Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 18, 2025

CHROMSCAN

RRID:SCR_013131
Type: Tool

Proper Citation

CHROMSCAN (RRID:SCR_013131)

Resource Information

URL: http://www.som.soton.ac.uk/research/geneticsdiv/epidemiology/chromscan/

Proper Citation: CHROMSCAN (RRID:SCR_013131)

Description: A statistical based program for association mapping of disease genes. It utilises the Malecot model and the linkage disequilibrium (LD) map for the candidate region to analyse the genotypes derive from large sample of matched cases and controls. (entry from Genetic Analysis Software)

Abbreviations: CHROMSCAN

Resource Type: software resource, software application

Keywords: gene, genetic, genomic

Funding:

Resource Name: CHROMSCAN

Resource ID: SCR_013131

Alternate IDs: nlx_154272

Record Creation Time: 20220129T080314+0000

Record Last Update: 20250416T063637+0000

Ratings and Alerts

No rating or validation information has been found for CHROMSCAN.

No alerts have been found for CHROMSCAN.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Zhang W, et al. (2007) Impact of marker density on the accuracy of association mapping. BMC proceedings, 1 Suppl 1(Suppl 1), S166.

Kuo TY, et al. (2007) Association mapping of susceptibility loci for rheumatoid arthritis. BMC proceedings, 1 Suppl 1(Suppl 1), S15.