

# Biomolecular Mass Spectrometry and Proteomics group



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# Biomolecular Mass Spectrometry and Proteomics group

A word cloud of roles within the Biomolecular Mass Spectrometry and Proteomics group. The roles are arranged in a circular pattern around a central point. The roles include: Structural biologists, Research program coordinator, Postdocs, Assistant professors, Cancer biologists, AIO's, Bioinformaticians, Professors, Virologists, Teachers, Analytical chemists, Immunologists, Students, IT, and Researchers. The words are in a sans-serif font, with varying sizes and orientations.

Structural biologists

Research program coordinator

Postdocs

Assistant professors

Cancer biologists

AIO's

Bioinformaticians

Professors

Virologists

Teachers

Analytical chemists

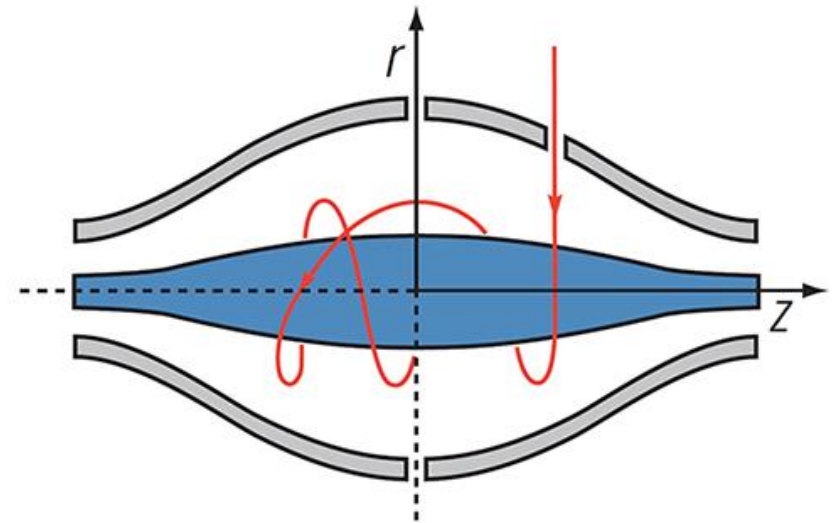
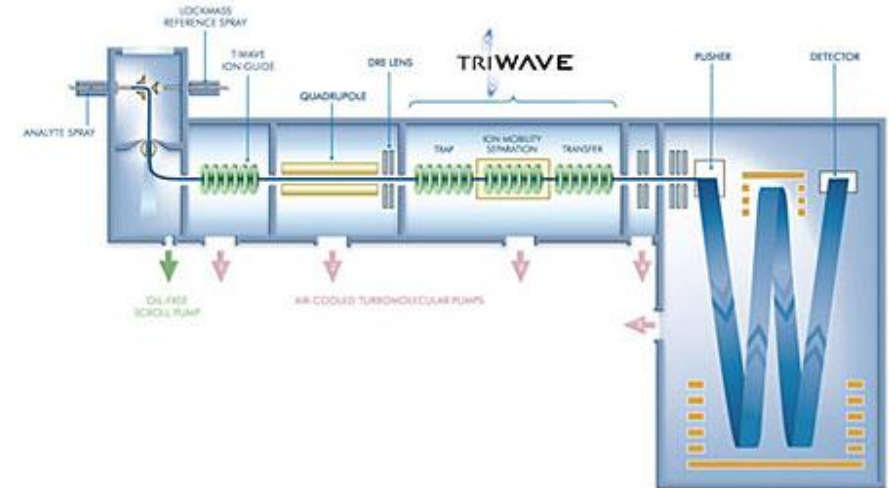
Immunologists

Students

IT

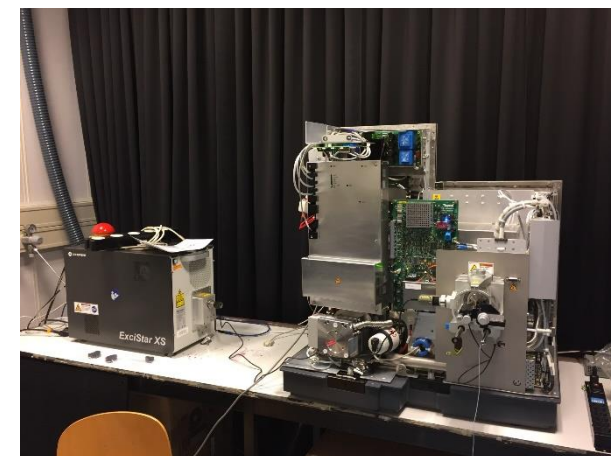
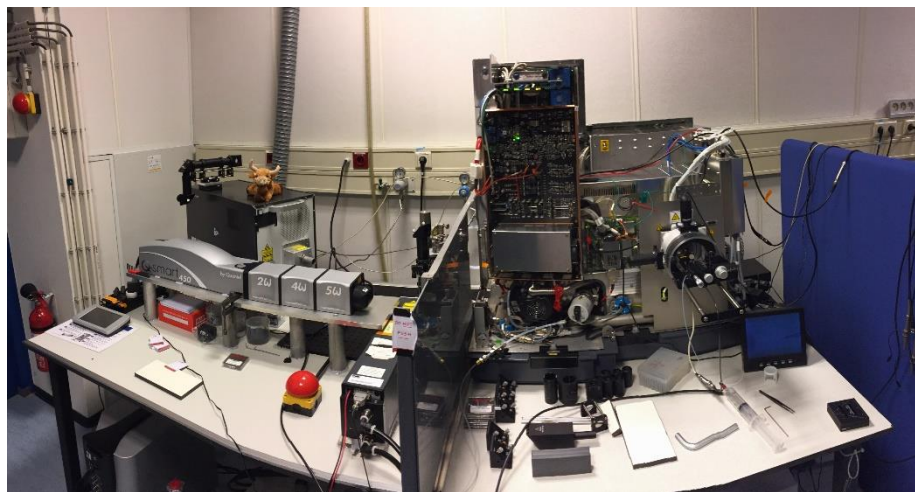
Researchers

