Resource Summary Report

Generated by <u>NIF</u> on May 4, 2025

SIGNOR

RRID:SCR_018485 Type: Tool

Proper Citation

SIGNOR (RRID:SCR_018485)

Resource Information

URL: https://signor.uniroma2.it/

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Description: Software application to organize and store in structured format signaling information published in scientific literature. Information is stored as binary causative relationships between biological entities and can be represented graphically as activity flow. Each relationship is linked to literature reporting experimental evidence. Each node is annotated with chemical inhibitors that modulate its activity. Signaling information is mapped to human proteome. SIGNOR 2.0 stores manually annotated causal relationships between proteins and other biologically relevant entities including chemicals, phenotypes, complexes, etc with compliance to FAIR data principles.

Synonyms: SIGnaling Network Open Resource, SIGNOR 2.0

Resource Type: database, storage service resource, data repository, service resource, data or information resource

Defining Citation: PMID:31665520

Keywords: Signal transduction data, signaling information, published data collection, activity flow, chemical inhibitor, human proteome, manually annotated data, protein, protein relationship, FAIR data, bio.tools

Funding: Italian Association for Cancer Research ; ELIXIR-IIB ; Italian Node of the European ELIXIR infrastructure ; EMBL-EBI Availability: Free, Available for download, Freely available

Resource Name: SIGNOR

Resource ID: SCR_018485

Alternate IDs: biotools:signor

Alternate URLs: https://bio.tools/signor

Record Creation Time: 20220129T080340+0000

Record Last Update: 20250503T060816+0000

Ratings and Alerts

No rating or validation information has been found for SIGNOR.

No alerts have been found for SIGNOR.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 30 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>NIF</u>.

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

Chen XY, et al. (2024) Integrative transcriptome-proteome approach reveals key hypoxiarelated features involved in the neuroprotective effects of Yang Xue oral liquid on Alzheimer's and Parkinson's disease. Frontiers in pharmacology, 15, 1411273.

Arora C, et al. (2024) The landscape of cancer-rewired GPCR signaling axes. Cell genomics, 4(5), 100557.

Liu X, et al. (2024) Activation of GPR81 by lactate drives tumour-induced cachexia. Nature metabolism, 6(4), 708.

Zeng X, et al. (2024) RNA demethylase FTO participates in malignant progression of gastric cancer by regulating SP1-AURKB-ATM pathway. Communications biology, 7(1), 800.

Latini S, et al. (2024) Unveiling the signaling network of FLT3-ITD AML improves drug sensitivity prediction. eLife, 12.

Doroodgar F, et al. (2024) Inflammatory and genomic interactions within keratoconus susceptible patients: a nationwide registered case-control study. Eye and vision (London, England), 11(1), 40.

Su Z, et al. (2024) Mutation patterns in colorectal cancer and their relationship with prognosis. Heliyon, 10(17), e36550.

Lo Surdo P, et al. (2023) SIGNOR 3.0, the SIGnaling network open resource 3.0: 2022 update. Nucleic acids research, 51(D1), D631.

Stefanucci L, et al. (2023) The effects of pathogenic and likely pathogenic variants for inherited hemostasis disorders in 140?214 UK Biobank participants. Blood, 142(24), 2055.

Pillich RT, et al. (2023) NDEx IQuery: a multi-method network gene set analysis leveraging the Network Data Exchange. Bioinformatics (Oxford, England), 39(3).

Hammad R, et al. (2023) Monocytes subsets altered distribution and dysregulated plasma hsa-miR-21-5p and hsa-miR-155-5p in HCV-linked liver cirrhosis progression to hepatocellular carcinoma. Journal of cancer research and clinical oncology, 149(17), 15349.

Schlüter A, et al. (2023) ClinPrior: an algorithm for diagnosis and novel gene discovery by network-based prioritization. Genome medicine, 15(1), 68.

Roberts KD, et al. (2022) A synthetic lipopeptide targeting top-priority multidrug-resistant Gram-negative pathogens. Nature communications, 13(1), 1625.

Fathima S, et al. (2022) Unraveling unique and common cell type-specific mechanisms in glioblastoma multiforme. Computational and structural biotechnology journal, 20, 90.

Chen X, et al. (2022) Integrative proteomic and phosphoproteomic profiling of invasive micropapillary breast carcinoma. Journal of proteomics, 257, 104511.

Wang LB, et al. (2021) Proteogenomic and metabolomic characterization of human glioblastoma. Cancer cell, 39(4), 509.

Levchenko A, et al. (2021) A genome-wide association study identifies a gene network associated with paranoid schizophrenia and antipsychotics-induced tardive dyskinesia. Progress in neuro-psychopharmacology & biological psychiatry, 105, 110134.

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

Palma A, et al. (2021) Integrating Patient-Specific Information into Logic Models of Complex Diseases: Application to Acute Myeloid Leukemia. Journal of personalized medicine, 11(2).