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| --- | --- | --- | --- |
| **I – General customer information** | | | |
| Company |  | | Date |
| Department |  | | |
| Address |  | | |
| Contact person |  | | |
| Email |  | Phone |  |
| Addresses of account department **(if different)** Invoices are only sent by email! |  | Email |  |
| VAT number (EU customer only) |  |  | |
| General email(s) for analytical results |  | | |

Please note that we are happy to bear the EU-tax. All other costs must be borne by the sender.

Recommended carriers are World courier, DHL, FedEx. Please take care that proforma invoice is < 20US$. Otherwise additional custom fees will be charged. In addition shipments <20US$ usually would pass the custom without delay.

Note, that samples are stored at shipping temperature, no matter what is written on the accompanying letter! It depends on the regulation of the customer if temperature control is necessary. Samples delivered with dry ice will be stored at -18°C.

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| **II – General sample information** | | | | | | | | | | |
| Sample name | |  | | | | | | | | |
| Commercial name | |  | | | | | | | | |
| Batch / Lot | |  | | | PO  (if necessary) | |  | | | |
| **If any offer or email correspondence for this shipment is availabe, please enclose these documents!** | | | | | | | | | | |
| **III – Required sample information** | | | | | | | | | | |
| Please enter detailed information in the required positions for determination of | | | | | | | | | | |
| * Enantiomeric purity * Quantitative analysis of amino acids / contaminanat amino acids / peptide content * Molecular weight / sequencing * Determination of conter ions (TFA / Ac / Cl …) * Determination of residuals of solvents | | | | | | | | | 1), 3), 4), 5), 6)  1), 2)(av only) , 3), 4), 5), 6)  1), 2)  4)  4) | |
| 1) | **Nominal Sequence**  (respectively amino acids composition and D/L configuration) | |  | | | | | | | |
| 2) | **Nominal molecular**  **Weight** | | (av)  (mi) | Molecular formular | |  | | Disulfid  bridge | | NO  YES 🡺 |
| 3) | If not elucidated by the sequence | | **Resin ?** | YES 🡺 acid cleavage possible?  YES  NO | | | | | | |
| **Protective groups ?** | YES 🡺 | | | | | | |
| 4) | **Counter ion ?** | YES 🡺 | | | | | | |
| 5) | **Expected peptide**  **Concentration** | | % or       mmol/g | | | | | | | |
| 6) | **Fomulated sample** | | YES  Please describe exact composition and concentration 🡺  Note:  If required, a clean-up procedure could be necessary and will be charged (A820). | | | | | | | |
| *Please enter any additional comments here* | | | | | | | | | | |

Please feel free to delete any unnecessary section **in exception of I. II. and III.**