# Biomolecular Mass Spectrometry and Proteomics group



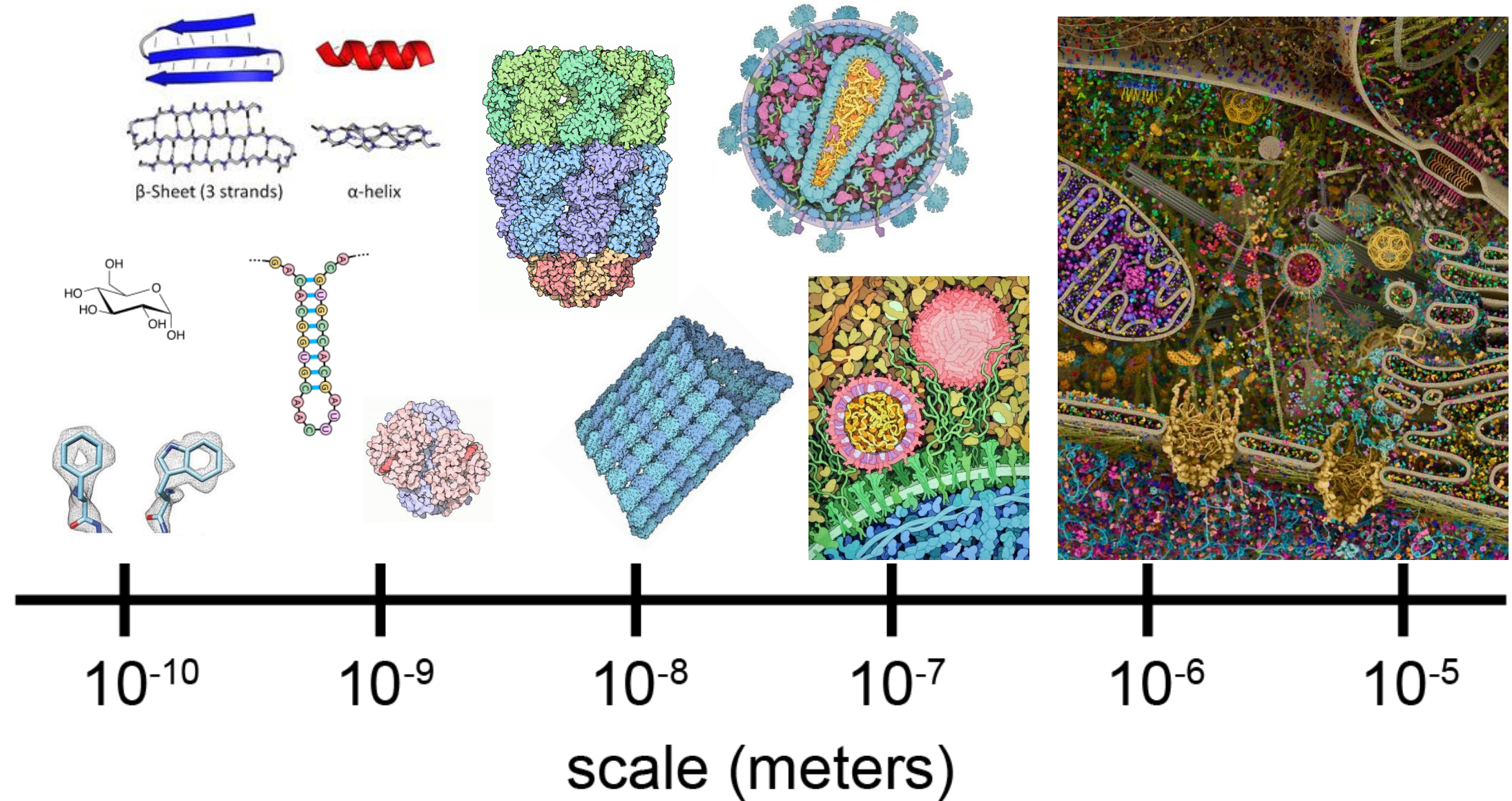


# Biomolecular Mass Spectrometry and Proteomics group: the lab (Kruytgebouw 6th