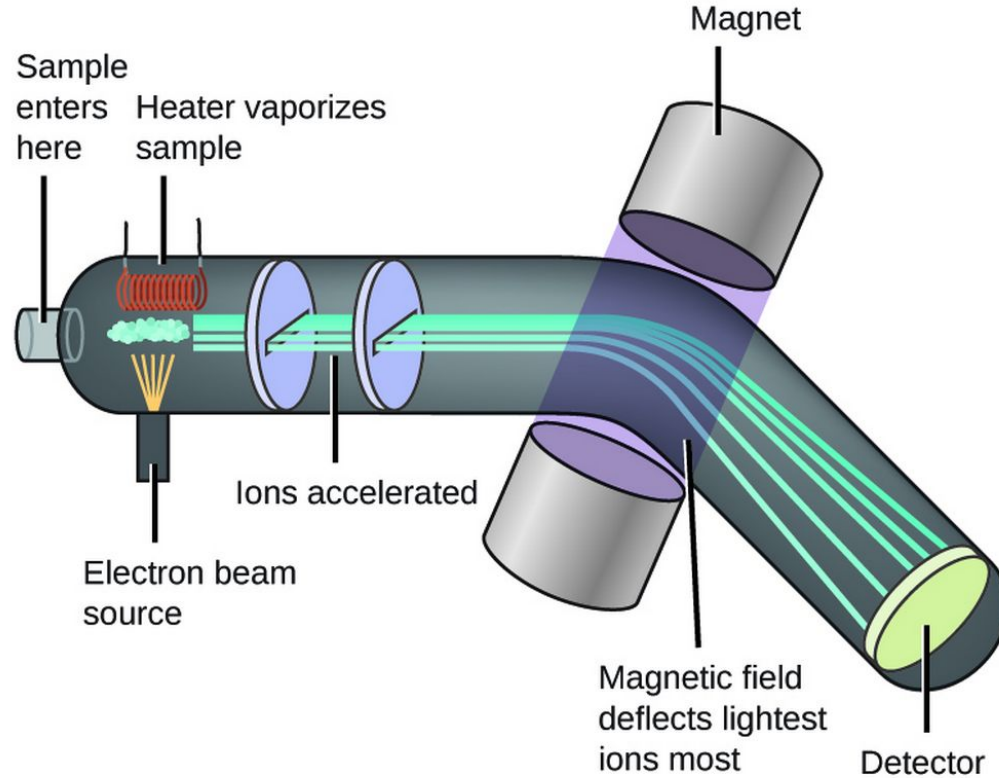


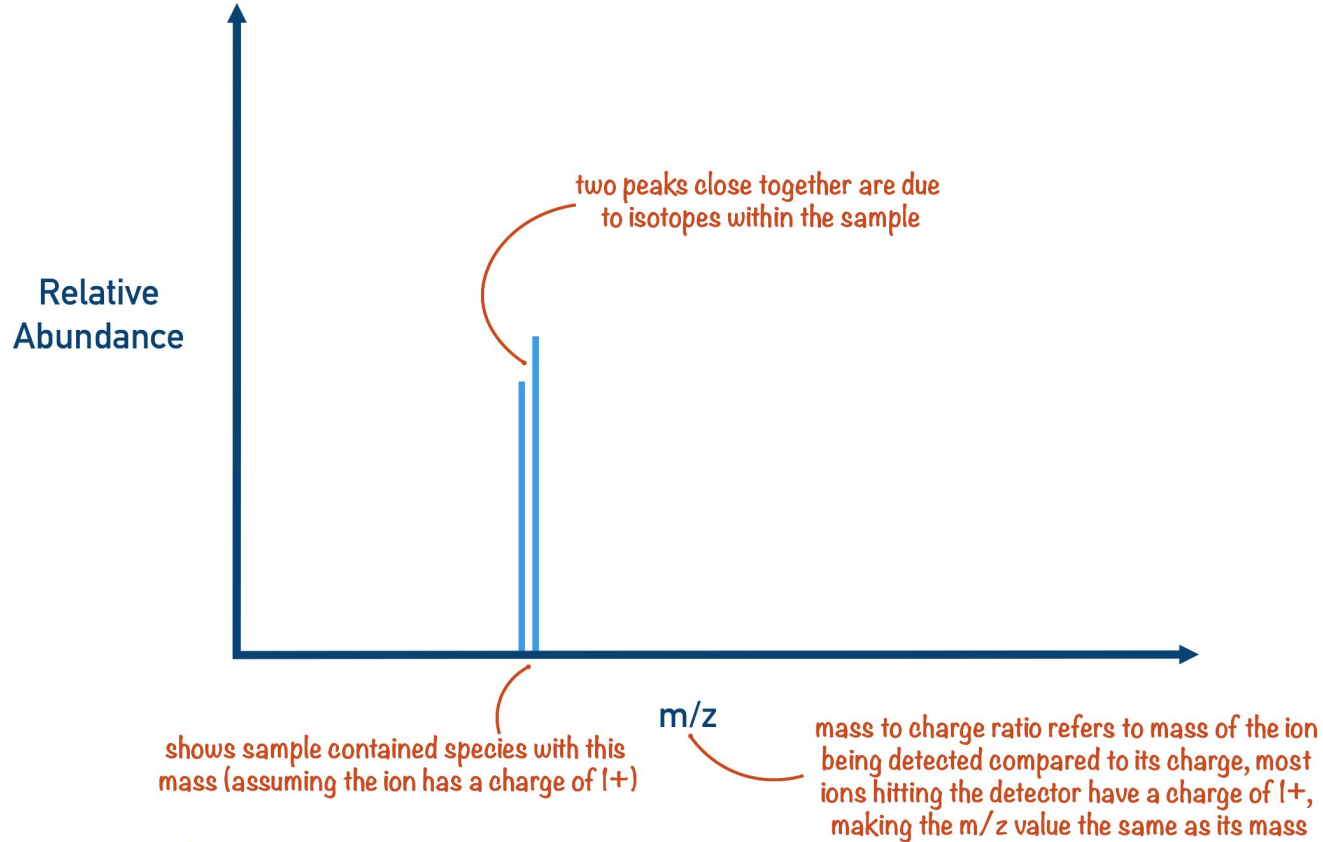
# Overview of Mass Spectrometry toolings and practices in neoantigen discovery

