Resource Summary Report

Generated by kravitz2 on Sep 5, 2026

SeqAnt

RRID:SCR_005186
Type: Tool

Proper Citation

SeqAnt (RRID:SCR_005186)

Resource Information

URL: http://seqant.genetics.emory.edu/

Proper Citation: SeqAnt (RRID:SCR_005186)

Description: A free web service and open source software package that performs rapid, automated annotation of DNA sequence variants (single base mutations, insertions, deletions) discovered with any sequencing platform. Variant sites are characterized with respect to their functional type (Silent, Replacement, 5' UTR, 3' UTR, Intronic, Intergenic), whether they have been previously submitted to dbSNP, and their evolutionary conservation. Annotated variants can be viewed directly on the web browser, downloaded in a tab delimited text file, or directly uploaded in a Browser Extended Data (BED) format to the UCSC genome browser. SeqAnt further identifies all loci harboring two or more coding sequence variants that help investigators identify potential compound heterozygous loci within exome sequencing experiments. In total, SeqAnt resolves a significant bottleneck by allowing an investigator to rapidly prioritize the functional analysis of those variants of interest.

Abbreviations: SeqAnt

Synonyms: SeqAnt - Sequence Annotator

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

Defining Citation: PMID:20854673

Keywords: annotation, dna sequence variant, single base mutation, insertion, deletion, sequencing, mutation, variant, sequence variant, perl, sequence, genome

Availability: GNU General Public License, v2

Resource Name: SeqAnt

Resource ID: SCR_005186

Alternate IDs: OMICS_00182

Record Creation Time: 20220129T080228+0000

Record Last Update: 20260903T234750+0000

Ratings and Alerts

No rating or validation information has been found for SeqAnt.

No alerts have been found for SeqAnt.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

Denson LA, et al. (2018) Clinical and Genomic Correlates of Neutrophil Reactive Oxygen Species Production in Pediatric Patients With Crohn's Disease. Gastroenterology, 154(8), 2097.

Pan F, et al. (2017) Tet2 loss leads to hypermutagenicity in haematopoietic stem/progenitor cells. Nature communications, 8, 15102.