Resource Summary Report

Generated by NIF on Aug 29, 2026

CUPSAT

RRID:SCR_010773
Type: Tool

Proper Citation

CUPSAT (RRID:SCR_010773)

Resource Information

URL: http://cupsat.tu-bs.de/

Proper Citation: CUPSAT (RRID:SCR_010773)

Description: A tool to predict changes in protein stability upon point mutations.

Abbreviations: CUPSAT

Synonyms: Cologne University Protein Stability Analysis Tool, CUPSAT: Cologne University Protein Stability Analysis Tool

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

Defining Citation: PMID:16845001

Keywords: bio.tools

Resource Name: CUPSAT

Resource ID: SCR_010773

Alternate IDs: biotools:cupsat, OMICS_00128

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

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260829T183038+0000

Ratings and Alerts

No rating or validation information has been found for CUPSAT.

No alerts have been found for CUPSAT.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 86 mentions in open access literature.

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

Ishaq S, et al. (2026) Pathogenic KRAS variants disrupt structure and dynamics: Insights from integrated computational analyses. PloS one, 21(2), e0341219.

Azmi MB, et al. (2026) Computational identification of rare pathogenic genomic variants in esophageal cancer markers: Transcript-level analysis, sequence-based insights, and structural-functional impacts of non-synonymous SNPs. Biochemistry and biophysics reports, 45, 102503.

Valentine AL, et al. (2026) Cancer mutations in RAD51 and its paralogues. PloS one, 21(5), e0349105.

Hoda A, et al. (2026) Computational analysis of non-synonymous SNPs in the sheep MC4R gene. Journal, genetic engineering & biotechnology, 24(2), 100709.

Ren Y, et al. (2026) Identification and Functional Characterization of Novel and Recurrent NTRK1 Variants in Chinese Families With Congenital Insensitivity to Pain With Anhidrosis: A Combined Clinical, Genetic, and Functional Study. European journal of neurology, 33(5), e70610.

Bliss HJ, et al. (2025) PRMT5 genetic interactions with DNA double strand break repair genes. PloS one, 20(10), e0331499.

Hashemi S, et al. (2025) Structure-guided design of a novel, stable, and soluble Cecropin A variant for antimicrobial therapeutic applications. Scientific reports, 15(1), 32836.

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).

Al-Marrawi M, et al. (2025) In silico protein structural analysis of PRMT5 and RUVBL1 mutations arising in human cancers. Cancer genetics, 292-293, 49.

Mosalanejad Z, et al. (2025) Designing an optimized theta-defensin peptide for HIV therapy using in-silico approaches. Journal of integrative bioinformatics, 22(1).

Tokatly Latzer I, et al. (2025) Central Dysmyelination in SSADH-Deficient Humans and Mice. Annals of clinical and translational neurology, 12(11), 2193.

Watson AE, et al. (2024) Target enrichment sequencing coupled with GWAS identifies MdPRX10 as a candidate gene in the control of budbreak in apple. Frontiers in plant

science, 15, 1352757.

Kaci A, et al. (2024) Functional characterization of HNF4A gene variants identify promoter and cell line specific transactivation effects. Human molecular genetics, 33(10), 894.

Khan MU, et al. (2024) Identification of novel natural compounds against CFTR p.Gly628Arg pathogenic variant. AMB Express, 14(1), 99.

Elamin G, et al. (2024) Integrative genomic analyses combined with molecular dynamics simulations reveal the impact of deleterious mutations of Bcl-2 gene on the apoptotic machinery and implications in carcinogenesis. Frontiers in genetics, 15, 1502152.

Lee YR, et al. (2023) Identification of a novel risk factor for chronic wasting disease (CWD) in elk: S100G single nucleotide polymorphism (SNP) of the prion protein gene (PRNP). Veterinary research, 54(1), 48.

Azmi MB, et al. (2023) Understanding the impact of structural modifications at the NNAT gene's post-translational acetylation site: in silico approach for predicting its drug-interaction role in anorexia nervosa. Eating and weight disorders : EWD, 28(1), 97.

Arribas-Carreira L, et al. (2023) Pathogenic variants in GCSH encoding the moonlighting H-protein cause combined nonketotic hyperglycinemia and lipoate deficiency. Human molecular genetics, 32(6), 917.

Mack AH, et al. (2023) A Proofreading Mutation with an Allosteric Effect Allows a Cluster of SARS-CoV-2 Viruses to Rapidly Evolve. Molecular biology and evolution, 40(10).

Azmi MB, et al. (2023) Transcript-Level In Silico Analysis of Alzheimer's Disease-Related Gene Biomarkers and Their Evaluation with Bioactive Flavonoids to Explore Therapeutic Interactions. ACS omega, 8(43), 40695.