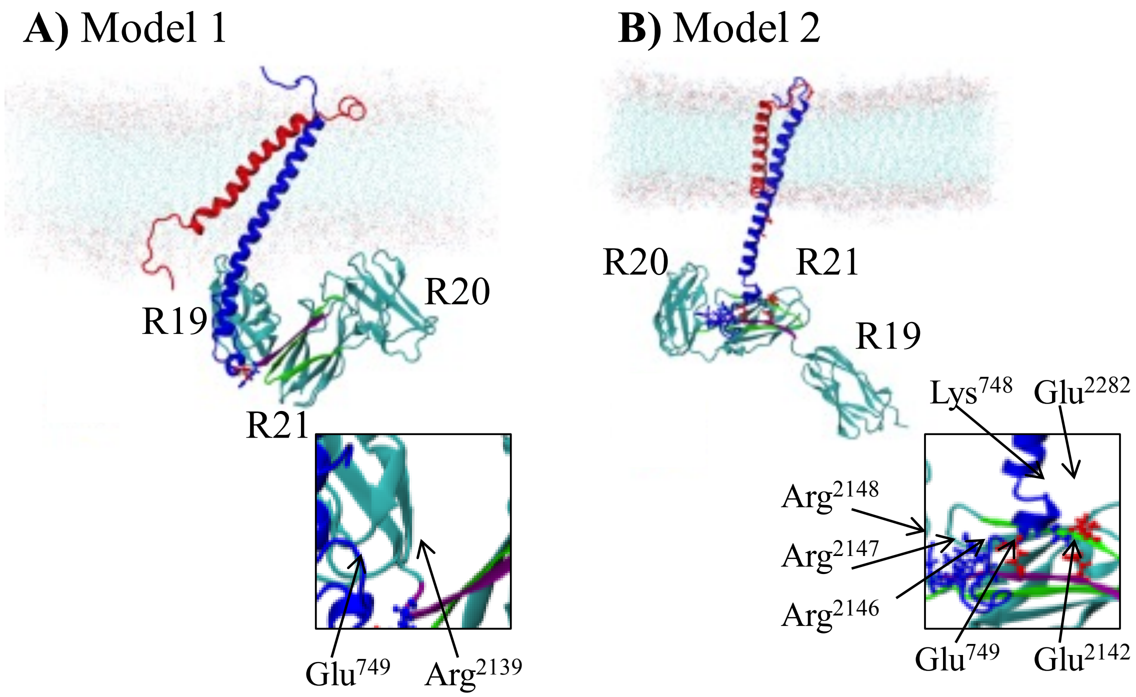
Supplementary Information:

Table S1 – The average energy of interaction across each trial of Model 1 and Model 2

Trial Number	Average Interaction Energy Between Integrin and CD Face of FLNa21 (kcal/mol)	
	Model 1	Model 2
1	-9	7
2	1	-4
3	-15	-67
4	-8	0.14
5	0	-42
	Average Interaction Energy Between Integrin and Autoinhibitory FLNa20 (kcal/mol)	
	Model 1	Model 2
1	-7	-40
2	-20	-33
3	-64	-42
4	-5	-11
5	1	-103



. **Figure S1– A)** Model 1 reveals one stable interaction from one of five trials. This interaction is between the integrin β_3 cytoplasmic tail and the auto-inhibitory strand at Glu^{749} and Arg^{2139}, respectively. **B)** Model 2 reveals two interactions, and integrin interacts more strongly at the auto-inhibitory strand than at the IgFLNa21 CD face in all four of five trials that demonstrated binding. The stronger interaction is between Lys^{748} and Glu^{2142} on the auto-inhibitory strand or Glu^{2282} on the IgFLNa21 CD face. There is also a weak interaction between Glu^{749} and a basic region consisting of Arg$^{2146-2148}$. Acidic residues are shown in red, basic residues in blue. The auto-inhibitory strand is depicted in purple and the IgFLNa21 CD face in green.

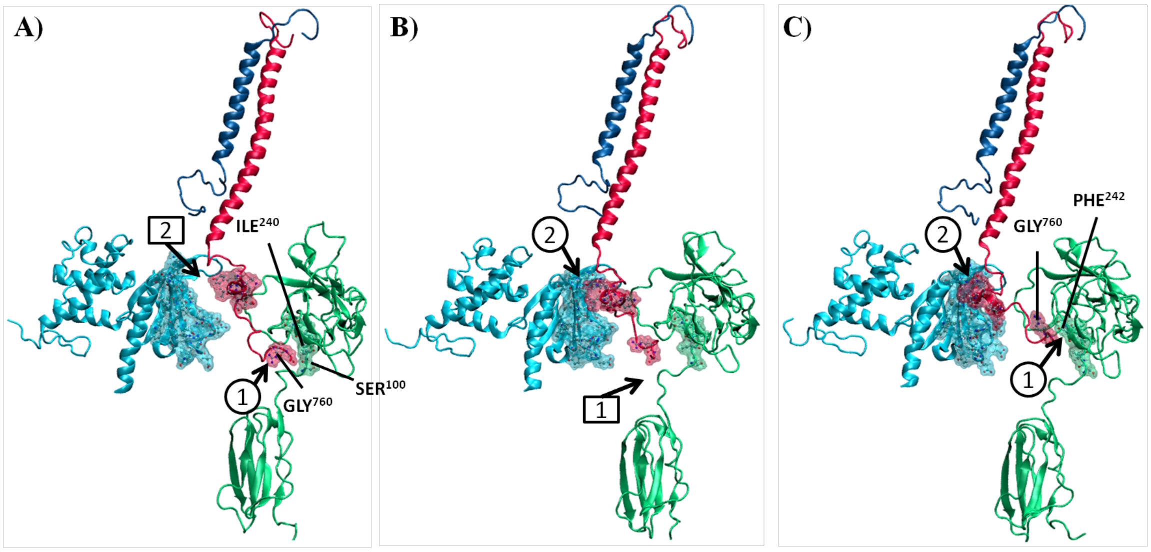


Figure S2 – The dynamics of filamin-bound simulations: A) In the beginning of simulations, GLY^{760} of β-integrin is associated with both SER^{100} and ILE^{240} of the distal portion of the CD face with respect to the lipid membrane (site 1). However, the small α-helix of β-integrin tail is not yet engaged with talin (site 2). B) As β-integrin binds talin, GLY^{760} is separated and pushed closer to the membrane and C) associates with PHE^{242} located on the proximal region of the filamin CD face. Circles and squares indicate association and dissociation, respectively.