# SILTMASS SOFTWARE

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## Background

Quantitation of relative or absolute amounts of proteins by mass spectrometry can be prone to large errors. The use of MS/MS ion intensities and stable isotope labeling, a method called isotope labeling tandem mass spectrometry (SILT), decreases the effects of contamination from unrelated compounds.

## Technology Summary

A software package (SILTmass) that automates protein identification and quantification using the SILT method. SILTmass has the ability to analyze the kinetics of protein turnover, in addition to relative and absolute protein quantitation. Using data-dependent scans, the labeling of multiple proteins can be quantified in a single chromatographic run, allowing the SILT method to be applied to more traditional proteomics experiments, including SILAC-style experiments. One major focus of the software development effort is the analysis of protein synthesis and degradation kinetics in animals, including humans. Overall, SILTmass provides a generalized method for the absolute and relative quantitation of protein labeling with a high degree of accuracy even for complex protein mixtures.

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