

Resource Summary Report

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SAINTexpress

RRID:SCR_018562

Type: Tool

Proper Citation

SAINTexpress (RRID:SCR_018562)

Resource Information

URL: <https://sourceforge.net/projects/saint-apms/files/>

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Description: Software tool for upgraded implementation of probabilistic scoring of affinity purification mass spectrometry data. Used for filtering high confidence interaction data from affinity purification mass spectrometry experiments. Used for assigning confidence scores to protein-protein interactions based on quantitative proteomics data in AP-MS experiments.

Synonyms: Significance Analysis of INteractome Express

Resource Type: software toolkit, software resource

Defining Citation: [PMID:24513533](#)

Keywords: Probabilistic scoring, affinity purification, mass spectrometry data, mass spectrometry experiment data, assigning confidence score, protein-protein interaction, quantitative proteomic data

Funding: NCRR R01 RR024031;
NIGMS R01 GM094231;
NCI R01 CA126239

Availability: Free, Freely available

Resource Name: SAINTexpress

Resource ID: SCR_018562

Record Creation Time: 20220129T080340+0000

Record Last Update: 20260729T044446+0000

Ratings and Alerts

No rating or validation information has been found for SAINTexpress.

No alerts have been found for SAINTexpress.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 13 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#).

Kaushal P, et al. (2024) Protocol for mapping differential protein-protein interaction networks using affinity purification-mass spectrometry. STAR protocols, 5(4), 103286.

Kravec M, et al. (2024) Carboxy-terminal polyglutamylation regulates signaling and phase separation of the Dishevelled protein. The EMBO journal, 43(22), 5635.

Xiong EH, et al. (2024) Functional genomic analysis of genes important for Candida albicans fitness in diverse environmental conditions. Cell reports, 43(8), 114601.

Lacoste J, et al. (2024) Pervasive mislocalization of pathogenic coding variants underlying human disorders. Cell, 187(23), 6725.

Segal D, et al. (2023) A central chaperone-like role for 14-3-3 proteins in human cells. Molecular cell, 83(6), 974.

Persaud R, et al. (2022) Clonamines stimulate autophagy, inhibit Mycobacterium tuberculosis survival in macrophages, and target Pik1. Cell chemical biology, 29(5), 870.

Xu C, et al. (2022) Comparative Network Biology Discovers Protein Complexes That Underline Cellular Differentiation in Anabaena sp. Molecular & cellular proteomics : MCP, 21(4), 100224.

Zhang Y, et al. (2022) An antibody-based proximity labeling map reveals mechanisms of SARS-CoV-2 inhibition of antiviral immunity. Cell chemical biology, 29(1), 5.

Chauhan JS, et al. (2022) The MITF regulatory network in melanoma. Pigment cell & melanoma research, 35(5), 517.

Yang Z, et al. (2022) Enhancing PD-L1 Degradation by ITCH during MAPK Inhibitor Therapy Suppresses Acquired Resistance. Cancer discovery, 12(8), 1942.

Gaspar VP, et al. (2021) Interactome Analysis of KIN (Kin17) Shows New Functions of This Protein. Current issues in molecular biology, 43(2), 767.

Marques JG, et al. (2020) NuRD subunit CHD4 regulates super-enhancer accessibility in rhabdomyosarcoma and represents a general tumor dependency. eLife, 9.

Aranda S, et al. (2020) Chromatin-Bound Proteome Profiling by Genome Capture. STAR protocols, 1(1), 100014.