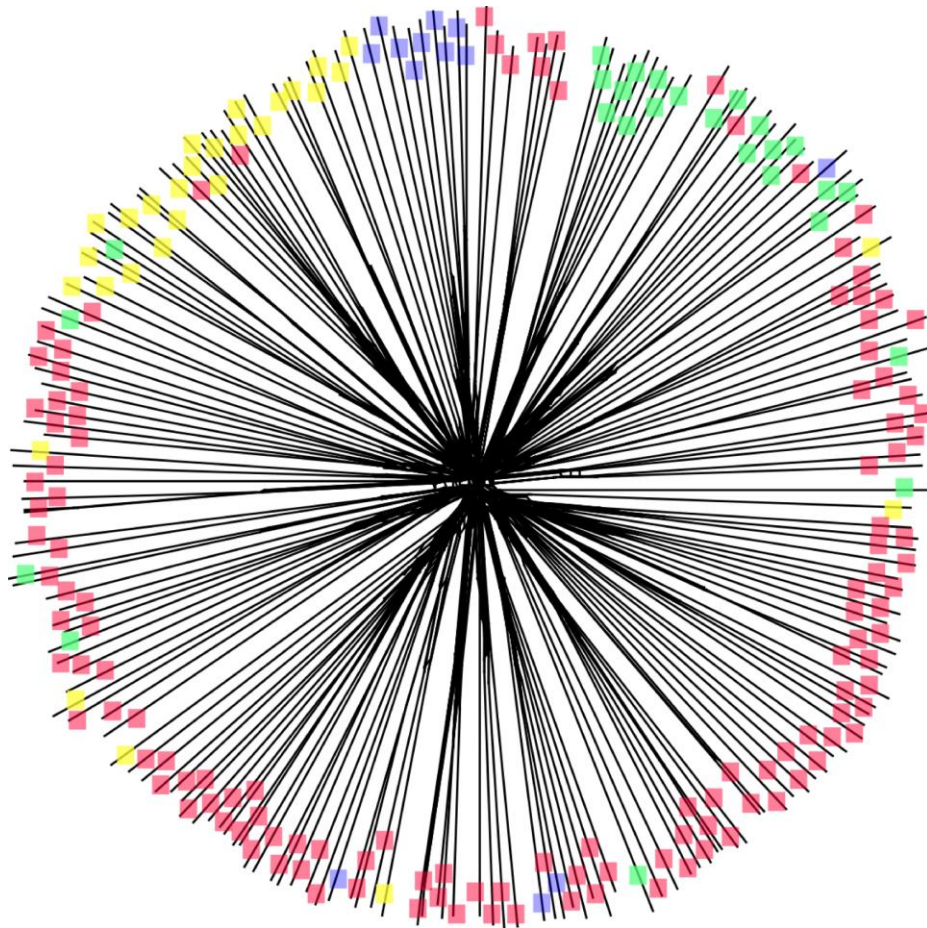**Supplemental Data** for "Functional Evolution of PLP-dependent Enzymes based on Active-Site Structural Similarities" Jonathan Catazaro, Adam Caprez, Ashu Guru, David Swanson and Robert Powers

Figure S1. **Sequence based network analysis of PLP-dependent enzymes.** A phylogenetic network of 139 PLP-dependent enzymes with ligand defined active sites in the PDB. The red, yellow, green, and blue markers indicate enzymes belonging to fold-types I, II, III, and IV, respectively. The network was built using a MSA from Clustal Omega and the Neighbor-net algorithm. The sequence-based network is completely random relative to the CPASS-based network depicted in Figure 1.
