Resource Summary Report

Generated by NIF on Aug 8, 2026

DNAnexus

RRID:SCR_011884
Type: Tool

Proper Citation

DNAnexus (RRID:SCR_011884)

Resource Information

URL: https://dnanexus.com/

Proper Citation: DNAnexus (RRID:SCR_011884)

Description: A cloud-based platform to support genomics at your organization.

Abbreviations: DNAnexus

Resource Type: service resource

Keywords: genomics, cloud computing, genomic analysis

Resource Name: DNAnexus

Resource ID: SCR_011884

Alternate IDs: OMICS_01217

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260801T190422+0000

Ratings and Alerts

No rating or validation information has been found for DNAnexus.

No alerts have been found for DNAnexus.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 136 mentions in open access literature.

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

Rhie A, et al. (2026) Biobank-scale genotyping of Robertsonian translocations reveals hidden structural variation on the human acrocentric chromosomes. bioRxiv : the preprint server for biology.

DeHaas D, et al. (2026) General, orders-of-magnitude faster whole-genome analysis with genotype representation graphs. bioRxiv : the preprint server for biology.

Kaur TC, et al. (2026) Sex-differential associations of MC3R p.F45S with human metabolic profile. Journal of neuroendocrinology, 38(6), e70214.

Tan J, et al. (2026) Potential regulators and metabolic networks of muscle fatty infiltration: genomic and radiomics investigation based on 33 300 participants. International journal of surgery (London, England), 112(1), 472.

Lin C, et al. (2026) Deep learning enhanced ALPS reveals genetic and environmental factors of brain glymphatic function. EBioMedicine, 124, 106133.

Lu J, et al. (2026) Impact of control selection strategies on GWAS results: a study of prostate cancer in the UK Biobank. Briefings in bioinformatics, 27(2).

Pounraja VK, et al. (2026) Population-scale repeat expansions elucidate disease risk and brain atrophy. Nature, 653(8115), 796.

Conry M, et al. (2026) Multiple myeloma risk linked to DNA damage response genes. Journal of hematology & oncology, 19(1), 10.

Halperin R, et al. (2025) Pseudohypoxia caused by germline genetic alterations in the VHL gene is associated with increased diabetes and cardiovascular risk: a UK biobank study. Cardiovascular diabetology, 24(1), 239.

Jung M, et al. (2025) High-throughput 3D engineered paediatric tumour models for precision medicine. Molecular systems biology, 21(12), 1748.

Park E, et al. (2025) Scalable and accurate rare variant meta-analysis with Meta-SAIGE. Nature genetics, 57(12), 3185.

Reeve MP, et al. (2025) Loss of CFHR5 function reduces the risk for age-related macular degeneration. Nature communications, 16(1), 5766.

Zhang S, et al. (2025) Re-Evaluating Acceptable Intake: A Comparative Study of N-Nitrosomorpholine and N-Nitroso Reboxetine Potency. Environmental and molecular mutagenesis, 66(3), 80.

LeBlanc DPM, et al. (2025) Duplex sequencing identifies unique characteristics of ENU-induced mutations in male mouse germ cells???. Biology of reproduction, 112(5), 1015.

Mudra Rakshasa-Loots A, et al. (2025) Affective disorders and chronic inflammatory conditions: analysis of 1.5 million participants in Our Future Health. BMJ mental health,

28(1).

Renatino Canevarolo R, et al. (2025) Epigenetic Plasticity Drives Carcinogenesis and Multi-Therapy Resistance in Multiple Myeloma. Research square.

Zhang S, et al. (2025) Transferability, Reproducibility and Sensitivity of Mutation Quantification by Duplex Sequencing. Environmental and molecular mutagenesis, 66(6-7), 311.

Jen HI, et al. (2025) Residual DNA impurities in AAV vectors-nature and transcription. Molecular therapy. Methods & clinical development, 33(3), 101503.

Lu J, et al. (2025) Association of heel bone mineral density with incident dementia among ageing adults: a population-based study from the UK Biobank. Aging clinical and experimental research, 37(1), 217.

Hastar N, et al. (2025) A pathogenic variant of AMOT leads to isolated X-linked congenital hydrocephalus due to N-terminal truncation. The Journal of clinical investigation, 135(17).