Structure *19*

Supplemental Information

Relative Solvent Accessible Surface Area Predicts Protein Conformational Changes upon Binding

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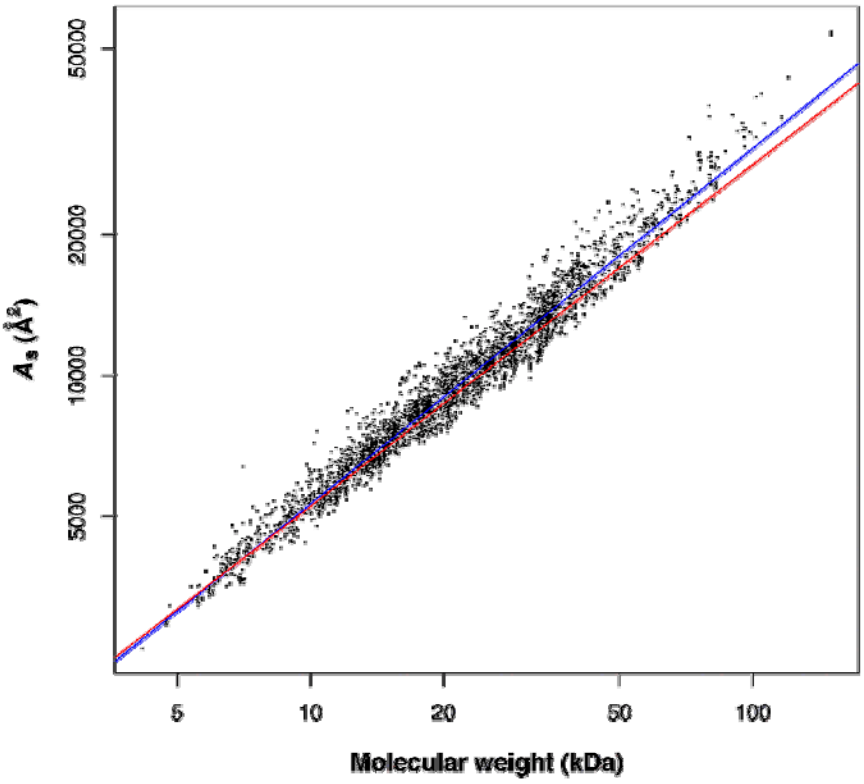

Figure S1, related to Figure 1. Relationship between protein molecular weight and solvent accessible surface area (A_s) for 4988 monomeric proteins. The blue line represents the fit in Equation 1 from this study, while the red line shows the fit derived in Miller et al. (1987a). These fits are very similar at low molecular weights but diverge above ~20 kDa due to the higher molecular weight proteins included in our study.

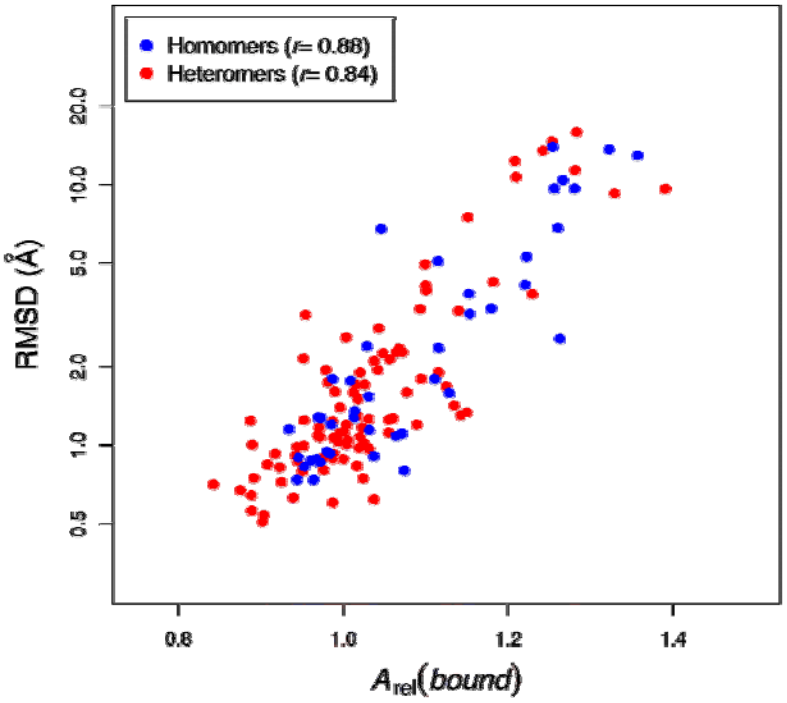

Figure S2, related to Figure 1. Correlation of $A_{rel}(bound)$ with RMSD for single-domain proteins as identified in SCOP 1.75 (Murzin et al., 1995).

