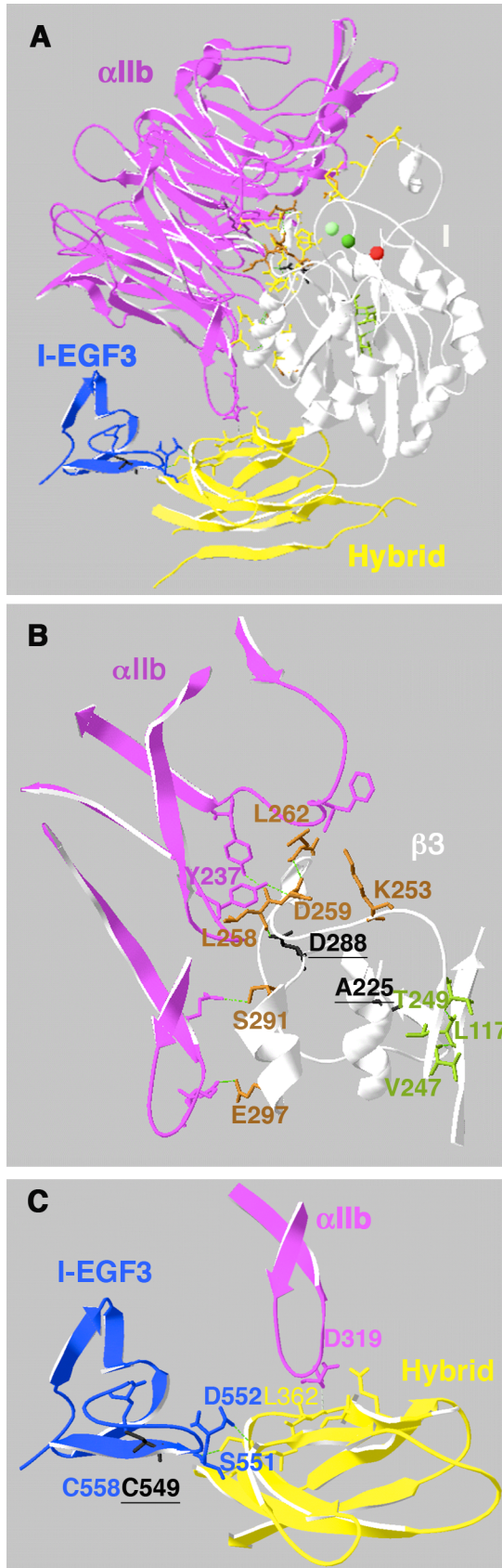


Supplemental Figure S1



**Fig. S1.** Mutants defective for expression are at the  $\alpha/\beta$  interface. *A.* Ribbon structure [from (28)] illustrating the location of the  $\alpha$ IIb head (magenta) the  $\beta$ 3 I (white), Hybrid (yellow) and I-EGF3 (blue) domains. SyMBS  $\text{Ca}^{2+}$  (light green), MIDAS  $\text{Mg}^{2+}$  (green), and ADMIDAS  $\text{Ca}^{2+}$  (red) cations are shown in the I domain. Side chains of  $\beta$  residues that are within 3 Å of  $\alpha$  are shown (brown) as are those within 3.5 Å (yellow). Side chains of the neighboring  $\alpha$  integrin residues are shown in magenta. *B.* Closer view of the interactions between  $\alpha$  and  $\beta$  in the region near **D288** and **A225** (black underlined; mutated in *mys*<sup>G12</sup> and *mys*<sup>b47</sup>). For simplicity, most contacts between 3 Å and 3.5 Å [including **R261** known to be key to  $\alpha/\beta$  interface (29)] have been removed and only the side chains of  $\beta$  amino acids within 3 Å of  $\alpha$  are shown (brown). **D288** precedes helix  $\alpha$ 5 that contains the **S291** and **E297** contacts. **D288** also hydrogen bonds (green dashed lines) with the  $3_{10}$  helix residue **L258** that is hydrogen bonded to  $\alpha$ IIb **Y237** (magenta). **A225** is closest to (within 3.5 Å) **L117** (green) that contacts (within 3 Å) **V247** and **T249** (green) in  $\beta$ 4 that precedes the loop containing the close  $\alpha/\beta$  contact **K253** and leading to the  $3_{10}$  helix. *C.* Closer view of the loop formed by I-EGF3 cysteines **C549** (black underlined; mutated in *mys*<sup>XN101</sup>) and **C558**. Loop residues **S551** and **D552** contact Hybrid residues and Hybrid **L362** in the Hybrid domain is hydrogen bonded to  $\alpha$ IIb **D319** (magenta).