

Resource Summary Report

Generated by SPARC SAWG on Jul 31, 2026

G-Anchor

RRID:SCR_016046

Type: Tool

Proper Citation

G-Anchor (RRID:SCR_016046)

Resource Information

URL: <https://github.com/vasilislenis/G-Anchor>

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Description: Software for comparing large genomes and exploiting highly conserved sequences as evolutionary-stable "anchors". The pipeline maps a newly sequenced genome (assembled in scaffolds) on a reference genome without the need of a supercomputer.

Abbreviations: G-Anchor

Synonyms: G-Anchor: A novel approach for cross-species comparison

Resource Type: data processing software, sequence analysis software, data analysis software, software resource, image analysis software, alignment software, software application

Keywords: anchor, comparison, scaffold, whole genome, alignment, sequence, mapping, anchoring, highly conserved elements, hce, evolution

Funding: HPC Wales ;
Biotechnology and Biological Sciences Research Council BB/J010170/1

Availability: Free, Available for download

Resource Name: G-Anchor

Resource ID: SCR_016046

License: MIT License

Record Creation Time: 20220129T080328+0000

Record Last Update: 20260731T042950+0000

Ratings and Alerts

No rating or validation information has been found for G-Anchor.

No alerts have been found for G-Anchor.

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 [SPARC SAWG](#) .

Lenis VPE, et al. (2018) G-Anchor: a novel approach for whole-genome comparative mapping utilizing evolutionary conserved DNA sequences. GigaScience, 7(5).