Resource Summary Report

Generated by dkNET on Apr 16, 2025

VAAST

RRID:SCR_002179
Type: Tool

Proper Citation

VAAST (RRID:SCR_002179)

Resource Information

URL: http://www.yandell-lab.org/software/vaast.html

Proper Citation: VAAST (RRID:SCR_002179)

Description: A probabilistic search tool for identifying damaged genes and their disease-causing variants in personal genome sequences. VAAST combines elements of phylogenetic conservation, amino acid substitution, and aggregative approaches to variant prioritization into a single unified likelihood-framework that allows users to accurately identify damaged genes and deleterious variants. The software can score both coding (SNV, indel and splice site) and non-coding variants (SNV), evaluating the cumulative impact of both types of variants simultaneously. It can identify rare variants causing rare genetic diseases and can also use both rare and common variants to identify genes responsible for common diseases.

Abbreviations: VAAST, VAAST 2

Synonyms: Variant Annotation Analysis and Search Tool, Variant Annotation Analysis & Search Tool

Resource Type: software resource, sequence analysis software, data analysis software, standalone software, software application, data processing software

Defining Citation: PMID:23836555, PMID:21700766

Keywords: sequence analysis software, genetic, variant classifier, amino acid substitution, disease, genome interpretation, variant prioritization, disease gene prioritization, genomic variation, bio.tools

Funding:

Availability: Free for academic use, Pay for commercial and clinical use, Contact sales at

Omicia Inc.

Resource Name: VAAST

Resource ID: SCR_002179

Alternate IDs: nlx_154686, SciRes_000138, biotools:vaast, OMICS_02134

Alternate URLs: https://bio.tools/vaast

License: Academic Free License from University of Utah, Commercial license from Omicia Inc.

Record Creation Time: 20220129T080212+0000

Record Last Update: 20250416T063257+0000

Ratings and Alerts

No rating or validation information has been found for VAAST.

No alerts have been found for VAAST.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 26 mentions in open access literature.

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

Diekhof EK, et al. (2024) The COVID-19 pandemic and changes in social behavior: Protective face masks reduce deliberate social distancing preferences while leaving automatic avoidance behavior unaffected. Cognitive research: principles and implications, 9(1), 2.

Pinnaro CT, et al. (2023) CRELD1 variants are associated with bicuspid aortic valve in Turner syndrome. Human genetics, 142(4), 523.

Wadsley M, et al. (2023) Restricting social networking site use for one week produces varied effects on mood but does not increase explicit or implicit desires to use SNSs: Findings from an ecological momentary assessment study. PloS one, 18(11), e0293467.

Wadsley M, et al. (2022) The roles of implicit approach motivation and explicit reward in excessive and problematic use of social networking sites. PloS one, 17(3), e0264738.

Hateley S, et al. (2021) The history and geographic distribution of a KCNQ1 atrial fibrillation risk allele. Nature communications, 12(1), 6442.

Cereghetti D, et al. (2021) Validation of New Methods of Using Simulated Whole-Body Movements as Implicit Indicators of Sound and Odor Preferences. Frontiers in psychology, 12, 659269.

Sweeney NM, et al. (2021) Rapid whole genome sequencing impacts care and resource utilization in infants with congenital heart disease. NPJ genomic medicine, 6(1), 29.

De La Vega FM, et al. (2021) Artificial intelligence enables comprehensive genome interpretation and nomination of candidate diagnoses for rare genetic diseases. Genome medicine, 13(1), 153.

James KN, et al. (2020) Partially automated whole-genome sequencing reanalysis of previously undiagnosed pediatric patients can efficiently yield new diagnoses. NPJ genomic medicine, 5, 33.

Bruders R, et al. (2020) A copy number variant is associated with a spectrum of pigmentation patterns in the rock pigeon (Columba livia). PLoS genetics, 16(5), e1008274.

Pinnaro CT, et al. (2020) Candidate modifier genes for immune function in 22q11.2 deletion syndrome. Molecular genetics & genomic medicine, 8(1), e1057.

Williams LB, et al. (2019) ALPK1 missense pathogenic variant in five families leads to ROSAH syndrome, an ocular multisystem autosomal dominant disorder. Genetics in medicine : official journal of the American College of Medical Genetics, 21(9), 2103.

Watkins WS, et al. (2019) De novo and recessive forms of congenital heart disease have distinct genetic and phenotypic landscapes. Nature communications, 10(1), 4722.

Kingsmore SF, et al. (2019) A Randomized, Controlled Trial of the Analytic and Diagnostic Performance of Singleton and Trio, Rapid Genome and Exome Sequencing in Ill Infants. American journal of human genetics, 105(4), 719.

Veyssiere M, et al. (2019) A novel nonsense variant in SUPT20H gene associated with Rheumatoid Arthritis identified by Whole Exome Sequencing of multiplex families. PloS one, 14(3), e0213387.

Nuel I, et al. (2019) "Science Manipulates the Things and Lives in Them": Reconsidering Approach-Avoidance Operationalization Through a Grounded Cognition Perspective. Frontiers in psychology, 10, 1418.

Wang J, et al. (2018) GRIPT: a novel case-control analysis method for Mendelian disease gene discovery. Genome biology, 19(1), 203.

Flygare S, et al. (2018) The VAAST Variant Prioritizer (VVP): ultrafast, easy to use whole genome variant prioritization tool. BMC bioinformatics, 19(1), 57.

Requena T, et al. (2017) A pipeline combining multiple strategies for prioritizing heterozygous variants for the identification of candidate genes in exome datasets. Human genomics, 11(1), 11.

Stelzer G, et al. (2016) VarElect: the phenotype-based variation prioritizer of the GeneCards Suite. BMC genomics, 17 Suppl 2(Suppl 2), 444.