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: data analysis software, software application, software resource, sequence analysis software, image analysis software, alignment software, data processing 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 Agency: NHGRI, NIGMS, 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


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 11388 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.


Song C, et al. (2024) eRNAbase: a comprehensive database for decoding the regulatory eRNAs in human and mouse. Nucleic acids research, 52(D1), D81.


Akiyama T, et al. (2024) ZSCAN4-binding motif-TGCACAC is conserved and enriched in CA/TG microsatellites in both mouse and human genomes. DNA research : an international journal for rapid publication of reports on genes and genomes, 31(1).

Carpenter M, et al. (2024) Assessing Reassortment between Bluetongue Virus Serotypes 10 and 17 at Different Coinfection Ratios in Culicoides sonorensis. Viruses, 16(2).


Huang X, et al. (2024) Transcriptomic and targeted metabolome analyses revealed the regulatory mechanisms of the synthesis of bioactive compounds in Citrus grandis 'tomentosa'. PeerJ, 12, e16881.


Suda K, et al. (2024) Aberrant Upregulation of RUNX3 Activates Developmental Genes to Drive Metastasis in Gastric Cancer. Cancer research communications, 4(2), 279.


Dexheimer S, et al. (2024) Characterization of Variant RNAs Encapsidated during Bromovirus Infection by High-Throughput Sequencing. Pathogens (Basel, Switzerland), 13(1).

Deng Y, et al. (2024) Aseptic loosening around total joint replacement in humans is regulated by miR-1246 and miR-6089 via the Wnt signalling pathway. Journal of orthopaedic surgery and research, 19(1), 94.


Zhang S, et al. (2024) Whole-Transcriptome Sequencing Reveals the Global Molecular Responses and NAC Transcription Factors Involved in Drought Stress in Dendrobium catenatum. Antioxidants (Basel, Switzerland), 13(1).