

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 8, 2026

Stanford SCG Bioinformatics Cluster

RRID:SCR_026876

Type: Tool

Proper Citation

Stanford SCG Bioinformatics Cluster (RRID:SCR_026876)

Resource Information

URL: <https://login.scg.stanford.edu>

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Description: High-performance computing facility. Its resources have been designed to support labs engaged in genetics and bioinformatics research, but are open to anyone on campus. The Stanford SCG Bioinformatics Cluster is optimized to support large memory, single-node threaded applications as well as applications and workflows that require many small files.

Abbreviations: SCG

Synonyms: SCG Cluster, Stanford University SCG Cluster, Stanford Genomics cluster, Stanford SCG Informatics Cluster

Resource Type: computational service resource

Keywords: high-performance computing, support large memory, single-node threaded applications

Availability: Restricted

Resource Name: Stanford SCG Bioinformatics Cluster

Resource ID: SCR_026876

Old URLs: <https://scg.stanford.edu>, <https://med.stanford.edu/gbsc/services/scg-cluster/scg-cluster.html>

Record Creation Time: 20250501T080713+0000

Record Last Update: 20260905T133533+0000

Ratings and Alerts

No rating or validation information has been found for Stanford SCG Bioinformatics Cluster.

No alerts have been found for Stanford SCG Bioinformatics Cluster.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Dupzyk AJ, et al. (2026) Dissecting the host determinants of orthoflavivirus infection using QIC-seq. PLoS pathogens, 22(6), e1014279.