Resource Summary Report

Generated by RRID on Aug 4, 2026

GREGOR

RRID:SCR_009165
Type: Tool

Proper Citation

GREGOR (RRID:SCR_009165)

Resource Information

URL: https://github.com/gaow/genetic-analysis-software/blob/master/pages/GREGOR.md

Proper Citation: GREGOR (RRID:SCR_009165)

Description: Software program that allows students and scientists to explore potential manifestations of genetic models and stochastic processes. It also provides a means to evaluate the effectiveness of statistical procedures such as linkage analysis or QTL detection. (entry from Genetic Analysis Software), THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: GREGOR

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, ms-dos

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: GREGOR

Resource ID: SCR_009165

Alternate IDs: nlx_154364

Old URLs: http://gnome.agrenv.mcgill.ca/tinker/gregor.htm

Record Creation Time: 20220129T080251+0000

Record Last Update: 20260801T191054+0000

Ratings and Alerts

No rating or validation information has been found for GREGOR.

No alerts have been found for GREGOR.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 47 mentions in open access literature.

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

Hlongwane N, et al. (2025) Quality of life in long-term care facilities in Gauteng, South Africa: an institutional ethnographic study of older adults' perspectives. BMJ open, 15(5), e099448.

Murdock DR, et al. (2025) Non-canonical splice variants in thoracic aortic dissection cases and Marfan syndrome with negative genetic testing. NPJ genomic medicine, 10(1), 25.

Chen X, et al. (2025) Genome-wide profiling of highly similar paralogous genes using HiFi sequencing. Nature communications, 16(1), 2340.

Arriaga MT, et al. (2025) Transcriptome-wide outlier approach identifies individuals with minor spliceopathies. medRxiv : the preprint server for health sciences.

Melino K, et al. (2025) Rhetorics and Realities of Access in Community Mental Health Care. Nursing inquiry, 32(2), e70014.

Stenton SL, et al. (2025) Mitochondrial DNA variant detection in over 6,500 rare disease families by the systematic analysis of exome and genome sequencing data resolves undiagnosed cases. HGG advances, 6(3), 100441.

Cupit C, et al. (2025) Mapping the Social Organisation of Neglect in the Case of Fibromyalgia: Using Smith's Sociology for People to Inform a Systems-Focused Literature Review. Sociology of health & illness, 47(2), e70008.

De Jonghe J, et al. (2025) Saturation genome editing of RNU4-2 reveals distinct dominant and recessive neurodevelopmental disorders. medRxiv : the preprint server for health sciences.

Chen Y, et al. (2024) De novo variants in the RNU4-2 snRNA cause a frequent neurodevelopmental syndrome. Nature, 632(8026), 832.

DeForest N, et al. (2024) Genome-wide discovery and integrative genomic characterization of insulin resistance loci using serum triglycerides to HDL-cholesterol ratio as a proxy. Nature communications, 15(1), 8068.

Stenton SL, et al. (2024) Mitochondrial DNA variant detection in over 6,500 rare disease families by the systematic analysis of exome and genome sequencing data resolves undiagnosed cases. medRxiv : the preprint server for health sciences.

Mahmoud M, et al. (2024) Closing the gap: Solving complex medically relevant genes at scale. medRxiv : the preprint server for health sciences.

Yuan J, et al. (2024) A compendium of genetic variations associated with promoter usage across 49 human tissues. Nature communications, 15(1), 8758.

Chen Y, et al. (2024) De novo variants in the non-coding spliceosomal snRNA gene RNU4-2 are a frequent cause of syndromic neurodevelopmental disorders. medRxiv : the preprint server for health sciences.

Du H, et al. (2024) VizCNV: An integrated platform for concurrent phased BAF and CNV analysis with trio genome sequencing data. bioRxiv : the preprint server for biology.

Savage SK, et al. (2024) Using a chat-based informed consent tool in large-scale genomic research. Journal of the American Medical Informatics Association : JAMIA, 31(2), 472.

Ungar RA, et al. (2024) Impact of genome build on RNA-seq interpretation and diagnostics. medRxiv : the preprint server for health sciences.

Dawood M, et al. (2024) GREGoR: Accelerating Genomics for Rare Diseases. ArXiv.

Pagadala M, et al. (2023) Germline modifiers of the tumor immune microenvironment implicate drivers of cancer risk and immunotherapy response. Nature communications, 14(1), 2744.

Gu Y, et al. (2023) Construction and evaluation of the functional polygenic risk score for gastric cancer in a prospective cohort of the European population. Chinese medical journal, 136(14), 1671.