Resource Summary Report

Generated by dkNET on Apr 19, 2025

HAP-SAMPLE

RRID:SCR_009234
Type: Tool

Proper Citation

HAP-SAMPLE (RRID:SCR_009234)

Resource Information

URL: http://www.hapsample.org/

Proper Citation: HAP-SAMPLE (RRID:SCR_009234)

Description: Web application for simulating SNP genotypes for case-control and affected-child trio studies by resampling from Phase I/II HapMap SNP data. The user provides a list of SNPs to be genotyped, along with a disease model file that describes causal SNPs and their effect sizes. The simulation tool is appropriate for candidate regions or whole-genome scans. (entry from Genetic Analysis Software)

Abbreviations: HAP-SAMPLE

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

Keywords: gene, genetic, genomic, web-based

Funding:

Resource Name: HAP-SAMPLE

Resource ID: SCR_009234

Alternate IDs: nlx_154392

Record Creation Time: 20220129T080251+0000

Record Last Update: 20250418T055215+0000

Ratings and Alerts

No rating or validation information has been found for HAP-SAMPLE.

No alerts have been found for HAP-SAMPLE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Fang G, et al. (2012) High-order SNP combinations associated with complex diseases: efficient discovery, statistical power and functional interactions. PloS one, 7(4), e33531.

Hou L, et al. (2011) Validation of a cost-efficient multi-purpose SNP panel for disease based research. PloS one, 6(5), e19699.

Aguiar-Pulido V, et al. (2010) Machine learning techniques for single nucleotide polymorphism--disease classification models in schizophrenia. Molecules (Basel, Switzerland), 15(7), 4875.

Liu Y, et al. (2008) A survey of genetic simulation software for population and epidemiological studies. Human genomics, 3(1), 79.