

Resource Summary Report

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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: service resource, data repository, data or information resource, database, storage service 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: 20260731T043035+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 40 mentions in open access literature.

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

Wu F, et al. (2025) TRIM13 prevents cardiomyocyte injury by affecting apoptosis through interacting with CD3D in myocardial infarction. iScience, 28(8), 113101.

Landowski M, et al. (2025) Mitochondrial fusion controls the development of specialized mitochondrial structure and metabolism in rod photoreceptor cells. bioRxiv : the preprint server for biology.

Alwadi D, et al. (2025) RNA-Seq Uncovers Association of Endocrine-Disrupting Chemicals with Hub Genes and Transcription Factors in Aggressive Prostate Cancer. International journal of molecular sciences, 26(12).

Jinesh GG, et al. (2025) FilaggrinHigh melanomas exhibit active FGFR and allergic signatures with impaired GNA14 and Th1 signatures. Frontiers in genetics, 16, 1569403.

Wawruszak A, et al. (2025) Selisistat, a SIRT1 inhibitor, enhances paclitaxel activity in luminal and triple-negative breast cancer: in silico, in vitro, and in vivo studies. Journal of enzyme inhibition and medicinal chemistry, 40(1), 2458554.

Liu D, et al. (2025) Polycystic ovary syndrome and epithelial-mesenchymal transition: Mendelian randomization and single-cell analysis insights. Journal of ovarian research, 18(1), 33.

Bourdakou MM, et al. (2025) Plasticity of Gene Expression in Spaceflight and Postflight in Relation to Cardiovascular Disease: Mechanisms and Candidate Repurposed Drugs.

Proteomics, 25(11-12), e202400241.

Xu X, et al. (2025) Suppression of SRC protein kinase activity alleviates the severity of aganglionosis by impairing CAV1/FLNA expression. *Science progress*, 108(2), 368504251336287.

Bravo JI, et al. (2025) A multi-omics analysis of human fibroblasts overexpressing an Alu transposon reveals widespread disruptions in aging-associated pathways. *bioRxiv : the preprint server for biology*.

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

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

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

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

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.

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

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

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.

Wager K, et al. (2024) Using bioinformatics and artificial intelligence to map the cyclin-dependent kinase 4/6 inhibitor biomarker landscape in breast cancer. *Future oncology (London, England)*, 20(40), 3519.

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.

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