floor, Oost and Zuid wings)

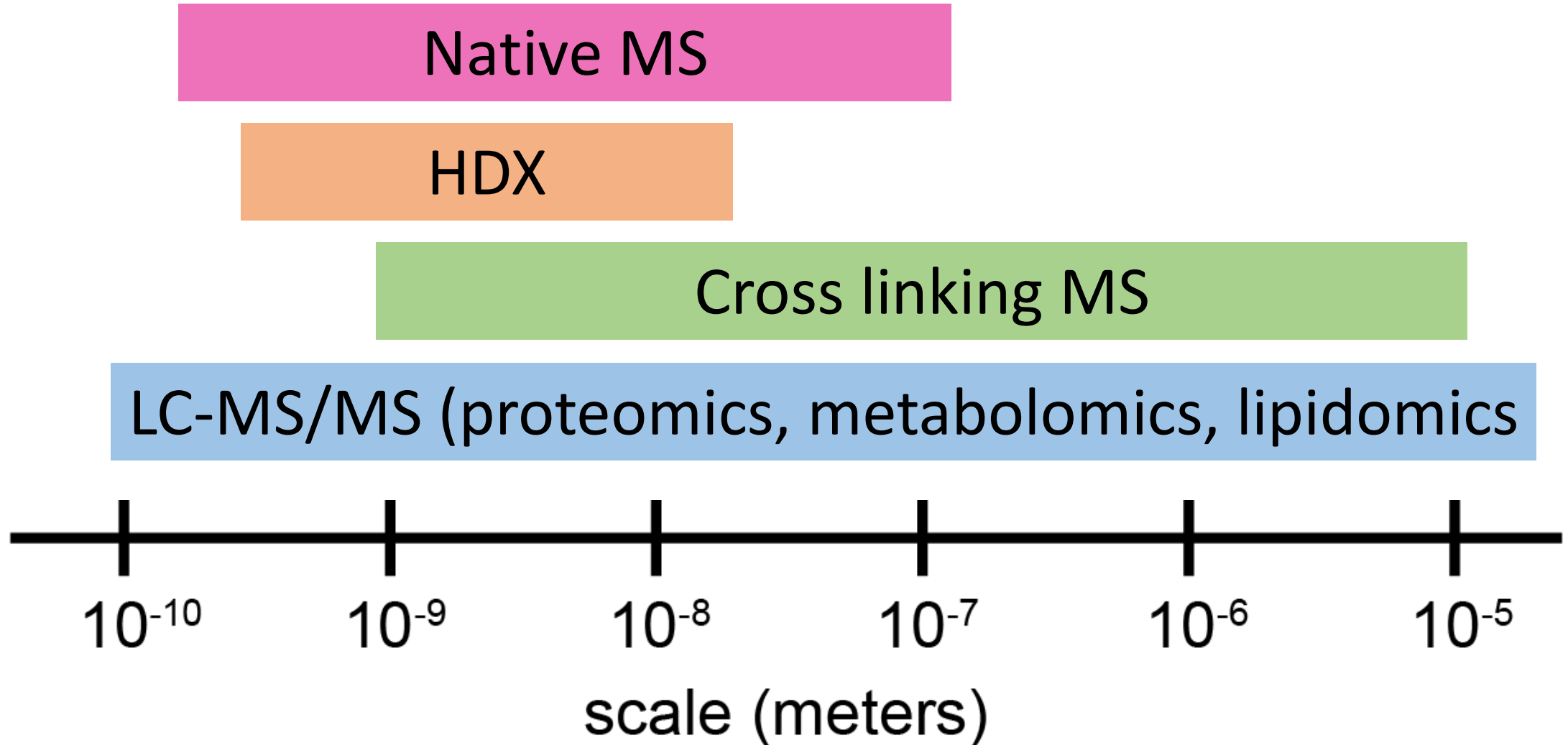




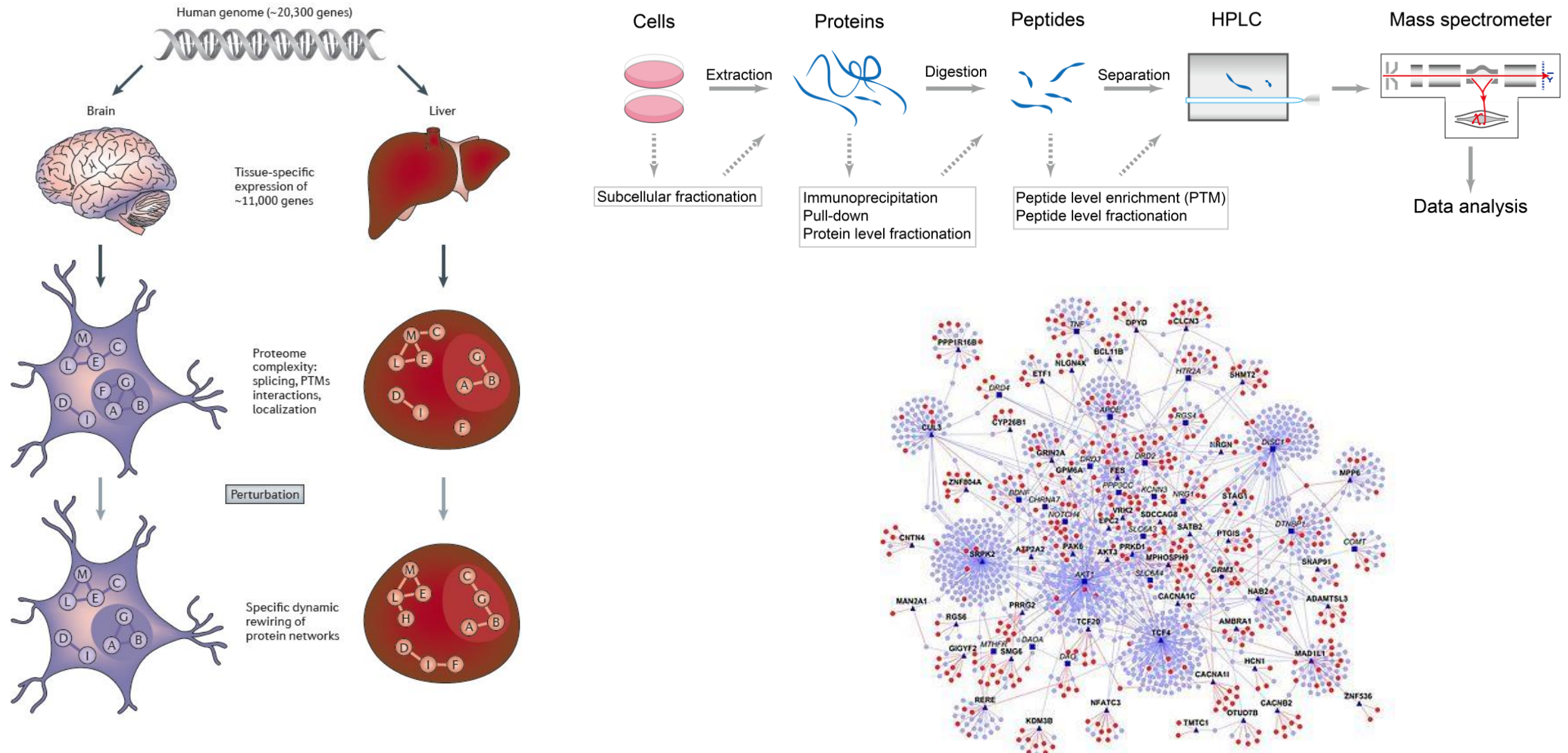
# Biomolecular structure across scales: from functional groups to cells



