

Supplemental Figure S4

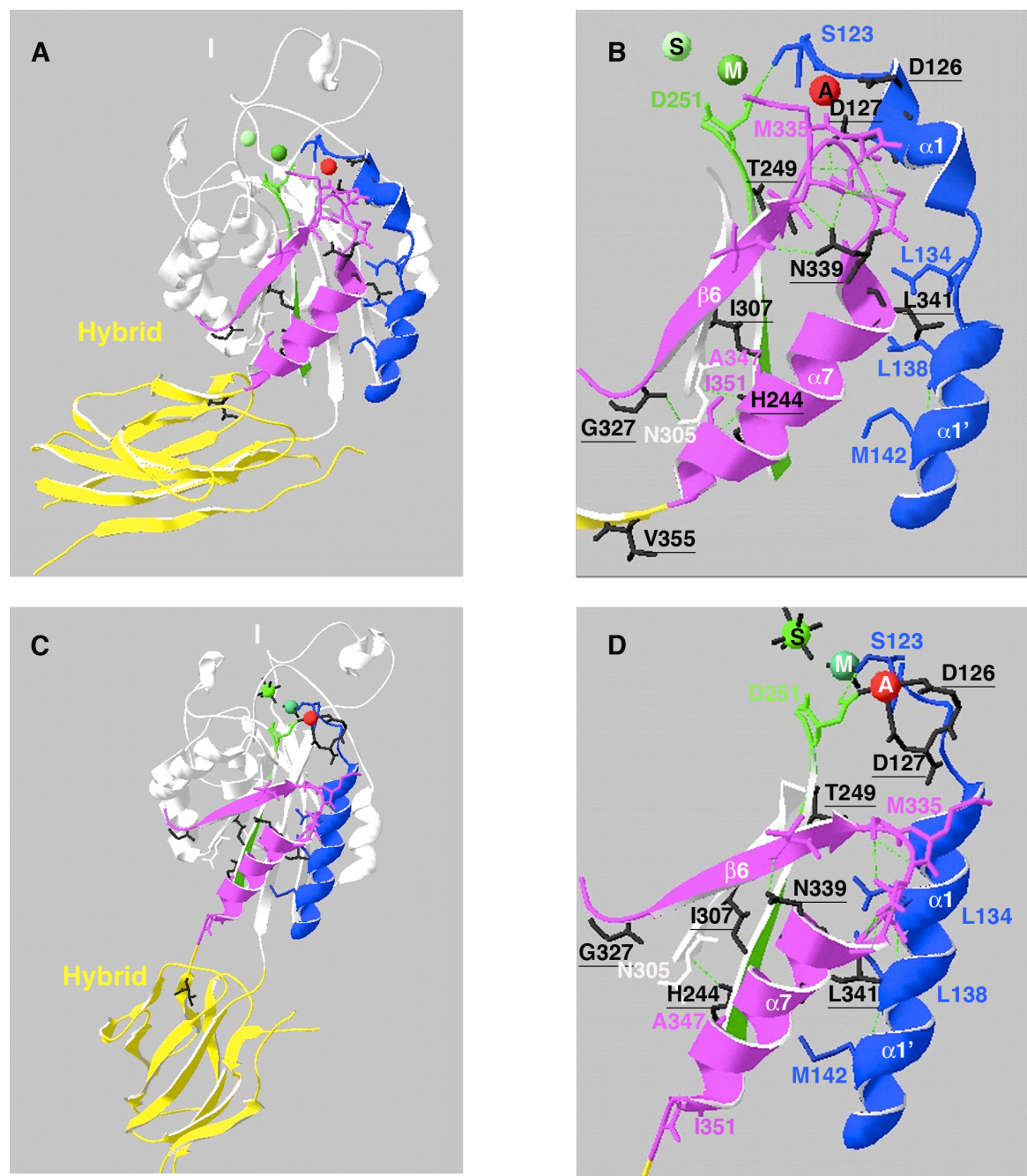


Fig. S4. Mutations that disrupt ADMIDAS increase ligand binding. *A* & *C*. Ribbon structure [from (28,30)] depicting the I and Hybrid (yellow) domains in the closed (*A*) and open (*C*) conformations. Loops with ADMIDAS coordinating residues are colored [loop- $\alpha 1,1'$ (blue), $\beta 6$ -loop- $\alpha 7$ (magenta), and $\beta 4$ -loop (green)] and expanded in *B* (closed) and *D* (open). Amino acids corresponding to those mutated in *Drosophila* β PS and analyzed for ligand binding are labeled (black and underlined). **D126**, **D127**, **M335**, and **D251** are ADMIDAS coordinating residues whose position relative to the ADMIDAS Ca^{2+} (A, red) are changed in the transition to the open state. The other divalent cations are SyMBBS Ca^{2+} (S, light green), and MIDAS Mg^{2+} (M, green). Hydrogen bonds are shown as green dashed lines in *B* and *D*.