0	22 999
Type C	0	0	0	2970

The substance/substance group *Quercetin dihydrate (H1130)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9284 %)	100.0000 % (> 92.5000 %)
Type B	100.0000 % (> 99.8687 %)	n/a (n/a)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
81442	81442	0.00	69.21
81530	81530	0.00	51.57

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Resveratrol (H1063)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 10006137-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Resveratrol (H1063)

Special notes

When selecting the *Resveratrol (H1063)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Resveratrol (H1063)	1	0	0

Second-stage model

For differentiation of the substance/substance group *Resveratrol (H1063)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Resveratrol (H1063)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Iron (H1015)	65.81	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Resveratrol (H1063)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Resveratrol (H1063)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Resveratrol (H1063)	23001206	81492	35	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 35 spectra of 1 reference samples from the substance/substance group *Resveratrol (H1063)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 1 different batches.
- 28 441 spectra from a total of 577 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 0 spectra of 0 reference samples from the substance/substance group *Resveratrol (H1063)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.
- 22 999 spectra from a total of 504 batches from further 78 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *Resveratrol (H1063)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Resveratrol (H1063)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Resveratrol (H1063)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	35	0	28 441
Type B	0	0	0	22 999
Type C	0	0	0	2970

The substance/substance group *Resveratrol (H1063)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9299 %)	100.0000 % (> 82.8571 %)
Type B	100.0000 % (> 99.8687 %)	n/a (n/a)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
81492	81492	0.00	87.35

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **s-Adenosyl-L-methionine (H1441)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 10006407-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

s-Adenosyl-L-methionine (H1441)

Special notes

When selecting the *s-Adenosyl-L-methionine (H1441)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
s-Adenosyl-L-methionine (H1441)	1	1	0

Second-stage model

For differentiation of the substance/substance group *S-Adenosyl-L-methionine (H1441)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *S-Adenosyl-L-methionine (H1441)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Antibiosis forte complex (H1115)	52.47	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *S-Adenosyl-L-methionine (H1441)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *S-Adenosyl-L-methionine (H1441)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	s-Adenosyl-L-methionine (...)	24000214/0	81537	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 40 spectra of 1 reference samples from the substance/substance group *S-Adenosyl-L-methionine (H1441)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 1 different batches.
- 28 436 spectra from a total of 577 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 40 spectra of 1 reference samples from the substance/substance group *s-Adenosyl-L-methionine (H1441)*.
- Among them are spectra of independent samples from 1 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	s-Adenosyl-L-methionine (...)	24002110/0	81559	40

- 22 959 spectra from a total of 503 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *s-Adenosyl-L-methionine (H1441)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *s-Adenosyl-L-methionine (H1441)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *s-Adenosyl-L-methionine (H1441)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	40	0	28 436
Type B	0	9	31	22 959
Type C	0	0	0	2970

The substance/substance group *s-Adenosyl-L-methionine (H1441)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9295 %)	100.0000 % (> 85.0000 %)
Type B	100.0000 % (> 99.8691 %)	22.5000 % (> 15.0000 %)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
81537	81537	0.00	52.47

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Silymarin (H1071)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80068-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Silymarin (H1071)

Special notes

When selecting the *Silymarin (H1071)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Silymarin (H1071)	3	3	18

Second-stage model

For differentiation of the substance/substance group *Silymarin (H1071)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Silymarin (H1071)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Calcium L-(+)-lactate complex (H1008)	17.86	—
ginkgo extract (H1024)	21.40	—
Carnitine (L-) (H1038)	21.89	—
OPC Proanthocyanidins (Pine Bark) (...)	22.30	—
Coenzyme Q10 (H1013)	25.32	—
Betaine hydrochloride (H1119)	25.85	—
Antioxidants NAT complex (H1004)	29.37	—
Orthocolon complex (H1800)	34.37	—
Rhodiola (H1064)	34.50	—
Arginine (L-) (H1036)	36.68	—
Aminomix NAC (H1002)	38.49	—
Garcinia cambogia (H1017)	41.35	—
Flavour orange (H1405)	41.71	—
Vitamin B1 (H1101)	42.73	—
Griffonia (H1035)	42.93	—
Glutathione (H1020)	46.96	—
Seabuckthorn (H1523)	47.00	—
Vitamin B6 (Pyridoxal 5'-phosphate)...	47.56	—
Antibiosis forte complex (H1115)	48.58	—
Sunflower seed protein (H1511)	49.81	—
Isoflavone (H1025)	50.07	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Silymarin (H1071)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Silymarin (H1071)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Silymarin (H1071)	15001046	80671	60	from supplier
Hepart	Silymarin (H1071)	16001084	80861	40	from supplier
Hepart	Silymarin (H1071)	21001429	81360	50	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 150 spectra of 3 reference samples from the substance/substance group *Silymarin (H1071)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 3 different batches.
- 28 326 spectra from a total of 575 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 120 spectra of 3 reference samples from the substance/substance group *Silymarin (H1071)*.
- Among them are spectra of independent samples from 3 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Silymarin (H1071)	067701	80375	40
Hepart	Silymarin (H1071)	16001084/0	81159	40
Hepart	Silymarin (H1071)	20002154	81322	40

- 22 879 spectra from a total of 501 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 34 spectra from 12 *Apo-Ident* customers from 19 batches from the substance/substance group *Silymarin (H1071)*.
- Among them are spectra of independent samples from 18 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
Flaigg Ag CH-4147 Ae...	Silymarin (H1071)	16001084/2	1
HCK	Silymarin (H1071)	15001046/0	1
HCK	Silymarin (H1071)	67701/7	1
Hepart AG, CH-8280 K...	Silymarin (H1071)	1241046101	1
Hepart AG, CH-8280 K...	Silymarin (H1071)	1241950401	1
Hepart AG, CH-8280 K...	Silymarin (H1071)	29901	2
Hepart AG	Silymarin (H1071)	1244029901	1
hepart ag	Silymarin (H1071)	1244950401	1
Hepart AG	Silymarin (H1071)	67701	1
Hepart	Silymarin (H1071)	15001046	1
Hepart	Silymarin (H1071)	16001084/1	1
Hepart	Silymarin (H1071)	16001084/2	2
Hepart	Silymarin (H1071)	16001084/3	1
Hepart	Silymarin (H1071)	20001783/0	1
Hepart	Silymarin (H1071)	20002154/0	2
Hepart	Silymarin (H1071)	20002154/1	2
Hepart	Silymarin (H1071)	60010841	1
Unisan/Hepart AG	Silymarin (H1071)	29901	1
Unisan	Silymarin (H1071)	15001046	2
Unisan	Silymarin (H1071)	15001046/1	1
Unisan	Silymarin (H1071)	29901	3
Unisan	Silymarin (H1071)	46101	1
Unisan	Silymarin (H1071)	67701	2
UNISAN	Silymarin (H1071)	67701	1
Unisan	Silymarin (H1071)	67701/7	1
Unisan	Silymarin (H1071)	950401	1

- 2936 spectra from 26 *Apo-Ident* customers from a total of 1441 batches from a further 62 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Silymarin (H1071)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Silymarin (H1071)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	150	0	28 326
Type B	0	86	34	22 879
Type C	0	20	14	2936

The substance/substance group *Silymarin (H1071)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9279 %)	100.0000 % (> 96.0000 %)
Type B	100.0000 % (> 99.8655 %)	71.6667 % (> 69.1667 %)
Type C	100.0000 % (> 98.8318 %)	58.8235 % (> 50.0000 %)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several

new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80671	80671	0.00	25.85
80861	80861	0.00	23.98
81360	81360	0.00	22.23

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Stomach complex (H1532)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 10006507-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Stomach complex (H1532)

Special notes

When selecting the *Stomach complex (H1532)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Stomach complex (H1532)	1	0	0

Second-stage model

For differentiation of the substance/substance group *Stomach complex (H1532)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Stomach complex (H1532)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Antioxidants NAT complex (H1004)	35.75	—
Antibiosis forte complex (H1115)	35.77	—
PET immune system (H1502)	37.63	—
Green coffee extract (H1433)	38.05	—
PET basis (H1503)	40.28	—
Carnitine (L-) (H1038)	40.72	—
Coenzyme Q10 (H1013)	42.51	—
Vitamin B1 (H1101)	46.41	—
Yeast organic (H1525)	46.56	—
a-Lipoic acid (H1000)	47.05	—
Vitamin C (H1104)	53.96	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Stomach complex (H1532)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Stomach complex (H1532)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Stomach complex (H1532)	24001421	81561	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 40 spectra of 1 reference samples from the substance/substance group *Stomach complex (H1532)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 1 different batches.
- 28 436 spectra from a total of 577 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a †. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 0 spectra of 0 reference samples from the substance/substance group *Stomach complex (H1532)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.
- 22 999 spectra from a total of 504 batches from further 78 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *Stomach complex (H1532)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Stomach complex (H1532)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Stomach complex (H1532)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	40	0	28 436
Type B	0	0	0	22 999
Type C	0	0	0	2970

The substance/substance group *Stomach complex (H1532)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9295 %)	100.0000 % (> 85.0000 %)
Type B	100.0000 % (> 99.8687 %)	n/a (n/a)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
81561	81561	0.00	35.77

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Sunflower seed protein (H1511)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 10006063-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Sunflower seed protein (H1511)

Special notes

When selecting the *Sunflower seed protein (H1511)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Sunflower seed protein (H1511)	1	0	0

Second-stage model

For differentiation of the substance/substance group *Sunflower seed protein (H1511)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Sunflower seed protein (H1511)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Coenzyme Q10 (H1013)	23.29	—
Carnitine (L-) (H1038)	24.69	—
Calcium L-(+) -lactate complex (H1008)	27.36	—
Vitamin B1 (H1101)	32.66	—
Silymarin (H1071)	32.85	—
Aminomix NAC (H1002)	34.47	—
Flavour orange (H1405)	34.73	—
ginkgo extract (H1024)	34.97	—
Arginine (L-) (H1036)	35.66	—
Leaky gut complex (H1802)	36.62	—
Pumpkin seed protein (H1509)	37.72	—
Isoflavone (H1025)	37.95	—
Antioxidants NAT complex (H1004)	39.10	—
Orthocolon complex (H1800)	39.12	—
Betaine hydrochloride (H1119)	40.69	—
Glutathione (H1020)	42.08	—
Antibiosis forte complex (H1115)	43.69	—
Oat bran beta-glucan (H1529)	44.38	—
OPC Proanthocyanidins (Pine Bark) (...)	46.28	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Sunflower seed protein (H1511)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Sunflower seed protein (H1511)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Sunflower seed protein (H1511)	22002178	81453	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 40 spectra of 1 reference samples from the substance/substance group *Sunflower seed protein (H1511)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 1 different batches.
- 28 436 spectra from a total of 577 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 0 spectra of 0 reference samples from the substance/substance group *Sunflower seed protein (H1511)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.
- 22 999 spectra from a total of 504 batches from further 78 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *Sunflower seed protein (H1511)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Sunflower seed protein (H1511)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Sunflower seed protein (H1511)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	40	0	28 436
Type B	0	0	0	22 999
Type C	0	0	0	2970

The substance/substance group *Sunflower seed protein (H1511)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9295 %)	100.0000 % (> 85.0000 %)
Type B	100.0000 % (> 99.8687 %)	n/a (n/a)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
81453	81453	0.00	29.95

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Taurine (H1084)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80071-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Taurine (H1084)

Special notes

When selecting the *Taurine (H1084)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Taurine (H1084)	6	5	15

Second-stage model

For differentiation of the substance/substance group *Taurine (H1084)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Taurine (H1084)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Antibiosis forte complex (H1115)	57.51	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Taurine (H1084)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Taurine (H1084)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Taurine (H1084)	14001767	80497	60	from supplier
Hepart	Taurine (H1084)	16000946	80809	40	from supplier
Hepart	Taurine (H1084)	16000946	80887	40	from supplier
Hepart	Taurine (H1084)	18000419	81063	40	from supplier
Hepart	Taurine (H1084)	21001444	81355	50	from supplier
Hepart	Taurine (H1084)	20001267	81382	50	from supplier
Hepart	Taurine (H1084)	22000694	81425	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 320 spectra of 7 reference samples from the substance/substance group *Taurine (H1084)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 6 different batches.

