

Resource Summary Report

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SALSA

RRID:SCR_022013

Type: Tool

Proper Citation

SALSA (RRID:SCR_022013)

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, software application, data analysis software, 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: 20260815T182704+0000

Ratings and Alerts

No rating or validation information has been found for SALSA.

No alerts have been found for SALSA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 46 mentions in open access literature.

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

Uliano-Silva M, et al. (2026) Elevated retrocopy burden and sloth-specific expansions illuminate mammalian genome evolution. *BMC biology*, 24(1).

Mochales-Riaño G, et al. (2026) Chromosome-level reference genome for the common wall gecko (*Tarentola mauritanica*) enables comparative and functional studies in geckos. *G3 (Bethesda, Md.)*, 16(5).

Nabeshima K, et al. (2026) A reference genome assembly of *Pteropus pselaphon*. *Scientific data*, 13(1).

van Rengs WMJ, et al. (2026) Wild tomato genome assemblies reveal structural variants and repeat content act as recombination barriers. *Nature communications*, 17(1).

Thomas WR, et al. (2026) Genomic comparisons and the adaptive basis of brain size plasticity and chromosomal instability in the Eurasian common shrew. *Molecular biology and evolution*, 43(2).

Sharma M, et al. (2026) Improved reference assembly and core collection resequencing to facilitate exploration of important agronomical traits for the improvement of oilseed crop, *Carthamus tinctorius* L. *GigaScience*, 15.

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

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.

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

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. *bioRxiv : the preprint server for biology*.

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.

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

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

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

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.