

# Resource Summary Report

Generated by [RRID](#) on Aug 8, 2026

## GraphML

RRID:SCR\_003545

Type: Tool

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### Proper Citation

GraphML (RRID:SCR\_003545)

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### Resource Information

**URL:** <http://graphml.graphdrawing.org/>

**Proper Citation:** GraphML (RRID:SCR\_003545)

**Description:** A file format for graphs that consists of a language core to describe the structural properties of a graph and a flexible extension mechanism to add application-specific data. It is based on XML and is ideally suited as a common denominator for all kinds of services generating, archiving, or processing graphs. Its main features include support of \* directed, undirected, and mixed graphs, \* hypergraphs, \* hierarchical graphs, \* graphical representations, \* references to external data, \* application-specific attribute data, and \* light-weight parsers.

**Abbreviations:** GraphML

**Synonyms:** The GraphML File Format

**Resource Type:** data or information resource, standard specification, narrative resource, markup language, interchange format

**Keywords:** xml, graph

**Availability:** Creative Commons Attribution License, v3

**Resource Name:** GraphML

**Resource ID:** SCR\_003545

**Alternate IDs:** nlx\_157666

**Record Creation Time:** 20220129T080219+0000

**Record Last Update:** 20260808T185800+0000

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### Ratings and Alerts

No rating or validation information has been found for GraphML.

No alerts have been found for GraphML.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Handke N, et al. (2025) TRAMbio: a flexible python package for graph rigidity analysis of macromolecules. BMC bioinformatics, 26(1), 266.

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

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

Gao M, et al. (2023) EasyGraph: A multifunctional, cross-platform, and effective library for interdisciplinary network analysis. Patterns (New York, N.Y.), 4(10), 100839.

Tomaszuk D, et al. (2023) MMLKG: Knowledge Graph for Mathematical Definitions, Statements and Proofs. Scientific data, 10(1), 791.

Patelli A, et al. (2022) Integrated database for economic complexity. Scientific data, 9(1), 628.

Balaur I, et al. (2022) GraphML-SBGN bidirectional converter for metabolic networks. Journal of integrative bioinformatics, 19(4).

Calle E, et al. (2021) Optimal selection of monitoring sites in cities for SARS-CoV-2 surveillance in sewage networks. Environment international, 157, 106768.

Rudolph JD, et al. (2019) A Network Module for the Perseus Software for Computational Proteomics Facilitates Proteome Interaction Graph Analysis. Journal of proteome research, 18(5), 2052.

Aryani A, et al. (2018) A Research Graph dataset for connecting research data repositories using RD-Switchboard. Scientific data, 5, 180099.

Rodríguez-García MÁ, et al. (2018) Inferring ontology graph structures using OWL reasoning. BMC bioinformatics, 19(1), 7.

Tomaszuk D, et al. (2018) Reducing vertices in property graphs. PloS one, 13(2), e0191917.

Hume S, et al. (2017) Visualizing and Validating Metadata Traceability within the CDISC Standards. AMIA Joint Summits on Translational Science proceedings. AMIA Joint Summits on Translational Science, 2017, 158.

Scharm M, et al. (2016) An algorithm to detect and communicate the differences in computational models describing biological systems. Bioinformatics (Oxford, England), 32(4), 563.

Wang R, et al. (2014) Network-based analysis of software change propagation. TheScientificWorldJournal, 2014, 237243.