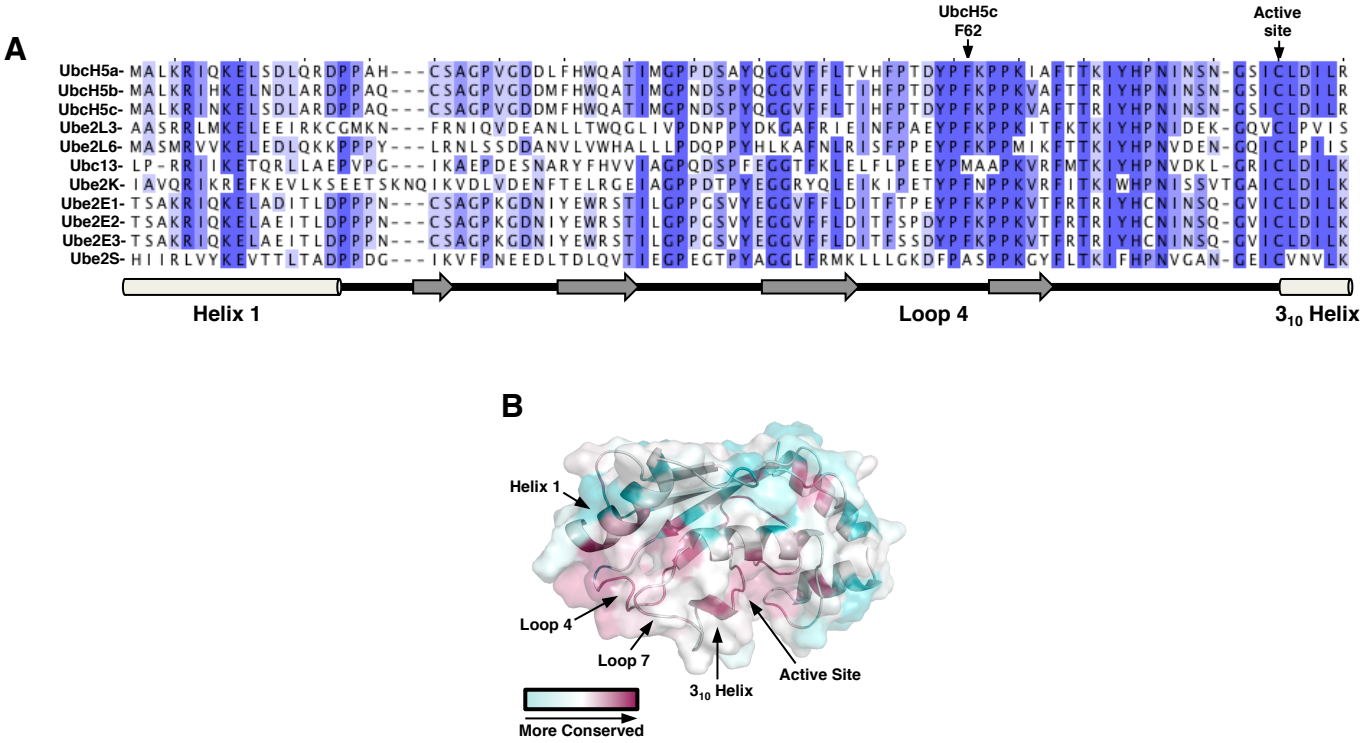
Supplemental Figure 3: ConSurf analysis of OspG interacting E2s



Supplemental Figure 3: ConsSurf analysis of OspG interacting E2s. a) Primary sequence alignment of all OspG-interacting E2s identified by yeast 2-hybrid (Kim et al., 2005) or mass spectrometry experiments and confirmed by *in vitro* pulldown experiments. The conserved hydrophobic residues analogous to UbcH5c F62 and the active site cysteine are marked with arrows. Residues are colored by conservation, where blue is the most conserved. Ube2S, which lacks the required hydrophobic residue analogous to UbcH5c F62 and does not interact with OspG, is also shown. **b)** ConSurf (Ashkenazy et al., 2010) analysis of OspG interacting E2s. Residue conservation is mapped onto a surface representation of the UbcH5c solution structure (PDB 2FUH). Key structural features are marked. The active site and E3-binding interface (magenta) are the most conserved regions among all OspG-interacting E2s.