Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 2, 2025

ProtParam Tool

RRID:SCR_018087
Type: Tool

Proper Citation

ProtParam Tool (RRID:SCR_018087)

Resource Information

URL: https://web.expasy.org/protparam/

Proper Citation: ProtParam Tool (RRID:SCR_018087)

Description: Software tool to calculate various physicochemical parameters for given protein stored in Swiss-Prot or TrEMBL or for user entered protein sequence. Protein can either be pecified as Swiss-Prot/TrEMBL accession number or ID, or in form of raw sequence. Computed parameters include molecular weight, theoretical pI, amino acid composition, atomic composition, extinction coefficient, estimated half-life, instability index, aliphatic index and grand average of hydropathicity.

Synonyms: ProtParam

Resource Type: analysis service resource, software application, service resource, production service resource, sequence analysis software, data processing software, data analysis software, software resource

Defining Citation: PMID:10027275

Keywords: Calculate phycicochemical parameter, protein, Swiss-Prot, TrEMBL, protein sequence, molecular weight, theortical pI, amino acid composition, atomic composition, extinction coefficient, bio.tools

Funding: NHGRI U01 HG02712;
Swiss Federal Government through Federal Office of Education and Science

Availability: Free, Freely available

Resource Name: ProtParam Tool

Resource ID: SCR_018087

Alternate IDs: biotools:protparam

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

Record Creation Time: 20220129T080338+0000

Record Last Update: 20250402T061535+0000

Ratings and Alerts

No rating or validation information has been found for ProtParam Tool.

No alerts have been found for ProtParam Tool.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4802 mentions in open access literature.

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

Walvekar AS, et al. (2025) Failure to repair damaged NAD(P)H blocks de novo serine synthesis in human cells. Cellular & molecular biology letters, 30(1), 3.

Wang J, et al. (2025) LC-AMP-I1, a novel venom-derived antimicrobial peptide from the wolf spider Lycosa coelestis. Antimicrobial agents and chemotherapy, 69(1), e0042424.

Knechtel JW, et al. (2025) KMT5C leverages disorder to optimize cooperation with HP1 for heterochromatin retention. EMBO reports, 26(1), 153.

Espinheira RP, et al. (2025) Discovery and Characterization of Mannan-Specialized GH5 Endo-1,4-?-mannanases: a Strategy for Açaí (Euterpe oleracea Mart.) Seeds Upgrading. Journal of agricultural and food chemistry, 73(1), 625.

Guillou MC, et al. (2025) Phytocytokine genes newly discovered in Malus domestica and their regulation in response to Erwinia amylovora and acibenzolar-S-methyl. The plant genome, 18(1), e20540.

Wang Y, et al. (2025) Identification of the CaCRT gene family and function of CaCRT1 under low-temperature stress in pepper (Capsicum annuum L.). Scientific reports, 15(1), 90.

Wang P, et al. (2025) The StbHLH47 transcription factor negatively regulates drought tolerance in potato (Solanum tuberosum L.). BMC plant biology, 25(1), 14.

Wang HW, et al. (2025) Identification, characterization, and expression of Oryza sativa tryptophan decarboxylase genes associated with fluroxypyr-meptyl metabolism. The plant genome, 18(1), e20547.

Zubair S, et al. (2025) Computational design of multi-epitope vaccine against Hepatitis C Virus infection using immunoinformatics techniques. PloS one, 20(1), e0317520.

Islam MSU, et al. (2025) Genome-wide identification and characterization of cation-proton antiporter (CPA) gene family in rice (Oryza sativa L.) and their expression profiles in response to phytohormones. PloS one, 20(1), e0317008.

Uddin ME, et al. (2025) Identification and Characterization of a Protease Producing Bacillus cereus Strain From Tannery Waste for Efficient Dehairing of Goat Skin. BioMed research international, 2025, 7639181.

Guo Y, et al. (2025) TaWI12 may be involved in pistillody and leaf cracking in wheat. BMC plant biology, 25(1), 123.

Yang X, et al. (2025) The Pyrus sinkiangensis Yu PsLEA4 Gene Enhances the Cold Resistance of Solanum lycopersicum. Plants (Basel, Switzerland), 14(2).

Sarwar S, et al. (2025) Genome-Wide Identification and In Silico Expression Analysis of CCO Gene Family in Citrus clementina (Citrus) in Response to Abiotic Stress. Plants (Basel, Switzerland), 14(2).

Wu X, et al. (2025) Genome-Wide Identification, Phylogenetic Evolution, and Abiotic Stress Response Analyses of the Late Embryogenesis Abundant Gene Family in the Alpine Cold-Tolerant Medicinal Notopterygium Species. International journal of molecular sciences, 26(2).

Bian X, et al. (2025) Genome-Wide Identification and Expression Profile of Farnesyl Pyrophosphate Synthase (FPS) Gene Family in Euphorbia Hirta L. International journal of molecular sciences, 26(2).

Feng X, et al. (2025) Genome-Wide Analysis of bZIP Transcription Factors and Expression Patterns in Response to Salt and Drought Stress in Vaccinium corymbosum. International journal of molecular sciences, 26(2).

Naveed M, et al. (2025) Scrutinizing the evidence of anthracene toxicity on adrenergic receptor beta-2 and its bioremediation by fungal manganese peroxidase via in silico approaches. Scientific reports, 15(1), 3795.

López CM, et al. (2025) CRISPR/Cas9 editing of two adenine phosphoribosyl transferase coding genes reveals the functional specialization of adenine salvage proteins in common bean. Journal of experimental botany, 76(2), 346.

O'Brien JH, et al. (2025) Cryo-EM Structure of Recombinantly Expressed hUGDH Unveils a Hidden, Alternative Allosteric Inhibitor. Biochemistry, 64(1), 92.