Resource Summary Report

Generated by dkNET on Apr 16, 2025

ANNOVAR

RRID:SCR_012821
Type: Tool

Proper Citation

ANNOVAR (RRID:SCR_012821)

Resource Information

URL: http://www.openbioinformatics.org/annovar/

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Description: An efficient software tool to utilize update-to-date information to functionally annotate genetic variants detected from diverse genomes (including human genome hg18, hg19, as well as mouse, worm, fly, yeast and many others). Given a list of variants with chromosome, start position, end position, reference nucleotide and observed nucleotides, ANNOVAR can perform: 1. gene-based annotation. 2. region-based annotation. 3. filter-based annotation. 4. other functionalities. (entry from Genetic Analysis Software)

Abbreviations: ANNOVAR

Synonyms: functional ANNOtation of genetic VARiants, ANNOVAR: Functional annotation of genetic variants

Resource Type: software resource, software application

Defining Citation: PMID:20601685

Keywords: genomic analysis, imaging genomics, next generation sequencing, snp, gene, bio.tools

Funding:

Availability: Free

Resource Name: ANNOVAR

Resource ID: SCR_012821

Alternate IDs: nlx_154225, biotools:annovar, OMICS_00165

Alternate URLs: https://bio.tools/annovar, https://bio.tools/annovar

Record Creation Time: 20220129T080312+0000

Record Last Update: 20250416T063634+0000

Ratings and Alerts

No rating or validation information has been found for ANNOVAR.

No alerts have been found for ANNOVAR.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 5240 mentions in open access literature.

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

Parada CM, et al. (2025) Growth-dependent concentration gradient of the oscillating Min system in Escherichia coli. The Journal of cell biology, 224(2).

Hsiao YJ, et al. (2025) Tp53 determines the spatial dynamics of M1/M2 tumor-associated macrophages and M1-driven tumoricidal effects. Cell death & disease, 16(1), 38.

Chen W, et al. (2025) Evolutionary trajectories of immune escape across cancers. bioRxiv : the preprint server for biology.

Arai Y, et al. (2025) Novel OTOG Variants and Clinical Features of Hearing Loss in a Large Japanese Cohort. Genes, 16(1).

Zhao W, et al. (2025) GoFCards: an integrated database and analytic platform for gain of function variants in humans. Nucleic acids research, 53(D1), D976.

Chen YC, et al. (2025) Multiomics Analysis Reveals Molecular Changes during Early Progression of Precancerous Lesions to Lung Adenocarcinoma in Never-Smokers. Cancer research, 85(3), 602.

Huang Y, et al. (2025) RMVar 2.0: an updated database of functional variants in RNA

modifications. Nucleic acids research, 53(D1), D275.

Ren Q, et al. (2025) Clinical features and search for genetic determinants of postprandial hypoglycaemia. Endocrine connections, 14(1).

Yalcouyé A, et al. (2025) Whole-exome sequencing reveals known and candidate genes for hearing impairment in Mali. HGG advances, 6(1), 100391.

Wang G, et al. (2025) Comparative genomic analysis unveiling the mutational landscape associated with premalignant lesions and early-stage gastric cardia cancer. Medicine, 104(2), e40332.

Liao R, et al. (2025) Characterization of the genomic landscape in liver oligometastatic NSCLC. BMC cancer, 25(1), 93.

Zhou Y, et al. (2025) Telomere-to-telomere genome and resequencing of 254 individuals reveal evolution, genomic footprints in Asian icefish, Protosalanx chinensis. GigaScience, 14.

Petrohilos C, et al. (2025) AMPed up immunity: 418 whole genomes reveal intraspecific diversity of koala antimicrobial peptides. Immunogenetics, 77(1), 11.

Sun H, et al. (2025) Elite Alleles of EPE1 Identified via Genome-wide Association Studies Increase Panicle Elongation Length in Rice. Rice (New York, N.Y.), 18(1), 4.

Minniakhmetov IR, et al. (2025) Genetic Structure of Hereditary Forms of Diabetes Mellitus in Russia. International journal of molecular sciences, 26(2).

Yang C, et al. (2025) stSNV: a comprehensive resource of SNVs in spatial transcriptome. Nucleic acids research, 53(D1), D1224.

Lei Y, et al. (2025) Population sequencing of cherry accessions unravels the evolution of Cerasus species and the selection of genetic characteristics in edible cherries. Molecular horticulture, 5(1), 6.

Sui Z, et al. (2025) Mesenchymal stromal cells promote the formation of lung cancer organoids via Kindlin-2. Stem cell research & therapy, 16(1), 7.

Leko V, et al. (2025) Utilization of primary tumor samples for cancer neoantigen discovery. Journal for immunotherapy of cancer, 13(1).

Jo T, et al. (2025) LD-informed deep learning for Alzheimer's gene loci detection using WGS data. Alzheimer's & dementia (New York, N. Y.), 11(1), e70041.