

Resource Summary Report

Generated by [kravitz2](#) on Sep 4, 2026

[halSynteny](#)

RRID:SCR_018127

Type: Tool

Proper Citation

halSynteny (RRID:SCR_018127)

Resource Information

URL: <https://github.com/ComparativeGenomicsToolkit/hal/tree/master/synteny>

Proper Citation: halSynteny (RRID:SCR_018127)

Description: Software tool as conserved synteny block construction method for multiple whole-genome alignments. Implementation of DAG-based for reconstruction of synteny blocks from genome alignment.

Synonyms: Hierarchical Alignment Format Synteny

Resource Type: data processing software, software application, software resource

Keywords: Conserved synteny, block construction method, genome alignment, DAG based reconstruction, synteny block, chromosome, bio.tools

Availability: Free, Freely available

Resource Name: halSynteny

Resource ID: SCR_018127

Alternate IDs: biotools:halSynteny

Alternate URLs: <https://bio.tools/halSynteny>

Record Creation Time: 20220129T080338+0000

Record Last Update: 20260903T235959+0000

Ratings and Alerts

No rating or validation information has been found for halSynteny.

No alerts have been found for halSynteny.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Totikov AA, et al. (2026) Comparative Genomics and Phylogenomics of the Mustelinae Lineage (Mustelidae, Carnivora). *Genome biology and evolution*, 18(3).

DeWeese K, et al. (2025) Scaffolded and annotated nuclear and organelle genomes of the North American brown alga *Saccharina latissima*. *Frontiers in genetics*, 16, 1494480.

Romanenko SA, et al. (2023) Integration of fluorescence in situ hybridization and chromosome-length genome assemblies revealed synteny map for guinea pig, naked mole-rat, and human. *Scientific reports*, 13(1), 21055.

Krasheninnikova K, et al. (2020) halSynteny: a fast, easy-to-use conserved synteny block construction method for multiple whole-genome alignments. *GigaScience*, 9(6).