

Supplemental Figure S9

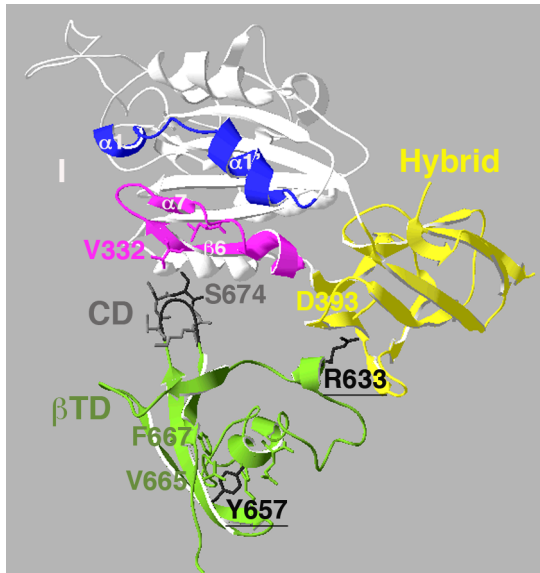


Fig. S9. β TD residues of $\beta 3$ in the closed conformation. The ribbon structure [from (29)] suggesting the “deadbolt” hypothesis (31) where the CD loop (gray) of the β TD domain (green), specifically **S674**, is located within 2.8 Å of **V332** of the $\beta 6$ strand. The $\beta 6$ - $\alpha 7$ (magenta) and $\alpha 1,1'$ (blue) of the $\beta 3$ integrin I domain (white) are highlighted as is the Hybrid domain (yellow). Residues mutated in the genetic screen *mys*^{b29} (F743>I;**Y657**) or in testing of the deadbolt hypothesis, **R633**, are labeled (underlined and in black). D393 in the Hybrid domain and within 3.5 Å of R633 is also shown. The side chains of CD loop residues deleted in testing deadbolt hypothesis are shown in gray but not labeled. The side chains of residues in the β strand prior to the CD loop and within 3.9 Å of **Y657** (**V665** and **F667**) are labeled.