

Resource Summary Report

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INTERSNP

RRID:SCR_009244

Type: Tool

Proper Citation

INTERSNP (RRID:SCR_009244)

Resource Information

URL: <http://intersnp.meb.uni-bonn.de/>

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Description: Software application for genome-wide interaction analysis (GWIA) of case-control SNP data. SNPs are selected for joint analysis using a priori information. Sources of information to define meaningful strategies can be statistical evidence (single marker association at a moderate level, computed from the own data) and genetic/biologic relevance (genomic location, function class or pathway information). (entry from Genetic Analysis Software)

Abbreviations: INTERSNP

Synonyms: genome-wide association and INTERaction analysis of SNP

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, c/c++, unix, ms-windows, macos

Resource Name: INTERSNP

Resource ID: SCR_009244

Alternate IDs: nlx_154409

Record Creation Time: 20220129T080251+0000

Record Last Update: 20260727T040447+0000

Ratings and Alerts

No rating or validation information has been found for INTERSNP.

No alerts have been found for INTERSNP.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 18 mentions in open access literature.

Listed below are recent publications. The full list is available at [nidm-terms](#) .

Xu X, et al. (2022) Systems Genetic Identification of Mitochondrion-Associated Alzheimer's Disease Genes and Implications for Disease Risk Prediction. *Biomedicines*, 10(8).

Ghasemi S, et al. (2022) Discovery of novel eGFR-associated multiple independent signals using a quasi-adaptive method. *Frontiers in genetics*, 13, 997302.

Yashin AI, et al. (2021) Roles of interacting stress-related genes in lifespan regulation: insights for translating experimental findings to humans. *Journal of translational genetics and genomics*, 5(4), 357.

Ukrainitseva S, et al. (2021) Interactions Between Genes From Aging Pathways May Influence Human Lifespan and Improve Animal to Human Translation. *Frontiers in cell and developmental biology*, 9, 692020.

Slim L, et al. (2020) Novel methods for epistasis detection in genome-wide association studies. *PloS one*, 15(11), e0242927.

Mangelson H, et al. (2019) The genome of *Chenopodium pallidicaule*: An emerging Andean super grain. *Applications in plant sciences*, 7(11), e11300.

Maughan PJ, et al. (2019) Genomic insights from the first chromosome-scale assemblies of oat (*Avena* spp.) diploid species. *BMC biology*, 17(1), 92.

Chattopadhyay S, et al. (2018) Enrichment of B cell receptor signaling and epidermal growth factor receptor pathways in monoclonal gammopathy of undetermined significance: a genome-wide genetic interaction study. *Molecular medicine (Cambridge, Mass.)*, 24(1), 30.

Lightfoot DJ, et al. (2017) Single-molecule sequencing and Hi-C-based proximity-guided assembly of amaranth (*Amaranthus hypochondriacus*) chromosomes provide insights into genome evolution. *BMC biology*, 15(1), 74.

Page JT, et al. (2016) DNA Sequence Evolution and Rare Homoeologous Conversion in Tetraploid Cotton. *PLoS genetics*, 12(5), e1006012.

Hohman TJ, et al. (2016) Discovery of gene-gene interactions across multiple independent data sets of late onset Alzheimer disease from the Alzheimer Disease Genetics Consortium. *Neurobiology of aging*, 38, 141.

Yan J, et al. (2015) Hippocampal transcriptome-guided genetic analysis of correlated episodic memory phenotypes in Alzheimer's disease. *Frontiers in genetics*, 6, 117.

Grigoriu-Serbanescu M, et al. (2015) Association of age-of-onset groups with GWAS significant schizophrenia and bipolar disorder loci in Romanian bipolar I patients. *Psychiatry research*, 230(3), 964.

Musameh MD, et al. (2015) Analysis of gene-gene interactions among common variants in candidate cardiovascular genes in coronary artery disease. *PloS one*, 10(2), e0117684.

Huang Y, et al. (2015) Molecular Basis of Gene-Gene Interaction: Cyclic Cross-Regulation of Gene Expression and Post-GWAS Gene-Gene Interaction Involved in Atrial Fibrillation. *PLoS genetics*, 11(8), e1005393.

Li J, et al. (2015) Genetic Interactions Explain Variance in Cingulate Amyloid Burden: An AV-45 PET Genome-Wide Association and Interaction Study in the ADNI Cohort. *BioMed research international*, 2015, 647389.

Meda SA, et al. (2013) Genetic interactions associated with 12-month atrophy in hippocampus and entorhinal cortex in Alzheimer's Disease Neuroimaging Initiative. *Neurobiology of aging*, 34(5), 1518.e9.

Herold C, et al. (2013) A one-degree-of-freedom test for supra-multiplicativity of SNP effects. *PloS one*, 8(10), e78038.