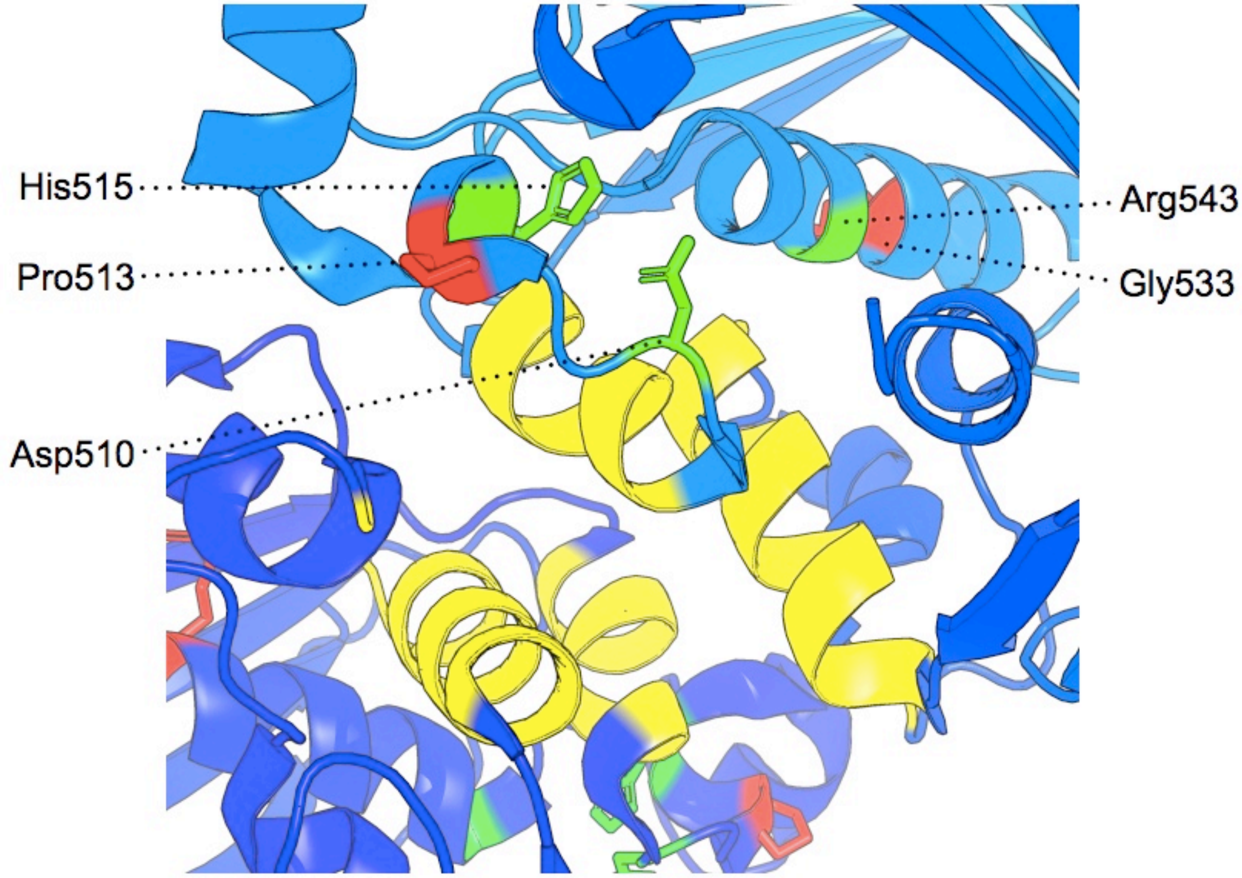
Supplementary Figure 1. Location of mutations within DBP hydratase domain



Catalytic residues are shown in green; two alpha-helices forming the hydratase domain's dimerization surface are depicted in yellow. Proline 513 is situated between / adjacent to active site residues aspartate 510 and histidine 515. Arginine 543 resides in an alpha-helix located centrally within the hydratase domain's C-terminal 'hot dog' fold, adjacent to active site residue glycine 533. Both changes abolish or create (respectively) a proline residue at the position indicated, and are therefore likely to have significant local conformational effects. Image is based on PDB structure 1S9C (http://www.rcsb.org/pdb/explore.do?structureId=1S9C).