

# 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 analysis software, data processing software, network analysis software, software application, software resource

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

**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:** 20260905T132814+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

## Usage and Citation Metrics

We found 132 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [PRECISE-TBI](#) .

Robson JM, et al. (2026) Toehold-VISTA: a machine learning approach to decipher programmable RNA sensor-target interactions. *Nucleic acids research*, 54(4).

Yu Q, et al. (2026) Diversity and evolution of a phase-variable multi-locus antigen in *Neisseria gonorrhoeae*. *bioRxiv : the preprint server for biology*.

Saito N, et al. (2026) Kuroshio Corridor: larval dispersal networks explain geographically independent connectivity among coral habitats in Japan. *Scientific reports*, 16(1).

Bacong JRC, et al. (2026) NOVAGene: a nonlinear approach to improve biological resolution in weighted gene co-expression networks for low-variability datasets. *Frontiers in bioinformatics*, 6, 1813626.

Ding W, et al. (2026) A Multimodal Single-Cell Epigenomic and 3D Genome Atlas of the Human Basal Ganglia. *bioRxiv : the preprint server for biology*.

Yu Q, et al. (2026) Diversity and evolution of a phase-variable multi-locus antigen in *Neisseria gonorrhoeae*. *PLoS pathogens*, 22(5), e1013962.

Ishiguro S, et al. (2026) A multi-kingdom genetic barcoding system for precise clone isolation. *Nature biotechnology*, 44(4), 616.

Ryu S, et al. (2026) Transcriptional regulation of neuropeptide receptors underlies context-dependent adaptation in *Drosophila melanogaster*. *FEBS open bio*, 16(1), 90.

Pendyala S, et al. (2026) Image-based, pooled phenotyping reveals multidimensional, disease-specific variant effects. *Cell*, 189(13), 4040.

Ceballos C, et al. (2026) The *Drosophila* connectome reveals axo-axonic synapses on descending neurons. *iScience*, 29(5), 115624.

Dos Santos Corrêa M, et al. (2026) Neuronal networks in the dorsal hippocampus causally regulate rescue behavior in mice. *Cell reports*, 45(2), 116923.

Caldarelli M, et al. (2026) Pupillometry and brain-wide c-Fos mapping uncover multimodal mirror emotional contagion related networks of mice. *iScience*, 29(2), 114827.

Robson JM, et al. (2025) Toehold-VISTA: A machine learning approach to decipher programmable RNA sensor-target interactions. *bioRxiv : the preprint server for biology*.

Zhai J, et al. (2025) Differential brain activation and network connectivity in social interactions presence and absence of physical contact. *Communications biology*, 8(1), 986.

Villette R, et al. (2025) Human gut microbiome gene co-expression network reveals a loss in taxonomic and functional diversity in Parkinson's disease. NPJ biofilms and microbiomes, 11(1), 142.

Villette R, et al. (2025) Integrated multi-omics highlights alterations of gut microbiome functions in prodromal and idiopathic Parkinson's disease. Microbiome, 13(1), 200.

Kennard AS, et al. (2025) Tubulin sequence divergence is associated with the use of distinct microtubule regulators. Current biology : CB, 35(2), 233.

Xue HC, et al. (2025) A unified cell atlas of vascular plants reveals cell-type foundational genes and accelerates gene discovery. Cell.

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.