

Resource Summary Report

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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: data analysis service, service resource, production service resource, analysis 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: 20260801T191017+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 74 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#) .

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

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.

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).

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.

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.

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

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.

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.

Ebhohimen IE, et al. (2023) Evaluation of the Antioxidant Properties of Carvacrol as a Prospective Replacement for Crude Essential Oils and Synthetic Antioxidants in Food Storage. *Molecules* (Basel, Switzerland), 28(3).

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.

Wu F, et al. (2023) Glycosylated, Lipid-Binding, CDR-Like Domains of SARS-CoV-2 ORF8 Indicate Unique Sites of Immune Regulation. *Microbiology spectrum*, 11(4), e0123423.

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).

Ali Y, et al. (2023) Association of IL-17F rs2397084 (E126G), rs11465553 (V155I) and rs763780 (H161R) variants with rheumatoid arthritis and their effects on the stability of protein. *PloS one*, 18(9), e0285874.

Pathak RK, et al. (2022) Unraveling structural and conformational dynamics of DGAT1 missense nsSNPs in dairy cattle. *Scientific reports*, 12(1), 4873.

Mehra R, et al. (2022) Structural heterogeneity and precision of implications drawn from cryo-electron microscopy structures: SARS-CoV-2 spike-protein mutations as a test case. *European biophysics journal : EBJ*, 51(7-8), 555.

Kanwal A, et al. (2022) RGS3 and IL1RAPL1 missense variants implicate defective neurotransmission in early-onset inherited schizoprenias. *Journal of psychiatry & neuroscience : JPN*, 47(6), E379.