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Variant: NM_000155.4(GALT):c.199C>T (p.Arg67Cys)

Version: 1.0

CA259339

25137 (ClinVar)

Gene: GALT (HGNC:2592)
Condition: galactosemia (MONDO:0018116)
Inheritance Mode: Autosomal recessive inheritance
UUID: 72582cf9-faed-4a34-af88-3d042662c417
Approved on: 2026/6/9
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HGVS expressions

NM_000155.4(GALT):c.199C>T (p.Arg67Cys)
NM_000155.4:c.199C>T
NC_000009.12:g.34647205C>T
CM000671.2:g.34647205C>T
NC_000009.11:g.34647202C>T
CM000671.1:g.34647202C>T
NC_000009.10:g.34637202C>T
NG_009029.1:g.5568C>T
NG_028966.1:g.21C>T
NG_009029.2:g.5617C>T
ENST00000691183.1:c.199C>T
ENST00000378842.8:c.199C>T
ENST00000378842.7:c.199C>T
ENST00000450095.6:c.-4C>T
ENST00000465543.6:n.538C>T
ENST00000468099.2:n.239C>T
ENST00000472111.5:n.240C>T
ENST00000473506.6:c.199C>T
ENST00000473529.5:n.246C>T
ENST00000485531.1:n.192C>T
ENST00000487381.5:n.225C>T
ENST00000489643.6:n.229C>T
ENST00000554085.5:c.199C>T
ENST00000554139.5:n.252C>T
ENST00000554330.5:n.196C>T
ENST00000554550.5:c.199C>T
ENST00000554638.5:n.223C>T
ENST00000554897.5:c.199C>T
ENST00000554944.5:n.229C>T
ENST00000555020.5:n.229C>T
ENST00000555086.5:n.203C>T
ENST00000555214.5:n.208C>T
ENST00000556157.1:n.306C>T
ENST00000556244.1:c.83C>T
ENST00000556278.1:c.199C>T
ENST00000556403.5:n.212C>T
ENST00000556494.5:n.231C>T

ENST00000557541.5:n.392C>T
ENST00000557706.5:n.313C>T
NM_000155.3:c.199C>T
NM_001258332.1:c.-4C>T
NM_001258332.2:c.-4C>T

Likely Pathogenic

Met criteria codes 4

PM3 PP4_Moderate PM2_Supporting PS3_Supporting

Evidence Links 1

Expert Panel

Galactosemia VCEP

Criteria Specification Information

- **Criteria Specification:** *ClinGen Galactosemia Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines for GALT Version 1.0.0*
- **Criteria Specification Approval History**
- **Criteria Specifications for this VCEP**

Evidence submitted by expert panel

Galactosemia VCEP

The c.199C>T variant in GALT is a missense variant predicted to cause substitution of arginine by cysteine at amino acid 67 (p.Arg67Cys). At least one patient with this variant displayed GALT activity of <10%, which is highly specific for galactosemia (PP4_moderate, PMID: 8598637, PMID: 22944367). This variant has been detected in at least 2 individuals with galactosemia. Of those individuals,1 individual was homozygous for the variant and 1 individual was compound heterozygous for the variant and a pathogenic variant and was confirmed in trans by parental testing, (1.5 PM3 points, PMID: 8598637, PMID: 22944367, PM3_moderate).The filtering allele frequency (the upper threshold of the 95% CI of (1/8,702) of the c.199C>T variant in GALT is 0.0001 for African chromosomes by gnomAD v4.1.0, which is lower than the ClinGen Galactosemia threshold (≤ 0.0005) for PM2_Supporting, and therefore meets this criterion (PM2_Supporting). The computational predictor REVEL gives a SCORE of 0.835, which is equal to or above the threshold of 0.7, evidence that correlates with impact to GALT function (PP3). Galt activity assays in yeast showed < 5% activity indicating that this variant impacts protein function (PMID:11152465, PS3_Supporting). In summary, this variant meets the criteria to be classified as likely pathogenic for galactosemia based on the ACMG/AMP criteria applied, as specified by the ClinGen Galactosemia VCEP: PP4_moderate, PM3_moderate, PM2_supporting, PP3, PS3_supporting (GALT specifications v1.0.0)

Met criteria codes

PM3	✔	1.5 points
PP4_Moderate	✔	2 individuals with GALT activity <10%.
PM2_Supporting	✔	<0.05%
PS3_Supporting	✔	Yeast activity assay <5% activity

Yeast activity assay <5% **PubMed:11152465**

Curation History

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See Report	Preferred Variant Title	Classification	Condition	Published Date	Version	Criteria Specification	Gene
View	NM_000155.4(GALT):c.199C>T (p.Arg6...	Likely Pathogenic	Galactosemia	2026-06-09	1.0	ClinGen Galactosemia Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines for GALT Version 1.0.0	GALT

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