

N-TERMINAL SEQUENCING



Since 2001 SYMBIOSIS provides you with a variety of automated Edman sequencing services in a GMP regulated environment:

- Determination of the N-terminal amino acid sequence of peptides and proteins/antibodies according to ICH guideline Q6B
- N -terminal sequence analysis of Erythropoietin according to Ph. Eur.
 - Feasibility studies and method validation of Edman sequencing assays according to ICH guideline Q2
 - Follow-up techniques such as MALDI-TOF MS and peptide mapping to generate supporting protein data on the complete sequence and the secondary structure (disulfide bridges)
- Determination of the C-terminal amino acid sequence of proteins or antibodies by complete N-terminal sequencing of the C-terminal peptide generated by peptide mapping

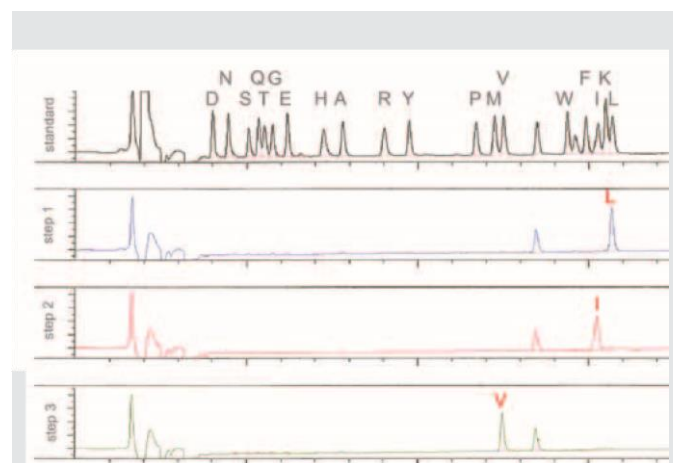
Automated Edman sequencing is a key technique for characterisation and quality control of peptides and proteins:

- As a direct sequencing technology, the sequencing of not more than 10 to 15 N-terminal amino acids is usually sufficient for the positive identification of a protein, regardless of its size or structure
- Included in the Ph. Eur. monograph of the glycoprotein Erythropoietin
- Essential part of characterisation and comparability programs of antibodies

As one of the key sequencing technologies automated Edman sequencing is a focus area within the service portfolio of SYMBIOSIS. Our expertise and techniques combined with the equipment available at SYMBIOSIS ensure highest quality in the performance and documentation of N-terminal sequencing to meet your specific requirements. Now and in the future.

Automated Edman sequencing offers several advantages over competing mass spectrometry based sequencing technologies:

- It clearly distinguishes between equal-mass amino acids (L/I and K/Q)
- Provides a straightforward and better result traceability on the basis of HPLC chromatograms compared to the rather elaborate interpretation of highly complex fragmentation data



Easy interpretation of acquired data:
Steps 1 to 3 of β -Lactoglobulin sequencing (L – I – V)

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