

Resource Summary Report

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Mass spectrometry Interactive Virtual Environment (MassIVE)

RRID:SCR_013665

Type: Tool

Proper Citation

Mass spectrometry Interactive Virtual Environment (MassIVE) (RRID:SCR_013665)

Resource Information

URL: <https://massive.ucsd.edu/ProteoSAFe/static/massive.jsp>

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Description: Mass spectrometry Interactive Virtual Environment (MassIVE) is a community resource developed by the NIH-funded Center for Computational Mass Spectrometry to promote the global, free exchange of mass spectrometry data. Data repository for proteomics data.

Abbreviations: MassIVE

Synonyms: Mass spectrometry Interactive Virtual Environment (MassIVE), MassIVE, Mass spectrometry Interactive Virtual Environment

Resource Type: data or information resource, data repository, database, service resource, storage service resource

Keywords: Proteomics, Mass Spec, FASEB list

Resource Name: Mass spectrometry Interactive Virtual Environment (MassIVE)

Resource ID: SCR_013665

Alternate IDs: r3d100012858

Alternate URLs: <https://massive.ucsd.edu/>

Record Creation Time: 20220129T080317+0000

Record Last Update: 20260905T132739+0000

Ratings and Alerts

No rating or validation information has been found for Mass spectrometry Interactive Virtual Environment (MassIVE).

No alerts have been found for Mass spectrometry Interactive Virtual Environment (MassIVE).

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1409 mentions in open access literature.

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

Nail AN, et al. (2026) Deficient arsenic methylation and global proteomic reprogramming in human keratinocytes during arsenic-induced skin carcinogenesis. Archives of toxicology.

Balamurugan K, et al. (2026) 3D "Emboli" Culture Models Epithelial Breast Cancer Cell Oxidative Mitochondrial Metabolism with Relevance for Lung Metastasis. Cancer research communications, 6(3), 600.

Gadad SS, et al. (2026) X-linked cancer-associated polypeptide (XCP) from lncRNA1456 modulates PHF8 histone demethylase activity to regulate the epigenome, gene expression, and cellular pathways in breast cancer. Oncogene, 45(17), 1557.

Sanchez KM, et al. (2026) Dynamic acetylation of a conserved lysine impacts glycerol kinase activity and abundance in the haloarchaeon Haloferax volcanii. The Journal of biological chemistry, 302(1), 110960.

Lin CP, et al. (2026) The Mechanism of Histone Ubiquitylation by the ASB9-CUL5 Ubiquitin Ligase. Molecular & cellular proteomics : MCP, 25(2), 101471.

Jung H, et al. (2026) Autism-associated ARHGEF9 variants impair GABAergic synapses and ultrasonic communication by reducing gephyrin phosphorylation. Molecular psychiatry, 31(3), 1757.

Relano-Rodriguez I, et al. (2026) Rapid elicitation of neutralizing Asn332-glycan-independent antibodies to the V3-glycan epitope of HIV-1 Env in nonhuman primates. Nature immunology, 27(3), 586.

Sasidharan V, et al. (2026) Extracellular vesicles mediate stem cell signaling and systemic RNAi in planarians. Science advances, 12(6), eady1461.

Preußer C, et al. (2026) Isolation Defines Identity: Functional Consequences of Extracellular Vesicle Purification Strategies. Advanced healthcare materials, 15(13), e04684.

Lin Y, et al. (2026) Intermittent fasting inhibits Tp53-driven glioma through gut microbiota-mediated methionine-m6A regulation. *Nature communications*, 17(1), 1804.

Raval S, et al. (2026) Nanoscaled, Fully Automated Hydrogen/Deuterium Exchange for Analysis of Macromolecular Assemblies Reaching the MDa Scale. *Molecular & cellular proteomics : MCP*, 25(3), 101519.

Mannocho-Russo H, et al. (2026) Community Curation of Microbial Metabolites Enables Biological Insights of Metabolomics Data. *bioRxiv : the preprint server for biology*.

Fellers RT, et al. (2026) PSLite Online: A Portable, Modern Web Application to Analyze Top-Down Mass Spectrometry Fragmentation Data. *Journal of mass spectrometry : JMS*, 61(3), e70037.

McLaughlin CN, et al. (2026) Endocytome profiling uncovers cell-surface protein dynamics underlying neuronal connectivity. *Neuron*, 114(11), 1935.

Mbabala L, et al. (2026) Proteomic Snapshots of Structural Cross-Linking Rearrangements in Ca²⁺/Calmodulin-Dependent Kinase-1-Delta Associated with Its Regulation by ATP, Ca²⁺/Calmodulin, and Reduction Potential. *Journal of proteome research*, 25(4), 1914.

Kang SWS, et al. (2026) PLIN5 phosphorylation orchestrates mitochondria lipid-droplet coupling to control hepatic lipid flux and steatosis. *Nature metabolism*, 8(3), 587.

Fisher RJ, et al. (2026) CoREST complex inhibition alters RNA splicing to promote neoantigen expression and enhance tumor immunity. *JCI insight*, 11(2).

Miller SC, et al. (2026) Signal recognition particle-dependent secretome in humans. *Scientific reports*, 16(1).

Noble JT, et al. (2026) Mammarenaviruses depend on endogenous fatty acid synthesis in cell culture systems. *Journal of lipid research*, 67(5), 101038.

Liu J, et al. (2026) A Dimeric Rocaglate Promotes Multivalent eIF4A-RNA Assembly. *bioRxiv : the preprint server for biology*.