Comments:

1 In the first paragraph, the second sentence may need to rephrase. It seems to have some grammar mistakes. “Among their many roles, MTs represent the principal structural components of the mitotic spindle, are essential in maintaining cell shape, motility and to facilitate intracellular transport and intracellular communication.”

2 “Beta tubulin is of critical function because most of the available data in the literature deals with this protein as a target for drug action and protein-protein interactions (Huzil et al, 2007).” The first sentence in the second paragraph seems misunderstanding for me: how beta tubulin’s critical function is due to it is the target of extensive research? The “phylogenetic relationship” should be the critical function of beta tubulin make it a target for extensive investigations or the target of drugs.

3 In the third paragraph, you mentioned that “To date, mammalian beta tubulin has been grouped into 9 classes, class I, IIa, IIb, III, IVa, IVb, V, VI, VIII (HUGO Gene Nomenclature Commitee). However, searching through literature, no phylogenic study has been done/found categorizing these genes in their respective classes like it was done with α-tubulin partners (Varsha K. Khodiyar et al, 2007). Thus, the basis of beta tubulin classification is not yet clear.” I am curious what is the basis of the current classification of beta tubulins into 9 groups and why you think this classification is not clear.

4 In your second part “this proposal is set to” (a) Validate the nomenclature of human beta tubulins by phylogenetic construction of molecular data using maximum likelihood (nucleotide sequences) I hypothesize beta isotypes to be orthologous to each other and expect them to form 08 clades of evolutionary relationships as reported in the literature.

First of all, I am not sure if “orthologous” would be appropriate to describe the relationship among different beta tubulin isotypes in the same species (I assume you mean the same species since you also mention isotypes), and if so, I feel “homologous” maybe more accurate. Second, you mentioned in the third paragraph in “introduction section” “However, searching through literature, no phylogenic study has been done/found categorizing these genes in their respective classes like it was done with α-tubulin partners (Varsha K. Khodiyar et al, 2007).” Is this conflicted with your hypothesis A “I hypothesize beta isotypes to be orthologous to each other and expect them to form 08 clades of evolutionary relationships as reported in the literature”. You need to be consistent.

5 (b) Replicate phylogenetic analysis of mammalian alpha-tubulin as presented by V.K. Khodiyar et al. 2007, in their paper entitled " A revised nomenclature for the human and rodent α-tubulin gene family) which categorized the 09 alpha tubulin genes into 4 major groups using neighbor joining. I would like to use maximum likelihood instead of NJ to construct phylogeny of alpha tubulins and compare it with their results. (nucleotide).

If you are not going to use exactly the same method what the previous researchers have used, “replicate” maybe not accurate.

6 The method section “nucleotide sequence” “Only the protein-coding portion of each cDNA will be used” could be rephrased to “only the cDNA sequence of each gene will be used” or “only the protein-coding sequence of each gene will be used”.