

Resource Summary Report

Generated by [SPARC SAWG](#) on Jul 29, 2026

IBDLD

RRID:SCR_013043

Type: Tool

Proper Citation

IBDLD (RRID:SCR_013043)

Resource Information

URL: <http://sourceforge.net/projects/ibdld/>

Proper Citation: IBDLD (RRID:SCR_013043)

Description: A C++ software program for multipoint IBD estimation based on high density SNP genotype data.

Abbreviations: IBDLD

Resource Type: software resource

Defining Citation: [PMID:21769932](#)

Keywords: c++

Availability: Free

Resource Name: IBDLD

Resource ID: SCR_013043

Alternate IDs: OMICS_00204

Record Creation Time: 20220129T080314+0000

Record Last Update: 20260725T190742+0000

Ratings and Alerts

No rating or validation information has been found for IBDLD.

No alerts have been found for IBDLD.

Data and Source Information

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Chen J, et al. (2025) Investigating the genetic imprint of long body length, high lean meat rate, high fertility and long gestation period in Danish Landrace pigs. BMC genomics, 26(1), 869.

Kang Z, et al. (2023) Genome-wide single-nucleotide polymorphism data and mitochondrial hypervariable region 1 nucleotide sequence reveal the origin of the Akhal-Teke horse. Animal bioscience, 36(10), 1499.

Thumma BR, et al. (2022) Genomic studies with preselected markers reveal dominance effects influencing growth traits in Eucalyptus nitens. G3 (Bethesda, Md.), 12(1).

Mollon J, et al. (2021) Genetic influences on externalizing psychopathology overlap with cognitive functioning and show developmental variation. European psychiatry : the journal of the Association of European Psychiatrists, 64(1), e29.

Knowles EEM, et al. (2021) Genetic Overlap Profiles of Cognitive Ability in Psychotic and Affective Illnesses: A Multisite Study of Multiplex Pedigrees. Biological psychiatry, 90(6), 373.

Peypoch O, et al. (2020) The TAGA Study: A Study of Factors Determining Aortic Diameter in Families at High Risk of Abdominal Aortic Aneurysm Reveal Two New Candidate Genes. Journal of clinical medicine, 9(4).

Ma H, et al. (2019) The Origin of a Coastal Indigenous Horse Breed in China Revealed by Genome-Wide SNP Data. Genes, 10(3).

Johnson MP, et al. (2019) Glycated Serum Protein Genetics and Pleiotropy with Cardiometabolic Risk Factors. Journal of diabetes research, 2019, 2310235.

Wang X, et al. (2018) Methods and results from the genome-wide association group at GAW20. BMC genetics, 19(Suppl 1), 79.

Zhao P, et al. (2018) Evidence of evolutionary history and selective sweeps in the genome of Meishan pig reveals its genetic and phenotypic characterization. GigaScience, 7(5).

Blackburn NB, et al. (2018) Heritability and genetic associations of triglyceride and HDL-C levels using pedigree-based and empirical kinships. BMC proceedings, 12(Suppl 9), 34.

Porto A, et al. (2018) Reliability of genomic predictions of complex human phenotypes. BMC proceedings, 12(Suppl 9), 51.

Peralta JM, et al. (2018) Genome-wide linkage scan for loci influencing plasma triglyceride levels. BMC proceedings, 12(Suppl 9), 52.

Chiang CW, et al. (2016) Conflation of Short Identity-by-Descent Segments Bias Their Inferred Length Distribution. G3 (Bethesda, Md.), 6(5), 1287.