Resource Summary Report

Generated by NIF on Apr 22, 2025

ASOoViR

RRID:SCR_005161
Type: Tool

Proper Citation

ASOoViR (RRID:SCR_005161)

Resource Information

URL: http://sourceforge.net/projects/asoovir/

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Description: A set of Ruby modules to annotate consequence terms, defined by the Sequence Ontology, of variants (SNP/SNVs, INDELs, SVs, CNAs) using Ensembl gene sets. Prior to annotation of variants an Ensembl gene set and reference coding sequences are loaded into memory from a database file, which can be downloaded or generated by the user from reference files. This allows rapid annotation of variants, making it suitable for annotation of whole genome scale calls. Annotation is performed on a transcript level basis, identifying associated sequence ontology terms for affected and nearby transcripts. Default output can be obtained on a gene basis, summarising the consequences for each gene affected, or on a transcript level basis. Output information is also readily customisable using user-generated scripts.

Abbreviations: ASOoViR

Synonyms: Annotating Sequence Ontology of Variants in Ruby, ASOoViR - Annotating Sequence Ontology of Variants in Ruby

Resource Type: software resource

Keywords: ruby, annotate

Funding:

Resource Name: ASOoViR

Resource ID: SCR_005161

Alternate IDs: OMICS_00167

Record Creation Time: 20220129T080228+0000

Record Last Update: 20250420T014245+0000

Ratings and Alerts

No rating or validation information has been found for ASOoViR.

No alerts have been found for ASOoViR.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We have not found any literature mentions for this resource.