

Resource Summary Report

Generated by T1D on Sep 18, 2026

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

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: 20260912T195744+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 [T1D](#) .

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 α 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 β 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.

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

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

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.