Criteria Specification

ClinGen Hereditary Breast, Ovarian and Pancreatic Cancer Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines for ATM Version 1.1

Affiliation: Hereditary Breast, Ovarian and Pancreatic Cancer VCEP
Description : ACMG-modified rules specifications for ATM (autosomal dominant and autosomal recessive disorders)
Version : 1.1.0
Pilot Rules Submitted : 11/17/2023
Release Notes :
Corrected combining rules for LP to include PVS1 + PM2_Supporting = LP

PDF

Rules for ATM

Gene: ATM (HGNC:795)
Preferred Transcript: NM_000051.3

HGNC Name: ATM serine/threonine kinase
Disease:
hereditary breast carcinoma (MONDO:0016419) **Mode of Inheritance:** Autosomal dominant inheritance
ataxia telangiectasia (MONDO:0008840) **Mode of Inheritance:** Autosomal recessive inheritance
ataxia - telangiectasia variant (MONDO:0018266) **Mode of Inheritance:** Autosomal recessive inheritance

Criteria & Strength Specifications

PVS1

Original ACMG Summary

Null variant (nonsense, frameshift, canonical +/−1 or 2 splice sites, initiation codon, single or multi-exon deletion) in a gene where loss of function (LOF) is a known mechanism of disease.
Caveats:
- Beware of genes where LOF is not a known disease mechanism (e.g. GFAP, MYH7).
- Use caution interpreting LOF variants at the extreme 3’ end of a gene.
- Use caution with splice variants that are predicted to lead to exon skipping but leave the remainder of the protein intact.
- Use caution in the presence of multiple transcripts.

Very Strong

Use ATM PVS1 Decision Tree

Modification Type: Gene-specific,Strength

Strong

Use ATM PVS1 Decision Tree.

Modification Type: Gene-specific,Strength

Moderate

Use ATM PVS1 Decision Tree.

Modification Type: Gene-specific,Strength

Supporting

Use ATM PVS1 Decision Tree

Modification Type: Gene-specific,Strength

Instructions: Use ATM PVS1 Decision Tree.

PS1

Original ACMG Summary

Same amino acid change as a previously established pathogenic variant regardless of nucleotide change.
Example: Val->Leu caused by either G>C or G>T in the same codon.
Caveat: Beware of changes that impact splicing rather than at the amino acid/protein level.

Strong

Use for protein changes as long as splicing is ruled-out for both alterations.

Modification Type: General recommendation

Moderate

Use for RNA changes as code PS1_RNA_Moderate if predictions or observations are similar or worse for the variant under consideration. Close matches must be VCEP approved LP/P variants.

Modification Type: Strength,General recommendation

Instructions: Use as ascribed for protein changes as long as a splice defect is ruled out for both variants; Use as PS1_RNA_Moderate for close-match splicing variants with similar predictions or observations of splice defect. Close matches must be VCEP approved as LP/P.

PS2

Original ACMG Summary

De novo (both maternity and paternity confirmed) in a patient with the disease and no family history.
Note: Confirmation of paternity only is insufficient. Egg donation, surrogate motherhood, errors in embryo transfer, etc. can contribute to non-maternity.

Not Applicable

PS3

Original ACMG Summary

Well-established in vitro or in vivo functional studies supportive of a damaging effect on the gene or gene product.
Note: Functional studies that have been validated and shown to be reproducible and robust in a clinical diagnostic laboratory setting are considered the most well-established.

Strong

Do not use as strong.

Modification Type: Gene-specific

Moderate

Use when a variant fails to rescue both an ATM specifc feature (e.g. phosphorylation of ATM-specific targets) AND radiosensitivity.

Modification Type: Gene-specific,Strength

Supporting

Use when a variant fails to rescue an ATM specifc feature, only (e.g. phosphorylation of ATM-specific targets). Do not use for radiosensitivity-only as that is not a feature specific to ATM deficiency

Modification Type: Gene-specific,Strength

Instructions: For protein, see detailed notes on ATM-specific assays; For RNA use code PVS1_O and modulate strength based on assay quality and quantity (curator discretion).

PS4

Original ACMG Summary

The prevalence of the variant in affected individuals is significantly increased compared to the prevalence in controls.
Note 1: Relative risk (RR) or odds ratio (OR), as obtained from case-control studies, is >5.0 and the confidence interval around the estimate of RR or OR does not include 1.0. See manuscript for detailed guidance.
Note 2: In instances of very rare variants where case-control studies may not reach statistical significance, the prior observation of the variant in multiple unrelated patients with the same phenotype, and its absence in controls, may be used as moderate level of evidence.

Strong

Use for case control studies that reflect an OR ≥2, p≤.05 and lower 95% CI ≥1.5.

Modification Type: General recommendation

Moderate

Do not use for proband counting.

