

Resource Summary Report

Generated by [ASWG](#) on Aug 25, 2026

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

Funding: NCRR RR018522;
NCRR 1-P41-RR024851;
NIAID ;
W.R. Wiley Environmental Molecular Science Laboratory

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: 20260815T182506+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 159 mentions in open access literature.

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

Skubitz APN, et al. (2026) Repurposing the liquid-based Pap test for the detection of ovarian cancer protein biomarkers. *Clinical proteomics*, 23(1).

Montalvo RN, et al. (2026) Ampk alpha2 T172 activation dictates exercise performance and energy transduction in skeletal muscle. *Science advances*, 12(9), eaeb3338.

Brahadeeswaran S, et al. (2026) Proteomic mapping of Rosa damascena nanovesicles reveals plastid mitochondrial metabolic convergence and antimicrobial peptides. *Plant signaling & behavior*, 21(1), 2641285.

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

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*.

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.

Uychoco P, et al. (2025) Structural, functional, and regulatory evaluation of a cysteine post-translationally modified Gcn5-related N-acetyltransferase. *Biochemical and biophysical research communications*, 748, 151299.

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.

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.

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

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

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*.

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.

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.

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.

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