

Resource Summary Report

Generated by [kravitz2](#) on Sep 19, 2026

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>

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

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

Resource Type: software resource, source code

Defining Citation: [PMID:11591649](#)

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

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Sequence Search and Alignment by Hashing Algorithm

Resource ID: SCR_000544

Alternate IDs: biotools:ssaha2, OMICS_00690, nlx_93831

Alternate URLs: <https://bio.tools/ssaha2>

License: GNU General Public License

Record Creation Time: 20220129T080202+0000

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 [kravitz2](#) .

Thangam M, et al. (2015) CRCDA--Comprehensive resources for cancer NGS data analysis. Database : the journal of biological databases and curation, 2015.

Wei X, et al. (2015) Genetic discovery for oil production and quality in sesame. Nature communications, 6, 8609.

Casbon JA, et al. (2013) Reflex: intramolecular barcoding of long-range PCR products for sequencing multiple pooled DNAs. Nucleic acids research, 41(10), e112.

Kurt K, et al. (2013) Subpopulations of Staphylococcus aureus clonal complex 121 are associated with distinct clinical entities. PloS one, 8(3), e58155.

Coppe A, et al. (2012) Sequencing and characterization of striped venus transcriptome expand resources for clam fishery genetics. PloS one, 7(9), e44185.

Ning Z, et al. (2001) SSAHA: a fast search method for large DNA databases. Genome research, 11(10), 1725.