

Resource Summary Report

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GWAPOWER

RRID:SCR_009216

Type: Tool

Proper Citation

GWAPOWER (RRID:SCR_009216)

Resource Information

URL: <http://www.stats.ox.ac.uk/~marchini/software.html>

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Description: A R package for assessing the power of genome-wide association studies using commercially available genotyping chips. The package encapsulates extensive simulation results generated by our program HAPGEN. (entry from Genetic Analysis Software)

Synonyms: R/GWAPOWER, Genome-Wide Association POWER

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, r

Resource Name: GWAPOWER

Resource ID: SCR_009216

Alternate IDs: nlx_154369, nlx_154586, SCR_000847

Record Creation Time: 20220129T080251+0000

Record Last Update: 20260729T044217+0000

Ratings and Alerts

No rating or validation information has been found for GWAPOWER.

No alerts have been found for GWAPOWER.

Data and Source Information

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Schott BH, et al. (2022) Single-cell genome-wide association reveals that a nonsynonymous variant in ERAP1 confers increased susceptibility to influenza virus. *Cell genomics*, 2(11).

Kou N, et al. (2020) A Mendelian Randomization Analysis to Expose the Causal Effect of IL-18 on Osteoporosis Based on Genome-Wide Association Study Data. *Frontiers in bioengineering and biotechnology*, 8, 201.

Ogawa D, et al. (2018) Haplotype-based allele mining in the Japan-MAGIC rice population. *Scientific reports*, 8(1), 4379.

Wilkie H, et al. (2017) A candidate gene approach to study nematode resistance traits in naturally infected sheep. *Veterinary parasitology*, 243, 71.

Mozaffarian D, et al. (2017) Genome-wide association meta-analysis of fish and EPA+DHA consumption in 17 US and European cohorts. *PLoS one*, 12(12), e0186456.

Cassiano GC, et al. (2016) Immunogenetic markers associated with a naturally acquired humoral immune response against an N-terminal antigen of *Plasmodium vivax* merozoite surface protein 1 (PvMSP-1). *Malaria journal*, 15, 306.

Rockman MV, et al. (2009) Recombinational landscape and population genomics of *Caenorhabditis elegans*. *PLoS genetics*, 5(3), e1000419.

Mu J, et al. (2005) Recombination hotspots and population structure in *Plasmodium falciparum*. *PLoS biology*, 3(10), e335.