

SV PTECH PTP-PCF



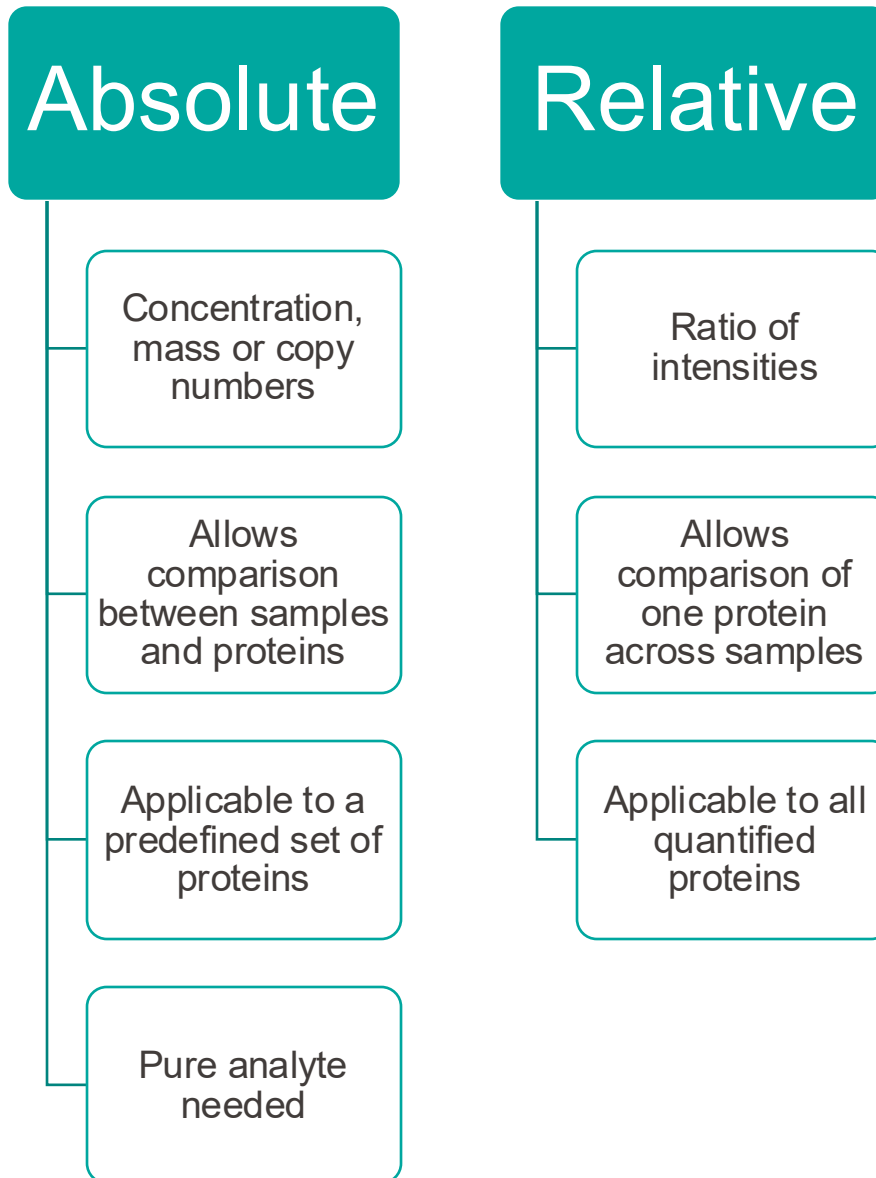
# Lab Methods (BIOENG-519) Methods: omics methods in biomedical research

## Proteomics: Bioinformatic session

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# Quantitation strategies



# Main assumptions for relative quantitation

- Equal total protein across samples
- Consistent sample preparation
- Stable instrument performance
- Peptide signal intensity reflects protein abundance
- Representative peptide selection (the quantified peptides represent the whole protein's abundance)
- Linear dynamic range
- Minimal missing values

