

Clinical Proteogenomics & Biomarker Panels — Hands-on

Design and operate clinical-grade proteogenomics workflows that connect variants and expression to protein evidence. This module covers MS-based discovery (DDA/DIA), peptide-spectrum matching, protein inference, PTM/phosphoproteomics, targeted assay development (PRM/SRM/MRM), quality metrics, and multi-omics integration for validated biomarker panels and reports.

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[Session 1](#)

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Proteomics Foundations & QC

Acquisition & data formats

[DDA vs DIA basics](#) [mzML/mzIdentML](#) [FASTA/decoys](#)

Quality metrics & controls

[mass accuracy/RT drift](#) [carryover/blank checks](#)
[iRT/standards](#)

Pipelines & toolchain

MaxQuant/MSFragger | FragPipe/Proteome Discoverer
DIA-NN/OpenSWATH

Session 2

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Discovery (DDA/DIA) & Protein Inference

PepID & FDR control

target-decoy | Percolator/PSM q-values | site-level FDR

Spectral libraries & DIA

library-free vs library-based | transition selection
interference handling

Protein inference & quant

razor/unique peptides | LFQ/iBAQ | missingness &
imputation

Session 3

Fee: Rs 27320 | Apply Now

PTMs/Phospho & Targeted Panels (PRM/SRM)

PTM identification (overview)

phospho enrichment | open searches | localization
scores

Targeted assay design

peptide uniqueness | stable isotope standards
transition optimization

Panel performance & QC

linearity/precision | LoD/LoQ | matrix effects

Session 4

Fee: Rs 32920 Apply Now

Proteogenomics, Validation & Reporting

Proteogenomic mapping

custom variant FASTA **RNA/Protein concordance**
neoantigen peptides (high-level)

Validation & governance

reference materials/QC charts **change control &**
SOPs **proficiency testing**

Clinical reporting & integration

evidence tables **FHIR/HL7 (overview)** **limitations &**
disclaimers