# 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

**Funding:**

**Resource Name:** GENETIC POWER CALCULATOR

**Resource ID:** SCR_009198

**Alternate IDs:** nlx_154340

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

**Record Last Update:** 20250412T055354+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 dkNET.


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.

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.

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

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.

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.

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

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.

Khan RAW, et al. (2016) A new risk locus in the ZEB2 gene for schizophrenia in the Han Chinese population. Progress in neuro-psychopharmacology & biological psychiatry, 66, 97.