

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 8, 2026

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/>

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

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: data or information resource, database, software resource

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

Record Last Update: 20260905T132528+0000

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 2729 mentions in open access literature.

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

Balamurugan K, et al. (2026) 3D "Emboli" Culture Models Epithelial Breast Cancer Cell Oxidative Mitochondrial Metabolism with Relevance for Lung Metastasis. Cancer research communications, 6(3), 600.

Dombaxe CP, et al. (2026) Proteomic Signatures of Regeneration: Uncovering Extracellular Matrix-Associated Cues in Goldfish Spinal Cord Repair. The Journal of comparative neurology, 534(5), e70170.

Sanchez KM, et al. (2026) Dynamic acetylation of a conserved lysine impacts glycerol kinase activity and abundance in the haloarchaeon Haloferax volcanii. The Journal of biological chemistry, 302(1), 110960.

Price HE, et al. (2026) Activity of Direct KRAS(G12C) Inhibitors in Preclinical Models of Pediatric Cancer. Molecular cancer therapeutics, 25(5), 727.

Niikura M, et al. (2026) Identification of serine/arginine-rich splicing factor 1-interacting proteins in Plasmodium berghei. Malaria journal, 25(1), 108.

Chianese U, et al. (2026) Glycolytic heterogeneity drives metabolic-targeted therapy in pancreatic ductal adenocarcinoma. Signal transduction and targeted therapy, 11(1), 25.

Malmhäll-Bah E, et al. (2026) Role of MNX1-mediated histone modifications and PBX gene family in MNX1-induced leukemogenesis. Scientific reports, 16(1), 2593.

Rodrigues-Junior DM, et al. (2026) The long noncoding RNA VIM-AS1 and nucleoporin Nup358/RanBP2 regulate SMAD nuclear accumulation during TGF- β signaling. Nucleic

acids research, 54(2).

Hovey OFJ, et al. (2026) LIN28A-Dependent Kinome and Phosphoproteome Reprogramming Promotes Imatinib Resistance. *Molecular & cellular proteomics : MCP*, 25(4), 101514.

Bathini M, et al. (2026) MHC1-TIP enables single-tube multimodal immunopeptidome profiling and uncovers intratumoral heterogeneity in antigen presentation. *Communications biology*, 9(1).

Ote M, et al. (2026) Envelope destabilization by AcrAB2NodT overexpression links antibiotic resistance to metal sensitivity in *Caulobacter vibrioides*. *Communications biology*, 9(1).

Bouwmeester R, et al. (2026) Transfer learning in DeepLC improves LC retention time prediction across substantially different modifications and setups. *Nature communications*, 17(1).

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.

Nishigori M, et al. (2026) Stress-induced OMA1-mediated cleavage of AIFM1 suppresses cell growth by controlling mitochondrial OXPHOS activity. *The EMBO journal*, 45(11), 3655.

Mihailovic M, et al. (2026) The coordinated action of UFMylation and the RQC pathways clears arrested polypeptides at the ER. *The EMBO journal*, 45(9), 3252.

Kang SWS, et al. (2026) PLIN5 phosphorylation orchestrates mitochondria lipid-droplet coupling to control hepatic lipid flux and steatosis. *Nature metabolism*, 8(3), 587.

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.

Schmidt T, et al. (2026) Synovial fluid potentiates local fibroblasts to drive monocyte activation in juvenile idiopathic arthritis. *Arthritis research & therapy*, 28(1).

Brahim S, et al. (2026) Kremen1 dependence receptor induces SEC24C and ATG9A-dependent cell death. *Cell communication and signaling : CCS*, 24(1).

Berlureau J, et al. (2026) An atypical F-type ATPase is necessary for the function of the antibody cleavage system MIB-MIP in mycoplasmas. *PLoS pathogens*, 22(3), e1014043.