# Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 23, 2025

## 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

**Funding:**

**Availability:** BSD License

**Resource Name:** AnnTools

**Resource ID:** SCR_005170

**Alternate IDs:** OMICS_00166

**Record Creation Time:** 20220129T080228+0000

**Record Last Update:** 20250420T014245+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 FDI Lab - SciCrunch.org.

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.