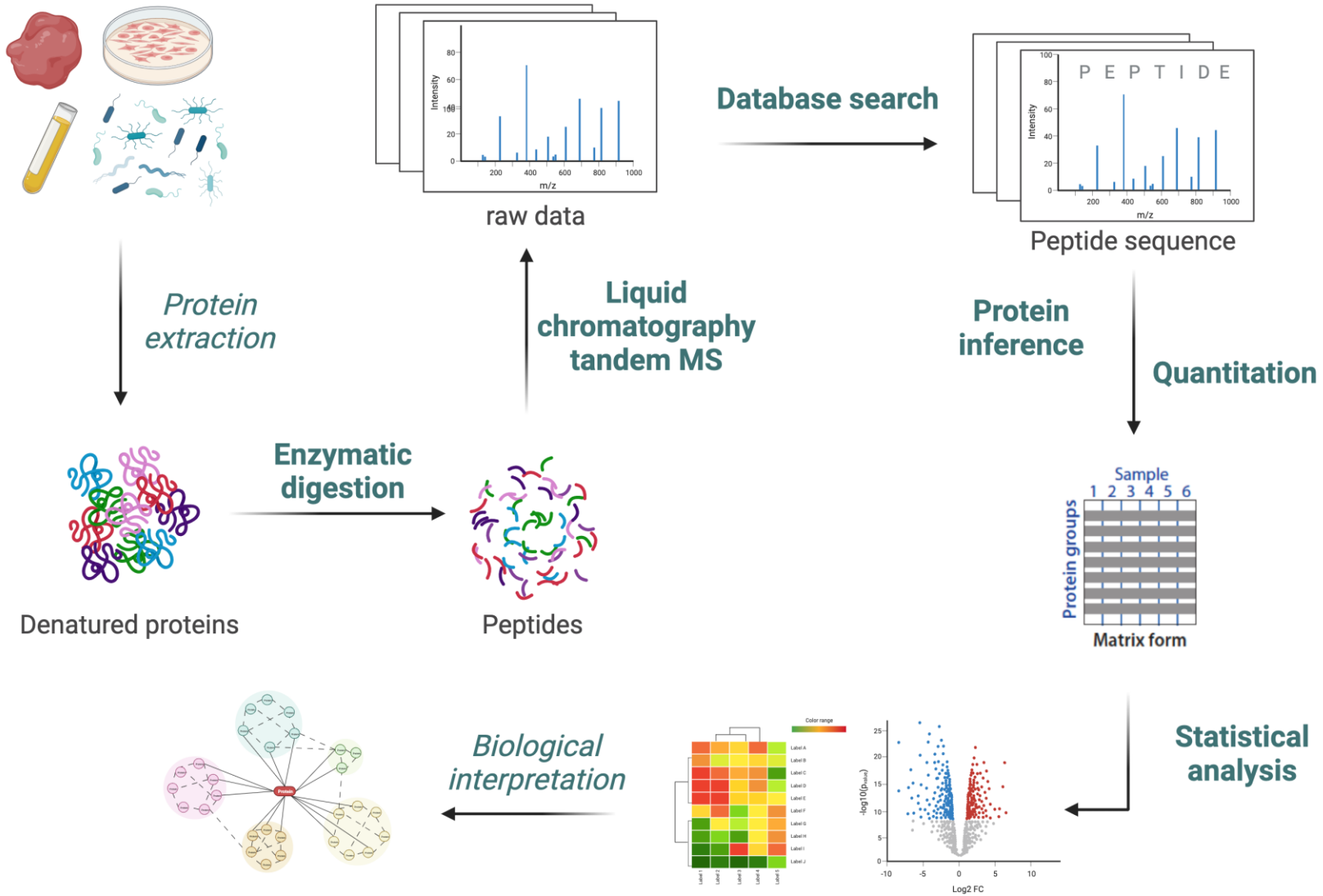
# Study example

# What are the proteomic differences between androgen receptor (AR) independent and AR dependent prostate cancer cell lines

