

Resource Summary Report

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ProtParam Tool

RRID:SCR_018087

Type: Tool

Proper Citation

ProtParam Tool (RRID:SCR_018087)

Resource Information

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

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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 specified 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: software application, service resource, data analysis software, sequence analysis software, data processing software, software resource, production service resource, analysis service resource

Defining Citation: [PMID:10027275](#)

Keywords: Calculate physicochemical parameter, protein, Swiss-Prot, TrEMBL, protein sequence, molecular weight, theoretical 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: 20260729T044449+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 5406 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Barajas JM, et al. (2026) Tandem Duplications in UBTF Create XPO1-Dependent Nuclear Export Signals that Reveal a Leukemic Therapeutic Dependency. *Blood cancer discovery*, 7(1), 51.

Martedì R, et al. (2026) De novo cysteine biosynthesis in *Pseudomonas aeruginosa*: Characterization of the two main cysteine synthase isoforms. *iScience*, 29(1), 114304.

Gao H, et al. (2026) Hydrogen-deuterium exchange reveals catalytically linked protein flexibility in myoglobin-mediated intramolecular C(sp³)-H activation. *Protein science : a publication of the Protein Society*, 35(1), e70410.

Verma HK, et al. (2026) Cystatin C prevents tissue injury after lung transplantation. *Life science alliance*, 9(2).

Khan A, et al. (2026) HMPV-TherResDB: Comprehensive human metapneumovirus (HMPV) database for sequence-structure annotations, vaccine resources, and therapeutics research. *Virus research*, 363, 199665.

Cleveland ME, et al. (2026) Toward the Bioremediation of Nylon Waste Materials: Genome Mining Leads to the Identification of a Thermostable Laurolactamase From *Thermopolyspora flexuosa*. *ChemSusChem*, 19(1), e202501964.

Smorodinsky-Atias K, et al. (2026) On the same side: VISTA and its ligands interact in cis on the cell surface. *Protein science : a publication of the Protein Society*, 35(1), e70415.

Grieben M, et al. (2026) Cloning, expression, purification, and structural modeling of the Chandipura virus matrix protein. *FEBS open bio*, 16(1), 41.

Farias FM, et al. (2026) Streptocyclin BTW is a novel member of a diverse family of circular bacteriocins in the genus *Streptococcus*. *Molecular nutrition & food research*, 70(1), e70290.

Lyu Y, et al. (2026) An open axial channel of the AAA ClpXP protease enhances degradation of specific classes of protein substrates. *Protein science : a publication of the Protein Society*, 35(1), e70372.

Pasha AVK, et al. (2026) Immunoinformatics-Based Multi-Epitope Vaccine Targeting *Helicobacter Pylori*. *Cancer reports (Hoboken, N.J.)*, 9(1), e70441.

De Coninck T, et al. (2025) OsAPSE modulates non-covalent interactions between arabinogalactan protein O-glycans and pectin in rice cell walls. *Frontiers in plant science*, 16, 1588802.

Graham LA, et al. (2025) Winter-active spiders (*Clubiona*) have a hyperactive antifreeze protein with a unique beta-solenoid fold. *The FEBS journal*.

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.

Song Y, et al. (2025) Genome-Wide Identification and Expression Analysis of the STAT Family in Reeve's Turtle (*Mauremys reevesii*). *Biochemical genetics*, 63(3), 2330.

Köller Z, et al. (2025) To be, or not to be cleaved: Directed evolution of a canonical serine protease inhibitor against active and inactive protease pair identifies binding loop residue critical for prevention of proteolytic cleavage. *Protein science : a publication of the Protein Society*, 34(5), e70146.

Huang Y, et al. (2025) Genome-wide identification of the interferon complex establishes IFNf in *Cypriniformes*. *BMC biology*, 23(1), 202.

Piao X, et al. (2025) *Schistosoma japonicum* cathepsin L1: A potential target for anti-schistosomiasis strategies. *PLoS neglected tropical diseases*, 19(7), e0013241.

Dai J, et al. (2025) Genome-wide identification and expression analysis of Dof gene family members in mulberry trees (*Morus notabilis* L.) under drought stress. *BMC genomics*, 26(1), 744.

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