Resource Summary Report

Generated by RRID on Apr 8, 2025

wANNOVAR

RRID:SCR_000565
Type: Tool

Proper Citation

wANNOVAR (RRID:SCR_000565)

Resource Information

URL: http://wannovar.usc.edu/

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Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 6,2023. Web interface to the ANNOVAR software, a tool to annotate functional consequences of genetic variation from high-throughput sequencing data, to help biologists without bioinformatics skills to easily submit a list of mutations (even whole-genome variants calls) to the web server, select the desired annotation categories, and receive functional annotation back by emails. Given a list of single nucleotide variants (SNVs) and insertions / deletions in VCF or ANNOVAR input format, wANNOVAR annotates their functional effects on genes (such as amino acid changes for non-synonymous SNPs), calculate their predicted functional importance scores (such as SIFT and PolyPhen scores), retrieve allele frequencies in public databases (such as the 1000 Genomes Project and NHLBI-ESP 6500 exomes), and implement a variants reduction protocol to identify a subset of potentially deleterious variants.

Abbreviations: wANNOVAR

Resource Type: service resource, analysis service resource, data analysis service, production service resource

Defining Citation: PMID:22717648

Keywords: annotate, function, genetic variant, high-throughput sequencing, single nucleotide variant, gene, variant, allele frequency, mutation, annotation, genome, insertion, deletion

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: wANNOVAR

Resource ID: SCR_000565

Alternate IDs: OMICS_00194

Record Creation Time: 20220129T080202+0000

Record Last Update: 20250407T215137+0000

Ratings and Alerts

No rating or validation information has been found for wANNOVAR.

No alerts have been found for wANNOVAR.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 21 mentions in open access literature.

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

van de Weijer LL, et al. (2023) A novel patient-derived meningioma spheroid model as a tool to study and treat epithelial-to-mesenchymal transition (EMT) in meningiomas. Acta neuropathologica communications, 11(1), 198.

Kowalik A, et al. (2018) BRCA1 founder mutations and beyond in the Polish population: A single-institution BRCA1/2 next-generation sequencing study. PloS one, 13(7), e0201086.

Bao X, et al. (2018) Targeted next-generation sequencing of malignant peripheral nerve sheath tumor of the pterygopalatine fossa with intracranial metastatic recurrence. Medicine, 97(4), e9636.

Yuan J, et al. (2018) Genetic Modulation of RNA Splicing with a CRISPR-Guided Cytidine Deaminase. Molecular cell, 72(2), 380.

Fedida J, et al. (2017) Contribution of exome sequencing for genetic diagnostic in arrhythmogenic right ventricular cardiomyopathy/dysplasia. PloS one, 12(8), e0181840.

Bardakjian T, et al. (2017) A recurrent, non-penetrant sequence variant, p.Arg266Cys in Growth/Differentiation Factor 3 (GDF3) in a female with unilateral anophthalmia and skeletal anomalies. American journal of ophthalmology case reports, 7, 102.

Ting SY, et al. (2017) Dual interaction of scaffold protein Tim44 of mitochondrial import motor with channel-forming translocase subunit Tim23. eLife, 6.

Lu Y, et al. (2017) A novel TUBB4A mutation G96R identified in a patient with hypomyelinating leukodystrophy onset beyond adolescence. Human genome variation, 4, 17035.

Lu Y, et al. (2017) A novel PLP1 mutation F240L identified in a patient with connatal type Pelizaeus-Merzbacher disease. Human genome variation, 4, 16044.

Rocha N, et al. (2017) Human biallelic MFN2 mutations induce mitochondrial dysfunction, upper body adipose hyperplasia, and suppression of leptin expression. eLife, 6.

Ullah E, et al. (2016) Genetic analysis of consanguineous families presenting with congenital ocular defects. Experimental eye research, 146, 163.

Damgaard RB, et al. (2016) The Deubiquitinase OTULIN Is an Essential Negative Regulator of Inflammation and Autoimmunity. Cell, 166(5), 1215.

Jinda W, et al. (2016) A novel start codon mutation of the MERTK gene in a patient with retinitis pigmentosa. Molecular vision, 22, 342.

Glanzmann B, et al. (2016) A new tool for prioritization of sequence variants from whole exome sequencing data. Source code for biology and medicine, 11, 10.

Subaran RL, et al. (2015) Pathogenic EFHC1 mutations are tolerated in healthy individuals dependent on reported ancestry. Epilepsia, 56(2), 188.

Nicchia E, et al. (2015) Identification of point mutations and large intragenic deletions in Fanconi anemia using next-generation sequencing technology. Molecular genetics & genomic medicine, 3(6), 500.

Schoeler NE, et al. (2015) Variants in KCNJ11 and BAD do not predict response to ketogenic dietary therapies for epilepsy. Epilepsy research, 118, 22.

Thangam M, et al. (2015) CRCDA--Comprehensive resources for cancer NGS data analysis. Database : the journal of biological databases and curation, 2015.

Liu W, et al. (2015) Prenatal diagnosis of complete maternal uniparental isodisomy of chromosome 4 in a fetus without congenital abnormality or inherited disease-associated variations. Molecular cytogenetics, 8, 85.

Orkunoglu-Suer F, et al. (2015) Targeted single molecule sequencing methodology for ovarian hyperstimulation syndrome. BMC genomics, 16(1), 264.