Resource Summary Report

Generated by NIF on Apr 21, 2025

GENECOUNTING

RRID:SCR_009189
Type: Tool

Proper Citation

GENECOUNTING (RRID:SCR_009189)

Resource Information

URL: http://www.mybiosoftware.com/genecounting-2-2-gene-counting-haplotype-analysis.html

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Description: THIS RESOURCE IS NO LONGER IN SERVCE, documented September 22, 2016. Software application for gene-counting for haplotype analysis with permutation tests for global association and specific haplotypes, accounting for missing data.

Abbreviations: GENECOUNTING

Resource Type: software resource, software application

Defining Citation: PMID:12490459

Keywords: gene, genetic, genomic, c, ms-windows, unix, solaris, linux

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: GENECOUNTING

Resource ID: SCR_009189

Alternate IDs: nlx_154329

Old URLs: http://www.mrc-epid.cam.ac.uk/Personal/jinghua.zhao/software/

Record Creation Time: 20220129T080251+0000

Record Last Update: 20250421T053722+0000

Ratings and Alerts

No rating or validation information has been found for GENECOUNTING.

No alerts have been found for GENECOUNTING.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Yan S, et al. (2021) The effect of common variants in GDF5 gene on the susceptibility to chronic postsurgical pain. Journal of orthopaedic surgery and research, 16(1), 420.

Liu B, et al. (2018) Common variants in the GNL3 contribute to the increasing risk of knee osteoarthritis in Han Chinese population. Scientific reports, 8(1), 9610.

Sun P, et al. (2018) MDM4 contributes to the increased risk of glioma susceptibility in Han Chinese population. Scientific reports, 8(1), 11093.

Wang N, et al. (2017) Additional evidence supports association of common genetic variants in VTI1A and ETFA with increased risk of glioma susceptibility. Journal of the neurological sciences, 375, 282.

Liu B, et al. (2017) Association of common genetic variants in VEGFA with biliary atresia susceptibility in Northwestern Han Chinese. Gene, 628, 87.

Guan F, et al. (2016) Two-stage association study to identify the genetic susceptibility of a novel common variant of rs2075290 in ZPR1 to type 2 diabetes. Scientific reports, 6, 29586.

Zhi L, et al. (2016) Association of common variants in MTAP with susceptibility and overall survival of osteosarcoma: a two-stage population-based study in Han Chinese. Journal of Cancer, 7(15), 2179.

Guan F, et al. (2016) Evaluation of association of common variants in HTR1A and HTR5A with schizophrenia and executive function. Scientific reports, 6, 38048.

Chang M, et al. (2015) Evaluation of relationship between GRM3 polymorphisms and cognitive function in schizophrenia of Han Chinese. Psychiatry research, 229(3), 1043.

Guan F, et al. (2015) Evaluation of genetic susceptibility of common variants in CACNA1D with schizophrenia in Han Chinese. Scientific reports, 5, 12935.

Hua T, et al. (2014) Nuclear factor-kappa B1 is associated with gastric cancer in a Chinese population. Medicine, 93(28), e279.

Lochman J, et al. (2013) Preliminary evidence for association between schizophrenia and polymorphisms in the regulatory Regions of the ADRA2A, DRD3 and SNAP-25 Genes. Psychiatry research, 205(1-2), 7.