

Variant: *NM_000173.7(GP1BA):c.1077G>A (p.Trp359Ter)*

Version: 1.0

CA116657 [↗](#)

4151 (ClinVar) [↗](#)

Gene: GP1BA ([HGNC:2811](#))

Condition: Bernard-Soulier syndrome ([MONDO:0009276](#))

Inheritance Mode: Autosomal recessive inheritance

UUID: d8a22472-b2b9-48f1-a1ac-21cf7211b306

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HGVS expressions

NM_000173.7:c.1077G>A

NM_000173.7(GP1BA):c.1077G>A (p.Trp359Ter)

NC_000017.11:g.4933681G>A

CM000679.2:g.4933681G>A

NC_000017.10:g.4836976G>A

CM000679.1:g.4836976G>A

NC_000017.9:g.4777756G>A

NG_008767.2:g.6387G>A

ENST00000329125.6:c.1077G>A

ENST00000649830.1:c.-888+661C>T

ENST00000329125.5:c.1077G>A

ENST00000611961.1:c.1077G>A

NM_000173.6:c.1077G>A

Likely Pathogenic

Met criteria codes 4

PP1

PP4

PVS1_Strong

PM2_Supporting

Not Met criteria codes 1

PM3

Evidence Links 0

Expert Panel

Platelet Disorders VCEP [↗](#)

Criteria Specification Information

[↗](#) **Criteria Specification:** ClinGen Platelet Disorders Expert

Panel Specifications to the ACMG/AMP Variant

Interpretation Guidelines for GP1BA Version 1.1.0

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

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

Evidence submitted by expert panel

Platelet Disorders VCEP

The c.1077G>A (p.Trp359Ter) variant in GP1BA is a nonsense variant that may cause loss of function of the protein, however it is predicted to escape nonsense mediated decay and remove >10% of the protein (PVS1_Strong). At least one patient (Proband in PMID: 2308962) with this variant had absent expression of GPIba measured by flow cytometry or Western blot, which is highly specific for Bernard-Soulier syndrome. Additionally, the patient had excessive mucocutaneous bleeding and macrothrombocytopenia which are consistent with Bernard-Soulier syndrome (PP4). The variant has been reported to segregate in the proband plus 2 heterozygous children and the

heterozygous mother, all had significantly reduced surface expression of GP1BA (PP1). The largest MAF allele frequency in gnomAD v4.0.1 is 0.0000008476 (based on 1/1179860 alleles) in the European (non-Finnish) population, which is lower than the ClinGen PD VCEP threshold (<0.0001114; PM2_Supporting). In summary, this variant meets the criteria to be classified as Likely Pathogenic for autosomal recessive Bernard-Soulier syndrome based on the ACMG/AMP criteria applied, as specified by the ClinGen PD VCEP: PVS1_Strong, PP4, PP1, and PM2_Supporting (VCEP specifications version 1.1).

Met criteria codes

PP1			The variant has been reported to segregate in the proband plus 2 additional heterozygous children and the heterozygous mother, all had significantly reduced surface expression of GP1BA by immunoblot (PP1).
PP4			At least one patient (Proband in PMID: 2308962) with this variant had absent expression of GPIba measured by flow cytometry or Western blot, which is highly specific for Bernard-Soulier syndrome. Additionally, the patient had excessive mucocutaneous bleeding and macrothrombocytopenia which are consistent with Bernard-Soulier syndrome (PP4).
PVS1_Strong			The c.1077G>A (p.Trp359Ter) variant in GP1BA is a nonsense variant that may cause loss of function of the protein, however it is predicted to escape nonsense mediated decay and remove >10% of the protein (PVS1_Strong).
PM2_Supporting			The largest MAF allele frequency in gnomAD v4.0.1 is 0.0000008476 (based on 1/1179860 alleles) in the European (non-Finnish) population, which is lower than the ClinGen PD VCEP threshold (<0.0001114; PM2_Supporting).

Not Met criteria codes

PM3			Proband in PMID: 2308962 is compound heterozygous for the c.1077G>A (p.Trp359Ter) and another variant that the authors were unable to detect
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Curation History

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