# MS toolkit in molecular life science

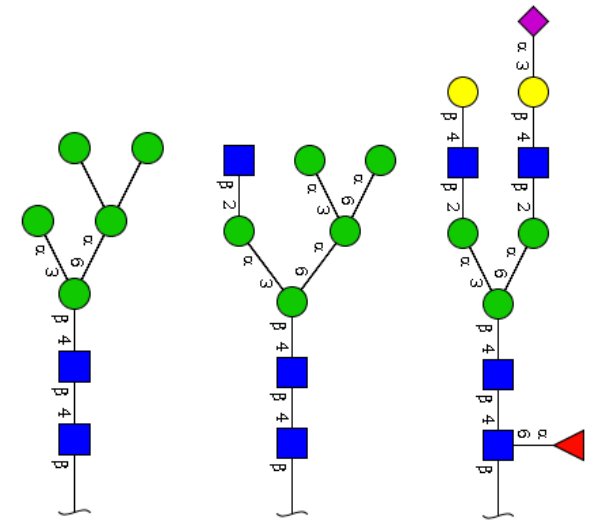
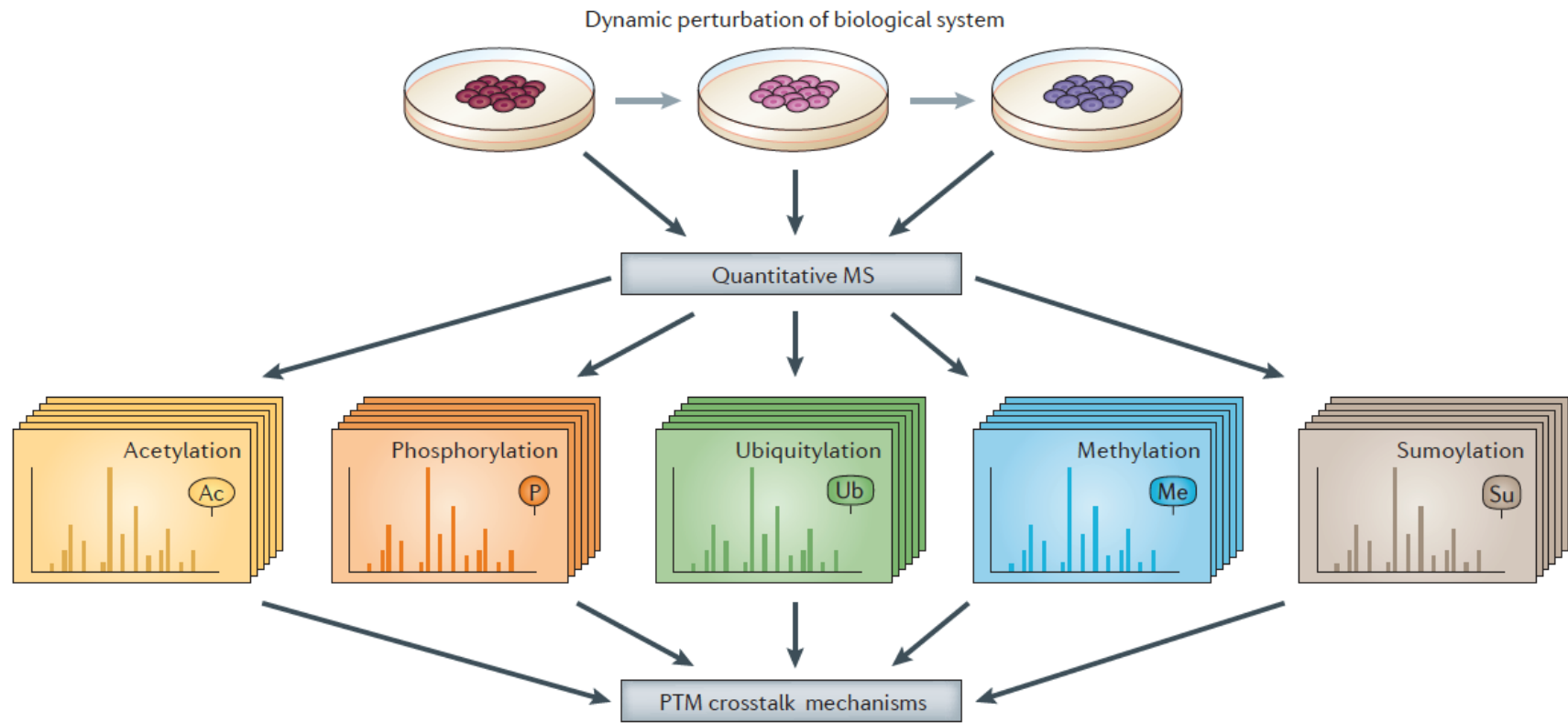