- 28 156 spectra from a total of 572 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 200 spectra of 5 reference samples from the substance/substance group *Taurine (H1084)*.
- Among them are spectra of independent samples from 5 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Taurine (H1084)	16000947	80810	40
Hepart	Taurine (H1084)	19000847	81160	40
Hepart	Taurine (H1084)	20001002	81288	40
Hepart	Taurine (H1084)	22002118	81454	40
Hepart	Taurine (H1084)	23001634	81498	40

- 22 799 spectra from a total of 499 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 47 spectra from 18 *Apo-Ident* customers from 18 batches from the substance/substance group *Taurine (H1084)*.
- Among them are spectra of independent samples from 15 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
HCK	Taurine (H1084)	14001767-6	1
Hepart AG, CH-8280 K...	Taurine (H1084)	25710	3
Hepart ag/Unisan	Taurine (H1084)	19000847	1
Hepart AG	Taurine (H1084)	14001767/3	4
Hepart AG	Taurine (H1084)	16000947/0	1
Hepart AG	Taurine (H1084)	16000947/2	1
Hepart AG	Taurine (H1084)	2656905/0	2
Hepart AG	Taurine (H1084)	28001	2

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Supplier	Substance	Batch	Spectra
Hepart/Unisan	Taurine (H1084)	14001767/3	1
Hepart	Taurine (H1084)	16000946	1
Hepart	Taurine (H1084)	16000946/1	2
Hepart	Taurine (H1084)	160009460/2	1
Hepart	Taurine (H1084)	16000947	5
Hepart	Taurine (H1084)	16000947/0	1
Hepart	Taurine (H1084)	16000947/2	2
Hepart	Taurine (H1084)	160009470	1
Hepart	Taurine (H1084)	20001002	1
Hepart	Taurine (H1084)	21001444	1
Unisan/Hepart AG	Taurine (H1084)	28001	1
Unisan	Taurine (H1084)	1294960201	2
unisan	Taurine (H1084)	14001767	2
Unisan	Taurine (H1084)	14001767/0	1
Unisan	Taurine (H1084)	16000946	1
Unisan	Taurine (H1084)	16000946/1	1
Unisan	Taurine (H1084)	28001	8

- 2923 spectra from 26 *Apo-Ident* customers from a total of 1442 batches from a further 62 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Taurine (H1084)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Taurine (H1084)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	320	0	28 156
Type B	0	200	0	22 799
Type C	0	46	1	2923

The substance/substance group *Taurine (H1084)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9275 %)	100.0000 % (> 98.1250 %)
Type B	100.0000 % (> 99.8648 %)	100.0000 % (> 97.0000 %)
Type C	100.0000 % (> 98.8288 %)	97.8723 % (> 91.4894 %)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra ([Rule of Three](#) [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80497	80497	0.00	59.85
80809	80809	0.00	62.37
80887	80887	0.00	61.86
81063	81063	0.00	60.76
81355	81355	0.00	61.45
81382	81382	0.00	62.76
81425	81425	0.00	57.51

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Threonine (L-) (H1052)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80107-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Threonine (L-) (H1052)

Special notes

When selecting the *Threonine (L-) (H1052)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Threonine (L-) (H1052)	1	2	15

Second-stage model

For differentiation of the substance/substance group *Threonine (L-) (H1052)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Threonine (L-) (H1052)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Glycine (H1021)	48.49	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Threonine (L-) (H1052)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Threonine (L-) (H1052)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Threonine (L-) (H1052)	14001718	80496	60	from supplier
Hepart	Threonine (L-) (H1052)	14001718	81018	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 100 spectra of 2 reference samples from the substance/substance group *Threonine (L-) (H1052)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 1 different batches.
- 28 376 spectra from a total of 577 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with

the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 80 spectra of 2 reference samples from the substance/substance group *Threonine (L-) (H1052)*.
- Among them are spectra of independent samples from 2 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Threonine (L-) (H1052)	17000875	80920	40
Hepart	Threonine (L-) (H1052)	18001023	81077	40

- 22919 spectra from a total of 502 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 25 spectra from 11 *Apo-Ident* customers from 16 batches from the substance/substance group *Threonine (L-) (H1052)*.
- Among them are spectra of independent samples from 15 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
HCK	Threonine (L-) (H1052)	14001718/2	1
HCK	Threonine (L-) (H1052)	14001718/9	1
HCK	Threonine (L-) (H1052)	14001718-4	2
HCK	Threonine (L-) (H1052)	14001718-5	2
Hedinger	Threonine (L-) (H1052)	25708	3
Hepart AG	Threonine (L-) (H1052)	1700875/5	1
Hepart/Unisan	Threonine (L-) (H1052)	14001718/3	1
Hepart/Unisan	Threonine (L-) (H1052)	14001718/9	1
Hepart	Threonine (L-) (H1052)	14001718-6	1
Hepart	Threonine (L-) (H1052)	14001718-7	1
Hepart	Threonine (L-) (H1052)	14001718-9	1
Hepart	Threonine (L-) (H1052)	17000875	1
Hepart	Threonine (L-) (H1052)	17000875/1	1
Purren Apotheke	Threonine (L-) (H1052)	1833014901	1
Unisan	Threonine (L-) (H1052)	14001718	2
Unisan	Threonine (L-) (H1052)	14001718/1	1

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Supplier	Substance	Batch	Spectra
Unisan	Threonine (L-) (H1052)	14001718/7	1
unisan	Threonine (L-) (H1052)	25708	1
Unisan	Threonine (L-) (H1052)	25708	1
UNISAN	Threonine (L-) (H1052)	25708	1

- 2945 spectra from 26 *Apo-Ident* customers from a total of 1444 batches from a further 62 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Threonine (L-) (H1052)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Threonine (L-) (H1052)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	100	0	28 376
Type B	0	80	0	22 919
Type C	0	19	6	2945

The substance/substance group *Threonine (L-) (H1052)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9282 %)	100.0000 % (> 94.0000 %)
Type B	100.0000 % (> 99.8664 %)	100.0000 % (> 92.5000 %)
Type C	100.0000 % (> 98.8358 %)	76.0000 % (> 64.0000 %)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra ([Rule of Three](#) [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the [Mahalanobis distance](#) to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80496	80496	0.00	55.85
81018	81018	0.00	59.24

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Trace elements BAG (H1078) / Zinc (H1110)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80503-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Trace elements BAG (H1078) / Zinc (H1110); Trace elements BAG (H1078); Zinc (H1110)

Special notes

When selecting the *Trace elements BAG (H1078) / Zinc (H1110)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Trace elements BAG (H1078) / Zinc (H1110)	9	4	28

Second-stage model

For differentiation of the substance/substance group *Trace elements BAG (H1078) / Zinc (H1110)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Trace elements BAG (H1078) / Zinc (H1110)* in the substance class *HCK - nutritional supplements (Hep-art)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Vitamin B12 (H1102)	15.14	—
Selenium (H1067)	18.72	—
Magnesium (H1060)	20.20	—
Biotin (H1007)	23.45	—
Ginseng (H1018)	23.64	—
Chromium (H1012)	24.23	—
Vitamin D3 (H1105)	24.55	—
Saffron style (H1434)	30.92	—
Selenium yeast (H1068)	31.39	—
Trace elements JK (H1080)	31.56	—
Vitamin K2 (75µg Mono) (H1108)	31.60	—
Artichoke extract (H1440)	34.63	—
Lycopene (H1058)	34.77	—
Gentian extract (H1438)	35.45	—
Chondroitin sulfate (H1065)	37.79	—
Marshmallow extract (H1439)	38.28	—
Boron (H1005)	38.72	—
Coenzyme Q10 (H1013)	38.80	—
Ashwagandha (H1132)	40.67	—
Vitamin E NAT (H1107)	42.29	—
Guar (H1023)	44.07	—
Orthovimin Neutral Complex (H1404)	48.40	—
Artemisia annua extract (H1118)	49.93	—
Levomefolic acid (L-5-MTHF) (H1128)	50.02	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Trace elements BAG (H1078) / Zinc (H1110)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Trace elements BAG (H1078) / Zinc (H1110)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Trace elements BAG (H1078)	16000795	80799	40	from supplier
Hepart	Trace elements BAG (H1078)	16000796	80800	40	from supplier
Hepart	Zinc (H1110)	14001803	80503	60	from supplier
Hepart	Zinc (H1110)	16000196	80761	60	from supplier
Hepart	Zinc (H1110)	16000518	80789	40	from supplier
Hepart	Zinc (H1110)	18001012	81068	40	from supplier
Hepart	Zinc (H1110)	18000559	81069	40	from supplier
Hepart	Zinc (H1110)	21001425	81358	50	from supplier
Hepart	Zinc (H1110)	22000935	81431	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 410 spectra of 9 reference samples from the substance/substance group *Trace elements BAG (H1078) / Zinc (H1110)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 9 different batches.
- 28 066 spectra from a total of 569 batches from further 129 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 180 spectra of 4 reference samples from the substance/substance group *Trace elements BAG (H1078) / Zinc (H1110)*.
- Among them are spectra of independent samples from 4 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Trace elements BAG (H1078)	16000797	80801	40
Hepart	Zinc (H1110)	14001753	80489	60
Hepart	Zinc (H1110)	16000519	80790	40
Hepart	Zinc (H1110)	20002833	81353	40

