

Resource Summary Report

Generated by [nidm-terms](#) on Sep 21, 2026

HapFABIA

RRID:SCR_010793

Type: Tool

Proper Citation

HapFABIA (RRID:SCR_010793)

Resource Information

URL: <http://www.bioinf.jku.at/research/short-IBD/>

Proper Citation: HapFABIA (RRID:SCR_010793)

Description: Software that identifies short identity by descent (IBD) segments that are tagged by rare variants in large sequencing data.

Abbreviations: HapFABIA

Synonyms: HapFABIA: Identification of very short segments of identity by descent characterized by rare variants in large sequencing data

Resource Type: software resource

Defining Citation: [PMID:24174545](#)

Keywords: bio.tools

Resource Name: HapFABIA

Resource ID: SCR_010793

Alternate IDs: biotools:hapfabia, OMICS_00203

Alternate URLs: <https://bio.tools/hapfabia>

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260919T195159+0000

Ratings and Alerts

No rating or validation information has been found for HapFABIA.

No alerts have been found for HapFABIA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Clevert DA, et al. (2017) Rectified factor networks for biclustering of omics data. Bioinformatics (Oxford, England), 33(14), i59.

Povysil G, et al. (2016) IBD Sharing between Africans, Neandertals, and Denisovans. Genome biology and evolution, 8(12), 3406.

Hochreiter S, et al. (2013) HapFABIA: identification of very short segments of identity by descent characterized by rare variants in large sequencing data. Nucleic acids research, 41(22), e202.