

Resource Summary Report

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TransRate

RRID:SCR_017034

Type: Tool

Proper Citation

TransRate (RRID:SCR_017034)

Resource Information

URL: <http://hibberdlab.com/transrate/>

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Description: Open source software tool for de novo transcriptome assembly reference free quality analysis. Used to examine assembly in detail and compare it to sequencing reads, reporting quality scores for contigs and assemblies to allow to choose between assemblers and parameters, filter out bad contigs from an assembly, and help decide when to stop trying to improve assembly.

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

Defining Citation: [PMID:27252236](#)

Keywords: de novo, transcriptome, assembly, reference, free, quality, analysis, sequencing, read, contig, parameter

Funding: BBSRC ;
Bill & Melinda Gates Foundation ;
European Union Horizon 2020 research and innovation program ;
Millennium Seed Bank ;
Royal Society University Research

Availability: Free, Available for download, Freely available

Resource Name: TransRate

Resource ID: SCR_017034

Alternate URLs: <https://github.com/Blahah/transrate>

License: MIT

Record Creation Time: 20220129T080333+0000

Record Last Update: 20260912T195847+0000

Ratings and Alerts

No rating or validation information has been found for TransRate.

No alerts have been found for TransRate.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 51 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Wu G, et al. (2026) Physiological and transcriptome analyses for revealing the mechanism of adventitious root formation in *Camellia luteoflora*. *BMC plant biology*, 26(1).

Xue H, et al. (2025) Comparative Transcriptomics of Olfactory Rosettes Reveals Expression Divergence and Adaptive Evolution in Herbivorous and Carnivorous Xenocyprididae Fishes. *Animals : an open access journal from MDPI*, 15(18).

Zhi L, et al. (2025) Metabolic Remodeling of the Tricarboxylic Acid Cycle and Glycolysis Reveals Cold-Induced Respiratory Adaptations in *Streltzoviella insularis* (Staudinger) (Lepidoptera: Cossidae) Larvae. *Insects*, 16(8).

Wu F, et al. (2025) Transcriptional analysis of *Camellia Huana* under low-phosphorus stress. *Scientific reports*, 15(1), 15796.

Chen X, et al. (2025) Elucidating the Molecular Basis of Thermal Stress Response in Juvenile Turbot (*Scophthalmus maximus*) via an Integrative Transcriptome-Metabolome Approach. *Biology*, 14(10).

Liu Z, et al. (2025) Physiological and transcriptomic analyses revealed the alleviating effects of exogenous Ca²⁺ and NO compound treatment on high salt stress in *Reaumuria soongorica*. *BMC genomics*, 26(1), 179.

Chen L, et al. (2025) Transcriptome Analysis of Potential Genes Involved in Innate Immunity in Mudflat Crab (*Helice tientsinensis*). *Animals : an open access journal from MDPI*, 15(19).

Peng Z, et al. (2025) Integrated physiological, biochemical, and transcriptomic analysis of the cold-sensitive response in *Mussaenda anomala*. *BMC genomics*, 26(1), 1023.

- Zhao X, et al. (2025) Interaction of host gene-gut microbiota in male grading of *Macrobrachium rosenbergii*. *Microbiology spectrum*, 13(10), e0129025.
- Feng L, et al. (2025) Functional characterization of PcMYB25, a candidate regulator of Patchouli alcohol biosynthesis in *Pogostemon cablin*, via exogenous hormone-elicited transcriptome analysis. *BMC plant biology*, 25(1), 1538.
- Li L, et al. (2024) Effects of supplementary light treatment on saffron: integrated physiological, metabolomic, and transcriptome analyses. *BMC plant biology*, 24(1), 1247.
- Zhong M, et al. (2024) Integrative analyses of the transcriptome and metabolome reveal comprehensive mechanisms of monolignol biosynthesis in response to bioclimatic factors in *Magnolia officinalis*. *BMC plant biology*, 24(1), 1210.
- Long X, et al. (2024) Photoheterotroph improved the growth and nutrient levels of *Chlorella vulgaris* and the related molecular mechanism. *Applied microbiology and biotechnology*, 108(1), 269.
- Lv X, et al. (2024) Gut commensal *Agathobacter rectalis* alleviates microglia-mediated neuroinflammation against pathogenesis of Alzheimer disease. *iScience*, 27(11), 111116.
- Niu J, et al. (2024) Integration of Transcriptomics and WGCNA to Characterize *Trichoderma harzianum*-Induced Systemic Resistance in *Astragalus mongholicus* for Defense against *Fusarium solani*. *Genes*, 15(9).
- Liu MJ, et al. (2023) Transcriptomics Reveal the Effects of Breeding Temperature on Growth and Metabolism in the Early Developmental Stage of *Platax teira*. *Biology*, 12(9).
- Shen C, et al. (2023) Integration of Transcriptomics and Proteomics Analysis Reveals the Molecular Mechanism of *Eriocheir sinensis* Gills Exposed to Heat Stress. *Antioxidants* (Basel, Switzerland), 12(12).
- Cai Y, et al. (2023) Long-Term *Phellodendri* Cortex Supplementation in the Tiger Grouper (*Epinephelus fuscoguttatus*): Dual Effects on Intestinal Health Revealed by Transcriptome Analysis. *Life* (Basel, Switzerland), 13(12).
- Wu N, et al. (2023) PPAR Signaling Maintains Metabolic Homeostasis under Hypothermia in Freshwater Drum (*Aplodinotus grunniens*). *Metabolites*, 13(1).
- Jiao J, et al. (2023) Identification and expression profile analysis of chemosensory genes in pine needle gall midge, *Thecodiplosis japonensis* (Diptera: Cecidomyiidae). *Frontiers in physiology*, 14, 1123479.