BIOCHEMISTRY
including biophysical chemistry & molecular biology
Addition and Correction

Correction to Solution Structural Dynamics of HIV-1 Reverse Transcriptase Heterodimer [(2009) *Biochemistry 48,* 7646. DOI: 10.1021/bi900790x]. James M. Seckler, Kathryn J. Howard, Mary D. Barkley,* and Patrick L. Wintrode*

The H−D exchange data for peptide 518−533 in the RNase H domain of the p66 subunit are incorrect. Peptide 518−533 cochromatographed with an impurity in early experiments but separated from the impurity when the chromatography conditions were changed in subsequent experiments. Figures 4A, 5A,B, and 6 and Tables 1 and S1 require changes to incorporate the correct data for this peptide. This does not affect the conclusions of the paper. The corrections to the figures and tables follow.

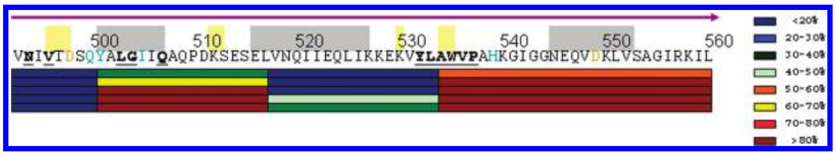

FIGURE 4: Panel A (last vertical bar only).

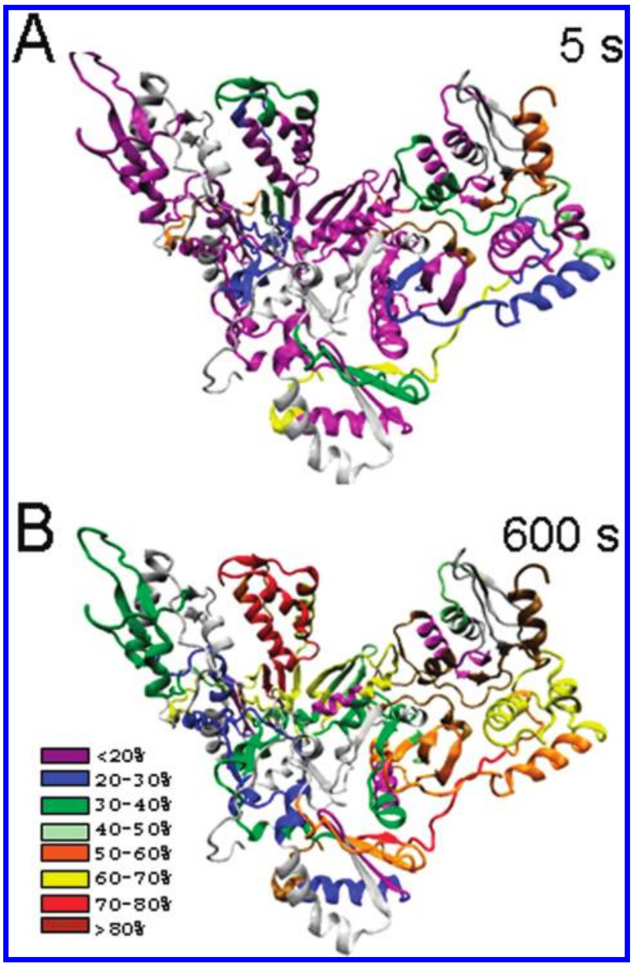

FIGURE 5: Panels A and B only.

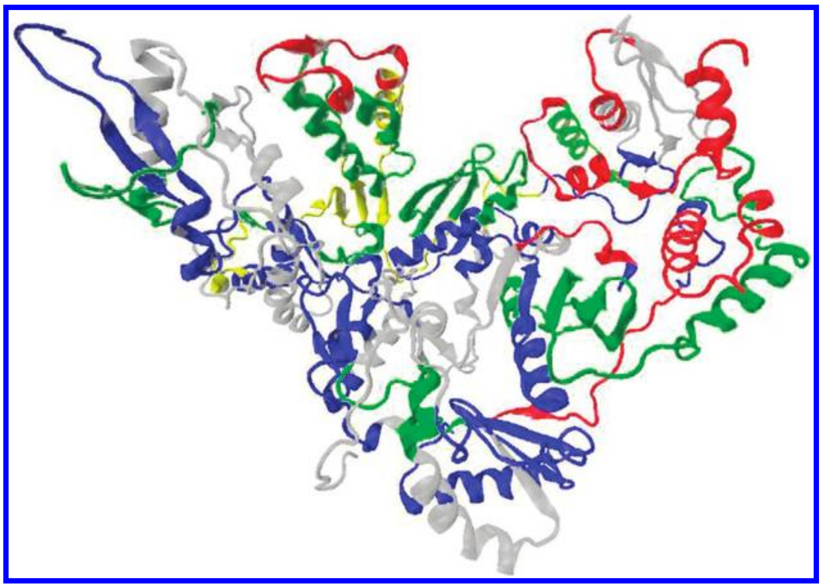

FIGURE 6

In Table 1, for VNQIIEQLIKKEKVYL (next to last row), the correct values in columns 3 and 5 are as follows: n-slow = 10 and ratio = 0.77. In Table S1, for VNQIIEQLIKKEKVYL (next to last row), the correct entries for n-slow, k-slow, n-medium, k-medium, n-fast, and k-fast (columns 5−10) are all dashes.

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