Modification Type: Gene-specific,Disease-specific

Instructions: Do not use for 'proband counting' method. Use for case control studies that reflect an OR ≥2, p≤.05 and lower 95% CI ≥1.5.

PM1

Original ACMG Summary

Located in a mutational hot spot and/or critical and well-established functional domain (e.g. active site of an enzyme) without benign variation.

Not Applicable

PM2

Original ACMG
Summary

Absent from controls (or at extremely low frequency if recessive) in Exome Sequencing Project, 1000 Genomes or Exome Aggregation Consortium.
Caveat: Population data for indels may be poorly called by next generation sequencing.

Supporting

Frequency ≤.001% when N>1 in a large general population database (e.g. gnomAD 2.1.1)

Modification Type: Gene-specific,Strength

Instructions: Use as PM2_Supporting for variants with a general population frequency ≤.001% in all sub-populations when N>1.

PM3

Original ACMG
Summary

For recessive disorders, detected in trans with a pathogenic variant
Note: This requires testing of parents (or offspring) to determine phase.

Very Strong

Use ATM PM3/BP2 table.

Modification Type: Gene-specific,Disease-specific,Strength,General recommendation

Strong

Use ATM PM3/BP2 table.

Modification Type: Gene-specific,Disease-specific,Strength,General recommendation

Moderate

Use ATM PM3/BP2 table.

Modification Type: Gene-specific,Disease-specific,Strength,General recommendation

Supporting

Use ATM PM3/BP2 table

Modification Gene-specific,Disease-specific,Strength,General recommendation

Type:

Instructions: Use ATM PM3/BP2 table.

PM4

Original ACMG Summary

Protein length changes due to in-frame deletions/insertions in a non-repeat region or stop-loss variants.

Moderate

Use for stop-loss variants.

Modification Type: Gene-specific,General recommendation

Instructions: Do not use for in-frame insertions or deletions less than a single exon; Use for stop-loss variants, only.

PM5

Original ACMG Summary

Novel missense change at an amino acid residue where a different missense change determined to be pathogenic has been seen before.
Example: Arg156His is pathogenic; now you observe Arg156Cys.
Caveat: Beware of changes that impact splicing rather than at the amino acid/protein level.

Supporting

Use for genomic frameshift and truncating variants with PTC upstream of p.R3047. Do not use for splice or start-loss variants

Modification Type: Gene-specific,Strength

Instructions: Do not use for 'hotspot'. Can be used for genomic frameshift and truncating variants with PTC upstream of p.R3047 as PM5_Supporting.

PM6

Original ACMG Summary

Assumed de novo, but without confirmation of paternity and maternity.

Not Applicable

PP1

Original ACMG Summary

Co-segregation with disease in multiple affected family members in a gene definitively known to cause the disease.
Note: May be used as stronger evidence with increasing segregation data.

Not Applicable

Comments: Informative pedigrees for segregation in families with AR Ataxia-Telangiectasia are not available. However, this VCEP would consider rules similar to the Glanzman and Hearing Loss VCEP rules if a pedigree becomes available.

PP2

Original ACMG Summary

Missense variant in a gene that has a low rate of benign missense variation and where missense variants are a common mechanism of disease.

Not Applicable

PP3

Original ACMG Summary

Multiple lines of computational evidence support a deleterious effect on the gene or gene product (conservation, evolutionary, splicing impact, etc.).
Caveat: As many in silico algorithms use the same or very similar input for their predictions, each algorithm should not be counted as an independent criterion. PP3 can be used only once in any evaluation of a variant.

Supporting

Protein: REVEL >.7333; RNA: multiple in silico predictors agree to a smilar effect

Instructions: Protein: REVEL >.7333; RNA: multiple in silico predictors agree to a similar effect.

PP4

Original ACMG Summary

Patient’s phenotype or family history is highly specific for a disease with a single genetic etiology.

Not Applicable

PP5

Original ACMG Summary

Reputable source recently reports variant as pathogenic, but the evidence is not available to the laboratory to perform an independent evaluation.

Not Applicable

This criterion is not for use as recommended by the ClinGen Sequence Variant Interpretation VCEP Review Committee. PubMed : 29543229

BA1

Original ACMG Summary

Allele frequency is above 5% in Exome Sequencing Project, 1000 Genomes or Exome Aggregation Consortium.

Stand Alone

Filtering Allele Frequency >.5%.

Instructions: Filtering Allele Frequency >.5%.

BS1

Original ACMG Summary

Allele frequency is greater than expected for disorder.

Strong

Filtering Allele Frequency >.05%.

Instructions: Filtering Allele Frequency >.05%.

BS2

Original ACMG Summary

Observed in a healthy adult individual for a recessive (homozygous), dominant (heterozygous), or X-linked (hemizygous) disorder, with full penetrance expected at an early age.

Not Applicable

BS3

Original ACMG Summary

Well-established in vitro or in vivo functional studies show no damaging effect on protein function or splicing.

