

## Sample Submission Form - Amino Acid Analysis

Please print this form and include it with your sample(s) and MSDS where applicable.

### Customer information:

Contact Name \_\_\_\_\_  
Company Name \_\_\_\_\_  
Address \_\_\_\_\_  
\_\_\_\_\_  
\_\_\_\_\_  
e-mail \_\_\_\_\_  
Phone \_\_\_\_\_

### Invoice information:

Quote reference (if any) \_\_\_\_\_  
Purchase order number \_\_\_\_\_  
Invoice address (if different) \_\_\_\_\_  
\_\_\_\_\_  
\_\_\_\_\_  
\_\_\_\_\_  
\_\_\_\_\_

### Analysis details (complete or tick as appropriate):

Sample ID	Approx. protein conc. (please supply if known)	Amino acid analysis		Separate analysis			Internal standard
		Free	Total	Tryptophan	Cysteine	Hydroxyproline	
Lab ID							
Lab ID							
Lab ID							
Lab ID							
Lab ID							

### Options (additional charges may apply, please contact us or see our website for details):

- ☐ Express service  
☐ Excel reports  
☐ Premium analysis  
☐ Duplicate analysis  
☐ Sample return – please supply address below if different to above

For internal use only:

Date and time samples received:

Received by:

#### Additional information/requirements:

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## Guide to submitting samples for analysis

To enable us to process your samples more efficiently please read the following guidelines. If you have requirements outside our standard specification, or any other queries, please contact us to discuss your needs.

### Shipping

Please ship samples to:

Amino Acid Analysis Department  
AltaBioscience,  
37, Walkers Road  
Manor Side  
Redditch  
B98 9HE  
UK

### Sample Quantities

Please see below for minimum quantities for analysis. If you are unable to supply these weights/volumes, please contact us to discuss your needs.

#### Total amino acid analysis

##### *Dry samples*

- For peptides at least 5mg of material is required if the sample is to be weighed in house, although we can process pre weighed peptides if required. Please inform us if you are aware of any of the following:
  - o Any known solubility issues.
  - o Any Ile-Ile, Ile-Val or Val-Val bonds as these are abnormally stable to the hydrolysis process and we will need to perform additional validation.
- We also require the following information for peptides:
  - o The salt form of the peptide, e.g. TFA or HCl salt.
  - o The theoretical ratios of the amino acids.
  - o Information regarding any modifications e.g. acetylated or modified amino acids.
- For other sample types including food at least 1g is typically required, unless the sample needs to be homogenised prior to analysis (please contact us for further information).

### *Solutions*

- For peptides and proteins, we can calculate accurate minimum sample volumes if the sequence is known.
- For other sample types including drink products 2mL is typically required.

Analysis of cysteine and tryptophan will require a separate hydrolysis and analysis operation and additional quantities of sample, please contact us for more information.

## **Free amino acid analysis**

### *Dry samples*

- For most sample types we require at least 1g of material, but can work with less depending on the sample type.
- If the sample needs to be homogenised prior to analysis more than 1g may be required, please contact us for further information.

### *Solutions*

- For most sample types including drink products 2mL is typically required.
- For physiological samples including cell culture media and plasma, 200uL is typically required but please contact us if you are unable to supply this.

## **Sample Considerations**

Analyses can be performed on amino acids and proteins coming from a wide range of sources. However, to obtain maximum accuracy, some points should be noted when supplying samples for analysis.

- If samples are hygroscopic, it may not be possible to obtain a steady weighing and hence an accurate value for amino acid content.
- Samples containing Glycerol, Acrylamide and Mannitol cannot be processed due to risk of explosion when hydrolysed.
- PEG can react with some amino acids during hydrolysis, affecting recovery, and should therefore be avoided.

- Samples with a high salt content can affect the ion exchange column. Ammonium salts should also be avoided in the last stage of purification as large amounts of ammonia will cause the analysis reagent to precipitate out in the reaction coil.
- Glycine buffers should never be used during the work up of proteins that have to be amino acid analysed. Glycine is very difficult to remove afterwards, with obvious effect on the accuracy of the measurement of glycine.
- Proteins adsorbed on nitrocellulose membranes cannot be analysed (use PVDF filters instead).