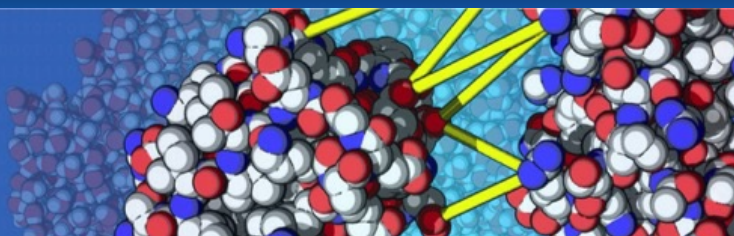


# PRODIGY

## @BonvinLab



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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., Kastiris 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 ( $\Delta G$ ) and dissociation constant ( $K_d$ ) predicted values are:

Protein-protein complex	$\Delta G$ (kcal mol <sup>-1</sup> )	$K_d$ (M)
cluster3_1	-14.4	7.2e-11

**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:	16
ICs charged-polar:	16
ICs charged-apolar:	37
ICs polar-polar:	8
ICs polar-apolar:	27
ICs apolar-apolar:	17

**Non Interacting Surface (NIS) per property:**

%NIS charged:	32.44
%NIS apolar:	36.67

**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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