Resource Summary Report

Generated by dkNET on Sep 5, 2026

SeattleSNPs - Variation Discovery Resource

RRID:SCR_001859
Type: Tool

Proper Citation

SeattleSNPs - Variation Discovery Resource (RRID:SCR_001859)

Resource Information

URL: http://pga.gs.washington.edu

Proper Citation: SeattleSNPs - Variation Discovery Resource (RRID:SCR_001859)

Description: The SeattleSNPs PGA is focused on identifying, genotyping, and modeling the associations between single nucleotide polymorphisms (SNPs) in candidate genes and pathways that underlie inflammatory responses in humans. SeattleSNPs is focused on variation analysis in genes related to the inflammatory response. These gene targets are found in specific pathways and from interacting molecules contributing to this response. Available Resources: - Baseline assembled and complete genomic sequence and chromosomal location for candidate gene targets - Mapping of exon and repeat structure for candidate genes - Amplification primers and conditions - SNPs mapped by location in gene structure - SNPs with immediate surrounding sequence for genotype assay design - Genotypes and relative allele frequencies of the SNPs - Special features of SNPs - location (5', coding, etc.), amino acid substitutions, recurrent variation - Manuals on all protocols, data analysis procedures, and use of software tools - Workshop on genetic variation analysis and a gene submission program for variation analysis Sponsors: SeattleSNPs is funded as part of the National Heart Lung and Blood Institute's (NHLBI) Programs for Genomic Applications (PGA).

Synonyms: SeattleSNPs

Resource Type: data or information resource, narrative resource, portal, software resource, topical portal, training material

Keywords: exon, gene, gene target, allele, amino acid, amplification, assay, chromosomal, genomic sequence, genotyping, humans, inflammatory response, molecule, pathway, primer, recurrent varation, repeat structure, singe nucleotide polymorphism (snp), substitution, variation analysis

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: SeattleSNPs - Variation Discovery Resource

Resource ID: SCR_001859

Alternate IDs: nif-0000-10423

Old URLs: http://pga.mbt.washington.edu/

Record Creation Time: 20220129T080210+0000

Record Last Update: 20260903T234505+0000

Ratings and Alerts

No rating or validation information has been found for SeattleSNPs - Variation Discovery Resource.

No alerts have been found for SeattleSNPs - Variation Discovery Resource.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 62 mentions in open access literature.

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

Xie Y, et al. (2023) Variants in genes related to inflammation and endothelial function can increase the risk for carotid atherosclerosis in southwestern China. Frontiers in neurology, 14, 1174425.

Johri P, et al. (2023) Developing an evolutionary baseline model for humans: jointly inferring purifying selection with population history. bioRxiv : the preprint server for biology.

Johri P, et al. (2023) Developing an Evolutionary Baseline Model for Humans: Jointly Inferring Purifying Selection with Population History. Molecular biology and evolution, 40(5).

Wysocka A, et al. (2021) The Relevance of Noncoding DNA Variations of Paraoxonase Gene Cluster in Atherosclerosis-Related Diseases. International journal of molecular sciences, 22(4).

Yi X, et al. (2020) Variants in clopidogrel-relevant genes and early neurological deterioration in ischemic stroke patients receiving clopidogrel. BMC neurology, 20(1), 159.

Liu CW, et al. (2020) The association of inflammasome and TLR2 gene polymorphisms with susceptibility to tuberculosis in the Han Taiwanese population. Scientific reports, 10(1), 10184.

Yi X, et al. (2020) Inflammation and Endothelial Function Relevant Genetic Polymorphisms and Carotid Plaque in Chinese Population. Journal of atherosclerosis and thrombosis, 27(9), 978.

Pirim D, et al. (2019) Apolipoprotein E-C1-C4-C2 gene cluster region and inter-individual variation in plasma lipoprotein levels: a comprehensive genetic association study in two ethnic groups. PloS one, 14(3), e0214060.

Lin CJ, et al. (2019) Polymorphisms of suppressor of cytokine signaling-3 associated with susceptibility to tuberculosis among Han Taiwanese. Cytokine, 114, 11.

Yasmin , et al. (2018) The matrix proteins aggrecan and fibulin-1 play a key role in determining aortic stiffness. Scientific reports, 8(1), 8550.

Yi X, et al. (2018) Interactions among variants in TXA2R, P2Y12 and GPIIIa are associated with carotid plaque vulnerability in Chinese population. Oncotarget, 9(25), 17597.

Liang Y, et al. (2017) Shared polymorphisms and modifiable behavior factors for myocardial infarction and high cholesterol in a retrospective population study. Medicine, 96(37), e7683.

Yi X, et al. (2016) Concomitant Use of Proton Pump Inhibitors and Clopidogrel Is Not Associated with Adverse Outcomes after Ischemic Stroke in Chinese Population. Journal of stroke and cerebrovascular diseases : the official journal of National Stroke Association, 25(12), 2859.

Oliveira-Paula GH, et al. (2016) Endothelial nitric oxide synthase tagSNPs influence the effects of enalapril in essential hypertension. Nitric oxide : biology and chemistry, 55-56, 62.

Yi X, et al. (2016) Interaction between COX-1 and COX-2 Variants Associated with Aspirin Resistance in Chinese Stroke Patients. Journal of stroke and cerebrovascular diseases : the official journal of National Stroke Association, 25(9), 2136.

Mackness M, et al. (2015) Human paraoxonase-1 (PON1): Gene structure and expression, promiscuous activities and multiple physiological roles. Gene, 567(1), 12.

Bressler J, et al. (2015) Sequence variation in telomerase reverse transcriptase (TERT) as a determinant of risk of cardiovascular disease: the Atherosclerosis Risk in Communities (ARIC) study. BMC medical genetics, 16, 52.

Wu F, et al. (2015) Interaction between arsenic exposure from drinking water and genetic polymorphisms on cardiovascular disease in Bangladesh: a prospective case-cohort study. Environmental health perspectives, 123(5), 451.

Farzan SF, et al. (2015) Gene-arsenic interaction in longitudinal changes of blood pressure: Findings from the Health Effects of Arsenic Longitudinal Study (HEALS) in Bangladesh. Toxicology and applied pharmacology, 288(1), 95.

Wu F, et al. (2014) Interaction between arsenic exposure from drinking water and genetic susceptibility in carotid intima-media thickness in Bangladesh. Toxicology and applied pharmacology, 276(3), 195.