

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

HapCompass

RRID:SCR_000942

Type: Tool

Proper Citation

HapCompass (RRID:SCR_000942)

Resource Information

URL: http://www.brown.edu/Research/Istrail_Lab/hapcompass.php

Proper Citation: HapCompass (RRID:SCR_000942)

Description: Software that utilizes a fast cycle basis algorithm for the accurate haplotype assembly of sequence data. It is able to create pairwise SNP phasings.

Resource Type: algorithm

Keywords: algorithm, haplotype, sequence, genome, dna, rna, snp

Funding: NSF 1048831;
NSF 1321000

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: HapCompass

Resource ID: SCR_000942

Alternate IDs: OMICS_00197

Record Creation Time: 20220129T080204+0000

Record Last Update: 20260905T132427+0000

Ratings and Alerts

No rating or validation information has been found for HapCompass.

No alerts have been found for HapCompass.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at [Kravitz](#) .

Berger E, et al. (2014) HapTree: a novel Bayesian framework for single individual polyplotyping using NGS data. PLoS computational biology, 10(3), e1003502.