

Resource Summary Report

Generated by [NIF](#) on Aug 30, 2026

MitoProteome

RRID:SCR_000739

Type: Tool

Proper Citation

MitoProteome (RRID:SCR_000739)

Resource Information

URL: <http://www.mitoproteome.org>

Proper Citation: MitoProteome (RRID:SCR_000739)

Description: A database of object-relational mitochondrial protein sequences, which contains both mitochondrial and nuclear encoded entries. This database that was generated from experimental evidence and other public databases. Each protein is annotated with data from external databases, including: Locuslink, Ensembl, OMIM, MINT, DIP, PFAM, InterPro, PRINTS and NCBI NR.

Resource Type: data or information resource, database

Defining Citation: [PMID:14681458](#)

Keywords: mitochondrial protein, nuclear, annotation, entries, object relational, object-relational

Resource Name: MitoProteome

Resource ID: SCR_000739

Alternate IDs: nif-0000-03146

Record Creation Time: 20220129T080203+0000

Record Last Update: 20260829T182910+0000

Ratings and Alerts

No rating or validation information has been found for MitoProteome.

No alerts have been found for MitoProteome.

Data and Source Information

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Levy S, et al. (2016) Identification of LACTB2, a metallo-β-lactamase protein, as a human mitochondrial endoribonuclease. Nucleic acids research, 44(4), 1813.

Mao L, et al. (2015) A constraint-based modelling approach to metabolic dysfunction in Parkinson's disease. Computational and structural biotechnology journal, 13, 484.

Lam C, et al. (2014) Two novel compound heterozygous mutations in OPA3 in two siblings with OPA3-related 3-methylglutaconic aciduria. Molecular genetics and metabolism reports, 1, 114.

Doyle SR, et al. (2013) Evidence of evolutionary constraints that influences the sequence composition and diversity of mitochondrial matrix targeting signals. PloS one, 8(6), e67938.

Narita K, et al. (2012) Proteomic analysis of multiple primary cilia reveals a novel mode of ciliary development in mammals. Biology open, 1(8), 815.

Galperin MY, et al. (2005) The Molecular Biology Database Collection: 2005 update. Nucleic acids research, 33(Database issue), D5.