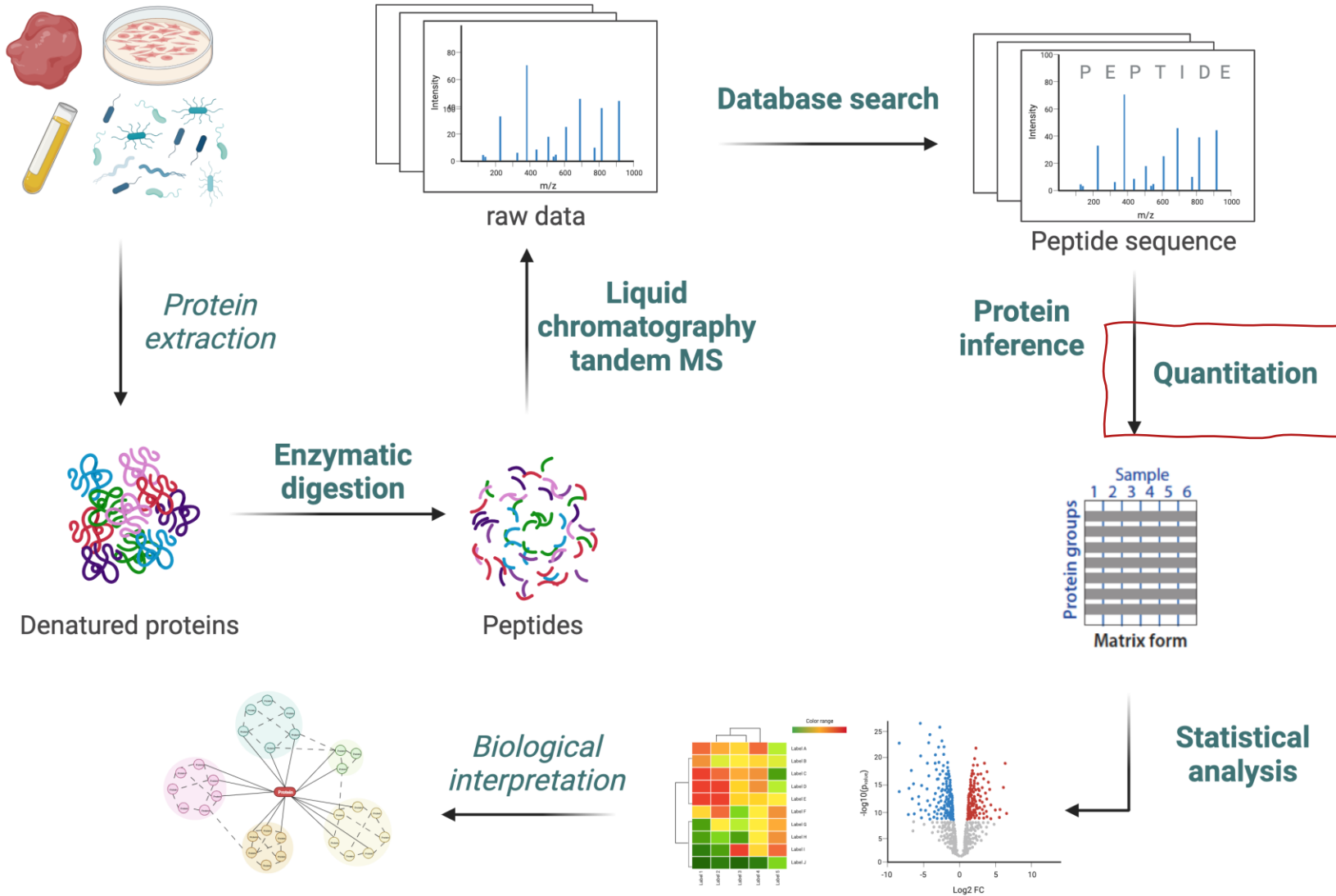
# What are the proteomic differences between androgen receptor (AR) independent and AR dependent prostate cancer cell lines

