Resource Summary Report

Generated by RRID on Apr 17, 2025

DynaMut

RRID:SCR_021849
Type: Tool

Proper Citation

DynaMut (RRID:SCR_021849)

Resource Information

URL: http://biosig.unimelb.edu.au/dynamut/

Proper Citation: DynaMut (RRID:SCR_021849)

Description: Web server for predicting impact of mutations on protein conformation, flexibility and stability.

Resource Type: web service, software resource, data access protocol

Defining Citation: PMID:29718330

Keywords: mutation, mutation impacts on protein conformation, protein flexibility, protein stability

Funding:

Availability: Free, Freely available

Resource Name: DynaMut

Resource ID: SCR_021849

Record Creation Time: 20220129T080357+0000

Record Last Update: 20250416T063918+0000

Ratings and Alerts

No rating or validation information has been found for DynaMut .

No alerts have been found for DynaMut .

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 41 mentions in open access literature.

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

Ahmad N, et al. (2024) A novel missense mutation of CCDC34 causes male infertility with oligoasthenoteratozoospermia in a consanguineous Pakistani family. Asian journal of andrology, 26(6), 605.

Liu P, et al. (2024) Characteristics of SARS-CoV-2 Omicron BA.5 variants in Shanghai after ending the zero-COVID policy in December 2022: a clinical and genomic analysis. Frontiers in microbiology, 15, 1372078.

Mahmood HR, et al. (2024) Epidemiological trends, antifungal drug susceptibility and SQLE point mutations in etiologic species of human dermatophytosis in Al-Diwaneyah, Iraq. Scientific reports, 14(1), 12669.

Saharkhiz S, et al. (2024) The State-of-the-Art Overview to Application of Deep Learning in Accurate Protein Design and Structure Prediction. Topics in current chemistry (Cham), 382(3), 23.

Kim OH, et al. (2024) Exploring novel MYH7 gene variants using in silico analyses in Korean patients with cardiomyopathy. BMC medical genomics, 17(1), 225.

Wang Y, et al. (2024) NRDE2 deficiency impairs homologous recombination repair and sensitizes hepatocellular carcinoma to PARP inhibitors. Cell genomics, 4(5), 100550.

Huang X, et al. (2024) The clinical and genetic aspects of six individuals with GH1 variants and isolated growth hormone deficiency type II. Frontiers in endocrinology, 15, 1363050.

Chkioua L, et al. (2024) Respiratory Chain Complex I Deficiency in Leber Hereditary Optic Neuropathy: Insights from Ophthalmologic and Molecular Investigations in Tunisia. BMC genomics, 25(1), 1133.

Jeong DW, et al. (2023) Palmitoylation-driven PHF2 ubiquitination remodels lipid metabolism through the SREBP1c axis in hepatocellular carcinoma. Nature communications, 14(1), 6370.

Litso I, et al. (2023) Structural Evolution of Primate Glutamate Dehydrogenase 2 as

Revealed by In Silico Predictions and Experimentally Determined Structures. Biomolecules, 14(1).

Dehnavi AZ, et al. (2023) Phenotype and genotype heterogeneity of PLA2G6-associated neurodegeneration in a cohort of pediatric and adult patients. Orphanet journal of rare diseases, 18(1), 177.

Yoo S, et al. (2023) The first case of novel variants of the FSHR mutation causing primary amenorrhea in 2 siblings in Korea. Annals of pediatric endocrinology & metabolism, 28(1), 54.

Ogun OJ, et al. (2023) An In Silico Functional Analysis of Non-Synonymous Single-Nucleotide Polymorphisms of Bovine CMAH Gene and Potential Implication in Pathogenesis. Pathogens (Basel, Switzerland), 12(4).

Chen H, et al. (2023) CTCF variant begets to short stature by down-regulation of IGF1. Journal of molecular endocrinology, 70(4).

Chen H, et al. (2023) Novel pathogenic NPR2 variants in short stature patients and the therapeutic response to rhGH. Orphanet journal of rare diseases, 18(1), 221.

Wang X, et al. (2023) Purifying selection leads to low protein diversity of the mitochondrial cyt b gene in avian malaria parasites. BMC ecology and evolution, 23(1), 49.

Ajith A, et al. (2023) In silico screening of non-synonymous SNPs in human TUFT1 gene. Journal, genetic engineering & biotechnology, 21(1), 95.

Akter S, et al. (2023) Spike protein mutations and structural insights of pangolin lineage B.1.1.25 with implications for viral pathogenicity and ACE2 binding affinity. Scientific reports, 13(1), 13146.

Mohammed F, et al. (2022) Missense Mutations in Desmoplakin Plakin Repeat Domains Have Dramatic Effects on Domain Structure and Function. International journal of molecular sciences, 23(1).

Pfeiffer A, et al. (2022) Phosphorylation of SHP2 at Tyr62 Enables Acquired Resistance to SHP2 Allosteric Inhibitors in FLT3-ITD-Driven AML. Cancer research, 82(11), 2141.