

**Points system for assigning weight of evidence for PM3**  
**ClinGen Lysosomal Diseases Variant Curation Expert Panel**

Date: June 7, 2024

Based on ClinGen Sequence Variant Interpretation Working Group guidance-  
[https://clinicalgenome.org/site/assets/files/3717/svi\\_proposal\\_for\\_pm3\\_criterion\\_-\\_version\\_1.pdf](https://clinicalgenome.org/site/assets/files/3717/svi_proposal_for_pm3_criterion_-_version_1.pdf)

<b>Classification/Zygoty of other variant</b>	<b>Points per Proband</b>	
	<b>Confirmed in trans</b>	<b>Phase unknown</b>
<i>Pathogenic or Likely pathogenic variant</i>	1.0	0.5 (P) 0.25 (LP)
<i>Homozygous occurrence (max points = 1.0)</i>	0.5	N/A

Note: The VCEP does not give points for compound heterozygotes if the second variant is a VUS.

<b>PM3 Point Table</b>			
<b>PM3_Supporting</b>	<b>PM3</b>	<b>PM3_Strong</b>	<b>PM3_VeryStrong</b>
<b>0.5 points</b>	<b>1.0 points</b>	<b>2.0 points</b>	<b>4.0 points</b>