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Supplemental Data

An Unusual Allosteric Mobility of the C-Terminal Helix of a High-Affinity α_L Integrin I Domain Variant Bound to ICAM-5

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Figure S1. Packing of ICAM-5/dm-I in the crystals

Symmetry related complexes are shown along a screw axis 2_1. α7 helix of the I domain swings out and fits into the groove of a symmetry related I domain.

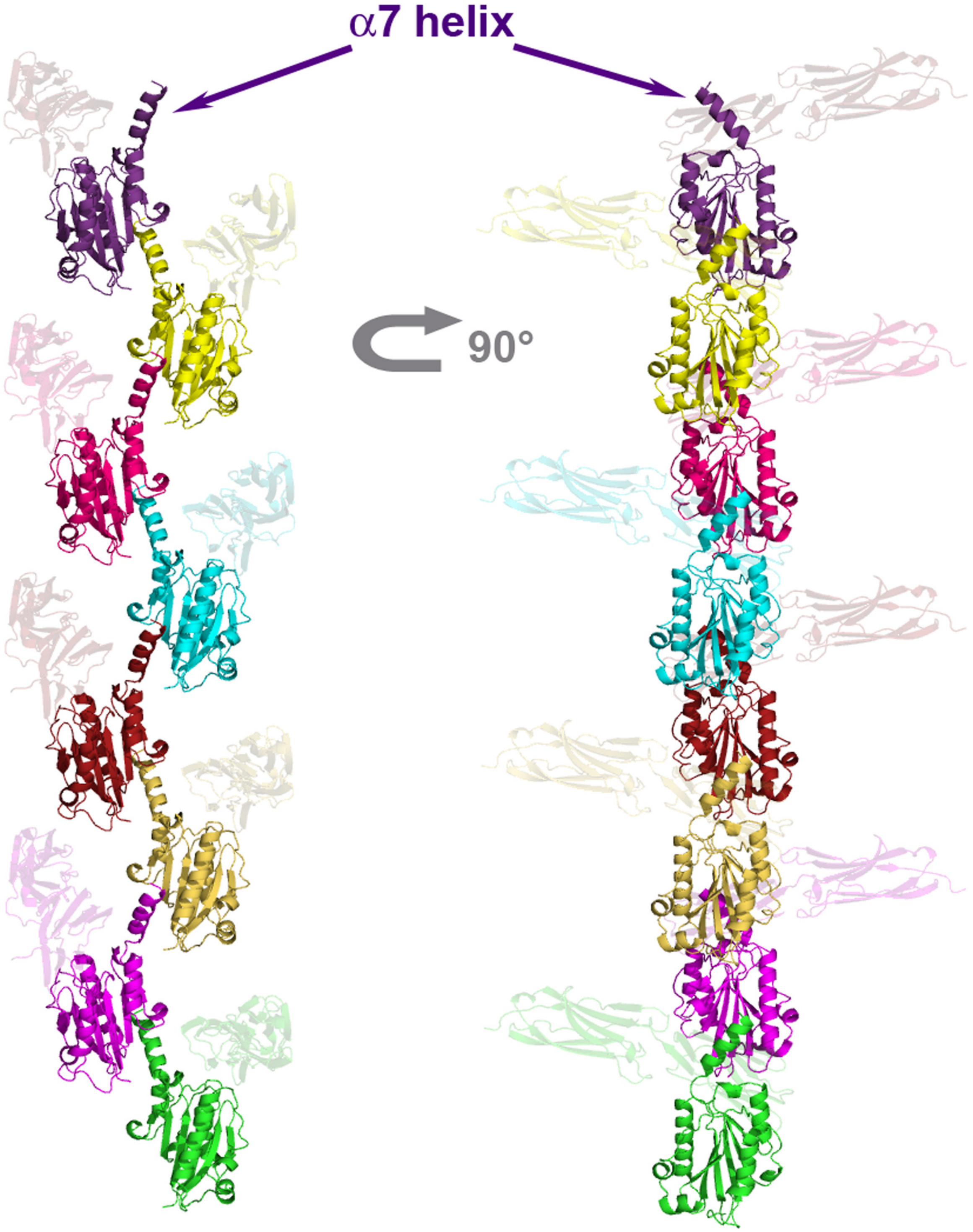
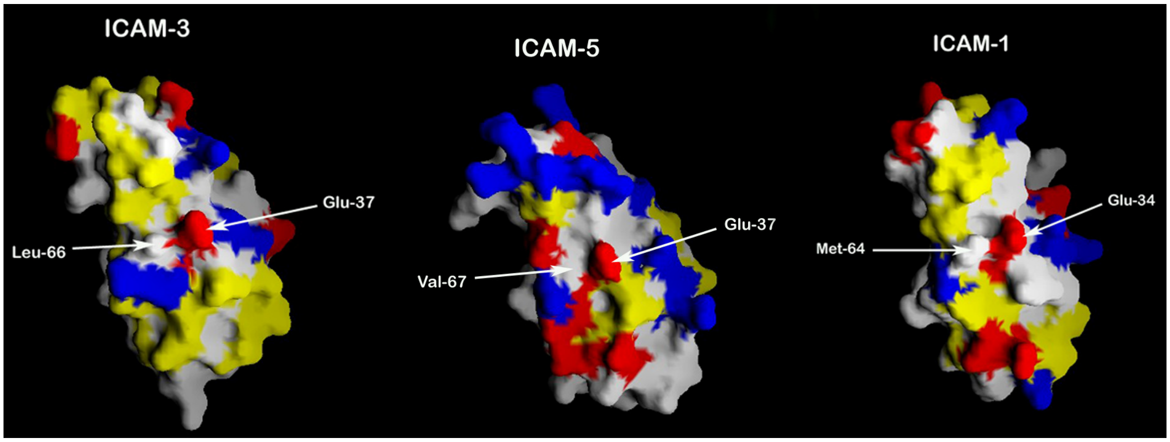

α7 helix
90°

Figure S2. Surface representations of the binding face of ICAM-1, ICAM-3 and ICAM-5

Negatively and positively charged residues are colored red and blue, respectively. Hydrophobic and neutral hydrophilic residues are colored grey and yellow, respectively. Some important residues are labeled. This figure is prepared with GRASP (Nicholls et al., 1991).



Supplemental Reference

Nicholls, A., Sharp, K.A., and Honig, B. (1991). Protein folding and association: insights from the interfacial and thermodynamic properties of hydrocarbons. Proteins *11*, 281–296.