Resource Summary Report

Generated by NIF on Aug 9, 2026

Align-GVGD

RRID:SCR_010772
Type: Tool

Proper Citation

Align-GVGD (RRID:SCR_010772)

Resource Information

URL: http://agvgd.iarc.fr/index.php

Proper Citation: Align-GVGD (RRID:SCR_010772)

Description: A freely available, web-based program that combines the biophysical characteristics of amino acids and protein multiple sequence alignments to predict where missense substitutions in genes of interest fall in a spectrum from enriched delterious to enriched neutral.

Abbreviations: Align-GVGD

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

Availability: Free

Resource Name: Align-GVGD

Resource ID: SCR_010772

Alternate IDs: OMICS_00125

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260808T190428+0000

Ratings and Alerts

No rating or validation information has been found for Align-GVGD.

No alerts have been found for Align-GVGD.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 93 mentions in open access literature.

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

Priya M, et al. (2026) Computational Prediction of Deleterious SNPs in the GALNS Gene Implicated in Morquio A Syndrome (MPS IVA). ACS omega, 11(7), 11183.

Arachchige NDS, et al. (2025) Comprehensive bioinformatics analysis of selected germline variants of uncertain significance identified in a cohort of Sri Lankan hereditary breast cancer patients. Human genomics, 19(1), 12.

van Ravensteijn SG, et al. (2025) Cemiplimab in Locally Advanced or Metastatic Secondary Angiosarcomas (CEMangio): A Phase II Clinical Trial and Biomarker Analyses. Clinical cancer research : an official journal of the American Association for Cancer Research, 31(17), 3678.

Huang H, et al. (2025) Functional evaluation and clinical classification of BRCA2 variants. Nature, 638(8050), 528.

S V, et al. (2025) A pro-angiogenic and hypoxic zebrafish model as a novel platform for anti-angiogenic drug testing. Biology open, 14(8).

Casoli T, et al. (2024) Association of Inflammatory Mediators with Mitochondrial DNA Variants in Geriatric COVID-19 Patients. Aging and disease, 15(6), 2665.

Martínez Duncker I, et al. (2024) Case report: Novel genotype of ALG2-CDG and confirmation of the heptasaccharide glycan (NeuAc-Gal-GlcNAc-Man2-GlcNAc2) as a specific diagnostic biomarker. Frontiers in genetics, 15, 1363558.

Bensenane R, et al. (2024) Safety of the Breast Cancer Adjuvant Radiotherapy in Ataxia-Telangiectasia Mutated Variant Carriers. Cancers, 16(7).

Almakhari M, et al. (2024) In-silico identification of deleterious non-synonymous SNPs of TBX1 gene: Functional and structural impact towards 22q11.2DS. PloS one, 19(6), e0298092.

Schäfer J, et al. (2023) The Usher syndrome 1C protein harmonin regulates canonical Wnt signaling. Frontiers in cell and developmental biology, 11, 1130058.

Madarász K, et al. (2022) Deep Molecular and In Silico Protein Analysis of p53 Alteration in Myelodysplastic Neoplasia and Acute Myeloid Leukemia. Cells, 11(21).

Abdelwahed M, et al. (2022) Autosomal dominant polycystic kidney disease (ADPKD) in Tunisia: From molecular genetics to the development of prognostic tools. Gene, 817, 146174.

Wolf J, et al. (2022) Final efficacy and safety data, and exploratory molecular profiling from the phase III ALUR study of alectinib versus chemotherapy in crizotinib-pretreated ALK-positive non-small-cell lung cancer. ESMO open, 7(1), 100333.

Clark KA, et al. (2022) Comprehensive evaluation and efficient classification of BRCA1 RING domain missense substitutions. American journal of human genetics, 109(6), 1153.

Montenegro LR, et al. (2021) Performance of mutation pathogenicity prediction tools on missense variants associated with 46,XY differences of sex development. Clinics (Sao Paulo, Brazil), 76, e2052.

Castells-Roca L, et al. (2021) Clinical consequences of BRCA2 hypomorphism. NPJ breast cancer, 7(1), 117.

Lesueur F, et al. (2021) TUMOSPEC: A Nation-Wide Study of Hereditary Breast and Ovarian Cancer Families with a Predicted Pathogenic Variant Identified through Multigene Panel Testing. Cancers, 13(15).

Özkan S, et al. (2021) Towards a New, Endophenotype-Based Strategy for Pathogenicity Prediction in BRCA1 and BRCA2: In Silico Modeling of the Outcome of HDR/SGE Assays for Missense Variants. International journal of molecular sciences, 22(12).

Secolin R, et al. (2021) Exploring a Region on Chromosome 8p23.1 Displaying Positive Selection Signals in Brazilian Admixed Populations: Additional Insights Into Predisposition to Obesity and Related Disorders. Frontiers in genetics, 12, 636542.

Pellikaan K, et al. (2021) The Diagnostic Journey of a Patient with Prader-Willi-Like Syndrome and a Unique Homozygous SNURF-SNRPN Variant; Bio-Molecular Analysis and Review of the Literature. Genes, 12(6).