

### High Confidence Rates using Mass Spectrometry

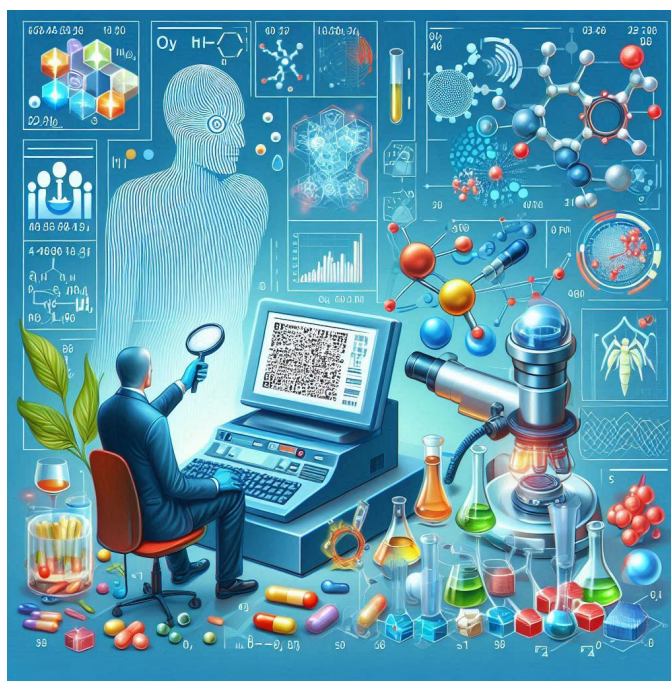
Peptide-bound new biomolecules are determined with high confidence rates, using a computer algorithm and clustering program in combination with mass spectrometric analysis. This process compares native polypeptide sequences to enzymatically derived or chemically fragmented polypeptide sequences.

#### Advantages:

- Large scale analyses and elucidation of high-confidence peptide from complex mixtures of proteins
- Aimed at large scale sequence determination of multiple native peptides from complex samples
- Generates a computed *de novo* polypeptide sequence
- Python-based algorithm combines clustering and alignment data from parallel analyses of polypeptide samples

#### Ideal Applications

This exciting process identifies new bioactive peptides from species underrepresented in available genomic, transcriptomic and proteomic data, as well as peptides that are not represented in the available data.



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