

# Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

## EULER-SR

RRID:SCR\_010485

Type: Tool

### Proper Citation

EULER-SR (RRID:SCR\_010485)

### Resource Information

**URL:** <http://cseweb.ucsd.edu/~ppevzner/software.html#EULER-short>

**Proper Citation:** EULER-SR (RRID:SCR\_010485)

**Description:** Assembly package that contains a suite of software programs for correcting errors in short reads and assembling them. The assembler may take as input classical Sanger reads, 454 sequences, and Illumina reads.

**Abbreviations:** EULER-SR

**Synonyms:** EULER: short reads assembler

**Resource Type:** software resource

**Defining Citation:** [PMID:18083777](#), [DOI:10.1101/gr.7088808](#)

**Keywords:** fragment assembly, short read, read

**Resource Name:** EULER-SR

**Resource ID:** SCR\_010485

**Alternate IDs:** OMICS\_00015

**Old URLs:** <http://ngslib.i-med.ac.at/node/64>, <https://sources.debian.org/src/euler-sr/>

**Record Creation Time:** 20220129T080259+0000

**Record Last Update:** 20260905T132642+0000

### Ratings and Alerts

No rating or validation information has been found for EULER-SR.

No alerts have been found for EULER-SR.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 17 mentions in open access literature.

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

Seoane P, et al. (2018) TransFlow: a modular framework for assembling and assessing accurate de novo transcriptomes in non-model organisms. BMC bioinformatics, 19(Suppl 14), 416.

Jimenez-Lopez JC, et al. (2016) Identification and Assessment of the Potential Allergenicity of 7S Vicilins in Olive (*Olea europaea* L.) Seeds. BioMed research international, 2016, 4946872.

Benzekri H, et al. (2014) De novo assembly, characterization and functional annotation of Senegalese sole (*Solea senegalensis*) and common sole (*Solea solea*) transcriptomes: integration in a database and design of a microarray. BMC genomics, 15(1), 952.

Doroghazi JR, et al. (2014) A roadmap for natural product discovery based on large-scale genomics and metabolomics. Nature chemical biology, 10(11), 963.

Chen K, et al. (2014) TIGRA: a targeted iterative graph routing assembler for breakpoint assembly. Genome research, 24(2), 310.

Yadav NK, et al. (2014) Next generation sequencing: potential and application in drug discovery. TheScientificWorldJournal, 2014, 802437.

Uchiyama K, et al. (2013) Development of 32 EST-SSR markers for *Abies firma* (Pinaceae) and their transferability to related species. Applications in plant sciences, 1(2).

Ueno S, et al. (2012) A second generation framework for the analysis of microsatellites in expressed sequence tags and the development of EST-SSR markers for a conifer, *Cryptomeria japonica*. BMC genomics, 13, 136.

Ren X, et al. (2012) Evaluating de Bruijn graph assemblers on 454 transcriptomic data. PloS one, 7(12), e51188.

Ronen R, et al. (2012) SEQuel: improving the accuracy of genome assemblies. Bioinformatics (Oxford, England), 28(12), i188.

Barrero RA, et al. (2011) De novo assembly of *Euphorbia fischeriana* root transcriptome identifies prostratin pathway related genes. BMC genomics, 12, 600.

Hu H, et al. (2011) Characterization of the *Conus bullatus* genome and its venom-duct transcriptome. BMC genomics, 12, 60.

Meriaux C, et al. (2011) Multiple changes in peptide and lipid expression associated with regeneration in the nervous system of the medicinal leech. *PloS one*, 6(4), e18359.

Kuroda M, et al. (2010) Characterization of quasispecies of pandemic 2009 influenza A virus (A/H1N1/2009) by de novo sequencing using a next-generation DNA sequencer. *PloS one*, 5(4), e10256.

Nagarajan H, et al. (2010) De Novo assembly of the complete genome of an enhanced electricity-producing variant of *Geobacter sulfurreducens* using only short reads. *PloS one*, 5(6), e10922.

Sirota-Madi A, et al. (2010) Genome sequence of the pattern forming *Paenibacillus vortex* bacterium reveals potential for thriving in complex environments. *BMC genomics*, 11, 710.

Ueno S, et al. (2010) Bioinformatic analysis of ESTs collected by Sanger and pyrosequencing methods for a keystone forest tree species: oak. *BMC genomics*, 11, 650.