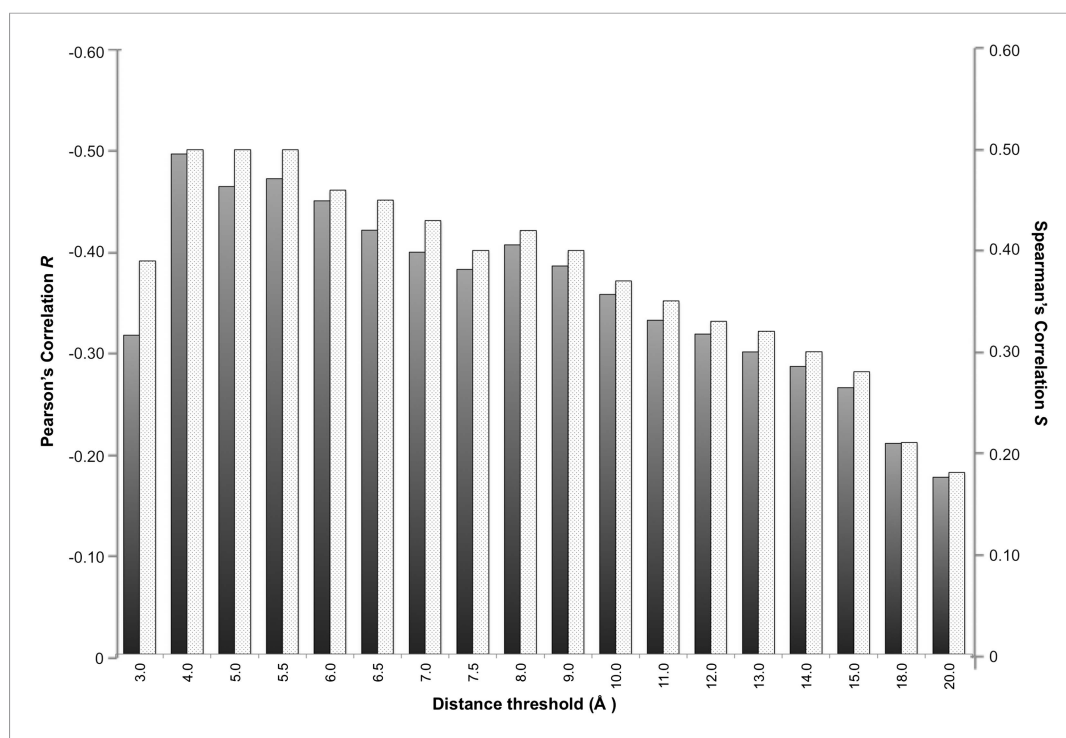


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## Figures and figure supplements

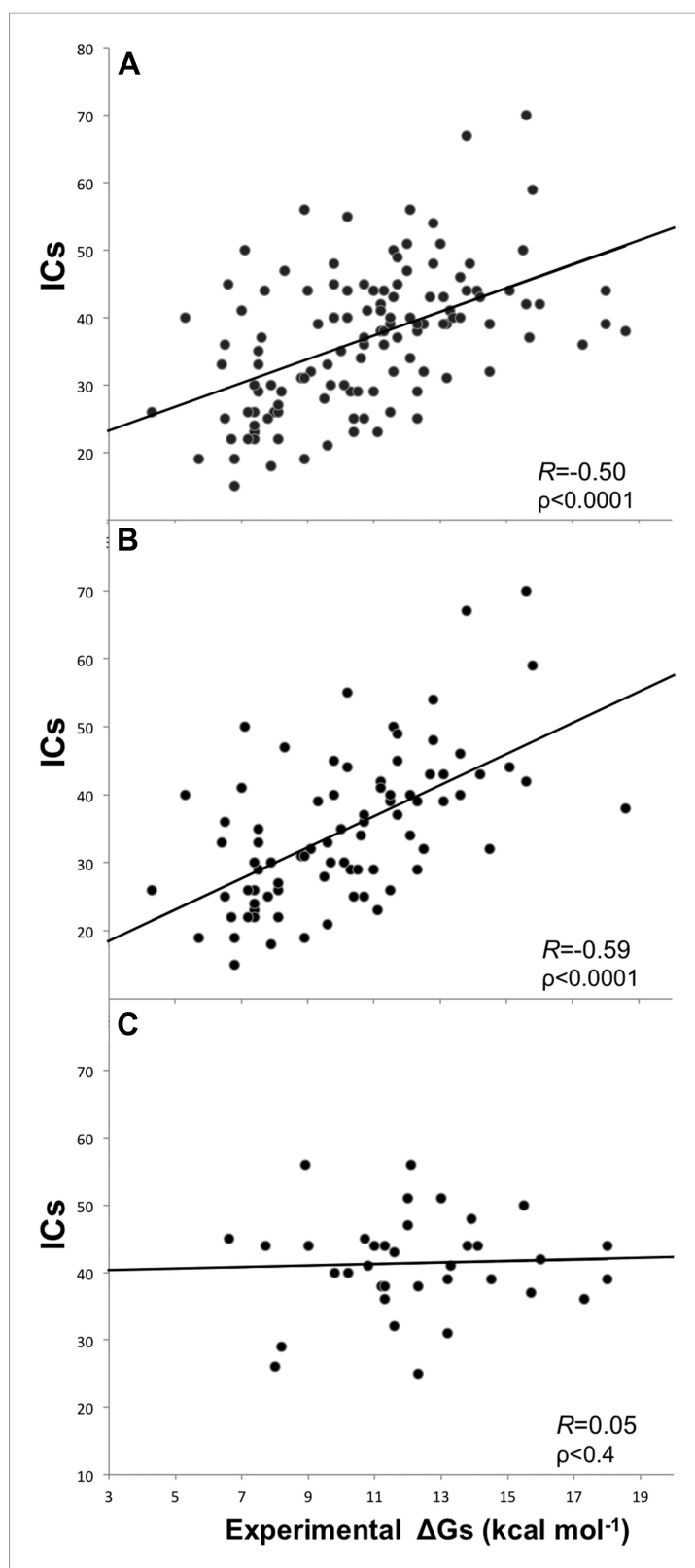
Contacts-based prediction of binding affinity in protein–protein complexes

