Resource Summary Report

Generated by RRID on Apr 11, 2025

Kinase Enrichment Analysis 3

RRID:SCR_023623
Type: Tool

Proper Citation

Kinase Enrichment Analysis 3 (RRID:SCR_023623)

Resource Information

URL: https://maayanlab.cloud/kea3

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Description: Web server application that infers overrepresentation of upstream kinases whose putative substrates are in user inputted list of proteins. Used to analyze data from phosphoproteomics and proteomics studies to predict upstream kinases responsible for observed differential phosphorylations.

Abbreviations: KEA3

Resource Type: software resource, data access protocol, web service

Defining Citation: PMID:34019655

Keywords: overrepresentation of upstream kinases, upstream kinases, upstream kinases substrates, user inputted list of proteins,

Funding: NHLBI U54 HL127624;
NCI U24 CA224260;
NIGMS T32 GM062754;
NIH Office of the Director OT3 OD025467

Availability: Free, Freely available

Resource Name: Kinase Enrichment Analysis 3

Resource ID: SCR_023623

Record Creation Time: 20230527T050216+0000

Record Last Update: 20250410T071629+0000

Ratings and Alerts

No rating or validation information has been found for Kinase Enrichment Analysis 3.

No alerts have been found for Kinase Enrichment Analysis 3.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Deng EZ, et al. (2024) Multiomics2Targets identifies targets from cancer cohorts profiled with transcriptomics, proteomics, and phosphoproteomics. Cell reports methods, 4(8), 100839.

Pichol-Thievend C, et al. (2024) VC-resist glioblastoma cell state: vessel co-option as a key driver of chemoradiation resistance. Nature communications, 15(1), 3602.

Arifin MZ, et al. (2024) BTLA and PD-1 signals attenuate TCR-mediated transcriptomic changes. iScience, 27(7), 110253.

Marino GB, et al. (2024) Protocol for using Multiomics2Targets to identify targets and driver kinases for cancer cohorts profiled with multi-omics assays. STAR protocols, 5(4), 103457.

Nguyen JH, et al. (2023) Developmental pyrethroid exposure disrupts molecular pathways for circadian rhythms and MAP kinase in mouse brain. bioRxiv : the preprint server for biology.

Thom CS, et al. (2023) Phosphoproteomics reveals content and signaling differences between neonatal and adult platelets. bioRxiv : the preprint server for biology.

Gamradt P, et al. (2023) Stiffness-induced cancer-associated fibroblasts are responsible for immunosuppression in a platelet-derived growth factor ligand-dependent manner. PNAS nexus, 2(12), pgad405.