Resource Summary Report

Generated by dkNET on Apr 17, 2025

HEGESMA

RRID:SCR_013304
Type: Tool

Proper Citation

HEGESMA (RRID:SCR_013304)

Resource Information

URL: http://biomath.med.uth.gr

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Description: Software application for performing genome scan meta-analysis, a quantitative method to identify genetic regions (bins) with consistently increased linkage score across multiple genome scans, and for testing the heterogeneity of the results of each bin across scans. The program provides as an output the average of ranks and three heterogeneity statistics, as well as corresponding significance levels. (entry from Genetic Analysis Software)

Synonyms: HEterogeneity and GEnome Search Meta Analysis

Resource Type: software resource, software application

Keywords: gene, genetic, genomic

Funding:

Resource Name: HEGESMA

Resource ID: SCR_013304

Alternate IDs: nlx_154396

Record Creation Time: 20220129T080315+0000

Record Last Update: 20250416T063639+0000

Ratings and Alerts

No rating or validation information has been found for HEGESMA.

No alerts have been found for HEGESMA.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Ding X, et al. (2021) Association of Immune and Inflammatory Gene Polymorphism With the Risk of IgA Nephropathy: A Systematic Review and Meta-Analysis of 45 Studies. Frontiers in immunology, 12, 683913.

Tziastoudi M, et al. (2021) Serpin Family E Member 1 Tag Single-Nucleotide Polymorphisms in Patients with Diabetic Nephropathy: An Association Study and Meta-Analysis Using a Genetic Model-Free Approach. Genes, 12(12).

Tziastoudi M, et al. (2020) The genetic map of diabetic nephropathy: evidence from a systematic review and meta-analysis of genetic association studies. Clinical kidney journal, 13(5), 768.

Bastami M, et al. (2019) Evidences from a Systematic Review and Meta-Analysis Unveil the Role of MiRNA Polymorphisms in the Predisposition to Female Neoplasms. International journal of molecular sciences, 20(20).

Stefanidis I, et al. (2018) The contribution of genetic variants of SLC2A1 gene in T2DM and T2DM-nephropathy: association study and meta-analysis. Renal failure, 40(1), 561.

Tziastoudi M, et al. (2017) A systematic review and meta-analysis of genetic association studies for the role of inflammation and the immune system in diabetic nephropathy. Clinical kidney journal, 10(3), 293.

Sun J, et al. (2015) Obstructive Sleep Apnea Susceptibility Genes in Chinese Population: A Field Synopsis and Meta-Analysis of Genetic Association Studies. PloS one, 10(8), e0135942.

Zhong A, et al. (2014) An updated meta-analysis of the association between tumor necrosis factor-? -308G/A polymorphism and obstructive sleep apnea-hypopnea syndrome. PloS one, 9(9), e106270.

Zeng Z, et al. (2014) Three single nucleotide variants of the HDAC gene are associated with

type 2 diabetes mellitus in a Chinese population: a community-based case-control study. Gene, 533(1), 427.

Liao YC, et al. (2013) Lack of association between a functional variant of the BRCA-1 related associated protein (BRAP) gene and ischemic stroke. BMC medical genetics, 14, 17.

Ziakas PD, et al. (2013) The role of TLR4 896 A>G and 1196 C>T in susceptibility to infections: a review and meta-analysis of genetic association studies. PloS one, 8(11), e81047.

Jin C, et al. (2013) GAB2 polymorphism rs2373115 confers susceptibility to sporadic Alzheimer's disease. Neuroscience letters, 556, 216.

Zintzaras E, et al. (2011) Estimating the mode of inheritance in genetic association studies of qualitative traits based on the degree of dominance index. BMC medical research methodology, 11, 171.

Partsinevelou A, et al. (2009) Quality of reporting of randomized controlled trials in polycystic ovary syndrome. Trials, 10, 106.