

Variant: *NM\_000277.2(PAH):c.464G>C (p.Arg155Pro)*

Version: 1.0

[CA229561](#) 

[102687 \(ClinVar\)](#) 

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

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

**Inheritance Mode:** Autosomal recessive inheritance

**UID:** a532eae1-862f-4d90-b69e-5e590a9f7512

**Approved on:** 2018-08-10

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### *HGVS expressions*

**NM\_000277.2:c.464G>C**

NM\_000277.2(PAH):c.464G>C (p.Arg155Pro)

NC\_000012.12:g.102866641C>G

CM000674.2:g.102866641C>G

NC\_000012.11:g.103260419C>G

CM000674.1:g.103260419C>G

NC\_000012.10:g.101784549C>G

NG\_008690.1:g.55962G>C

NG\_008690.2:g.96770G>C

NM\_000277.1:c.464G>C

NM\_001354304.1:c.464G>C

NM\_000277.3:c.464G>C

ENST00000307000.7:c.449G>C

ENST00000549111.5:n.560G>C

ENST00000551988.5:n.530+10821G>C

ENST00000553106.5:c.464G>C

**Likely Pathogenic**

Met criteria codes **4**

**PP3** **PM3** **PM2** **PP4\_Moderate**

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: PM2: absent from ExAC, gnomAD, 1000G, ESP. PAGE MAF=0.00066; PP3: Deleterious effect predicted in SIFT, Polyphen-2, MutationTaster. REVEL=0.967; PP4\_Moderate: Detected in a patient with classic PKU. Cofactor deficiency excluded. (PMID:10679941); PM3: Detected in trans with R408W (P) (PMID:10679941). 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).

#### Met criteria codes

<b>PP3</b>	✓	Deleterious effect predicted in SIFT, Polyphen-2, MutationTaster. REVEL=0.967
<b>PM3</b>	✓	Detected in trans with R408W (P) Detected in trans with R408W <a href="#">PubMed:10679941</a>
<b>PM2</b>	✓	absent from ExAC, gnomAD, 1000G, ESP. PAGE MAF=0.00066
<b>PP4_Moderate</b>	✓	Detected in a patient with classic PKU. Cofactor deficiency excluded. 302 PKU or HPA patients in 290 families were analyzed. Most of the patients were identified by neonatal screening. Cofactor deficiency was excluded by the BH4 test. Detected in a patient (SD) with classic PKU. <a href="#">PubMed:10679941</a>

#### Curation History [↗](#)

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