

Resource Summary Report

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Network Data Exchange (NDEx)

RRID:SCR_003943

Type: Tool

Proper Citation

Network Data Exchange (NDEx) (RRID:SCR_003943)

Resource Information

URL: <http://www.ndexbio.org/>

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Description: Repository where scientists and organizations can share, store, manipulate, and publish biological network data. Users can also run their own copies of NDEx Server software in cases where stored networks must be kept in highly secure environment (such as for HIPAA compliance) or where high application load is incompatible with shared public resource. Open source software system that is part of Cytoscape family. Project of Cytoscape Consortium in conjunction with Ideker lab at UCSD School of Medicine. Public forum where biologists can exchange and publish computable network models in many types and formats. NDEx is based on REST web API which can be accessed by any application, including NDEx website and NDEx Cytoscape App. NDEx networks are assigned stable, globally unique URIs and so can be referenced by publications, by other networks, and by analytic applications.

Abbreviations: NDEx

Synonyms: ndex bio, NDEx, Network Data Exchange, UCSD NDEx, ndex biology, the Network Data Exchange

Resource Type: data or information resource, database

Defining Citation: [PMID:34570431](#), [PMID:28150243](#)

Keywords: network, pathway, network model, web service, FASEB list

Availability: Free, Freely available

Resource Name: Network Data Exchange (NDEx)

Resource ID: SCR_003943

Alternate IDs: nlx_158334, r3d100000028

Alternate URLs: <http://ndexbio.org/>, <http://www.home.ndexbio.org/disclaimer-license/>, <http://www.ndexbio.org/#/>, <https://api.datacite.org/doi?prefix=10.18119>, <https://doi.org/10.17616/R3PP4D>

Record Creation Time: 20220129T080221+0000

Record Last Update: 20260821T193724+0000

Ratings and Alerts

No rating or validation information has been found for Network Data Exchange (NDEx).

No alerts have been found for Network Data Exchange (NDEx).

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 87 mentions in open access literature.

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

van Beek D, et al. (2026) Beyond Single Variants: A Pathway-Based Approach to Explore the Genetic Basis of Memory. *Molecular neurobiology*, 63(1), 364.

Wright SN, et al. (2026) Common and rare genetic variants show network convergence for a majority of human traits. *EMBO reports*, 27(8), 1918.

Ono K, et al. (2025) Cytoscape Web: bringing network biology to the browser. *Nucleic acids research*, 53(W1), W203.

Sun G, et al. (2025) Identifying novel therapeutic targets in cystic fibrosis through advanced single-cell transcriptomics analysis. *Computers in biology and medicine*, 187, 109748.

Pio-Lopez L, et al. (2025) Universal multilayer network embedding reveals a causal link between GABA neurotransmitter and cancer. *BMC bioinformatics*, 26(1), 149.

Lenkiewicz J, et al. (2025) Cell Mapping Toolkit: an end-to-end pipeline for mapping subcellular organization. *Bioinformatics (Oxford, England)*, 41(6).

Yin X, et al. (2025) Global siRNA screen identifies human host factors critical for SARS-CoV-2 replication and late stages of infection. *PLoS biology*, 23(6), e3002738.

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

Wright SN, et al. (2025) Common and rare genetic variants show network convergence for a majority of human traits. medRxiv : the preprint server for health sciences.

Mei H, et al. (2025) Network analysis of multivariate time series data in biological systems: methods and applications. Briefings in bioinformatics, 26(3).

Lin E, et al. (2025) Gene clusters linked to insulin resistance identified in a genome-wide study of the Taiwan Biobank population. Nature communications, 16(1), 3525.

Espada CR, et al. (2025) Computational discovery of conserved RNA structures and functional characterization of a structured lncRNA in *Leishmania braziliensis*. Non-coding RNA research, 14, 51.

Avasthi KK, et al. (2025) Different plasma exosome isolation methods generated distinct microRNA and protein profiles in healthy controls and patients with advanced prostate and lung cancer. BMC cancer, 26(1), 160.

Wang B, et al. (2025) Rare coding mutations identify 36 large-effect risk genes in obsessive-compulsive disorder and chronic tic disorders. medRxiv : the preprint server for health sciences.

Schaffer LV, et al. (2025) Multimodal cell maps as a foundation for structural and functional genomics. Nature, 642(8066), 222.

Farías MA, et al. (2025) HSV-1 alters lipid metabolism and induces lipid droplet accumulation in functionally impaired mouse dendritic cells. iScience, 28(5), 112441.

Garibaldi-Ríos AF, et al. (2025) Genomic Landscape of Breast Cancer: Study Across Diverse Ethnic Groups. Diseases (Basel, Switzerland), 13(3).

Kübler K, et al. (2025) Tamoxifen induces PI3K activation in uterine cancer. Nature genetics, 57(9), 2192.

Shan L, et al. (2024) Statistical and network analyses reveal mechanisms for the enhancement of macrophage immunity by manganese in *Mycobacterium tuberculosis* infection. Biochemistry and biophysics reports, 37, 101602.

Yin X, et al. (2024) Global siRNA Screen Reveals Critical Human Host Factors of SARS-CoV-2 Multicycle Replication. bioRxiv : the preprint server for biology.