

Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 2026

Chromosome Scale Assembler

RRID:SCR_017960

Type: Tool

Proper Citation

Chromosome Scale Assembler (RRID:SCR_017960)

Resource Information

URL: <https://github.com/HMPNK/CSA2.6>

Proper Citation: Chromosome Scale Assembler (RRID:SCR_017960)

Description: Software pipeline for high-throughput chromosome level vertebrate genome assembly. Pipeline, which after contig assembly performs post assembly improvements by ordering assembly and closing gaps, as well as splitting of low supported regions.

Abbreviations: CSA

Synonyms: Chromosome Scale Assembler

Resource Type: software application, software resource

Keywords: Assembly, chromosome, vertebrate, genome, contig, closing, gap, splitting, low, supported, region, bio.tools

Funding: German Research foundation

Availability: Free, Available for download, Freely available

Resource Name: Chromosome Scale Assembler

Resource ID: SCR_017960

Alternate IDs: biotools:csa2.6

Alternate URLs: <https://bio.tools/CSA2.6>

License: MIT License

Record Creation Time: 20220129T080337+0000

Record Last Update: 20260905T133303+0000

Ratings and Alerts

No rating or validation information has been found for Chromosome Scale Assembler.

No alerts have been found for Chromosome Scale Assembler.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Kono T, et al. (2025) Protocol for characterizing craniopharyngioma subtypes and their microenvironments using single-cell RNA sequencing and immunohistochemistry. STAR protocols, 6(2), 103760.

Kuhl H, et al. (2020) CSA: A high-throughput chromosome-scale assembly pipeline for vertebrate genomes. GigaScience, 9(5).

Kaya H, et al. (2018) SCCmecFinder, a Web-Based Tool for Typing of Staphylococcal Cassette Chromosome mec in Staphylococcus aureus Using Whole-Genome Sequence Data. mSphere, 3(1).

Lienau EK, et al. (2013) Phylogenomic analysis identifies gene gains that define Salmonella enterica subspecies I. PLoS one, 8(10), e76821.

Dodd KA, et al. (2011) Ancient ancestry of KFDV and AHFV revealed by complete genome analyses of viruses isolated from ticks and mammalian hosts. PLoS neglected tropical diseases, 5(10), e1352.