- 22 819 spectra from a total of 500 batches from further 76 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the

substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 96 spectra from 20 *Apo-Ident* customers from 32 batches from the substance/substance group *Trace elements BAG (H1078) / Zinc (H1110)*.
- Among them are spectra of independent samples from 28 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
HCK	Zinc (H1110)	14001753/1	1
HCK	Zinc (H1110)	14001803/2	1
HCK	Zinc (H1110)	14001803-3	1
HCK	Zinc (H1110)	16000196/0	1
HCK	Zinc (H1110)	16000196-1	1
Hepart ag /Unisan	Zinc (H1110)	18001012	2
Hepart AG, CH-8280 K...	Zinc (H1110)	1164991001	1
Hepart AG	Zinc (H1110)	1164991001	3
Hepart AG	Zinc (H1110)	14001803/2	1
Hepart AG	Zinc (H1110)	16000518/1	1
Hepart AG	Zinc (H1110)	16000519/0	9
Hepart AG	Zinc (H1110)	18000559/1	1
Hepart AG	Zinc (H1110)	41501	7
Hepart AG	Zinc (H1110)	991001	3
Hepart/Unisan	Zinc (H1110)	14001803/2	1
Hepart/Unisan	Zinc (H1110)	18001012/0	1
Hepart	Zinc (H1110)	14001803	1
Hepart	Zinc (H1110)	16000196	3
Hepart	Zinc (H1110)	16000518	2
Hepart	Zinc (H1110)	16000518/1	3
Hepart	Zinc (H1110)	16000518-1	1
Hepart	Zinc (H1110)	16000519	1
Hepart	Zinc (H1110)	16000519/0	2
Hepart	Zinc (H1110)	16000519/1	1
Hepart	Zinc (H1110)	18000559/0	3
Hepart	Zinc (H1110)	18000559/1	2
Hepart	Zinc (H1110)	18000559/2	2
Hepart	Zinc (H1110)	18001012/0	2
Hepart	Zinc (H1110)	18001012/1	1
Hepart	Zinc (H1110)	18001012/2	3
Hepart	Zinc (H1110)	1800559/0	1
Hepart	Zinc (H1110)	20002833/0	2
Hepart	Zinc (H1110)	21001425/0	1
Hepart	Zinc (H1110)	21001425/1	1
Hepart	Zinc (H1110)	xxxx	1
Unisan GmbH, 78465 K...	Zinc (H1110)	991001	1
Unisan	Zinc (H1110)	1164949701	1
Unisan	Zinc (H1110)	1164991001	2
Unisan	Zinc (H1110)	14001753	1
Unisan	Zinc (H1110)	14001753/0	1
Unisan	Zinc (H1110)	14001803	3
Unisan	Zinc (H1110)	14001803/1	1
Unisan	Zinc (H1110)	16000196	3
Unisan	Zinc (H1110)	16000196/0	2
Unisan	Zinc (H1110)	16000518	1
Unisan	Zinc (H1110)	41501	5

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Supplier	Substance	Batch	Spectra
Unisan	Zinc (H1110)	991001	7

- 2874 spectra from 26 *Apo-Ident* customers from a total of 1428 batches from a further 62 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Trace elements BAG (H1078) / Zinc (H1110)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Trace elements BAG (H1078) / Zinc (H1110)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	410	0	28 066
Type B	0	176	4	22 819
Type C	0	93	3	2874

The substance/substance group *Trace elements BAG (H1078) / Zinc (H1110)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9275 %)	100.0000 % (> 98.5366 %)
Type B	100.0000 % (> 99.8649 %)	97.7778 % (> 96.1111 %)
Type C	100.0000 % (> 98.8247 %)	96.8750 % (> 93.7500 %)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80503	80503	0.00	29.40
80761	80761	0.00	23.64
80789	80789	0.00	19.86
80799	80799	0.00	35.76

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Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80800	80800	0.00	34.27
81068	81068	0.00	21.96
81069	81069	0.00	24.20
81358	81358	0.00	20.53
81431	81431	0.00	22.82

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Trace elements BAG complex (H1079)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 10006318-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Trace elements BAG complex (H1079)

Special notes

When selecting the *Trace elements BAG complex (H1079)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Trace elements BAG complex (H1079)	1	0	0

Second-stage model

For differentiation of the substance/substance group *Trace elements BAG complex (H1079)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Trace elements BAG complex (H1079)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Magnesium (H1060)	16.34	—
Garcinia cambogia (H1017)	21.45	—
Trace elements JK (H1080)	32.45	—
Copper (H1032)	34.25	—
Trace elements SE complex (H1082)	34.27	—
Potassium (H1030)	45.73	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Trace elements BAG complex (H1079)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Trace elements BAG complex (H1079)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Trace elements BAG comple...	23002044	81511	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 40 spectra of 1 reference samples from the substance/substance group *Trace elements BAG complex (H1079)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 1 different batches.
- 28 436 spectra from a total of 577 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the

substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 0 spectra of 0 reference samples from the substance/substance group *Trace elements BAG complex (H1079)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.
- 22 999 spectra from a total of 504 batches from further 78 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *Trace elements BAG complex (H1079)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Trace elements BAG complex (H1079)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Trace elements BAG complex (H1079)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	40	0	28 436
Type B	0	0	0	22 999
Type C	0	0	0	2970

The substance/substance group *Trace elements BAG complex (H1079)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate* (*specificity*) and the weighted *true positive rate* (*recognition rate*) are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9295 %)	100.0000 % (> 85.0000 %)
Type B	100.0000 % (> 99.8687 %)	n/a (n/a)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
81511	81511	0.00	20.89

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Trace elements SE complex (H1082)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 10005866-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Trace elements SE complex (H1082)

Special notes

When selecting the *Trace elements SE complex (H1082)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Trace elements SE complex (H1082)	14	15	13

Second-stage model

For differentiation of the substance/substance group *Trace elements SE complex (H1082)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Trace elements SE complex (H1082)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Copper (H1032)	21.44	—
Magnesium (H1060)	24.88	—
Garcinia cambogia (H1017)	30.12	—
Iron (H1015)	35.62	—
Chaga (H1011)	36.62	—
Argentum (H1116)	40.50	—
Potassium (H1030)	45.74	—
Walnut leaf (H1114)	49.12	—
Trace elements BAG complex (H1079)	57.93	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Trace elements SE complex (H1082)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Trace elements SE complex (H1082)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Trace elements SE complex...	14000722	80459	40	from supplier
Hepart	Trace elements SE complex...	14000721	80461	40	from supplier
Hepart	Trace elements SE complex...	14000721	80464	40	from supplier
Hepart	Trace elements SE complex...	15000555	80588	60	from supplier
Hepart	Trace elements SE complex...	15000555 (F2)	80590	60	from supplier
Hepart	Trace elements SE complex...	15000556 (B1)	80592	60	from supplier
Hepart	Trace elements SE complex...	15000557	80594	60	from supplier
Hepart	Trace elements SE complex...	15000557 (B1)	80595	60	from supplier
Hepart	Trace elements SE complex...	15000558 (B1)	80598	60	from supplier
Hepart	Trace elements SE complex...	15000553	80600	60	from supplier
Hepart	Trace elements SE complex...	15000553 (F2)	80602	60	from supplier
Hepart	Trace elements SE complex...	17000888	80961	40	from supplier
Hepart	Trace elements SE complex...	17000887	80962	40	from supplier
Hepart	Trace elements SE complex...	19001260	81187	40	from supplier
Hepart	Trace elements SE complex...	21000339	81407	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 760 spectra of 15 reference samples from the substance/substance group *Trace elements SE complex (H1082)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 14 different batches.
- 27716 spectra from a total of 564 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 860 spectra of 18 reference samples from the substance/substance group *Trace elements SE complex (H1082)*.
- Among them are spectra of independent samples from 15 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Trace elements SE complex...	14000720	80460	40
Hepart	Trace elements SE complex...	15000555(B1)	80589	60
Hepart	Trace elements SE complex...	15000556	80591	60
Hepart	Trace elements SE complex...	15000556(F2)	80593	60
Hepart	Trace elements SE complex...	15000557(F2)	80596	60
Hepart	Trace elements SE complex...	15000558	80597	60
Hepart	Trace elements SE complex...	15000558(F2)	80599	60
Hepart	Trace elements SE complex...	15000553(B1)	80601	60
Hepart	Trace elements SE complex...	17000886	80960	40
Hepart	Trace elements SE complex...	19001256	81186	40
Hepart	Trace elements SE complex...	20000407	81260	40
Hepart	Trace elements SE complex...	20001880	81277	40
Hepart	Trace elements SE complex...	20002693	81296	40
Hepart	Trace elements SE complex...	21000339-338-261	81339	40
Hepart	Trace elements SE complex...	23001536	81504	40
Hepart	Trace elements SE complex...	14000722	80462	40
Hepart	Trace elements SE complex...	14000720	80463	40
Hepart	Trace elements SE complex...	15000558	80979	40

- 22 139 spectra from a total of 488 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 24 spectra from 9 *Apo-Ident* customers from 14 batches from the substance/substance group *Trace elements SE complex (H1082)*.
- Among them are spectra of independent samples from 13 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
Hepart AG/Unisan	Trace elements SE complex...	19001256/0	1
Hepart AG/Unisan	Trace elements SE complex...	20001880/0	1
Hepart AG	Trace elements SE complex...	17000886/0	1
Hepart AG	Trace elements SE complex...	17000887/0	2
Hepart AG	Trace elements SE complex...	19001256/0	1
Hepart/Unisan	Trace elements SE complex...	20001880/0	1
Hepart	Trace elements SE complex...	15000555/0	1
Hepart	Trace elements SE complex...	17000886/0	1
Hepart	Trace elements SE complex...	17000886/1	3
Hepart	Trace elements SE complex...	17000887/0	2
Hepart	Trace elements SE complex...	17000888/0	1
Hepart	Trace elements SE complex...	19001256	2
Hepart	Trace elements SE complex...	19001260/0	1
Hepart	Trace elements SE complex...	20000407	1
Hepart	Trace elements SE complex...	20001880	1
Hepart	Trace elements SE complex...	31301	2
Unisan	Trace elements SE complex...	15000555	1
Unisan	Trace elements SE complex...	15000556/0	1

- 2946 spectra from 26 *Apo-Ident* customers from a total of 1446 batches from a further 62 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Trace elements SE complex (H1082)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Trace elements SE complex (H1082)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	760	0	27 716
Type B	0	860	0	22 139
Type C	0	22	2	2946

