Resource Summary Report

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Genome Aggregation Database

RRID:SCR_014964
Type: Tool

Proper Citation

Genome Aggregation Database (RRID:SCR_014964)

Resource Information

URL: http://gnomad.broadinstitute.org/

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Description: Database that aggregates exome and genome sequencing data from large-scale sequencing projects. The gnomAD data set contains individuals sequenced using multiple exome capture methods and sequencing chemistries. Raw data from the projects have been reprocessed through the same pipeline, and jointly variant-called to increase consistency across projects.

Abbreviations: gnomAD

Synonyms: gnomAD 2.0, gnomAD Browser, gnomAD version 2.0, Exome Aggregation Consortium

Resource Type: data or information resource, database

Keywords: database, genome, , bio.tools, FASEB list

Funding: Broad Institute

Availability: Open source, Available to the biomedical community, The community can contribute to this resource

Resource Name: Genome Aggregation Database

Resource ID: SCR_014964

Alternate IDs: biotools:gnomad

Alternate URLs: https://github.com/macarthur-lab/gnomad_browser/issues, https://bio.tools/gnomad

License: ODC Open Database License

License URLs: http://gnomad.broadinstitute.org/terms

Record Creation Time: 20220129T080323+0000

Record Last Update: 20260905T133211+0000

Ratings and Alerts

No rating or validation information has been found for Genome Aggregation Database.

No alerts have been found for Genome Aggregation Database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 5310 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Huang KK, et al. (2026) Mutational Signatures and Clonal Hematopoiesis in Intestinal Metaplasia across Countries with Varying Stomach Cancer Incidence. Cancer discovery, 16(3), 497.

Gurjao C, et al. (2026) Germline Predisposition to Oncogenic Alkylating Damage in Colorectal Cancer. Cancer epidemiology, biomarkers & prevention : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology, 35(3), 420.

Avolio M, et al. (2026) The Molecular and Functional Landscape of Resistance to FOLFIRI Chemotherapy in Metastatic Colorectal Cancer. Cancer discovery, 16(2), 270.

Yun KH, et al. (2026) Phase IB/II Trial with Correlative Analyses of Doxorubicin plus Durvalumab Combination in Patients with Advanced Soft Tissue Sarcoma. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(9), 1686.

Meng X, et al. (2026) Characterization of Genetic Etiologic Factors for Pediatric Acute Lymphoblastic Leukemia in Large Childhood Cancer Survivorship Cohorts. Cancer epidemiology, biomarkers & prevention : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology, 35(7), 1100.

Lee S, et al. (2026) Functional characterization of SDHB variants clarifies hereditary pheochromocytoma and paraganglioma risk and genotype-phenotype relationships. The Journal of clinical investigation, 136(4).

Gatz SA, et al. (2026) Phase I/II Study of the PARP Inhibitor Olaparib and Irinotecan in Children and Young Adults with Recurrent/Refractory Malignancies: Arm D of the AcSé-ESMART Trial. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(7), 1210.

Hang JF, et al. (2026) Out-of-frame CBX3::ALK fusion drives ALK activation and therapy response. Cell reports. Medicine, 7(4), 102697.

Gupta I, et al. (2026) Correlation of the differential expression of PIK3R1 and its spliced variant, p55?, in pan-cancer. Molecular oncology, 20(5), 1299.

Monti M, et al. (2026) Integrating interferon gamma receptor pathways, antigenicity, and immune contexture as predictors of immunotherapeutic strategies for mucosal melanomas. Journal for immunotherapy of cancer, 14(3).

Pehrsson M, et al. (2026) Opportunistic Screening of High-Risk Breast Cancer Variants in Hospital Biobank Setting. Cancer epidemiology, biomarkers & prevention : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology, 35(6), 883.

Smolen C, et al. (2026) Protocol for identifying genetic modifiers of phenotypes in individuals with disease-associated variants. STAR protocols, 7(2), 104546.

Radovich M, et al. (2026) Broader gene representation by whole-exome sequencing improves accuracy of tumor mutational burden assessment for selection of pembrolizumab immunotherapy. Cancer immunology, immunotherapy : CII, 75(6).

Tang C, et al. (2026) Investigating the determinants of immunotherapy response in the primary tumour of clear cell renal cell carcinoma (RCC). BMJ oncology, 5(2), e001031.

Lange LM, et al. (2026) Rare but Relevant? Assessing Variants in Dystonia-Linked Genes in Parkinson's Disease. Movement disorders : official journal of the Movement Disorder Society, 41(1), 247.

Labat-de-Hoz L, et al. (2026) Structural and functional dissection of the WH2/DAD motif of INF2, a formin linked to human inherited degenerative disorders. The FEBS journal, 293(3), 825.

Jiang Q, et al. (2026) Beyond the genome: clinical challenges in diagnosing LONP1-related mitochondrial disorders. Frontiers in cell and developmental biology, 14, 1779332.

Shalom S, et al. (2026) The Genetic Landscape of Inherited Retinal Diseases in the Israeli Population. Investigative ophthalmology & visual science, 67(4), 24.

Wu G, et al. (2026) Pathogenicity and Functional Analysis of Multi-Variant Allele of RPE65 Causing Retinitis Pigmentosa. Translational vision science & technology, 15(2), 1.

Carretero-Vilarroig L, et al. (2026) Diagnostic Yield and Genotype-Phenotype Correlations of Clinical Exome Sequencing in Hereditary Spastic Paraparesis: Experience From Eastern Spain. European journal of neurology, 33(1), e70475.