**HISAT2**

RRID:SCR_015530
Type: Tool

### Proper Citation

HISAT2 (RRID:SCR_015530)

### Resource Information

**URL:** [http://ccb.jhu.edu/software/hisat2/index.shtml](http://ccb.jhu.edu/software/hisat2/index.shtml)

**Description:** Graph-based alignment of next generation sequencing reads to a population of genomes.

**Resource Name:** HISAT2

**Proper Citation:** HISAT2 (RRID:SCR_015530)

**Resource Type:** Resource, source code, data analysis software, data processing software, software application, sequence analysis software, software resource

**Keywords:** alignment program, mapping reads, population genomics, human genome

**Resource ID:** SCR_015530

**Parent Organization:** Johns Hopkins University; Maryland; USA

**Funding Agency:** NIGMS, NLM, NSF

**Related resources:** TopHat

**References:** [PMID:25751142](http://www.ncbi.nlm.nih.gov/pubmed/25751142)

**Availability:** Available for download

**Website Status:** Last checked up

**Alternate URLs:** [https://github.com/infphilo/hisat2](https://github.com/infphilo/hisat2)

**Mentions Count:** 1331
Ratings and Alerts

No rating or validation information has been found for HISAT2.

No alerts have been found for HISAT2.

Data and Source Information
Source: SciCrunch Registry

Usage and Citation Metrics

We found 1331 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch Infrastructure.


Zhang Q, et al. (2020) Apoptotic SKOV3 cells stimulate M0 macrophages to differentiate into
M2 macrophages and promote the proliferation and migration of ovarian cancer cells by activating the ERK signaling pathway. International journal of molecular medicine, 45(1), 10-22.