The substance/substance group *Trace elements SE complex (H1082)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9274 %)	100.0000 % (> 99.2105 %)
Type B	100.0000 % (> 99.8640 %)	100.0000 % (> 99.3023 %)
Type C	100.0000 % (> 98.8364 %)	91.6667 % (> 79.1667 %)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80459	80459	0.00	31.62
80461	80461	0.00	32.09
80464	80464	0.00	32.98
80588	80588	0.00	50.20
80590	80590	0.00	49.22
80592	80592	0.00	44.30
80594	80594	0.00	45.85
80595	80595	0.00	44.70
80598	80598	0.00	53.03
80600	80600	0.00	45.63
80602	80602	0.00	45.11
80961	80961	0.00	48.39
80962	80962	0.00	47.12
81187	81187	0.00	25.57
81407	81407	0.00	51.85

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Tryptophan (L-) (H1053)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80127-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Tryptophan (L-) (H1053)

Special notes

When selecting the *Tryptophan (L-) (H1053)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Tryptophan (L-) (H1053)	6	2	30

Second-stage model

For differentiation of the substance/substance group *Tryptophan (L-) (H1053)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Tryptophan (L-) (H1053)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Phenylalanine (L-) (H1049)	31.27	—
Antibiosis forte complex (H1115)	63.05	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Tryptophan (L-) (H1053)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Tryptophan (L-) (H1053)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Tryptophan (L-) (H1053)	074501	80401	40	from supplier
Hepart	Tryptophan (L-) (H1053)	15000441	80581	60	from supplier
Hepart	Tryptophan (L-) (H1053)	16001394	80845	40	from supplier
Hepart	Tryptophan (L-) (H1053)	16001404	80846	40	from supplier
Hepart	Tryptophan (L-) (H1053)	20001589	81284	40	from supplier
Hepart	Tryptophan (L-) (H1053)	21001643	81379	50	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 270 spectra of 6 reference samples from the substance/substance group *Tryptophan (L-) (H1053)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 6 different batches.

- 28 206 spectra from a total of 572 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 100 spectra of 2 reference samples from the substance/substance group *Tryptophan (L-) (H1053)*.
- Among them are spectra of independent samples from 2 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Tryptophan (L-) (H1053)	15000443	80582	60
Hepart	Tryptophan (L-) (H1053)	19001101	81219	40

- 22 899 spectra from a total of 502 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 64 spectra from 16 *Apo-Ident* customers from 33 batches from the substance/substance group *Tryptophan (L-) (H1053)*.
- Among them are spectra of independent samples from 30 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
Caelo	Tryptophan (L-) (H1053)	15000441/4	1
Caelo	Tryptophan (L-) (H1053)	15000443/0	1
HCK	Tryptophan (L-) (H1053)	15000441	2
HCK	Tryptophan (L-) (H1053)	15000441/2	1
HCK	Tryptophan (L-) (H1053)	15000441-2	1
HCK	Tryptophan (L-) (H1053)	15000443	2
HCK	Tryptophan (L-) (H1053)	15000443-0	2
HCK	Tryptophan (L-) (H1053)	15000443-1	2
HCK	Tryptophan (L-) (H1053)	16001404	1
Hepart AG, CH-8280 K...	Tryptophan (L-) (H1053)	27901	1
Hepart ag/Unisan	Tryptophan (L-) (H1053)	19001101/0	1

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Supplier	Substance	Batch	Spectra
Hepart AG	Tryptophan (L-) (H1053)	160001404/3	1
Hepart AG	Tryptophan (L-) (H1053)	16001394/2	1
Hepart AG	Tryptophan (L-) (H1053)	16001404/3	3
Hepart AG	Tryptophan (L-) (H1053)	1824027901	2
Hepart AG	Tryptophan (L-) (H1053)	27901	4
Hepart AG	Tryptophan (L-) (H1053)	27902	1
Hepart	Tryptophan (L-) (H1053)	15000443-2	3
Hepart	Tryptophan (L-) (H1053)	15000443-3	1
Hepart	Tryptophan (L-) (H1053)	15000443-4	1
Hepart	Tryptophan (L-) (H1053)	16001394/0	3
Hepart	Tryptophan (L-) (H1053)	16001394/2	1
Hepart	Tryptophan (L-) (H1053)	16001404-0	5
Hepart	Tryptophan (L-) (H1053)	16001404-1	1
Hepart	Tryptophan (L-) (H1053)	19001101	1
Hepart	Tryptophan (L-) (H1053)	19001101/0	1
Hepart	Tryptophan (L-) (H1053)	20001589/0	1
Hepart	Tryptophan (L-) (H1053)	9001101/01	1
Purren Apotheke	Tryptophan (L-) (H1053)	1825950001	1
Purren Apotheke	Tryptophan (L-) (H1053)	978501	1
Unisan/Hepart AG	Tryptophan (L-) (H1053)	27901	1
unisan	Tryptophan (L-) (H1053)		1
Unisan	Tryptophan (L-) (H1053)	150000441	1
Unisan	Tryptophan (L-) (H1053)	15000441/4	1
Unisan	Tryptophan (L-) (H1053)	15000443	2
Unisan	Tryptophan (L-) (H1053)	15000443/0	1
Unisan	Tryptophan (L-) (H1053)	1824950001	2
Unisan	Tryptophan (L-) (H1053)	27901	1
Unisan	Tryptophan (L-) (H1053)	27902	2
Unisan	Tryptophan (L-) (H1053)	74501	2
Unisan	Tryptophan (L-) (H1053)	74501/4	1
Unisan	Tryptophan (L-) (H1053)	950001	1

- 2906 spectra from 26 *Apo-Ident* customers from a total of 1428 batches from a further 62 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Tryptophan (L-) (H1053)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Tryptophan (L-) (H1053)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	270	0	28 206
Type B	0	100	0	22 899
Type C	0	47	17	2906

The substance/substance group *Tryptophan (L-) (H1053)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9276 %)	100.0000 % (> 97.7778 %)
Type B	100.0000 % (> 99.8659 %)	100.0000 % (> 94.0000 %)
Type C	100.0000 % (> 98.8267 %)	73.4375 % (> 68.7500 %)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80401	80401	0.00	33.40
80581	80581	0.00	45.49
80845	80845	0.00	63.05
80846	80846	0.00	58.10
81284	81284	0.00	50.26
81379	81379	0.00	66.82

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Tyrosine (L-) (H1054)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80121-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Tyrosine (L-) (H1054)

Special notes

When selecting the *Tyrosine (L-) (H1054)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Tyrosine (L-) (H1054)	3	2	11

Second-stage model

For differentiation of the substance/substance group *Tyrosine (L-) (H1054)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Tyrosine (L-) (H1054)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Glycine (H1021)	63.64	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Tyrosine (L-) (H1054)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Tyrosine (L-) (H1054)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Tyrosine (L-) (H1054)	074601	80386	100	from supplier
Hepart	Tyrosine (L-) (H1054)	15001380	80704	60	from supplier
Hepart	Tyrosine (L-) (H1054)	18000412	81050	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 200 spectra of 3 reference samples from the substance/substance group *Tyrosine (L-) (H1054)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 3 different batches.
- 28 276 spectra from a total of 575 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with

the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 80 spectra of 2 reference samples from the substance/substance group *Tyrosine (L-) (H1054)*.
- Among them are spectra of independent samples from 2 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Tyrosine (L-) (H1054)	20000220	81267	40
Hepart	Tyrosine (L-) (H1054)	23001739	81506	40

- 22919 spectra from a total of 502 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 25 spectra from 9 *Apo-Ident* customers from 11 batches from the substance/substance group *Tyrosine (L-) (H1054)*.
- Among them are spectra of independent samples from 11 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
HCK	Tyrosine (L-) (H1054)	1380	1
Hepart AG	Tyrosine (L-) (H1054)	15001380/0	2
Hepart AG	Tyrosine (L-) (H1054)	29502	1
Hepart AG	Tyrosine (L-) (H1054)	74601	1
Hepart	Tyrosine (L-) (H1054)	15001380-1	5
Hepart	Tyrosine (L-) (H1054)	15001380-4	2
Hepart	Tyrosine (L-) (H1054)	18000412/0	2
Hepart	Tyrosine (L-) (H1054)	20000220	1
Unisan	Tyrosine (L-) (H1054)	29501	3
Unisan	Tyrosine (L-) (H1054)	29502	4
UNISAN	Tyrosine (L-) (H1054)	74601	1
Unisan	Tyrosine (L-) (H1054)	74601/3	1
Unisan	Tyrosine (L-) (H1054)	979102	1

- 2945 spectra from 26 *Apo-Ident* customers from a total of 1449 batches from a further 62 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Tyrosine (L-) (H1054)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Tyrosine (L-) (H1054)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	200	0	28 276
Type B	0	80	0	22 919
Type C	0	16	9	2945

The substance/substance group *Tyrosine (L-) (H1054)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9277 %)	100.0000 % (> 97.0000 %)
Type B	100.0000 % (> 99.8664 %)	100.0000 % (> 92.5000 %)
Type C	100.0000 % (> 98.8358 %)	64.0000 % (> 52.0000 %)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra ([Rule of Three](#) [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the [Mahalanobis distance](#) to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80386	80386	0.00	91.07
80704	80704	0.00	95.38
81050	81050	0.00	91.77

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Valine (L-) (H1056)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80145-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Valine (L-) (H1056)

Special notes

When selecting the *Valine (L-) (H1056)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Valine (L-) (H1056)	4	1	9

Second-stage model

For differentiation of the substance/substance group *Valine (L-) (H1056)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Valine (L-) (H1056)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Leucine (L-) (H1046)	54.93	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Valine (L-) (H1056)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Valine (L-) (H1056)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Valine (L-) (H1056)	14001947	80520	60	from supplier
Hepart	Valine (L-) (H1056)	16001380/0	80844	40	from supplier
Hepart	Valine (L-) (H1056)	21002275	81401	50	from supplier
Hepart	Valine (L-) (H1056)	23000774	81494	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 190 spectra of 4 reference samples from the substance/substance group *Valine (L-) (H1056)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 4 different batches.
- 28 286 spectra from a total of 574 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples

are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 60 spectra of 1 reference samples from the substance/substance group *Valine (L-) (H1056)*.
- Among them are spectra of independent samples from 1 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Valine (L-) (H1056)	15001436	80670	60

- 22939 spectra from a total of 503 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 15 spectra from 8 *Apo-Ident* customers from 11 batches from the substance/substance group *Valine (L-) (H1056)*.
- Among them are spectra of independent samples from 9 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
HCK	Valine (L-) (H1056)	15001436-1	1
HCK	Valine (L-) (H1056)	7016659	1
Hepart AG	Valine (L-) (H1056)		1
Hepart AG	Valine (L-) (H1056)	15001436	1
Hepart AG	Valine (L-) (H1056)	16001380/0	1
Hepart AG	Valine (L-) (H1056)	16001380/2	1
Hepart AG	Valine (L-) (H1056)	1807025012	1
Purren Apotheke	Valine (L-) (H1056)	1807936701	1
Unisan	Valine (L-) (H1056)	15001436	2
Unisan	Valine (L-) (H1056)	15001436/1	1
Unisan	Valine (L-) (H1056)	1807961101	2
Unisan	Valine (L-) (H1056)	25012	2

