Corrections

Evolution of Enzymatic Activities in the Enolase Superfamily: Stereochemically Distinct Mechanisms in Two Families of *cis*,*cis*-Muconate Lactonizing Enzymes, by Ayano Sakai, Alexander A. Fedorov, Elena V. Fedorov, Alexandra M. Schnoes, Margaret E. Glasner, Shoshana Brown, Marc E. Rutter, Kevin Bain, Shawn Chang, Tarun Gheyi, J. Michael Sauder, Stephen K. Burley, Patricia C. Babbitt, Steven C. Almo, and John A. Gerlt,* Volume 48, Number 7, 2009, pages 1445–1453.

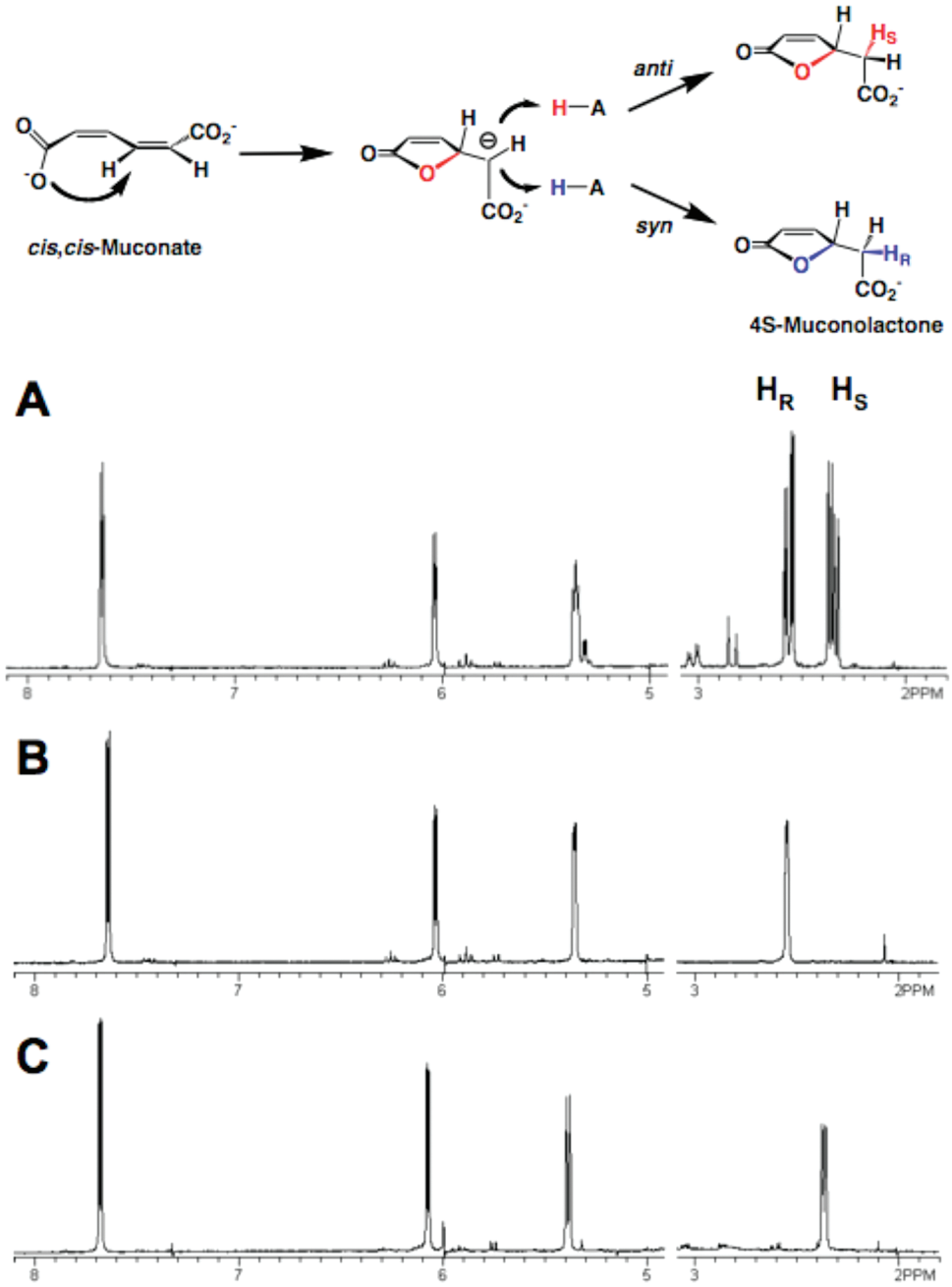

FIGURE 3: Stereochemical course of the MLE-catalyzed reaction. The facial relationships of the carboxylate group and active site acid/base catalyst in *anti*- and *syn*-cycloisomerization reactions are shown at the top. (A) ^{1}H NMR spectrum of (4*S*)-muconolactone obtained in H_2O. (B) ^{1}H NMR spectrum of (4*S*)-muconolactone obtained in D_2O with the MLE from *M. smegmatis*. (C) ^{1}H NMR spectrum of (4*S*)-muconolactone obtained in D_2O with the MLE from *P. fluorescens*.

Three errors in assignment of absolute configurations were made in this article, none of which alters the conclusion that the two families of *cis*,*cis*-muconate lactonizing enzymes (MLEs) catalyze their reactions with opposite stereochemical courses.

On page 1449, we incorrectly stated that solvent-derived deuterium is incorporated into the 5-pro-*S* hydrogen of (+)-(4*S*)-muconolactone by the MLEs from both *Pseudomonas putida* and *Pseudomonas fluorescens*; both MLEs incorporate solvent-derived deuterium into the 5-pro-*R* hydrogen [Avigad, G., and England, S. (1984) *Fed. Proc. 28*, 345, Abstract 486; Chari, R. V. J., Whitman, C. P., Kozarich, J. W., Ngai, K.-L., and Ornston, L. N. (1987) *J. Am. Chem. Soc. 109*, 5514−5519]. We also incorrectly stated that solvent-derived deuterium is incorporated into the 5-pro-*R* hydrogen of (+)-(4*S*)-muconolactone by the MLE from *Mycobacterium smegmatis*; this MLE incorporates solvent-derived deuterium into the 5-pro-*S* hydrogen.

