

Resource Summary Report

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Percolator: Semi-supervised learning for peptide identification from shotgun proteomics datasets

RRID:SCR_005040

Type: Tool

Proper Citation

Percolator: Semi-supervised learning for peptide identification from shotgun proteomics datasets (RRID:SCR_005040)

Resource Information

URL: <http://noble.gs.washington.edu/proj/percolator/>

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Description: Percolator post-processes the results of a shotgun proteomics database search program, re-ranking peptide-spectrum matches so that the top of the list is enriched for correct matches. Shotgun proteomics uses liquid chromatography-tandem mass spectrometry to identify proteins in complex biological samples. We describe an algorithm, called Percolator, for improving the rate of peptide identifications from a collection of tandem mass spectra. Percolator uses semi-supervised machine learning to discriminate between correct and decoy spectrum identifications, correctly assigning peptides to 17% more spectra from a tryptic dataset and up to 77% more spectra from non-tryptic digests, relative to a fully supervised approach. The yeast-01 data is available in tab delimited format. The SEQUEST parameter file and target database for the yeast and worm data are also available.

Synonyms: Percolator

Resource Type: software resource, data or information resource, database

Defining Citation: [PMID:17952086](#)

Keywords: worm, yeast, bio.tools

Resource Name: Percolator: Semi-supervised learning for peptide identification from shotgun proteomics datasets

Resource ID: SCR_005040

Alternate IDs: biotools:percolator, nlx_98814

Alternate URLs: <https://bio.tools/percolator>

Record Creation Time: 20220129T080228+0000

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Ratings and Alerts

No rating or validation information has been found for Percolator: Semi-supervised learning for peptide identification from shotgun proteomics datasets.

No alerts have been found for Percolator: Semi-supervised learning for peptide identification from shotgun proteomics datasets.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2482 mentions in open access literature.

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

Schmidt A, et al. (2026) Gas plasma therapy of murine and human diabetic wounds is associated with junctional and hippo signaling and oxidative protein modifications. Redox biology, 89, 103951.

Lee E, et al. (2026) Streptococcus pneumoniae HtrA is a dynamic and monomeric virulence factor capable of forming larger oligomeric complexes. Protein science : a publication of the Protein Society, 35(1), e70411.

Thilmany S, et al. (2026) Hormonal Contraceptives and Depression: A Proteomic Analysis Using Neuronal Models. Proteomics. Clinical applications, 20(1), e70017.

Luciani M, et al. (2026) Muscle proteomics reveals biomarkers of stress and meat quality in organic versus conventional broiler chickens. Poultry science, 105(1), 106164.

Gao H, et al. (2026) Hydrogen-deuterium exchange reveals catalytically linked protein flexibility in myoglobin-mediated intramolecular C(sp³)-H activation. Protein science : a publication of the Protein Society, 35(1), e70410.

Bisseling Q, et al. (2026) Altered Mechanical Properties of Astrocytes Lacking MLC1: Implications for the Leukodystrophy MLC. Glia, 74(2), e70104.

Liao SC, et al. (2025) CHCHD2 mutant mice link mitochondrial deficits to PD pathophysiology. Science advances, 11(46), eadu0726.

Pan Y, et al. (2025) Functional-proteomics-based investigation of the cellular response to farnesyltransferase inhibition in lung cancer. iScience, 28(2), 111864.

Morais LH, et al. (2025) The gut microbiome promotes mitochondrial respiration in the brain of a Parkinson's disease mouse model. *NPJ Parkinson's disease*, 11(1), 301.

Kasai T, et al. (2025) In-Source Collision-Induced Dissociation (CID) Improves Higher-Energy Collisional Dissociation (HCD)-Dependent Fragmentation of ADP-Ribosyl Peptides. *Rapid communications in mass spectrometry : RCM*, 39(4), e9961.

Lei C, et al. (2025) Chemical Glycoproteomic Profiling in Rice Seedlings Reveals N-glycosylation in the ERAD-L Machinery. *Molecular & cellular proteomics : MCP*, 24(2), 100883.

Kowalczyk J, et al. (2025) Ubiquitin-like and ubiquitinated proteins associated with the maternal cell walls of *Scenedesmus obliquus* 633 as identified by immunochemistry and LC-MS/MS proteomics. *Protoplasma*, 262(2), 299.

Monteiro R, et al. (2025) Molecular properties of the RmlT wall teichoic acid rhamnosyltransferase that modulates virulence in *Listeria monocytogenes*. *Nature communications*, 16(1), 24.

Fischer A, et al. (2025) Targeting pleuro-alveolar junctions reverses lung fibrosis in mice. *Nature communications*, 16(1), 173.

Errico A, et al. (2025) In vitro effect of hCG on cryptorchid patients' gubernacular cells: a predictive model for adjuvant personalized therapy. *Cell communication and signaling : CCS*, 23(1), 19.

Biel N, et al. (2025) Reducing Cofilin dosage makes embryos resilient to heat stress. *bioRxiv : the preprint server for biology*.

Tang W, et al. (2025) Cohesin positions the epigenetic reader Phf2 within the genome. *The EMBO journal*, 44(3), 736.

Petrone BL, et al. (2025) A pilot study of metaproteomics and DNA metabarcoding as tools to assess dietary intake in humans. *Food & function*, 16(1), 282.

Li X, et al. (2025) Systematic Evaluation of Isolation Techniques and Freeze-Thaw Effects on Plasma Extracellular Vesicle Heterogeneity and Subpopulation Profiling. *Journal of extracellular biology*, 4(6), e70058.

Bertrand L, et al. (2025) Unveiling conserved HIV-1 open reading frames encoding T cell antigens using ribosome profiling. *Nature communications*, 16(1), 1707.