

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 3, 2026

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 resource, software toolkit, source code

Defining Citation: [PMID:36522651](#)

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

Funding: European Research Council ;
Howard Hughes Medical Institutes ;
NIH Office of the Director S10OD028632;
NSF ;
Swiss National Science Foundation

Resource Name: RagTag

Resource ID: SCR_027293

License: MIT license

Record Creation Time: 20250811T213301+0000

Record Last Update: 20260829T183514+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 91 mentions in open access literature.

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

Cortez J, et al. (2026) Reference genome of an irruptive migrant, the pine siskin (*Spinus pinus*). *The Journal of heredity*, 117(3), 469.

Liu H, et al. (2026) Genomics of rafting crustaceans reveals adaptation to climate change in tropical oceans. *Nature communications*, 17(1).

Kim S, et al. (2026) Tetraopes Milkweed Beetle Genomes Elucidate the Adaptive Basis of a Temperate Coevolutionary Radiation. *Molecular ecology resources*, 26(3), e70117.

Kim S, et al. (2026) Chromosome-Scale Reference Genome Assemblies for Two Anoplophora Longhorned Beetle Species (Coleoptera: Cerambycidae). *Genome biology and evolution*, 18(3).

De Vega JJ, et al. (2026) A haplotype-complete chromosome-level assembly of octoploid *Urochloa humidicola* cv. Tully reveals multiple genomic compositions and evolutionary histories in the species. *G3 (Bethesda, Md.)*, 16(4).

Al-Hasan BA, et al. (2026) Complete genome sequence and functional characterization of *Bacillus amyloliquefaciens* NJF-55: a sheep-derived probiotic candidate. *Scientific reports*, 16(1), 6408.

Li X, et al. (2026) Genomic insights into dominant lactic acid bacteria in spoiled plant-based meat analogues. *Current research in food science*, 12, 101332.

Albillos-Arenal S, et al. (2026) Lineage-Specific Adaptive Strategies Shape the Response of de Novo Lager Yeast Hybrids to High-Gravity Fermentation. *Microbial biotechnology*, 19(5), e70375.

Osorio-Navarro Y, et al. (2026) Whole Genome Sequence of *Xylaria chamelensis* (Xylariales, Ascomycota), A New Species Associated with Fabaceae Pods. *Mycobiology*, 54(3), 384.

Sessi IR, et al. (2026) First whole-genome assembly of the Galápagos Petrel (*Pterodroma phaeopygia*) using Oxford Nanopore sequencing to advance conservation genomics in a critically endangered seabird. *G3 (Bethesda, Md.)*, 16(3).

Sedaghatkish A, et al. (2026) A contamination-reduced genome of *Plasmodiophora brassicae* with comprehensive functional annotation. *BMC microbiology*, 26(1), 118.

Nawae W, et al. (2026) Genome Assembly of Three Shrub Mangroves in the Genus *Acanthus* Reveals Two Polyploidy Events and Expansion of Genes Linked to Root Adaptation in Coastal Habitats. *GigaScience*, 15.

Rivarola M, et al. (2026) Chromosome-scale genome assembly of the South American fruit fly, *Anastrepha fraterculus* sp.1. *Insect science*, 33(2), 640.

Liang J, et al. (2026) Complex temporal dynamics of phage-bacteria populations in an animal-associated marine system. *Nature communications*, 17(1).

Enabuele EE, et al. (2026) Misleading inference of schistosome epidemiology from ribosomal internal transcribed spacer (ITS) and mitochondrial DNA. *bioRxiv : the preprint server for biology*.

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

Dean LL, et al. (2026) The tiger who came to T2T: Telomere-to-Telomere genome assembly of the Sumatran tiger (*Panthera tigris sumatrae*) using nanopore simplex reads. *BMC genomics*, 27(1).

Kosushkin SA, et al. (2026) Genome sequencing uncovers the history of the Russian desman's gradual population decline and contributes to the evolutionary history of *Talpidae*. *BMC ecology and evolution*, 26(1), 12.

Méndez M, et al. (2026) First draft genome and genomic analysis of *Neofusicoccum parvum* isolated from mango (*Mangifera indica* L.) in Paraguay. *Frontiers in fungal biology*, 7, 1813584.

Abbà S, et al. (2026) Multi-Omics Profiling of the *Scaphoideus titanus* Yeast-Like Symbiont Guides the Bioinformatic Discovery of Related Fungal Symbioses in Insects. *Environmental microbiology*, 28(7), e70361.