VAGrENT

RRID:SCR_005180
Type: Tool

Proper Citation

VAGrENT (RRID:SCR_005180)

Resource Information

URL: http://www.sanger.ac.uk/resources/software/vagrent/

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Description: Software tool set for calculating the biological consequences of genomic variations. The suite of perl modules compares genomic variations with reference genome annotations and generates the possible effects each variant may have on the transcripts it overlaps. It evaluates each variation/transcript combination and describes the effects in the mRNA, CDS and protein sequence contexts. It provides details of the sequence and position of the change within the transcript / protein as well as Sequence Ontology terms to classify its consequences.

Abbreviations: VAGrENT

Synonyms: Variation Annotation Generator, VAGrENT: Variation Annotation Generator

Resource Type: software resource, software toolkit

Keywords: perl, genomic variation, transcript, mrna, cds, protein sequence, protein, sequence

Resource Name: VAGrENT

Resource ID: SCR_005180

Alternate IDs: OMICS_00192

Ratings and Alerts
No rating or validation information has been found for VAGrENT.

No alerts have been found for VAGrENT.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Epstein-Peterson ZD, et al. (2022) De Novo myelodysplastic syndromes in patients 20-50 years old are enriched for adverse risk features. Leukemia research, 117, 106857.


