

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 8, 2026

GraphClust2

RRID:SCR_017286

Type: Tool

Proper Citation

GraphClust2 (RRID:SCR_017286)

Resource Information

URL: <https://github.com/BackofenLab/GraphClust-2>

Proper Citation: GraphClust2 (RRID:SCR_017286)

Description: Software tool for scalable clustering of RNAs based on sequence and secondary structures similarities. Implemented within Galaxy framework. Used for studying RNA function.

Synonyms: GraphClust, GraphClust-2

Resource Type: data analysis software, data processing software, software application, software resource, web application

Defining Citation: [PMID:31808801](#), [PMID:22689765](#)

Keywords: scalable, clustering, RNA, sequence, secondary, structure, function, bio.tools

Funding: German Federal Ministry of Education and Research ;
German Research Foundation Collaborative Research Centre 992 Medical Epigenetics

Availability: Free, Available for download, Freely available

Resource Name: GraphClust2

Resource ID: SCR_017286

Alternate IDs: biotools:GraphClust2

Alternate URLs: <https://bio.tools/GraphClust2>

License: GNU GPL v3

Record Creation Time: 20220129T080334+0000

Record Last Update: 20260905T132822+0000

Ratings and Alerts

No rating or validation information has been found for GraphClust2.

No alerts have been found for GraphClust2.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Ram-Mohan N, et al. (2020) Comparative Metatranscriptomics of Periodontitis Supports a Common Polymicrobial Shift in Metabolic Function and Identifies Novel Putative Disease-Associated ncRNAs. *Frontiers in microbiology*, 11, 482.

Buongermino Pereira M, et al. (2020) A comprehensive survey of integron-associated genes present in metagenomes. *BMC genomics*, 21(1), 495.

Miladi M, et al. (2019) GraphClust2: Annotation and discovery of structured RNAs with scalable and accessible integrative clustering. *GigaScience*, 8(12).

Middleton SA, et al. (2014) NoFold: RNA structure clustering without folding or alignment. *RNA (New York, N.Y.)*, 20(11), 1671.