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 idenitification, peptide sequence, ms, ms spectrum, proteomic, bio.tools, FASEB list

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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: 20250410T070649+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 141 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

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. (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).

Niksirat H, et al. (2024) The quantification of zebrafish ocular-associated proteins provides hints for sex-biased visual impairments and perception. Heliyon, 10(12), e33057.

Arikan M, et al. (2024) gNOMO2: a comprehensive and modular pipeline for integrated multi-omics analyses of microbiomes. GigaScience, 13.

Song KJ, et al. (2024) Proteogenomic analysis reveals non-small cell lung cancer subtypes predicting chromosome instability, and tumor microenvironment. Nature communications, 15(1), 10164.

Geng Z, et al. (2024) The Open Pediatric Cancer Project. bioRxiv : the preprint server for biology.

Wen B, et al. (2024) Assessment of false discovery rate control in tandem mass spectrometry analysis using entrapment. bioRxiv : the preprint server for biology.

Son J, et al. (2023) DbyDeep: Exploration of MS-Detectable Peptides via Deep Learning. Analytical chemistry, 95(30), 11193.

Miller SE, et al. (2023) Metaproteomics reveals functional partitioning and vegetational variation among permafrost-affected Arctic soil bacterial communities. mSystems, 8(3), e0123822.

Xu W, et al. (2023) HyperSpec: Ultrafast Mass Spectra Clustering in Hyperdimensional Space. Journal of proteome research, 22(6), 1639.

Wacholder A, et al. (2023) Biological factors and statistical limitations prevent detection of most noncanonical proteins by mass spectrometry. PLoS biology, 21(12), e3002409.

Feng S, et al. (2023) A Phosphoproteomics Data Resource for Systems-level Modeling of Kinase Signaling Networks. bioRxiv : the preprint server for biology.

McDaniel EA, et al. (2023) Diverse electron carriers drive syntrophic interactions in an enriched anaerobic acetate-oxidizing consortium. The ISME journal, 17(12), 2326.

Shen S, et al. (2023) Quantitative Proteomics of Human Retinal Pigment Epithelium Reveals Key Regulators for the Pathogenesis of Age-Related Macular Degeneration. International journal of molecular sciences, 24(4).

Volkening JD, et al. (2023) Viral proteogenomic and expression profiling during productive replication of a skin-tropic herpesvirus in the natural host. PLoS pathogens, 19(6), e1011204.

Bedran G, et al. (2023) The Immunopeptidome from a Genomic Perspective: Establishing the Noncanonical Landscape of MHC Class I-Associated Peptides. Cancer immunology research, 11(6), 747.