Resource Summary Report

Generated by dkNET on May 19, 2025

MFPaQ

RRID:SCR_012049
Type: Tool

Proper Citation

MFPaQ (RRID:SCR_012049)

Resource Information

URL: http://mfpaq.sourceforge.net/

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Description: Software that allows fast and user-friendly verification of Mascot result files, as well as data quantification using isotopic labeling methods (SILAC/ICAT) or label free approaches (spectral counting, MS signal comparison).

Synonyms: Mascot File Parsing and Quantification

Resource Type: software resource

Defining Citation: PMID:17533220

Keywords: standalone software, bio.tools

Funding:

Resource Name: MFPaQ

Resource ID: SCR_012049

Alternate IDs: biotools:mfpaq, OMICS_02495

Alternate URLs: https://bio.tools/mfpaq

Record Creation Time: 20220129T080308+0000

Record Last Update: 20250420T014604+0000

Ratings and Alerts

No rating or validation information has been found for MFPaQ.

No alerts have been found for MFPaQ.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 14 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Tang J, et al. (2020) ANPELA: analysis and performance assessment of the label-free quantification workflow for metaproteomic studies. Briefings in bioinformatics, 21(2), 621.

Khazaei G, et al. (2019) Proteomics evaluation of MDA-MB-231 breast cancer cells in response to RNAi-induced silencing of hPTTG. Life sciences, 239, 116873.

Dezest M, et al. (2017) Mechanistic insights into the impact of Cold Atmospheric Pressure Plasma on human epithelial cell lines. Scientific reports, 7, 41163.

Miller M, et al. (2017) Control of RUNX-induced repression of Notch signaling by MLF and its partner DnaJ-1 during Drosophila hematopoiesis. PLoS genetics, 13(7), e1006932.

Ramus C, et al. (2016) Spiked proteomic standard dataset for testing label-free quantitative software and statistical methods. Data in brief, 6, 286.

Ramus C, et al. (2016) Benchmarking quantitative label-free LC-MS data processing workflows using a complex spiked proteomic standard dataset. Journal of proteomics, 132, 51.

Pichereaux C, et al. (2016) Comparative shotgun proteomic analysis of wild and domesticated Opuntia spp. species shows a metabolic adaptation through domestication. Journal of proteomics, 143, 353.

Chantalat E, et al. (2016) The AF-1-deficient estrogen receptor ER?46 isoform is frequently expressed in human breast tumors. Breast cancer research : BCR, 18(1), 123.

Spinner CA, et al. (2015) Substrates of the ASB2? E3 ubiquitin ligase in dendritic cells. Scientific reports, 5, 16269.

Ainaoui N, et al. (2015) Promoter-Dependent Translation Controlled by p54nrb and hnRNPM during Myoblast Differentiation. PloS one, 10(9), e0136466.

Zaccaria A, et al. (2015) Accessing to the minor proteome of red blood cells through the influence of the nanoparticle surface properties on the corona composition. International journal of nanomedicine, 10, 1869.

Moulédous L, et al. (2015) Phosphoproteomic analysis of the mouse brain mu-opioid (MOP) receptor. FEBS letters, 589(18), 2401.

Fabre B, et al. (2015) Deciphering preferential interactions within supramolecular protein complexes: the proteasome case. Molecular systems biology, 11(1), 771.

Galiacy SD, et al. (2011) Deeper in the human cornea proteome using nanoLC-Orbitrap MS/MS: An improvement for future studies on cornea homeostasis and pathophysiology. Journal of proteomics, 75(1), 81.