Michał Rembalski

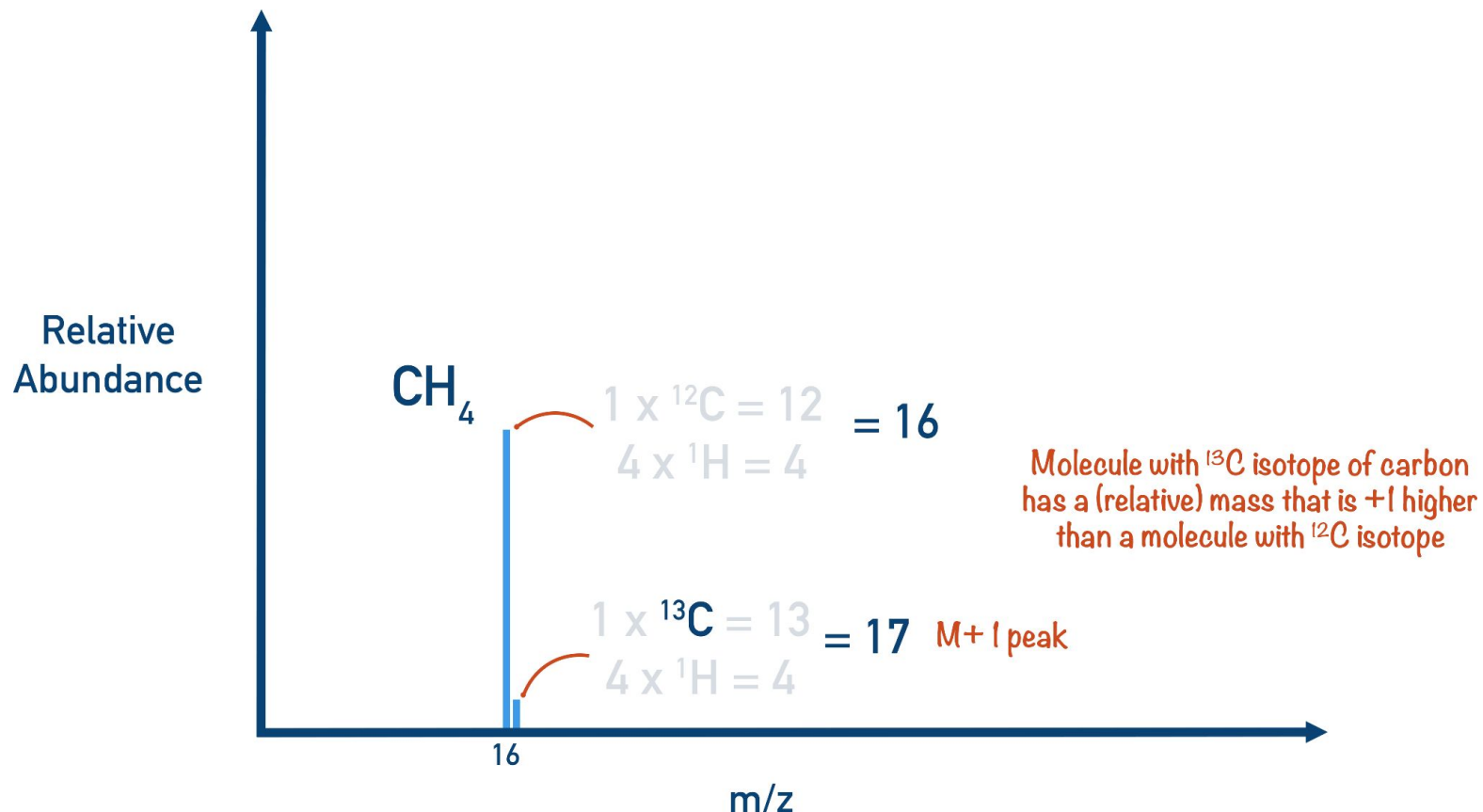
# Mass spectrometry introduction



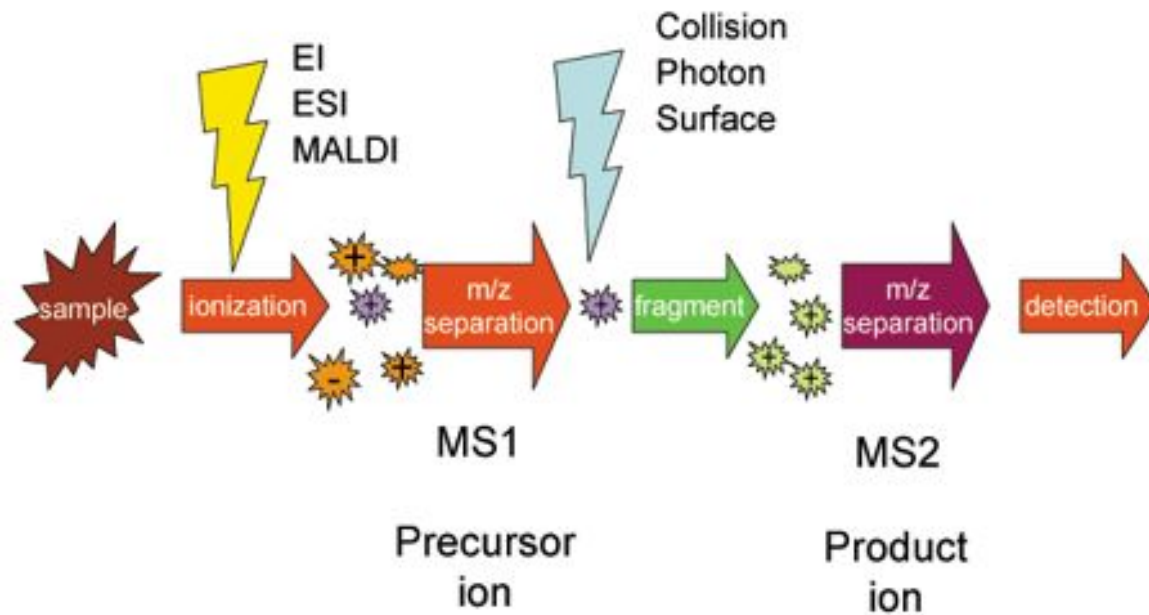
