

Resource Summary Report

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PremierBiosoft Proteo IQ Software

RRID:SCR_018072

Type: Tool

Proper Citation

PremierBiosoft Proteo IQ Software (RRID:SCR_018072)

Resource Information

URL: http://www.premierbiosoft.com/protein_quantification_software/index.html

Proper Citation: PremierBiosoft Proteo IQ Software (RRID:SCR_018072)

Description: Software package as comprehensive qualitative and quantitative suite for proteomics. Used to validate and quantify proteins by combining results from popular mass spectrometry platforms and database search engines. Provides customizable interface to support any form of biological annotation. Used to compare protein quantitative results in relation to biological pathways, protein localization, protein function, or to transcript abundance. Every protein identification can be linked to any external or internal knowledge database. Custom links are provided to GenBank, UniProt, IPI, and SwissProt databases or in-house LIMS.

Synonyms: ProteoIQ

Resource Type: data analysis software, data analytics software, data processing software, software application, software resource

Keywords: Proteomic, qualitative, quantitative, protein identification, data, PREMIER Biosoft, mass spectrometry data, database search engine

Availability: Restricted

Resource Name: PremierBiosoft Proteo IQ Software

Resource ID: SCR_018072

Record Creation Time: 20220129T080338+0000

Record Last Update: 20260821T194139+0000

Ratings and Alerts

No rating or validation information has been found for PremierBiosoft Proteo IQ Software.

No alerts have been found for PremierBiosoft Proteo IQ Software.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 35 mentions in open access literature.

Listed below are recent publications. The full list is available at [NIF](#) .

Xiao W, et al. (2026) Metabolite-gated vascular contractility switch: OXGR1 activation mechanism enables agonist therapy for rosacea erythema. *Cell*, 189(7), 1990.

Agany DD, et al. (2025) Multi-omics of cockroaches infected with *Salmonella Typhimurium* identifies molecular signatures of vector colonization. *BMC genomics*, 26(1), 1118.

Adams TM, et al. (2022) Sequential in vitro enzymatic N-glycoprotein modification reveals site-specific rates of glycoenzyme processing. *The Journal of biological chemistry*, 298(10), 102474.

Zhao P, et al. (2020) Virus-Receptor Interactions of Glycosylated SARS-CoV-2 Spike and Human ACE2 Receptor. *Cell host & microbe*, 28(4), 586.

Zhao P, et al. (2020) Virus-Receptor Interactions of Glycosylated SARS-CoV-2 Spike and Human ACE2 Receptor. *bioRxiv : the preprint server for biology*.

Park SB, et al. (2019) Silver-coated magnetic nanocomposites induce growth inhibition and protein changes in foodborne bacteria. *Scientific reports*, 9(1), 17499.

Yu WH, et al. (2018) Exploiting glycan topography for computational design of Env glycoprotein antigenicity. *PLoS computational biology*, 14(4), e1006093.

Abou-Antoun TJ, et al. (2018) Molecular and functional analysis of anchorage independent, treatment-evasive neuroblastoma tumorspheres with enhanced malignant properties: A possible explanation for radio-therapy resistance. *PloS one*, 13(1), e0189711.

Park YJ, et al. (2017) Uncovering stem cell differentiation factors for salivary gland regeneration by quantitative analysis of differential proteomes. *PloS one*, 12(2), e0169677.

Balinsky CA, et al. (2017) IRAV (FLJ11286), an Interferon-Stimulated Gene with Antiviral Activity against Dengue Virus, Interacts with MOV10. *Journal of virology*, 91(5).

Yilmaz O, et al. (2017) Scrambled eggs: Proteomic portraits and novel biomarkers of egg quality in zebrafish (*Danio rerio*). *PloS one*, 12(11), e0188084.

Cunningham CB, et al. (2017) Ethological principles predict the neuropeptides co-opted to influence parenting. *Nature communications*, 8, 14225.

Gajdošik Šrajer M, et al. (2017) Data set of proteomic analysis of food borne pathogens after treatment with the disinfectants based on pyridoxal oxime derivatives. *Data in brief*, 15, 738.

Akpalu D, et al. (2017) Matrix Signaling Subsequent to a Myocardial Infarction: A Proteomic Profile of Tissue Factor Microparticles. *JACC. Basic to translational science*, 2(5), 529.

Li X, et al. (2017) Structural Analysis of the Glycosylated Intact HIV-1 gp120-b12 Antibody Complex Using Hydroxyl Radical Protein Footprinting. *Biochemistry*, 56(7), 957.

Jimenez L, et al. (2017) miR-375 Regulates Invasion-Related Proteins Vimentin and L-Plastin. *The American journal of pathology*, 187(7), 1523.

Weatherly DB, et al. (2016) Recombination-driven generation of the largest pathogen repository of antigen variants in the protozoan *Trypanosoma cruzi*. *BMC genomics*, 17(1), 729.

Ji W, et al. (2016) Comparative Proteomic Analysis of Soybean Leaves and Roots by iTRAQ Provides Insights into Response Mechanisms to Short-Term Salt Stress. *Frontiers in plant science*, 7, 573.

Zhang M, et al. (2016) Critical Role of COI1-Dependent Jasmonate Pathway in AAL toxin induced PCD in Tomato Revealed by Comparative Proteomics. *Scientific reports*, 6, 28451.

Benard O, et al. (2016) Impact of high-fat diet on the proteome of mouse liver. *The Journal of nutritional biochemistry*, 31, 10.