



SDI Review Form 1.6

Journal Name:	International Journal of Biochemistry Research & Review
Manuscript Number:	2014_IJBcRR_14873
Title of the Manuscript:	The E1 Copper Binding Domain of Full-length Amyloid Precursor Protein Promotes Epithelial to Mesenchymal Transition in DU145 Cells in an Isoform-specific Manner
Type of the Article	

General guideline for Peer Review process:

This journal's peer review policy states that **NO** manuscript should be rejected only on the basis of '**lack of Novelty**', provided the manuscript is scientifically robust and technically sound.

To know the complete guideline for Peer Review process, reviewers are requested to visit this link:

(<http://www.sciencedomain.org/page.php?id=sdi-general-editorial-policy#Peer-Review-Guideline>)



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PART 1: Review Comments

	Reviewer's comment	Author's comment <i>(if agreed with reviewer, correct the manuscript and highlight that part in the manuscript. It is mandatory that authors should write his/her feedback here)</i>
<u>Compulsory</u> REVISION comments	1. The key funding of APP₆₉₅ on EMT are based on the light microscopy and dendricity analysis. I am not sure if this method is enough powerful and convictive for the EMT assay. Whatever, I think you should describe in detail or verify this by citing paper. In addition to this, the author needs another classic or traditional method to verify this important result, such as migration or invasion tranwell experiments. 2. The results show that both the extracellular E1 copper binding domain and the cytosolic domain tyrosine687 account for the APP₆₉₅ function on EMT. However, the title of paper did not accurately describe the key finding. Why did the author only emphasize the E1 copper binding domain in title? 3. There are some confusing about the function of APP isoform. According to the results, the E1 copper binding domain and tyrosine687 of APP₆₉₅ is key domain to promote EMT. However, the APP₇₅₁ or APP₇₇₀ also consist the two domains. Why they did not have the same function as APP₆₉₅. The author should gave the reasonable explain about this phenomenon. This should be addressed in the discussion.	
<u>Minor</u> REVISION comments	1. Fig 1, although the author addressed that it was not necessary to perform real time quantitative PCR, I thinks this results is important for demonstrating the expression of APP isoforms in prostate cancer cell line, so it is recommended to apply the real time quantitative PCR to quantify the expression of APP isoform. 2. Table 1, should analyze the statistical significant data between a series APP molecular constructs and	



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	APP695, which will show the role of key domains. 3. N-cadherin is the key marker of EMT, so in Fig 2B the author should add the N-cadherin protein expression data by WB.	
<u>Optional/General</u> comments	The authors in this manuscript describe a new function for the amyloid precursor protein (APP), and identified the key functional domain of APP on EMT of prostate cell line by isoform-specific manner. Using a range of APP molecular constructs, they demonstrate that the full-length 695 amino acid isoform (APP₆₉₅) can promote EMT via a mechanism requiring an intact extracellular E1 copper binding domain and tyrosine687 within the cytosolic domain of the protein. The data are new and original. These findings deepen the understanding of how APP promote EMT, and therefore have impact on the how targeting APP contributes to therapeutic strategies for prevention of prostate cancer metastasis. However, there are a couple minor points that should be addressed. Otherwise, this paper is suited for this journal.	

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