

# Resource Summary Report

Generated by [NIF](#) on Sep 12, 2026

## MDBLOCKS

RRID:SCR\_009280

Type: Tool

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### Proper Citation

MDBLOCKS (RRID:SCR\_009280)

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### Resource Information

**URL:** [http://ib.berkeley.edu/labs/slatkin/eriq/software/mdb\\_web/](http://ib.berkeley.edu/labs/slatkin/eriq/software/mdb_web/)

**Proper Citation:** MDBLOCKS (RRID:SCR\_009280)

**Description:** Software application using the minimum description length model to delineate haplotype blocks (entry from Genetic Analysis Software)

**Abbreviations:** MDBLOCKS

**Synonyms:** Minimum Description length method for haplotype BLOCKS

**Resource Type:** software application, software resource

**Keywords:** gene, genetic, genomic

**Resource Name:** MDBLOCKS

**Resource ID:** SCR\_009280

**Alternate IDs:** nlx\_154461

**Record Creation Time:** 20220129T080252+0000

**Record Last Update:** 20260912T200243+0000

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### Ratings and Alerts

No rating or validation information has been found for MDBLOCKS.

No alerts have been found for MDBLOCKS.

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### Data and Source Information

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

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## Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Indap AR, et al. (2005) Analysis of concordance of different haplotype block partitioning algorithms. BMC bioinformatics, 6, 303.