

Resource Summary Report

Generated by T1D on Aug 1, 2026

EMLD

RRID:SCR_009171

Type: Tool

Proper Citation

EMLD (RRID:SCR_009171)

Resource Information

URL: <https://github.com/gaow/genetic-analysis-software/blob/master/pages/EMLD.md>

Proper Citation: EMLD (RRID:SCR_009171)

Description: Software application to calculate pair-wise linkage disequilibrium based on SNP genotype data from unrelated individuals. EM algorithm is used to estimate pair-wise haplotype frequencies. The output file is in the format of input file for GOLD program, thus it can be directly plug into GOLD to get LD plots. (entry from Genetic Analysis Software)

Abbreviations: EMLD

Synonyms: EM estimation of haplotype frequencies and LD calculation

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, java, unix, ms-windows

Resource Name: EMLD

Resource ID: SCR_009171

Alternate IDs: nlx_154298

Old URLs: <http://epi.mdanderson.org/~qhuang/Software/pub.htm>

Record Creation Time: 20220129T080251+0000

Record Last Update: 20260731T042809+0000

Ratings and Alerts

No rating or validation information has been found for EMLD.

No alerts have been found for EMLD.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Rehberger Likozar A, et al. (2021) LPA Genotypes and Haplotypes Are Associated with Lipoprotein(a) Levels but Not Arterial Wall Properties in Stable Post-Coronary Event Patients with Very High Lipoprotein(a) Levels. *Journal of cardiovascular development and disease*, 8(12).

Lee Y, et al. (2020) Evidence for Divergent Selection on Immune Genes between the African Malaria Vectors, *Anopheles coluzzii* and *A. gambiae*. *Insects*, 11(12).

Ria M, et al. (2011) A common polymorphism in the promoter region of the TNFSF4 gene is associated with lower allele-specific expression and risk of myocardial infarction. *PloS one*, 6(3), e17652.

Costas J, et al. (2005) Relative efficiency of the linkage disequilibrium mapping approach in detecting candidate genes for schizophrenia in different European populations. *Genomics*, 86(3), 280.