Resource Summary Report

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F-SNP: a collection of functional SNPs, specifically prioritized for disease association studies

RRID:SCR_007653
Type: Tool

Proper Citation

F-SNP: a collection of functional SNPs, specifically prioritized for disease association studies (RRID:SCR_007653)

Resource Information

URL: http://compbio.cs.queensu.ca/F-SNP/

Proper Citation: F-SNP: a collection of functional SNPs, specifically prioritized for disease association studies (RRID:SCR_007653)

Description: F-SNP database provides integrated information about the functional effects of SNPs obtained from 16 bioinformatics tools and databases. The functional effects are predicted and indicated at the splicing, transcriptional, translational, and post-translational level. As such, the F-SNP database helps identify and focus on SNPs with potential pathological effect to human health. Users can find SNP's based on ID, associated disease, gene, or chromosomal region.

Synonyms: F-SNP

Resource Type: data or information resource, database

Keywords: functional snp, disease-associated snp, snp, snp functional effect, snp pathogenicity, FASEB list

Resource Name: F-SNP: a collection of functional SNPs, specifically prioritized for disease association studies

Resource ID: SCR_007653

Alternate IDs: nif-0000-02832

Record Creation Time: 20220129T080243+0000

Record Last Update: 20260806T054445+0000

Ratings and Alerts

No rating or validation information has been found for F-SNP: a collection of functional SNPs, specifically prioritized for disease association studies.

No alerts have been found for F-SNP: a collection of functional SNPs, specifically prioritized for disease association studies.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 131 mentions in open access literature.

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

Wu P, et al. (2024) MiRNA polymorphisms affect the prognosis of gastric cancer: insights from Xianyou, Fujian. Frontiers in oncology, 14, 1355270.

Wang H, et al. (2022) Circulating Inflammatory Mediators and Genetic Polymorphisms of Inflammation Mediators and Their Association with Factors Related to Abdominal Aortic Aneurysm: A Systemic Review and Meta-Analysis. Reviews in cardiovascular medicine, 23(8), 270.

Shinwari K, et al. (2021) Predicting the Most Deleterious Missense Nonsynonymous Single-Nucleotide Polymorphisms of Hennekam Syndrome-Causing CCBE1 Gene, In Silico Analysis. TheScientificWorldJournal, 2021, 6642626.

Kuang D, et al. (2021) SOCS3 Gene Polymorphism and Hypertension Susceptibility in Chinese Population: A Two-Center Case-Control Study. BioMed research international, 2021, 8445461.

Wang Y, et al. (2021) Polygenic risk of genes involved in the catecholamine and serotonin pathways for ADHD in children. Neuroscience letters, 760, 136086.

Li D, et al. (2020) The functional variant of NTN1 contributes to the risk of nonsyndromic cleft lip with or without cleft palate. European journal of human genetics : EJHG, 28(4), 453.

Hu WN, et al. (2020) Relationship between Long Noncoding RNA H19 Polymorphisms and Risk of Coronary Artery Disease in a Chinese Population: A Case-Control Study. Disease markers, 2020, 9839612.

Pourmoshir N, et al. (2020) hsa-miR-423 rs6505162 Is Associated with The Increased Risk of Breast Cancer in Isfahan Central Province of Iran. Cell journal, 22(Suppl 1), 110.

Miyamoto Y, et al. (2020) A polymorphism in the cachexia-associated gene INHBA predicts efficacy of regorafenib in patients with refractory metastatic colorectal cancer. PloS one, 15(9), e0239439.

Chatterjee M, et al. (2020) Folate System Gene Variant rs1801394 66A>G may have a Causal Role in Down Syndrome in the Eastern Indian Population. International journal of molecular and cellular medicine, 9(3), 215.

Guo F, et al. (2020) Correlation Between TNFAIP2 Gene Polymorphism and Prediction/Prognosis for Gastric Cancer and Its Effect on TNFAIP2 Protein Expression. Frontiers in oncology, 10, 1127.

Caja F, et al. (2020) DNA Mismatch Repair Gene Variants in Sporadic Solid Cancers. International journal of molecular sciences, 21(15).

Siasi E, et al. (2020) Associations of Single Nucleotide Polymorphism in miR-146a Gene with Susceptibility to Breast Cancer in the Iranian Female. Asian Pacific journal of cancer prevention : APJCP, 21(6), 1585.

Sio YY, et al. (2020) The Asthma-associated PER1-like domain-containing protein 1 (PERLD1) Haplotype Influences Soluble Glycosylphosphatidylinositol Anchor Protein (sGPI-AP) Levels in Serum and Immune Cell Proliferation. Scientific reports, 10(1), 715.

Suenaga M, et al. (2020) Single Nucleotide Polymorphisms in MiRNA Binding Sites of Nucleotide Excision Repair-Related Genes Predict Clinical Benefit of Oxaliplatin in FOLFOXIRI Plus Bevacizumab: Analysis of the TRIBE Trial. Cancers, 12(7).

Chen X, et al. (2019) Stress response genes associated with attention deficit hyperactivity disorder: A case-control study in Chinese children. Behavioural brain research, 363, 126.

Chen G, et al. (2019) Association Study of Myosin Heavy Chain 15 Polymorphisms with Asthma Susceptibility in Chinese Han. BioMed research international, 2019, 3805405.

Ding D, et al. (2019) Polymorphisms in DNA methylation-related genes are linked to the phenotype of Machado-Joseph disease. Neurobiology of aging, 75, 225.e1.

Xie X, et al. (2019) Polymorphisms of Ionotropic Glutamate Receptor-Related Genes and the Risk of Autism Spectrum Disorder in a Chinese Population. Psychiatry investigation, 16(5), 379.

Hsieh FI, et al. (2019) Combined Effects of MMP-7, MMP-8 and MMP-26 on the Risk of Ischemic Stroke. Journal of clinical medicine, 8(11).