

# Resource Summary Report

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## MitoRes

RRID:SCR\_008208

Type: Tool

### Proper Citation

MitoRes (RRID:SCR\_008208)

### Resource Information

**URL:** <http://mitores.ba.itb.cnr.it>

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**Description:** MitoRes, is a comprehensive and reliable resource for massive extraction of sequences and sub-sequences of nuclear genes and encoded products targeting mitochondria in metazoa. It has been developed for supporting high-throughput in-silico analyses aimed to studies of functional genomics related to mitochondrial biogenesis, metabolism and to their pathological dysfunctions. It integrates information from the most accredited world-wide databases to bring together gene, transcript and encoded protein sequences associated to annotations on species name and taxonomic classification, gene name, functional product, organelle localization, protein tissue specificity, Enzyme Classification (EC), Gene Ontology (GO) classification and links to other related public databases. The section Cluster, has been dedicated to the collection of data on protein clustering of the entire catalogue of MitoRes protein sequences based on all versus all global pair-wise alignments for assessing putative intra- and inter-species functional relationships. The current version of MitoRes is based on the UniProt release 4 and contains 64 different metazoan species. The incredible explosion of knowledge production in Biology in the past two decades has created a critical need for bioinformatic instruments able to manage data and facilitate their retrieval and analysis. Hundreds of biological databases have been produced and the integration of biological data from these different resources is very important when we want to focus our efforts towards the study of a particular layer of biological knowledge. MitoRes is a completely rebuilt edition of MitoNuc database, which has been extensively modified to deal successfully with the challenges of the post genomic era. Its goal is to represent a comprehensive and reliable resource supporting high-quality in-silico analyses aimed to the functional characterization of gene, transcript and amino acid sequences, encoded by the nuclear genome and involved in mitochondrial biogenesis, metabolism and pathological dysfunctions in metazoa. The central features of MitoRes are: # an integrated catalogue of protein, transcript and gene sequences and sub-sequences # a Web-based application composed of a wide spectrum of search/retrieval facilities # a sequence export manager allowing massive extraction of bio-sequences (genes, introns, exons, gene flanking regions, transcripts, UTRs, CDS,

proteins and signal peptides) in FASTA, EMBL and GenBank formats. It is an interconnected knowledge management system based on a MySQL relational database, which ensures data consistency and integrity, and on a Web Graphical User Interface (GUI), built in Seagull PHP Framework, offering a wide range of search and sequence extraction facilities. The database is compiled extracting and integrating information from public resources and data generated by the MitoRes team. The MitoRes database consists of comprehensive sequence entries whose core data are protein, transcript and gene sequences and taxonomic information describing the biological source of the protein. Additional information include: bio-sequences structure and location, biological function of protein product and dynamic links to both, external public databases used as data resources and public databases reporting complementary information. The core entity of the MitoRes database is represented by the protein so that each MitoRes entry is generated for each protein reported in the UniProt database as a nuclear encoded protein involved in mitochondrial biogenesis and function. Sponsors: MitoRes has been supported by Ministero Universit e Ricerca Scientifica, Italy (PRIN, Programma Biotechnologie legge 95/95-MURST 5, Project MURST Cluster C03/2000, CEGBA). Currently it is supported by operating grants from the Ministero dell'Istruzione, dell'Universit e della Ricerca (MIUR), Italy (PNR 2001-2003 (FIRB art.8) D.M. 199, Strategic Program: Post-genome, grant 31-063933 and Project n.2, Cluster C03 L. 488/929).

**Abbreviations:** MitoRes

**Resource Type:** data acquisition software, data analysis software, data processing software, software application, software resource

**Keywords:** dysfunction, encode, enzyme, exon, extraction, function, functional, gene, alignment, amino acid, biogenesis, bioinformatic, biological, biology, cds, classification, disfunctional, genome, genomic, genomics, intron, localization, location, metabolic process, metabolism, metazoa, mitochondria, mitochondrial, mitochondrial genes and proteins databases, nuclear, nuclear\_gene, nuclear\_mitochondrial, nuclear\_sequence, organelle, organelle localization, pathological, peptide, protein, protein\_coding, protein structure classification, region, sequence, signal, signal\_peptide, specie, specificity, structure, sub-sequence, taxonomic, tissue, transcript, utr

**Resource Name:** MitoRes

**Resource ID:** SCR\_008208

**Alternate IDs:** nif-0000-21269

**Old URLs:** <http://www2.ba.itb.cnr.it/MitoNuc/>

**Record Creation Time:** 20220129T080246+0000

**Record Last Update:** 20260905T132619+0000

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## Ratings and Alerts

No rating or validation information has been found for MitoRes.

No alerts have been found for MitoRes.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 1 mentions in open access literature.

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

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