

# Resource Summary Report

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## SALSA

RRID:SCR\_022013

Type: Tool

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### Proper Citation

SALSA (RRID:SCR\_022013)

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### Resource Information

**URL:** <https://github.com/marbl/salsa>

**Proper Citation:** SALSA (RRID:SCR\_022013)

**Description:** Software tool for scaffold long read assemblies with Hi-C data.

**Synonyms:** SALSA2

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

**Defining Citation:** [DOI:10.1371/journal.pcbi.1007273](https://doi.org/10.1371/journal.pcbi.1007273), [DOI:10.1186/s12864-017-3879-z](https://doi.org/10.1186/s12864-017-3879-z)

**Keywords:** scaffolding, Hi-C data, scaffold long read assemblies

**Funding:** NHGRI R44 HG009584;  
NIAID R01 AI100947;  
Ministry of Health and Welfare ;  
Republic of Korea

**Availability:** Free, Available for download, Freely available

**Resource Name:** SALSA

**Resource ID:** SCR\_022013

**License:** MIT License

**Record Creation Time:** 20220421T050138+0000

**Record Last Update:** 20260801T042845+0000

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### Ratings and Alerts

No rating or validation information has been found for SALSA.

No alerts have been found for SALSA.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 40 mentions in open access literature.

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

Mochales-Riaño G, et al. (2025) Chromosome-level reference genome for the medically important Arabian horned viper (*Cerastes gasperettii*). *GigaScience*, 14.

Márquez R, et al. (2025) A draft genome assembly for the dart-poison frog *Phyllobates terribilis*. *GigaByte* (Hong Kong, China), 2025, gigabyte157.

Xu Y, et al. (2025) High-quality genome of black wolfberry (*Lycium ruthenicum* Murr.) provides insights into the genetics of anthocyanin biosynthesis regulation. *Horticulture research*, 12(2), uhae298.

Han H, et al. (2025) A telomere-to-telomere phased genome of an octoploid strawberry reveals a receptor kinase conferring anthracnose resistance. *GigaScience*, 14.

Brown T, et al. (2025) Chromosome-scale genome assembly reveals how repeat elements shape non-coding RNA landscapes active during newt limb regeneration. *Cell genomics*, 5(2), 100761.

Rey Redondo E, et al. (2024) Genomic characterisation and ecological distribution of *Mantoniella tinhouana*: a novel Mamiellophycean green alga from the Western Pacific. *Frontiers in microbiology*, 15, 1358574.

Rives N, et al. (2024) Diverse Origins of Near-Identical Antifreeze Proteins in Unrelated Fish Lineages Provide Insights Into Evolutionary Mechanisms of New Gene Birth and Protein Sequence Convergence. *Molecular biology and evolution*, 41(9).

Canesin LEC, et al. (2024) A reference genome for the Harpy Eagle reveals steady demographic decline and chromosomal rearrangements in the origin of Accipitriformes. *Scientific reports*, 14(1), 19925.

Rives N, et al. (2024) Diverse origins of near-identical antifreeze proteins in unrelated fish lineages provide insights into evolutionary mechanisms of new gene birth and protein sequence convergence. *bioRxiv : the preprint server for biology*.

Webster CF, et al. (2024) The genome sequence of *Tadarida brasiliensis* I. Geoffroy Saint-Hilaire, 1824 [Molossidae; Tadarida]. *Wellcome open research*, 9, 98.

Mutemi KN, et al. (2024) A genome resource for the marine annelid *Platynereis dumerilii*. bioRxiv : the preprint server for biology.

Ang G, et al. (2024) A high-quality genome of the convergent lady beetle, *Hippodamia convergens*. G3 (Bethesda, Md.), 14(6).

Mata-Sucre Y, et al. (2024) Repeat-based holocentromeres of the woodrush *Luzula sylvatica* reveal insights into the evolutionary transition to holocentricity. Nature communications, 15(1), 9565.

Warren WC, et al. (2024) *Astyanax mexicanus* surface and cavefish chromosome-scale assemblies for trait variation discovery. G3 (Bethesda, Md.), 14(8).

Shekhar MS, et al. (2024) Genome assembly, Full-length transcriptome, and isoform diversity of Red Snapper, *Lutjanus argentimaculatus*. Scientific data, 11(1), 796.

Jiang L, et al. (2024) The Bioinformatic Applications of Hi-C and Linked Reads. Genomics, proteomics & bioinformatics, 22(4).

Grewal S, et al. (2024) Chromosome-scale genome assembly of bread wheat's wild relative *Triticum timopheevii*. Scientific data, 11(1), 420.

Bickerstaff JRM, et al. (2024) Chromosome Structural Rearrangements in Invasive Haplodiploid *Ambrosia* Beetles Revealed by the Genomes of *Euwallacea fornicatus* (Eichhoff) and *Euwallacea similis* (Ferrari) (Coleoptera, Curculionidae, Scolytinae). Genome biology and evolution, 16(11).

Rueda-M N, et al. (2024) Genomic evidence reveals three W-autosome fusions in *Heliconius* butterflies. PLoS genetics, 20(7), e1011318.

Tamura K, et al. (2023) A highly contiguous genome assembly of red perilla (*Perilla frutescens*) domesticated in Japan. DNA research : an international journal for rapid publication of reports on genes and genomes, 30(1).