The ClinGen Evidence Repository is an **FDA-recognized human genetic variant database** containing expert-curated assertions regarding variants' pathogenicity and supporting evidence summaries. [Disclaimer]

Variant: NC_012920.1(MT-ATP6):m.8783G>A

Version: 1.1

CA414798058

692983 (ClinVar)

Gene: MT-ATP6 (HGNC:4508)
Condition: mitochondrial disease (MONDO:0044970)
Inheritance Mode: Mitochondrial inheritance
UUID: 3bb82672-99f3-4d9d-8909-d6b9559b3339
Approved on: 2024-12-09
Published on: 2025-05-19

HGVS expressions

NC_012920.1:m.8783G>A
J01415.2:m.8783G>A
ENST00000361899.2:c.257G>A

Uncertain Significance

Met criteria codes 1

PP3

Not Met criteria codes 6

PM6 PM2 PS2 PS3 PS4 PP1

Evidence Links 0

Expert Panel

Mitochondrial Diseases VCEP

Criteria Specification Information

- **Criteria Specification:** *ClinGen Mitochondrial Disease Nuclear and Mitochondrial Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines Version 1_mtDNA*
- **Criteria Specification Approval History**
- **Criteria Specifications for this VCEP**

Evidence submitted by expert panel

Mitochondrial Diseases VCEP

The m.8783G>A (p.G86E) variant in MT-ATP6 has been reported in one individual with primary mitochondrial disease to date however clinical details are not provided (PMID: 32652755). There are no reports of large families with this variant segregating with disease. There are no reported de novo occurrences of this variant to our knowledge. This variant is present in population databases (0.002%; one homoplasmic occurrence in MITOMAP; one homoplasmic and six heteroplasmic occurrences in gnomAD v3.1.2; four homoplasmic and nine heteroplasmic occurrences in the Helix database). The computational predictor APOGEE gives a consensus rating of pathogenic with a score of 0.59 (Min=0, Max=1; APOGEE2 score is 0.819), which predicts a damaging effect on gene function (PP3). There are no cybrids, single fiber studies, or other functional assays reported on this variant. In summary, this variant meets criteria to be classified as uncertain significance for primary mitochondrial disease inherited in a mitochondrial manner. This classification was approved by the NICHD/NINDS U24 ClinGen Mitochondrial Disease Variant Curation Expert Panel on December 9, 2024. Mitochondrial DNA-specific ACMG/AMP criteria applied (PMID: 32906214): PP3.

Met criteria codes

PP3	✔	The computational predictor APOGEE gives a consensus rating of pathogenic with a score of 0.59 (Min=0, Max=1; APOGEE2 score is 0.819), which predicts a damaging effect on gene function (PP3).

Not Met criteria codes

PM6	✖	There are no reported de novo occurrences of this variant to our knowledge.
PM2	✖	This variant is present in population databases (0.002%; one homoplasmic occurrence in MITOMAP; one homoplasmic and six heteroplasmic occurrences in gnomAD v3.1.2; four homoplasmic and nine heteroplasmic occurrences in the Helix database).
PS2	✖	There are no reported de novo occurrences of this variant to our knowledge.
PS3	✖	There are no cybrids, single fiber studies, or other functional assays reported on this variant.
PS4	✖	The m.8783G>A (p.G86E) variant in MT-ATP6 has been reported in one individual with primary mitochondrial disease to date however clinical details are not provided (PMID: 32652755).
PP1	✖	There are no reports of large families with this variant segregating with disease.

Curation History

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