Variant: NM_001110792.2(MECP2):c.1214C>T (p.Pro405Leu)

Version: 1.0

CA232923

143418 (ClinVar)

Gene: MECP2 (HGNC:4204)
Condition: Rett syndrome (MONDO:0010726)
Inheritance Mode: X-linked inheritance
UUID: 2983b3c7-626e-495d-81be-dcdb05e3c83d
Approved on: 2024-10-30
Published on: 2024-11-29

HGVS expressions

NM_001110792.2:c.1214C>T
NM_001110792.2(MECP2):c.1214C>T (p.Pro405Leu)
NC_000023.11:g.154030650G>A
CM000685.2:g.154030650G>A
NC_000023.10:g.153296101G>A
CM000685.1:g.153296101G>A
NC_000023.9:g.152949295G>A
NG_007107.2:g.111478C>T
NG_007107.3:g.111454C>T
ENST00000303391.11:c.1178C>T
ENST00000453960.7:c.1214C>T
ENST00000303391.10:c.1178C>T
ENST00000407218.5:c.*550C>T
ENST00000453960.6:c.1214C>T
ENST00000619732.4:c.1178C>T
ENST00000628176.2:c.*550C>T
NM_001110792.1:c.1214C>T
NM_001316337.1:c.899C>T
NM_004992.3:c.1178C>T
NM_001316337.2:c.899C>T
NM_001369391.2:c.899C>T
NM_001369392.2:c.899C>T
NM_001369393.2:c.899C>T
NM_001369394.1:c.899C>T
NM_001369394.2:c.899C>T
NM_001386137.1:c.509C>T
NM_001386138.1:c.509C>T
NM_001386139.1:c.509C>T
NM_004992.4:c.1178C>T

Likely Benign

Met criteria codes 2

BS2 BP5

Not Met criteria codes 5

Expert Panel

Rett and Angelman-like Disorders VCEP

PM1 BS1 BP4 PP3 PP4

Evidence Links 0

Criteria Specification Information

Criteria Specification: *ClinGen Rett and Angelman-like Disorders Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines for MECP2 Version 3.0.0*

Criteria Specification Approval History

Criteria Specifications for this VCEP

Evidence submitted by expert panel

Rett and Angelman-like Disorders VCEP

The p.Pro393Leu variant in MECP2 (NM_004992.4) is observed in at least 2 unaffected individuals (internal database - Ambry, internal database - Invitae) (BS2). The p.Pro393Leu variant is found in a patient with an alternate molecular basis of disease (internal database - Ambry) (BP5). The highest population minor allele frequency of the p.Pro393Leu variant in MECP2 in gnomAD v4.1 is 0.00002210 in Admixed American population (not sufficient to meet BS1 criteria). In summary, the p.Pro393Leu variant in MECP2 is classified as Likely Benign based on the ACMG/AMP criteria (BS2, BP5).

Met criteria codes

BS2	✔	The p.Pro393Leu variant is observed in at least 2 unaffected individuals (internal database - Ambry, internal database - Invitae) (BS2).
BP5	✔	The p.Pro393Leu variant is found in a patient with an alternate molecular basis of disease (internal database - Ambry) (BP5).

Not Met criteria codes

PM1	✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline
BS1	✖	The highest population minor allele frequency of the p.Pro393Leu variant in MECP2 (NM_004992.4) in gnomAD v4.1 is 0.00002210 in Admixed American population (not sufficient to meet BS1 criteria).
BP4	✖	The computational predictor REVEL gives a score of 0.38.
PP3	✖	The computational predictor REVEL gives a score of 0.38.
PP4	✖	No code specific comments provided, please refer to the summary above or general recommendations provided in the guideline

Curation History

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