

Resource Summary Report

Generated by [SPARC SAWG](#) on Aug 3, 2026

Bowtie

RRID:SCR_005476

Type: Tool

Proper Citation

Bowtie (RRID:SCR_005476)

Resource Information

URL: <http://bowtie-bio.sourceforge.net/index.shtml>

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Description: Software ultrafast memory efficient tool for aligning sequencing reads. Bowtie is short read aligner.

Resource Type: software resource, data processing software, sequence analysis software, alignment software, software application, data analysis software, image analysis software

Defining Citation: [PMID:19261174](#), [DOI:10.1186/gb-2009-10-3-r25](#)

Keywords: sequence, analysis, long, reference, read, alignment, gap, local, pair, end, rna, rnaseq, bio.tools

Funding: NHGRI R01 HG006102;
NIGMS R01 GM083873;
Amazon Web Services in Education Research

Availability: Free, Available for download, Freely available

Resource Name: Bowtie

Resource ID: SCR_005476

Alternate IDs: biotools:bowtie, OMICS_00653

Alternate URLs: <https://github.com/BenLangmead/bowtie>, <https://bio.tools/bowtie>, <https://sources.debian.org/src/bowtie/>

License: GNU GPL v3.0

Record Creation Time: 20220129T080230+0000

Ratings and Alerts

No rating or validation information has been found for Bowtie.

No alerts have been found for Bowtie.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 13226 mentions in open access literature.

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

Crnovrsanin N, et al. (2026) Combining cell-free DNA fragmentomes and total tumour volume improves prognostication and tumour response evaluation in patients with colorectal cancer liver metastases. *EBioMedicine*, 123, 106081.

Pan L, et al. (2026) tRNA-Derived Fragment tRF-22 Promotes Immunosuppression by Inhibiting HnRNPA1 Ubiquitination in Esophageal Squamous Cell Carcinoma. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(1), e05806.

Kunzelman GW, et al. (2026) Chromatin Profiling Reveals Distinct Male and Female Trajectories for Developmental Learning Potential. *Developmental neurobiology*, 86(1), e23017.

Kärkkäinen M, et al. (2026) Integrative omics approaches to uncover liquid-based cancer-predicting biomarkers in Lynch syndrome. *International journal of cancer*, 158(1), 243.

Lucetti G, et al. (2026) RNAi-mediated gene silencing of a 26S proteasome subunit increases mortality of the Japanese beetle *Popillia japonica*. *Pest management science*, 82(1), 1066.

Leichter SM, et al. (2026) Polycomb misregulation in enterocytes drives tissue decline in the aging *Drosophila* intestine. *Genome research*, 36(1), 102.

Mohn RA, et al. (2026) Variant Calling in the Goldilocks Zone: How Reference Genome Choice and Read Mapping Stringency Impact Heterozygosity Estimates and Phylogenetic Analyses. *Molecular ecology resources*, 26(1), e70079.

Santos M, et al. (2026) Comprehensive Mapping of Functional Enhancers in Chinese Hamster Ovary Cells. *Biotechnology and bioengineering*, 123(1), 196.

Matchett CL, et al. (2026) Discovery and Validation of Molecular Biomarkers for Differentiation of Nondysplastic Barrett's Esophagus from High-grade Dysplasia and Esophageal Adenocarcinoma. *Cancer prevention research (Philadelphia, Pa.)*, 19(1), 49.

Liu X, et al. (2026) Investigation into the Pancreatic Pathogenesis of SFTSV across Multiple Levels. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(1), e15862.

Xu Y, et al. (2026) Lipid Droplet-Driven Ribosome Collisions Trigger ZAK?-p38 Signaling to Accelerate Testicular Aging. *Aging cell*, 25(1), e70359.

Lemonnier C, et al. (2026) Comparison of Metabarcoding and Shotgun Sequencing Confirms the Relevance of Chloroplastic rRNA Genes to Assess Community Structure of Lake Phytoplankton. *Molecular ecology resources*, 26(1), e70077.

Yuan C, et al. (2026) Zoonotic *Streptococcus* imports glucose to inhibit stringent response and promote growth during meningitis. *Nature microbiology*, 11(1), 125.

Kama Y, et al. (2026) Notch interaction with RUNX factors regulates initiation of the T-lineage program. *The Journal of experimental medicine*, 223(2).

Xiong EH, et al. (2025) Protocol to identify genes important for *Candida albicans* fitness in diverse environmental conditions using pooled bar-seq screening approach. *STAR protocols*, 6(1), 103645.

Ramponi V, et al. (2025) H4K20me3-Mediated Repression of Inflammatory Genes Is a Characteristic and Targetable Vulnerability of Persister Cancer Cells. *Cancer research*, 85(1), 32.

Weichert-Leahey N, et al. (2025) KAT6A/B inhibition synergizes with retinoic acid and enhances the efficacy of GD2-targeted immunotherapy in neuroblastoma. *bioRxiv* : the preprint server for biology.

Figuerola-Bou E, et al. (2025) KDM6 Demethylases Contribute to EWSR1::FLI1-Driven Oncogenic Reprogramming in Ewing Sarcoma. *Cancer research*, 85(22), 4485.

Sørhus E, et al. (2025) Transcriptomics uncover inhibition of repair and wound healing pathways in Atlantic halibut (*Hippoglossus hippoglossus*) after crude oil exposure. *Ecotoxicology and environmental safety*, 296, 118151.

Mokhtari A, et al. (2025) Using multiomic integration to improve blood biomarkers of major depressive disorder: a case-control study. *EBioMedicine*, 113, 105569.