## Abstract Submitted for the MAR07 Meeting of The American Physical Society

Dependence of Localized Electronic Structure on Ligand Configuration in the [2Fe] Hydrogenase Catalytic Core<sup>\*</sup> CHRISTOPHER H. CHANG, KWISEON KIM, National Renewable Energy Laboratory — The [FeFe] hydrogenase enzyme is found in a variety of organisms, including Archaea, Eubacteria, and green algae<sup>1,2</sup>, and crystallographically determined atomic position data is available for two examples. The biologically unusual catalytic H-cluster, responsible for proton reduction to  $H_2$  in vivo, is conserved in the known structures and includes two *bis*-thiolato bridged iron ions with extensive cyano- and carbonyl ligation. To address the configurational specificity of the diatomic ligand ligation, density functional theoretical calculations were done on [2Fe] core models of the active center, with varying CO and CN<sup>-</sup> ligation patterns. Bonding in each complex has been characterized within the Natural Bond Orbital formalism. The effect of ligand configuration on bonding and charge distribution as well as Kohn-Sham orbital structure will be presented. [1] M. Forestier, P. King, L. Zhang, M. Posewitz, S. Schwarzer, T. Happe, M.L. Ghirardi, and M. Seibert, Eur. J. Biochem. 270, 2750 (2003). [2] Posewitz, M.C., P.W. King, S.L. Smolinski, R.D. Smith, II, A.R. Ginley, M.L. Ghirardi, and M. Seibert, Biochem. Soc. Trans. 33, 102 (2005). \*This work was supported by the US DOE-SC-BES Hydrogen Fuels Initiative, and done in collaboration with the NREL Chemical and Biosciences Center.

> Kwiseon Kim National Renewable Energy Laboratory

Date submitted: 13 Nov 2006

Electronic form version 1.4