

Shotgun Proteomics — Peptide Identification & FDR — Hands-on

Learn the complete peptide and protein identification workflow used in modern shotgun proteomics. You will configure search spaces, run and tune peptide spectrum matching, understand scoring and target decoy based validation, control FDR at PSM, peptide and protein levels, and generate reviewer ready identification reports.

Shotgun Proteomics — Peptide Identification & FDR

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Session 1

Fee: Rs 12320 [Apply Now](#)

Spectra, Search Space & Search Setup

Understanding tandem MS spectra for IDs

[fragment series \(b y\)](#) [charge states & isotopes](#) [noise and intensity patterns](#)

Database and search space definition

[UniProt Swiss Prot vs TrEMBL](#) [contaminant databases](#) [enzyme rules & missed cleavages](#)

Search parameter setup and export

precursor and fragment tolerances **fixed and variable modifications** **open vs narrow searches overview**

Session 2

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Peptide Spectrum Matching & Scoring

Search engines and score types

Comet MS GF plus X Tandem **SEQUEST like scores**
XCorr, E values, hyperscore ideas

Spectrum pre processing and matching

peak picking and filtering **matching theoretical vs experimental ions** **handling chimeric spectra**

Score distributions and diagnostics

decoy vs target score curves **delta score concepts**
search quality checks

Session 3

Fee: Rs 20720 Apply Now

Target Decoy, FDR & Validation

Target decoy strategies and pitfalls

reversed vs shuffled decoys **concatenated vs separate** **decoy inflation issues**

Multi level FDR estimation

PSM FDR and q values **peptide and protein FDR**
percolator like rescoring ideas

Confidence thresholds and validation workflows

one percent FDR conventions **site level vs peptide**

level control **manual spectrum review guidelines**

Session 4

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Protein Inference, Reports & Reproducibility

Protein inference and parsimony rules

shared peptides handling **razor peptides concept**
protein grouping and sub grouping

Export tables, evidence tracking and checklists

PSM, peptide and protein tables **sequence coverage**
plots **minimal information for proteomics reports**

Reproducibility and repository submission overview

search parameter documentation **pipeline versioning**
PRIDE submission concepts