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| **IV – Required Analysis** | | | | | | | | | | | | |
|  | | | | | | | | **sample amount** (per analysis)  [mg] | **regular**  **TAT**  [working days] | **in**  **duplicate** | **Expanded report**  (surcharge) | **Urgent**  (30% sur-charge) |
| **Enantiomeric purity** |  | **Substance specific validated method A.0.**       ⭠ *enter number* | | | | | | | |  |  |  |
|  | **A.0.1.(X)** (A440 / A430 / A450)  Free amino acids, -derivatives or resin bonds **via GC-FID in duplicate** | | | | 2 | | | 5 | **-** |  |  |
|  | **A.0.8.** (A525)  Some amino acids via **HPLC-UV** **in duplicate**  *(if method available)* | | | | 2 | | | 7 | **-** |  |  |
|  | **A.0.3**. (A790 / A791 / A793)  Free amino acids, -derivatives and peptides via **GC-MS** | | free amino acids or derivatives | | 1-2 | | | 5 |  |  |  |
| peptides | | 2–5 | | | 8-12 |
| Amino acids to be determined | |  | | | | | | |
|  | **A.0.10.** (A769)  Accurate determination of **amino acid derivatives** via **GC-MS** **in duplicate (not available for peptides)** | | | | 1-2 | | | 5-7 | **-** |  |  |
| **Quantitative amino**  **acid analyses**  **&**  **peptide content** |  | **Substance specific validated method A.0.4.**       ⭠ *enter number* | | | | | | | |  |  |  |
|  | **A.0.4.** (A400 / A401/ if resin bond A461)  Determination of all amino acids including determination of blind values. Most accurate! **If peptide content need to be determined mark below.** | | | | | | 4 | 10-15 |  |  |  |
|  | **A.0.4.** (A400 / A401/ if resin bond A461)  Determination of **peptide content**, **calculated using onlys 5 acids** including determination of blind values. | | | | | | 4 | 10 |  |  |  |
|  | **A.0.4.0.** (A420 / A421 // if resin bond A455)  Determination of all amino acids without determination of blind values. Results could be falsified when blind values are present. **If peptide content need to be determined mark below.** | | | | | | 3 | 10-15 |  |  |  |
|  | **A.0.4.0.** (A420 / A421 // if resin bond A455)  Determination of **peptide content, calculated using only 5 amino acids** without determination of blind values | | | | | | 4 | 10 |  |  |  |
|  | **A.0.4.12.** (A770 / A771)  If the peptide content is low or complex matrix is present, it could be necessary to determination the amino acids including determination of blind values by GC-MS. | | | | | | 4 | 10-15 |  |  |  |
| **Additional**  **services** | | Determination of **peptide content** (A402) | | YES | | | **-** | +1 |  | | |
| **Amino**  **acids as contaminants** |  | **Substance specific validated method A.0.6.3.**       ⭠ *enter number* | | | | | | | |  |  |  |
|  | **A.0.6.3.** (A785 / A786)  Most reliable quantitative determination of contaminant amino acids via GC-MS | | | | | 5 | | 8-12 |  |  |  |

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|  | | | | | | | **sample amount** (per analysis)  [mg] | **regular**  **TAT**  [working days] | **in**  **duplicate** | **Expanded report**  (surcharge) | **Urgent**  (30% sur-charge) |
| **Molecular weight**  **and**  **sequencing**  **using HR-MS** |  | **Substance specific validated method X.0.8.**       ⭠ *enter number* | | | | | | | - |  |  |
|  | **X.0.8.1.** (A814)  Determination of molecular weight of peptides (identity) | | | | | 1 | 10 | - |  |  |
|  | **X.0.8.** (A804 / A806 / A803)  Sequencing of peptides | | | | | 1 | 10-15 | - |  |  |
| **Additional**  **services** | | | **A.0.7.4.** (A811)  Cleavage of cyclic peptides (disulfide bond) | | YES | 2 | +1 | **-** | | |
| **Counter ions** |  | **Substance specific validated method C.27.**       ⭠ *enter number*  **Substance specific validated method C.32.**       ⭠ *enter number* | | | | | | | **-** |  |  |
|  | **C.27.1**. (A210 / 211 / 212)  Determination **in duplicate** via **GC-FID** | | | | TFA  acetate | 3 | 6-8 | **-** |  |  |
|  | **C.32.** (A213 / A214)  Determination of anions  **in duplicate via IC**  *(please select)* | | | | TFA  acetate  chloride  fluoride  phosphate | 3 | 10-12 | **-** |  |  |
| **Other**  **services** | | | **Single analysis only !**  (Reduced reliability and OOS investigation) | | YES | | | - | | |
| **Water** |  | **Substance specific validated method C.28.**       ⭠ *enter number* | | | | | | | - |  |  |
|  | **C.28.1.** (A200)  Determination of water **(in duplicate)** | | | | | 3 | 6-8 | - |  |  |
| **Other**  **services** | | | | **Single analysis only !**  (Reduced reliability and OOS investigation) | ☐ YES | | | **-** | | |
| **Residuals of solvents** |  | **Substance specific validated method C.26.**       ⭠ *enter number* | | | | | | | - |  |  |
|  | **C.26.1.** (A229 / A230 / A231 / A232)  Determination of residual of solvents **(in duplicate)** | | | | | 3-5 | 7 | - |  |  |
|  | Reduced Solvent screening - higher reporting limit (A227) | | | | | 3 | 10 |  |  | **-** |
|  | Regular Solvent screening( A235) | | | | | 3 | 10 |  |  | **-** |
|  | Expanded solvent screening (A236) | | | | | 5 | 12 |  |  | **-** |
| **Other services** | | **Single analysis only !**  (Reduced reliability and OOS investigation) | | | YES | | | **-** | | |
| Blank before and after analysis (A228) | | | YES | - | +1 |
| *please enter solvents here, or mark them in the attached list* | | | | | | | | | | |