## Proteomics: mapping out all proteins and interactions in cells and tissues



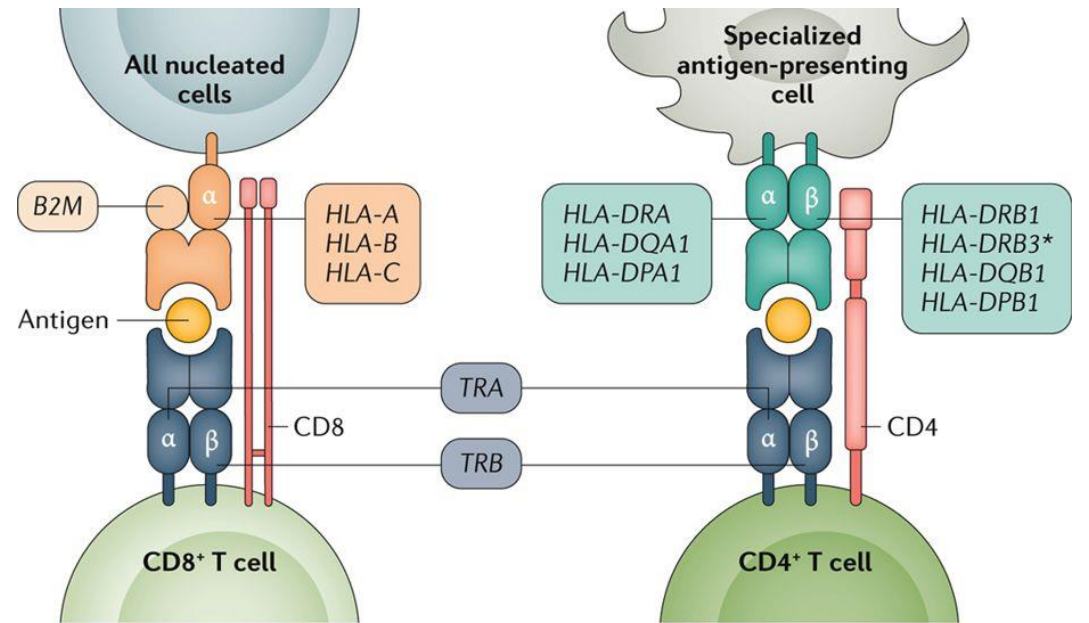
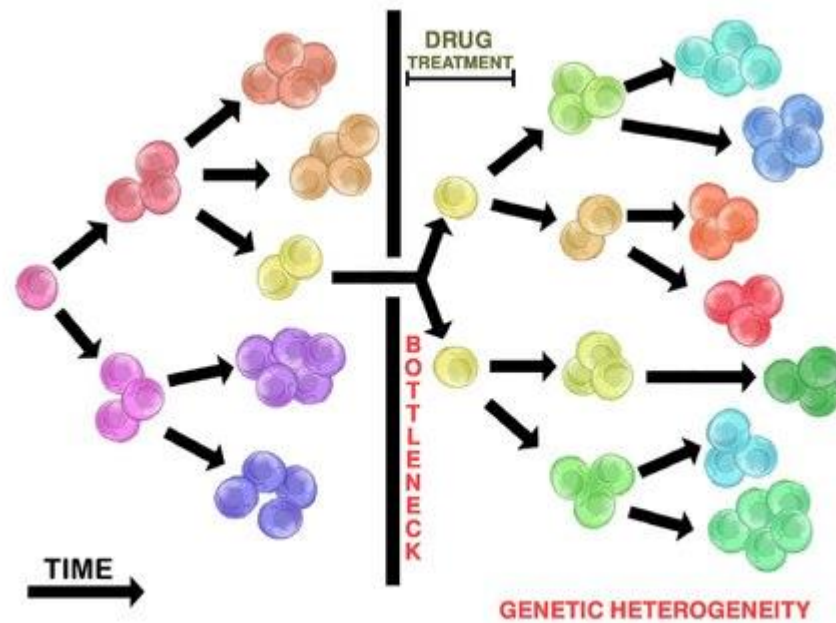


# Proteomics: mapping out all post-translational modifications



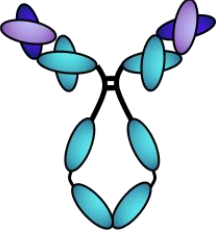
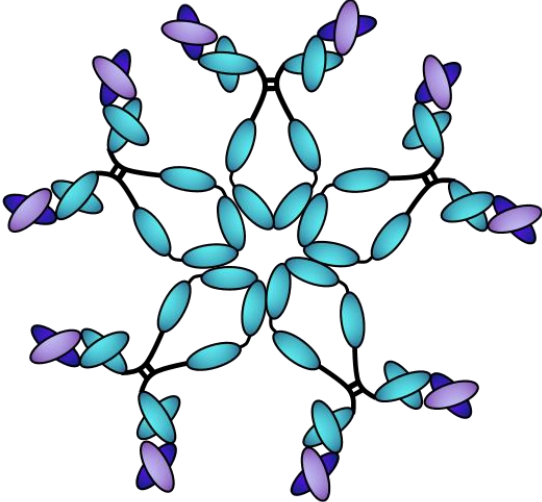
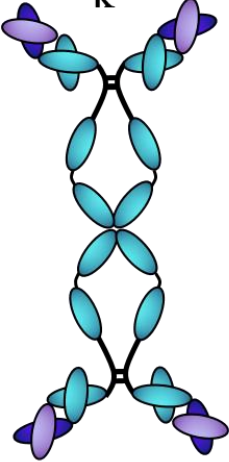
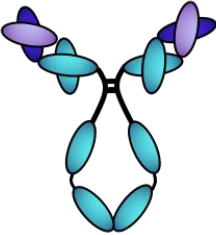
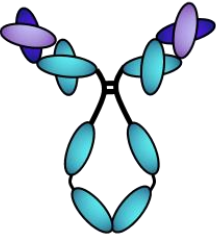
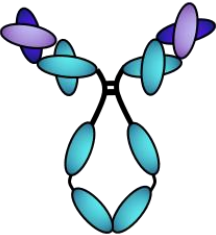


# Cancer biology and immunology



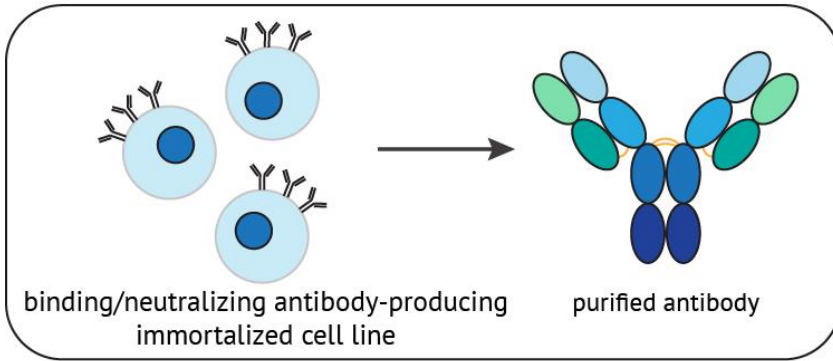
# Antibody characterization

## The five major classes of immunoglobulin.

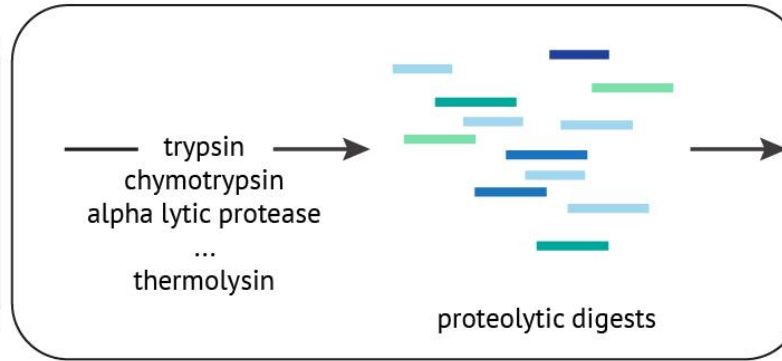
Antibody classes	IgG	IgM	IgA		IgE	IgD
Heavy chain	$\gamma$	$\mu$	$\alpha$		$\epsilon$	$\delta$
Light chain	$\kappa$ or $\lambda$	$\kappa$ or $\lambda$	$\kappa$	$\lambda$	$\kappa$ or $\lambda$	$\kappa$ or $\lambda$
Structure						
Relative MW	$146 \leq X \leq 170$ kDa	$\sim 900$ kDa	$\sim 320$ kDa	$\sim 160$ kDa	$\sim 184$ kDa	$\sim 190$ kDa

