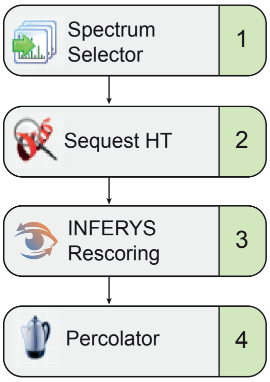
INFERYS RESCORING
BY MSAID

The powerful enhancement for classical search engines

- Powerful AI-enhancement to well-established classical search-engines
- Prediction-based scoring of all candidate PSMs generated by Sequest™ HT prior to FDR control
- Increased sensitivity of analysis through better separation of target and decoy identifications
- Streamlined implementation and fast computation on your local computer
- Available in Thermo Scientific™ Proteome Discoverer™ 3.0 software

Workflow



Classical search engine (SE) Sequest™ HT functions as candidate generator. All candidate PSMs are predicted using INFERYS® and scored against experimental spectra using intensity-based figures of merit. Classical SE scores and intensity-based scores are aggregated by Percolator.

Recommended for

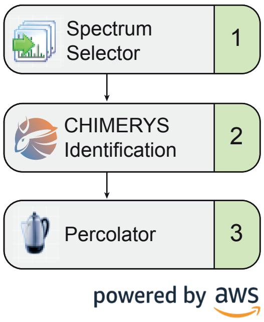
- Sparse data and vast search spaces
- Single cell data & low input amounts
- Immunopeptidomics

CHIMERYS
BY MSAID

The AI-driven, cloud-native, intelligent search algorithm

- Intelligent search algorithm for next generation DDA data analysis
- Prediction-based scoring of full isolation window and deconvolution of chimeric spectra
- Substantially increased PSM, peptide and protein identification and quantification
- Cloud-native microservice to streamline processing
- Available in Thermo Scientific™ Proteome Discoverer™ 3.0 software

Workflow



CHIMERYS aims to best explain the experimental spectrum using the fewest number of peptides. All reasonable peptides within the isolation window are scored in a concerted step and compete for experimental intensity, thereby deconvoluting the spectrum. FDR estimation is performed by Percolator.

Recommended for

- Comprehensive knowledge extraction
- Complex data & high input amounts
- High-throughput samples

Compatibilities

- CID and HCD
- 7-30 amino acids
- Label-free, TMT™, and TMTpro™
- IonTrap and Orbitrap™ data
- Met(Ox) and Cys(Cam)
- Multiple proteases

For more information, please visit us at msaid.de and thermofisher.com/proteomediscoverer.