Resource Summary Report

Generated by kravitz2 on Sep 18, 2026

DGENE

RRID:SCR_009158
Type: Tool

Proper Citation

DGENE (RRID:SCR_009158)

Resource Information

URL: http://www.biomath.medsch.ucla.edu/faculty/klange/software.html

Proper Citation: DGENE (RRID:SCR_009158)

Description: THIS RESOURCE IS NO LOGER IN SERVICE. Documented on May 16,2023. A simple dBASE III program for the management of pedigree and locus data. It permits easy extraction of genetic data for use with MENDEL and FISHER. (entry from Genetic Analysis Software)

Abbreviations: DGENE

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, dbase iii, ms-dos

Availability: THIS RESOURCE IS NO LOGER IN SERVICE

Resource Name: DGENE

Resource ID: SCR_009158

Alternate IDs: nlx_154281

Record Creation Time: 20220129T080251+0000

Record Last Update: 20260912T200241+0000

Ratings and Alerts

No rating or validation information has been found for DGENE.

No alerts have been found for DGENE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 7 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

Lee S, et al. (2026) Large-scale blood pressure GWAS accounting for gene-depression interactions in 564,680 individuals from diverse populations. HGG advances, 7(2), 100566.

Feitosa M, et al. (2026) Discovery of gene-alcohol interaction loci influencing blood pressure in 1.1 million individuals from multiple populations. Research square.

Bentley AR, et al. (2025) Multi-ancestry genome-wide association analyses incorporating SNP-by-psychosocial interactions identify novel loci for serum lipids. Translational psychiatry, 15(1), 207.

Nagarajan P, et al. (2024) A Large-Scale Genome-Wide Study of Gene-Sleep Duration Interactions for Blood Pressure in 811,405 Individuals from Diverse Populations. medRxiv : the preprint server for health sciences.

Todisco E, et al. (2022) Hematological disorders after salvage PARPi treatment for ovarian cancer: Cytogenetic and molecular defects and clinical outcomes. International journal of cancer, 151(10), 1791.

He X, et al. (2019) Identification of functional butanol-tolerant genes from Escherichia coli mutants derived from error-prone PCR-based whole-genome shuffling. Biotechnology for biofuels, 12, 73.

Kumar RD, et al. (2013) Prioritizing Potentially Druggable Mutations with dGene: An Annotation Tool for Cancer Genome Sequencing Data. PloS one, 8(6), e67980.