- 2955 spectra from 26 *Apo-Ident* customers from a total of 1449 batches from a further 62 sub-

stances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Valine (L-) (H1056)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Valine (L-) (H1056)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	190	0	28 286
Type B	0	54	6	22 939
Type C	0	14	1	2955

The substance/substance group *Valine (L-) (H1056)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9277 %)	100.0000 % (> 96.8421 %)
Type B	100.0000 % (> 99.8673 %)	90.0000 % (> 85.0000 %)
Type C	100.0000 % (> 98.8458 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra ([Rule of Three](#) [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the [Mahalanobis distance](#) to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80520	80520	0.00	73.84
80844	80844	0.00	64.30
81401	81401	0.00	59.95
81494	81494	0.00	64.52

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Vitamin B6 (Pyridoxal 5'-phosphate) (H1136)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 10006320-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Vitamin B6 (Pyridoxal 5'-phosphate) (H1136)

Special notes

When selecting the *Vitamin B6 (Pyridoxal 5'-phosphate) (H1136)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Vitamin B6 (Pyridoxal 5'-phosphate) (H1136)	2	0	0

Second-stage model

For differentiation of the substance/substance group *Vitamin B6 (Pyridoxal 5'-phosphate) (H1136)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Vitamin B6 (Pyridoxal 5'-phosphate) (H1136)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Vitamin C (H1104)	29.28	—
Flavour orange (H1405)	33.35	—
Garcinia cambogia (H1017)	34.95	—
Calcium L-(+) -lactate complex (H1008)	36.92	—
Antioxidants NAT complex (H1004)	38.62	—
ginkgo extract (H1024)	43.36	—
Potassium (H1030)	44.91	—
Pathogene complex (H1803)	47.75	—
Magnesium (H1060)	47.76	—
Antibiosis forte complex (H1115)	47.85	—
PET basis (H1503)	49.21	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Vitamin B6 (Pyridoxal 5'-phosphate) (H1136)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Vitamin B6 (Pyridoxal 5'-phosphate) (H1136)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Vitamin B6 (Pyridoxal 5'-...	22000703	81523	30	from supplier
Hepart	Vitamin B6 (Pyridoxal 5'-...	23002378	81524	30	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 60 spectra of 2 reference samples from the substance/substance group *Vitamin B6 (Pyridoxal 5'-phosphate) (H1136)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 2 different batches.
- 28 416 spectra from a total of 576 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 0 spectra of 0 reference samples from the substance/substance group *Vitamin B6 (Pyridoxal 5'-phosphate) (H1136)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.
- 22 999 spectra from a total of 504 batches from further 78 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *Vitamin B6 (Pyridoxal 5'-phosphate) (H1136)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Vitamin B6 (Pyridoxal 5'-phosphate) (H1136)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Vitamin B6 (Pyridoxal 5'-phosphate) (H1136)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	60	0	28 416
Type B	0	0	0	22 999
Type C	0	0	0	2970

The substance/substance group *Vitamin B6 (Pyridoxal 5'-phosphate) (H1136)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9288 %)	100.0000 % (> 90.0000 %)
Type B	100.0000 % (> 99.8687 %)	n/a (n/a)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
81523	81523	0.00	41.68
81524	81524	0.00	37.11

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Vitamin C (H1104)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80009-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Vitamin C (H1104)

Special notes

When selecting the *Vitamin C (H1104)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Vitamin C (H1104)	14	21	37

Second-stage model

For differentiation of the substance/substance group *Vitamin C (H1104)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Vitamin C (H1104)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Antioxidants NAT complex (H1004)	31.12	—
Flavour orange (H1405)	32.84	—
ginkgo extract (H1024)	34.63	—
Calcium L-(+)-lactate complex (H1008)	34.86	—
Vitamin B6 (Pyridoxal 5'-phosphate)...	39.77	—
PET basis (H1503)	40.57	—
Green coffee extract (H1433)	43.31	—
Potassium (H1030)	43.42	—
Antibiosis forte complex (H1115)	43.81	—
Arginine (L-) (H1036)	49.17	—
PET immune system (H1502)	52.92	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Vitamin C (H1104)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Vitamin C (H1104)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Vitamin C (H1104)	044502	80363	40	from supplier
Hepart	Vitamin C (H1104)	074201	80394	40	from supplier
Hepart	Vitamin C (H1104)	074001	80395	40	from supplier
Hepart	Vitamin C (H1104)	073901	80396	40	from supplier
Hepart	Vitamin C (H1104)	074101	80397	40	from supplier
Hepart	Vitamin C (H1104)	074201	80418	38	from supplier
Hepart	Vitamin C (H1104)	044602	80438	40	from supplier
Hepart	Vitamin C (H1104)	14001780	80499	60	from supplier
Hepart	Vitamin C (H1104)	14001788	80500	60	from supplier
Hepart	Vitamin C (H1104)	14001794	80501	60	from supplier
Hepart	Vitamin C (H1104)	14001797	80502	60	from supplier
Hepart	Vitamin C (H1104)	16000200	80751	60	from supplier

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Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Vitamin C (H1104)	16000198	80753	60	from supplier
Hepart	Vitamin C (H1104)	16000229	80756	60	from supplier
Hepart	Vitamin C (H1104)	16000230	80760	60	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 758 spectra of 15 reference samples from the substance/substance group *Vitamin C (H1104)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 14 different batches.
- 27 718 spectra from a total of 564 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 970 spectra of 21 reference samples from the substance/substance group *Vitamin C (H1104)*.
- Among them are spectra of independent samples from 21 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Vitamin C (H1104)	16000197	80752	60
Hepart	Vitamin C (H1104)	16000199	80754	60
Hepart	Vitamin C (H1104)	16000201	80755	60
Hepart	Vitamin C (H1104)	16000203	80757	60
Hepart	Vitamin C (H1104)	16000202	80758	60
Hepart	Vitamin C (H1104)	16000231	80759	60
Hepart	Vitamin C (H1104)	17000915	80963	40
Hepart	Vitamin C (H1104)	17000916	80964	40
Hepart	Vitamin C (H1104)	17000917	80965	40
Hepart	Vitamin C (H1104)	17000918	80966	40
Hepart	Vitamin C (H1104)	17000919	80967	40
Hepart	Vitamin C (H1104)	17000920	80968	40
Hepart	Vitamin C (H1104)	19001003	81195	40
Hepart	Vitamin C (H1104)	19001004	81196	40
Hepart	Vitamin C (H1104)	19001005	81197	40
Hepart	Vitamin C (H1104)	19001006	81198	40

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Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Vitamin C (H1104)	19000134	81199	40
Hepart	Vitamin C (H1104)	20001591	81269	40
Hepart	Vitamin C (H1104)	20001556	81274	40
Hepart	Vitamin C (H1104)	20002432	81320	40
Hepart	Vitamin C (H1104)	2100112-6-9	81361	50

- 22 029 spectra from a total of 483 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 94 spectra from 20 *Apo-Ident* customers from 42 batches from the substance/substance group *Vitamin C (H1104)*.
- Among them are spectra of independent samples from 37 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
Fagron	Vitamin C (H1104)	44502	1
Falcento	Vitamin C (H1104)	44602	1
HCK	Vitamin C (H1104)	14001794/0	1
HCK	Vitamin C (H1104)	14001797/0	2
HCK	Vitamin C (H1104)	16000197-0	2
HCK	Vitamin C (H1104)	16000198-0	2
HCK	Vitamin C (H1104)	16000203/0	2
Hepart / Unisan	Vitamin C (H1104)	170009170	1
Hepart AG, CH-8280 K...	Vitamin C (H1104)	1084025019	1
Hepart AG	Vitamin C (H1104)	1084025020	3
Hepart AG	Vitamin C (H1104)	1085025020	1
Hepart AG	Vitamin C (H1104)	16000197/0	1
Hepart AG	Vitamin C (H1104)	16000198	1
Hepart AG	Vitamin C (H1104)	16000231/0	1
Hepart AG	Vitamin C (H1104)	17000915/0	2
Hepart AG	Vitamin C (H1104)	17000917/0	1
Hepart AG	Vitamin C (H1104)	17000920/0	1
Hepart AG	Vitamin C (H1104)	19001004/0	1
Hepart AG	Vitamin C (H1104)	44501	3
Hepart AG	Vitamin C (H1104)	44502	3
Hepart AG	Vitamin C (H1104)	44601	2
Hepart AG	Vitamin C (H1104)	73901	3
Hepart AG	Vitamin C (H1104)	74201	2
Hepart/Unisan	Vitamin C (H1104)	19001006/0	1
Hepart	Vitamin C (H1104)	14001794	1
Hepart	Vitamin C (H1104)	16000199-0	1
Hepart	Vitamin C (H1104)	16000201-0	2
Hepart	Vitamin C (H1104)	16000203/0	2
Hepart	Vitamin C (H1104)	16000230-0	1
Hepart	Vitamin C (H1104)	16000231/0	1
Hepart	Vitamin C (H1104)	170009150	1
Hepart	Vitamin C (H1104)	17000919/0	2
Hepart	Vitamin C (H1104)	17000920/0	1

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Supplier	Substance	Batch	Spectra
Hepart	Vitamin C (H1104)	19001004	1
Hepart	Vitamin C (H1104)	19001004/0	3
Hepart	Vitamin C (H1104)	19001005/0	4
Hepart	Vitamin C (H1104)	19001006/0	3
Hepart	Vitamin C (H1104)	20001556/0	1
Hepart	Vitamin C (H1104)	21001126	2
Hepart	Vitamin C (H1104)	21001126/0	2
Unisan Gmbh, 78465 K...	Vitamin C (H1104)	25020	1
Unisan/Hepart AG	Vitamin C (H1104)	44501	1
Unisan/Hepart AG	Vitamin C (H1104)	44602	2
Unisan	Vitamin C (H1104)	1084025020	1
Unisan	Vitamin C (H1104)	1085025020	3
Unisan	Vitamin C (H1104)	14001780/0	1
Unisan	Vitamin C (H1104)	14001788	1
unisan	Vitamin C (H1104)	14001794	1
Unisan	Vitamin C (H1104)	14001797	1
Unisan	Vitamin C (H1104)	16000198	1
Unisan	Vitamin C (H1104)	16000200	1
Unisan	Vitamin C (H1104)	16000203	1
Unisan	Vitamin C (H1104)	16000203/0	1
Unisan	Vitamin C (H1104)	16000231	1
Unisan	Vitamin C (H1104)	25020	1
Unisan	Vitamin C (H1104)	44501	3
Unisan	Vitamin C (H1104)	44502	1
Unisan	Vitamin C (H1104)	73901	3
Unisan	Vitamin C (H1104)	74001	1
UNISAN	Vitamin C (H1104)	74001	1

