

Variant: NM_000277.2(PAH):c.561G>A (p.Trp187Ter)

CA229624 [↗](#)

102736 (ClinVar) [↗](#)

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

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

Inheritance Mode: Autosomal recessive inheritance

UUID: c75a3cc6-1a5e-4837-b431-6e2b2a14c0b1

Approved on: 2018-08-10

Published on: 2018-12-10

HGVS expressions

NM_000277.2:c.561G>A

NM_000277.2(PAH):c.561G>A (p.Trp187Ter)

NC_000012.12:g.102855281C>T

CM000674.2:g.102855281C>T

NC_000012.11:g.103249059C>T

CM000674.1:g.103249059C>T

NC_000012.10:g.101773189C>T

NG_008690.1:g.67322G>A

NG_008690.2:g.108130G>A

NM_000277.1:c.561G>A

NM_001354304.1:c.561G>A

NM_000277.3:c.561G>A

ENST00000307000.7:c.546G>A

ENST00000549111.5:n.657G>A

ENST00000551988.5:n.582G>A

ENST00000553106.5:c.561G>A

Pathogenic

Met criteria codes **3**

PVS1

PP4_Moderate

PM2

Evidence Links **1**

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: PVS1: Nonsense variant; PM2: Extremely low frequency in gnomAD. MAF=0.00002.; PP4_Moderate: Detected in 3 chromosomes of patients with PAH deficiency. BH4 deficiency ruled out. (PMID:8268925). In summary this variant meets criteria to be classified as pathogenic for phenylketonuria in an autosomal recessive manner based on the ACMG/AMP criteria applied as specified by the PAH Expert Panel: (PVS1, PM2, PP4_Moderate).

Met criteria codes

PVS1			Nonsense variant
PP4_Moderate			Detected in 3 chromosomes of patients with PAH deficiency. BH4 deficiency ruled out. W187X detected in 3 chromosomes. All patients were presenting with blood phenylalanine levels persistently above 150 umol/l, and diagnosis of PAH deficiency was made when other potential causes of hyperphenylalaninemia had been ruled out. The criteria for inclusion were: normal serum tyrosine, normal urinary excretion of biopterin and neopterin, and no indication of acquired hyperphenylalaninemia. PubMed:8268925 
PM2			Extremely low frequency in gnomAD. MAF=0.00002.

Curation History 











See Report 

Preferred Variant Title 

Classification 

Condition 

Published Date 

Version 

Criteria Specification 

Gene

No matching records found

The information on this website is not intended for direct diagnostic use or medical decision-making without review by a genetics professional. Individuals should not change their health behavior solely on the basis of information contained on this website. If you have questions about the information contained on this website, please see a health care professional.