

Resource Summary Report

Generated by [dkNET](#) on Aug 28, 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: 20260821T193731+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 [dkNET](#) .

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.

Huang W, et al. (2026) Gut microbiota-derived xanthohumol protects against heatstroke by inhibiting macrophage pyroptosis in mice. Journal of advanced research, 82, 967.

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.

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.

Courcelles M, et al. (2026) Noncanonical Transcription and Splicing Shape the Colorectal Cancer Immunopeptidome in MSI and MSS Tumors. Molecular & cellular proteomics : MCP, 25(6), 101581.

Xie T, et al. (2026) Region-Resolved Integrative Multi-Omic Characterization Reveals Diverse Tumor and Microenvironment Features of Pituitary Neuroendocrine Tumors. Molecular & cellular proteomics : MCP, 25(6), 101583.

Clements J, et al. (2026) HDAC11 Regulates RNA Splicing via De-Fatty Acylation of SF3B2. *bioRxiv : the preprint server for biology*.

Carnielli JBT, et al. (2026) Chemical genetics reveals Leishmania KKT2 and CRK9 kinase activity is required for cell cycle progression. *PLoS pathogens*, 22(5), e1014194.

Borghi E, et al. (2026) Microbiota-gut-brain axis and treatment resistance in epilepsy: a multicentre prospective study protocol (CARE). *BMJ open*, 16(6), e111607.

Robinson L, et al. (2026) ALS-FTD-linked CCFNFS621G drives increased hippocampal astrocyte ramification and mitochondrial dysfunction and impairs motor neuron excitability. *Journal of neuroinflammation*, 23(1).

Kong F, et al. (2026) Isolation of small extracellular vesicles from small volumes of blood plasma using size exclusion chromatography and density gradient ultracentrifugation. *eLife*, 13.

Park SM, et al. (2026) Therapeutic targeting of blood-derived protein infiltration to modulate neuroinflammation in cerebellar ataxia. *Journal of neuroinflammation*, 23(1).

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

Mozes C, et al. (2026) Covalent Reprogramming of Kinase Binders to Modulate Protein Abundance. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(36), e75153.

Liu Y, et al. (2026) DNA O-MAP uncovers the molecular neighborhoods associated with specific genomic loci. *eLife*, 13.

Ramirez-Zavala B, et al. (2026) Inducible gene deletion reveals essentiality of protein kinases and a septation initiation network in *Candida albicans*. *PLoS genetics*, 22(4), e1012118.

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.

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

Raheja M, et al. (2026) A microprotein encoded by FERMT3 modulates endothelial cell protein catabolism and induces cell cycle arrest and senescence. *Cell communication and signaling : CCS*, 24(1).