Resource Summary Report

Generated by NIF on Apr 18, 2025

MAP-O-MAT

RRID:SCR_008197
Type: Tool

Proper Citation

MAP-O-MAT (RRID:SCR_008197)

Resource Information

URL: https://bioinformatics.oxfordjournals.org/content/21/4/557.full.pdf

Proper Citation: MAP-O-MAT (RRID:SCR_008197)

Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented August 18, 2016. MAP-O-MAT is a web-based server for automated linkage mapping of human polymorphic DNA markers. The server uses publicly available genotype data for over 15,000 markers. It facilitates the verification of order and map distances for custom mapping sets using genotype data from the CEPH database, and from the Marshfield, SNP Consortium and Rutgers linkage maps. The CRI-MAP program is used for likelihood calculations and some mapping algorithms, and physical map positions are provided from the human genome assembly.

Synonyms: MAP-O-MAT

Resource Type: analysis service resource, data analysis service, service resource, production service resource

Keywords: general human genetics databases, automated, distance, dna, genotype, human, linkage, map, mapping, marker, polymorphic, position, verification

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: MAP-O-MAT

Resource ID: SCR_008197

Alternate IDs: nif-0000-21251

Old URLs: http://compgen.rutgers.edu/mapomat/

Record Creation Time: 20220129T080246+0000

Record Last Update: 20250418T055156+0000

Ratings and Alerts

No rating or validation information has been found for MAP-O-MAT.

No alerts have been found for MAP-O-MAT.

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 NIF.

Christiansen M, et al. (2014) Mutations in Danish patients with long QT syndrome and the identification of a large founder family with p.F29L in KCNH2. BMC medical genetics, 15, 31.

Silveira AC, et al. (2010) Convergence of linkage, gene expression and association data demonstrates the influence of the RAR-related orphan receptor alpha (RORA) gene on neovascular AMD: a systems biology based approach. Vision research, 50(7), 698.