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Supplementary Material for: "Characterization of the Zinc Binding Site in Methionine Synthase Enzymes of *Escherichia coli* : The Role of Zinc in the Methylation of Homocysteine" K. Peariso, C.W. Goulding, S. Huang, R.G. Matthews, and J.E. Penner-Hahn

Figure S1 k^3-weighted zinc EXAFS spectra of native methionine synthase enzymes. Bottom) MetE; and Top) MetH(2-649). Solid line = unfiltered EXAFS data; dashed line = best fits using parameters in Table 1. The EXAFS oscillations are normalized to the zinc concentration, as determined by the magnitude of the edge jump. Spectra are plotted on the same scale, offset vertically for clarity.

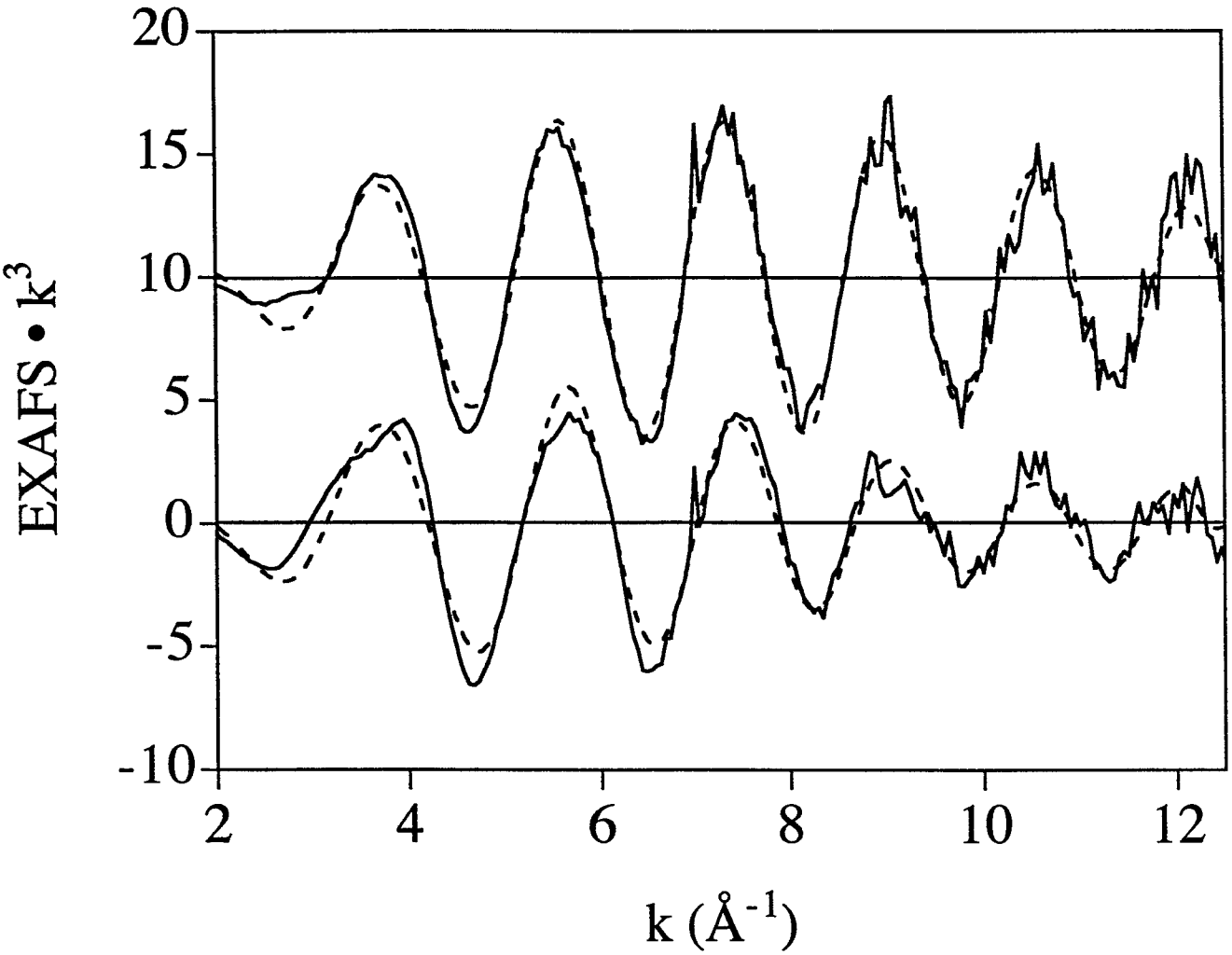

Figure S2 Formation of cob(I)alamin from methylcobalamin form of MetH(2-1227) and L-homocysteine monitored at 386 nm. Solid line: Wild-type MetH(2-1227); Dashed line: Cys247Ala mutant MetH(2-1227).

