

Variant: *NM_000277.1:c.772C>T*

Version: 1.0

[CA6748843](#)

[590340 \(ClinVar\)](#)

Gene: PAH ([HGNC:5053](#))

Condition: phenylketonuria ([MONDO:0009861](#))

Inheritance Mode: Autosomal recessive inheritance

UUID: 254ed141-a219-404a-8c94-1fd2aceb8103

Approved on: 2018-08-13

Published on: 2019-04-06

HGVS expressions

NM_000277.1:c.772C>T

NC_000012.12:g.102852885G>A

CM000674.2:g.102852885G>A

NC_000012.11:g.103246663G>A

CM000674.1:g.103246663G>A

NC_000012.10:g.101770793G>A

NG_008690.1:g.69718C>T

NG_008690.2:g.110526C>T

NM_000277.2:c.772C>T

NM_001354304.1:c.772C>T

NM_000277.3:c.772C>T

ENST00000307000.7:c.757C>T

ENST00000549247.6:n.531C>T

ENST00000553106.5:c.772C>T

Likely Benign

Met criteria codes **2**

BS1 **BP7**

Not Met criteria codes **1**

PM2

Evidence Links **0**

Expert Panel

[Phenylketonuria VCEP](#)

Criteria Specification Information **!**

[Criteria Specifications for this VCEP](#)

Evidence submitted by expert panel

Phenylketonuria VCEP

PAH-specific ACMG/AMP criteria applied: **BS1:** > PAH specific guidelines of AF-0.0002 (0.02%); **BP7:** No deleterious effect predicted.. In summary this variant meets criteria to be classified as likely benign for phenylketonuria in an autosomal recessive manner based on the ACMG/AMP criteria applied as specified by the PAH Expert Panel: (BS1, BP7).

Met criteria codes

BS1



> PAH specific guidelines of AF-0.0002 (0.02%)

BP7



No deleterious effect predicted.

Not Met criteria codes

PM2



> PAH specific guidelines of AF-0.0002 (0.02%)

Curation History [↗](#)



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