Resource Summary Report

Generated by RRID on May 18, 2025

Mitoprot

RRID:SCR_019023 Type: Tool

Proper Citation

Mitoprot (RRID:SCR_019023)

Resource Information

URL: https://ihg.gsf.de/ihg/mitoprot.html

Proper Citation: Mitoprot (RRID:SCR_019023)

Description: Web server for prediction of mitochondrial targeting sequences.

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

Keywords: Mitochondrial targeting sequence, sequence prediction, mitochondrial sequence, prediction

Funding:

Availability: Free, Freely available

Resource Name: Mitoprot

Resource ID: SCR_019023

Record Creation Time: 20220129T080343+0000

Record Last Update: 20250517T060409+0000

Ratings and Alerts

No rating or validation information has been found for Mitoprot.

No alerts have been found for Mitoprot.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 48 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>RRID</u>.

Liu X, et al. (2024) Salmonella enterica serovar Typhimurium remodels mitochondrial dynamics of macrophages via the T3SS effector SipA to promote intracellular proliferation. Gut microbes, 16(1), 2316932.

Shrivastava D, et al. (2024) ATM1, an essential conserved transporter in Apicomplexa, bridges mitochondrial and cytosolic [Fe-S] biogenesis. PLoS pathogens, 20(9), e1012593.

Calabrese C, et al. (2024) Mitochondrial translocation of TFEB regulates complex I and inflammation. EMBO reports, 25(2), 704.

Silva MF, et al. (2023) Functional and biochemical characterization of the Toxoplasma gondii succinate dehydrogenase complex. PLoS pathogens, 19(12), e1011867.

Cui Z, et al. (2023) Reconfiguration of the reductive TCA cycle enables high-level succinic acid production by Yarrowia lipolytica. Nature communications, 14(1), 8480.

Kahie MA, et al. (2023) Evolution and expression analysis of the caffeoyl-CoA 3-Omethyltransferase (CCoAOMT) gene family in jute (Corchorus L.). BMC genomics, 24(1), 204.

Lucero RA, et al. (2021) Deletion of the natural inhibitory protein Inh1 in Ustilago maydis has no effect on the dimeric state of the F1FO-ATP synthase but increases the ATPase activity and reduces the stability. Biochimica et biophysica acta. Bioenergetics, 1862(7), 148429.

Pyrih J, et al. (2021) The iron-sulfur scaffold protein HCF101 unveils the complexity of organellar evolution in SAR, Haptista and Cryptista. BMC ecology and evolution, 21(1), 46.

Peng GX, et al. (2021) The human tRNA taurine modification enzyme GTPBP3 is an active GTPase linked to mitochondrial diseases. Nucleic acids research, 49(5), 2816.

Jiang X, et al. (2021) Human Herpesvirus 6B U26 Inhibits the Activation of the RLR/MAVS Signaling Pathway. mBio, 12(1).

Horváthová L, et al. (2021) Analysis of diverse eukaryotes suggests the existence of an ancestral mitochondrial apparatus derived from the bacterial type II secretion system. Nature communications, 12(1), 2947.

Song L, et al. (2021) Characterization and expression analysis of mitochondrial localization

molecule: NOD-like receptor X1 (NIrx1) in mucosal tissues of turbot (Scophthalmus maximus) following bacterial challenge. Developmental and comparative immunology, 116, 103944.

Pyrih J, et al. (2021) Vestiges of the Bacterial Signal Recognition Particle-Based Protein Targeting in Mitochondria. Molecular biology and evolution, 38(8), 3170.

Sharma N, et al. (2021) Mycobacterium tuberculosis Protein PE6 (Rv0335c), a Novel TLR4 Agonist, Evokes an Inflammatory Response and Modulates the Cell Death Pathways in Macrophages to Enhance Intracellular Survival. Frontiers in immunology, 12, 696491.

Choi M, et al. (2021) Mitochondrial Targeting of the Ammonia-Sensitive Uncoupler SLC4A11 by the Chaperone-Mediated Carrier Pathway in Corneal Endothelium. Investigative ophthalmology & visual science, 62(12), 4.

Boonyakida J, et al. (2021) Identification of antigenic domains and peptides from VP15 of white spot syndrome virus and their antiviral effects in Marsupenaeus japonicus. Scientific reports, 11(1), 12766.

Costa JH, et al. (2021) Genome-wide identification of ascorbate-glutathione cycle gene families in soybean (Glycine max) reveals gene duplication events and specificity of gene members linked to development and stress conditions. International journal of biological macromolecules, 187, 528.

Saxena R, et al. (2021) Human neurotropic polyomavirus, JC virus, agnoprotein targets mitochondrion and modulates its functions. Virology, 553, 135.

Wang H, et al. (2021) Genome-wide identification, characterization, and expression analysis of tea plant autophagy-related genes (CsARGs) demonstrates that they play diverse roles during development and under abiotic stress. BMC genomics, 22(1), 121.

Haeussler S, et al. (2021) Genome-wide RNAi screen for regulators of UPRmt in Caenorhabditis elegans mutants with defects in mitochondrial fusion. G3 (Bethesda, Md.), 11(7).