**Anna Vangone and Alexandre MJJ Bonvin**



**Figure 1.** Correlation between number of inter-residue contacts and binding affinity ( $\Delta G$ s) as a function of the distance cut-off used to calculate the contacts. Both the Pearson's  $R$  (dark grey bars) and the Spearman's  $S$  (light grey-patterned bars) correlation coefficient are reported.

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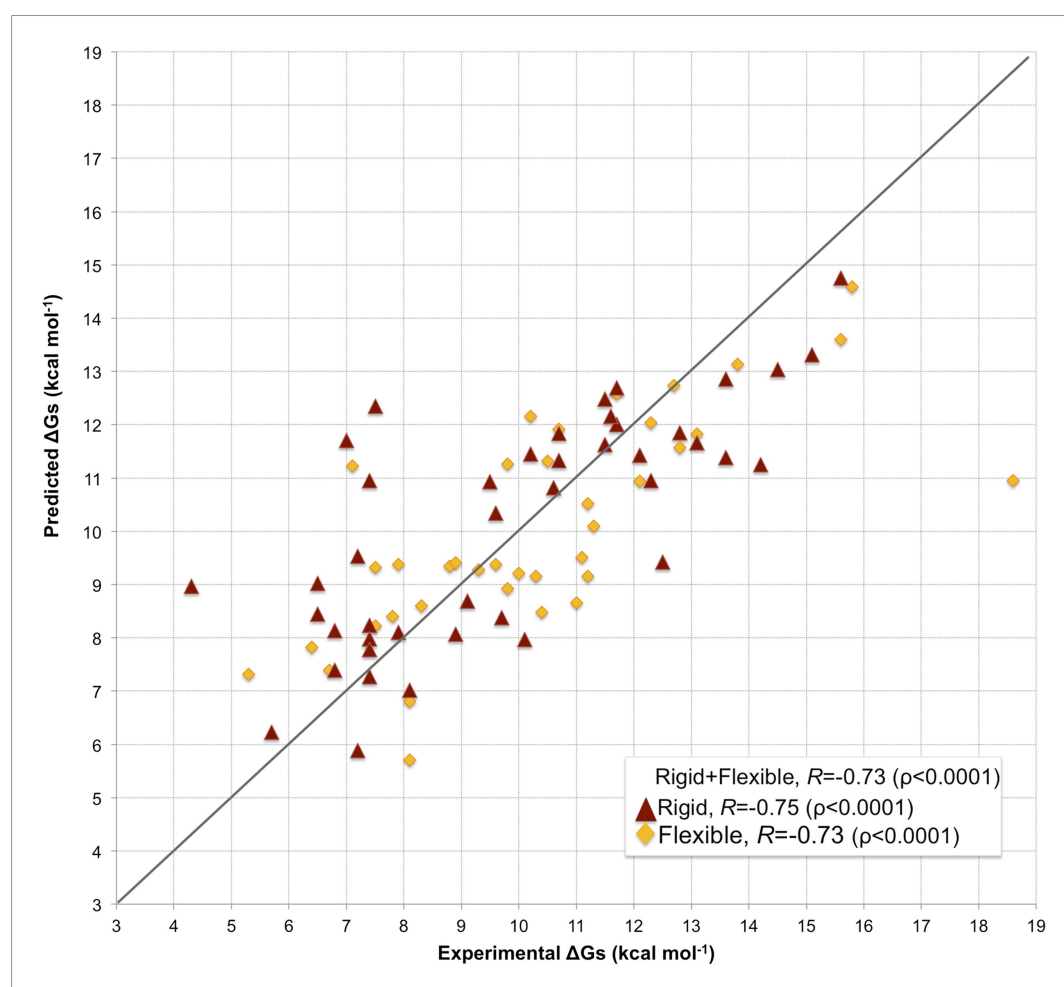


