

Resource Summary Report

Generated by [dkNET](#) on Aug 6, 2026

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>

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

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, storage service resource, 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: 20260806T054603+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 1132 mentions in open access literature.

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

Durot S, et al. (2026) Multi-omics analysis reveals metabolic diversity underlying endothelial cell functions. *Life science alliance*, 9(3).

Bisseling Q, et al. (2026) Altered Mechanical Properties of Astrocytes Lacking MLC1: Implications for the Leukodystrophy MLC. *Glia*, 74(2), e70104.

Dupuis S, et al. (2026) Acclimation to high and low diurnal light is flexible in *Chlamydomonas reinhardtii*. *Proceedings of the National Academy of Sciences of the United States of America*, 123(1), e2523996123.

Zhou MH, et al. (2026) Spinal α -1 induces GluA3 degradation to regulate assembly of calcium-permeable AMPA receptors and pain hypersensitivity. *The Journal of clinical investigation*, 136(1).

Gilani A, et al. (2026) Secretory kinase FAM20C triggers adipocyte dysfunction, inciting insulin resistance and inflammation in obesity. *The Journal of clinical investigation*, 136(1).

Almási ÉDH, et al. (2025) *Klebsiella oxytoca* facilitates microbiome recovery via antibiotic degradation and restores colonization resistance in a diet-dependent manner. *Nature communications*, 16(1), 551.

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

Kim MW, et al. (2025) Endogenous self-peptides guard immune privilege of the central nervous system. *Nature*, 637(8044), 176.

Swensen AC, et al. (2025) Increased inflammation as well as decreased endoplasmic reticulum stress and translation differentiate pancreatic islets from donors with pre-symptomatic stage 1 type 1 diabetes and non-diabetic donors. *Diabetologia*, 68(7), 1463.

Schnizlein MK, et al. (2025) Non-redundant cardiolipin synthases shape membrane composition and support stress resilience in *Bacteroides fragilis*. *bioRxiv : the preprint server for biology*.

Lin CP, et al. (2025) The Mechanism of Histone Ubiquitylation by the ASB9-CUL5 Ubiquitin Ligase. *bioRxiv : the preprint server for biology*.

Daba SD, et al. (2025) Proteomics analysis of round and wrinkled pea (*Pisum sativum* L.) seeds during different development periods. *Proteomics*, 25(3), e2300363.

Reynolds TS, et al. (2025) Proteomic Analysis of Hsp90 α -Selective Inhibitors Against Triple-Negative Breast Cancer to Gain a Mechanistic Insight. *Molecular & cellular proteomics : MCP*, 24(9), 101043.

Corcoran CJ, et al. (2025) A glyoxal-specific aldehyde signaling axis in *Pseudomonas aeruginosa* that influences quorum sensing and infection. *Nature communications*, 16(1), 6616.

Vuille JA, et al. (2025) The E3 ligase HECTD4 regulates COX-2-dependent tumor progression and metastasis. *Proceedings of the National Academy of Sciences of the United States of America*, 122(32), e2425621122.

Yu F, et al. (2025) PepCentric Enables Fast Repository-Scale Proteogenomics Searches. *bioRxiv : the preprint server for biology*.

Lee YZ, et al. (2025) Rational design of next-generation filovirus vaccines with glycoprotein stabilization, nanoparticle display, and glycan modification. *bioRxiv : the preprint server for biology*.

Chapman A, et al. (2025) Honey bee egg composition changes seasonally and after acute maternal virus infection. *Scientific reports*, 15(1), 10418.

Hart CE, et al. (2025) Defining the limits of plant chemical space: challenges and estimations. *GigaScience*, 14.

Kirchhoffer OA, et al. (2025) Prioritization of novel anti-infective stilbene derivatives by combining metabolomic data organization and a stringent 3R-infection model in a knowledge graph. *RSC advances*, 15(17), 13010.