

Resource Summary Report

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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: data or information resource, database

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

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: 20260829T182922+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 59 mentions in open access literature.

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

An X, et al. (2025) Exploring the Regulatory Effect of Hydroxytyrosol on Ovarian Inflammation Through Autophagy-Targeted Mechanisms: A Bioinformatics Approach. *Nutrients*, 17(9).

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.

Song J, et al. (2025) DriverSub-SVM: a machine learning approach for cancer subtype classification by integrating patient-specific and global driver genes. *BMC bioinformatics*, 26(1), 297.

Taoma K, et al. (2025) Interpretable prediction of drug synergy for breast cancer by random forest with features from Boolean modeling of signaling pathways. *Scientific reports*, 15(1), 17735.

Kupsco A, et al. (2025) Newborn mitochondrial DNA copy number is associated with changes to DNA methylation that persist into childhood and are associated with cognitive development. *Clinical epigenetics*, 17(1), 112.

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.

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.

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).

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.