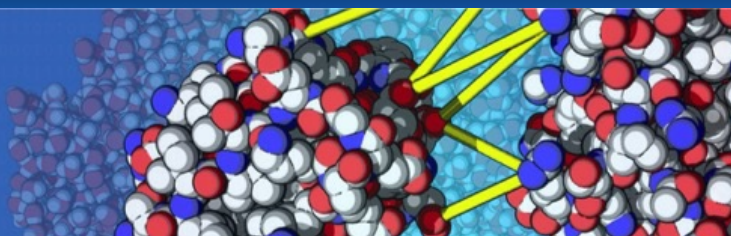


PRODIGY

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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) |
|-------------------------|--------------------------------------|-----------|
| cluster1_1 | -14.9 | 3.2e-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: | 20 |
| ICs charged-polar: | 24 |
| ICs charged-apolar: | 42 |
| ICs polar-polar: | 4 |
| ICs polar-apolar: | 23 |
| ICs apolar-apolar: | 27 |

Non Interacting Surface (NIS) per property:

| | |
|---------------|-------|
| %NIS charged: | 32.59 |
| %NIS apolar: | 37.92 |

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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