

Resource Summary Report

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MS-GF+

RRID:SCR_015646

Type: Tool

Proper Citation

MS-GF+ (RRID:SCR_015646)

Resource Information

URL: <https://omics.pnl.gov/software/ms-gf>

Proper Citation: MS-GF+ (RRID:SCR_015646)

Description: Software that performs peptide identification by scoring MS/MS spectra against peptides derived from a protein sequence database.

Synonyms: MSGF+, MSGFPlus

Resource Type: software resource

Defining Citation: [PMID:25358478](#)

Keywords: protein identification, peptide sequence, ms, ms spectrum, proteomic, bio.tools, FASEB list

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NIAID ;
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Availability: Free, Available for download, Acknowledgment requested

Resource Name: MS-GF+

Resource ID: SCR_015646

Alternate IDs: biotools:ms-gf

Alternate URLs: <https://github.com/sangtaekim/msgfplus>, <https://bio.tools/ms-gf>

Record Creation Time: 20220129T080326+0000

Record Last Update: 20260801T190526+0000

Ratings and Alerts

No rating or validation information has been found for MS-GF+.

No alerts have been found for MS-GF+.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 155 mentions in open access literature.

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

Butkovich LV, et al. (2025) Untargeted GC-MS Metabolic Profiling of Anaerobic Gut Fungi Reveals Putative Terpenoids and Strain-Specific Metabolites. *Metabolites*, 15(9).

Weil BR, et al. (2025) Persistent Fibrosis and Left Ventricular Chamber Stiffening Despite Cessation of Repetitive Pressure Overload in Swine. *JACC. Basic to translational science*, 10(6), 844.

Veličković M, et al. (2025) Advanced multi-modal mass spectrometry imaging reveals functional differences of placental villous compartments at microscale resolution. *Nature communications*, 16(1), 2061.

Geng Z, et al. (2025) The Open Pediatric Cancer Project. *GigaScience*, 14.

Klaes S, et al. (2025) De novo peptide databases enable protein-based stable isotope probing of microbial communities with up to species-level resolution. *Environmental microbiome*, 20(1), 111.

Pan Y, et al. (2025) Functional-proteomics-based investigation of the cellular response to farnesyltransferase inhibition in lung cancer. *iScience*, 28(2), 111864.

Chatterjee P, et al. (2025) Quorum sensing mediates morphology and motility transitions in the model archaeon *Haloferax volcanii*. *bioRxiv : the preprint server for biology*.

Liao SC, et al. (2025) CHCHD2 mutant mice link mitochondrial deficits to PD pathophysiology. *Science advances*, 11(46), eadu0726.

Wen B, et al. (2025) Assessment of false discovery rate control in tandem mass spectrometry analysis using entrapment. *Nature methods*, 22(7), 1454.

Chatterjee P, et al. (2025) Quorum sensing mediates morphology and motility transitions in the model archaeon *Haloferax volcanii*. *mBio*, 16(7), e0090625.

Hackl S, et al. (2025) PTMVision: An Interactive Visualization Webserver for Post-translational Modifications of Proteins. *Journal of proteome research*, 24(2), 919.

Bonilauri B, et al. (2025) The Long Non-coding RNA Landscape of Endurance Exercise Training. *bioRxiv : the preprint server for biology*.

Lee EM, et al. (2025) Syntrophic bacterial and host-microbe interactions in bacterial vaginosis. *The ISME journal*, 19(1).

Lindback MM, et al. (2025) Virocell resource manipulation under nutrient limitation. *mSystems*, 10(7), e0052125.

Ghosh S, et al. (2025) Production of triacetic acid lactone from oleic acid by engineering the yeast *Candida viswanathii*. *Microbial cell factories*, 24(1), 215.

Liao SC, et al. (2024) CHCHD2 mutant mice display mitochondrial protein accumulation and disrupted energy metabolism. *bioRxiv : the preprint server for biology*.

Schiller H, et al. (2024) Identification of structural and regulatory cell-shape determinants in *Haloferax volcanii*. *Nature communications*, 15(1), 1414.

Kruk ME, et al. (2024) An integrated metaproteomics workflow for studying host-microbe dynamics in bronchoalveolar lavage samples applied to cystic fibrosis disease. *mSystems*, 9(7), e0092923.

Yang T, et al. (2024) Introducing ?-HelixNovo for practical large-scale de novo peptide sequencing. *Briefings in bioinformatics*, 25(2).

Howard-Varona C, et al. (2024) Environment-specific virocell metabolic reprogramming. *The ISME journal*, 18(1).