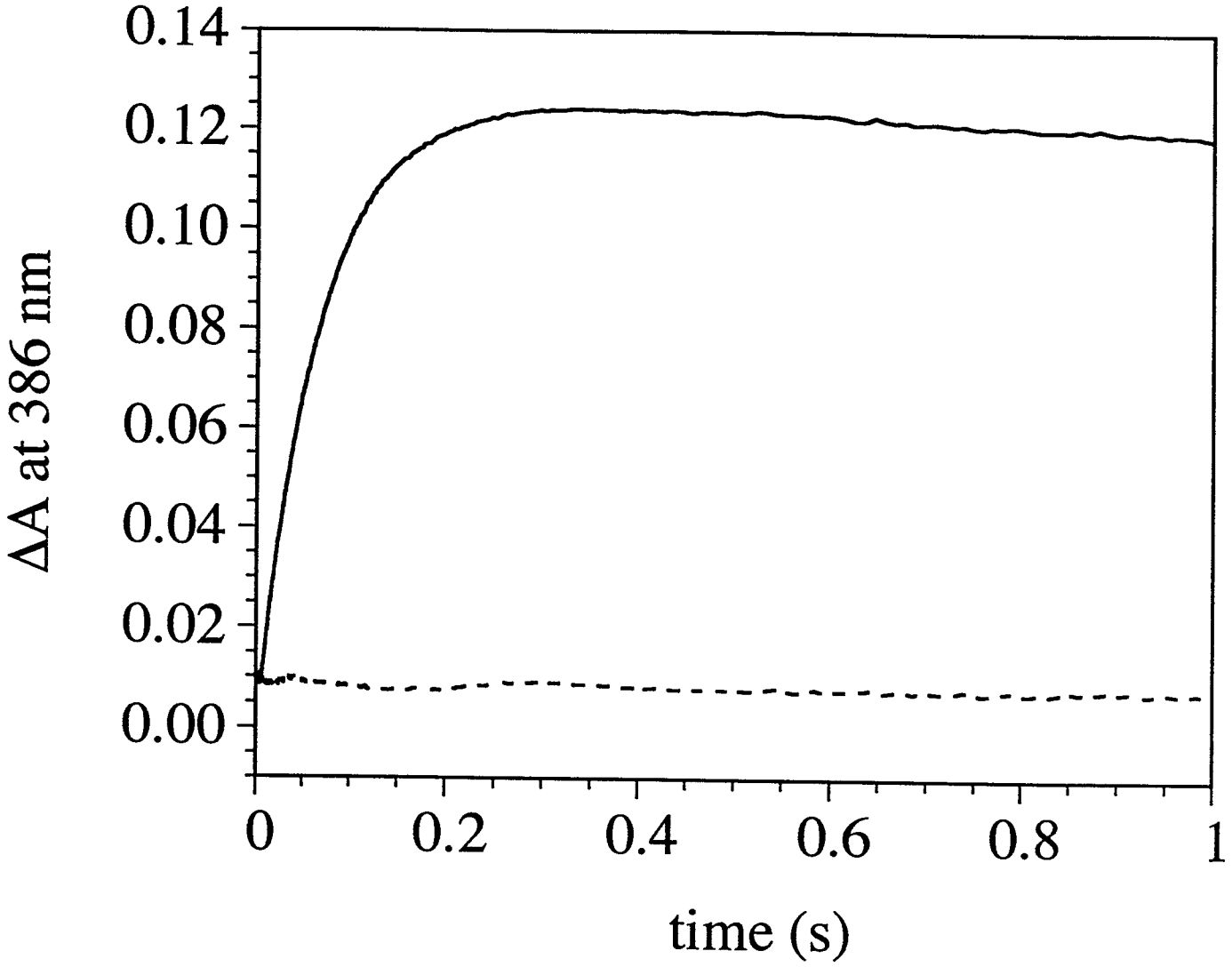

Figure S3 Zinc EXAFS spectra of native methionine synthase enzymes (solid line) and enzymes + homocysteine (dashed line). Top) MetE and MetE + L-homocysteine; Middle) MetH(2-649) and MetH(2-649) + L-homocysteine; Bottom) MetH(2-649) and MetH(2-649) + D-homocysteine. All spectra are plotted on the same scale, offset vertically for clarity.