### 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

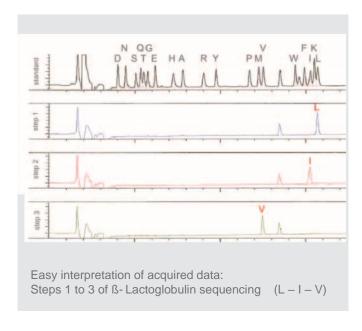
  Follow-up techniques such as MALDI-TOF MS and peptide mapping to generate supporting protein data on
- the complete sequence and the secondary structure (disulfide bridges)
- Determination of the C-terminal amino acid sequence of proteins or antibodies by complete N-terminal sequencing of the C-terminal 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
- Essential part of characterisation and comparability programs of antibodies

# 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



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.

#### **SYMBIOSIS GmbH**

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