Supporting Figures for:

Predicting evolutionary site variability from structure in viral proteins: buriedness, packing, flexibility, and design

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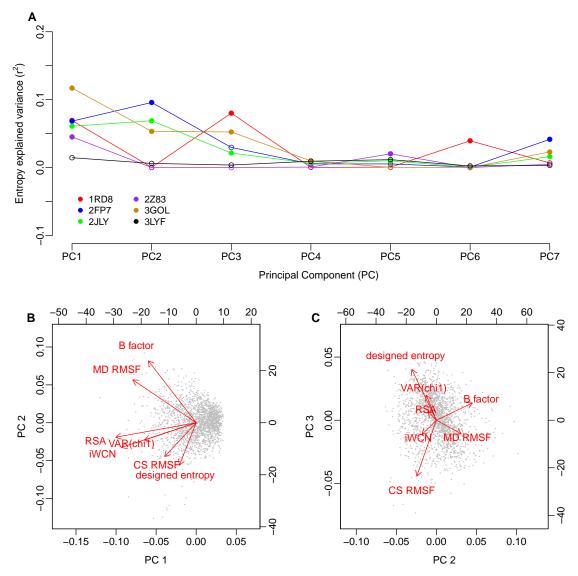


Fig. S1 Principal Component (PC) Regression of sequence entropy against the structural variables, including CS RMSF. (A) Variance in entropy explained by each principal component. For most proteins, PC1 and either PC2 or PC3 show the strongest correlations with sequence entropy. Significant correlations (P < 0.05) are shown as filled symbols, and insignificant correlations ($P \ge 0.05$) are shown as open symbols. (B) and (C) Composition of the three leading components. Red arrows represent the loadings of each of the structural variables on the principal components; black dots represent the amino acid sites in the PC coordinate system.

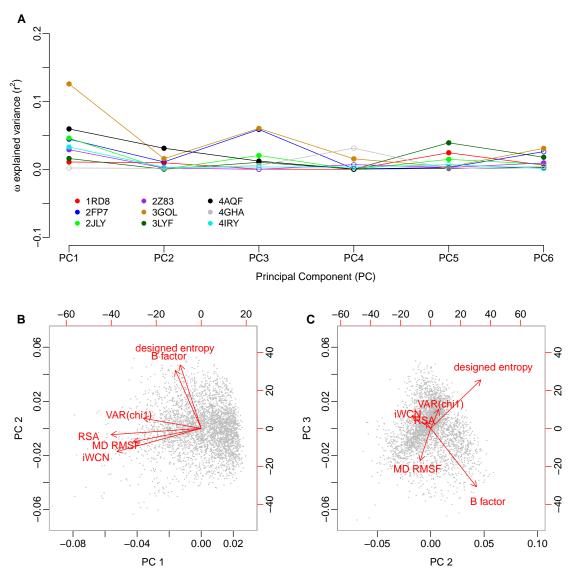


Fig. S2 Principal Component (PC) Regression of ω against the structural variables. (A) Variance in ω explained by each principal component. For most proteins, PC1 and PC3 show the strongest correlations with ω . Significant correlations (P < 0.05) are shown as filled symbols, and insignificant correlations ($P \ge 0.05$) are shown as open symbols. (B) and (C) Composition of the three leading components. Red arrows represent the loadings of each of the structural variables on the principal components; black dots represent the amino acid sites in the PC coordinate system. Note that parts B and C are identical to those shown in Figure 6.

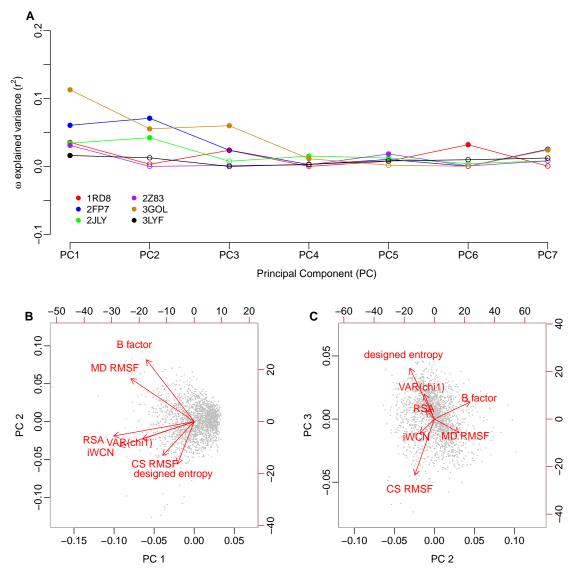


Fig. S3 Principal Component (PC) Regression of ω against the structural variables, including CS RMSF. (A) Variance in ω explained by each principal component. For most proteins, PC1 and either PC2 or PC3 show the strongest correlations with ω . Significant correlations (P < 0.05) are shown as filled symbols, and insignificant correlations ($P \ge 0.05$) are shown as open symbols. (B) and (C) Composition of the three leading components. Red arrows represent the loadings of each of the structural variables on the principal components; black dots represent the amino acid sites in the PC coordinate system. Note that parts B and C are identical to those shown in Figure S1.