

Resource Summary Report

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X2K Web

RRID:SCR_023624

Type: Tool

Proper Citation

X2K Web (RRID:SCR_023624)

Resource Information

URL: <https://maayanlab.cloud/X2K>

Proper Citation: X2K Web (RRID:SCR_023624)

Description: Web service to predict involvement of upstream cell signaling pathways, given signature of differentially expressed genes. Used to linking expression signatures to upstream cell signaling networks.

Abbreviations: X2K

Synonyms: eXpression2Kinases (X2K) Web

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

Defining Citation: [PMID:29800326](#)

Keywords: predicts involvement of upstream cell signaling pathways, differentially expressed genes, linking expression signatures, upstream cell signaling networks,

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

Availability: Free, Freely available

Resource Name: X2K Web

Resource ID: SCR_023624

Alternate URLs: https://github.com/MaayanLab/x2k_web

Record Creation Time: 20230527T050216+0000

Record Last Update: 20260801T190810+0000

Ratings and Alerts

No rating or validation information has been found for X2K Web.

No alerts have been found for X2K Web.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Dos Santos FM, et al. (2025) Dynamic Cellular Proteome Remodeling during SARS-CoV-2 Infection. Identification of Plasma Protein Readouts. Journal of proteome research, 24(1), 171.

Liu H, et al. (2025) Optineurin Cooperates With NRF2 to Regulate Tooth Root Morphogenesis by Controlling Mitochondrial Dynamics and Apoptosis. Cell proliferation, 58(5), e13799.

Elbatarny M, et al. (2025) Systems biology approaches investigating mitochondrial dysfunction in cyanotic heart disease: a systematic review. EBioMedicine, 118, 105839.

Payva F, et al. (2025) Systems biology approach delineates critical pathways associated with papillary thyroid cancer: a multi-omics data analysis. Thyroid research, 18(1), 15.

Wang J, et al. (2024) Targeting c-Myc transactivation by LMNA inhibits tRNA processing essential for malate-aspartate shuttle and tumour progression. Clinical and translational medicine, 14(5), e1680.

Ajiboye BO, et al. (2024) In silico exploration of anti-prostate cancer compounds from differential expressed genes. BMC urology, 24(1), 138.

Bhuiyan P, et al. (2024) System biology approaches to identify hub genes linked with ECM organization and inflammatory signaling pathways in schizophrenia pathogenesis. Heliyon, 10(3), e25191.

Alharbi M, et al. (2024) The ameliorative effect of pioglitazone against colistin-induced nephrotoxicity is mediated by inhibition of NF- κ B and restoration of Nrf2 signaling: An integrative bioinformatics prediction-guided in vitro study. PloS one, 19(12), e0314092.

Liu L, et al. (2024) Suppression of DNMT1 combined with ATM or ATR inhibitor as a therapeutic combination of acute myeloid leukemia. Anti-cancer drugs, 35(3), 251.

Wang M, et al. (2024) KIF18A and CDK1 as combined therapeutic targets in cervical and endometrial carcinomas: based on bioinformatics analysis and in vitro experiments. Translational cancer research, 13(12), 6880.