

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: data or information resource, data repository, database, service resource, 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: ELIXIR-IIB ;
EMBL-EBI ;
Italian Association for Cancer Research ;
Italian Node of the European ELIXIR infrastructure

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: 20260912T200021+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 61 mentions in open access literature.

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

Jinesh G, et al. (2026) Pericentromeric Transcription of Novel Pathogen-Related Human GPS Genes in Cancers is Regulated by C19MC miRNAs, CEBPB, IFN- γ , and IFN- α . Research square.

Shu Y, et al. (2026) Integrated network pharmacology and comprehensive bioinformatics analysis to identify the mechanisms and molecular targets of ketamine in ischemic stroke-depression comorbidity. PloS one, 21(3), e0343918.

Peng X, et al. (2026) Integrated Phosphoproteomics Identifies TGF β -Dependent Phosphorylation Events Linking Kinase Signaling to Autophagy in Palatogenesis. Proteomes, 14(1).

Zhou X, et al. (2026) Stratified signaling network remodeling of kinase-transcription factors' interactions in Parkinson's disease. Bioinformatics advances, 6(1), vbag059.

Sanchez M, et al. (2026) Large scale compound selection guided by cell painting reveals activity cliffs and functional relationships. Communications biology, 9(1), 225.

Laman Trip DS, et al. (2026) A tissue-specific atlas of protein-protein associations enables prioritization of candidate disease genes. Nature biotechnology, 44(4), 654.

Lo Surdo P, et al. (2026) SIGNOR 4.0: the 2025 update with focus on phosphorylation data. Nucleic acids research, 54(D1), D682.

Fernandez KJ, et al. (2026) Endocrine therapy reprogramming of breast cancer facilitates metastatic escape via upregulation of P-Rex1/Rac1 signalling. *Nature communications*, 17(1).

Landowski M, et al. (2026) Mitofusins are required for specialized mitochondrial morphology and function of rod photoreceptor cells. *Frontiers in cell and developmental biology*, 14, 1724328.

Fatima N, et al. (2025) Profiling HIV1-host protein-protein interaction networks in patient-derived exosome proteins: impact on pathophysiology and innate immune pathways. *Virology journal*, 22(1), 259.

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

Zhang C, et al. (2025) Single-cell/spatial integration reveals an MES2-like glioblastoma program orchestrated by immune communication and regulatory networks. *Frontiers in immunology*, 16, 1699134.

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).

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.

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

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.

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.

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*.