

Resource Summary Report

Generated by [dkNET](#) on Sep 19, 2026

Bowtie 2

RRID:SCR_016368

Type: Tool

Proper Citation

Bowtie 2 (RRID:SCR_016368)

Resource Information

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

Proper Citation: Bowtie 2 (RRID:SCR_016368)

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, data analysis software, data processing software, image analysis software, sequence analysis software, software application, software resource

Defining Citation: [PMID: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: 20260919T195300+0000

Ratings and Alerts

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

No alerts have been found for Bowtie 2.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1993 mentions in open access literature.

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

Shu X, et al. (2026) S6K1 overexpression enhances autophagy in breast cancer cells by inducing the translation of CLU. Chinese medical journal, 139(8), 1210.

Wi?cek K, et al. (2026) An in vitro transcription-based protocol for mapping HIV integration sites using lentiviral integration site sequencing. STAR protocols, 7(1), 104284.

Jang Y, et al. (2026) Enhancer RNA-mediated transcriptional regulation of TDP-43 during early neural lineage specification. Animal cells and systems, 30(1), 320.

Yang Y, et al. (2026) Elucidating the therapeutic efficacy and mechanisms of arctigenin in ameliorating renal fibrosis: a combined transcriptomic and proteomic study. Frontiers in pharmacology, 17, 1796732.

van der Elst A, et al. (2026) Molecular and Immune Landscape of Recurrent and/or Distant Metastatic Squamous Cell Carcinoma of the Head and Neck: An EORTC/IMMUCAN Project. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(13), 2732.

Kempynck N, et al. (2026) CREsted: modeling genomic and synthetic cell-type-specific enhancers across tissues and species. Nature methods, 23(5), 946.

Wang F, et al. (2026) Multi-omics integration to elucidate the antibacterial mechanism of Streptomyces sp. strain PBSH9. BMC microbiology, 26(1).

Hu Y, et al. (2026) Invasive patterns of Biomphalaria straminea revealed by genetic mapping in the Greater Bay Area, China. Infectious diseases of poverty, 15(1), 9.

Pan W, et al. (2026) Analysis of chloroplast genomes and SSR classification and identification of Agropyron species and closely related species. Scientific reports, 16(1), 3579.

De Napoli S, et al. (2026) Severity of Depressive Symptoms by Perceived Stress and Gut Microbiota Composition: A Sex-Stratified Bayesian Approach in a Non-Clinical Sample. *Stress and health : journal of the International Society for the Investigation of Stress*, 42(1), e70152.

Deol KK, et al. (2026) Vitamin B2 metabolism promotes FSP1 stability to prevent ferroptosis. *Nature structural & molecular biology*, 33(3), 525.

Luo S, et al. (2026) Chromatin-intrinsic mechanisms determine orientation-specific class switch recombination. *Nature communications*, 17(1).

Zhang T, et al. (2026) Study on the mechanism of hinokitiol in inhibiting the biofilm activity of *Staphylococcus epidermidis*. *Frontiers in microbiology*, 17, 1811623.

Behrouz Sharif S, et al. (2026) WSTF deficiency reprograms regulatory networks by linking locus-specific chromatin remodeling to altered isoform expression and misdirected signaling. *Nucleic acids research*, 54(11).

Park J, et al. (2026) Innate immune priming by n-dodecyl- β -D-maltoside in murine models of bacterial and viral infection. *EBioMedicine*, 124, 106143.

Liu H, et al. (2026) The genomes of 5 mantises provide insights into sex chromosome evolution and Mantodea phylogeny clarification. *GigaScience*, 15.

Kong Y, et al. (2026) Prebiotics as adjunctive treatment ameliorates DSS-induced colitis and gut microbiota. *Microbiology spectrum*, 14(1), e0150225.

van der Elst A, et al. (2026) Genomic and Immune Landscape of Recurrent and/or Metastatic Squamous Cell Carcinoma of the Head and Neck Progressing on Anti-PD-1 Treatment. *Cancer immunology research*, 14(4), 608.

Gorin A, et al. (2026) IFN γ -induced memory in human macrophages is sustained by the durability of cytokine signaling itself. *The Journal of experimental medicine*, 223(4).

Hu S, et al. (2026) MicroRNA210 regulated brain pericyte dysfunction exacerbates hypoxic-ischemic brain injury in neonatal mice. *Fluids and barriers of the CNS*, 23(1), 4.