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: NM_000277.2(PAH):c.547_548delGAinsTT (p.Glu183Leu)

Version: 1.0

CA267658

120278 (ClinVar)

Gene: PAH
Condition: phenylketonuria (MONDO:0009861)
Inheritance Mode: Autosomal recessive inheritance
UUID: 3e905683-806d-4709-8aaf-b71562b3bf03
Approved on: 2019/8/11
Published on: 2019/8/11

HGVS expressions

NM_000277.2:c.547_548delGAinsTT
NM_000277.2(PAH):c.547_548delGAinsTT (p.Glu183Leu)
NC_000012.12:g.102855294_102855295delinsAA
CM000674.2:g.102855294_102855295delinsAA
NC_000012.11:g.103249072_103249073delinsAA
CM000674.1:g.103249072_103249073delinsAA
NC_000012.10:g.101773202_101773203delinsAA
NG_008690.1:g.67308_67309delinsTT
NG_008690.2:g.108116_108117delinsTT
ENST00000553106.6:c.547_548delinsTT
ENST00000307000.7:c.532_533delinsTT
ENST00000549111.5:n.643_644delinsTT
ENST00000551988.5:n.568_569delinsTT
ENST00000553106.5:c.547_548delinsTT
NM_000277.1:c.547_548delinsTT
NM_000277.2:c.547_548delinsTT
NM_001354304.1:c.547_548delinsTT
NM_000277.3:c.547_548delinsTT
NM_001354304.2:c.547_548delinsTT

Likely Pathogenic

Met criteria codes 4

PP3 PP4 PM3 PM2

Evidence Links 1

Expert Panel

Phenylketonuria VCEP

Criteria Specification Information

Criteria Specifications for this VCEP

Evidence submitted by expert panel

Phenylketonuria VCEP

The c.547_548delGAinsTT PAH variant has been identified in at least one patient with classic PKU (PMID: 26666653). It was detected in trans with the pathogenic variant c.143T>C; p.Leu48Ser (ClinVar 608). This variant is absent from 1000G, ESP, and gnomAD databases. It is

predicted deleterious in multiple in silico models. In summary, this variant meets criteria to be classified as likely pathogenic for PAH. PAH-specific ACMG/AMP criteria applied: PP4, PM2, PM3, PP3.

Met criteria codes

PP3	✔	MutationTaster: Disease Causing; PolyPhen-2: Probably Damaging; PROVEAN: Deleterious; SIFT: Damaging
PP4	✔	A compound heterozygous proband with this variant was described with the classic PKU phenotype and PHE >1200umol/L. Defects in BH4 cofactor metabolism were not excluded.
		A compound heterozygous proband with this variant was described with the classic PKU phenotype and PHE >1200umol/L. Defects in BH4 cofactor metabolism were not excluded. PubMed:26666653
PM3	✔	This variant has been observed in trans with the previously assessed pathogenic variant c.143T>C; p.Leu48Ser (ClinVar 608, Pathogenic).
		This variant has been observed in trans with the previously assessed pathogenic variant c.143T>C; p.Leu48Ser (ClinVar 608, Pathogenic). PubMed:26666653
PM2	✔	The variant is absent from ExAC, gnomAD, 1000G, and ESP.

Curation History

Showing 1 to 1 of 1 rows

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.

ClinGen Terms of Use.
¤ Powered by BCM's Genboree.