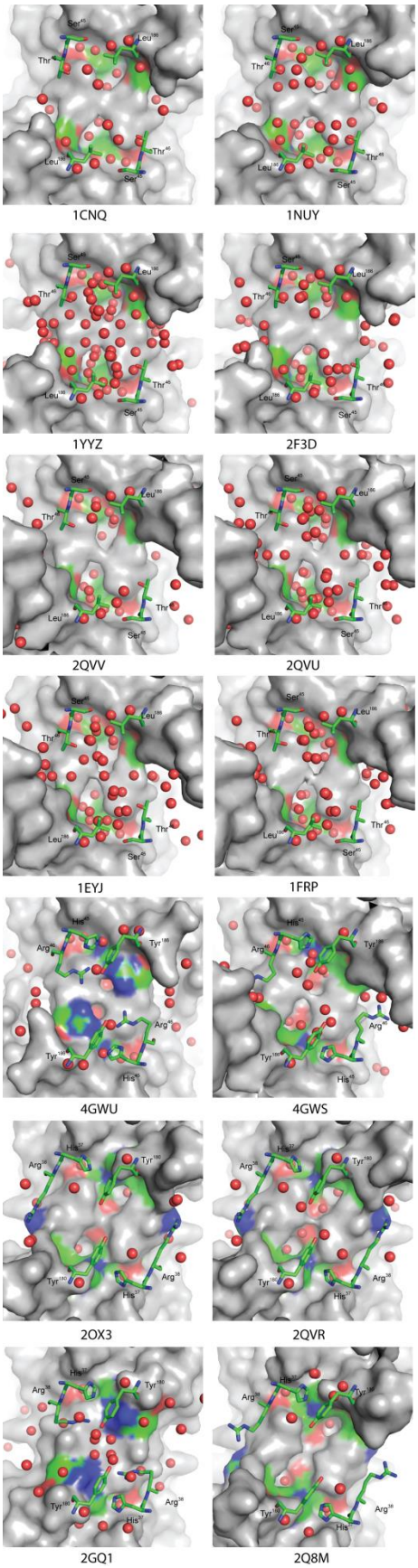

Supplemental Figure 1. Hydration levels of the central regions of *p*FBPase and *e*FBPase. Central cavities from PDB ID 1CNQ (R-state *p*FBPase, product complex, 2.3 Å), PDB ID 1NUY (R-state *p*FBPase, product complex, 1.3 Å), PDB ID 1YYZ (I_R-state Leu^{54} *p*FBPase, AMP complex, 1.9 Å), PDB ID 2F3D (I_T-state Asp^{10} *p*FBPase, AMP complex, 1.8 Å), PDB ID 2QVV (*p*FBPase, Fru-2,6-P_2 complex, 2 Å), PDB ID 2QVU (*p*FBPase, Fru-2,6-P_2 complex, 1.5 Å), PDB ID 1EYJ (T-state *p*FBPase, AMP complex, 2.3 Å), PDB ID 1FRP (T-state *p*FBPase, AMP complex, 2.0 Å), PDB ID 4GWU (Cav^- *p*FBPase, Fru-2,6-P_2 complex, 3.0 Å), PDB ID 4GWS (T-state Cav^- *p*FBPase, AMP complex, 2.8 Å), PDB ID 2OX3 (R-state *e*FBPase, product complex, 2.2 Å), PDB ID 2QVR (*e*FBPase, Fru-2,6-P_2 complex, 2.2 Å), PDB ID 2GQ1 (*e*FBPase, ammonium sulfate complex, 1.5 Å), and PDB ID 2Q8M (*e*FBPase, AMP-Glc-6-P complex, 2.1 Å) are displayed. The surface renderings are of subunits C1 and C4 of the tetramer, with ball-and-stick models representing selected residues from subunits C2 and C3 and water molecules as red spheres. The top 8 images are of *p*FBPase at various resolutions and conformational states, wheres the subsequent pair of images are of Cav^- *p*FBPase and the last four are of complexes of *e*FBPase, again at various resolutions and conformational states.