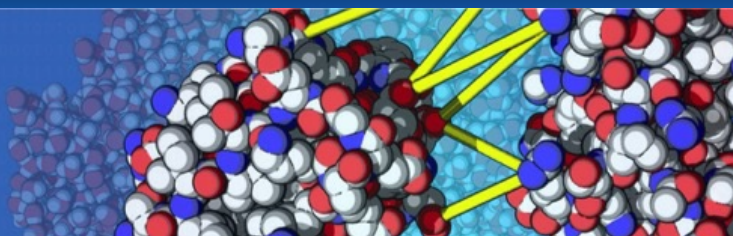


PRODIGY

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Your PRODIGY prediction has finished successfully.

Please note that the results will be deleted after two weeks.

To cite PRODIGY, please refer to:

Vangone A. and Bonvin A.M.J.J. "**Contact-based prediction of binding affinity in protein-protein complexes**", *eLife*, 4, e07454 (2015).

Xue L., Rodrigues J., Kastitis P., Bonvin A.M.J.J.*, Vangone A.*, "**PRODIGY: a web-server for predicting the binding affinity in protein-protein complexes**", *Bioinformatics*, doi:10.1093/bioinformatics/btw514.

For more information about the **predictive model** please check the [PRODIGY prediction method page](#).

Further information can be found in the [PRODIGY Manual](#) and an example of the PRODIGY output can be found [here](#).

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B I N D I N G P R A E F I C I E N T I I T O Y N A N D

The binding affinity (ΔG) and dissociation constant (K_d) predicted values are:

Protein-protein complex	ΔG (kcal mol ⁻¹)	K_d (M)
cluster2_1	-13.5	3.3e-10

Please note! The K_d is calculated at the default temperature of 25 °C, unless a different value has been provided in the input page -> Parameters

P R E D I C T I O N D E T A I L S

Number of Interfacial Contacts (ICs) per property:

ICs charged-charged:	14
ICs charged-polar:	16
ICs charged-apolar:	34
ICs polar-polar:	7
ICs polar-apolar:	28
ICs apolar-apolar:	27

Non Interacting Surface (NIS) per property:

%NIS charged:	32.93
%NIS apolar:	40.92

Table of the ICs at the interface:

[List of residue-residue pairs at the interface \(.txt\)](#)

D O W N L O A D O U T P U T S

[Pymol ICs-based representation script \(.pml\)](#)

[Archive file of all the outputs \(.tgz\)](#)

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