Resource Summary Report

Generated by NIF on May 7, 2025

pFind

RRID:SCR_003011
Type: Tool

Proper Citation

pFind (RRID:SCR_003011)

Resource Information

URL: http://pfind.ict.ac.cn/software/pFind/index.html

Proper Citation: pFind (RRID:SCR_003011)

Description: A search engine system for automated peptide and protein identification from tandem mass spectra.

Resource Type: software resource

Defining Citation: PMID:17702057

Keywords: mass spectrometry, proteomics

Funding:

Resource Name: pFind

Resource ID: SCR_003011

Alternate IDs: OMICS_02467

Record Creation Time: 20220129T080216+0000

Record Last Update: 20250420T014133+0000

Ratings and Alerts

No rating or validation information has been found for pFind.

No alerts have been found for pFind.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 90 mentions in open access literature.

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

Fan L, et al. (2025) CICADA: a circRNA effort toward the ghost proteome. Nucleic acids research, 53(1).

Zhao Q, et al. (2025) Nonenzymatic lysine D-lactylation induced by glyoxalase II substrate SLG dampens inflammatory immune responses. Cell research, 35(2), 97.

Gou J, et al. (2025) O-GlcNAcylated FTO promotes m6A modification of SOX4 to enhance MDS/AML cell proliferation. Cell communication and signaling : CCS, 23(1), 43.

Kuang W, et al. (2025) Eupalinolide B inhibits periodontitis development by targeting ubiquitin conjugating enzyme UBE2D3. MedComm, 6(1), e70034.

Guan X, et al. (2024) Blocking Ubiquitin-Specific Protease 7 Induces Ferroptosis in Gastric Cancer via Targeting Stearoyl-CoA Desaturase. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 11(18), e2307899.

Dong X, et al. (2024) Quantitative chemical proteomics reveals that phenethyl isothiocyanate covalently targets BID to promote apoptosis. Cell death discovery, 10(1), 456.

Liu Z, et al. (2024) Bioorthogonal photocatalytic proximity labeling in primary living samples. Nature communications, 15(1), 2712.

Xu N, et al. (2024) CircCDC42-encoded CDC42-165aa regulates macrophage pyroptosis in Klebsiella pneumoniae infection through Pyrin inflammasome activation. Nature communications, 15(1), 5730.

Zhao Y, et al. (2024) Catalyst-free late-stage functionalization to assemble ?-acyloxyenamide electrophiles for selectively profiling conserved lysine residues. Communications chemistry, 7(1), 31.

Yu J, et al. (2024) Ribosome External Electric Field Regulates Metabolic Enzyme Activity: The RAMBO Effect. The journal of physical chemistry. B, 128(29), 7002.

Liu DD, et al. (2024) Characterize direct protein interactions with enrichable, cleavable and latent bioreactive unnatural amino acids. Nature communications, 15(1), 5221.

Fan X, et al. (2024) Analysis of RNA translation with a deep learning architecture provides new insight into translation control. bioRxiv : the preprint server for biology.

Li M, et al. (2024) KHSRP ameliorates acute liver failure by regulating pre-mRNA splicing through its interaction with SF3B1. Cell death & disease, 15(8), 618.

Shao X, et al. (2024) ZASP: A Highly Compatible and Sensitive ZnCl2 Precipitation-Assisted Sample Preparation Method for Proteomic Analysis. Molecular & cellular proteomics : MCP, 23(10), 100837.

Damm M, et al. (2024) Venomics and Peptidomics of Palearctic Vipers: A Clade-Wide Analysis of Seven Taxa of the Genera Vipera, Montivipera, Macrovipera, and Daboia across Türkiye. Journal of proteome research, 23(8), 3524.

Wang J, et al. (2024) Pulmonary and renal long COVID at two-year revisit. iScience, 27(7), 110344.

Liu X, et al. (2024) Oxygen enhances antiviral innate immunity through maintenance of EGLN1-catalyzed proline hydroxylation of IRF3. Nature communications, 15(1), 3533.

Wu XX, et al. (2024) Cryo-EM structures of the plant plastid-encoded RNA polymerase. Cell, 187(5), 1127.

Liu R, et al. (2023) Dynamic phosphorylation of CENP-N by CDK1 guides accurate chromosome segregation in mitosis. Journal of molecular cell biology, 15(6).

Cheng K, et al. (2023) MetaLab-MAG: A Metaproteomic Data Analysis Platform for Genome-Level Characterization of Microbiomes from the Metagenome-Assembled Genomes Database. Journal of proteome research, 22(2), 387.