Title (en)
AUTOMATED IDENTIFICATION OF PEPTIDES

Title (de)
AUTOMATISIERTE PEPTIDERKENNUNG

Title (fr)
IDENTIFICATION AUTOMATISEE DE PEPTIDES

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Application
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Abstract (en)
[origin: WO0221139A2] A fully automated, computer-mediated and user-independent method is described to identify and characterize a peptide sequence present in a peptide database that corresponds to an experimental peptide. The method identifies the corresponding sequence if it is present in the database, without the need for a skilled observer to choose from amongst a list of possible matches. By using an automated back-read process, the present method can uniquely identify a corresponding peptide sequence in a database based on a single matching peptide sequence. The method also permits mapping of mass spectral data to sequences in peptide or nucleotide databases for unambiguous identification of exons; determining a correct reading frame; identifying artefacts and errors in sequences; identifying mutations and polymorphisms; identifying post-translational modifications; and identifying exon-intron boundaries. Also provided are a computer-readable medium comprising instructions for causing a computer to perform the disclosed methods; a computer comprising such instructions; and a peptide or nucleic acid database, a computer-readable file or list, or a display comprising information obtained by performing the disclosed methods.

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