LC MS MS Methods — DDA DIA PRM SRM — Hands-on

Develop an intuitive understanding of the major LC–MS/MS acquisition strategies used in proteomics. This module focuses on how DDA, DIA, PRM and SRM work at a conceptual level, how method parameters influence coverage, sensitivity and throughput, and how to choose and plan acquisition modes for discovery and targeted studies.

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Session Index

Session 1

Fee: Rs 8800 Apply Now

LC MS MS Fundamentals & Scan Logic

Signal path and key terms in LC–MS/MS

MS1 and MS2 **precursor and fragment ions** **scan events and cycles**

Chromatography and mass spectrometry together

retention time and peak shape **gradient overview** **resolution vs run time**

Cycle time, duty cycle and trade offs

points across a peak **coverage vs sensitivity**

throughput considerations

Session 2

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DDA Methods & Optimization Concepts

DDA precursor selection logic

intensity based top N view | isolation window concept | charge state preferences

Dynamic exclusion and sampling the chromatogram

repeat sequencing avoidance | exclusion windows | complex vs simple samples

Using pilot runs to refine DDA methods

adjusting gradients | mass range choices | cycle settings sanity checks

Session 3

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DIA & PRM Design Logic

DIA acquisition concepts

segmented mass window view | coverage vs interference | library based vs library free ideas

PRM for targeted quant conceptually

monitoring selected precursors | high resolution MS2 focus | panel size and cycle time

When to choose DDA vs DIA vs PRM

discovery vs verification | cohort size and depth needs | instrument and time constraints

Session 4

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SRM Panels & Method Planning

SRM concept for highly targeted assays

theory plus planning exercise

Transitions, scheduling and dwell time logic

precursor and fragment choice **time window scheduling** **panel size vs data quality**

Designing a simple acquisition plan across modes

linking study goals to modes **instrument time budgeting** **documenting method settings**