

Resource Summary Report

Generated by [dkNET](#) on Aug 31, 2026

LDMAP

RRID:SCR_006308

Type: Tool

Proper Citation

LDMAP (RRID:SCR_006308)

Resource Information

URL: <http://cedar.genetics.soton.ac.uk/pub/PROGRAMS/LDMAP>

Proper Citation: LDMAP (RRID:SCR_006308)

Description: Software program for constructing linkage disequilibrium (LD) maps. (entry from Genetic Analysis Software)

Abbreviations: LDMAP

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, c, unix, solaris

Resource Name: LDMAP

Resource ID: SCR_006308

Alternate IDs: nlx_154425

Record Creation Time: 20220129T080235+0000

Record Last Update: 20260829T183048+0000

Ratings and Alerts

No rating or validation information has been found for LDMAP.

No alerts have been found for LDMAP.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Senju C, et al. (2023) Deep intronic founder mutations identified in the ERCC4/XPF gene are potential therapeutic targets for a high-frequency form of xeroderma pigmentosum. Proceedings of the National Academy of Sciences of the United States of America, 120(27), e2217423120.

Lin M, et al. (2019) Haplotype analysis of SERPINE1 gene: Risk for aneurysmal subarachnoid hemorrhage and clinical outcomes. Molecular genetics & genomic medicine, 7(8), e737.

Andrade ACB, et al. (2019) Linkage disequilibrium and haplotype block patterns in popcorn populations. PloS one, 14(9), e0219417.

Sinoquet C, et al. (2018) A method combining a random forest-based technique with the modeling of linkage disequilibrium through latent variables, to run multilocus genome-wide association studies. BMC bioinformatics, 19(1), 106.

Segr?? AV, et al. (2010) Common inherited variation in mitochondrial genes is not enriched for associations with type 2 diabetes or related glycemic traits. PLoS genetics, 6(8).

Sandovici I, et al. (2006) Human imprinted chromosomal regions are historical hot-spots of recombination. PLoS genetics, 2(7), e101.

Gibson J, et al. (2005) Cosmopolitan linkage disequilibrium maps. Human genomics, 2(1), 20.

Maniatis N, et al. (2004) Positional cloning by linkage disequilibrium. American journal of human genetics, 74(5), 846.