

Resource Summary Report

Generated by SPARC SAWG on Sep 4, 2026

TMHMM Server

RRID:SCR_014935

Type: Tool

Proper Citation

TMHMM Server (RRID:SCR_014935)

Resource Information

URL: <http://www.cbs.dtu.dk/services/TMHMM/>

Proper Citation: TMHMM Server (RRID:SCR_014935)

Description: Web application for the prediction of transmembrane helices in proteins using Hidden Markov Models. FASTA formatted sequences can be uploaded via file or copy-paste, and output can be formatted as extensive with graphics, extensive without graphics, or one line per protein. Submissions are limited to 10,000 sequences and 4,000,000 amino acids - each sequence is limited to no more than 8,000 amino acids.

Synonyms: TMHMM Server v 2.0

Resource Type: software resource, web application

Keywords: sequence, amino acid, web application, transmembrane helices, hidden markov model, fasta

Availability: Open source

Resource Name: TMHMM Server

Resource ID: SCR_014935

Record Creation Time: 20220129T080323+0000

Record Last Update: 20260903T235900+0000

Ratings and Alerts

No rating or validation information has been found for TMHMM Server.

No alerts have been found for TMHMM Server.

Data and Source Information

Usage and Citation Metrics

We found 2154 mentions in open access literature.

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

Telford MS, et al. (2026) Antibacterial microcins self-assemble to promote biofilm formation in *Acinetobacter baumannii*. *Cell reports*, 45(4), 117156.

Feng C, et al. (2026) Identification and analysis of the crucial holin domain and sites and the bactericidal activity of a holin-endolysin lysis cassette from phage PZL-Ah152 against *Aeromonas hydrophila*. *Journal of virology*, 100(1), e0083225.

Kesawat MS, et al. (2026) Genome-wide analysis of the pleiotropic drug resistance (PDR) gene family and putative PDR specific miRNAs: deciphering their functions in development processes and varied stresses in *Triticum aestivum* L. *BMC genomics*, 27(1), 108.

Wang L, et al. (2026) Genome-Wide Analysis of *Nelumbo nucifera* UXS Family Genes: Mediating Dwarfing and Aquatic Salinity Tolerance. *Plants (Basel, Switzerland)*, 15(1).

Ye Q, et al. (2026) Molecular Characterization and Expression Analysis of CD22 in Nile Tilapia (*Oreochromis niloticus*) and Its Potential Role in Immune Responses. *Biology*, 15(2).

Yu R, et al. (2026) Identification, cloning and expression analysis of chloroplast TOC-TIC complex components in a C4 halophyte *Suaeda aralocaspica* without Kranz anatomy. *BMC plant biology*, 26(1).

Xie Y, et al. (2026) Reversible S-palmitoylation of C4 protein encoded by TYLCCxV orchestrates geminiviral pathogenesis. *Stress biology*, 6(1).

Li P, et al. (2026) Secreted proteins from *Bacillus subtilis* K1 induce apple resistance against gray mold. *Frontiers in plant science*, 17, 1825616.

Reneer ZB, et al. (2026) Antigenic mapping of H2 influenza viruses recognized by ferret and human sera and predicting antigenically significant sites. *mSphere*, 11(6), e0002226.

Yang X, et al. (2026) Genome-wide identification of the ADF gene family and expression analysis of responses to cold stress in bitter melon. *BMC plant biology*, 26(1).

Yang X, et al. (2026) Knockout of aminopeptidase N3 confers resistance to low concentrations of *Bacillus thuringiensis* Cry4Ba protoxin in *Aedes aegypti*. *Parasites & vectors*, 19(1).

Kang B, et al. (2026) Identification and characterization of salt-, drought-, and combined salt-drought stress-responsive NHX gene family in *Medicago sativa*. *Plant signaling & behavior*, 21(1), 2657741.

Wang G, et al. (2026) Correlation and expression pattern analyses of immune receptor genes in cotton. *BMC genomics*, 27(1).

Koramutla MK, et al. (2026) Genome-wide identification of ethylene receptor protein-coding gene families in wheat and their regulated expression during development and under multiple abiotic stresses. *BMC plant biology*, 26(1), 347.

Ren J, et al. (2026) Comparative analysis of seven types of phosphate transporters in forty species from the phylogenetic and transcriptomic perspective. *PloS one*, 21(5), e0349574.

Cao X, et al. (2026) The vacuolar transporters MaMATE11 and MaMATE14 affect blue flower coloration in grape hyacinth (*Muscari*). *Horticulture research*, 13(1), uhaf270.

Fu Y, et al. (2026) Disruption of yellow-e3 impairs both adult molting and cuticular melanization in the honeybee (*Apis mellifera*). *Frontiers in zoology*, 23(1).

Zhang Y, et al. (2026) Nuclear Localization of Effector BPE159: A Pivotal Mechanism for Intracellular Persistence of *Brucella* by Hampering Host Autophagy. *Microorganisms*, 14(3).

Liu CP, et al. (2026) A brain-gut excitatory peptide/CCHamide homolog regulates satiation and motivational state transitions in the *Aplysia* feeding circuit. *The Journal of biological chemistry*, 302(3), 111257.

Wang X, et al. (2026) Transcriptomic divergences of larval labial salivary glands facilitate host-plant range oscillations between specialist and generalist *Helicoverpa* species. *BMC genomics*, 27(1).