

Resource Summary Report

Generated by [T1D](#) on Aug 9, 2026

[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

Resource Name: pFind

Resource ID: SCR_003011

Alternate IDs: OMICS_02467

Record Creation Time: 20220129T080216+0000

Record Last Update: 20260808T185750+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 132 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Ma ZH, et al. (2026) Nucleophagy is promoted by two autophagy receptors and inhibited by chromatin-nuclear envelope tethering in fission yeast. *Nature communications*, 17(1).

Indeglia A, et al. (2026) Protocol for identification of protein citrullination by immunoprecipitation followed by mass spectrometry. *STAR protocols*, 7(1), 104326.

Li J, et al. (2026) Sustainable Phosphorylated Cellulose Nanocrystals: A Dual-Affinity Platform for High-Efficiency Enrichment of Intact Glycopeptides and Phosphopeptides. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(27), e23858.

Cao Z, et al. (2026) DiNovo enables high-coverage and high-confidence de novo peptide sequencing via mirror proteases and deep learning. *Nature communications*, 17(1).

Li N, et al. (2026) Single-Position Peptide Clustering for Peptidomics Reveals Novel Disease Biomarkers and Dysregulated Proteolytic Characteristics. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(5), e10910.

Xu C, et al. (2026) Analysis of MHC class II-bound CyHV-2 peptides in *Carassius gibelio* using mass spectrometry. *Journal of virology*, 100(2), e0187025.

Yang X, et al. (2026) A Brief Progress in Methods for Deciphering Protein-Protein Interaction Networks. *International journal of molecular sciences*, 27(4).

Bai J, et al. (2026) TGM2-mediated serotonylation of GPX4 confers ferroptosis resistance to promote gastric tumorigenesis. *Cell discovery*, 12(1).

Fu Q, et al. (2026) Enamel proteins from six *Homo erectus* specimens across China. *Nature*, 655(8121), 141.

de-Dios T, et al. (2025) Bone Adhered Sediments as a Source of Target and Environmental DNA and Proteins. *Molecular biology and evolution*, 42(9).

Yu J, et al. (2025) In Vivo Ribosome-Amplified MetaBOLism, RAMBO, Effect Observed by Real Time Pulse Chase, RTPC, NMR Spectroscopy. *Biochemistry*, 64(12), 2660.

Gou J, et al. (2025) Targeting O-GlcNAcylated METTL3 impedes MDS/AML progression via diminishing SRSF1 m6A modification. *Molecular therapy : the journal of the American Society of Gene Therapy*, 33(12), 6146.

He H, et al. (2025) Inhibition Peroxiredoxin-2 by Capsaicin Ameliorates Rheumatoid Arthritis via ROS-Mediated Apoptosis in Fibroblast-Like Synoviocytes. *MedComm*, 6(6), e70209.

Song Y, et al. (2025) Identification of Unknown Biological Toxin Proteins Using Mass Spectrometry: A Case Study on De Novo Sequencing of Ricin. *Toxins*, 17(11).

Zhu S, et al. (2025) Unraveling the Central Role of Global Regulator PprI in *Deinococcus radiodurans* Through Label-Free Quantitative Proteomics. *Proteomes*, 13(2).

Li L, et al. (2025) Spatiotemporal single-cell architecture of gene expression in the *Caenorhabditis elegans* germ cells. *Cell discovery*, 11(1), 26.

Zhu TY, et al. (2025) Genetically encoding ϵ -N-methacryllysine into proteins in live cells. *Nature communications*, 16(1), 2623.

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

Xiao C, et al. (2025) Oncogenic roles of young human de novo genes and their potential as neoantigens in cancer immunotherapy. *Cell genomics*, 5(9), 100928.

Wang C, et al. (2025) MCM7 promotes liver fibrosis by transcriptionally regulating IL11 via the SHCBP1-RACGAP1-STAT3 axis. *Cell death & disease*, 16(1), 608.