

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 19, 2026

Traph

RRID:SCR_005119

Type: Tool

Proper Citation

Traph (RRID:SCR_005119)

Resource Information

URL: <http://www.cs.helsinki.fi/en/gsa/traph/>

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Description: A software tool for transcript identification and quantification with RNA-Seq. The method has a two-fold advantage: on the one hand, it translates the problem as an established one in the field of network flows, which can be solved in polynomial time, with different existing solvers; on the other hand, it is general enough to encompass many of the previous proposals under the least sum of squares model.

Abbreviations: Traph

Synonyms: Transcripts in gRAPHS - Traph: A tool for transcript identification and quantification with RNA-Seq, Transcripts in gRAPHS

Resource Type: software resource

Defining Citation: [PMID:23734627](#)

Availability: Acknowledgement requested

Resource Name: Traph

Resource ID: SCR_005119

Alternate IDs: OMICS_01295

Record Creation Time: 20220129T080228+0000

Record Last Update: 20260919T195048+0000

Ratings and Alerts

No rating or validation information has been found for Traph.

No alerts have been found for Traph.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Tung LH, et al. (2019) Quantifying the benefit offered by transcript assembly with Scallop-LR on single-molecule long reads. Genome biology, 20(1), 287.

Gatter T, et al. (2019) Ry?t?: network-flow based transcriptome reconstruction. BMC bioinformatics, 20(1), 190.

Canzar S, et al. (2016) CIDANE: comprehensive isoform discovery and abundance estimation. Genome biology, 17, 16.