# Isotopes



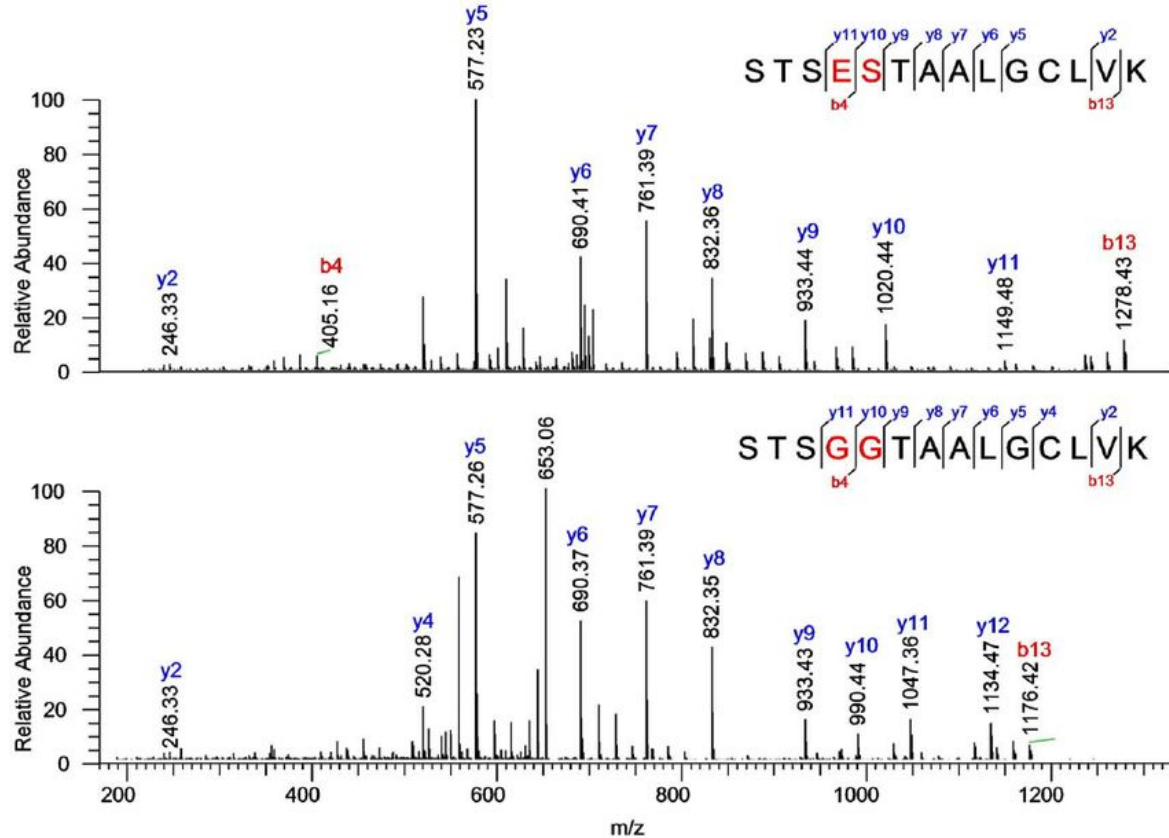
# Isotopes



# MS vs MS/MS



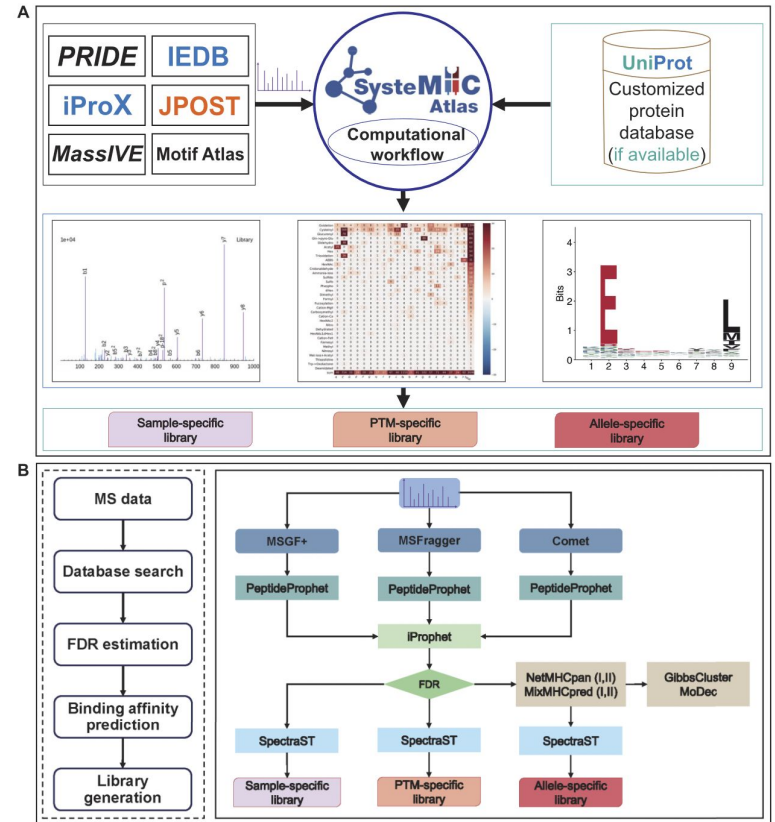
