



SDI Review Form 1.6

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

Note: Anonymous Reviewer