Resource Summary Report

Generated by SPARC SAWG on Sep 12, 2026

AnnTools

RRID:SCR_005170
Type: Tool

Proper Citation

AnnTools (RRID:SCR_005170)

Resource Information

URL: http://anntools.sourceforge.net/

Proper Citation: AnnTools (RRID:SCR_005170)

Description: Software tool for annotating single nucleotide substitutions (SNP/SNV), small insertions/deletions (indels), and copy number variations (CNV) calls generated from sequencing and microarray data. Only human genome build 37/hg19 can be annotated at this time.

Abbreviations: AnnTools

Resource Type: software resource

Keywords: single nucleotide substitution, snp, snv, indel, copy number variation, sequencing, microarray, linux, unix, mac osx, python, mysql, genome annotation, genome, annotation

Availability: BSD License

Resource Name: AnnTools

Resource ID: SCR_005170

Alternate IDs: OMICS_00166

Record Creation Time: 20220129T080228+0000

Record Last Update: 20260912T195622+0000

Ratings and Alerts

No rating or validation information has been found for AnnTools.

No alerts have been found for AnnTools.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Umar M, et al. (2020) Genome sequencing unveils mutational landscape of the familial Mediterranean fever: Potential implications of IL33/ST2 signalling. Journal of cellular and molecular medicine, 24(19), 11294.

Klimiankou M, et al. (2019) Ultra-Sensitive CSF3R Deep Sequencing in Patients With Severe Congenital Neutropenia. Frontiers in immunology, 10, 116.

Fakhro KA, et al. (2015) Copy number variations in the genome of the Qatari population. BMC genomics, 16, 834.

Tavassoli T, et al. (2014) De novo SCN2A splice site mutation in a boy with Autism spectrum disorder. BMC medical genetics, 15, 35.