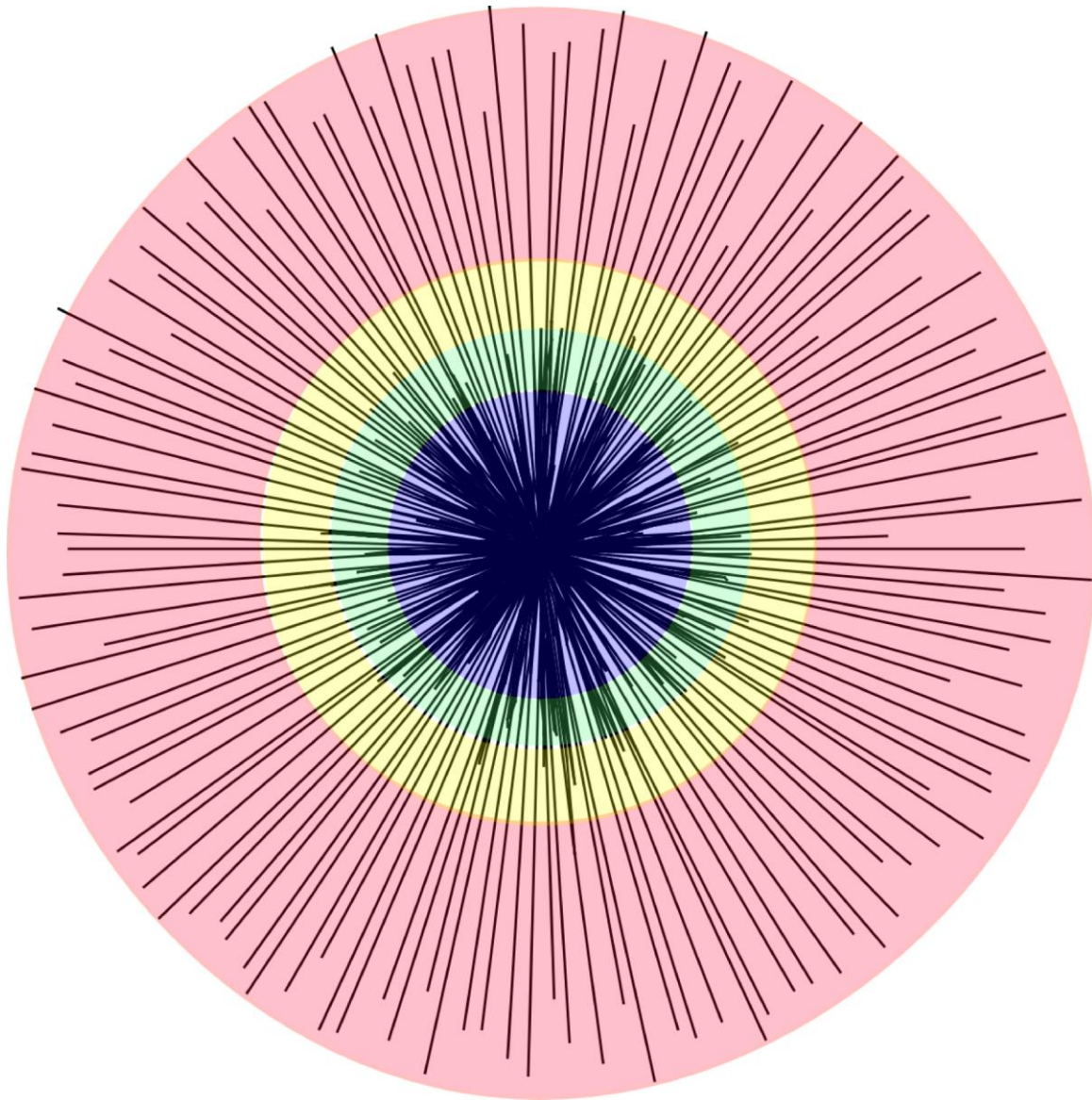
Figure S2. Structure based network analysis of PLP-dependent enzymes. A phylogenetic network of 139 PLP-dependent enzymes with ligand defined active sites in the PDB. The network was built using pairwise TMalign scores and the Neighbor-net algorithm. Red, yellow, green, and blue regions correspond to fold-types I, II, III, and IV, respectively. The struture-based network is random, except for fold-type, relative to the CPASS-based network depicted in Figure 1.