Resource Summary Report

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NetSurfP

RRID:SCR_018781
Type: Tool

Proper Citation

NetSurfP (RRID:SCR_018781)

Resource Information

URL: http://www.cbs.dtu.dk/services/NetSurfP/

Proper Citation: NetSurfP (RRID:SCR_018781)

Description: Web tool for prediction of surface accessibility, secondary structure, disorder, and phi/psi dihedral angles of amino acids in amino acid sequence. Used to predict solvent accessibility, secondary structure, structural disorder, and backbone dihedral angles for each residue of input sequences.

Synonyms: NetSurfP-2.0

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

Defining Citation: PMID:30785653

Keywords: Surface accessibility prediction, solvent accessibility prediction, secondary structure prediction, disorder prediction, dihedral angel, amino acid, amino acid sequence, backbone dihedral angels, residue, input sequence

Funding:

Availability: Free, Freely available

Resource Name: NetSurfP

Resource ID: SCR_018781

Record Creation Time: 20220129T080341+0000

Record Last Update: 20250412T060239+0000

Ratings and Alerts

No rating or validation information has been found for NetSurfP.

No alerts have been found for NetSurfP.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 32 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Tanshee RR, et al. (2024) A comprehensive in silico investigation into the pathogenic SNPs in the RTEL1 gene and their biological consequences. PloS one, 19(9), e0309713.

Sarkar B, et al. (2024) Comprehensive characterization of high-risk coding and non-coding single nucleotide polymorphisms of human CXCR4 gene. PloS one, 19(12), e0312733.

Pancaldi F, et al. (2023) Syntenic Cell Wall QTLs as Versatile Breeding Tools: Intraspecific Allelic Variability and Predictability of Biomass Quality Loci in Target Plant Species. Plants (Basel, Switzerland), 12(4).

Holcomb DD, et al. (2022) Protocol to identify host-viral protein interactions between coagulation-related proteins and their genetic variants with SARS-CoV-2 proteins. STAR protocols, 3(3), 101648.

Qian P, et al. (2022) Chronic exercise remodels the lysine acetylome in the mouse hippocampus. Frontiers in molecular neuroscience, 15, 1023482.

Soltani I, et al. (2021) Comprehensive in-silico analysis of damage associated SNPs in hOCT1 affecting Imatinib response in chronic myeloid leukemia. Genomics, 113(1 Pt 2), 755.

Tamrakar A, et al. (2021) Biophysical characterization of the homodimers of HomA and HomB, outer membrane proteins of Helicobacter pylori. Scientific reports, 11(1), 24471.

Pal A, et al. (2021) RIGI, TLR7, and TLR3 Genes Were Predicted to Have Immune Response Against Avian Influenza in Indigenous Ducks. Frontiers in molecular biosciences, 8, 633283.

Li G, et al. (2021) Global analysis of lysine acetylation in soybean leaves. Scientific reports, 11(1), 17858.

Wan J, et al. (2021) Lysine Acetylation in the Proteome of Renal Tubular Epithelial Cells in

Diabetic Nephropathy. Frontiers in genetics, 12, 767135.

Rawat K, et al. (2021) Ovine CD14- an Immune Response Gene Has a Role Against Gastrointestinal Nematode Haemonchus contortus-A Novel Report. Frontiers in immunology, 12, 664877.

Goud TS, et al. (2021) Molecular characterization of coat color gene in Sahiwal versus Karan Fries bovine. Journal, genetic engineering & biotechnology, 19(1), 22.

Attri S, et al. (2021) Dissecting role of founder mutation p.V727M in GNE in Indian HIBM cohort. Open medicine (Warsaw, Poland), 16(1), 1733.

Rozario LT, et al. (2021) In silico analysis of deleterious SNPs of human MTUS1 gene and their impacts on subsequent protein structure and function. PloS one, 16(6), e0252932.

Tsu BV, et al. (2021) Diverse viral proteases activate the NLRP1 inflammasome. eLife, 10.

Asmani F, et al. (2021) In Silico designing and immunogenic production of the multimeric CfaB*ST, CfaE, LTB antigen as a peptide vaccine against Enterotoxigenic Escherichia coli. Microbial pathogenesis, 158, 105087.

Shinwari K, et al. (2021) Predicting the Most Deleterious Missense Nonsynonymous Single-Nucleotide Polymorphisms of Hennekam Syndrome-Causing CCBE1 Gene, In Silico Analysis. TheScientificWorldJournal, 2021, 6642626.

Li WJ, et al. (2021) Insulin signaling regulates longevity through protein phosphorylation in Caenorhabditis elegans. Nature communications, 12(1), 4568.

Liaci AM, et al. (2021) Structure of the human signal peptidase complex reveals the determinants for signal peptide cleavage. Molecular cell, 81(19), 3934.

Almutairi ZM, et al. (2021) Molecular characterization and expression analysis of ribosomal L18/L5e gene in Pennisetum glaucum (L.) R. Br. Saudi journal of biological sciences, 28(6), 3585.