

# Resource Summary Report

Generated by T1D on Sep 19, 2026

## GenoViewer

RRID:SCR\_001203

Type: Tool

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### Proper Citation

GenoViewer (RRID:SCR\_001203)

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### Resource Information

**URL:** <http://www.genoviewer.com/>

**Proper Citation:** GenoViewer (RRID:SCR\_001203)

**Description:** THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 23,2022. Open source viewer / browser software for the SAM / BAM format commonly used in the assembly tasks of Next Generation Sequencing data.

**Abbreviations:** GenoViewer

**Resource Type:** software resource

**Defining Citation:** [PMID:22359445](https://pubmed.ncbi.nlm.nih.gov/22359445/)

**Keywords:** next-generation sequencing, sequence, mutation, windows, linux, mac os x, genome, browser, sam, bam, fasta, gff, read error, snp, mnp, insertion, deletion

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** GenoViewer

**Resource ID:** SCR\_001203

**Alternate IDs:** OMICS\_02146

**Alternate URLs:** <https://github.com/astrid/GenoViewer>

**Record Creation Time:** 20220129T080206+0000

**Record Last Update:** 20260919T194936+0000

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### Ratings and Alerts

No rating or validation information has been found for GenoViewer.

No alerts have been found for GenoViewer.

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## Data and Source Information

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

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## Usage and Citation Metrics

We have not found any literature mentions for this resource.