

Resource Summary Report

Generated by [ASWG](#) on Aug 3, 2026

[wANNOVAR](#)

RRID:SCR_000565

Type: Tool

Proper Citation

wANNOVAR (RRID:SCR_000565)

Resource Information

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

Proper Citation: wANNOVAR (RRID:SCR_000565)

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., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: wANNOVAR

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

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: 20260803T040254+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 [ASWG](#) .

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.

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

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

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

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.

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

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.

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

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

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

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

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.