Resource Summary Report

Generated by T1D on Aug 1, 2026

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: VAGrENT: Variation Annotation Generator, 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

Record Creation Time: 20220129T080228+0000

Record Last Update: 20260801T042603+0000

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 14 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Domenico D, et al. (2025) Enabling whole genome sequencing analysis from FFPE specimens in clinical oncology. Nature communications, 16(1), 10649.

Mitchell E, et al. (2025) The long-term effects of chemotherapy on normal blood cells. Nature genetics, 57(7), 1684.

Persaud N, et al. (2025) Clinical Significance of TERT Promoter Mutations in Neuroblastoma. JCO precision oncology, 9, e2500074.

McCarter JGW, et al. (2023) Interaction between myelodysplasia-related gene mutations and ontogeny in acute myeloid leukemia. Blood advances, 7(17), 5000.

Mitchell E, et al. (2022) Clonal dynamics of haematopoiesis across the human lifespan. Nature, 606(7913), 343.

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.

Skead K, et al. (2021) Interacting evolutionary pressures drive mutation dynamics and health outcomes in aging blood. Nature communications, 12(1), 4921.

Fittall MW, et al. (2020) Drivers underpinning the malignant transformation of giant cell tumour of bone. The Journal of pathology, 252(4), 433.

Brunner SF, et al. (2019) Somatic mutations and clonal dynamics in healthy and cirrhotic human liver. Nature, 574(7779), 538.

Xu J, et al. (2019) Abnormal oxidative metabolism in a quiet genomic background underlies clear cell papillary renal cell carcinoma. eLife, 8.

Fittall MW, et al. (2018) Recurrent rearrangements of FOS and FOSB define osteoblastoma. Nature communications, 9(1), 2150.

Diolaiti D, et al. (2018) A recurrent novel MGA-NUTM1 fusion identifies a new subtype of high-grade spindle cell sarcoma. Cold Spring Harbor molecular case studies, 4(6).

Abelson S, et al. (2018) Prediction of acute myeloid leukaemia risk in healthy individuals. Nature, 559(7714), 400.

Wegert J, et al. (2018) Recurrent intragenic rearrangements of EGFR and BRAF in soft tissue tumors of infants. Nature communications, 9(1), 2378.