# 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)

**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.

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

**Keywords:** sequence, genomic, analysis, search, alignment, algorithm, mapping

**Resource ID:** SCR_000544

**Parent Organization:** Wellcome Trust Sanger Institute; Hinxton; United Kingdom

**Related resources:** SMALT

**References:** [PMID:11591649](https://pubmed.ncbi.nlm.nih.gov/11591649)

**Availability:** Open Source

**Website Status:** Last checked up

**Alternate IDs:** nlx_93831, OMICS_00690
Abbreviations: SSAHA2

Mentions Count: 6

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 scicrunch.


