

# Resource Summary Report

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## GENETIC POWER CALCULATOR

RRID:SCR\_009198

Type: Tool

### Proper Citation

GENETIC POWER CALCULATOR (RRID:SCR\_009198)

### Resource Information

**URL:** <http://pngu.mgh.harvard.edu/~purcell/gpc/>

**Proper Citation:** GENETIC POWER CALCULATOR (RRID:SCR\_009198)

**Description:** Software application for automated power analysis for variance components (VC) quantitative trait locis (QTL) linkage and association tests in sibships, and other common tests (entry from Genetic Analysis Software)

**Abbreviations:** GENETIC POWER CALCULATOR

**Resource Type:** software application, software resource

**Keywords:** gene, genetic, genomic

**Resource Name:** GENETIC POWER CALCULATOR

**Resource ID:** SCR\_009198

**Alternate IDs:** nlx\_154340

**Record Creation Time:** 20220129T080251+0000

**Record Last Update:** 20260805T044219+0000

### Ratings and Alerts

No rating or validation information has been found for GENETIC POWER CALCULATOR.

No alerts have been found for GENETIC POWER CALCULATOR.

### Data and Source Information

**Source:** [SciCrunch Registry](#)

## Usage and Citation Metrics

We found 219 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [RRID](#) .

Sopori S, et al. (2024) CLOCK gene 3'UTR and exon 9 polymorphisms show a strong association with essential hypertension in a North Indian population. *BMC medical genomics*, 17(1), 289.

Sequera HDG, et al. (2023) Variants of CARD8 in *Leishmania guyanensis*-cutaneous leishmaniasis and influence of the variants genotypes on circulating plasma cytokines IL-1 ?, TNF? and IL-8. *PLoS neglected tropical diseases*, 17(6), e0011416.

Buraczynska M, et al. (2021) LDLR gene polymorphism (rs688) affects susceptibility to cardiovascular disease in end-stage kidney disease patients. *BMC nephrology*, 22(1), 316.

Xiang H, et al. (2020) Relationships of interleukin-17 polymorphisms with recurrent aphthous ulcer risk in a Han Chinese population. *The Journal of international medical research*, 48(12), 300060520976833.

van Dijk BJ, et al. (2020) Complement C5 Contributes to Brain Injury After Subarachnoid Hemorrhage. *Translational stroke research*, 11(4), 678.

Oka A, et al. (2020) Alopecia areata susceptibility variant in MHC region impacts expressions of genes contributing to hair keratinization and is involved in hair loss. *EBioMedicine*, 57, 102810.

Hong EP, et al. (2019) Genomic Variations in Susceptibility to Intracranial Aneurysm in the Korean Population. *Journal of clinical medicine*, 8(2).

Fan BJ, et al. (2018) Family-Based Genome-Wide Association Study of South Indian Pedigrees Supports WNT7B as a Central Corneal Thickness Locus. *Investigative ophthalmology & visual science*, 59(6), 2495.

Visconti A, et al. (2018) Genome-wide association study in 176,678 Europeans reveals genetic loci for tanning response to sun exposure. *Nature communications*, 9(1), 1684.

Hong EP, et al. (2017) Risk prediction of pulmonary tuberculosis using genetic and conventional risk factors in adult Korean population. *PloS one*, 12(3), e0174642.

Chang CH, et al. (2017) Arterial stiffness and blood pressure improvement in aldosterone-producing adenoma harboring KCNJ5 mutations after adrenalectomy. *Oncotarget*, 8(18), 29984.

Kantojärvi K, et al. (2017) Variants in calcium voltage-gated channel subunit Alpha1 C-gene (CACNA1C) are associated with sleep latency in infants. *PloS one*, 12(8), e0180652.

Ishizuka K, et al. (2017) Rare genetic variants in CX3CR1 and their contribution to the increased risk of schizophrenia and autism spectrum disorders. *Translational psychiatry*, 7(8), e1184.

Son CN, et al. (2017) ABCG2 Polymorphism Is Associated with Hyperuricemia in a Study of a Community-Based Korean Cohort. *Journal of Korean medical science*, 32(9), 1451.

Robinson PC, et al. (2016) Exome-wide study of ankylosing spondylitis demonstrates additional shared genetic background with inflammatory bowel disease. *NPJ genomic medicine*, 1, 16008.

Buraczynska M, et al. (2016) Effect of G(-174)C polymorphism in interleukin-6 gene on cardiovascular disease in type 2 diabetes patients. *Cytokine*, 79, 7.

Fuchsberger C, et al. (2016) The genetic architecture of type 2 diabetes. *Nature*, 536(7614), 41.

Binder MD, et al. (2016) Common and Low Frequency Variants in MERTK Are Independently Associated with Multiple Sclerosis Susceptibility with Discordant Association Dependent upon HLA-DRB1\*15:01 Status. *PLoS genetics*, 12(3), e1005853.

Buraczynska M, et al. (2016) Association between functional variant of inflammatory system gene (PSMA6) and end-stage kidney disease. *International urology and nephrology*, 48(12), 2083.

Banday MZ, et al. (2016) Tumor necrosis factor- $\alpha$  (TNF- $\alpha$ )-308G/A promoter polymorphism in colorectal cancer in ethnic Kashmiri population - A case control study in a detailed perspective. *Meta gene*, 9, 128.