

# Resource Summary Report

Generated by [dkNET](#) on Aug 12, 2026

## Assemblytics

RRID:SCR\_023967

Type: Tool

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### Proper Citation

Assemblytics (RRID:SCR\_023967)

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### 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:** web service, software resource, data access protocol

**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:** 20260812T044431+0000

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### Ratings and Alerts

No rating or validation information has been found for Assemblytics.

No alerts have been found for Assemblytics.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Jiang K, et al. (2026) Macrolide resistance trajectories across three *Bordetella pertussis* genetic backgrounds under stepwise erythromycin exposure. *Frontiers in microbiology*, 17, 1803864.

Pawar PY, et al. (2026) De novo genome assemblies of threatened Asian hornbills (*Bucerotidae*) reveal declining population trajectories during the late Pleistocene. *BMC ecology and evolution*, 26(1).

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.

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

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

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.

Oresegun DR, et al. (2022) De Novo Assembly of *Plasmodium knowlesi* Genomes From Clinical Samples Explains the Counterintuitive Intrachromosomal Organization of Variant SICavar and kir Multiple Gene Family Members. *Frontiers in genetics*, 13, 855052.