**Figure 2.** Plots of inter-residue contacts (ICs) vs experimentally determined binding affinities ( $\Delta G$ s) of protein–protein complexes. **(A)** Full dataset (122 complexes), **(B)** reliable experimental methods only (stopped-flow, surface plasmon resonance, spectroscopy, isothermal titration calorimetry) (81 complexes), and **(C)** non-reliable experimental methods (inhibition assay and fluorescence) (36 complexes). The trend line and corresponding Pearson

*Figure 2. continued on next page*

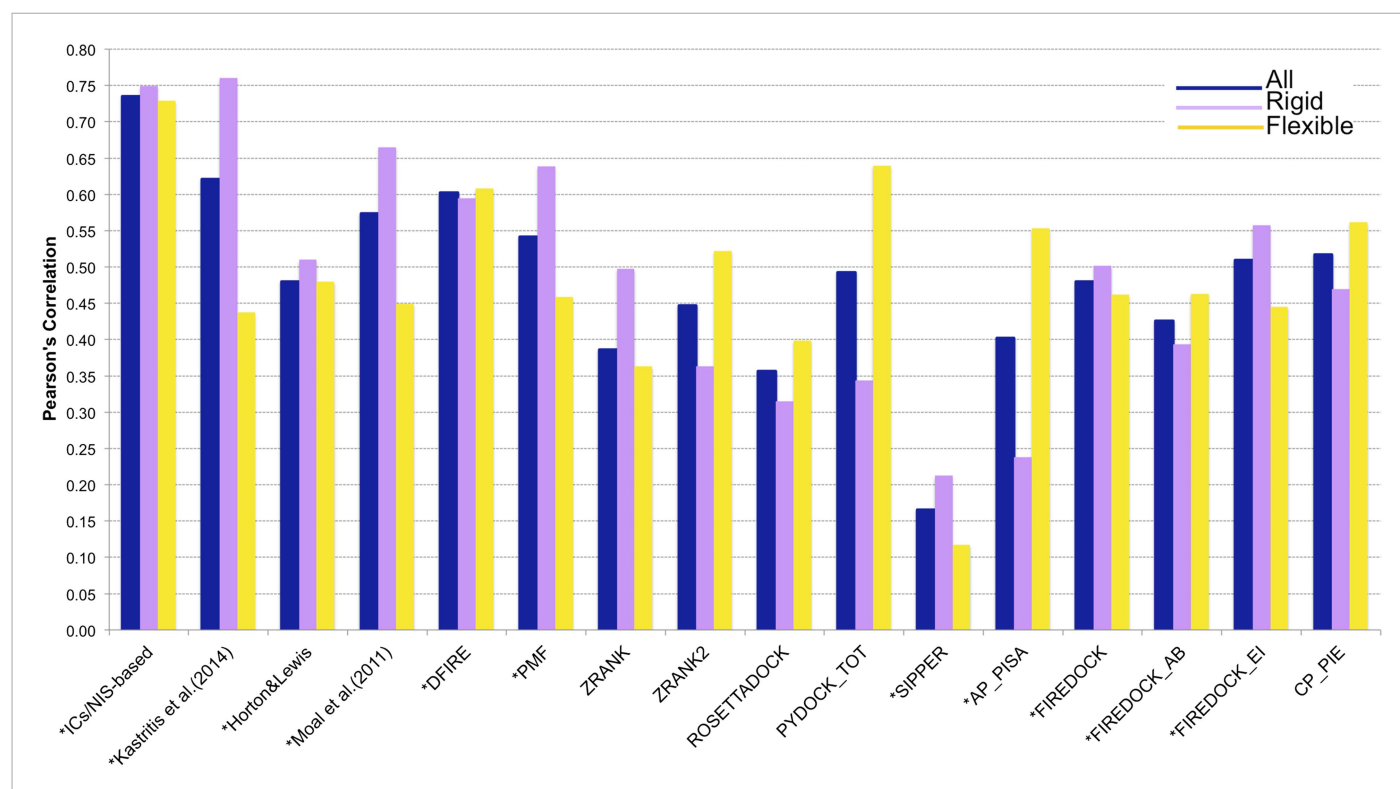
Figure 2. Continued

correlation coefficients and p-values ( $p$ ) are reported in each plot; binding affinities are reported as absolute values.  
DOI: [10.7554/eLife.07454.005](https://doi.org/10.7554/eLife.07454.005)