# Antibody characterization

Stable isotope labelling of leucine/isoleucine



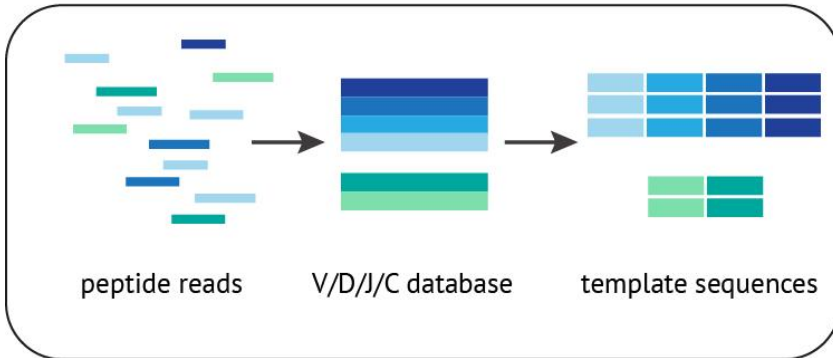
Optimize panel of proteases



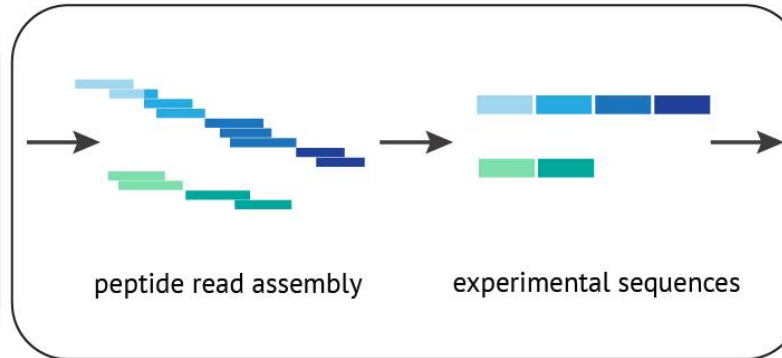
Optimize LC gradient, fragmentation scheme, MS parameters



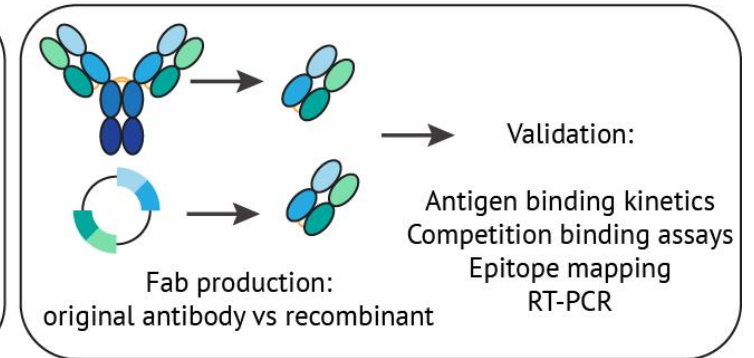
Assemble Ig databases for template construction