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| **V – Additional infomation** | | | | |
| ***Recommendations for the different types of products discussed with the German Authoritities*** | | | | |
| *Drug product* | | | * *analysis in duplicate should be perfomed* * *expanded report should be perfomed* * *6x SST should be considered*   *substance specific validation may be necessary* | |
| *Drug substance / API* | | | * *analysis in duplicate may be required* * *expanded report is recommended for not substance specific validated methods* * *substance specific validation may be necessary (depends on the status of the studies and submission)* | |
| *Others* | | | *as required eg. research and development* | |
|  | | | | |
| ***Further information*** | | | | |
| *Sample amount* | | | *Sample amount is the amount of peptide.*  *If samples are liquid please contact us.*  *The amount needed for sample handling depends on the physical properties.*  *A freeze dried product needs nearly no additional amount whereas an oily product some 10mg’s.*  *These amounts are necessary to obtain the required accuracy of the weighing process (minimum weight in accordance to USP) and the required LOQ’s.*  *Please ask if these sample amounts are not available.* | |
| *Shipment* | | | *Any container is possible (Eppendorf tubes, Screw cap vials, ….)*  *To prevent evaporation of low boiling solvents it is highly recommended to send about 10 mg*  *in a small sample container.* | |
|  | | | | |
| ***More detailed method information*** | | | | |
| ***Enantiomeric***  ***purity*** | ***A.0.1.(X).*** | ***GC-FID*** | | *For free amino acids the method is appropriate because no hydrolysis is performed and no side products are expected.*  *Also for many of the amino acid derivatives the method is suitable. If however the cleavage leads to high concentration of by-product or the sample itself is contaminated, co-elution with any contamination is possible and leads to incorrect results. Very seldom racemization is observed during sample preparation. These draw backs are minimized by the GC-MS analysis. For derivatives the method is only suitable for higher specifications, e.g.<0.5% enantiomeric purity.* |
| ***A.0.3.*** | ***GC-MS*** | | *This method can be used for peptides and amino acids /amino acid derivatives to determine the enantiomeric purity of the amino acids in the peptide.*  *The result is the mean value of the enantiomeric purity of each amino acid.* |
| ***A.0.8.*** | ***HPLC-UV*** | | *The method uses chiral columns for HPLC.*  *A couple of derivatives can be separated on chiral HPLC columns without derivatization, if they have a chromophoric group like Fmoc.*  *The lower selectivity of the chromatographic column is often compensated by the higher selectivity of FID detector.*  *HPLC and GC(-MS) results may differ if the sample is contaminated by any other derivative of the same amino acid with different enantiomeric purity. GC(-MS) gives as result the mean value of the enantiomers of all these derivatives, HPLC analyzes the enantiomeric purity of the specified amino acid derivative only.* |
| ***A.0.10.*** | ***GC-MS*** | | *Determination of the Enantiomeric Purity of the Amino Acid derivatives via GC MS. This method is similar to A.0.3. but specifications and requirements are more tight.*  *LOQ of 0.05% with standard deviation of 0.03% should be determined. In order to achieve this, additional performance qualification of primary standard with known high enantiomeric purity is necessary in parallel to the analysis in duplicate.* |

