Antibody & Binder Engineering Informatics — Hands-on

Learn practical informatics workflows for antibody and binder engineering. From sequence and structural analysis of CDRs and frameworks through humanization strategies, paratope epitope mapping and developability assessment, you will design candidate variants that balance affinity, specificity, stability and manufacturability for therapeutic, diagnostic and research applications.

Antibody & Binder Engineering Informatics

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Session Index

Session 1

Fee: Rs 12320 Apply Now

Antibody Formats, Numbering & Architecture

Antibody and binder types overview

- IgG, Fab, scFv, VHH and related formats
- multispecific and fusion formats overview
- binders beyond antibodies (DARPins like)

Numbering schemes and annotation

- Kabat, Chothia, IMGT, AHo schemes
- framework vs CDR boundaries
- heavy and light chain pairing

Sequence databases and repertoire mining public antibody sequence resources germline gene usage patterns clonotypes and lineage views

Session 2

Fee: Rs 16520 Apply Now

CDR Design, Humanization & Liability Assessment

Framework and CDR level analysis

identifying key CDR residues canonical structures ideas backbone and packing constraints

Humanization and germline reversion strategies

germline selection and liability reduction backmutations and contact residues maintaining affinity while reducing risk

Sequence liabilities and post translational motifs

deamidation, isomerization, oxidation motifs glycosylation sites in CDRs and frameworks simple redesign strategies for liabilities

Session 3

Fee: Rs 20720 Apply Now

Paratope, Epitope & Structure Guided Optimization

Paratope mapping and contact analysis

interface mapping from complex structures hot spots and key interaction residues H bond, salt bridge and hydrophobic networks

Epitope level views and escape variants (concepts)

epitope classification and mapping sequence variability and escape prone positions multi epitope and cocktail thinking

Structure guided affinity and specificity tuning

CDR side chain redesign ideas clashes, gaps and complementarity views linking docking and MD insights to design

Session 4

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Developability, Workflows & Reporting Packages

Developability assessment panels

stability, aggregation and viscosity indicators charge, pI and surface property views simple scores and traffic light style summaries

End to end antibody informatics workflows

from sequence to shortlisted variants integrating stability and liability filters handoffs to expression and biophysical teams

Figures, tables and documentation for teams and reviewers

variant comparison tables with rationale interface maps and liability heatmaps clear design story from wild type to lead