In Figure 3 on page 1450, we reversed the stereochemical assignments of the 5-hydrogens in (4*S*)-muconolactone; the corrected Figure 3 is shown below.

BI900265W

10.1021/bi900265w
Published on Web 02/25/2009

Structure and Inhibition of Orotidine 5′-Monophosphate Decarboxylase from *Plasmodium falciparum*, by David B. Langley, Maryam Shojaei, Camilla Chan, Hiu Chuen Lok, Joel P. Mackay, Thomas W. Traut, J. Mitchell Guss, and Richard I. Christopherson,* Volume 47, Number 12, 2008, pages 3842–3854.

Our structure is discussed in light of other structures of the enzyme present in the Protein Data Bank, some of which became available just prior to submission of the manuscript. Brief comparison with these more recent structures was discussed in footnote 3 which was accidentally omitted from the article in the version published on the Web on February 28, 2008 (ASAP), and in the March 25, 2008, issue (Vol. 47, No. 12, pp 3842–3854). It should appear at the bottom of the left column of page 3852. The correct electronic version of the paper was published February 27, 2009.

[3]Our conclusion is also supported by low-resolution *Pf*ODCase structures published by Tokuoka et al., just prior to the submission of this paper (*42*). PDB entries 2ZA2, 2ZA1, and 2ZA3, all at ∼2.65 Å resolution and comprising apo, OMP-, and UMP-complexed *Pf*ODCase, also have the $\beta\alpha$5-loop in the active conformation. The apoenzyme has disordered phosphate-binding loops, while in the OMP and UMP complexes they are closed. The OMP and UMP ligands overlay almost perfectly with the UMP ligand modeled in Figures 3 and 4. The carboxylate moiety of OMP is accommodated by a subtle rotation of the side chain of D136. In contrast, other fine-detail features, such as the expected bifurcated hydrogen bonding between Q269 and the substrate/product, are not apparent in these lower-resolution structures.

BI900043P

10.1021/bi900043p
Published on Web 03/02/2009