- LNCaP
- H660
- Five replicates per condition
- Relative quantitation

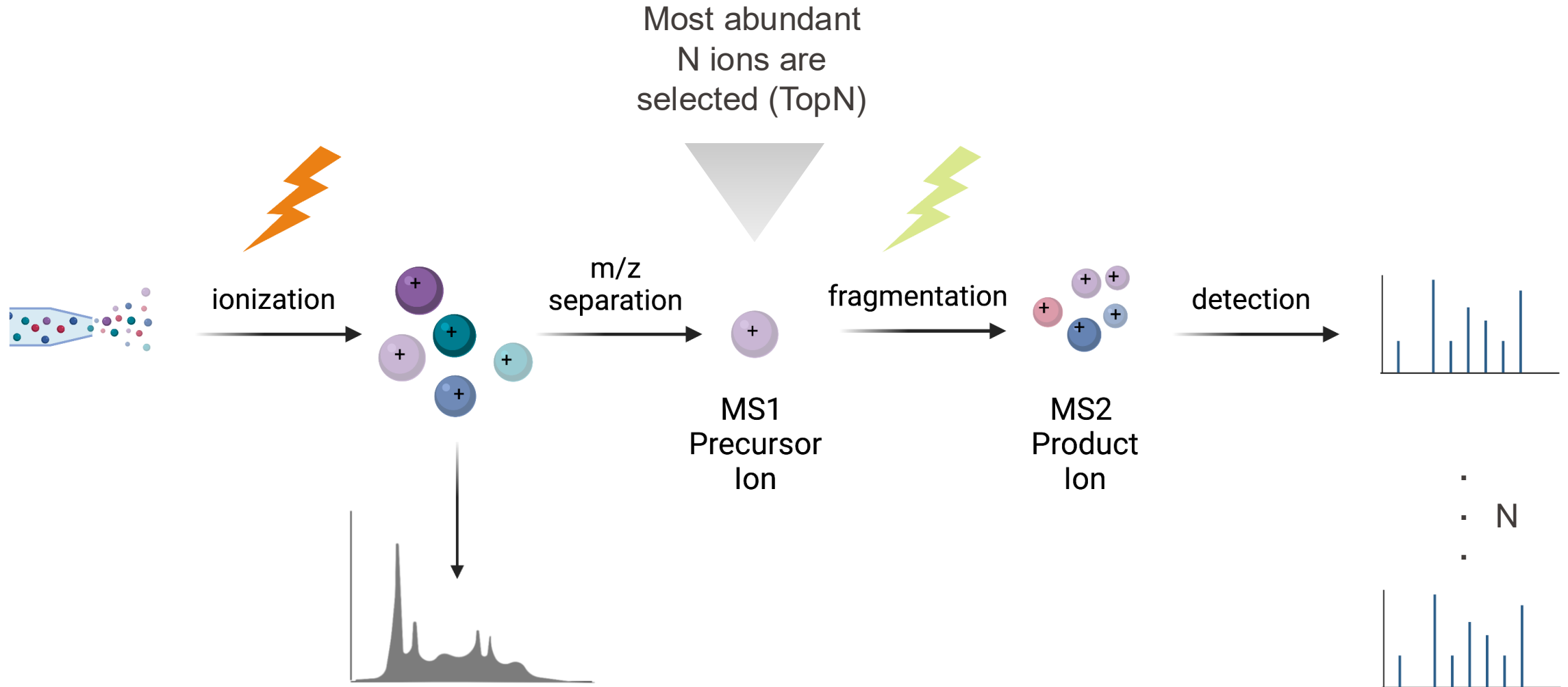
# Typical bottom-up workflow



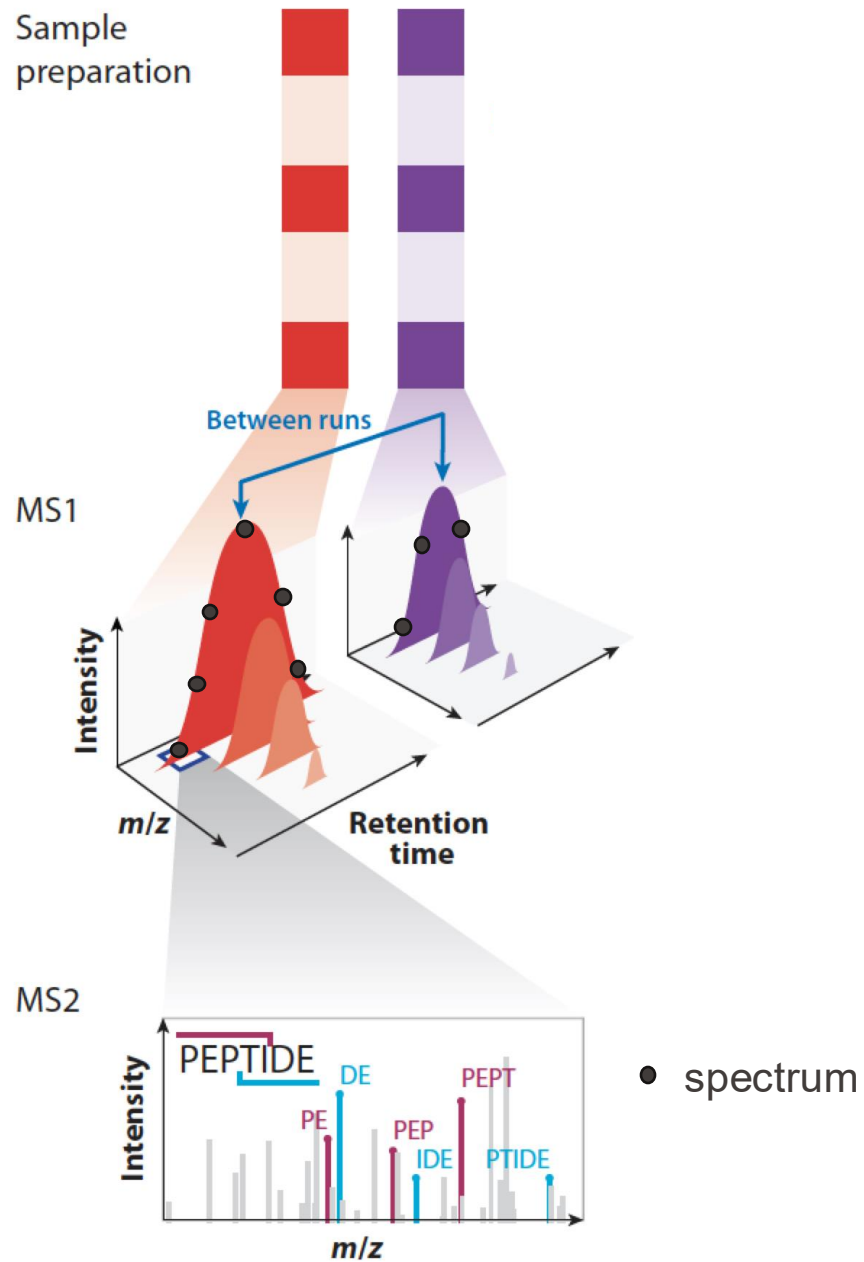
# Typical bottom-up workflow



# Tandem MS and Data Dependent Acquisition (DDA)

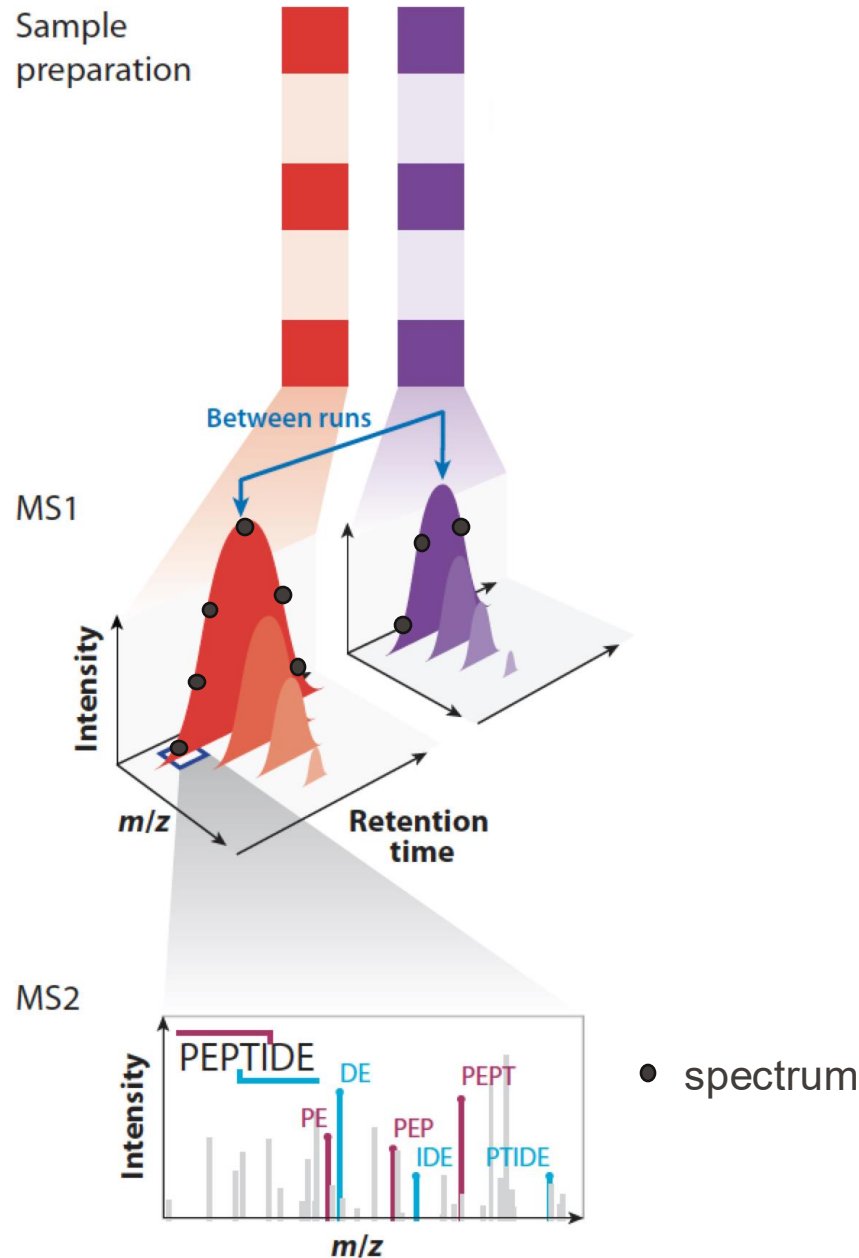


# Label-free Quantitation (LFQ)



# Label-free Quantitation (LFQ)

Sample preparation



MaxQuant & Perseus

Tyanova, S., Temu, T. & Cox, J. [The MaxQuant computational platform for mass spectrometry-based shotgun proteomics](#). *Nature Protocols* **11**, 2301–2319 (2016).

Tyanova, Stefka, and Juergen Cox. 2018. “Perseus: A Bioinformatics Platform for Integrative Analysis of Proteomics Data in Cancer Research.” In, 133–48. Springer New York. [https://doi.org/10.1007/978-1-4939-7493-1\\_7](https://doi.org/10.1007/978-1-4939-7493-1_7).