



**SDI Review Form 1.6**

Journal Name:	<b><u>British Journal of Medicine and Medical Research</u></b>
Manuscript Number:	<b>2013_BJMMR_7449</b>
Title of the Manuscript:	<b>High frequency of non-B HIV-1 subtypes specific mutations at the protease gene among treatment-naïve HIV-1 infected individuals in Jos, Nigeria</b>
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**

	<b>Reviewer's comment</b>	<b>Author's comment</b> <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>
<b><u>Compulsory</u></b> REVISION comments		
<b><u>Minor</u></b> REVISION comments		
<b><u>Optional/General</u></b> comments	<p>The manuscript is confusing. For example, the authors do not clearly distinguish observed polymorphisms that are known to be associated with drug resistance, those that are not associated with resistance, and those that are subtype-specific; the data and discussion mixes them together creating confusion. In addition, the authors do not appear to understand their own data. In figures 1-4 are plotted the % frequency of mutations by subtype. For subtype A there are only 5 sequences in their data set therefore the frequency of a mutation found in one sequence is 1 in 5 or 20% - cannot have frequencies of 1-5% as shown in the figure. Similarly, for the other CRF and subtypes.</p> <p>The data presented here is nearly identical to a previous publication and several sentences are taken word for word from it. The publication is: Anejo Okopi JA, et al, J. HIV Hum. Reprod. (2013) 1:8-14. "Prevalence of minor mutations and natural polymorphisms at the protease gene among treatment-naïve human immunodeficiency virus-1 infected individuals in Jos, Nigeria."</p>	<p>It might be true, if one reads our previous paper, but here we only try to segment the description in line with subtype-specific mutations and individuals mutations were discussed in line with the current IAS-USA drug resistance update list ref -31</p> <p>We got our percentages in the figures the way we did because, for each subtype, the number of mutations cannot be greater than the number of isolates</p> <p>The data here is truly identical but we shifted focus to re-analyse the data to capture a segment that has never being reported in Nigeria. We have been able to attend to some sentences considered close which are highlighted in the ms</p>