Moderate

Use when a variant rescues both an ATM specifc feature (e.g. phosphorylation of ATM-specific targets) AND radiosensitivity.

Modification Type: Gene-specific,Disease-specific,Strength,General Recommendation

Supporting

Use when a variant rescues EITHER an ATM specifc feature OR rescues radiosensitivity.

Modification Type: Gene-specific,Disease-specific,Strength,General Recommendation

Instructions: For protein, see detailed notes on ATM-specific assays; For RNA use code BP7_O and modulate strength based on assay quality and quantity (curator discretion).

BS4

Original ACMG Summary

Lack of segregation in affected members of a family.
Caveat: The presence of phenocopies for common phenotypes (i.e. cancer, epilepsy) can mimic lack of segregation among affected individuals. Also, families may have more than one pathogenic variant contributing to an autosomal dominant disorder, further confounding an apparent lack of segregation.

Not Applicable

Comments: AD Condition: Co-segregation analysis in lowpenetrance genes can lead to false positive results (PMID 32773770) . AR Condition: informative

instances of lack of co-segregation in A-T families are too rare to be considered for weight at this time and can also be considered for BP2 if biallelic unaffected patients are observed in an A-T family.

BP1

Original ACMG Summary

Missense variant in a gene for which primarily truncating variants are known to cause disease.

Not Applicable

BP2

Original ACMG Summary

Observed in trans with a pathogenic variant for a fully penetrant dominant gene/disorder or observed in cis with a pathogenic variant in any inheritance pattern.

Strength

Use ATM PM3/BP2 table.

Modification Type: Gene-specific,Disease-specific,Strength,General recommendation

Strength

Use ATM PM3/BP2 table.

Modification Type: Gene-specific,Disease-specific,Strength,General recommendation

Strength

Use ATM PM3/BP2 table

Modification Type: Gene-specific,Disease-specific,Strength,General recommendation

Instructions: Use ATM PM3/BP2 table.

BP3

Original ACMG Summary

In frame-deletions/insertions in a repetitive region without a known function.

Not Applicable

BP4

Original ACMG Summary

Multiple lines of computational evidence suggest no impact on gene or gene product (conservation, evolutionary, splicing impact, etc)
Caveat: As many in silico algorithms use the same or very similar input for their predictions, each algorithm cannot be counted as an independent criterion. BP4 can be used only once in any evaluation of a variant.

Supporting

- **Protein** Analysis: Metapredictor REVEL score ≤.249
- **RNA** Analysis: Concordance of ≥2 predictors reflecting no predicted splice defect
  - **NOTE**: Splice analysis needs to be considered for all variant types (including missense, frameshift, nonsense, etc. as any variant has the potential to impact splicing which may preclude any expected protein effects)
  - **NOTE**: BP4 for splice predictions may not be applied in conjunction with BP7_O_Variable (a lack of observed RNA defect)
  - **NOTE**: BP4 for protein predictors may be applied to BS3_Variable for protein effects.
  - **NOTE**: BP4 could be used towards an RNA impact, a protein impact or both, as applicable. However, a variant's classification should be the sum of evidence for RNA or protein as tallied independently and should not mix-and-match evidence from RNA and protein evidence bodies.
    - Example: Do not apply BP4 for in silico splice predictions toward the classification of a missense variant where all other evidence points towards a benign protein effect (instead apply PP3 or BP4, as applicable, for a protein predictor).

Modification Type: General recommendation

Instructions: Protein: REVEL <.249; RNA: multiple in silico predictors agree to a lack of splice defect.

BP5

Original ACMG Summary

Variant found in a case with an alternate molecular basis for disease.

Not Applicable

BP6

Original ACMG Summary

Reputable source recently reports variant as benign, but the evidence is not available to the laboratory to perform an independent evaluation.

Not Applicable

This criterion is not for use as recommended by the ClinGen Sequence Variant Interpretation VCEP Review Committee. PubMed : 29543229

BP7

Original ACMG Summary

A synonymous variant for which splicing prediction algorithms predict no impact to the splice consensus sequence nor the creation of a new splice site AND the nucleotide is not highly conserved.

Strong

Can be considered for BP7_O with curator discretion of quality.

Modification Type: General recommendation

Moderate

Can be considered for BP7_O with curator discretion of quality.

Modification Type: General recommendation

Supporting

Can be considered for BP7_O with curator discretion of quality; Use for synonymous and deep intronic variants defined as further than (but not including) +7 and further than (but not including) -40 at donor and acceptor sites, respectively

Modification Type: General recommendation

Instructions: Use for synonymous and deep intronic variants defined as further than (but not including) +7 and further than (but not including) -40 at donor and acceptor sites, respectively. Use as BP7_O for synonymous and intronic variants with no splice defect observed. Weight for BP7_O is variable based on curator impression fo assay quality (not specified).