

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

Defining Citation: [PMID:30321304](#)

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

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

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: 20260903T235840+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 161 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

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.

Gao C, et al. (2026) Genomic divergence, introgression and KASP fingerprinting panel development in five cultivar groups of sweet osmanthus. *BMC plant biology*, 26(1).

Zhu K, et al. (2026) Genomic Evaluation of the Genetic Structure and Analysis of Selective Evolutionary Signatures of Xupu Goose. *Biology*, 15(6).

Babaei M, et al. (2026) Genetic architecture of phenological, morphological, and phytochemical traits in Cannabis landraces. *The plant genome*, 19(2), e70243.

Sun J, et al. (2026) An integrated QTL-GWAS approach fine-maps a major locus (qMWS3 - 2) for stable resistance to maize white spot in tropical germplasm. *BMC plant biology*, 26(1).

Amat G, et al. (2026) Whole-Genome Resequencing Reveals Deep Genomic Differentiation and Highly Differentiated Segments Between a Composite Domestic Cattle Population and Yak from the Ili River Valley and Other Xinjiang Regions. *Animals : an open access journal from MDPI*, 16(11).

Yan J, et al. (2026) Uncovering novel loci and developing functional Kompetitive Allele Specific PCR markers for chilling requirement in peach via genome-wide association study. *Horticulture research*, 13(6), uhag069.

Jiang B, et al. (2026) Whole genome sequencing revealed genetic diversity, population structure, and selective signature of Tianhua mutton sheep. *BMC genomics*, 27(1).

Mei D, et al. (2026) Genetic diversity analysis of Xizang Sophora Moorcroftiana (Benth.) Baker based on whole-genome resequencing. *BMC genomics*, 27(1), 152.

Luo X, et al. (2026) Genomic divergence, adaptation, and the genetic basis of quality traits in ancient walnut landraces and wild relatives. *Horticulture research*, 13(7), uhag082.

Huo G, et al. (2026) Genome-wide association study in a lettuce core collection from 811 accessions reveals genetic loci for anthocyanin accumulation and cultivar development. *Horticulture research*, 13(1), uhaf258.

Zhu J, et al. (2026) Unlocking tropical adaptation: novel flowering time genes implicate JA and ROS signaling in maize. *BMC plant biology*, 26(1), 195.

Chu SJ, et al. (2026) Genetic recovery in an alpine climate-sensitive pika species during upward treeline shift. *BMC genomics*, 27(1).

Bernini F, et al. (2026) An analysis of the genomic architecture of the worldwide Irish Wolfhound dogs. *Scientific reports*, 16(1).

Xue Y, et al. (2026) Identification of candidate genes involved in root gall formation during early infection of *Plasmodiophora brassicae* in *B.napus*. *Frontiers in plant science*, 17, 1847458.

Yao Y, et al. (2026) Genome-Wide Resequencing Reveals High Connectivity and Localized Adaptive Signals in Manila Clam (*Ruditapes philippinarum*) Populations Along the Southeastern Coast of China. *Animals : an open access journal from MDPI*, 16(12).

Yang CJ, et al. (2026) Natural selection and recombination interact to structure genome-wide variation in pines. *The Plant journal : for cell and molecular biology*, 126(1), e70866.

Liu C, et al. (2026) Genomic signatures of rapid local selection and introgression drive adaptive phylogeography in the European river skater. *BMC biology*, 24(1), 45.

Espitia-Buitrago P, et al. (2026) Integrating image-based phenotyping and GWAS to map resistance to spittlebug nymphs in interspecific *Urochloa* grasses. *G3 (Bethesda, Md.)*, 16(6).

Xie H, et al. (2026) Large-scale multi-omics profiling reveals environmental and evolutionary drivers of fungal phylogeographic and metabolic diversity. *Nature communications*, 17(1).