# Resource Summary Report

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# NetworkX

RRID:SCR_016864
Type: Tool

## Proper Citation

NetworkX (RRID:SCR_016864)

## Resource Information

**URL:** https://networkx.github.io/

**Proper Citation:** NetworkX (RRID:SCR_016864)

**Description:** Software Python package for the creation, manipulation, and study of the structure, dynamics, and functions of complex networks.

**Resource Type:** data processing software, software application, network analysis software, data analysis software, software resource

**Keywords:** create, analysis, structure, dynamic, function, complex, network, data

**Funding:**

**Availability:** Free, Available for download, Freely available

**Resource Name:** NetworkX

**Resource ID:** SCR_016864

**Alternate URLs:** https://github.com/networkx/networkx

**License:** 3-clause BSD license

**Record Creation Time:** 20220129T080332+0000

**Record Last Update:** 20250418T055459+0000

## Ratings and Alerts

No rating or validation information has been found for NetworkX.

No alerts have been found for NetworkX.

## Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 105 mentions in open access literature.

**Listed below are recent publications.** The full list is available at FDI Lab - SciCrunch.org.

Skorupka A, et al. (2024) Detecting anomalies in graph networks on digital markets. PloS one, 19(12), e0315849.

Wei L, et al. (2024) Systems-level reconstruction of kinase phosphosignaling networks regulating endothelial barrier integrity using temporal data. NPJ systems biology and applications, 10(1), 134.

Vishwanathan A, et al. (2024) Predicting modular functions and neural coding of behavior from a synaptic wiring diagram. Nature neuroscience, 27(12), 2443.

Nilsen AS, et al. (2024) Exploring effects of anesthesia on complexity, differentiation, and integrated information in rat EEG. Neuroscience of consciousness, 2024(1), niae021.

Wei L, et al. (2024) Systems-level reconstruction of kinase phosphosignaling networks regulating endothelial barrier integrity using temporal data. bioRxiv : the preprint server for biology.

Sadowski M, et al. (2024) Characterizing the genetic architecture of drug response using gene-context interaction methods. Cell genomics, 4(12), 100722.

Brempou D, et al. (2024) Using parenclitic networks on phaeochromocytoma and paraganglioma tumours provides novel insights on global DNA methylation. Scientific reports, 14(1), 29958.

Köhler CA, et al. (2024) Facilitating the Sharing of Electrophysiology Data Analysis Results Through In-Depth Provenance Capture. eNeuro, 11(6).

Wei L, et al. (2024) Using machine learning to dissect host kinases required for Leishmania internalization and development. bioRxiv : the preprint server for biology.

Xie X, et al. (2024) IL-1?-induced epithelial cell and fibroblast transdifferentiation promotes neutrophil recruitment in chronic rhinosinusitis with nasal polyps. Nature communications, 15(1), 9101.

Newsham I, et al. (2024) Early detection and diagnosis of cancer with interpretable machine learning to uncover cancer-specific DNA methylation patterns. Biology methods & protocols, 9(1), bpae028.

Gupta M, et al. (2023) Critical mechanistic features of HIV-1 viral capsid assembly. Science advances, 9(1), eadd7434.

Fan P, et al. (2023) Combination of antidepressants and antipsychotics as a novel treatment option for psychosis in Alzheimer's disease. CPT: pharmacometrics & systems pharmacology, 12(8), 1119.

Lu M, et al. (2023) Effect of intracranial electrical stimulation on dynamic functional connectivity in medically refractory epilepsy. Frontiers in human neuroscience, 17, 1295326.

Nanda P, et al. (2023) Multicellular growth as a dynamic network of cells. bioRxiv : the preprint server for biology.

Wu CG, et al. (2023) Extended regulation interface coupled to the allosteric network and disease mutations in the PP2A-B56? holoenzyme. bioRxiv : the preprint server for biology.

Wright SN, et al. (2023) Genome-wide association studies of human and rat BMI converge on synapse, epigenome, and hormone signaling networks. Cell reports, 42(8), 112873.

Iranzo J, et al. (2023) Protocol for comparing gene-level selection on coding mutations between two groups of samples with Coselens. STAR protocols, 4(1), 102117.

Collier M, et al. (2022) Pathogen transmission modes determine contact network structure, altering other pathogen characteristics. Proceedings. Biological sciences, 289(1989), 20221389.

Domingo-Fernández D, et al. (2022) Causal reasoning over knowledge graphs leveraging drug-perturbed and disease-specific transcriptomic signatures for drug discovery. PLoS computational biology, 18(2), e1009909.