Sequence Search and Alignment by Hashing Algorithm
RRID:SCR_000544
Type: Tool

Proper Citation

Sequence Search and Alignment by Hashing Algorithm (RRID:SCR_000544)

Resource Information

URL: http://www.sanger.ac.uk/science/tools/ssaha2-0

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Description: A program designed for the efficient mapping of sequence reads onto genomic references. The software is capable of reading most sequencing platforms and giving a range of outputs are supported.

Abbreviations: SSAHA2

Synonyms: Sequence Search and Alignment by Hashing Algorithm, ssaha2, ssaha

Resource Type: source code, software resource

Defining Citation: PMID:11591649

Keywords: sequence, genomic, analysis, search, alignment, algorithm, mapping, bio.tools

Availability: Open Source

Resource Name: Sequence Search and Alignment by Hashing Algorithm

Resource ID: SCR_000544

Alternate IDs: nlx_93831, OMICS_00690, biotools:ssaha2

Alternate URLs: https://bio.tools/ssaha2
Ratings and Alerts

No rating or validation information has been found for Sequence Search and Alignment by Hashing Algorithm.

No alerts have been found for Sequence Search and Alignment by Hashing Algorithm.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 6 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.


