

Resource Summary Report

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PEAKS Studio

RRID:SCR_022841

Type: Tool

Proper Citation

PEAKS Studio (RRID:SCR_022841)

Resource Information

URL: <https://www.bioinfor.com/peaks-studio/>

Proper Citation: PEAKS Studio (RRID:SCR_022841)

Description: Software platform with complete solutions for discovery proteomics, including protein identification and quantification, analysis of post translational modifications and sequence variants (mutations), and peptide/protein de novo sequencing.

Synonyms: PEAKS Studio Xpro

Resource Type: software resource

Defining Citation: [PMID:14558135](#)

Keywords: Bioinformatics Solutions Inc., peptide de novo sequencing, mass spectrometry, discovery proteomics, protein identification and quantification, analysis, post translational modifications, sequence variants, mutations,

Availability: Restricted

Resource Name: PEAKS Studio

Resource ID: SCR_022841

Record Creation Time: 20221008T050158+0000

Record Last Update: 20260912T200030+0000

Ratings and Alerts

No rating or validation information has been found for PEAKS Studio.

No alerts have been found for PEAKS Studio.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 18 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Nishiuchi T, et al. (2026) Paleoproteomics of pottery food residues reveals plant cupin superfamily proteins preserved for thousands of years. *iScience*, 29(5), 115637.

Goldman A, et al. (2026) An LRRK2 variant blocks NCOA4 trafficking upon iron overload, leading to ferroptotic death. *Journal of cell science*, 139(14).

Fahmy AM, et al. (2026) STING dampens the unfolded protein response to enable the presentation of self-antigens on MHC-I during inflammation. *Cell reports*, 45(6), 117497.

Basse V, et al. (2025) Regulation of respiratory syncytial virus nucleoprotein oligomerization by phosphorylation. *The Journal of biological chemistry*, 301(3), 108256.

Manara P, et al. (2025) Blocking NRF2 Translation by Inhibition of Cap-Dependent Initiation Sensitizes Lymphoma Cells to Ferroptosis and CAR T-cell Immunotherapy. *Cancer research*.

Juanes-Velasco P, et al. (2024) Crucial Parameters for Immunopeptidome Characterization: A Systematic Evaluation. *International journal of molecular sciences*, 25(17).

Kasso T, et al. (2024) A queen's tale: An experimental palaeoproteomic study of a honey bee queen cell specimen from Natural History Museum Denmark. *Open research Europe*, 4, 227.

Gil-Pitarch C, et al. (2024) Neddylation inhibition prevents acetaminophen-induced liver damage by enhancing the anabolic cardiolipin pathway. *Cell reports. Medicine*, 5(7), 101653.

Aguilan JT, et al. (2024) Effect of dynamic exclusion and the use of FAIMS, DIA and MALDI-mass spectrometry imaging with ion mobility on amyloid protein identification. *Clinical proteomics*, 21(1), 47.

Choi S, et al. (2024) pXg: Comprehensive Identification of Noncanonical MHC-I-Associated Peptides From De Novo Peptide Sequencing Using RNA-Seq Reads. *Molecular & cellular proteomics : MCP*, 23(4), 100743.

Jackson M, et al. (2024) Quantitative proteomic profiling in brain subregions of mice exposed to open-field low-intensity blast reveals position-dependent blast effects. *Shock waves*, 34, 381.

Sun W, et al. (2023) Glycopeptide database search and de novo sequencing with PEAKS GlycanFinder enable highly sensitive glycoproteomics. *Nature communications*, 14(1), 4046.

Olari LR, et al. (2023) The C-terminal 32-mer fragment of hemoglobin alpha is an amyloidogenic peptide with antimicrobial properties. *Cellular and molecular life sciences : CMLS*, 80(6), 151.

Lozano-Rabella M, et al. (2023) Exploring the Immunogenicity of Noncanonical HLA-I Tumor Ligands Identified through Proteogenomics. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 29(12), 2250.

Sapiro AL, et al. (2023) Longitudinal map of transcriptome changes in the Lyme pathogen *Borrelia burgdorferi* during tick-borne transmission. *eLife*, 12.

Mayer RL, et al. (2023) Immunopectidomics in the Era of Single-Cell Proteomics. *Biology*, 12(12).

Meyer S, et al. (2023) Prevalent and immunodominant CD8 T cell epitopes are conserved in SARS-CoV-2 variants. *Cell reports*, 42(1), 111995.

Kumar P, et al. (2022) Tumour-associated antigenic peptides are present in the HLA class I ligandome of cancer cell line derived extracellular vesicles. *Immunology*, 166(2), 249.