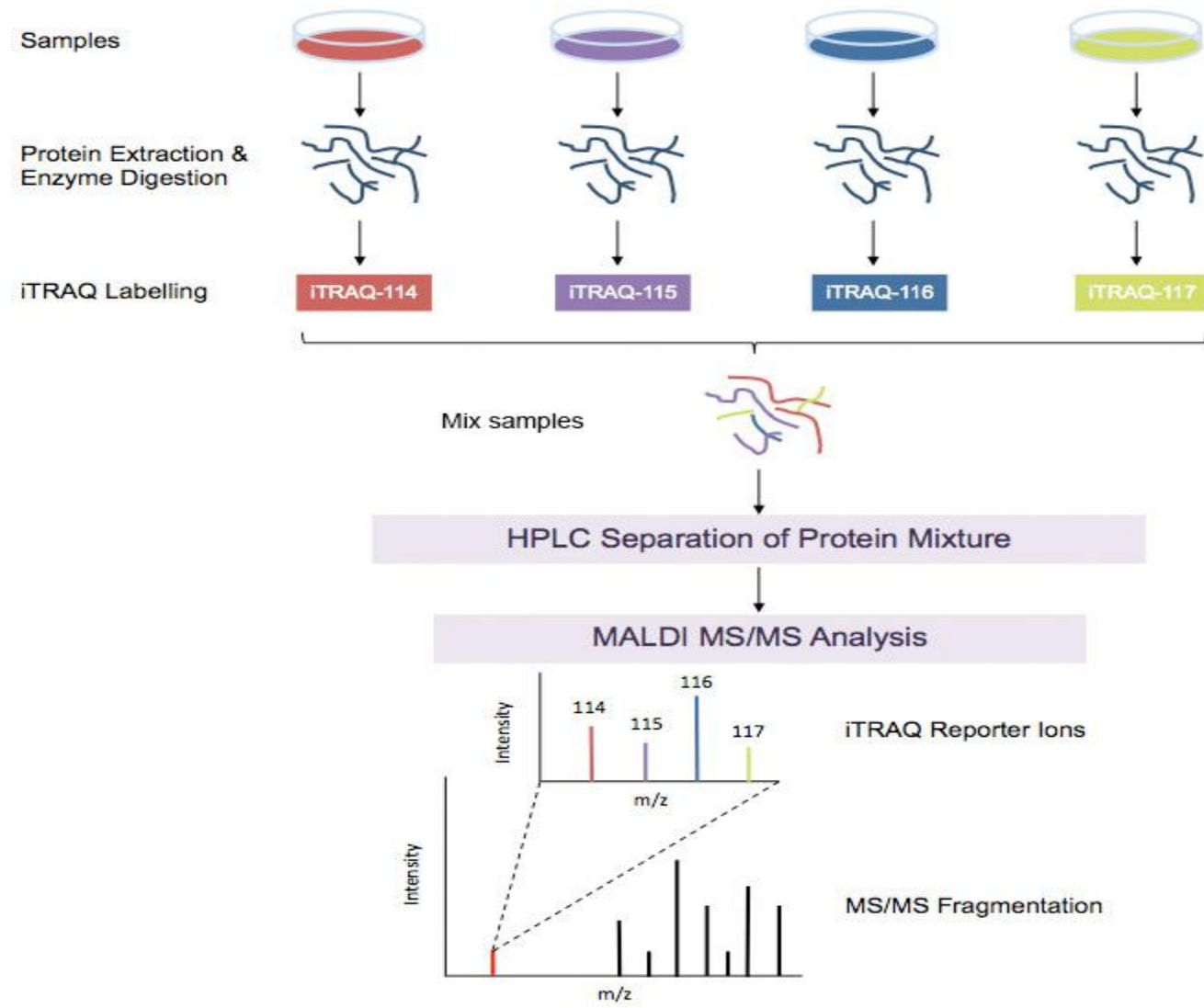




itraq proteomics

Creative Proteomics offers iTRAQ protein quantification service suited for unbiased untargeted biomarker discovery. Relative quantification of proteins for biomarker discovery in complex mixtures by mass spectrometry can easily and quickly be achieved using iTRAQ technology. iTRAQ is ideally suited for comparing normal, diseased, and drug-treated samples, time course studies, biological replicates and provides relative quantitation.

iTRAQ technology utilizes isobaric reagents to label the primary amines of peptides and proteins. The iTRAQ reagents usually consist of an N-methyl piperazine reporter group, a balance group, and an N-hydroxy succinimide ester group that is reactive with the primary amines of peptides. The balance groups present in each of the iTRAQ reagents function to make the labeled peptides from each sample isobaric and the quantification is facilitated through analysis of reporter groups that are generated upon fragmentation in the mass spectrometer. There are currently two mainly used reagents: 4-plex and 8-plex, which can be used to label all peptides from different samples/treatments. These samples are then pooled and usually fractionated by nano liquid chromatography and analyzed by tandem mass spectrometry (MS/MS).



Contact information

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