

Resource Summary Report

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MSstats

RRID:SCR_014353

Type: Tool

Proper Citation

MSstats (RRID:SCR_014353)

Resource Information

URL: <http://msstats.org/>

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Description: A package for statistical relative quantification of proteins and peptides in global, targeted, and data-independent proteomics. It handles shotgun, label-free, and label-based Selected Reaction Monitoring, as well as SWATH/DIA (Data Independent Acquisition) experiments. MSStats provide functionality for data processing and visualization, model-based statistical analysis, and model-based sample size calculations.

Synonyms: MSStats

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

Defining Citation: [DOI:10.1186/1471-2105-13-S16-S6](https://doi.org/10.1186/1471-2105-13-S16-S6)

Keywords: data independent acquisition, statistical relative quantification, protein, peptide, data analysis software, data processing, data visualization, proteomics

Funding: National Science Foundation CAREER award 1054826

Availability: Acknowledgement requested, Available for download

Resource Name: MSstats

Resource ID: SCR_014353

Alternate URLs: <http://www.bioconductor.org/packages/release/bioc/html/MSstats.html>

Record Creation Time: 20220129T080320+0000

Record Last Update: 20260803T040630+0000

Ratings and Alerts

No rating or validation information has been found for MSstats.

No alerts have been found for MSstats.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 214 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#).

Sajic T, et al. (2025) Depletion-dependent activity-based protein profiling using SWATH/DIA-MS detects serine hydrolase lipid remodeling in lung adenocarcinoma progression. Nature communications, 16(1), 4889.

Wang M, et al. (2025) Distinct gene regulatory dynamics drive skeletogenic cell fate convergence during vertebrate embryogenesis. Nature communications, 16(1), 2187.

Taggi V, et al. (2025) Targeted and Untargeted Proteomics-based Comparison of Adenoviral Infected hCMEC/D3 and hBMEC as a Human Brain Endothelial Cells to Study the OATP2B1 Transporter. Molecular neurobiology, 62(7), 9074.

Cheng Z, et al. (2025) PeiTuQingXin formula alleviated atopic dermatitis symptoms via inhibiting TRADD/TRAF2/RIP1 complex mediated NF- κ B signaling pathway activation. Archives of dermatological research, 317(1), 535.

Furrer R, et al. (2025) Metabolic dysregulation contributes to the development of dysferlinopathy. Life science alliance, 8(5).

Martín-Arana J, et al. (2025) Whole-exome tumor-agnostic ctDNA analysis enhances minimal residual disease detection and reveals relapse mechanisms in localized colon cancer. Nature cancer, 6(6), 1000.

Iwata T, et al. (2025) Monoallelic mutations in MMD2 cause autosomal dominant aggressive periodontitis. The Journal of experimental medicine, 222(9).

Wang J, et al. (2025) Cerebellar Mechanisms Underlying Autism-like Cognitive Deficits in Mouse Offspring with Prenatal Valproic Acid Exposure. Toxics, 13(10).

Fay A, et al. (2025) A split ALFA tag-nanobody system for protein localization and proximity proteomics in mycobacteria. bioRxiv : the preprint server for biology.

Clarke S, et al. (2025) The Incoming Influenza Genome Assembles a Host RBP Network that Orchestrates Viral RNA Synthesis. bioRxiv : the preprint server for biology.

Tejada-Arranz A, et al. (2025) Mechanisms of Pseudomonas aeruginosa resistance to type VI secretion system attacks. Nature communications, 16(1), 10744.

Neumann S, et al. (2025) Cytoplasmic and nuclear protein interaction networks of the synapto-nuclear messenger CRT1 in neurons reveal cooperative chromatin binding between CRT1 and CRT1, MEF2C and RFX3. *bioRxiv : the preprint server for biology*.

Hoffmann UA, et al. (2025) A Cyanobacterial Screening Platform for Rubisco Mutant Variants. *ACS synthetic biology*, 14(7), 2619.

Lee C, et al. (2025) DMXL1 promotes recruitment of V1-ATPase to lysosomes upon TRPML1 activation. *Nature structural & molecular biology*.

Jin Y, et al. (2025) Exploring the Mechanism of Luteolin in Protecting Chickens from Ammonia Poisoning Based on Proteomic Technology. *Metabolites*, 15(5).

Zuazo-Gaztelu I, et al. (2025) A nonenzymatic dependency on inositol-requiring enzyme 1 controls cancer cell cycle progression and tumor growth. *PLoS biology*, 23(4), e3003086.

Donald AMH, et al. (2025) Longitudinal Proteomic Profiling of Cognition across an Aerobic Exercise Intervention. *Annals of neurology*, 97(5), 1007.

Chazal M, et al. (2025) Nuclear activities and interactome of the NS5 protein of Tick-Borne Encephalitis Virus. *bioRxiv : the preprint server for biology*.

Lafranchi L, et al. (2025) Pooled overexpression screening identifies PIPPI as a novel microprotein involved in the ER stress response. *Nucleic acids research*, 53(20).

González A, et al. (2025) Multi-omic assessment of mRNA translation dynamics in liver cancer cell lines. *Scientific data*, 12(1), 1520.