

Variant: *NM_001204.7(BMPR2):c.1178A>G (p.Asn393Ser)*

Version: 1.0

CA350341785 [↗](#)

812825 (ClinVar) [↗](#)

Gene: BMPR2 ([HGNC:659](#))

Condition: pulmonary arterial hypertension ([MONDO:0015924](#))

Inheritance Mode: Autosomal dominant inheritance

UUID: e098d725-2e47-436a-91f1-bdbf8009f446

Approved on: 2025/1/3

Published on: 2025/1/3

HGVS expressions

NM_001204.7:c.1178A>G

NM_001204.7(BMPR2):c.1178A>G (p.Asn393Ser)

NC_000002.12:g.202532634A>G

CM000664.2:g.202532634A>G

NC_000002.11:g.203397357A>G

CM000664.1:g.203397357A>G

NC_000002.10:g.203105602A>G

NG_009363.1:g.161308A>G

ENST00000374580.10:c.1178A>G

ENST00000638587.1:c.1109A>G

ENST00000374574.2:c.1178A>G

ENST00000374580.8:c.1178A>G

NM_001204.6:c.1178A>G

Uncertain Significance

Met criteria codes **2**

PM1

PM2_Supporting

Not Met criteria codes **7**

PM4

BS1

PVS1

PS4

BP4

BA1

PP3

Evidence Links **0**

Expert Panel

Pulmonary Hypertension VCEP [↗](#)

Criteria Specification Information

[↗](#) **Criteria Specification:** ClinGen Pulmonary Hypertension

Expert Panel Specifications to the ACMG/AMP Variant

Interpretation Guidelines for BMPR2 Version 1.1.0

[↗](#) **Criteria Specification Approval History**

[↗](#) **Criteria Specifications for this VCEP**

Evidence submitted by expert panel

Pulmonary Hypertension VCEP

The c.1178A>G (p.Asn393Ser) variant is a missense variant harboured in exon 9 of the BMPR2 gene, predicted to cause substitution of asparagine to serine encoding the functionally relevant catalytic kinase domain but without functional evidence indicating critical or non-critical (PM1_moderate). This variant is absent from gnomAD v2.1.1 (controls) and v4.1 (PM2_supporting). The REVEL prediction algorithm score is 0.68, AlphaMissense is 0.79, both below our thresholds for pathogenicity (PP3_not met) but above our thresholds for benignity (BP4 not met). The variant has been reported only once in a PAH subject (PMID: 32581362) (PS4 not met). Functional studies have not

been conducted for this variant (PS3 not assessed). In summary, this variant meets the criteria to be classified as a variant of unknown significance for pulmonary arterial hypertension based on the ACMG/AMP criteria applied, as specified by the ClinGen Pulmonary Hypertension VCEP: PM1_moderate, PM2_supporting (VCEP specification version 1.1.0, 1/18/2024).

Met criteria codes

PM1			p.Asn393Ser is located in the catalytic kinase domain without benign variation.
PM2_Supporting			The variant is absent from gnomAd v2.1.1 controls and v4.1.

Not Met criteria codes

PM4			The variant is a missense variant.
BS1			The variant is absent from gnomAd v2.1.1 controls and v4.1.
PVS1			The variant is a missense variant.
PS4			The variant has been identified in a single individual diagnosed with PAH (PMID: 32581362).
BP4			The REVEL score of 0.68 is bellow the PH VCEP threshold of >=0.75 for pathogenicity and above the threshold of <=0.25 for benignity.
BA1			The variant is absent from gnomAd v2.1.1 controls and v4.1.
PP3			The REVEL score of 0.68 is bellow the PH VCEP threshold of >=0.75 for pathogenicity and above the threshold of <=0.25 for benignity.

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.](#)