

Resource Summary Report

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PopLDdecay

RRID:SCR_022509

Type: Tool

Proper Citation

PopLDdecay (RRID:SCR_022509)

Resource Information

URL: <https://github.com/BGI-shenzhen/PopLDdecay>

Proper Citation: PopLDdecay (RRID:SCR_022509)

Description: Software tool for linkage disequilibrium decay analysis based on variant call format files.

Resource Type: software resource, data processing software, software application, data analysis software

Defining Citation: [PMID:30321304](#)

Keywords: linkage disequilibrium decay analysis, variant call format, VCF) files

Funding: National Natural Science Foundation of China ;
China Postdoctoral Science Foundation

Availability: Free, Available for download, Freely available

Resource Name: PopLDdecay

Resource ID: SCR_022509

License: MIT License

Record Creation Time: 20220623T050145+0000

Record Last Update: 20260804T043742+0000

Ratings and Alerts

No rating or validation information has been found for PopLDdecay .

No alerts have been found for PopLDdecay .

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 117 mentions in open access literature.

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

Huang X, et al. (2026) PMEL governs autosomal dominant inheritance of white-tail independent of yellow body plumage in chickens (*Gallus gallus domesticus*). *Poultry science*, 105(1), 106127.

Wang G, et al. (2025) Genomic evidence for hybridization and introgression between blue peafowl and endangered green peafowl and molecular foundation of leucistic plumage of blue peafowl. *GigaScience*, 14.

Li X, et al. (2025) High-resolution genome assembly and population genetic study of the endangered maple *Acer pentaphyllum* (Sapindaceae): implications for conservation strategies. *Horticulture research*, 12(4), uhae357.

Xu Z, et al. (2025) The genetic structure and selective sweep analysis of meat pigeon breeds raised in Hainan using whole genome resequencing technology. *Poultry science*, 104(11), 105731.

Peng S, et al. (2025) Whole genome resequencing uncovers candidate genes related to plumage color in Yuexi frizzled feather chicken. *Poultry science*, 104(11), 105680.

Muhetapa M, et al. (2025) Identification of Genomic Variants and Candidate Genes for Reproductive Traits and Growth Traits in Pishan Red Sheep Using Whole-Genome Resequencing. *Biology*, 14(6).

Yadav HK, et al. (2025) Telomere-to-telomere genome assembly of linseed (*Linum usitatissimum* L.) for functional genomics and accelerated genetic improvement. *Plant biotechnology journal*, 23(9), 3919.

Han J, et al. (2025) Genomic insights into the genetic diversity and genetic basis of body height in endangered Chinese Ningqiang ponies. *BMC genomics*, 26(1), 292.

Lai E, et al. (2025) Genome of root celery and population genomic analysis reveal the complex breeding history of celery. *Plant biotechnology journal*, 23(3), 946.

Qiu Y, et al. (2025) Origins, Dispersal, and Impact: Bidirectional Introgression Between Chinese and European Pig Populations. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 12(22), e2416573.

Feng C, et al. (2025) Genomic and genetic insights into Mendel's pea genes. *Nature*, 642(8069), 980.

Guo C, et al. (2025) Genomic selection with GWAS-identified QTL markers enhances prediction accuracy for quantitative traits in poplar (*Populus deltoides*). *Communications biology*, 8(1), 1242.

Long Z, et al. (2025) Evolutionary Genomics Unravels the Responses and Adaptation to Climate Change in a Key Alpine Forest Tree Species. *Molecular biology and evolution*, 42(7).

Konwar T, et al. (2025) Genome wide association analysis of flavour related metabolites in tea germplasm [*Camellia sinensis* (L.) Kuntze] from Assam using a genotyping by sequencing strategy. *BMC plant biology*, 25(1), 911.

Liu X, et al. (2025) A 14-bp motif in the KIT active promoter region is critical for melanin accumulation in yaks, mice, and humans. *BMC biology*, 23(1), 208.

Chen G, et al. (2025) Population Genomic Analysis Provides Insights Into the Evolution and Conservation of Two Critically Endangered Musk Deer Species. *Evolutionary applications*, 18(8), e70134.

Yuan Z, et al. (2025) High-quality phenotypic and genotypic dataset of barley genebank core collection to unlock untapped genetic diversity. *GigaScience*, 14.

Ding R, et al. (2025) Chromosome-Level Genome Assembly and Whole-Genome Resequencing Revealed Contrasting Population Genetic Differentiation of Black Bream (*Megalobrama skolkovii*) (Teleostei: Cyprinidae) Allopatric and Sympatric to Its Kin Species. *Ecology and evolution*, 15(1), e70874.

Wang Y, et al. (2025) Genetic diversity analysis and core germplasm construction of tea plants in Lu'an. *BMC plant biology*, 25(1), 253.

Chen B, et al. (2025) A system genetics analysis uncovers the regulatory variants controlling drought response in wheat. *Plant biotechnology journal*, 23(5), 1565.