

# Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

## [mitopred](#)

RRID:SCR\_006135

Type: Tool

### Proper Citation

mitopred (RRID:SCR\_006135)

### Resource Information

**URL:** <http://bioapps.rit.albany.edu/MITOPRED/>

**Proper Citation:** mitopred (RRID:SCR\_006135)

**Description:** THIS RESOURCE IS NO LONGER IN SERVICE, documented on July 16, 2013. It predicts nuclear-encoded mitochondrial proteins from all eukaryotic species including plants. Prediction is based on the occurrence patterns of Pfam domains (version 16.0) in different cellular locations, amino acid composition and pI value differences between mitochondrial and non-mitochondrial locations. Additionally, you may download MITOPRED predictions for complete proteomes. Re-calculated predictions are instantly accessible for proteomes of *Saccharomyces cerevisiae*, *Caenorhabditis elegans*, *Drosophila*, *Homo sapiens*, *Mus musculus* and *Arabidopsis* species as well as all the eukaryotic sequences in the Swiss-Prot and TrEMBL databases. Queries, at different confidence levels, can be made through four distinct options: (i) entering Swiss-Prot/TrEMBL accession numbers; (ii) uploading a local file with such accession numbers; (iii) entering protein sequences; (iv) uploading a local file containing protein sequences in FASTA format. The Mitopred algorithm works based on the differences in the Pfam domain occurrence patterns and amino acid composition differences in different cellular compartments. Location specific Pfam domains have been determined from the entire eukaryotic set of Swissprot database. Similarly, differences in the amino acid composition between mitochondrial and non-mitochondrial sequences were pre-calculated. This information is used to calculate location-specific amino acid weights that are used to calculate amino acid score. Similarly, pI average values of the N-terminal 25 residues in different cellular location were also determined. This knowledge-base is accessed by the program during execution.

**Abbreviations:** MITOPRED

**Synonyms:** A genome-scale method for predicting mitochondrial proteins

**Resource Type:** data analysis service, service resource, production service resource, analysis service resource

**Keywords:** yeast, c. elegans, drosophila, mouse, human, arabidopsis, bio.tools

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** mitopred

**Resource ID:** SCR\_006135

**Alternate IDs:** biotools:mitopred, nif-0000-03956, BioTools:mitopred

**Alternate URLs:** <https://bio.tools/mitopred>, <https://bio.tools/mitopred>, <https://bio.tools/mitopred>

**Record Creation Time:** 20220129T080234+0000

**Record Last Update:** 20260801T190930+0000

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## Ratings and Alerts

No rating or validation information has been found for mitopred.

No alerts have been found for mitopred.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Sun N, et al. (2019) Unique, Diverged, and Conserved Mitochondrial Functions Influencing *Candida albicans* Respiration. *mBio*, 10(3).

Denoeud F, et al. (2011) Genome sequence of the stramenopile *Blastocystis*, a human anaerobic parasite. *Genome biology*, 12(3), R29.

Cardol P, et al. (2011) Mitochondrial NADH:ubiquinone oxidoreductase (complex I) in eukaryotes: a highly conserved subunit composition highlighted by mining of protein databases. *Biochimica et biophysica acta*, 1807(11), 1390.

Prasad BD, et al. (2010) In silico identification of carboxylate clamp type tetratricopeptide repeat proteins in *Arabidopsis* and rice as putative co-chaperones of Hsp90/Hsp70. *PLoS one*, 5(9), e12761.

Desler C, et al. (2009) In Silico screening for functional candidates amongst hypothetical proteins. *BMC bioinformatics*, 10, 289.

Gaston D, et al. (2009) Predicting proteomes of mitochondria and related organelles from genomic and expressed sequence tag data. *Methods in enzymology*, 457, 21.

Chatre L, et al. (2009) Efficient mitochondrial targeting relies on co-operation of multiple protein signals in plants. *Journal of experimental botany*, 60(3), 741.