Protein Stability, Mutation Scanning & Aggregation — Hands-on

Learn how to evaluate and improve protein stability and aggregation behaviour using computational workflows. You will run in silico mutation scans, interpret ΔΔG predictions from multiple tools, map aggregation hot spots, and balance stability with function. The module focuses on practical decision support for enzyme engineering, antibodies, industrial proteins and biotherapeutics developability.

Protein Stability Mutation Scanning & Aggregation

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Session Index

Session 1

Fee: Rs 12320 Apply Now

Stability Concepts & Biophysical Determinants

Thermodynamic and kinetic stability basics

- folding free energy (ΔG) ideas
- melting temperature and unfolding profiles
- local vs global stability concepts

Sequence and structure features that drive stability hydrophobic core packing salt bridges and H bond networks disulfides, prolines and cavities

Experimental readouts and links to computation

DSC, DSF and CD overview activity vs stability trade offs connecting mutations to measured shifts

Session 2

Fee: Rs 16520 Apply Now

In Silico Mutagenesis & ΔΔG Prediction

Setting up mutation scanning campaigns

single site and saturation scans targeting cores, interfaces and loops sequence vs structure driven ideas

Using ΔΔG prediction tools

energy function and ML based predictors input preparation and constraints filtering obviously destabilising variants

Ranking and combining mutation effects

interpreting ΔΔG scales and cutoffs epistasis and double mutants (concepts) shortlisting candidates for wet lab testing

Session 3

Fee: Rs 20720 Apply Now

Aggregation, Solubility & Developability

Aggregation hot spots and sequence liabilities

aggregation predicting tools overview hydrophobic patches and beta propensities surface exposure and flexibility links

Solubility, charge and isoelectric point considerations

net charge and pI shifts charge patterning concepts surface polarity and patches

Developability panels for biotherapeutics and enzymes

stability, aggregation and liability flags expression and formulation perspectives multi parameter scoring ideas

Session 4

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Design Strategies, Workflows & Reporting

Balancing stability, aggregation and function

do and do not rules for mutations preserving active and binding sites combining beneficial substitutions

End to end computational workflow patterns

from structure and sequence to ranked variants integrating MD and free energy insights handoffs to wet lab and analytics

Figures, tables and documentation for projects

heatmaps of ΔΔG and aggregation scores variant shortlists with rationale checklists for reviewers and partners