

Biomimetic Modeling of Metalloenzyme Active Sites Using Computational Chemistry Methods

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- **Background:** Eubacterial proteins are synthesized with a formyl group at the N-terminus. Peptide deformylase (PDF), in a reaction catalyzed by an Fe(II) coordination complex in the active site, catalyzes the hydrolytic removal of the N-terminal formyl group from nascent proteins, making it of interest in antibacterial drug development.
- **The goal of this research** is to find a biomimetic ligand for the enzyme active site which gives the most thermodynamically and/or kinetically favorable deformylation reaction.
- **Key result:** The imidazole ligands give the lowest ΔG_{rxn} . The sulfur electron-donating group can allow for the ΔG^\ddagger to be lower with these ligands.

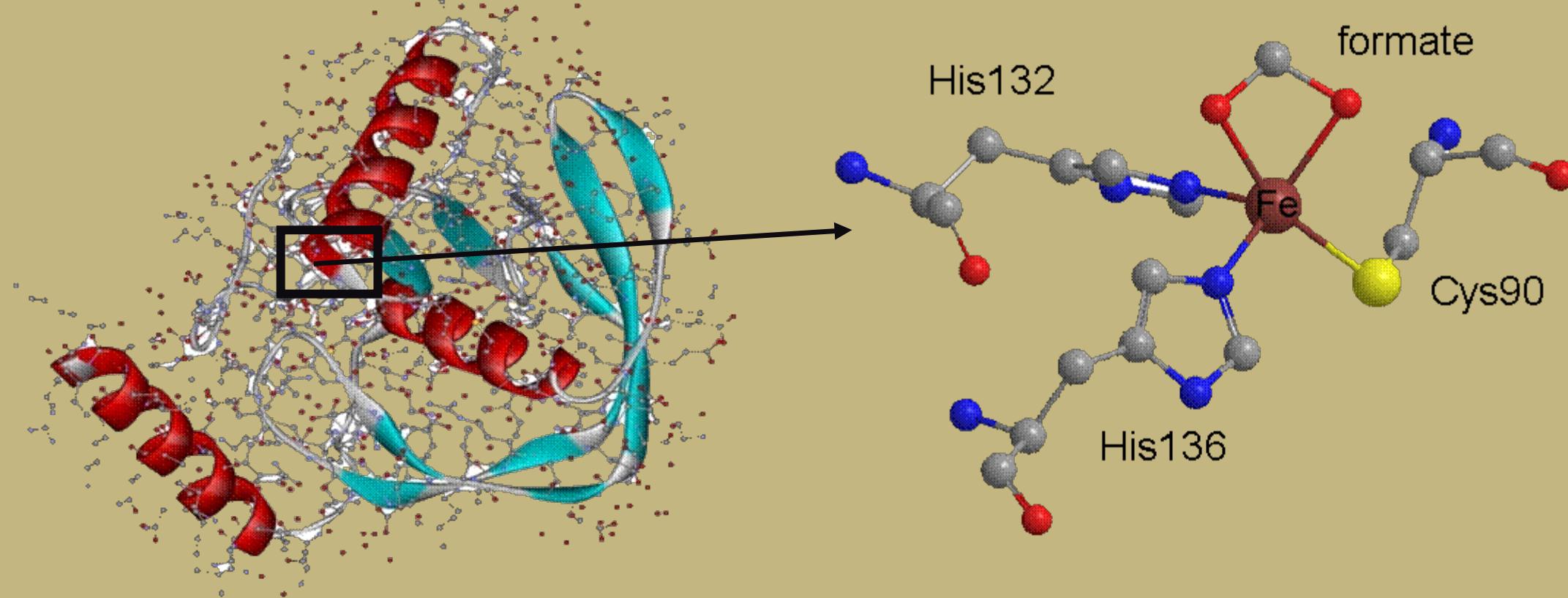
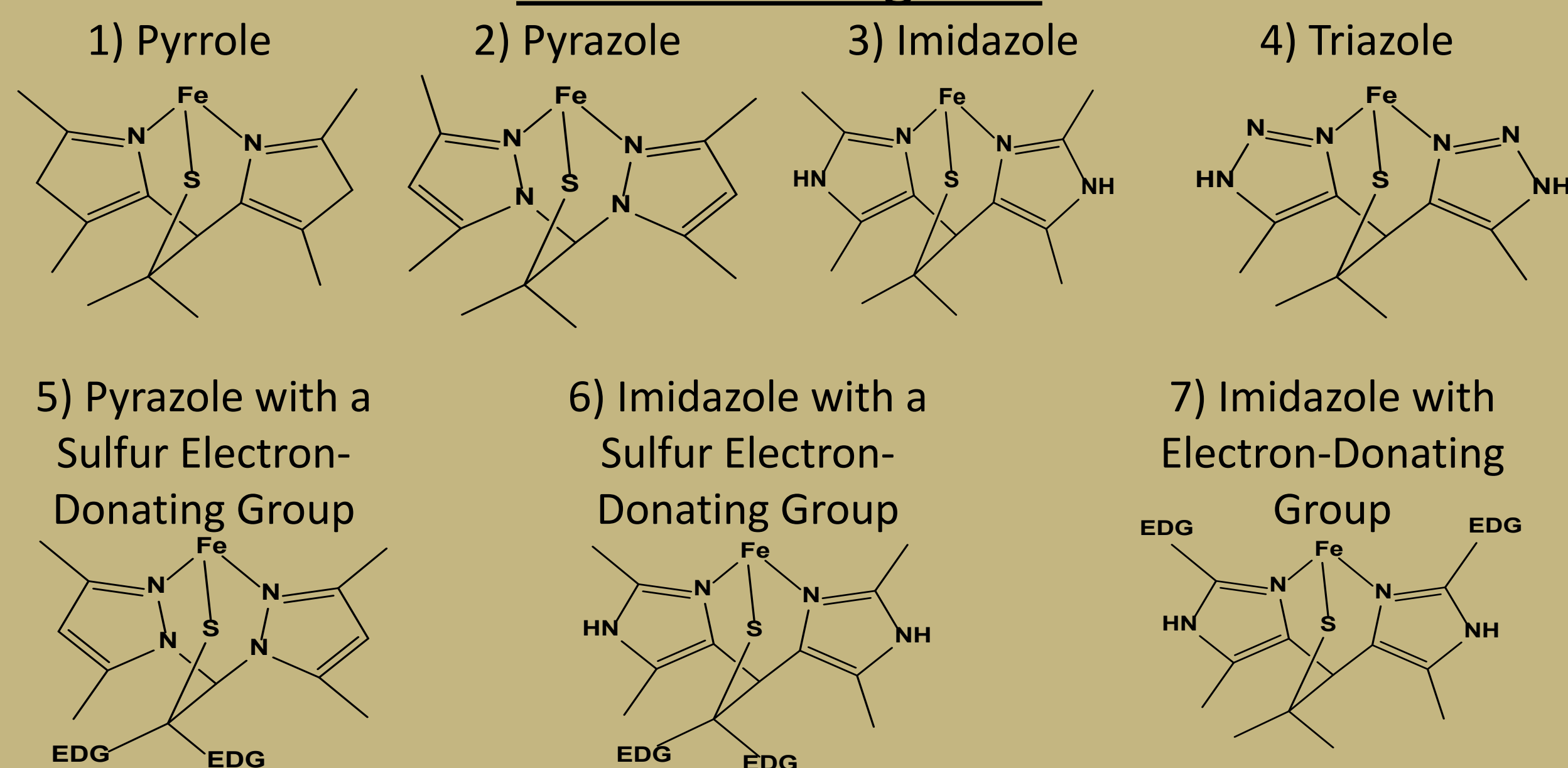


Figure 1. (left) PDF enzyme and (right) active site.

