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PEER-REVIEW REPORT

Name of journal: *World Journal of Clinical Cases*

Manuscript NO: 89436

Title: Genetic investigation of the ubiquitin-protein ligase A gene as putative target in Angelman syndrome

Provenance and peer review: Unsolicited Manuscript; Externally peer reviewed

Peer-review model: Single blind

Reviewer's code: 06251300
Position: Peer Reviewer
Academic degree: MD
Professional title: Doctor
Reviewer's Country/Territory: India
Author's Country/Territory: Tunisia

Manuscript submission date: 2023-10-31

Reviewer chosen by: AI Technique

Reviewer accepted review: 2023-11-14 08:23

Reviewer performed review: 2023-11-23 14:11

Review time: 9 Days and 5 Hours

Scientific quality	[ ] Grade A: Excellent [Y] Grade B: Very good [ ] Grade C: Good [ ] Grade D: Fair [ ] Grade E: Do not publish
Novelty of this manuscript	[ ] Grade A: Excellent [Y] Grade B: Good [ ] Grade C: Fair [ ] Grade D: No novelty
Creativity or innovation of this manuscript	[ ] Grade A: Excellent [Y] Grade B: Good [ ] Grade C: Fair [ ] Grade D: No creativity or innovation

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Scientific significance of the conclusion in this manuscript	[ ] Grade A: Excellent [Y] Grade B: Good [ ] Grade C: Fair [ ] Grade D: No scientific significance
Language quality	[ ] Grade A: Priority publishing [Y] Grade B: Minor language polishing [ ] Grade C: A great deal of language polishing [ ] Grade D: Rejection
Conclusion	[ ] Accept (High priority) [ ] Accept (General priority) [Y] Minor revision [ ] Major revision [ ] Rejection
Re-review	[Y] Yes [ ] No
Peer-reviewer statements	Peer-Review: [Y] Anonymous [ ] Onymous
	Conflicts-of-Interest: [ ] Yes [Y] No

SPECIFIC COMMENTS TO AUTHORS

• Please check for several grammatical errors • In the methods or results section, include a few sentences on how specifically these 50 were treated. • In the discussion session, implications of specific genes can be put together in a table for easy reading. • You can discuss and highlight the importance of performing patient-derived iPSC modelling (PMID: 33370574; PMID: 35316126) from these individual mutation types for a better understanding of these disease phenotypes and better targeting.