

Resource Summary Report

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Edena v3

RRID:SCR_013065

Type: Tool

Proper Citation

Edena v3 (RRID:SCR_013065)

Resource Information

URL: <http://www.genomic.ch/edena.php>

Proper Citation: Edena v3 (RRID:SCR_013065)

Description: Software providing a method that automatically determines suited overlaps cutoffs according to the contextual coverage, reducing thus the need for manual parameterization.

Abbreviations: Edena v3

Synonyms: Edena v3: de novo short reads assembler

Resource Type: software resource

Defining Citation: [PMID:24130309](#)

Availability: Commercial license, Free

Resource Name: Edena v3

Resource ID: SCR_013065

Alternate IDs: OMICS_00014

Record Creation Time: 20220129T080314+0000

Record Last Update: 20260725T190747+0000

Ratings and Alerts

No rating or validation information has been found for Edena v3.

No alerts have been found for Edena v3.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Mueller L, et al. (2017) One Year Genome Evolution of Lausannevirus in Allopatric versus Sympatric Conditions. *Genome biology and evolution*, 9(6), 1432.

Aung HL, et al. (2016) Draft Genome Sequences of Two Drug-Resistant *Mycobacterium tuberculosis* Isolates from Myanmar. *Genome announcements*, 4(5).

Yan L, et al. (2015) Analyses of the complete genome and gene expression of chloroplast of sweet potato [*Ipomoea batata*]. *PloS one*, 10(4), e0124083.

He B, et al. (2015) Optimal assembly strategies of transcriptome related to ploidies of eukaryotic organisms. *BMC genomics*, 16(1), 65.

Rodrigues FA, et al. (2012) Subtractive libraries for prospecting differentially expressed genes in the soybean under water deficit. *Genetics and molecular biology*, 35(1 (suppl)), 304.

Gui J, et al. (2011) Recent advances in molecular technologies and their application in pathogen detection in foods with particular reference to *Yersinia*. *Journal of pathogens*, 2011, 310135.

Narzisi G, et al. (2011) Comparing de novo genome assembly: the long and short of it. *PloS one*, 6(4), e19175.

Otero JM, et al. (2010) Whole genome sequencing of *Saccharomyces cerevisiae*: from genotype to phenotype for improved metabolic engineering applications. *BMC genomics*, 11, 723.

Davis BM, et al. (2009) High-throughput sequencing reveals suppressors of *Vibrio cholerae* *rpoE* mutations: one fewer porin is enough. *Nucleic acids research*, 37(17), 5757.