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, storage service resource, database, 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

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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 683 mentions in open access literature.

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

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.

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.

Ku AT, et al. (2025) Radiogenomic Profiling of Prostate Tumors prior to External Beam Radiotherapy Converges on a Transcriptomic Signature of TGF-? Activity Driving Tumor Recurrence. Clinical cancer research : an official journal of the American Association for Cancer Research, 31(24), 5211.

Sun Y, et al. (2025) TBK1 Targeting Is Identified as a Therapeutic Strategy to Enhance CAR T-Cell Efficacy Using Patient-Derived Organotypic Tumor Spheroids. Cancer immunology research, 13(2), 210.

Kelly RL, et al. (2025) The Breast Tumor Immune Microenvironment of DNA Double-Strand Break Repair Pathogenic Variant Carriers Is Enriched with Tumor-Associated Macrophages. Cancer epidemiology, biomarkers & prevention : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology, 34(6), 868.

Linder J, et al. (2025) Predicting RNA-seq coverage from DNA sequence as a unifying model of gene regulation. Nature genetics, 57(4), 949.

Wilson AC, et al. (2025) Novel risk loci encompassing genes influencing STAT3, GPCR, and oxidative stress signaling are associated with co-morbid GERD and COPD. PLoS genetics, 21(2), e1011531.

Han HJ, et al. (2025) Differential neuropilin isoform expressions highlight plasticity in macrophages in the heterogenous TME through in-silico profiling. Frontiers in immunology, 16, 1547330.

Xia P, et al. (2025) SCANER: robust and sensitive identification of malignant cells from the scRNA-seq profiled tumor ecosystem. Briefings in bioinformatics, 26(2).

Zhao W, et al. (2025) A prognostic signature for lung adenocarcinoma in people who have never smoked. bioRxiv : the preprint server for biology.

Yuan M, et al. (2025) Optimized phenotyping of complex morphological traits: enhancing discovery of common and rare genetic variants. Briefings in bioinformatics, 26(2).

Uusi-Mäkelä J, et al. (2025) Tumor-associated long non-coding RNAs show variable expression across diffuse gliomas and effect on cell growth upon silencing in glioblastoma. Scientific reports, 15(1), 16220.

Jung SY, et al. (2025) Epigenetic age and accelerated aging phenotypes: a tumor biomarker for predicting colorectal cancer. Aging, 17(7), 1624.

Lawrence ES, et al. (2025) Adaptive PRKAA1 variant in Andeans is associated with improved ventilation and sleep phenotypes. iScience, 28(8), 112911.

Gurevic I, et al. (2025) JAK inhibitor withdrawal causes a transient pro-inflammatory cascade: A potential mechanism for major adverse cardiac events. PloS one, 20(6), e0311706.

Hou Z, et al. (2025) Kinship estimation bias carries over to heritability estimation bias using variance components. bioRxiv : the preprint server for biology.

Ospina OE, et al. (2025) spatialGE Is a User-Friendly Web Application That Facilitates Spatial Transcriptomics Data Analysis. Cancer research, 85(5), 848.

Henriques G, et al. (2025) Integrating AI and genomics: predictive CNN models for schizophrenia phenotypes. Journal of integrative bioinformatics, 22(2).

Claps A, et al. (2025) High precision characterization of RCCX rearrangements in a 21-hydroxylase deficiency Latin American cohort using oxford nanopore long read sequencing. Scientific reports, 15(1), 24983.

Jurgens JA, et al. (2025) Gene Identification for Ocular Congenital Cranial Motor Neuron Disorders Using Human Sequencing, Zebrafish Screening, and Protein Binding Microarrays. Investigative ophthalmology & visual science, 66(3), 62.