The ClinGen Evidence Repository is an **FDA-recognized human genetic variant database** containing expert-curated assertions regarding variants' pathogenicity and supporting evidence summaries. [Disclaimer]

Variant: NM_000212.3(ITGB3):c.444C>G (p.Tyr148Ter)

Version: 1.0

CA400021992

1684354 (ClinVar)

Gene: ITGB3 (HGNC:3690)
Condition: Glanzmann thrombasthenia (MONDO:0100326)
Inheritance Mode: Autosomal recessive inheritance
UUID: 397bd7bc-6990-4e72-9a0a-ba7e9bdbba9e
Approved on: 2024/4/16
Published on: 2024/4/16

HGVS expressions

NM_000212.3:c.444C>G
NM_000212.3(ITGB3):c.444C>G (p.Tyr148Ter)
NC_000017.11:g.47284525C>G
CM000679.2:g.47284525C>G
NC_000017.10:g.45361891C>G
CM000679.1:g.45361891C>G
NC_000017.9:g.42716890C>G
NG_008332.2:g.35684C>G
ENST00000696963.1:c.444C>G
ENST00000559488.7:c.444C>G
ENST00000559488.5:c.444C>G
ENST00000560629.1:c.409C>G
ENST00000571680.1:c.444C>G
NM_000212.2:c.444C>G

Pathogenic

Met criteria codes 3

PM3_Supporting PVS1 PM2_Supporting

Not Met criteria codes 1

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.444C>G (p.Tyr148Ter) variant in exon 4 is a nonsense variant predicted to cause a premature stop codon in biologically-relevant-exon 4 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 0.000001799] (2/1112006 alleles) in the European (non-Finnish)

population, which is lower than the ClinGen PD VCEP threshold (<0.0001; PM2_Supporting). This variant is reported in ClinVar (SCV002515562.1) 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

PM3_Supporting	✔	One homozygous patient has been reported (SCV002515562.1) in the Gold Variants database (PM3_supporting).
PVS1	✔	The c.444C>G (p.Tyr148Ter) variant in exon 4 is a nonsense variant predicted to cause a premature stop codon in biologically-relevant-exon 4 and is predicted to lead to nonsense mediated decay in a gene in which loss-of-function is an established disease mechanism (PVS1)
PM2_Supporting	✔	The highest population minor allele frequency in gnomAD v4.0.0 is 0.000001799] (2/1112006 alleles) in the European (non-Finnish) population, which is lower than the ClinGen PD VCEP threshold (<0.0001; PM2_Supporting).

Not Met criteria codes

PP4	✖	This variant is reported in ClinVar in a Glanzmann thrombasthenia patient (ISTH-SSC Genomics in Thrombosis and Hemostasis, KU Leuven, Center for Molecular and Vascular Biology). No phenotypic information about this patient is provided, so PP4 could not 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.

ClinGen Terms of Use.
¤ Powered by BCM's Genboree.