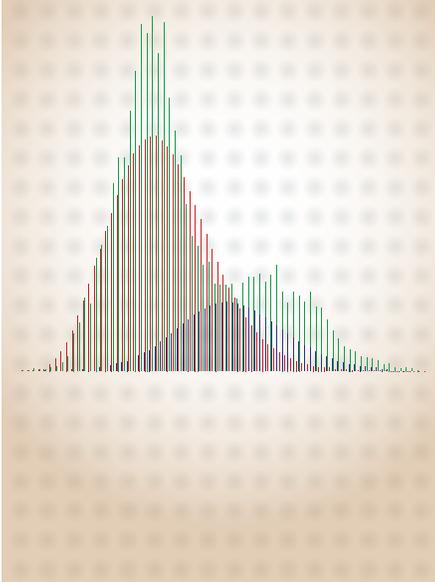


*Right from identification to quantification, a powerful software that supports the entire proteomic data analysis pipeline*



*Probability based scoring of peptides and proteins.*

*Calculate protein and peptide false discovery rates.*

*Apply NSAF normalization to your protein samples.*

*Robust label free quantification process by spectral counting, TIC and XIC.*

*Isobaric quantification using iTRAQ, TMT or any customized tags.*

*Isotopic quantification using SILAC, ICAT or any with a customized tags.*

*Compare by difference, intersection or union between various proteome sets.*

*Apply functions to two or more proteome sets.*

*Compare search results from multiple search engines like Mascot, SEQUEST and X!Tandem.*

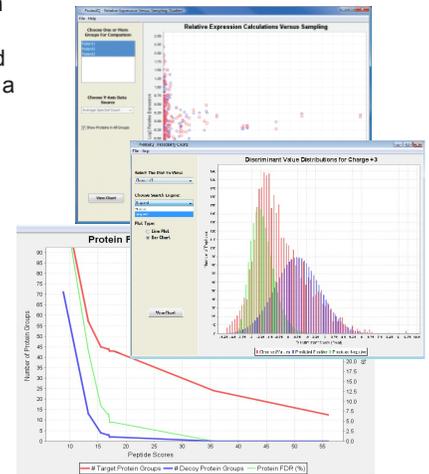
*Supports Sequest SQT and Proteome Discoverer v1.4 MSF file formats.*

*Compare relative protein expression across samples through heat maps.*

*Identify significant protein expression changes 15 interactive plots.*

*Export results in multiple formats including CSV and HTML and share with fellow researchers.*

ProteoIQ provides an easy-to-use and intuitive solution for combining results from popular database search engines to validate protein identifications, compare and quantify protein expression across 100's of samples in a single project. It supports all popular forms of peptide and protein quantification such as label free, isotopic and isobaric tag based quantification workflows. With label free quantification workflows, you can quantify proteins via Area Under Curve (AUC) from extracted ion chromatograms (XIC) of every detected peak, from Precursor Intensity of identified peptides from the MS/MS spectra or from Spectral Counting (SC) of identified MS/MS spectra. Further, ProteoIQ allows you to quantify protein expression using iTRAQ, TMT, SILAC, ICAT or any other isobaric or isotopic labels. With ProteoIQ, it is easy to view and interact with your proteomic data and locate significant changes in protein expression.



## Statistical Validation of Identified Peptides and Proteins

**Discriminant Score (F-value):** ProteoIQ calculates Discriminant score (F-value), a common scoring method that can be applied to all search engines. It removes dependency of the identified peptide on the charge state. This score is recommended for MALDI TOF-TOF workflows. ProteoIQ uses the F-value for FDR and probability analysis. Plots based on Mascot or SEQUEST scores or probabilities can also be generated. You can even use probability based measurements for verifying protein assignments and use sensitivity and error plots to maintain an acceptable error rate.

**False Discovery Rates:** The False Discovery Rate calculation is a powerful method to evaluate the error of an entire proteome. ProteoIQ provides automated false discovery rate analysis by comparing results searched against a target and a decoy database. False discovery rates can be assigned at the protein or peptide level. The interactive false discovery rate plot displays the number of peptide and protein identifications from a target and a decoy database search. You can choose an error rate that maximizes the number of good protein identifications, while limiting the frequency of random assignments.

## Quantification

**Label-Free Quantification:** ProteoIQ supports label free quantification using Spectral Counting, Extracted Ion Chromatogram and Area Under Curve methods.

**Isobaric Quantification:** Perform isobaric labeling quantification regardless of instrument type or search engine. ProteoIQ supports a wide array of experiment types including iTRAQ, Tandem Mass Tags (TMT) or custom modifications.

**Isotopic Quantification:** With ProteoIQ you define the type of isotopic label, making it extremely flexible for a wide array of experiment types, including SILAC, ICAT, Dimethyl labeling, 18O, 15N, and acetylation.

### To activate & evaluate, follow these steps

- Install ProteoIQ from our website or the CD
- Launch the program and click 'Activate' on the first window
- Enter the 'Registration Number' requested from us and your e-mail address. Click 'Next'
- Update the registration information following the on-screen prompts and click 'Submit'

### For a quick start

- Check the Multimedia Tutorial

### Order on-line

- E-mail: [sales@premierbiosoft.com](mailto:sales@premierbiosoft.com)
- Phone: 650-856-2703, Fax: 650-618-1773

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