

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 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: 20260725T190659+0000

Ratings and Alerts

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

No alerts have been found for EULER-SR.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 17 mentions in open access literature.

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

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.

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

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

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.

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.

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.

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.