- 2876 spectra from 26 *Apo-Ident* customers from a total of 1418 batches from a further 62 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Vitamin C (H1104)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Vitamin C (H1104)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	758	0	27 718
Type B	0	970	0	22 029
Type C	0	89	5	2876

The substance/substance group *Vitamin C (H1104)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9274 %)	100.0000 % (> 99.2084 %)
Type B	100.0000 % (> 99.8639 %)	100.0000 % (> 99.3814 %)
Type C	100.0000 % (> 98.8248 %)	94.6809 % (> 91.4894 %)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80363	80363	0.00	50.95
80394	80394	0.00	34.58
80395	80395	0.00	32.86
80396	80396	0.00	44.19
80397	80397	0.00	31.12
80418	80418	0.00	44.67
80438	80438	0.00	50.79
80499	80499	0.00	31.17
80500	80500	0.00	32.61
80501	80501	0.00	36.70
80502	80502	0.00	46.36
80751	80751	0.00	47.51
80753	80753	0.00	51.10
80756	80756	0.00	48.44
80760	80760	0.00	47.36

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group	Vitamin E NAT (H1107) / Lutein-Zeaxanthin-Astaxanthin (H1129)
Substance class	HCK - nutritional supplements (Hepart)
Report date	07/03/2025
Report number	80010-2025-03-07
Executing company	HiperScan GmbH Weißeritzstraße 3 01067 Dresden Germany

Relevant substance names

Vitamin E NAT (H1107) / Lutein-Zeaxanthin-Astaxanthin (H1129); Lutein-Zeaxanthin-Astaxanthin (H1129); Vitamin E NAT (H1107)

Special notes

When selecting the *Vitamin E NAT (H1107) / Lutein-Zeaxanthin-Astaxanthin (H1129)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Vitamin E NAT (H1107) / Lutein-Zeaxanthin-Astaxanthin (H1129)	13	22	38

Second-stage model

For differentiation of the substance/substance group *Vitamin E NAT (H1107) / Lutein-Zeaxanthin-Astaxanthin (H1129)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Vitamin E NAT (H1107) / Lutein-Zeaxanthin-Astaxanthin (H1129)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Coenzyme Q10 (H1013)	18.02	—
Glutathione (H1020)	23.39	—
Ginseng (H1018)	24.02	—
Flavour orange (H1405)	24.50	—
Oat bran beta-glucan (H1529)	25.11	—
Ginger extract (H1437)	26.89	—
PET coenzyme Q10 (H1505)	27.13	—
Aminomix NAC (H1002)	34.98	—
Coconut (H1522)	36.51	—
Leaky gut complex (H1802)	42.68	—
Chondroitin sulfate (H1065)	43.95	—
Glutamine (L-) (H1043)	45.59	—
Vitamin K2 (75µg Mono) (H1108)	46.56	—
Boron (H1005)	47.20	—
Calcium L-(+) -lactate complex (H1008)	48.25	—
α-Lipoic acid (H1000)	50.88	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Vitamin E NAT (H1107) / Lutein-Zeaxanthin-Astaxanthin (H1129)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Vitamin E NAT (H1107) / Lutein-Zeaxanthin-Astaxanthin (H1129)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Lutein-Zeaxanthin-Astaxan...	22000706	81438	40	from supplier
Hepart	Lutein-Zeaxanthin-Astaxan...	23002235	81517	40	from supplier
Hepart	Vitamin E NAT (H1107)	071601	80421	40	from supplier
Hepart	Vitamin E NAT (H1107)	071701	80426	35	from supplier
Hepart	Vitamin E NAT (H1107)	14001815	80512	60	from supplier
Hepart	Vitamin E NAT (H1107)	14001821	80513	60	from supplier

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Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Vitamin E NAT (H1107)	14001822	80514	60	from supplier
Hepart	Vitamin E NAT (H1107)	15001558	80688	60	from supplier
Hepart	Vitamin E NAT (H1107)	15001559(F2)	80690	60	from supplier
Hepart	Vitamin E NAT (H1107)	15001561	80693	60	from supplier
Hepart	Vitamin E NAT (H1107)	15001560(B1)	80694	60	from supplier
Hepart	Vitamin E NAT (H1107)	15001557	80697	60	from supplier
Hepart	Vitamin E NAT (H1107)	16001246	80826	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 675 spectra of 13 reference samples from the substance/substance group *Vitamin E NAT (H1107)* / *Lutein-Zeaxanthin-Astaxanthin (H1129)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 13 different batches.
- 27 801 spectra from a total of 565 batches from further 129 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 1200 spectra of 25 reference samples from the substance/substance group *Vitamin E NAT (H1107)* / *Lutein-Zeaxanthin-Astaxanthin (H1129)*.
- Among them are spectra of independent samples from 22 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Vitamin E NAT (H1107)	065001	80350	40
Hepart	Vitamin E NAT (H1107)	071501	80381	40
Hepart	Vitamin E NAT (H1107)	15001557(B1)	80686	60
Hepart	Vitamin E NAT (H1107)	15001558(F2)	80687	60
Hepart	Vitamin E NAT (H1107)	15001561(B1)	80689	60
Hepart	Vitamin E NAT (H1107)	15001559	80691	60
Hepart	Vitamin E NAT (H1107)	15001561(F2)	80692	60
Hepart	Vitamin E NAT (H1107)	15001560(F2)	80695	60
Hepart	Vitamin E NAT (H1107)	15001557(F2)	80696	60
Hepart	Vitamin E NAT (H1107)	15001559(B1)	80698	60
Hepart	Vitamin E NAT (H1107)	15001558(B1)	80699	60

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Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Vitamin E NAT (H1107)	15001560	80700	60
Hepart	Vitamin E NAT (H1107)	17000890	80958	40
Hepart	Vitamin E NAT (H1107)	17000891	80969	40
Hepart	Vitamin E NAT (H1107)	17000892	80970	40
Hepart	Vitamin E NAT (H1107)	18001024	81080	40
Hepart	Vitamin E NAT (H1107)	18001025	81081	40
Hepart	Vitamin E NAT (H1107)	18001026	81082	40
Hepart	Vitamin E NAT (H1107)	19001884	81209	40
Hepart	Vitamin E NAT (H1107)	19001496	81210	40
Hepart	Vitamin E NAT (H1107)	19001883	81211	40
Hepart	Vitamin E NAT (H1107)	22000723	81429	40
Hepart	Vitamin E NAT (H1107)	071501	80382	40
Hepart	Vitamin E NAT (H1107)	071501	80383	40
Hepart	Vitamin E NAT (H1107)	071501	80384	40

- 21 799 spectra from a total of 482 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 74 spectra from 19 *Apo-Ident* customers from 42 batches from the substance/substance group *Vitamin E NAT (H1107)* / *Lutein-Zeaxanthin-Astaxanthin (H1129)*.
- Among them are spectra of independent samples from 38 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.

Supplier	Substance	Batch	Spectra
	Vitamin E NAT (H1107)	25022	1
HCK	Vitamin E NAT (H1107)	14001822/0	1
HCK	Vitamin E NAT (H1107)	15001557-0	1
Hepart AG, CH-8280 K...	Vitamin E NAT (H1107)	1094017701	1
Hepart AG, CH-8280 K...	Vitamin E NAT (H1107)	65001	1
Hepart ag/ Unisan	Vitamin E NAT (H1107)	19001883/0	1
Hepart AG	Vitamin E NAT (H1107)	1094025022	1
Hepart AG	Vitamin E NAT (H1107)	15001557	1
Hepart AG	Vitamin E NAT (H1107)	15001557/0	2
Hepart AG	Vitamin E NAT (H1107)	16001246/0	1
Hepart AG	Vitamin E NAT (H1107)	17000890/0	4
Hepart AG	Vitamin E NAT (H1107)	17000891/0	1
Hepart AG	Vitamin E NAT (H1107)	25022	2
Hepart AG	Vitamin E NAT (H1107)	65101	3
Hepart/Unisan	Vitamin E NAT (H1107)	19001496	1
Hepart	Vitamin E NAT (H1107)	14001821	1
Hepart	Vitamin E NAT (H1107)	16000588	1
Hepart	Vitamin E NAT (H1107)	16000588-0	1
Hepart	Vitamin E NAT (H1107)	16000590/0	1
Hepart	Vitamin E NAT (H1107)	16000591/0	1
Hepart	Vitamin E NAT (H1107)	160005910	1
Hepart	Vitamin E NAT (H1107)	16000591-0	1
Hepart	Vitamin E NAT (H1107)	16001246	1
Hepart	Vitamin E NAT (H1107)	17000890	1

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Supplier	Substance	Batch	Spectra
Hepart	Vitamin E NAT (H1107)	17000891	1
Hepart	Vitamin E NAT (H1107)	17000891/0	2
Hepart	Vitamin E NAT (H1107)	17000892/0	1
Hepart	Vitamin E NAT (H1107)	18001024/0	3
Hepart	Vitamin E NAT (H1107)	18001026/0	1
Hepart	Vitamin E NAT (H1107)	19001496	1
Hepart	Vitamin E NAT (H1107)	19001496/0	2
Hepart	Vitamin E NAT (H1107)	19001883/0	1
Hepart	Vitamin E NAT (H1107)	19001884/0	2
Hepart	Vitamin E NAT (H1107)	210000619	1
Hepart	Vitamin E NAT (H1107)	21000619/0	1
Purren Apotheke	Vitamin E NAT (H1107)	945901	1
Unisan 02.04.2016	Vitamin E NAT (H1107)	15001558/0	1
Unisan 2.10.2015	Vitamin E NAT (H1107)	14001821/0	1
Unisan	Vitamin E NAT (H1107)	1094017701	1
Unisan	Vitamin E NAT (H1107)	1094025021	1
Unisan	Vitamin E NAT (H1107)	1095961301	1
Unisan	Vitamin E NAT (H1107)	14001821	1
Unisan	Vitamin E NAT (H1107)	14001821/0	1
Unisan	Vitamin E NAT (H1107)	15001557/0	1
Unisan	Vitamin E NAT (H1107)	15001558	1
Unisan	Vitamin E NAT (H1107)	15001659/0	1
Unisan	Vitamin E NAT (H1107)	16000589/0	2
Unisan	Vitamin E NAT (H1107)	16000591	2
Unisan	Vitamin E NAT (H1107)	16000591/0	1
Unisan	Vitamin E NAT (H1107)	16001246	1
Unisan	Vitamin E NAT (H1107)	25022	2
Unisan	Vitamin E NAT (H1107)	65001	3
Unisan	Vitamin E NAT (H1107)	71501	4
UNISAN	Vitamin E NAT (H1107)	71701	1

