Dear Franc Perdih,  
I agree with your Editorial corrections.

1.) Lines 116-117: Although you did use those values associated with the DFIX command, the refined values are almost always slightly different, as is the case also in your structures. Suggest rephrasing this sentence to be more general: "... with O‒H and N‒H groups refined fixing the bond lengths."

Response: The sentence has been corrected.   
2.) Line 134: Why you used mass concentration instead of molar concentration? In bioassay only molar concentration is logical since we study the activity of molecules.  
Response: To our knowledge, most of the literatures about bioassay are used mass concentration. Instead, only a small part of literatures used molar concentration.

3.) Line 144: This is unusual specification ...

Response: Corrected as 5% HCl (1 mol L–1).  
4.) Table 3: It seems this table was not updated with data from new cifs.  
Response: Table 3 has been updated.   
One more thing. Have you checked the possibility that structure 2 is orthorombic and not monoclinic? What is your comment regarding the Alert B  
(missing reflections) - did you try to refine with the ACTA 50 command?  
Response: The structure 2 is indeed monoclinic, instead of orthorhombic. The Alert B (missiong reflections) is due to the omit operation. The Most Disagreeable Reflections are removed with omit instruction.

Sincerely yours,  
Xiao-Yang Qiu, and Shu-Juan Liu