Resource Summary Report

Generated by dkNET on Apr 17, 2025

PL-EM

RRID:SCR_009329
Type: Tool

Proper Citation

PL-EM (RRID:SCR_009329)

Resource Information

URL: http://www.people.fas.harvard.edu/~junliu/plem/

Proper Citation: PL-EM (RRID:SCR_009329)

Description: Software application (entry from Genetic Analysis Software)

Abbreviations: PL-EM

Synonyms: Partition-Ligation EM algorithm for haplotype inference with single nucleotide polymorphisms

Resource Type: software resource, software application

Keywords: gene, genetic, genomic

Funding:

Resource Name: PL-EM

Resource ID: SCR_009329

Alternate IDs: nlx_154537

Record Creation Time: 20220129T080252+0000

Record Last Update: 20250416T063544+0000

Ratings and Alerts

No rating or validation information has been found for PL-EM.

No alerts have been found for PL-EM.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 7 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Poras I, et al. (2017) Haplotypes of the HLA-G 3' Untranslated Region Respond to Endogenous Factors of HLA-G+ and HLA-G- Cell Lines Differentially. PloS one, 12(1), e0169032.

Dias FC, et al. (2015) Human leucocyte antigen-G (HLA-G) and its murine functional homolog Qa2 in the Trypanosoma cruzi Infection. Mediators of inflammation, 2015, 595829.

Martelli-Palomino G, et al. (2013) Polymorphic sites at the 3' untranslated region of the HLA-G gene are associated with differential hla-g soluble levels in the Brazilian and French population. PloS one, 8(10), e71742.

Kim S, et al. (2008) TNFR1 promoter -329G/T polymorphism results in allele-specific repression of TNFR1 expression. Biochemical and biophysical research communications, 368(2), 395.

Thompson SR, et al. (2007) A common interleukin 18 haplotype is associated with higher body mass index in subjects with diabetes and coronary heart disease. Metabolism: clinical and experimental, 56(5), 662.

Weale ME, et al. (2004) A survey of current software for haplotype phase inference. Human genomics, 1(2), 141.

Qin ZS, et al. (2002) Partition-ligation-expectation-maximization algorithm for haplotype inference with single-nucleotide polymorphisms. American journal of human genetics, 71(5), 1242.