Corrections

Conformational Changes in the Active Site Loops of Dihydrofolate Reductase during the Catalytic Cycle, by Rani P. Venkitakrishnan, Eduardo Zaborowski, Dan McElheny, Stephen J. Benkovic, H. Jane Dyson, and Peter E. Wright*, Volume 43, Number 51, December 28, 2004, pages 16046−16055.

Page 16054. The correct version of Table 1 appears below.

Table 1: Conformational States of Wild-Type and G121V DHFR Complexes

complex[a]	wild-type DHFR	G121V DHFR
apoenzyme	disordered	disordered
E:folate	*occluded*	*occluded*
E:DHF	*occluded*	*occluded*
E:THF	*occluded*	nm[b]
E:NADPH	*closed*	*occluded* (+ *closed*)[c]
E:NADP$^+$	disordered	nm[b]
E:DHNADPH	disordered	nm[b]
E:folate:NADP$^+$	*closed*	*occluded*
E:folate:NADPH	*closed*	*occluded*
E:DHF:NADP$^+$	*closed*	nm[b]
E:DHF:DHNADPH	*occluded*	nm[b]
E:THF:NADP$^+$	*occluded*	*occluded*
E:THF:NADPH	*occluded*	*occluded*

[a] Intermediates in the steady-state cycle are in boldface type. Models for the Michaelis complex are in italic type. [b] Not measured. [c] The predominant conformation for the E:NADPH complex of G121V is occluded, with a small population of the closed state present.

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