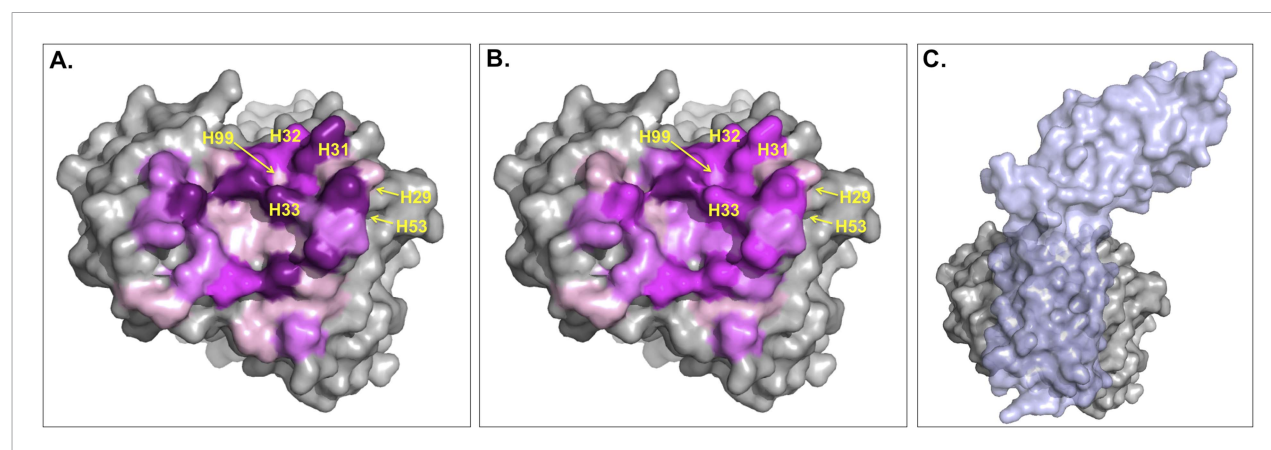
**Figure 3.** Scatter plot of predicted vs experimental binding affinities. The predictions were made according to the inter-residue contacts (ICs)/non-interacting surface (NIS)-based model (Model 6, Equation 2) for the cleaned dataset of 81 protein-protein complexes. The correlation for all 81 complexes yields an  $R$  of  $-0.73$  ( $p < 0.0001$ ) with a RMSE of  $1.89 \text{ kcal mol}^{-1}$ . When only rigid cases (interface RMSD between superimposed free and bound components  $\leq 1.0 \text{ \AA}$ , red triangles) are considered, the correlation increases to  $R = -0.75$  ( $p < 0.0001$ ) with a RMSE of  $1.88 \text{ kcal mol}^{-1}$ , while for flexible cases (interface RMSD  $> 1.0 \text{ \AA}$ ; yellow rhombus)  $R = -0.73$  ( $p < 0.0001$ ) with a RMSE of  $1.88 \text{ kcal mol}^{-1}$ . The  $x = y$  line is shown as reference; binding affinities are reported as absolute values.

