# Quantitative Proteogenomics — Genome Guided Searches — Hands-on

Learn how to conceptually connect genomic information with LC–MS/MS readouts through quantitative proteogenomics. This module focuses on genome guided database ideas, variant and junction peptide concepts, and how to interpret quantitative proteomics in the context of genomic alterations and pathways for discovery and translational projects.

## Quantitative Proteogenomics — Genome Guided Searches

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**Session Index**

**Session 1**

**Fee: Rs 8800** Apply Now

### Proteogenomics Foundations & Study Context

What proteogenomics tries to link conceptually

- genome and transcript information
- observed peptide and protein signals
- variant and novel sequence evidence

Typical proteogenomics study scenarios

- tumor and matched normal concepts
- cell line and

model system contexts | coordinated DNA, RNA and protein layers

Data layers and sample relationships on paper

matched genomic and proteomic samples | linking identifiers across layers | conceptual sample tracking map

Session 2

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## Genome Guided Database & Peptide Space

Concepts for building genome guided protein databases

reference protein sequences idea | incorporating sample specific variants | balancing database size and coverage

Variant and junction peptide concepts

amino acid changes from genomic variants | peptides spanning exon junction ideas | novel sequence windows conceptually

Controlling search space in proteogenomics at high level

limiting to sample relevant changes | separating canonical and extended entries | thinking about decoys and FDR impact

Session 3

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## Proteogenomic Search, FDR & Quant Concepts

Interpreting identifications against extended databases

canonical vs variant peptide evidence | novel peptide hit considerations | site and sequence level confidence

FDR and confidence thinking in proteogenomics

impact of larger search spaces | separate handling of novel classes | supporting evidence from multiple spectra

Quantitative layers in proteogenomics at high level

peptide and protein abundance patterns | linking to copy number and expression | thinking about outliers and concordance

Session 4
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## Biology, Pathways & Reporting in Proteogenomics

From variant peptides to biological hypotheses

theory plus planning worksheet

Pathway and network thinking with multi layer data

linking genomic changes to protein effects | pathway level consistency and conflicts | highlighting variant driven signatures

Reporting proteogenomics methods and results clearly

describing database construction concepts | tables of key variant peptides | summary figures for multi layer views