

Online Advanced Training on

Mass Spectrometry-based Proteomics with Post-Translational Modification Biology (Phospho & Glycoproteomics)

Date : 11 April to 10 May 2026 (Duration: 5 Weeks)

Schedule: Weekends (Saturday & Sunday)

Time: 6:00 PM – 8:00 PM IST, Session Length: 2 Hours Each

About the Training

This 5-week advanced training program focuses on mass spectrometry-based proteomics with Phospho- and Glycoproteomics. Participants will gain practical skills in MS workflows, quantitative proteomics, and PTM data analysis using real biological datasets. The course emphasizes phosphorylation and glycosylation-driven signaling in disease, supported by hands-on analysis and case studies. Learners will develop the ability to interpret proteomics data into pathways, networks, and biological insights, preparing them for research, biotech, and pharma R&D roles.

Target Audience

- B.Sc/M.Sc/B.Tech/M.Tech students in Biotechnology, Life Science, Biochemistry & Microbiology
- PhD Scholars working in proteomics, PTM biology, signaling, glycosylation
- Early-career researchers in mass spectrometry-based omics data analysis
- Professionals pursuing roles in bioinformatics, proteomics & translational research

Fee & Features

Indian Participants INR 1899

Other Participants US 110 \$

- E-Certificate to participants
- Live and Interactive Sessions
- Session Recordings
- E-material & Lecture PPTs to Participants

Resource Person



Hariprabu K Gopal

Institute of Bioinformatics,
Bangalore



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Course Outcomes

- Understand mass spec-based proteomics workflows and data generation principles.
- Perform quantitative comparison of proteomic datasets and interpret variation.
- Identify and interpret phosphorylation and glycosylation-based PTM signatures.
- Convert dataset findings into biological pathways, networks, and mechanisms.
- Gain applicability for roles in proteomics research labs, pharma & biotech R&D, and omics-based data analysis positions.

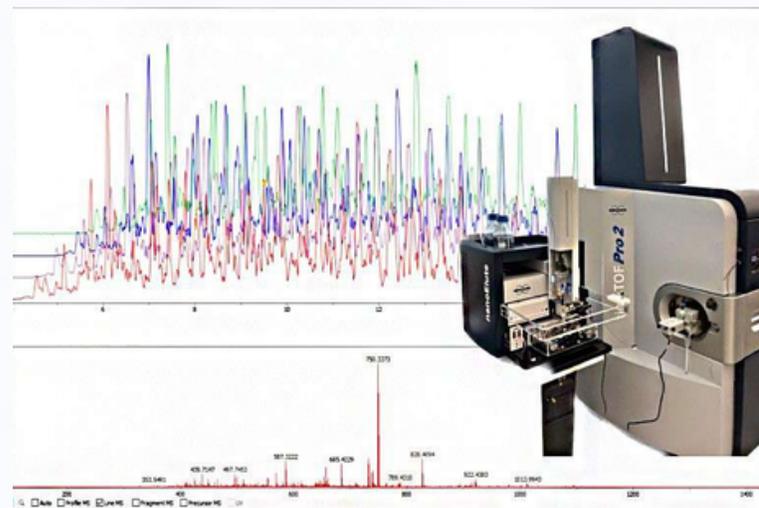
Date and Global Time

Date: 11 April to 10 May 2026

India (IST): 6:00 PM – 8:00 PM | Saudi Arabia (AST): 3:30 PM – 5:30 PM | UAE (GST): 4:30 PM – 6:30 PM | New York (ET): 7:30–9:30 AM | Malaysia (MYT): 8:30 PM – 10:30 PM | Singapore (SGT): 8:30 PM – 10:30 PM

Training Objectives

- To build a strong conceptual understanding of proteomics and peptide biology
- To train participants in mass spectrometry-based proteomics workflows
- To enable participants to analyse MS-derived proteomic datasets independently
- To provide deep exposure to Post-Translational Modifications (PTMs) – Phosphorylation & Glycosylation
- To develop competency in data interpretation, pathway inference & biological insight building



Course Module

Week 1

Session 1

Introduction to Proteomics – Top-down & Bottom-up approach
Fundamentals in Mass Spectrometry – Orbitrap

Session 2

Sample preparation in proteomics – \ Reduction, Alkylation, Digestion, Peptide cleanup, Peptide labeling & its importance

Week 2

Session 3

Data analysis in Proteomics – MaxQuant workflow and brief intro on Proteome Discoverer

Session 4

Quantitative proteomics – Normalization, Data Interpretation, Visualization in Perseus

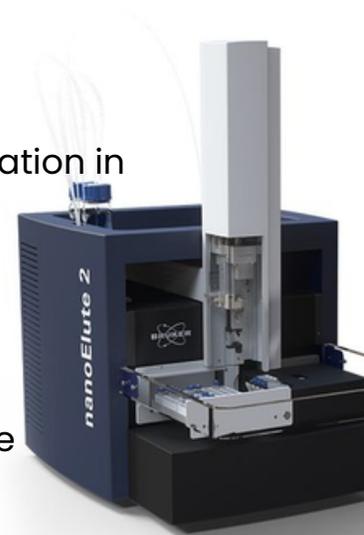
Week 3

Session 5

Introduction to Phosphoproteomics – Biology, site localization, disease signaling, case studies in cancer.

Session 6

Phosphoproteomic data analysis – KSEA analysis, Kinase substrate mapping, Kinome visualization.



Course Module

Week 4

Session 7

Introduction to Glycoproteomics and its role in disease biology, especially cancer.

Session 8

Glycoproteomic data analysis – Oxonium ions, MS behavior, identification of glycans and glycopeptides.

Week 5

Session 9

IBiological interpretation – Functional annotation, Gene Ontology, Pathway enrichment, and Cytoscape network mapping.

Session 10

Doubt clarification + Capstone project initiation (public dataset–based analysis: phospho and glyco).

Software/Tools

- MaxQuant
- Perseus
- Cytoscape
- pGlyco
- GlycoWorkbench
- Excel



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