

Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

[Assemblytics](#)

RRID:SCR_023967

Type: Tool

Proper Citation

Assemblytics (RRID:SCR_023967)

Resource Information

URL: <http://assemblytics.com/>

Proper Citation: Assemblytics (RRID:SCR_023967)

Description: Web analytics tool for detection of variants from assembly. Used to detect and analyze structural variants from genome assembly by comparing it to reference genome.

Synonyms: assemblytics

Resource Type: software resource, data access protocol, web service

Defining Citation: [PMID:27318204](#)

Keywords: structural variants, genome assembly, detection of variants, variant assembly, assembly analysis, reference genome comparison,

Availability: Free, Available for download, Freely available

Resource Name: Assemblytics

Resource ID: SCR_023967

Alternate IDs: OMICS_11402

Alternate URLs: <https://sources.debian.org/src/assemblytics/>,
<https://github.com/marianattestad/assemblytics>

License: MIT license

Record Creation Time: 20230824T050210+0000

Record Last Update: 20260801T190824+0000

Ratings and Alerts

No rating or validation information has been found for Assemblytics.

No alerts have been found for Assemblytics.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Hu M, et al. (2025) Benchmarking, detection, and genotyping of structural variants in a population of whole-genome assemblies using the SVGAP pipeline. bioRxiv : the preprint server for biology.

Hu M, et al. (2025) Accurate, Scalable Structural Variant Genotyping in Complex Genomes at Population Scales. Molecular biology and evolution, 42(8).

Miao H, et al. (2024) Genomic evolution and insights into agronomic trait innovations of Sesamum species. Plant communications, 5(1), 100729.

Zhang H, et al. (2024) A Haplotype-resolved, Chromosome-scale Genome for Malus domestica Borkh. 'WA 38'. G3 (Bethesda, Md.), 14(12).

Kong Q, et al. (2024) Biparental graph strategy to represent and analyze hybrid plant genomes. Plant physiology, 196(2), 1284.

Hu J, et al. (2024) Transposable elements cause the loss of self-incompatibility in citrus. Plant biotechnology journal, 22(5), 1113.

Toh H, et al. (2022) A haplotype-resolved genome assembly of the Nile rat facilitates exploration of the genetic basis of diabetes. BMC biology, 20(1), 245.