

Supplemental Figure S3

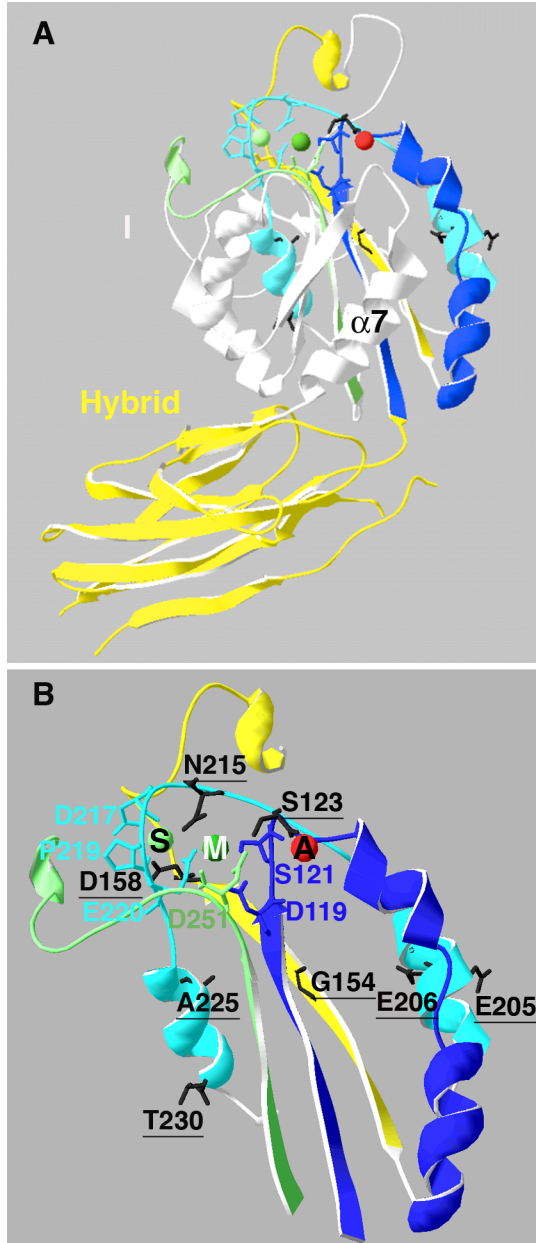


Fig. S3. Mutations reducing ligand binding map to MIDAS and SyMBS domains. *A.* Ribbon structure [from (28)] illustrating the location of the I and Hybrid (yellow) domains. Loops with residues that contribute to SyMBS, and MIDAS domains and the helices and β -strands flanking them are colored as are metal coordinating side chains. *B.* Enlarged MIDAS and SyMBS loops. β 1-loop- α 1,1' containing the MIDAS DXSXS (119-123) is in dark blue. β 4-loop- β 10 helix containing MIDAS D251 is green. SyMBS coordinating N215, D217, P219, and E220 (also a MIDAS residue) are between α 2 and α 3 (light blue). The loop following β 2 contributes SyMBS D158 (yellow). Amino acids corresponding to those mutated in *Drosophila* β PS and analyzed for ligand binding are labeled (black and underlined). E205 corresponds to the position of amino acids (following N204) that are inserted in *mys*^{b69} and *mys*^{b50}. Coloring of divalent cations is; SyMBS (S) Ca²⁺, light green; MIDAS (M) Mg²⁺, green; and ADMIDAS (A) Ca²⁺, red.