BIOCHEMISTRY
including biophysical chemistry & molecular biology

Addition/Correction

pubs.acs.org/biochemistry

Correction to Effect of Cofactor Binding and Loop Conformation on Side Chain Methyl Dynamics in Dihydrofolate Reductase

Jason R. Schnell, H. Jane Dyson, and Peter E. Wright*

Biochemistry, **2004**, *43* (2), 374−383. DOI: 10.1021/bi035464z

New experiments using improved pulse shaping indicate that the ${}^3J_{C\gamma CO}$ coupling constants for the E:folate:NADP$^+$ and E:folate complexes reported in Table 2 of the Supporting Information are in error. The reported ${}^3J_{C\gamma CO}$ coupling constants were systematically decreased in magnitude, apparently because of incomplete inversion of ^{13}CO resonances by the standard sinc-shaped 180° pulse used in the original pulse sequence. This problem led to errors in rotamer populations (Table 3 of the original paper) for several residues and affects one of the conclusions. The side chain of Ile14, which packs against the nicotinamide ring of the cofactor in the E:folate:NADP$^+$ complex, does not exhibit rotamer averaging, as originally reported, but fully populates the $\chi_1 = +60°$ rotamer. Ile94, which packs against the bound folate, displays rotamer averaging in the new data but with altered rotamer distribution; for the minor rotamer, $\chi_1 = -60°$ rather than $\chi_1 = 180°$ as in the original work. These new data do not support the model of conformational flexibility in the active site suggested by the original experiments. All other conclusions of the original paper remain valid.

The revised ${}^3J_{C\gamma CO}$ coupling constants for the E:folate:NADP$^+$ and E:folate complexes will be tabulated in a forthcoming paper, along with new data for six additional complexes of DHFR and a refined rotamer analysis (which replaces Table 3 of the original paper) based on improved parametrization of the Karplus equations.

Received: March 13, 2013
Published: March 22, 2013

dx.doi.org/10.1021/bi4003277 | *Biochemistry* 2013, 52, 2383−2383