Resource Summary Report

Generated by dkNET on Apr 18, 2025

LDSELECT

RRID:SCR_007010
Type: Tool

Proper Citation

LDSELECT (RRID:SCR_007010)

Resource Information

URL: http://droog.gs.washington.edu/ldSelect.html

Proper Citation: LDSELECT (RRID:SCR_007010)

Description: Software program that analyzes patterns of linkage disequilibrium (LD) between polymorphic sites in a locus, and bins the SNPs on the basis of a threshold level of LD as measured by r2. (entry from Genetic Analysis Software)

Abbreviations: LDSELECT

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, bio.tools

Funding:

Resource Name: LDSELECT

Resource ID: SCR_007010

Alternate IDs: biotools:ld_select, nlx_154426

Alternate URLs: https://bio.tools/ld_select

Record Creation Time: 20220129T080239+0000

Record Last Update: 20250416T063452+0000

Ratings and Alerts

No rating or validation information has been found for LDSELECT.

No alerts have been found for LDSELECT.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Shi Q, et al. (2023) rs66651343 and rs12909095 confer lung cancer risk by regulating CCNDBP1 expression. PloS one, 18(4), e0284347.

Shi Q, et al. (2022) Breast cancer-associated SNP rs72755295 is a cis-regulatory variation for human EXO1. Genetics and molecular biology, 45(4), e20210420.

Sandford AJ, et al. (2019) Adhesion molecule gene variants and plasma protein levels in patients with suspected obstructive sleep apnea. PloS one, 14(1), e0210732.

Li JX, et al. (2018) A functional SNP upstream of the ADRB2 gene is associated with COPD. International journal of chronic obstructive pulmonary disease, 13, 917.

Masalia RR, et al. (2018) Multiple genomic regions influence root morphology and seedling growth in cultivated sunflower (Helianthus annuus L.) under well-watered and water-limited conditions. PloS one, 13(9), e0204279.

Xie H, et al. (2016) Genetic variations in apoptosis pathway and the risk of ovarian cancer. Oncotarget, 7(35), 56737.

Wood AR, et al. (2015) Whole-genome sequencing to understand the genetic architecture of common gene expression and biomarker phenotypes. Human molecular genetics, 24(5), 1504.

Li H, et al. (2014) Pilot study demonstrating potential association between breast cancer image-based risk phenotypes and genomic biomarkers. Medical physics, 41(3), 031917.

Wang Y, et al. (2014) Integrative approach detected association between genetic variants of microRNA binding sites of TLRs pathway genes and OSCC susceptibility in Chinese Han population. PloS one, 9(7), e101695.

Yin J, et al. (2011) Genetic variants in TGF-? pathway are associated with ovarian cancer risk. PloS one, 6(9), e25559.

Yamada K, et al. (2011) Genome-wide association study of schizophrenia in Japanese population. PloS one, 6(6), e20468.

Haralambieva IH, et al. (2011) Genetic polymorphisms in host antiviral genes: associations with humoral and cellular immunity to measles vaccine. Vaccine, 29(48), 8988.

Haralambieva IH, et al. (2010) 2'-5'-Oligoadenylate synthetase single-nucleotide polymorphisms and haplotypes are associated with variations in immune responses to rubella vaccine. Human immunology, 71(4), 383.

Lee JC, et al. (2008) WW-domain-containing oxidoreductase is associated with low plasma HDL-C levels. American journal of human genetics, 83(2), 180.

Oliveira SA, et al. (2005) Identification of risk and age-at-onset genes on chromosome 1p in Parkinson disease. American journal of human genetics, 77(2), 252.