- 2896 spectra from 26 *Apo-Ident* customers from a total of 1418 batches from a further 62 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Vitamin E NAT (H1107)* / *Lutein-Zeaxanthin-Astaxanthin (H1129)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Vitamin E NAT (H1107)* / *Lutein-Zeaxanthin-Astaxanthin (H1129)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	675	0	27 801
Type B	0	1200	0	21 799
Type C	0	73	1	2896

The substance/substance group *Vitamin E NAT (H1107)* / *Lutein-Zeaxanthin-Astaxanthin (H1129)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9274 %)	100.0000 % (> 99.1111 %)
Type B	100.0000 % (> 99.8639 %)	100.0000 % (> 99.5000 %)
Type C	100.0000 % (> 98.8259 %)	98.6486 % (> 94.5946 %)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80421	80421	0.00	22.32
80426	80426	0.00	23.90
80512	80512	0.00	25.28
80513	80513	0.00	21.06
80514	80514	0.00	22.75
80688	80688	0.00	31.86
80690	80690	0.00	31.08
80693	80693	0.00	32.11
80694	80694	0.00	30.71
80697	80697	0.00	33.10
80826	80826	0.00	23.72
81438	81438	0.00	26.89
81517	81517	0.00	25.41

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Vitamins BAG complex (H1091)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 10006323-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Vitamins BAG complex (H1091)

Special notes

When selecting the *Vitamins BAG complex (H1091)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Vitamins BAG complex (H1091)	2	0	0

Second-stage model

For differentiation of the substance/substance group *Vitamins BAG complex (H1091)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Vitamins BAG complex (H1091)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Orthocolon complex (H1800)	17.97	—
Arginine (L-) (H1036)	21.66	—
Orthovimin Neutral Complex (H1404)	22.34	—
Rhodiola (H1064)	22.44	—
Vitamin B1 (H1101)	24.94	—
Boron (H1005)	25.12	—
Detox complex (H1111)	26.33	—
Zinc (H1110)	27.03	—
Ginseng (H1018)	27.81	—
Saffron style (H1434)	28.25	—
Artichoke extract (H1440)	32.01	—
Juniper (H1112)	32.16	—
Baobab (H1410)	32.19	—
Isoflavone (H1025)	32.89	—
Konjak Glucomannan (H1530)	34.30	—
Coenzyme Q10 (H1013)	34.83	—
Leaky gut complex (H1802)	35.19	—
Silicium (H1070)	35.47	—
Glutathione (H1020)	35.54	—
Marshmallow extract (H1439)	36.16	—
Green coffee extract (H1433)	36.49	—
Calcium L-(+) -lactate complex (H1008)	36.78	—
OPC Proanthocyanidins (Pine Bark) (...)	38.26	—
Lycopene (H1058)	38.70	—
Silymarin (H1071)	38.71	—
Selenium yeast (H1068)	39.71	—
Garcinia cambogia (H1017)	40.27	—
Gentian extract (H1438)	40.53	—
Magnesium (H1060)	43.51	—
Psyllium husks (H1527)	44.79	—
Vitamin K2 (75µg Mono) (H1108)	45.13	—
Selenium (H1067)	45.32	—
Flavour orange (H1405)	45.95	—
Antioxidants NAT complex (H1004)	48.41	—
Vitamin B12 (H1102)	49.51	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the sub-

stance/substance group *Vitamins BAG complex (H1091)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Vitamins BAG complex (H1091)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Vitamins BAG complex (H1091)	23002040	81528	40	from supplier
Hepart	Vitamins BAG complex (H1091)	24000713	81574	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 80 spectra of 2 reference samples from the substance/substance group *Vitamins BAG complex (H1091)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 2 different batches.
- 28 396 spectra from a total of 576 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 0 spectra of 0 reference samples from the substance/substance group *Vitamins BAG complex (H1091)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.
- 22 999 spectra from a total of 504 batches from further 78 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *Vitamins BAG complex (H1091)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Vitamins BAG complex (H1091)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Vitamins BAG complex (H1091)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	80	0	28 396
Type B	0	0	0	22 999
Type C	0	0	0	2970

The substance/substance group *Vitamins BAG complex (H1091)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9284 %)	100.0000 % (> 92.5000 %)
Type B	100.0000 % (> 99.8687 %)	n/a (n/a)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra ([Rule of Three](#) [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the [Mahalanobis distance](#) to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
81528	81528	0.00	22.34
81574	81574	0.00	25.08

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Walnut leaf (H1114)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 80904-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Walnut leaf (H1114)

Special notes

When selecting the *Walnut leaf (H1114)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Walnut leaf (H1114)	3	0	0

Second-stage model

For differentiation of the substance/substance group *Walnut leaf (H1114)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Walnut leaf (H1114)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Copper (H1032)	17.40	—
Chaga (H1011)	25.47	—
Trace elements SE complex (H1082)	25.99	—
Garcinia cambogia (H1017)	28.46	—
Artemisia annua extract (H1118)	31.68	—
Iron (H1015)	33.31	—
Pathogene complex (H1803)	34.50	—
Antibiosis mite complex (H1113)	39.58	—
Potassium (H1030)	41.26	—
Magnesium (H1060)	42.91	—
Argentum (H1116)	43.02	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Walnut leaf (H1114)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Walnut leaf (H1114)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Walnut leaf (H1114)	16001149	80904	40	from supplier
Hepart	Walnut leaf (H1114)	15001009	80908	40	from supplier
Hepart	Walnut leaf (H1114)	19000343/0	81162	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 120 spectra of 3 reference samples from the substance/substance group *Walnut leaf (H1114)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 3 different batches.
- 28 356 spectra from a total of 575 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a †. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 40 spectra of 1 reference samples from the substance/substance group *Walnut leaf (H1114)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.

Supplier	Substance	Batch	Sample ID	Spectra
Hepart	Walnut leaf (H1114)	16001149	80907	40

- 22 959 spectra from a total of 503 batches from further 77 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *Walnut leaf (H1114)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Walnut leaf (H1114)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose,

all relevant spectra of the various substances were compared with *Walnut leaf (H1114)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	120	0	28 356
Type B	0	40	0	22 959
Type C	0	0	0	2970

The substance/substance group *Walnut leaf (H1114)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9280 %)	100.0000 % (> 95.0000 %)
Type B	100.0000 % (> 99.8691 %)	100.0000 % (> 85.0000 %)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
80904	80904	0.00	25.47
80908	80908	0.00	34.50
81162	81162	0.00	30.66

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

VALIDATION REPORT

IdentModule 2.9-2025-01

Validated substance/substance group **Yeast organic (H1525)**
Substance class HCK - nutritional supplements (Hepart)
Report date 07/03/2025
Report number 10006098-2025-03-07
Executing company HiperScan GmbH
Weißeritzstraße 3
01067 Dresden
Germany

Relevant substance names

Yeast organic (H1525)

Special notes

When selecting the *Yeast organic (H1525)* substance/substance group, the following information is displayed to the user:

no information

Applicable documents

978-3-7692-8026-5 *European Pharmacopoeia 11th Edition, Basic Version 2022* [3]
Komm2.2.40 *Erfüllung von Ph. Eur. 2.2.40 durch Apo-Ident* [4]
AA004 *Erstellung und Validierung eines IdentModul-Updates*

Validation method

Validation is performed after every change to the chemometric model (also “database”) in three steps:

1. The chemometric model is calculated from the calibration spectra using a *PCA algorithm*. The calibration spectra originate from the calibration samples of all substances in this class.
2. In the *chemometric model* generated, the distances between all separable substances are checked for compliance with the specified safety distances.
3. All spectra are presented to the generated chemometric model for evaluation. In three runs, the reference spectra (*Type A*), spectra from independent samples (*Type B*), and spectra from the field (*Type C*) are presented successively. Here, no single *false positive* result is permitted.

Finally, a report is generated from the validation run results and is archived together with the parameters of the model generation in audit-compliant manner.

Number of independent samples (batches) in calibration and validation

A sample is considered independent if no sample from the same batch has been included in the calibration of the chemometric model.

Substance/substance group	Type A	Type B	Type C
Yeast organic (H1525)	1	0	0

Second-stage model

For differentiation of the substance/substance group *Yeast organic (H1525)* the following second-stage model is used:

no second-stage model

Nearest chemometric neighbors (distance to the nearest foreign sample)

The following table lists the nearest chemometric neighbors of the substance/substance group *Yeast organic (H1525)* in the substance class *HCK - nutritional supplements (Hepart)*. For *Mahalanobis distances* M that do not meet the criterion $M \geq 9$, the differentiation is questioned. However, it is often possible that substances that the main model could not reliably separate from each other can be differentiated in a second-stage model.

A necessary condition for the output of a clear result is therefore: All substances in the second-stage model must have a distance $M \geq 9$ from each other. All remaining substances must reach $M \geq 9$ in the main model.

Where this is not achieved, an ambiguous result is shown as result which includes at least the two substances that are too close to each other as possible identities (substance group). Alternatively these substances can be excluded from the list of substances identifiable with Apo-Ident.

Substance	Distance in main model	Distance in second-stage model
Antioxidants NAT complex (H1004)	30.71	—
Antibiosis forte complex (H1115)	34.20	—
PET basis (H1503)	39.05	—
Aminomix NAC (H1002)	39.34	—
Coenzyme Q10 (H1013)	42.86	—
α -Lipoic acid (H1000)	47.93	—
Vitamin B1 (H1101)	49.16	—
PET joints (H1501)	55.31	—

The list stops after the first substance with a *Mahalanobis distance* greater than 50. If the substance/substance group *Yeast organic (H1525)* is separated from critical neighbours in a second-stage model, all the remaining substances in the second-stage model follow.

Calibration samples

Only spectra which have been recorded by *HiperScan GmbH* from traceable samples are used for the generation of the [chemometric models](#). The following samples have been obtained from the substance/substance group *Yeast organic (H1525)*:

Supplier	Substance	Batch	Sample ID	Spectra	Certificate
Hepart	Yeast organic (H1525)	22002512	81469	40	from supplier

Validation samples

A total of 54 445 spectra were provided for validation. The results were evaluated separately according to the following sample categories:

Type A All calibration spectra.

- 40 spectra of 1 reference samples from the substance/substance group *Yeast organic (H1525)*. These samples are listed above in the [calibration samples](#) section. The reference samples come from 1 different batches.

- 28 436 spectra from a total of 577 batches from further 130 substances. These spectra were recorded by *HiperScan GmbH*. *Type A* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type A* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix A](#). The samples in [Appendix A](#) were added for model generation not with the intention to have the model identify these substances, but with the intention to make the model reject them despite their similarity to substances identifiable.