Biomimetic Ligands



- **Background:** CytC3 and SyrB2 are non-heme iron halogenase metalloenzymes that catalyze halogenation reactions of natural products. Halogenation is useful in synthesizing organic compounds; however, typical organic halogenation reactions involve toxic chemicals, posing environmental danger.
- **The goal of this research** is to determine the effect of ligand structure and metal spin state on the thermodynamics, kinetics, and chemoselectivity for the halogenation reaction catalyzed by these complexes.
- **Key result:** With the TQA ligand, reaction energetics for hydrogen atom abstraction and the overall reaction are more favorable with high-spin Fe^{IV}. Activation energy barriers are lower for halogenation versus hydroxylation, imparting chemoselectivity.

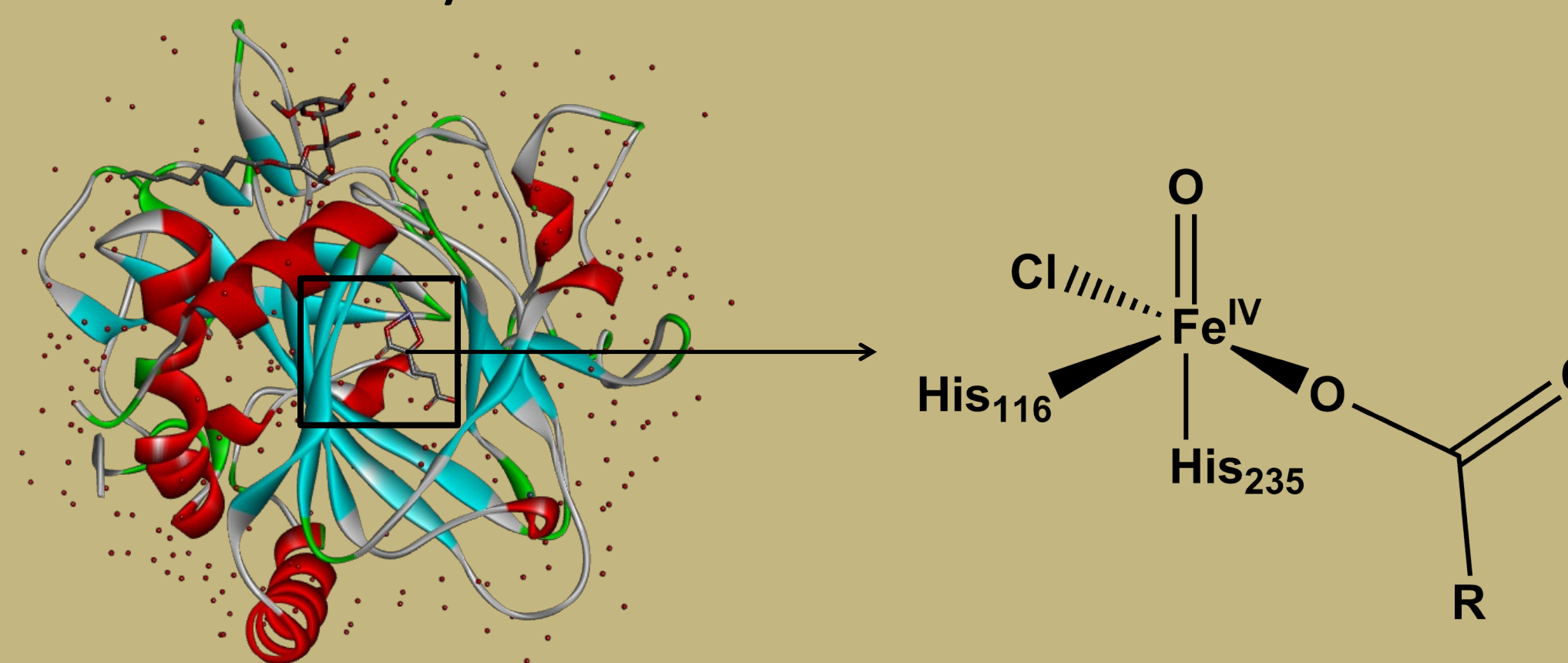


Figure 2. (left) SyrB2 enzyme and (right) active site.

Biomimetic Ligands

