

Variant: *NM_000212.3(ITGB3):c.1309G>T (p.Glu437Ter)*

Version: 1.0

CA8623244 [↗](#)

1695377 (ClinVar) [↗](#)

Gene: ITGB3 ([HGNC:3690](#))

Condition: Glanzmann thrombasthenia ([MONDO:0100326](#))

Inheritance Mode: Autosomal recessive inheritance

UUID: 6e67cd67-37d2-4bd3-b64e-97e9f51a835e

Approved on: 2024/4/16

Published on: 2024/4/16

HGVS expressions

NM_000212.3(ITGB3):c.1309G>T (p.Glu437Ter)

NM_000212.3:c.1309G>T

NC_000017.11:g.47292187G>T

CM000679.2:g.47292187G>T

NC_000017.10:g.45369553G>T

CM000679.1:g.45369553G>T

NC_000017.9:g.42724552G>T

NG_008332.2:g.43346G>T

ENST00000696963.1:c.1309G>T

ENST00000559488.7:c.1309G>T

ENST00000559488.5:c.1309G>T

ENST00000560629.1:c.1274G>T

NM_000212.2:c.1309G>T

Pathogenic

Met criteria codes **3**

PM2_Supporting

PVS1

PM3_Supporting

Not Met criteria codes **2**

BS2

PP4

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 Version 2.1*

[↗](#) **PDF**

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

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

Evidence submitted by expert panel

Platelet Disorders VCEP

The c.1309G>T (p.Glu437Ter) variant in exon 10 is a nonsense variant predicted to cause a premature stop codon in biologically-relevant-exon 10 and is predicted to lead to nonsense mediated decay in a gene in which loss-of-function is an established disease mechanism (PVS1). The highest population minor allele frequency in gnomAD v4.0.0 is 0.00002319 (2/86254 alleles) in the South Asian population, which is lower than the ClinGen PD VCEP threshold (<0.0001; PM2_Supporting). This variant is reported in ClinVar (SCV002546491.1) in a

homozygous Glanzmann thrombasthenia patient (PM3_Supporting). In summary, this variant meets the criteria to be classified as Pathogenic for autosomal recessive Glanzmann Thrombasthenia based on the ACMG/AMP criteria applied, as specified by the ClinGen PD VCEP: PVS1, PM3_Supporting, and PM2_Supporting (VCEP specifications version 2; date of approval 04/16/2024).

Met criteria codes

PM2_Supporting			The highest population minor allele frequency in gnomAD v4.0.0 is 0.00002319 (2/86254 alleles) in the South Asian population, which is lower than the ClinGen PD VCEP threshold (<0.0001; PM2_Supporting).
PVS1			The c.1309G>T (p.Glu437Ter) variant in exon 10 is a nonsense variant predicted to cause a premature stop codon in biologically-relevant-exon 10 and is predicted to lead to nonsense mediated decay in a gene in which loss-of-function is an established disease mechanism (PVS1).
PM3_Supporting			One homozygous patient has been reported (SCV002546491.1) in the Gold Variants database (PM3_supporting).

Not Met criteria codes

BS2			A homozygous patient is reported (PMID: 29143464) but not asserted to have GT, they have a platelet count of 208x10^9/L and MPV of 12.7 fl. No aggregation or bleeding information is provided.
PP4			Variant is reported in a GT case in ClinVar (ISTH-SSC Genomics in Thrombosis and Hemostasis, KU Leuven, Center for Molecular and Vascular Biology). No phenotypic details about the patient are provided, so PP4 cannot be applied.

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.