

Resource Summary Report

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RagTag

RRID:SCR_027293

Type: Tool

Proper Citation

RagTag (RRID:SCR_027293)

Resource Information

URL: <https://github.com/malonge/RagTag>

Proper Citation: RagTag (RRID:SCR_027293)

Description: Collection of software tools for scaffolding and improving modern genome assemblies. Reference-based scaffolder. Used for fast and flexible genome assembly scaffolding and improvement.

Resource Type: software toolkit, software resource, source code

Defining Citation: [PMID:36522651](#)

Keywords: Reference-based scaffolder, genome assembly scaffolding, scaffolding, genome assemblies,

Funding: NIH Office of the Director S10OD028632;
NSF ;
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Resource Name: RagTag

Resource ID: SCR_027293

License: MIT license

Record Creation Time: 20250811T213301+0000

Record Last Update: 20260804T043927+0000

Ratings and Alerts

No rating or validation information has been found for RagTag.

No alerts have been found for RagTag.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 66 mentions in open access literature.

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

Xing TF, et al. (2025) Extensive Recombination Suppression and Genetic Degeneration of a Young ZW Sex Chromosome System in Halfbeak Fish. *Molecular biology and evolution*, 42(7).

Brady MJ, et al. (2025) Antagonistic kinesin-14s within a single chromosomal drive haplotype. *bioRxiv : the preprint server for biology*.

Zeng Y, et al. (2025) Increased maize chromosome number by engineered chromosome fission. *Science advances*, 11(21), eadw3433.

Shearman JR, et al. (2025) Assembly of the salt-secreting mangrove *Avicennia rumphiana*. *PloS one*, 20(2), e0318091.

Abdirassilova AA, et al. (2025) Whole genome sequencing of *Yersinia pestis* isolates from Central Asian natural plague foci revealed the role of adaptation to different hosts and environmental conditions in shaping specific genotypes. *PLoS neglected tropical diseases*, 19(9), e0013533.

Igolkina AA, et al. (2025) A comparison of 27 *Arabidopsis thaliana* genomes and the path toward an unbiased characterization of genetic polymorphism. *Nature genetics*, 57(9), 2289.

Roshka YA, et al. (2025) Antimicrobial Potential of Secalonic Acids from Arctic-Derived *Penicillium chrysogenum* INA 01369. *Antibiotics (Basel, Switzerland)*, 14(1).

Platt li RN, et al. (2025) Genomic data reveal a north-south split and introgression history of blood fluke populations across Africa. *Nature communications*, 16(1), 3508.

Ziegler FMR, et al. (2025) A full genome assembly reveals drought stress effects on gene expression and metabolite profiles in blackcurrant (*Ribes nigrum* L.). *Horticulture research*, 12(2), uhae313.

Tonon E, et al. (2025) Chromosomal-level assembly of *Magnusiomyces clavatus*: novel genetic insights on an emerging fungal pathogen. *G3 (Bethesda, Md.)*, 15(11).

Naktang C, et al. (2025) Chromosome-level assemblies of two hexaploid bamboos, *Thyrsostachys oliveri* and *Thyrsostachys siamensis*, provide a foundation for functional and comparative genomics studies. *GigaScience*, 14.

Krueger M, et al. (2025) Phylogenomic associations among methicillin-resistant *Staphylococcus aureus* isolates derived from pets, dairies, and humans. *Microbiology spectrum*, 13(6), e0199524.

Sargent DJ, et al. (2025) A CACTA-like transposon in the Anthocyanidin synthase 1 (Ans-1) gene is responsible for apricot fruit colour in the raspberry (*Rubus idaeus*) cultivar 'Varnes'. *PloS one*, 20(2), e0318692.

Yaikhan T, et al. (2025) Probiogenomic analysis of *Limosilactobacillus fermentum* SD7, a probiotic candidate with remarkable aggregation abilities. *Heliyon*, 11(3), e42451.

Javier MCF, et al. (2025) Draft genome of the endangered visayan spotted deer (*Rusa alfredi*), a Philippine endemic species. *GigaByte (Hong Kong, China)*, 2025, gigabyte150.

Nachtigall PG, et al. (2025) A Segregating Structural Variant Defines Novel Venom Phenotypes in the Eastern Diamondback Rattlesnake. *Molecular biology and evolution*, 42(4).

Chen CC, et al. (2025) High-quality chromosome-level genome of three *Meretrix* species using Nanopore and Hi-C technologies. *Scientific data*, 12(1), 1141.

Luque-Jimenez E, et al. (2025) Discovery of a bacteriophage sequence in a mite genome assembly reveals bacterial contamination and opens new possibilities for exploring arthropod symbionts. *Microbial genomics*, 11(10).

Ritter EJ, et al. (2025) The assembly and annotation of two teinturier grapevine varieties, Dakapo and Rubired. *GigaByte (Hong Kong, China)*, 2025, gigabyte149.

Mohapatra S, et al. (2025) Comprehensive genome analysis of *Streptomyces caeruleatus* S14 isolated from rice rhizosphere. *Frontiers in plant science*, 16, 1526700.