Type B Spectra from independent samples not included in the database structure. Measurement is carried out by *HiperScan GmbH*.

Samples from batches of which no spectra have been included in the database structure are considered as independent samples. The number of batches from which independent samples supplied *Type B* spectra for validation is shown below, representing the number of independent *Type B* samples. Samples, of which some of the spectra have been included in the database structure and other spectra in the validation, are marked with a [†]. The following applies to the remaining unmarked samples: In the same batch, there was at least one additional sample (other sales container, other sample ID) from which reference spectra (*Type A*) were included in the database structure.

- 0 spectra of 0 reference samples from the substance/substance group *Yeast organic (H1525)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. They are sorted upwards in the following table and separated from the additional samples by a line.
- 22 999 spectra from a total of 504 batches from further 78 substances. These spectra were recorded by *HiperScan GmbH*. *Type B* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type B* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix B](#).

Type C Spectra of independent samples not included in the database structure. *Apo-Ident* customers carry out the measurements. *HiperScan GmbH* generally does not verify the information provided by the customer regarding manufacturer and batch number.

- 0 spectra from 0 *Apo-Ident* customers from 0 batches from the substance/substance group *Yeast organic (H1525)*.
- Among them are spectra of independent samples from 0 batches from which no spectra have been included in the database structure. These are sorted upwards in the following table.
- 2970 spectra from 26 *Apo-Ident* customers from a total of 1460 batches from a further 63 substances. These spectra were recorded by *Apo-Ident* customers. *Type C* samples are documented within this entire report. If the substance can be identified with this [chemometric model](#), the samples are listed in the *Type C* section of each substance page. If the substance cannot be identified by this model, the samples are listed in [Appendix C](#).

Validation results

The validation runs checked whether the substance/substance group *Yeast organic (H1525)* can clearly be distinguished from all other substances using NIR spectroscopy with *Apo-Ident*. For this purpose, all relevant spectra of the various substances were compared with *Yeast organic (H1525)* and it was evaluated how many matches (positive) and rejections (negative) were correct or incorrect. The following table breaks down the numbers of correct and incorrect results according to the expected result (*positive/negative*) and the validation spectrum type (*A/B/C*).

	False positive	True positive	False negative	True negative
Type A	0	40	0	28 436
Type B	0	0	0	22 999
Type C	0	0	0	2970

The substance/substance group *Yeast organic (H1525)* can be clearly distinguished from all other substances. In order to make these figures comparable, the weighted *true negative rate (specificity)* and the weighted *true positive rate (recognition rate)* are determined:

	Specificity	Recognition rate
Type A	100.0000 % (> 99.9295 %)	100.0000 % (> 85.0000 %)
Type B	100.0000 % (> 99.8687 %)	n/a (n/a)
Type C	100.0000 % (> 98.8776 %)	n/a (n/a)

In order to ensure that each substance is entered with the same weight irrespective of the number of spectra available, each spectrum is weighted with the reciprocal value of its number. (If several new spectra of a substance with a very distinctive spectrum are added, the values for *specificity* and *recognition rate* are safer, but are by no means idealised.)

In order to illustrate the impact of the number of spectra, a comparison is made in parentheses as to how the *specificity* or *recognition rate* would worsen if three additional incorrect results were to exist amongst the spectra (*Rule of Three* [10, 11]). The larger the number of spectra, the lower the deterioration if the three hypothetical *incorrect results* were added.

Where the number of spectra does not exceed 20, no *recognition rate* is provided.

Identity according to identity test using NIR spectroscopy

For each substance, a certificate of the correct identity is obtained from an independent GMP-certified test laboratory. If the identity of the sample can be provided using NIR on an independently tested reference sample, in the following table the *Mahalanobis distance* to the reference sample is specified as well as the *Mahalanobis distance* to the next non-identical substance:

Sample ID	Reference sample ID	Distance to reference sample	Distance to next foreign sample
81469	81469	0.00	34.20

The identity of a sample will be confirmed by NIR if the distance to the next foreign sample is at least 50 % greater than the distance to a reference sample whose identity has been established by laboratory testing. This criterion is always considered in the chemometric model, which contains all substances of the substance class, even if a second-stage dissolves a subgroup of similar substances, thereby increasing the distances between them. The samples confirmed by NIR support the statistical variance of the original reference substance, but cannot add new aspects or forms of the substance.

Appendix A: Additional calibration samples (Type A)

Not required.

Appendix B: Additional validation samples (Type B)

It is necessary that spectra also enter the validation which cannot be identified with this model. In this manner, it is verified that the model also rejects unknown substances. The spectra for these samples were recorded by *HiperScan GmbH*. They are allocated to the *Type B*. They also include the calibration spectra for other models.

The samples originate from 10 batches. From these 440 spectra were recorded. The spectra recorded on independent samples of substances which can be identified with the model are listed respectively in the section *Type B* for the individual substances and do not appear again elsewhere in this list.

Supplier	Substance	Batch	Spectra	Certificate
Hepart	Melatonin (H1061)	069101	40	from supplier
Hepart	Melatonin (H1061)	069101	60	from supplier
Hepart	Proline (-L) (H1051)	066401	40	from supplier
Hepart	TopFlora multi forte complex (H1119)	15001135	60	from supplier
Hepart	Vitamins BAG (H1090)	20000156	40	from supplier
Hepart	Vitamins BAG (H1090)	19002541/0	40	from supplier
Hepart	Vitamins BAG (H1090)	19002481	40	from supplier
Hepart	Vitamins BAG (H1090)	20001365	40	from supplier
Hepart	Vitamins BAG (H1090)	20001935	40	from supplier
Hepart	Vitamins BAG (H1090)	21000740	40	from supplier

Appendix C: Additional validation samples (*Type C*)

Spectra for substances from the field which cannot be identified with this model also enter the validation. In this manner, it is verified that the model also rejects unknown substances. The spectra for these samples were recorded by *Apo-Ident* customers. They belong to *Type C*. The information provided by the customer regarding the manufacturer and batch number is taken over by *HiperScan GmbH* to a large extent unchecked.

The samples originate from 4 batches. From these, 9 spectra were recorded. The spectra recorded on independent samples of substances from the field which can be identified with the model are listed respectively in the section *Type C* for the individual substances and do not appear again elsewhere in this list.

0 A B C D E F G H I J K L M N O P Q R S T U V W X Y Z

Supplier	Substance	Batch	Spectra
Hepart AG	Proline (-L) (H1051)	707801	2
Hepart AG	Proline (-L) (H1051)	25707	2
Unisan	Proline (-L) (H1051)	66401	3

V

Supplier	Substance	Batch	Spectra
Unisan	Vitamin K2-Ca-Mn complex (H...	69001	2

Appendix D: Requirements of validation

In order to ensure adherence to the safe scientific status, the individual methods for manufacturing and testing must be validated under certain circumstances (compare § 34 para. 1 no. 3, § 35 para. 1 no. 4 and para. 4 sentence 1 no. 2 b, para. 6 sentence 3 *ApoBetrO* [Pharmacies Rules and Regulations]). The *ApoBetrO* [Pharmacies Rules and Regulations] incorporates a legal definition in § 1 a para. 16 (quotation translated):

“Validation is the provision of documented proof which with a high degree of safety documents that, via a specific process or standard work process, a medicinal product is manufactured and tested, which is in accordance with previously determined quality features.”

Validation documentation can be used to prove that methods or devices which are not described in the Pharmacopoeia within the meaning of § 6 para. 1 sentence 3 *ApBetrO* [Pharmacies Rules and Regulations] achieve the same results as those in the Pharmacopoeia. On the other hand, with the requirements of the demanded validation it must be observed whether the respective testing method is already incorporated in the Pharmacopoeia.

NIR spectroscopy as a general testing method need not be validated in accordance with the express ruling in the *Ph. Eur. Section 1.1* [3], as it is already described in *Section 2.2.40* of the *Ph. Eur.* as an area of application for the identification of raw materials.

However, a special validation requirement exists for the reference database. This requirement is met with the existing document. Further requirements or rules as to how this proof must be furnished do not exist. It is required that the processes guarantee the same results as the methods and devices in the Pharmacopoeia [17].

Carrying out identity tests with *Apo-Ident* is therefore also possible if the NIR spectroscopy process is not required in the Pharmacopoeia monograph of the substance for identity testing. All NIR analyses with *Apo-Ident* prove several, often all molecule groups and are therefore comparable with a series of individual, targeted chemical proofs [4]. Therefore, the identity proof with *Apo-Ident* replaces the monograph test series (with two or more test combinations).

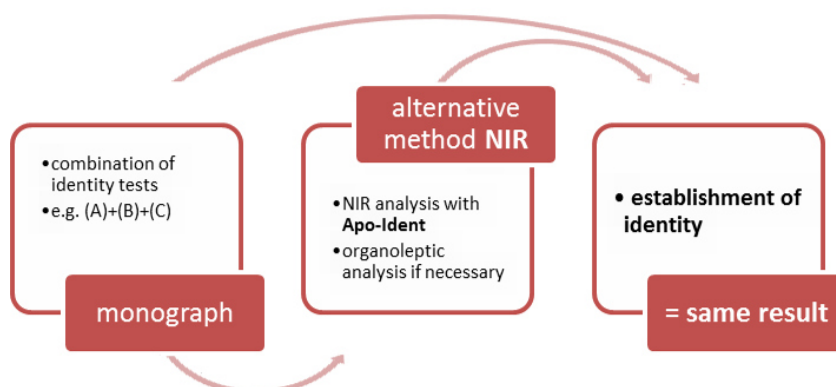


Figure 2: The combination of tests of the monograph is replaced by the alternative method NIR spectroscopy using *Apo-Ident*. This is permissible because both test procedures result in the establishment of the identity of the raw material.

With this validation documentation, proof is furnished that identical results are achieved with *Apo-Ident* and Pharmacopoeia methods, i.e. confirmation of the identity of the raw material [2].

Appendix E: Conformity of Apo-Ident with the European pharmacopeia

According to *Ph. Eur. Section 2.2.40*, NIR spectroscopy is basically suitable for: “Identification of agents, excipients, dosage forms, intermediate manufacturing products, chemical raw materials and packaging materials” ([3], quotation translated).

The fact that *Apo-Ident* meets the further criteria of the European Pharmacopoeia under the headings in *Section 2.2.40*

- Apparatus
- Measurement methods
- Sample preparation and presentation
- Testing the functionality of the instrument
- Identification and characterisation (qualitative analysis)
- Quantitative analysis
- Ongoing model evaluation
- Transfer of databases
- Data storage

can be proven based on the *HiperScan GmbH* documentation of “Meeting 2.2.40 *Ph. Eur.* by *Apo-Ident*” [4].

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