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

Keywords: Proteomics, Mass Spec, FASEB list

Funding:

Resource Name: Mass spectrometry Interactive Virtual Environment (MassIVE)

Resource ID: SCR_013665

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

Record Creation Time: 20220129T080317+0000

Record Last Update: 20250416T063648+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 863 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Zhang X, et al. (2025) ?-PrimeNovo: an accurate and efficient non-autoregressive deep learning model for de novo peptide sequencing. Nature communications, 16(1), 267.

Sengupta S, et al. (2025) Proteasome inhibition induces microtubule-dependent changes in nuclear morphology. iScience, 28(1), 111550.

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.

Singh A, et al. (2025) Cell-death induced immune response and coagulopathy promote cachexia in Drosophila. bioRxiv : the preprint server for biology.

Crissey MAS, et al. (2025) Divergent effects of acute and chronic PPT1 inhibition in melanoma. Autophagy, 21(2), 394.

Malaymar Pinar D, et al. (2025) Nuclear Factor I Family Members are Key Transcription Factors Regulating Gene Expression. Molecular & cellular proteomics : MCP, 24(1), 100890.

Bandura J, et al. (2025) Distinct Proteomic Brain States Underlying Long-Term Memory Formation in Aversive Operant Conditioning. Journal of proteome research, 24(1), 27.

Rios KT, et al. (2025) Widespread release of translational repression across Plasmodium's host-to-vector transmission event. PLoS pathogens, 21(1), e1012823.

Davis GJ, et al. (2025) Chemical tools to define and manipulate interferon-inducible Ubl protease USP18. Nature communications, 16(1), 957.

Christel S, et al. (2025) Catabolic pathway acquisition by rhizosphere bacteria readily enables growth with a root exudate component but does not affect root colonization. mBio, 16(1), e0301624.

Zhang QY, et al. (2025) Regulation of enzymatic lipid peroxidation in osteoblasts protects against postmenopausal osteoporosis. Nature communications, 16(1), 758.

Martá-Ariza M, et al. (2025) Comparison of the amyloid plaque proteome in Down syndrome, early-onset Alzheimer's disease, and late-onset Alzheimer's disease. Acta neuropathologica, 149(1), 9.

Gupta A, et al. (2025) Invasive lobular carcinoma integrated multi-omics analysis reveals silencing of Arginosuccinate synthase and upregulation of nucleotide biosynthesis in tamoxifen resistance. bioRxiv : the preprint server for biology.

de Oliveira ACFM, et al. (2025) A metabologenomics approach reveals the unexplored biosynthetic potential of bacteria isolated from an Amazon Conservation Unit. Microbiology spectrum, 13(1), e0099624.

Guise AJ, et al. (2024) TDP-43-stratified single-cell proteomics of postmortem human spinal motor neurons reveals protein dynamics in amyotrophic lateral sclerosis. Cell reports, 43(1), 113636.

Deinhardt-Emmer S, et al. (2024) Role of the Senescence-Associated Factor Dipeptidyl Peptidase 4 in the Pathogenesis of SARS-CoV-2 Infection. Aging and disease, 15(3), 1398.

Gui Y, et al. (2024) Fibroblast expression of transmembrane protein smoothened governs microenvironment characteristics after acute kidney injury. The Journal of clinical investigation, 134(13).

De Gasperi R, et al. (2024) Septin 7 interacts with Numb to preserve sarcomere structural organization and muscle contractile function. eLife, 12.