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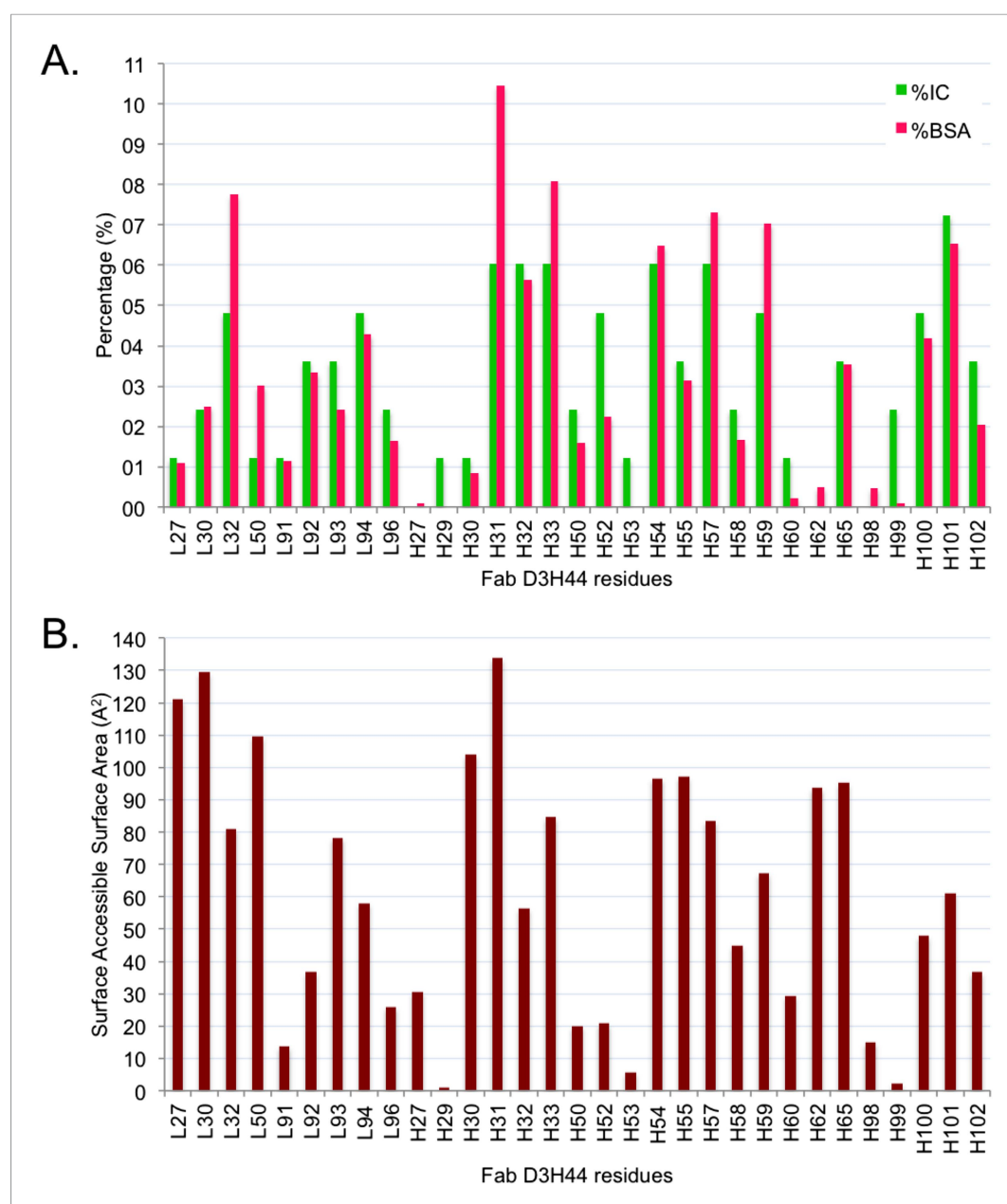
**Figure 4.** Comparison of the performance of our ICs/NIS-based model (Model 6, Equation 2) with other predictor models reported by *Moal et al. (2011)* and the CCharPPI (*Moal et al., 2015a, b*) webserver. The performance is expressed as Pearson's Correlation coefficient between experimental and predicted binding affinities. Predictions were made on the common set of 79 complexes between our cleaned dataset, the data tested by *Moal et al. (2011)* and the CCharPPI (*Moal et al., 2015a, b*) pre-calculated data. Correlations for the entire set and the rigid (43) and flexible (36) complexes are reported as absolute values for easier comparison (methods marked with asterisk showed original negative correlations).

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**Figure 5.** Surface representation of Fab D3H44; residues at the interface are colored according to their contribution (in percentage) to (A) the buried surface area (BSA) of Fab upon complex formation and (B) the total number of inter-residue contacts (ICs) made. Increasing graduation of pink is used for the ranges 0–2%, 2–4%, 4–6%, and above 6% of BSA/ICs contribution. (C) Surface representation of Fab D3H44 (gray) in complex with Tissue factor (light blue), PDB code: 1JPS (*Faelber et al., 2001*). Fab D3H44 is represented in all panels with the same orientation. Values of residues BSA/ICs contribution are reported in *Supplementary file 5*. The following figure supplement is available for *Figure 5*.

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**Figure 5—figure supplement 1.** Comparison between BSA and ICs relative contribution. **(A)** Relative contribution (percentage) of each Fab D3H44 interfacial residues to the total BSA (hot pink) and ICs (green). **(B)** Corresponding solvent-accessible surface area in Å<sup>2</sup> of the Fab D3H44 residues in the free form (separated proteins taken from the complex).

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