

# Resource Summary Report

Generated by [ASWG](#) on Aug 3, 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:** 20260801T190357+0000

### Ratings and Alerts

No rating or validation information has been found for HapFABIA.

No alerts have been found for HapFABIA.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 3 mentions in open access literature.

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

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.