

Resource Summary Report

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Global Proteome Machine Database (GPM DB)

RRID:SCR_006617

Type: Tool

Proper Citation

Global Proteome Machine Database (GPM DB) (RRID:SCR_006617)

Resource Information

URL: <http://www.thegpm.org/>

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Description: The Global Proteome Machine Organization was set up so that scientists involved in proteomics using tandem mass spectrometry could use that data to analyze proteomes. The projects supported by the GPMO have been selected to improve the quality of analysis, make the results portable and to provide a common platform for testing and validating proteomics results. The Global Proteome Machine Database was constructed to utilize the information obtained by GPM servers to aid in the difficult process of validating peptide MS/MS spectra as well as protein coverage patterns. This database has been integrated into GPM server pages, allowing users to quickly compare their experimental results with the best results that have been previously observed by other scientists.

Abbreviations: The GPM

Synonyms: GPM, The Global Proteome Machine Organization: Proteomics Database and Open Source Software, Global Proteome Machine Database, GPM DB, The Global Proteome Machine Database, The Global Proteome Machine, Global Proteome Machine Database (GPM DB), The Global Proteome Machine Organization

Resource Type: data analysis software, data or information resource, data processing software, data repository, database, service resource, software application, software resource, storage service resource

Keywords: mass spectrometry, pattern, peptide, protein, proteome, scientist, spectra, tandem, FASEB list

Resource Name: Global Proteome Machine Database (GPM DB)

Resource ID: SCR_006617

Alternate IDs: r3d100010883, nif-0000-10455

Alternate URLs: <https://www.thegpm.org/GPMDB/index.html>,
<https://researchdata.and.s.org.au/gpm-global-proteome-machine-database/11342>,
<https://doi.org/10.17616/R30C90>

Record Creation Time: 20220129T080237+0000

Record Last Update: 20260821T193751+0000

Ratings and Alerts

No rating or validation information has been found for Global Proteome Machine Database (GPM DB).

No alerts have been found for Global Proteome Machine Database (GPM DB).

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 282 mentions in open access literature.

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

Yang H, et al. (2026) Identification of menstrual blood markers by proteomic mass spectrometry. International journal of legal medicine, 140(2), 1183.

Larrea-Sebal A, et al. (2026) Blood proteomics: insights from public data. Genome biology, 27(1).

Mahmood S, et al. (2026) Blood feeding triggers the terminal differentiation of precursor cells in tick salivary glands. Science advances, 12(13), eaec7620.

Schmollinger S, et al. (2026) Client distribution between Chlamydomonas FDX1 and FDX2 in carbon, nitrogen and sulfur assimilation. bioRxiv : the preprint server for biology.

Wang B, et al. (2026) Efficacy of chitinases from mangrove wetland derived Penicillium oxalicum on powdered chitin. Frontiers in microbiology, 17, 1773725.

McAttee C, et al. (2026) Secreted exosomes induce filopodia formation. eLife, 13.

LeBleu G, et al. (2026) Mapping of PTP1B, TCPTP, SHP2, and Putative Substrates Reveals Novel Networks in Glomerular Podocytes. Journal of cellular physiology, 241(1), e70128.

Schilling V, et al. (2026) The State of Peptide Detectability in Computational Proteomics and Guidelines for AI Applications. Computational and structural biotechnology journal,

35(1), 0037.

Trifunovic S, et al. (2026) Acute E-Cigarette Aerosol Condensate Exposure Disrupts the Transcriptome and Proteome Profiles of Human Bronchial Epithelial BEAS-2B Cells. *Cells*, 15(6).

Hernandez-Ortiz S, et al. (2025) A co-conserved gene pair supports *Caulobacter* iron homeostasis during chelation stress. *Journal of bacteriology*, 207(4), e0048424.

Prost S, et al. (2025) The unexpected loss of the 'hunger hormone' ghrelin in true passerines: a game changer in migration physiology. *Royal Society open science*, 12(3), 242107.

Kale V, et al. (2025) FISH-FACS proteomics: enhanced label-free quantitative proteome analysis from low cell numbers of uncultured environmental microorganisms. *ISME communications*, 5(1), ycaf145.

Elrashedy A, et al. (2025) Advances in bioinformatics and multi-omics integration: transforming viral infectious disease research in veterinary medicine. *Virology journal*, 22(1), 22.

Mount HO, et al. (2025) The *Legionella pneumophila* effector PieF modulates mRNA stability through association with eukaryotic CCR4-NOT. *mSphere*, 10(1), e0089124.

McAtee C, et al. (2025) Secreted exosomes induce filopodia formation. *bioRxiv : the preprint server for biology*.

Liu B, et al. (2025) Identification of novel protein biomarkers of macrophage polarization using comparative proteomic analyses of murine primary macrophages. *Journal of immunology (Baltimore, Md. : 1950)*.

Ortiz SH, et al. (2025) A co-conserved gene pair supports *Caulobacter* iron homeostasis during chelation stress. *bioRxiv : the preprint server for biology*.

Aspinwall J, et al. (2025) Behavioral Manipulation of *Ixodes scapularis* by *Ehrlichia muris euclairensis*: Implications for Tick-Borne Disease Transmission. *bioRxiv : the preprint server for biology*.

Tefft NM, et al. (2025) Controlled Enzyme Cargo Loading in Engineered Bacterial Microcompartment Shells. *Biochemistry*, 64(6), 1285.

Gholami Z, et al. (2025) Comparative Proteomics of Resistant and Susceptible Strains of *Frankliniella occidentalis* to Abamectin. *Electrophoresis*, 46(1-2), 112.