Resource Summary Report

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GenGen

RRID:SCR_013447
Type: Tool

Proper Citation

GenGen (RRID:SCR_013447)

Resource Information

URL: http://www.openbioinformatics.org/gengen/

Proper Citation: GenGen (RRID:SCR_013447)

Description: A suite of free software tools to facilitate the analysis of high-throughput genomics data sets. The package is currently a work-in-progress and infrequently updated.

Abbreviations: GenGen

Synonyms: GenGen: Genetic Genomics Analysis of Complex Data

Resource Type: software resource, software application

Keywords: genomic analysis, imaging genomics, pathway, network, snp, gene, genetics, genomics

Availability: Free

Resource Name: GenGen

Resource ID: SCR_013447

Alternate IDs: nlx_155766

Alternate URLs: http://www.nitrc.org/projects/gengen

Record Creation Time: 20220129T080316+0000

Record Last Update: 20260808T190520+0000

Ratings and Alerts

No rating or validation information has been found for GenGen.

No alerts have been found for GenGen.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 26 mentions in open access literature.

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

Cornwell T, et al. (2025) Proactive adjustments to cued gait perturbations in people with and without chronic stroke. bioRxiv : the preprint server for biology.

Oliver KF, et al. (2020) Loci associated with conception rate in crossbred beef heifers. PloS one, 15(4), e0230422.

Jiao H, et al. (2019) Genome-Wide Interaction and Pathway Association Studies for Body Mass Index. Frontiers in genetics, 10, 404.

Oliver KF, et al. (2019) Genomic Analysis of Spontaneous Abortion in Holstein Heifers and Primiparous Cows. Genes, 10(12).

Law PJ, et al. (2019) Association analyses identify 31 new risk loci for colorectal cancer susceptibility. Nature communications, 10(1), 2154.

Michailidou K, et al. (2017) Association analysis identifies 65 new breast cancer risk loci. Nature, 551(7678), 92.

Neupane M, et al. (2017) Loci and pathways associated with uterine capacity for pregnancy and fertility in beef cattle. PloS one, 12(12), e0188997.

Chen M, et al. (2016) Pathway analysis of bladder cancer genome-wide association study identifies novel pathways involved in bladder cancer development. Genes & cancer, 7(7-8), 229.

Wei R, et al. (2016) Meta-dimensional data integration identifies critical pathways for susceptibility, tumorigenesis and progression of endometrial cancer. Oncotarget, 7(34), 55249.

Spain SL, et al. (2016) A genome-wide analysis of putative functional and exonic variation associated with extremely high intelligence. Molecular psychiatry, 21(8), 1145.

Jiao H, et al. (2015) Pathway-Based Genome-Wide Association Studies for Plasma Triglycerides in Obese Females and Normal-Weight Controls. PloS one, 10(8), e0134923.

Ram??rez O, et al. (2015) Genome data from a sixteenth century pig illuminate modern breed relationships. Heredity, 114(2), 175.

Rosenberger A, et al. (2015) META-GSA: Combining Findings from Gene-Set Analyses across Several Genome-Wide Association Studies. PloS one, 10(10), e0140179.

Li WD, et al. (2015) Pathway-Based Genome-wide Association Studies Reveal That the Rac1 Pathway Is Associated with Plasma Adiponectin Levels. Scientific reports, 5, 13422.

Todd JN, et al. (2015) Genetic Evidence for a Causal Role of Obesity in Diabetic Kidney Disease. Diabetes, 64(12), 4238.

Jin L, et al. (2014) Pathway-based analysis tools for complex diseases: a review. Genomics, proteomics & bioinformatics, 12(5), 210.

Sulovari A, et al. (2014) GACT: a Genome build and Allele definition Conversion Tool for SNP imputation and meta-analysis in genetic association studies. BMC genomics, 15, 610.

Jiang L, et al. (2013) Comparison of the performance of two commercial genome-wide association study genotyping platforms in Han Chinese samples. G3 (Bethesda, Md.), 3(1), 23.

Bishop MT, et al. (2013) Splice site SNPs of phospholipase PLCXD3 are significantly associated with variant and sporadic Creutzfeldt-Jakob disease. BMC medical genetics, 14, 91.

Jones AR, et al. (2013) Residual association at C9orf72 suggests an alternative amyotrophic lateral sclerosis-causing hexanucleotide repeat. Neurobiology of aging, 34(9), 2234.e1.