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 delimetered 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

Funding:

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: 20250422T055220+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 5 mentions in open access literature.

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

Zlatic SA, et al. (2022) Convergent cerebrospinal fluid proteomes and metabolic ontologies in humans and animal models of Rett syndrome. iScience, 25(9), 104966.

Kowalczyk JT, et al. (2021) Rigosertib Induces Mitotic Arrest and Apoptosis in RAS-Mutated Rhabdomyosarcoma and Neuroblastoma. Molecular cancer therapeutics, 20(2), 307.

Moulay G, et al. (2020) Alternative splicing of clathrin heavy chain contributes to the switch from coated pits to plaques. The Journal of cell biology, 219(9).

Kim JO, et al. (2017) The Ndc80 complex bridges two Dam1 complex rings. eLife, 6.

Phua SC, et al. (2017) Dynamic Remodeling of Membrane Composition Drives Cell Cycle through Primary Cilia Excision. Cell, 168(1-2), 264.