

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 17, 2026

LDHAT

RRID:SCR_006298

Type: Tool

Proper Citation

LDHAT (RRID:SCR_006298)

Resource Information

URL: <http://www.stats.ox.ac.uk/~mcvean/LDhat/>

Proper Citation: LDHAT (RRID:SCR_006298)

Description: Software package for the analysis of recombination rates from population genetic data (entry from Genetic Analysis Software)

Abbreviations: LDHAT

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, c, dos

Resource Name: LDHAT

Resource ID: SCR_006298

Alternate IDs: nlx_154423

Record Creation Time: 20220129T080235+0000

Record Last Update: 20260912T200235+0000

Ratings and Alerts

No rating or validation information has been found for LDHAT.

No alerts have been found for LDHAT.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 46 mentions in open access literature.

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

Cao L, et al. (2026) Augmented CENH3 loading is accompanied by transcriptional and epigenetic reprogramming at rice centromeres during meiosis. *Genome biology*, 27(1).

Magagula NA, et al. (2025) Exploring Meiotic Recombination and Its Potential Benefits in South African Beef Cattle: A Review. *Veterinary sciences*, 12(7).

Ferguson S, et al. (2024) Exploring the role of polymorphic interspecies structural variants in reproductive isolation and adaptive divergence in *Eucalyptus*. *GigaScience*, 13.

Dinh BL, et al. (2024) Recombination map tailored to Native Hawaiians may improve robustness of genomic scans for positive selection. *Human genetics*, 143(1), 85.

Akther S, et al. (2024) Natural selection and recombination at host-interacting lipoprotein loci drive genome diversification of Lyme disease and related bacteria. *mBio*, 15(9), e0174924.

Dinh BL, et al. (2023) Recombination map tailored to Native Hawaiians improves robustness of genomic scans for positive selection. *bioRxiv : the preprint server for biology*.

Krishnan S, et al. (2023) Rhometa: Population recombination rate estimation from metagenomic read datasets. *PLoS genetics*, 19(3), e1010683.

Epstein R, et al. (2023) Exploring impact of recombination landscapes on breeding outcomes. *Proceedings of the National Academy of Sciences of the United States of America*, 120(14), e2205785119.

Versoza CJ, et al. (2022) The recombination landscapes of spiny lizards (genus *Sceloporus*). *G3 (Bethesda, Md.)*, 12(2).

Wertheim JO, et al. (2022) Detection of SARS-CoV-2 intra-host recombination during superinfection with Alpha and Epsilon variants in New York City. *Nature communications*, 13(1), 3645.

Wang L, et al. (2022) Linked selection, differential introgression and recombination rate variation promote heterogeneous divergence in a pair of yellow croakers. *Molecular ecology*, 31(22), 5729.

Lynch M, et al. (2022) The Linkage-Disequilibrium and Recombinational Landscape in *Daphnia pulex*. *Genome biology and evolution*, 14(11).

Liu S, et al. (2022) Demographic History and Natural Selection Shape Patterns of Deleterious Mutation Load and Barriers to Introgression across *Populus* Genome. *Molecular biology and evolution*, 39(2).

Schreiber M, et al. (2022) Recombination landscape divergence between populations is marked by larger low-recombining regions in domesticated rye. *Molecular biology and evolution*, 39(6).

Ye Z, et al. (2022) Genetic Diversity, Heteroplasmy, and Recombination in Mitochondrial Genomes of *Daphnia pulex*, *Daphnia pulicaria*, and *Daphnia obtusa*. *Molecular biology and evolution*, 39(4).

Fuentes RR, et al. (2022) Domestication Shapes Recombination Patterns in Tomato. *Molecular biology and evolution*, 39(1).

do Socorro Fôro Ramos E, et al. (2021) High Heterogeneity of Echoviruses in Brazilian Children with Acute Gastroenteritis. *Viruses*, 13(4).

Patiño-Galindo JÁ, et al. (2021) Global Patterns of Recombination across Human Viruses. *Molecular biology and evolution*, 38(6), 2520.

Hassan S, et al. (2021) High-resolution population-specific recombination rates and their effect on phasing and genotype imputation. *European journal of human genetics : EJHG*, 29(4), 615.

Zanardo LG, et al. (2021) Experimental evolution of cowpea mild mottle virus reveals recombination-driven reduction in virulence accompanied by increases in diversity and viral fitness. *Virus research*, 303, 198389.