

Resource Summary Report

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BWA

RRID:SCR_010910

Type: Tool

Proper Citation

BWA (RRID:SCR_010910)

Resource Information

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

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

Abbreviations: BWA

Synonyms: Burrows-Wheeler Aligner (BWA), Burrows-Wheeler Aligner

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

Defining Citation: [PMID:19451168](#), [PMID:20080505](#), [DOI:10.1093/bioinformatics/btp324](#)

Keywords: sequence, alignment, reference, genome, human, short, long, read, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: BWA

Resource ID: SCR_010910

Alternate IDs: SCR_015853, biotools:bwa-sw, OMICS_00654

Alternate URLs: <https://sourceforge.net/projects/bio-bwa/files/>, <https://bio.tools/bwa-sw>, <https://sources.debian.org/src/bwa/>

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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 have not found any literature mentions for this resource.