

Supplemental Figure S8

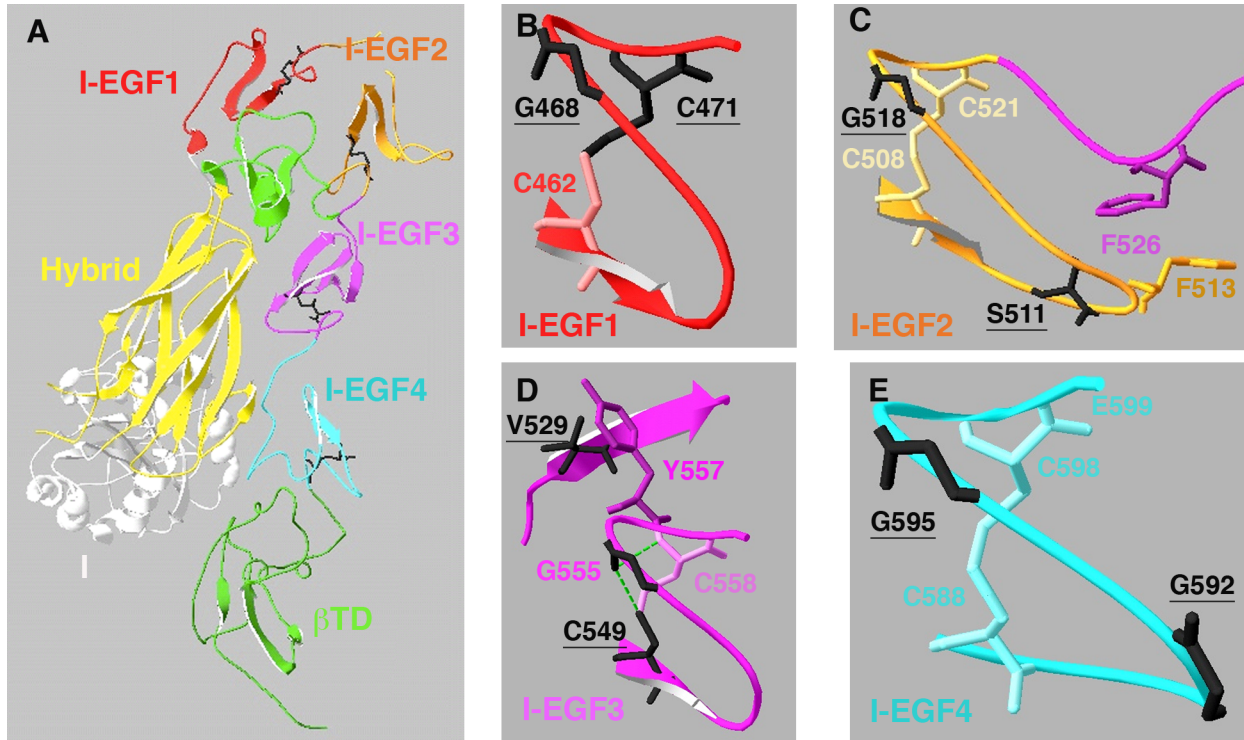


Fig. S8. Integrity of the I-EGF repeats' final disulfide loops maintains the low affinity conformation. *A*. Ribbon structure [from (28)] depicting the $\beta 3$ integrin I (white), Hybrid (yellow), I-EGF1 (red), I-EGF2 (orange), I-EGF3 (magenta), I-EGF4 (light blue) and the β TD (green) domains in the closed conformation. *B-E*. The final disulfide loop from each of the I-EGF repeats is shown with residues altered in mutants depicted in black and underlined. Disulfides are shown and labeled as is the highly conserved glycine three residues prior to the final cysteine. Note that 6 of the I-EGF repeat mutations are in either the final disulfide residues or in the glycine required for the final turn. Additionally, the *mys*^{b22}(R676>C;G592;*z*=5.9) mutation by introducing an additional unpaired cysteine may disrupt the disulfide in I-EGF4. Finally, *mys*^{b55}(R587>Q;S511;*z*=5.2) located in the first turn between C7-C8 in I-EGF2 is involved in positioning of I-EGF2/I-EGF3 junction as it, together with F513, is closely associated (within 3.5 Å) with F526 at the beginning of I-EGF3. The one activating I-EGF repeat mutation not in or contacting the final disulfide loop in the I-EGF repeats is *mys*^{b63}(G531>D;G458;*z*=4.6) and its location is shown in Fig. S2.