BWA
RRID:SCR_010910
Type: Tool

Proper Citation

BWA (RRID:SCR_010910)

Resource Information

URL: http://bio-bwa.sourceforge.net/

Description: Software for aligning sequencing reads against large reference genome. Consists of three algorithms: one for sequence reads up to 100bp, and other two for longer sequences ranged from 70bp to 1Mbp.

Resource Name: BWA

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

Keywords: sequence, alignment, reference, genome, human, short, long, read

Resource ID: SCR_010910

Parent Organization: SourceForge

Related resources: shovill, Proovread

References: PMID:19451168, PMID:20080505

Availability: Free, Available for download, Freely available

Website Status: Last checked up

Alternate IDs: OMICS_00654, SCR_015853
Alternate URLs: https://sourceforge.net/projects/bio-bwa/files/

Abbreviations: BWA

Mentions Count: 880

Ratings and Alerts

No rating or validation information has been found for BWA.

No alerts have been found for BWA.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 880 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch Infrastructure](https://sourceforge.net/projects/bio-bwa/files/).


Zhang XL, et al. (2020) Genetic Basis and Genotype-Phenotype Correlations in Han Chinese Patients with Idiopathic Dilated Cardiomyopathy. Scientific reports, 10(1), 2226.


