

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: 20260725T191022+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 13 mentions in open access literature.

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

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.

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.

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.

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.

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.

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.

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.

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) Immunopeptidomics 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.