Resource Summary Report

Generated by NIF on Apr 9, 2025

Spectrum Mill

RRID:SCR_022171
Type: Tool

Proper Citation

Spectrum Mill (RRID:SCR_022171)

Resource Information

URL: https://proteomics.broadinstitute.org/

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Description: Software tool for high throughput processing of MS/MS and MS spectra to provide protein and peptide identifications and relative quantitation.

Synonyms: Agilent Spectrum Mill MS Proteomics Workbench, Spectrum Mill v7.11

Resource Type: software toolkit, software resource, data processing software, software application

Keywords: mass spectrometry data, MS spectra, protein and peptide identifications, protein and peptide quantification,

Funding:

Availability: Free, Available for download

Resource Name: Spectrum Mill

Resource ID: SCR_022171

License URLs: https://proteomics.broadinstitute.org/eulaBI.htm

Record Creation Time: 20220421T050139+0000

Record Last Update: 20250409T061751+0000

Ratings and Alerts

No rating or validation information has been found for Spectrum Mill.

No alerts have been found for Spectrum Mill.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

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

Zhu QM, et al. (2024) Protein interaction networks in the vasculature prioritize genes and pathways underlying coronary artery disease. Communications biology, 7(1), 87.

Weingarten-Gabbay S, et al. (2024) The HLA-II immunopeptidome of SARS-CoV-2. Cell reports, 43(1), 113596.

Simpson MS, et al. (2024) IRE1? recognizes a structural motif in cholera toxin to activate an unfolded protein response. The Journal of cell biology, 223(7).

Lee SY, et al. (2024) Directed evolution of the multicopper oxidase laccase for cell surface proximity labeling and electron microscopy. bioRxiv : the preprint server for biology.

Mansur A, et al. (2023) Dynamic regulation of inter-organelle communication by ubiquitylation controls skeletal muscle development and disease onset. eLife, 12.

Hofman DA, et al. (2023) Translation of non-canonical open reading frames as a cancer cell survival mechanism in childhood medulloblastoma. bioRxiv : the preprint server for biology.

Phulphagar KM, et al. (2023) Sensitive, High-Throughput HLA-I and HLA-II Immunopeptidomics Using Parallel Accumulation-Serial Fragmentation Mass Spectrometry. Molecular & cellular proteomics : MCP, 22(6), 100563.

Farsi Z, et al. (2023) Brain-region-specific changes in neurons and glia and dysregulation of dopamine signaling in Grin2a mutant mice. Neuron, 111(21), 3378.

Howard EE, et al. (2022) Effects of Testosterone on Mixed-Muscle Protein Synthesis and Proteome Dynamics During Energy Deficit. The Journal of clinical endocrinology and metabolism, 107(8), e3254.