

Variant: NM_000277.2(PAH):c.511G>A (p.Gly171Arg)

CA229598 [↗](#)

102716 (ClinVar) [↗](#)

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

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

Inheritance Mode: Autosomal recessive inheritance

UUID: 0dbfb1dc-9c9b-4fbe-b1a1-37b190aafe51

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HGVS expressions

NM_000277.2(PAH):c.511G>A (p.Gly171Arg)

NM_000277.2:c.511G>A

NC_000012.12:g.102855331C>T

CM000674.2:g.102855331C>T

NC_000012.11:g.103249109C>T

CM000674.1:g.103249109C>T

NC_000012.10:g.101773239C>T

NG_008690.1:g.67272G>A

NG_008690.2:g.108080G>A

NM_000277.1:c.511G>A

NM_001354304.1:c.511G>A

NM_000277.3:c.511G>A

ENST00000307000.7:c.496G>A

ENST00000549111.5:n.607G>A

ENST00000551988.5:n.532G>A

ENST00000553106.5:c.511G>A

Likely Pathogenic

Met criteria codes **4**

PP4_Moderate

PP3

PM2

PM3_Strong

Evidence Links **2**

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: PM2: Absent from ExAC, gnomAD, 1000G, ESP; PP3: Deleterious effect predicted in SIFT, Polyphen-2, MutationTaster. REVEL=0.966; PP4_Moderate: Detected in PKU patients. BH4 deficiency assessed. Upgraded per ClinGen PAH EP. (PMID:26600521; PMID:23430918); PM3_Strong: Detected with c.611A>G (P/LP) and R408W (P). Upgraded per ClinGen SVI workgroup. (PMID:23430918; PMID:26600521). In summary this variant meets criteria to be classified as likely pathogenic for phenylketonuria in an autosomal recessive manner based on the ACMG/AMP criteria applied as specified by the PAH Expert Panel: (PM2, PP3, PP4_Moderate, PM3_Strong).

Met criteria codes

PP4_Moderate			Detected in PKU patients. BH4 deficiency assessed. Upgraded per ClinGen PAH EP.
			Detected in 1 PKU patient: PKU (>450 umol/L). PubMed:23430918 Phe>120 uM, no BH4 defect, in trans with EX6-96G>A PubMed:26600521
PP3			Deleterious effect predicted in SIFT, Polyphen-2, MutationTaster. REVEL=0.966
PM2			Absent from ExAC, gnomAD, 1000G, ESP
PM3_Strong			Detected with c.611A>G (P/LP) and R408W (P). Upgraded per ClinGen SVI workgroup.
			EX6-96G>A (c.611A>G) (P/LP) maternal, G171R paternal PubMed:26600521 Patient Genotype: p.G171R/ p.R408W PubMed:23430918

Curation History

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