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| ***More detailed method information*** | | | |
| ***Quantitative amino acid analysis (AAA)*** | ***A.0.4.*** | ***GC-FID*** | *Epimeric impurity is added as internal standard. Internal standard and amino acid from the sample have the identical behavior in achiral environment. Therefore, the method of enantiomer labeling is very robust in comparison to other methods.*  *The enantiomeric purity of the amino acids is taken into account because the enantiomers are added as multi-internal standard. The blind values correspond to the enantiomeric purity after hydrolysis.* |
| ***A.0.4.0.*** | *If quantitation is ordered without determination of blind values, the epimeric purity of the peptide is set to 100%; racemization during hydrolysis is estimated and taken into account. The result will be falsified if the peptide is contaminated by unspecified enantiomeric antipodes or if amino acids racemize to an extent other than expected. This is the case eg. for Cys or Cys-neighboring amino acids. These “blind values” cannot be estimated.* |
| ***A.0.4.12.*** | *If the peptide content is very low or if complex matrix is present, it could be possible that MS detection for the analysis is necessary. This method is similar to A.0.4 but with MS-detection.* |
| ***Peptide content*** | | *If AAA is used to quantify the peptide content respectively the content of amino acids and not for the relative composition, it is highly recommended to perform analysis in duplicate*  *Molecular weight of the determined molecule is needed. The content of the free peptide is lower than the content of the peptide incl. protective groups or counter ion.* |
| ***Amino acids***  ***as contaminants*** | ***A.0.6.3.*** | ***GC-MS*** | *Most accurate method. Detection is done by mass spectrometry. This is required due to the low amount in the sample.* |
| ***A.0.6.1.*** | ***GC-FID*** | *All proteinogenic amino acids can be quantitatively determined. Limit of quantitation is 0.1%. Results could be falsified by coelution.* |
| ***A.0.6.*** | *This is only possible as additional service to other analysis, e.g. enantiomeric purity.*  *All proteinogenic amino acids beside His can be qualitatively determined. The certificates states a sentence if other amino acids could be present in the sample.* |
| ***Molecular weight and sequencing*** | ***X.0.8.1.*** | | *Determination of the monoisotopic mass with high-resolution mass spectrometry* |
| ***X.0.8.*** | | *Sequencing by MSn using HR-MS. If the peptide is cyclic, disulfide-bridge must be cleaved before analysis. If the peptide is cyclic without disulfide-bridges, please contact us so we can evaluate another method.* |
| ***Counter ions*** | ***C.27.1.*** | ***GC-FID*** | *Even strongly adsorbed ions or covalently linked acetate and trifluoro acetate can be determined.*  *The sample is allowed to react with methyl alcohol/BF3, whereby the carboxyl groups including the trifluoro acetyl ions and acetyl ions are converted to their methyl esters. After careful extraction with hexane the esters are determined by capillary gas chromatography.* |
| ***C.32.*** | ***IC*** | *In comparison to C.27.1 primary free counter ions are determined.*  *Please note, that samples should be soluble in DMSO / water. If the samples are not soluble standard deviation can be increased.* |
| ***Water*** | ***C.28.1.*** | ***GC-TCD*** | *In contrast to the indirect methods of determination of water whereby products of reaction with water are quan­tified, our analytical method measures water directly. After thermal desorption at 140°C, water is separated from other volatile components and detected quantitatively.*  *The samples are preconditioned in a desiccator with silica over night without vacuum. In this case, environmental influences as humidity are reduced.*  *Quantitation is done by the external standard method. The amount of sample re­quired for single analysis is only about 1 mg.* |
| ***Residuals of solvents*** | ***C.26.1.*** | ***GC-FID*** | *The peptide is dissolved in dimethyl sulfoxide free of traces of solvent or another suitable solvent. The solvents are separated by capillary gas chromatography. The procedure follows closely the method of USP 467, but direct injection is used instead of headspace.* |
| ***Screening*** | | *We offer three different solvent screenings. For details please see additional list of solvents.* |