Resource Summary Report

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NCBI database of Genotypes and Phenotypes (dbGap)

RRID:SCR_002709
Type: Tool

Proper Citation

NCBI database of Genotypes and Phenotypes (dbGap) (RRID:SCR_002709)

Resource Information

URL: http://www.ncbi.nlm.nih.gov/gap

Proper Citation: NCBI database of Genotypes and Phenotypes (dbGap) (RRID:SCR_002709)

Description: Database developed to archive and distribute clinical data and results from studies that have investigated interaction of genotype and phenotype in humans. Database to archive and distribute results of studies including genome-wide association studies, medical sequencing, molecular diagnostic assays, and association between genotype and non-clinical traits.

Abbreviations: dbGaP

Synonyms: database of Genotypes and Phenotypes (dbGaP), dbGaP, NCBI, Database of Genotypes and Phenotypes

Resource Type: data or information resource, data repository, database, service resource, storage service resource

Defining Citation: PMID:24297256, PMID:17898773

Keywords: clinical, trial, genotype, interaction, homology, cell, morphology, interaction, phenotype, molecular diagnosis, genetic recombination, gold standard, bio.tools

Funding: NLM

Availability: Restricted

Resource Name: NCBI database of Genotypes and Phenotypes (dbGap)

Resource ID: SCR_002709

Alternate IDs: nif-0000-23342, OMICS_00263, biotools:dbgap, r3d100010788

Alternate URLs: http://www.ncbi.nlm.nih.gov/sites/entrez?db=gap, https://bio.tools/dbgap, https://doi.org/10.17616/R3GS4K

Record Creation Time: 20220129T080214+0000

Record Last Update: 20260905T132452+0000

Ratings and Alerts

No rating or validation information has been found for NCBI database of Genotypes and Phenotypes (dbGap).

No alerts have been found for NCBI database of Genotypes and Phenotypes (dbGap).

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 736 mentions in open access literature.

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

Zakarian C, et al. (2026) Long-read MitoScope reveals tissue-resolved somatic mitochondrial variation and landscape of nuclear-embedded mitochondrial sequences. bioRxiv : the preprint server for biology.

Kar A, et al. (2026) Lessons from single cell omics: admixed American ancestry and sex confer cardiometabolic disease risk in Mexicans. Genome medicine, 18(1).

Zhang Y, et al. (2026) Global mRNA 3'UTR lengthening in small-cell neuroendocrine carcinoma. bioRxiv : the preprint server for biology.

Wang Y, et al. (2026)

CDK1 depletion suppresses glioma malignancy through cell cycle pathway regulation: Mechanistic insights from functional and molecular profiling

. Oncology reports, 55(3).
Lu ZA, et al. (2026) Leveraging transdiagnostic genetic liability to psychiatric disorders to dissect clinical outcomes of anorexia nervosa. Molecular psychiatry, 31(3), 1475.

Banu K, et al. (2026) IRS4 is a PI3K-activating cancer dependency up-regulated through DNA rearrangements or epigenetic mechanisms in multiple solid tumors. Science advances, 12(18), eaeb3503.

Jiang L, et al. (2026) ImmuSeeker: deep mining of immune-related gene family signatures through lineage reconstruction. Genome biology, 27(1).

Sutcliffe MD, et al. (2026) Transcriptomic profiling of mouse mammary tumors enables prognostic and predictive biomarker discovery for human breast cancers. bioRxiv : the preprint server for biology.

Lawal B, et al. (2026) IMIREG: a lineage-resolved regulon signature unveiling immune engagement archetypes and predicting immunotherapy response across diverse cancers. NPJ precision oncology, 10(1).

Demontis D, et al. (2026) Rare genetic variants confer a high risk of ADHD and implicate neuronal biology. Nature, 649(8098), 909.

Wang C, et al. (2026) Unravelling genome-wide mosaic microsatellite mutations at single-cell resolution. bioRxiv : the preprint server for biology.

Bareghamyan Y, et al. (2026) Integrated analysis of the blood metallome and DNA methylation, gene expression, and protein levels of immune-associated genes in residents from mining region. Environmental geochemistry and health, 48(2), 81.

Starble RM, et al. (2026) Epigenetic priming promotes tyrosine kinase inhibitor resistance and oncogene amplification. Nature structural & molecular biology, 33(1), 7.

Fisher N, et al. (2026) Mitochondrial genetic variation across tissues of the human body. Nucleic acids research, 54(10).

Kang H, et al. (2026) Spatial GWAS Atlas: a knowledgebase for decoding the genetic architecture of complex traits in spatial resolution. Nucleic acids research, 54(D1), D1301.

Jiang T, et al. (2026) GENEasso: a curated resource of credible disease-gene associations across complex diseases from GWAS summary statistics. Nucleic acids research, 54(D1), D1415.

Li Y, et al. (2026) The contribution of short tandem repeats to splicing variation in the human cortex. bioRxiv : the preprint server for biology.

Pr??lot L, et al. (2026) ImmunoPepper: extracting personalized peptides from complex splicing graphs. Bioinformatics (Oxford, England), 42(1).

Kahlon S, et al. (2026) Reduced immunogenicity of MYC amplified, metastatic prostate cancer. Oncoscience, 13, 35.

Monteiro AC, et al. (2026) OPG-Producing B Cells and RANKL-Expressing T Cells Define Immune Signatures Predictive of Bone Metastases in Breast Cancer. Cancer research communications, 6(1), 85.