

# Resource Summary Report

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## 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 resource, software application

**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:** 20260731T043023+0000

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## Ratings and Alerts

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

No alerts have been found for Chromosome Scale Assembler.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 5 mentions in open access literature.

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

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.