

# Resource Summary Report

Generated by [NIF](#) on Aug 20, 2026

## Traph

RRID:SCR\_005119

Type: Tool

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### Proper Citation

Traph (RRID:SCR\_005119)

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### Resource Information

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

**Proper Citation:** Traph (RRID:SCR\_005119)

**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:** 20260815T182308+0000

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### Ratings and Alerts

No rating or validation information has been found for Traph.

No alerts have been found for Traph.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 3 mentions in open access literature.

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

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.