

# Resource Summary Report

Generated by [SPARC SAWG](#) on Jul 28, 2026

## 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 [SPARC SAWG](#) .

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.