Resource Summary Report

Generated by dkNET on Apr 29, 2025

HAPLOBLOCKFINDER

RRID:SCR_005844
Type: Tool

Proper Citation

HAPLOBLOCKFINDER (RRID:SCR_005844)

Resource Information

URL: http://cgi.uc.edu/cgi-bin/kzhang/haploBlockFinder.cgi

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Description: Software package for haplotype block identification, visualization and htSNP selection. It can also compare the haplotype block structure with local LD pattern. The program can be either run as a web service, or standalone executables on local machine. (entry from Genetic Analysis Software)

Abbreviations: HAPLOBLOCKFINDER

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, c and perl, unix, ms-windows

Funding:

Resource Name: HAPLOBLOCKFINDER

Resource ID: SCR_005844

Alternate IDs: nlx_154380

Record Creation Time: 20220129T080232+0000

Record Last Update: 20250429T055017+0000

Ratings and Alerts

No rating or validation information has been found for HAPLOBLOCKFINDER.

No alerts have been found for HAPLOBLOCKFINDER.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Chen X, et al. (2009) Molecular population genetics of human CYP3A locus: signatures of positive selection and implications for evolutionary environmental medicine. Environmental health perspectives, 117(10), 1541.

Zhang F, et al. (2006) HDC gene polymorphisms are associated with age at natural menopause in Caucasian women. Biochemical and biophysical research communications, 348(4), 1378.

Carrick DM, et al. (2006) Genetic variations in ZFP36 and their possible relationship to autoimmune diseases. Journal of autoimmunity, 26(3), 182.

Fang Y, et al. (2005) Promoter and 3'-untranslated-region haplotypes in the vitamin d receptor gene predispose to osteoporotic fracture: the rotterdam study. American journal of human genetics, 77(5), 807.

Crawford DC, et al. (2004) Haplotype diversity across 100 candidate genes for inflammation, lipid metabolism, and blood pressure regulation in two populations. American journal of human genetics, 74(4), 610.

Carlson CS, et al. (2004) Selecting a maximally informative set of single-nucleotide polymorphisms for association analyses using linkage disequilibrium. American journal of human genetics, 74(1), 106.