Resource Summary Report

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LINKDATAGEN

RRID:SCR_015625
Type: Tool

Proper Citation

LINKDATAGEN (RRID:SCR_015625)

Resource Information

URL: http://bioinf.wehi.edu.au/software/linkdatagen

Proper Citation: LINKDATAGEN (RRID:SCR_015625)

Description: Perl tool that generates linkage mapping input files using data from HAPMAP Phase III populations. It provides rudimentary error checks and is easily amended for personal linkage mapping preferences.

Resource Type: data processing software, sequence analysis software, data analysis software, software resource, software application

Defining Citation: PMID:19435744, PMID:21917141

Keywords: annotation, snp, sequencing, genome, linkage, mapping, perl, hapmap phase iii

Funding: NHMRC 461269;
NHMRC 490037;
NHMRC 406657

Availability: Free, Available for download

Resource Name: LINKDATAGEN

Resource ID: SCR_015625

Record Creation Time: 20220129T080326+0000

Record Last Update: 20250429T055747+0000

Ratings and Alerts

No rating or validation information has been found for LINKDATAGEN.

No alerts have been found for LINKDATAGEN.

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 FDI Lab - SciCrunch.org.

Carrion-Castillo A, et al. (2021) Whole-genome sequencing identifies functional noncoding variation in SEMA3C that cosegregates with dyslexia in a multigenerational family. Human genetics, 140(8), 1183.

Toma C, et al. (2020) Using linkage studies combined with whole-exome sequencing to identify novel candidate genes for familial colorectal cancer. International journal of cancer, 146(6), 1568.

Toma C, et al. (2019) Identification of a Novel Candidate Gene for Serrated Polyposis Syndrome Germline Predisposition by Performing Linkage Analysis Combined With Whole-Exome Sequencing. Clinical and translational gastroenterology, 10(10), e00100.

Rafehi H, et al. (2019) Bioinformatics-Based Identification of Expanded Repeats: A Non-reference Intronic Pentamer Expansion in RFC1 Causes CANVAS. American journal of human genetics, 105(1), 151.

Marsh AP, et al. (2015) Complete callosal agenesis, pontocerebellar hypoplasia, and axonal neuropathy due to AMPD2 loss. Neurology. Genetics, 1(2), e16.

Guimier A, et al. (2015) MMP21 is mutated in human heterotaxy and is required for normal left-right asymmetry in vertebrates. Nature genetics, 47(11), 1260.

Doi H, et al. (2014) Late-onset spastic ataxia phenotype in a patient with a homozygous DDHD2 mutation. Scientific reports, 4, 7132.