

# Resource Summary Report

Generated by [FDI Lab - SciCrunch.org](http://FDI Lab - SciCrunch.org) on Apr 1, 2025

## Bowtie 2

RRID:SCR\_016368

Type: Tool

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### Proper Citation

Bowtie 2 (RRID:SCR\_016368)

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### Resource Information

**URL:** <http://bowtie-bio.sourceforge.net/bowtie2/index.shtml>

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**Description:** Ultrafast and memory efficient tool for aligning sequencing reads to long reference sequences. Supports gapped, local, and paired end alignment modes. More suited to finding longer, gapped alignments in comparison with original Bowtie method.

**Synonyms:** , bowtie 2, bowtie2 v 2.2.3

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

**Defining Citation:** [PMID:22388286](https://pubmed.ncbi.nlm.nih.gov/22388286/)

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

**Funding:** NHGRI R01 HG006102;  
NIGMS R01 GM083873

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

**Resource Name:** Bowtie 2

**Resource ID:** SCR\_016368

**Alternate IDs:** biotools:bowtie2

**Alternate URLs:** <http://bowtie-bio.sourceforge.net/bowtie2/index.shtml>,

<https://github.com/BenLangmead/bowtie2>, <https://bio.tools/bowtie2>

**License:** GNU General Public License v3.0

**Record Creation Time:** 20220129T080321+0000

**Record Last Update:** 20250401T061126+0000

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## Ratings and Alerts

No rating or validation information has been found for Bowtie 2.

No alerts have been found for Bowtie 2.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 1524 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch.org](#).

Zhou Y, et al. (2025) Cellular senescence-associated gene IFI16 promotes HMOX1-dependent evasion of ferroptosis and radioresistance in glioblastoma. *Nature communications*, 16(1), 1212.

Zhang N, et al. (2025) Deciphering the molecular logic of WOX5 function in the root stem cell organizer. *The EMBO journal*, 44(1), 281.

Wen J, et al. (2025) Complete Mitochondrial Genome of King Threadfin, *Polydactylus macrochir* (Günther, 1867): Genome Characterization and Phylogenetic Analysis. *Genes*, 16(1).

Demond H, et al. (2025) Transcriptome and DNA methylation profiling during the NSN to SN transition in mouse oocytes. *BMC molecular and cell biology*, 26(1), 2.

Sasaki M, et al. (2025) Efficacy of CBP/p300 Dual Inhibitors against Derepression of KREMEN2 in cBAF-Deficient Cancers. *Cancer research communications*, 5(1), 24.

Gregorova P, et al. (2025) Purification of micrococcal nuclease for use in ribosomal profiling of high-salinity extremophiles. *The Journal of biological chemistry*, 301(1), 108020.

Yang JT, et al. (2025) Non-adapted bacterial infection suppresses plant reproduction. *Science advances*, 11(2), eads7738.

Albuquerque-Wendt A, et al. (2025) TransLeish: Identification of membrane transporters essential for survival of intracellular Leishmania parasites in a systematic gene deletion screen. *Nature communications*, 16(1), 299.

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.

Zhou L, et al. (2025) Targeted antimicrobial self-assembly peptide hydrogel with in situ bio-mimic remineralization for caries management. *Bioactive materials*, 44, 428.

Bayam E, et al. (2025) Bi-allelic variants in WDR47 cause a complex neurodevelopmental syndrome. *EMBO molecular medicine*, 17(1), 129.

Ye GC, et al. (2025) Comprehensive analysis of the interaction microbiome and prostate cancer: an initial exploration from multi-cohort metagenome and GWAS studies. *Journal of translational medicine*, 23(1), 130.

Wu C, et al. (2025) Analysis of glutamate-dependent mechanism and optimization of fermentation conditions for poly-gamma-glutamic acid production by *Bacillus subtilis* SCP017-03. *PLoS one*, 20(1), e0310556.

Marchand V, et al. (2025) Monocytes generated by interleukin-6-treated human hematopoietic stem and progenitor cells secrete calprotectin that inhibits erythropoiesis. *iScience*, 28(1), 111522.

Bryan E, et al. (2025) Nucleosomal asymmetry shapes histone mark binding and promotes poising at bivalent domains. *Molecular cell*, 85(3), 471.

Biedler JK, et al. (2024) On the Origin and Evolution of the Mosquito Male-determining Factor Nix. *Molecular biology and evolution*, 41(1).

Chen Z, et al. (2024) Use of pus metagenomic next-generation sequencing for efficient identification of pathogens in patients with sepsis. *Folia microbiologica*, 69(5), 1003.

Liao R, et al. (2024) Integrated metabolomic and metagenomic strategies shed light on interactions among planting environments, rhizosphere microbiota, and metabolites of tobacco in Yunnan, China. *Frontiers in microbiology*, 15, 1386150.

Caradec T, et al. (2024) Small molecule MarR modulators potentiate metronidazole antibiotic activity in aerobic *E. coli* by inducing activation by the nitroreductase NfsA. *The Journal of biological chemistry*, 300(7), 107431.

Noonan HR, et al. (2024) A chronic signaling TGF $\beta$  zebrafish reporter identifies immune response in melanoma. *eLife*, 13.