# An example spectrum of a peptide



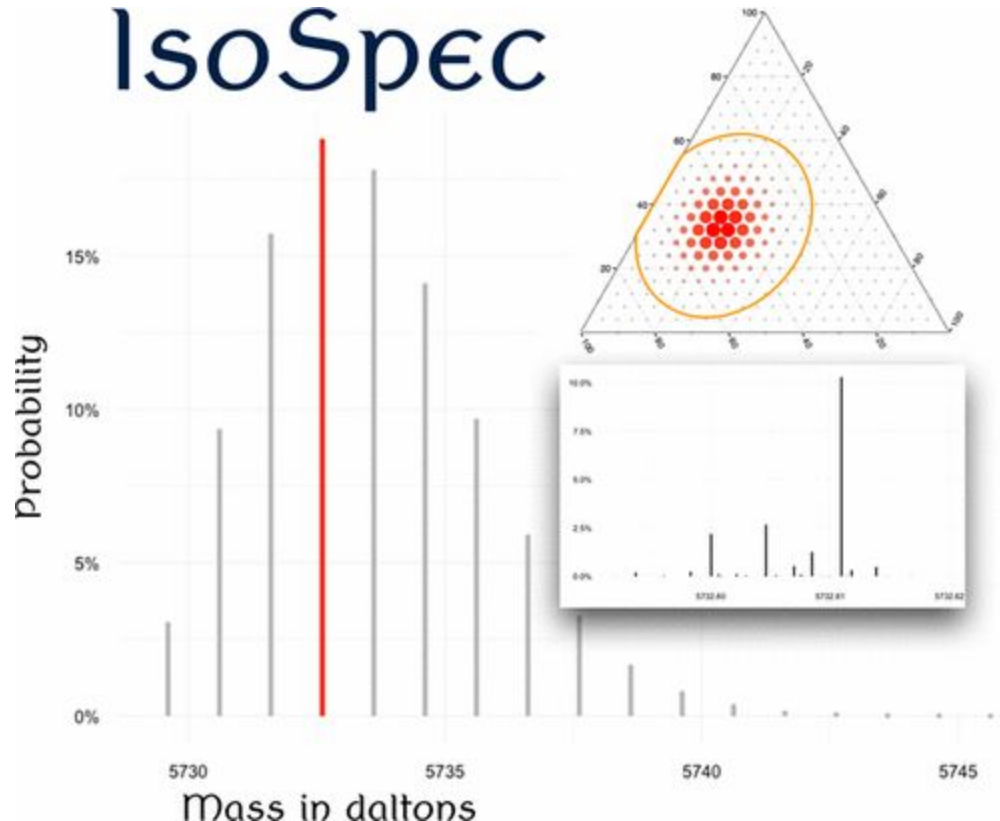
# MSGF+/MSFragger/Comet (targeted search)

