



## Protein Biosynthesis and its Mechanisms in Mammalian Mitochondria

Henry Benjamin\*

Department of Biomolecules, University of Cambridge, Cambridge, UK

### DESCRIPTION

Protein synthesis in mammalian mitochondria results in the production of 13 proteins that serve as key subunits of oxidative phosphorylation complexes. The each stage of mitochondrial translation, including initiation, elongation, termination and ribosome recycling. The critical proteins involved in each phase are discussed. In mammals all of the products of mitochondrial protein production are introduced into the inner membrane. Several proteins that may aid in the binding of ribosomes to the membrane during translation are characterised although much remains unknown about this process. Mutations in mitochondrial or nuclear genes encoding translation system components frequently result in significant impairments in oxidative phosphorylation and a list of these mutations is presented. Through oxidative phosphorylation, mitochondria generate more than 90% of the energy utilized by mammalian cells. They also perform important processes such as heme biosynthesis a section of the urea cycle and play a role in apoptosis [1].

Mitochondria are oblong-shaped organelles that are enclosed by two membranes. The Outer Membrane (OM) defines the general structure and forms an envelope, creating a barrier that prevents tiny molecules from passing through. The Inner Membrane (IM) is heavily invaginated, generating cristae and surrounds the matrix the interior soluble component. The IM is divided into two halves. The Inner Membrane Boundary (IMB) is intimately linked to the OM which it shares a number of contact points [2]. The majority of the IM's surface is made up of Crystal Membranes (CM). The IMB and CM are linked by narrow, ring-like structures that act as a barrier between the intra crystal and intramembranous spaces. For clarity, we shall refer to the Inner Membrane (IM) as including both the IMB and the CM throughout this. The IM is the site of oxidative phosphorylation which produces the majority of ATP required by aerobic cells. Systems are found in the IM and serve as components in the electron transport and ATP synthase complexes. All of the mitochondrial proteins are produced. Several particular phases of mammalian mitochondrial protein

synthesis however have been successfully performed in providing insight on unique aspects of this system. It concentrates on research into the auxiliary elements needed for mammalian mitochondrial protein synthesis. Major distinctions in translational systems in lower eukaryotes Proteomics has been used to identify the majority of mitochondrial ribosomal proteins [3]. The small subunit of the bovine mitochondrial ribosome contains approximately 29 proteins, 14 of which have homologs in prokaryotic ribosomes and 15 of which are unique to mitochondrial ribosomes. Only six of these mitochondrial-specific proteins have yeast mitochondrial ribosome homologs. The big subunit contains around 48 proteins. The remaining 20 are unique to mitochondrial ribosomes and are homologs of bacterial ribosomal proteins. Again just nine of these mitochondrial specific ribosomal proteins have yeast homologs, demonstrating that the protein composition of mitochondrial ribosomes differs significantly between higher and lower eukaryotes [4].

Many proteins with bacterial homologs are substantially bigger than their equivalents. According to database study the human mitochondrial ribosome has a similar protein range to the bovine system. Protein biosynthesis occurs in four stages each needing a different collection of auxiliary elements. During initiation the mRNA's start site is chosen and the initiator tRNA is base-paired to the mRNA in the ribosome's P-site. The codons in the mRNA are read consecutively during elongation while the amino acids are integrated into the expanding polypeptide chain. The finished polypeptide is released and the ribosome complex is dissociated during termination and ribosome recycling [5].

### REFERENCES

1. Nissen P, Thirup S, Kjeldgaard M, Nyborg J. The crystal structure of Cys-tRNA<sup>Cys</sup>-EF-Tu-GDPNP reveals general and specific features in the ternary complex and in tRNA. *Structure*.1999; 7(2):143-56.
2. Hunter SE, Spremulli LL. Effects of mutagenesis of residue 221 on the properties of bacterial and mitochondrial elongation factor EF-Tu. *Biochim Biophys Acta*. 2004; 1699(1-2):173-82.

**Correspondence to:** Henry Benjamin, Department of Biomolecules, University of Cambridge, Cambridge, UK, E-mail: benjamin@gmail.com

**Received:** 25-Nov-2022, Manuscript No. BOM-22-19265; **Editor assigned:** 28-Nov-2022, Pre QC No. BOM-22-19265(PQ); **Reviewed:** 15-Dec-2022, QC No. BOM-22-19265; **Revised:** 22-Dec-2022, Manuscript No. BOM-22-19265(R); **Published:** 29-Dec-2022, DOI: 10.35248/2167-7956.22.11.246.

**Citation:** Benjamin H (2022) Protein Biosynthesis and its Mechanisms in Mammalian Mitochondria. *J Biol Res Ther*. 11:246.

**Copyright:** © 2022 Benjamin H. This is an open access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

3. Hunter SE, Spremulli LL. Mutagenesis of glutamine 290 in *Escherichia coli* and mitochondrial elongation factor Tu affects interactions with mitochondrial aminoacyl-tRNAs and GTPase activity. *Biochemistry*. 2004; 43(22):6917-27.
4. Hunter SE, Spremulli LL. Mutagenesis of Arg335 in bovine mitochondrial elongation factor Tu and the corresponding residue in the *Escherichia coli* factor affects interactions with mitochondrial aminoacyl-tRNAs. *RNA Biol*. 2004;1(2):95-102.
5. Kumazawa Y, Schwartzbach CJ, Liao HX, Mizumoto K, Kaziro Y, Miura KI, et al. Interactions of bovine mitochondrial phenylalanyl-tRNA with ribosomes and elongation factors from mitochondria and bacteria. *Biochim Biophys Acta*. 1991; 1090(2):167-72.