SUPPORTING INFORMATION

Towards a sample metadata standard in public proteomics repositories

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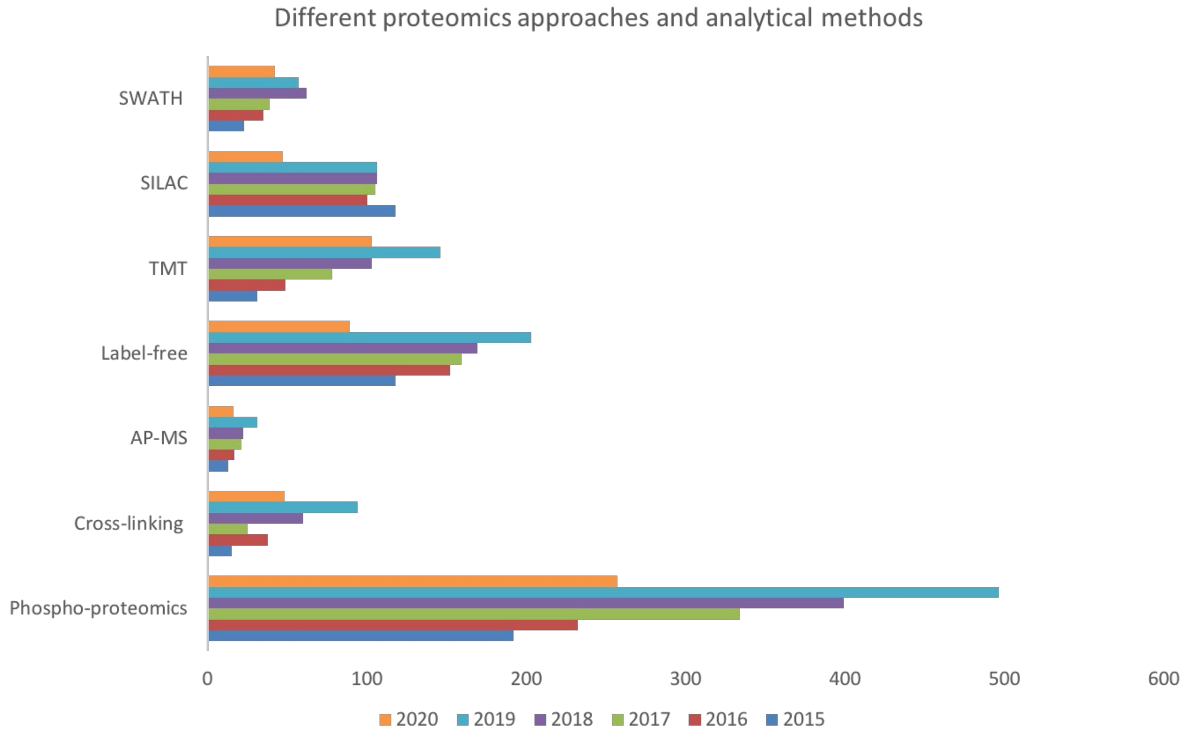
Supplementary Note 1: Number of datasets in PRIDE by experiment type



Supplementary Figure 1: PRIDE experiments by different keywords (e.g. Cross-linking. TMT). The plot shows the number of studies divided by seven major experiment types: Phosphoproteomics, crosslinking, affinity purification mass spectrometry (AP-MS, Label free, Tandem mass tag (TMT), Stable isotope labeling by amino acids in cell culture (SILAC), SAWTH proteomics.