

Resource Summary Report

Generated by [NIF](#) on Sep 3, 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 [NIF](#) .

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.