

Variant: *NM_000531.6(OTC):c.621C>T (p.Ser207=)*

Version: 1.0

CA10385896 [↗](#)

368259 (ClinVar) [↗](#)

Gene: OTC ([HGNC:5009](#))

Condition: ornithine carbamoyltransferase deficiency ([MONDO:0010703](#))

Inheritance Mode: X-linked inheritance (recessive (HP:0001419))

UUID: 412b662e-dec2-45af-ba81-64507e94994c

Approved on: 2026/5/21

Published on: 2026/5/29

HGVS expressions

NM_000531.6:c.621C>T

NM_000531.6(OTC):c.621C>T (p.Ser207=)

NC_000023.11:g.38403698C>T

CM000685.2:g.38403698C>T

NC_000023.10:g.38262951C>T

CM000685.1:g.38262951C>T

NC_000023.9:g.38147895C>T

NG_008471.1:g.56216C>T

ENST00000039007.5:c.621C>T

ENST000000643344.1:c.*371C>T

ENST00000039007.4:c.621C>T

ENST000000465127.1:c.172-262423C>T

NM_000531.5:c.621C>T

Benign

Met criteria codes **2**

BA1

BP7

Not Met criteria codes **3**

PP4

PM2

PM1

Evidence Links **0**

Expert Panel

Urea Cycle Disorders VCEP [↗](#)

Criteria Specification Information

[↗](#) **Criteria Specification:** *ClinGen Urea Cycle Disorders Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines for OTC Version 1.0.0*

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

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

Evidence submitted by expert panel

Urea Cycle Disorders VCEP

The NM_000531.6: c.621C>T (p.Ser207=) variant is a synonymous (silent) variant that is not predicted by SpliceAI to impact splicing (BP4, BP7). The highest population minor allele frequency in gnomAD v4.1.0 is 0.0008888 (30/33752 alleles) in the East Asian population and there are 13 hemizygotes across all populations, which is higher than the ClinGen OTC VCEP threshold (≥ 10 male hemizygotes) for BA1, and therefore meets this criterion (BA1). In summary, this variant meets the criteria to be classified as Benign for X-linked ornithine

carbamoyltransferase deficiency. ACMG/AMP criteria met, as specified by the ClinGen Urea Cycle Disorders VCEP (OTC specifications version 1.0.0): BA1, BP4, BP7.			
Met criteria codes			
BA1			There are 13 total hemizygotes in gnomAD v4.1.0 which is higher than the ClinGen OTC VCEP threshold (≥ 10 male hemizygotes) for BA1, and therefore meets this criterion (BA1).
BP7			The c.621C>T (p.Ser207=) variant is a synonymous (silent) variant that is not predicted by SpliceAI to impact splicing (BP7). SpliceAI delta scores 0.00-0.01 (Donor Loss).
Not Met criteria codes			
PP4			Not reported in cases in the literature 4/8/23
PM2			No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
PM1			This variant is not at one of the well-established hotspots: Carbamoylphosphate binding site - amino acids: Ser-90, Thr-91, Arg-92, Thr-93, His-117, Arg-141, His-168 and Arg-330 Ornithine binding site - amino acids: Asn-199, Asp-263, Ser-267, Met-268, Gly-269 Catalytic site - amino acids: His-302, Cys-303, Leu-304, Pro-305 Salt bridge - Arg-92 and Glu-122

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.