**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](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:** ssaha2, ssaha, Sequence Search and Alignment by Hashing Algorithm

**Resource Type:** source code, software resource

**Defining Citation:** [PMID:11591649](https://www.ncbi.nlm.nih.gov/pubmed/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:** biotools:ssaha2, OMICS_00690, nlx_93831

**Alternate URLs:** [https://bio.tools/ssaha2](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 FDI Lab - SciCrunch.org.