Test *de novo* and template-matching assembly tools

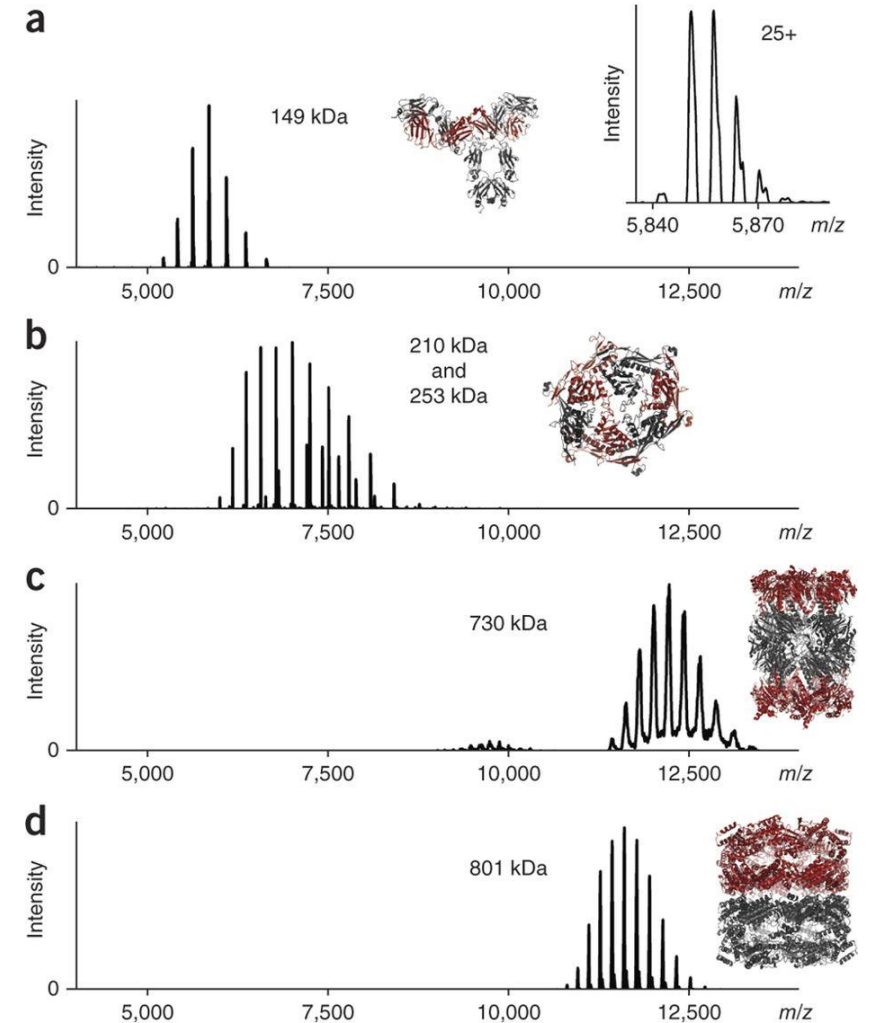
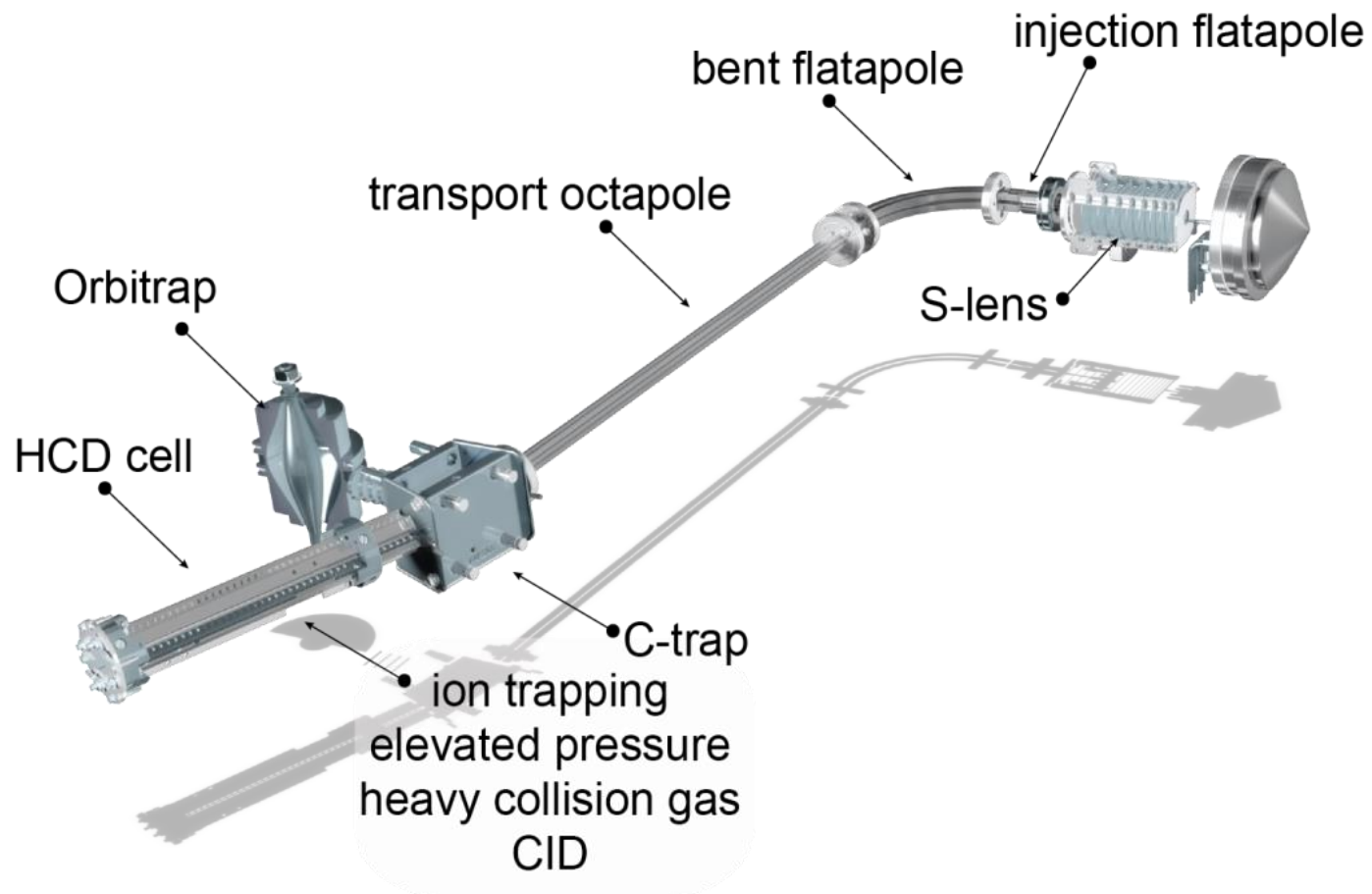


