

Resource Summary Report

Generated by SPARC SAWG on Sep 16, 2026

HIA

RRID:SCR_006865

Type: Tool

Proper Citation

HIA (RRID:SCR_006865)

Resource Information

URL: <http://sourceforge.net/projects/hiahia/>

Proper Citation: HIA (RRID:SCR_006865)

Description: A sequence alignment tool to align both short and long reads to a reference genome. HIA has two indexes, a hash table index and a suffix array index. The hash table is capable of the direct lookup of a q-gram and the suffix array is very fast in the lookup of a variable length q-gram. Our experiments show that the hybrid of hash table and suffix array is useful at the perspective of speed to map NGS sequencing reads to a reference genome sequence.

Abbreviations: HIA

Synonyms: Hybrid Index based sequence Alignment, HIA - Hybrid Index based sequence Alignment

Resource Type: software resource

Keywords: matlab, java, command-line

Resource Name: HIA

Resource ID: SCR_006865

Alternate IDs: OMICS_00666

Record Creation Time: 20220129T080238+0000

Record Last Update: 20260912T195646+0000

Ratings and Alerts

No rating or validation information has been found for HIA.

No alerts have been found for HIA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.