

SEQUIT! NCE

de novo sequencing of peptides

Sequit! is a new computer program for *de novo* peptide sequencing by tandem mass spectrometry. Sequit! provides precise sequencing of tryptic as well as nontryptic peptides using fragmentation spectra even with incomplete b- or y-fragment series and erroneous peaks.

- *de novo* peptide sequencing

Sequencing using *collision-induced dissociation* (CID) or *laser-induced dissociation* (LID) (*post-source decay* (PSD) and *in-source decay* (ISD)) data provided by MALDI-TOF, MALDI-TOF/TOF, MALDI-QTOF, ESI-QTOF, ESI-TRAP or ESI/MALDI-FTICR mass spectrometers
Sequencing of post-translationally or chemically modified peptides
Batch analyses

- Database search

Automatic submission of the sequencing results for automated BLAST searches in local sequence databases
Readout and visualisation of the database search results

- Peptide mass fingerprint (PMF) analysis

Analysis of trypsin digests of complex protein mixtures
Automatic correlation of PMF analyses and peptide sequences
Identification of mutated and modified peptides

Reference: Demine R., Walden P. Sequit: software for *de novo* peptide sequencing by matrix-assisted laser desorption/ionization post-source decay mass spectrometry. *Rapid Commun Mass Spectrom.* 2004; **18**: 907-913.

More information is available at www.sequit.org