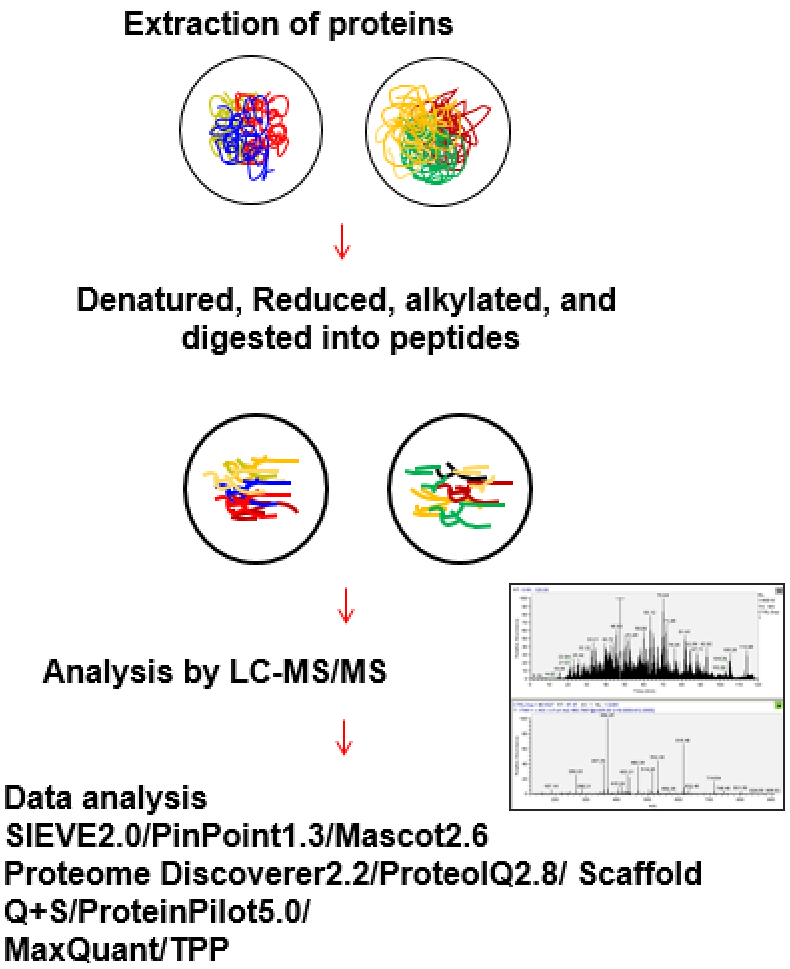
# Label-Free Shotgun Proteomics



**Extraction of proteins**

**Denatured, Reduced, alkylated, and digested into peptides**

**Analysis by LC-MS/MS**

**Data analysis**
**SIEVE2.0/PinPoint1.3/Mascot2.6**
**Proteome Discoverer2.2/ProteolQ2.8/ Scaffold Q+S/ProteinPilot5.0/**
**MaxQuant/TPP**

Recently, many studies have provided a relationship between protein abundance and sampling statistics based on sequence coverage, peptide count, and spectral count using label-free liquid chromatography−tandem mass spectrometry (LC−MS/MS) shotgun proteomics. The use of sampling statistics offers a promising method of measuring relative protein abundance and detecting differentially expressed or co-expressed proteins. Finally, this method supports robust quantification of relative protein abundance and for sensitive detection of biologically significant differential protein expression under multiple experimental conditions.