Antibody production and product validation

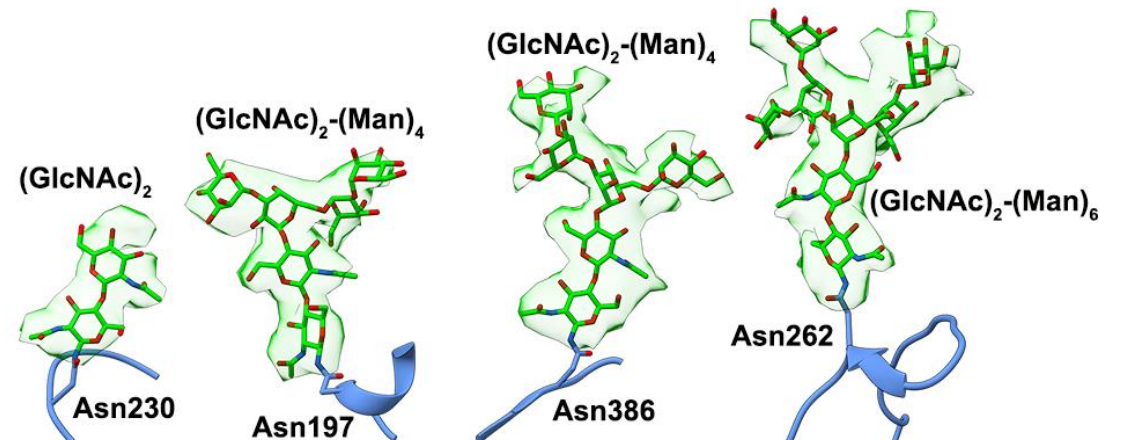
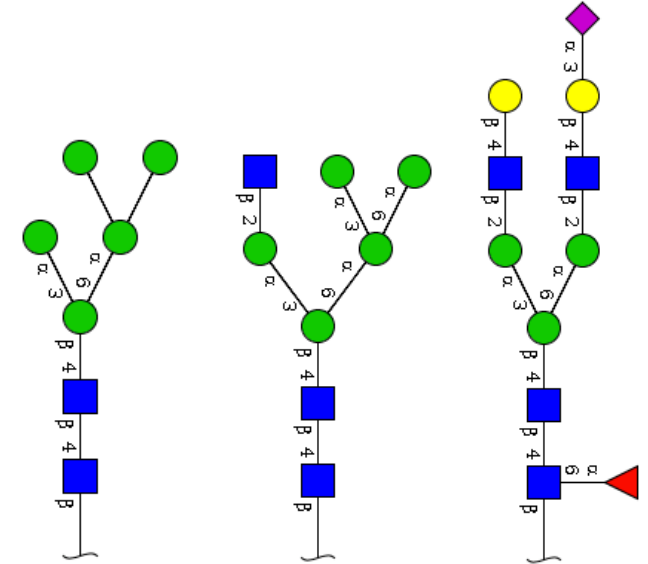
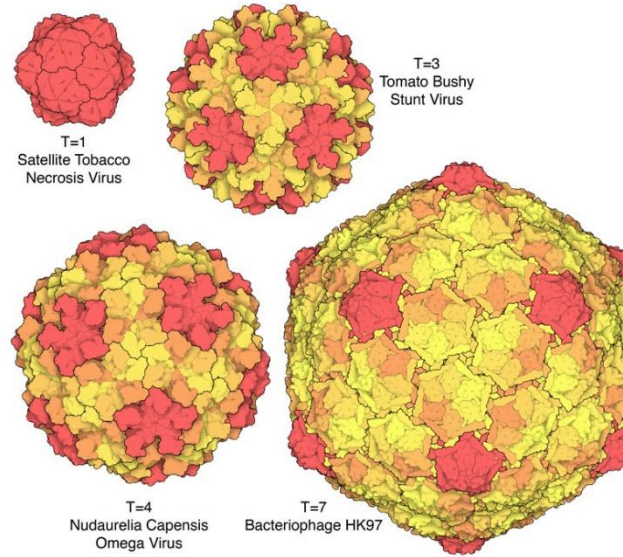
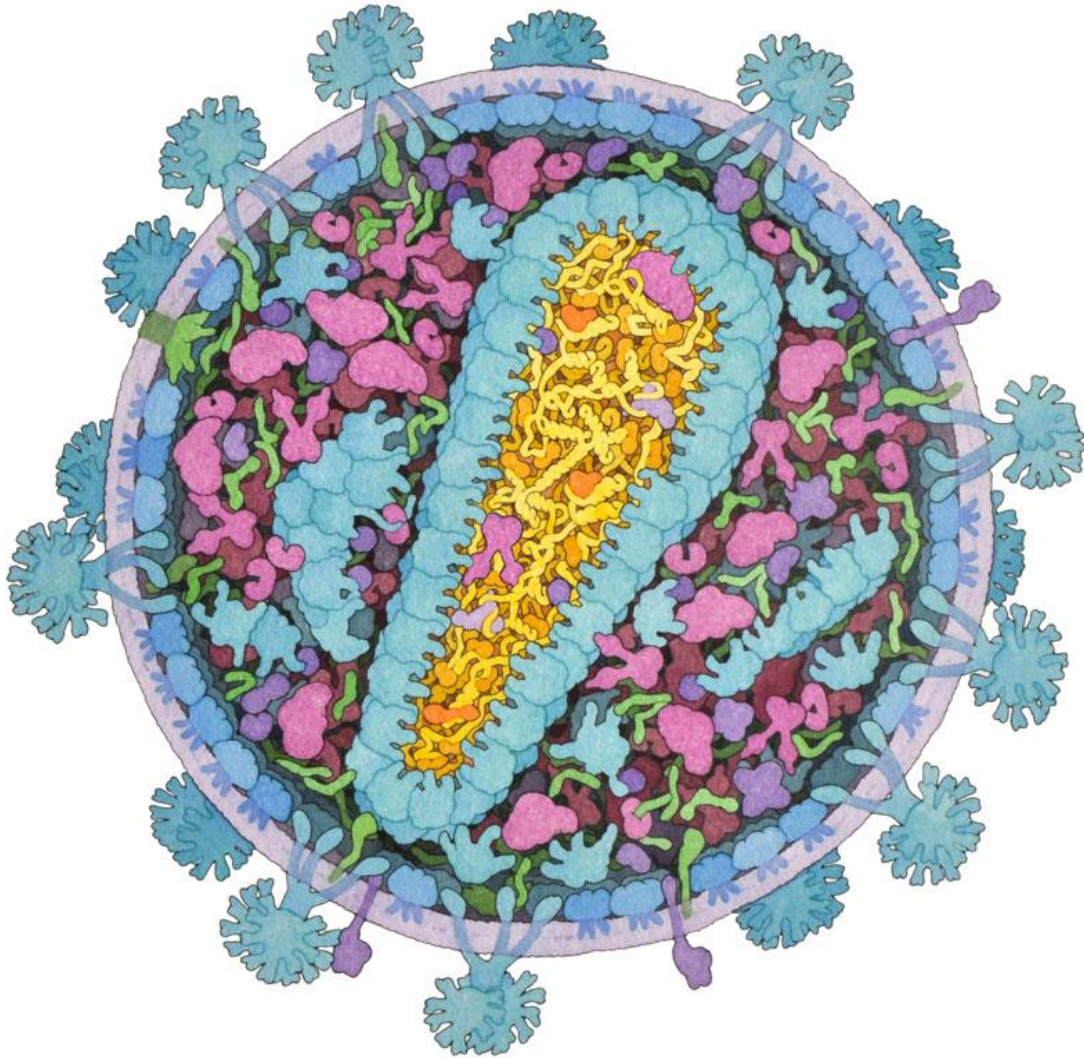




# Native MS – studying assembly of large protein complexes



# Viruses – native MS, structure and immunity





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