

Antigen Processing & Presentation — MHC I & II — Hands-on

Develop a working, computation-ready understanding of how peptides are generated, processed and displayed on MHC class I and II molecules. This module connects cell biology and genetics of MHC pathways to the kinds of peptide sets, restrictions and features used in immunoinformatics, epitope prediction and reverse vaccinology pipelines.

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Session 1

Fee: Rs 8800 [Apply Now](#)

MHC Genetics, Polymorphism & Expression

MHC loci, class I vs class II regions and nomenclature

[HLA-A, -B, -C](#) [HLA-DR, -DQ, -DP](#) [alleles, supertypes, haplotypes](#)

Polymorphism, linkage and population diversity

[peptide binding groove variation](#) [frequency](#)
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coverage

MHC expression, regulation and induction by infection

constitutive vs induced expression **IFN driven**

upregulation **immune evasion by downregulation**

Session 2

Fee: Rs 11800 Apply Now

Antigen Processing Pathways — Class I

Endogenous antigen sources and proteasomal processing

cytosolic proteins & DRiPs **constitutive vs**

immunoproteasome **peptide length distributions**

TAP transport, ER trimming and peptide loading complex

TAP specificity and transport **ERAP trimming** **tapasin and loading complex**

Cell surface display and CD8 T cell recognition

stability and half life of pMHC I **anchor residues and motifs** **link to CTL epitopes**

Session 3

Fee: Rs 14800 Apply Now

Antigen Processing Pathways — Class II & Cross-Presentation

Exogenous antigen uptake and endosomal processing

phagocytosis & endocytosis **endosomal/lysosomal proteases** **pH dependence & peptide pools**

Invariant chain, CLIP exchange and HLA-DM/HLA-DO

biosynthesis of MHC II **Ii/CLIP removal** **peptide editing and selection**

Cross-presentation routes and CD4/CD8 coordination

vacuolar vs cytosolic routes **dendritic cell specialization** **helper T cell support for CTL**

Session 4

Fee: Rs 18800 Apply Now

From Peptide Repertoires to Epitope Pipelines

Conceptual link between processing pathways and epitope features

anchor motifs and pockets **length preferences and flanking regions** **processing-aware scoring**

Interpreting mass-spectrometry ligandomics / immunopeptidomes (conceptual)

eluted ligand datasets **motif extraction** **benchmarking prediction tools**

Mini exercise: sketching a processing-aware vaccine design workflow

from proteome to candidate peptides **MHC coverage and filtering** **handoff to B/T epitope modules**