Database search tools developed to identify peptides by matching tandem mass spectrometry (MS/MS) data to a database of known protein sequences.

Comet is open source and based on SEQUEST.

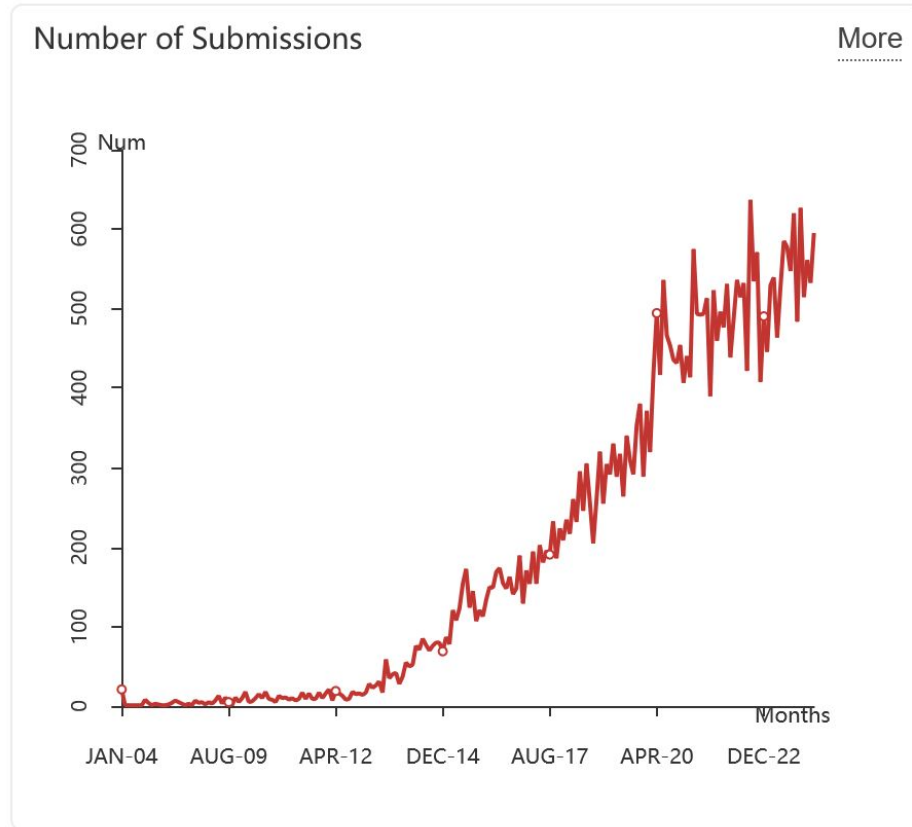


# IsoSpec (an infinite resolution of a spectrum)



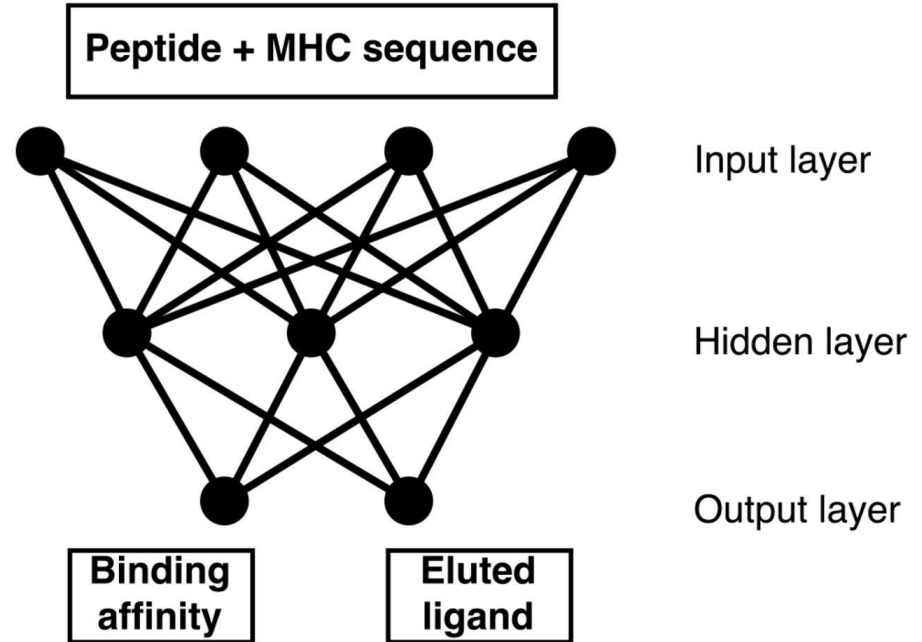


# PRIDE database

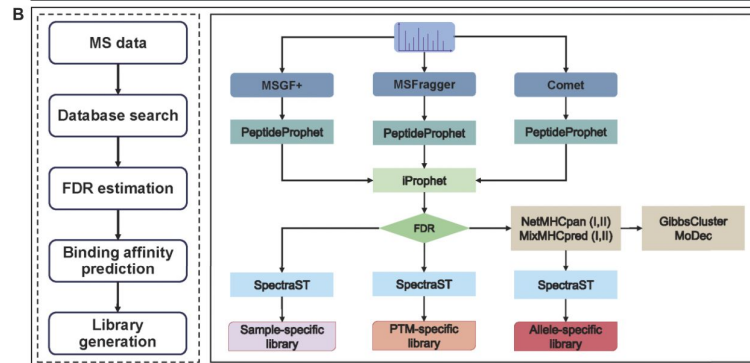
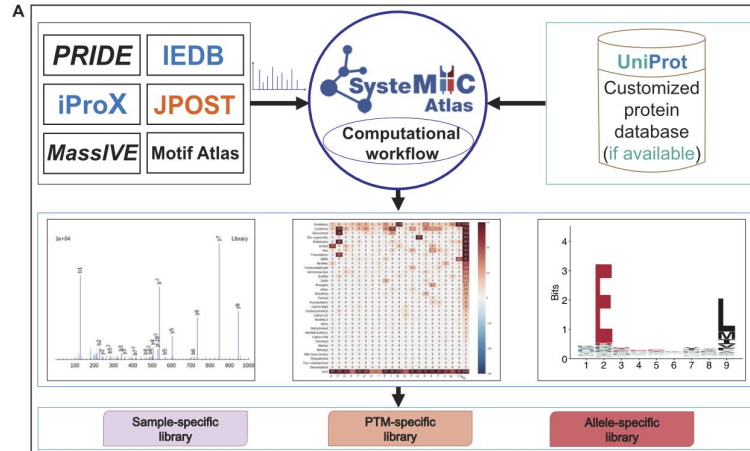


# NetMHCpan (and targeted vs non-targeted searches)

‘Improved predictions of MHC antigen presentation by concurrent motif deconvolution and integration of MS MHC eluted ligand data’



# SystemMHCAtlas v2.0



# Bibliography

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<https://nationalmaglab.org/user-facilities/icr/techniques/fragmentation-techniques/tandem-ms>

<https://www.x-mol.net/paper/article/234107>

<https://www.ebi.ac.uk/pride/>

[https://www.researchgate.net/publication/375913575\\_The\\_SystemHC\\_Atlas\\_v20\\_an\\_updated\\_resource\\_for\\_mass\\_spectrometry-based\\_immunopeptidomics](https://www.researchgate.net/publication/375913575_The_SystemHC_Atlas_v20_an_updated_resource_for_mass_spectrometry-based_immunopeptidomics)

<https://services.healthtech.dtu.dk/services/NetMHCpan-4.1/>

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