**BWA**

**RRID:** SCR_010910  
**Type:** Tool

### Proper Citation

BWA (RRID:SCR_010910)

### Resource Information


**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  
**Proper Citation:** BWA (RRID:SCR_010910)  
**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.


Suo Y, et al. (2020) A high-quality chromosomal genome assembly of Diospyros


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


