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

References: PMID:19261174

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

Parent Organization: Johns Hopkins University; Maryland; USA

Funding Agency: Amazon Web Services in Education Research, NHGRI, NIGMS

Related resources: Bowtie 2

Availability: Free, Available for download, Freely available

Website Status: Last checked up

Resource Name: Bowtie

Resource ID: SCR_005476
**Alternate IDs:** OMICS_00653, biotools:bowtie

**Alternate URLs:** https://github.com/BenLangmead/bowtie, https://bio.tools/bowtie

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**Ratings and Alerts**

No rating or validation information has been found for Bowtie.

No alerts have been found for Bowtie.

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**Data and Source Information**

**Source:** [SciCrunch Registry](https://scicrunch.org)

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**Usage and Citation Metrics**

We found 7665 mentions in open access literature.

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


Ebelt ND, et al. (2020) 5-Azacytidine Potentiates Anti-tumor Immunity in a Model of

Dunican DS, et al. (2020) Bivalent promoter hypermethylation in cancer is linked to the H327me3/H3K4me3 ratio in embryonic stem cells. BMC biology, 18(1), 25.


Ding X, et al. (2020) Genome sequence of the agarwood tree Aquilaria sinensis (Lour.) Spreng: the first chromosome-level draft genome in the Thymelaeceae family. GigaScience, 9(3).
