Resource Summary Report

Generated by dkNET on Apr 23, 2025

SignaLink

RRID:SCR_003569
Type: Tool

Proper Citation

SignaLink (RRID:SCR_003569)

Resource Information

URL: http://signalink.org/

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Description: An integrated resource to analyze signaling pathway cross-talks, transcription factors, miRNAs and regulatory enzymes. The multi-layered database structure is made up of signaling pathways, their pathway regulators (e.g., scaffold and endocytotic proteins) and modifier enzymes (e.g., phosphatases, ubiquitin ligases), as well as transcriptional and post-transcriptional regulators of all of these components. The website allows the interactive exploration of how each signaling protein is regulated. Features * experimental data not only from humans but from two invertebrate model organisms, C. elegans and D. melanogaster; * combines manual curation with large-scale datasets; * provides confidence scores for each interaction; * operates a customizable download page with multiple file formats (e.g., BioPAX, Cytoscape, SBML).

Abbreviations: SignaLink

Resource Type: database, data or information resource

Defining Citation: PMID:23331499, PMID:20542890

Keywords: analyze, signaling, pathway, cross-talk, transcription factor, mirna, regulatory enzyme, protein, interaction, regulatory network, signaling pathway, scaffold protein, enzyme, signaling, drug discovery, regulatory, network, post-transcriptional regulator, transcriptional regulator, protein-protein interaction, post-translational modification, pathway regulator, FASEB list

Funding:

Availability: Acknowledgement requested, Free for non-profit use

Resource Name: SignaLink

Resource ID: SCR_003569

Alternate IDs: nlx_157704

Record Creation Time: 20220129T080219+0000

Record Last Update: 20250423T060133+0000

Ratings and Alerts

No rating or validation information has been found for SignaLink.

No alerts have been found for SignaLink.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 55 mentions in open access literature.

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

Wright SN, et al. (2025) State of the interactomes: an evaluation of molecular networks for generating biological insights. Molecular systems biology, 21(1), 1.

Kim J, et al. (2025) Transcription factors and hormone receptors: Sex?specific targets for cancer therapy (Review). Oncology letters, 29(2), 93.

Kong C, et al. (2024) Transcriptomic Evidence Reveals the Dysfunctional Mechanism of Synaptic Plasticity Control in ASD. Genes, 16(1).

Taoma K, et al. (2024) Boolean modeling of breast cancer signaling pathways uncovers mechanisms of drug synergy. PloS one, 19(2), e0298788.

Iida M, et al. (2024) A network-based trans-omics approach for predicting synergistic drug combinations. Communications medicine, 4(1), 154.

Kumar S, et al. (2023) konnect2prot: a web application to explore the protein properties in a functional protein-protein interaction network. Bioinformatics (Oxford, England), 39(1).

Mo J, et al. (2023) Network medicine framework identified drug-repurposing opportunities of pharmaco-active compounds of Angelica acutiloba (Siebold & Zucc.) Kitag. for skin aging. Aging, 15(11), 5144.

Jennings P, et al. (2023) Capturing time-dependent activation of genes and stress-response pathways using transcriptomics in iPSC-derived renal proximal tubule cells. Cell biology and toxicology, 39(4), 1773.

Paul I, et al. (2023) Parallelized multidimensional analytic framework applied to mammary epithelial cells uncovers regulatory principles in EMT. Nature communications, 14(1), 688.

Hwang KW, et al. (2023) Unveiling the Molecular Landscape of FOXA1 Mutant Prostate Cancer: Insights and Prospects for Targeted Therapeutic Strategies. International journal of molecular sciences, 24(21).

Yun R, et al. (2023) N-linked glycosylation is essential for anti-tumor activities of KIAA1324 in gastric cancer. Cell death & disease, 14(8), 546.

Jaskiewicz K, et al. (2023) The Impaired Wound Healing Process Is a Major Factor in Remodeling of the Corneal Epithelium in Adult and Adolescent Patients With Keratoconus. Investigative ophthalmology & visual science, 64(2), 22.

Catozzi S, et al. (2022) Reconstruction and analysis of a large-scale binary Ras-effector signaling network. Cell communication and signaling : CCS, 20(1), 24.

Liu Z, et al. (2022) SLC4A4 promotes prostate cancer progression in vivo and in vitro via AKT-mediated signalling pathway. Cancer cell international, 22(1), 127.

ElHarouni D, et al. (2022) iTReX: Interactive exploration of mono- and combination therapy dose response profiling data. Pharmacological research, 175, 105996.

Csabai L, et al. (2022) SignaLink3: a multi-layered resource to uncover tissue-specific signaling networks. Nucleic acids research, 50(D1), D701.

Thomas JP, et al. (2021) Network Biology Approaches to Achieve Precision Medicine in Inflammatory Bowel Disease. Frontiers in genetics, 12, 760501.

Ravichandran S, et al. (2021) VB10, a new blood biomarker for differential diagnosis and recovery monitoring of acute viral and bacterial infections. EBioMedicine, 67, 103352.

Hou Y, et al. (2021) Multimodal single-cell omics analysis identifies epithelium-immune cell interactions and immune vulnerability associated with sex differences in COVID-19. Signal transduction and targeted therapy, 6(1), 292.

Ge Y, et al. (2021) An integrative drug repositioning framework discovered a potential therapeutic agent targeting COVID-19. Signal transduction and targeted therapy, 6(1), 165.