A gene expression profiling assay based on the direct measurement of a reduced representation of the transcriptome of 1000 genes and computational inference of the rest genes by a linear model.

A gene expression assay that uses [next-generation sequencing](https://en.wikipedia.org/wiki/Next-generation_sequencing) (NGS) to reveal the presence and quantity of [RNA](https://en.wikipedia.org/wiki/RNA) in a biological sample at a given moment in time.

A mass spectrometry-based assay to identify and quantify post-translational modifications on histone proteins from bulk chromatin.

An assay used in [molecular biology](https://en.wikipedia.org/wiki/Molecular_biology) to study [chromatin accessibility](https://en.wikipedia.org/wiki/Chromatin). It aims to identify accessible [DNA](https://en.wikipedia.org/wiki/DNA) regions, equivalent to [DNase I hypersensitive sites](https://en.wikipedia.org/wiki/DNase_I_hypersensitive_site).

A targeted phosphoproteomic assay based on the direct measurement of a reduced representation of the Phosphoprofiling of 96 phosphopeptide probes .

SWATH MS a data independent acquisition (DIA) method which aims to complement traditional mass spectrometry-based proteomics techniques such as shotgun and SRM methods. In essence, it allows a complete and permanent recording of all fragment ions of the detectable peptide precursors present in a biological sample. It thus combines the advantages of shotgun (high throughput) with those of SRM (high reproducibility and consistency).