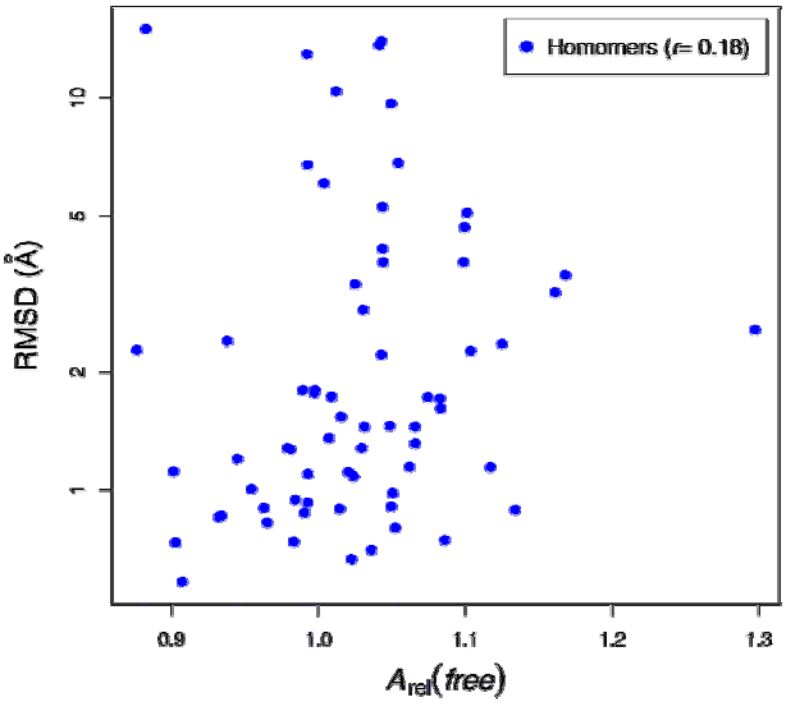

Figure S3, related to Figure 4. Comparison of $A_{rel}(free)$ values for monomeric proteins vs. RMSD between unbound and homomeric conformations.

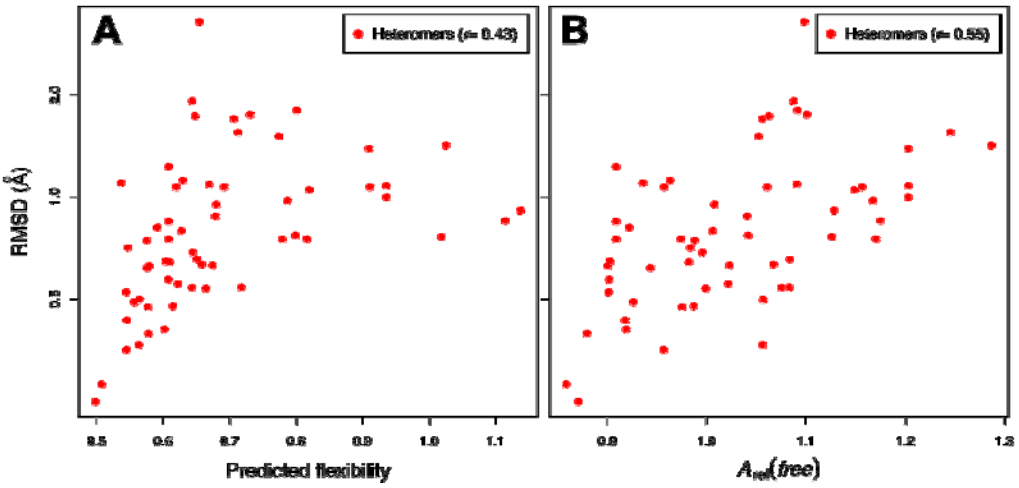

Figure S4, related to Figure 5. *(A)* Correlation between predicted flexibility from normal model analysis and RMSD for 60 monomeric proteins from Dobbins *et al*. *(B)* Correlation between A_{rel}(*free*) and RMSD for the same set of proteins.