

HADDOCK2.2

WeNMR/West-Life GRID-enabled web portal

[WeNMR home](#) [West-Life home](#) [West-Life services](#) [HADDOCK2.2](#) [HADDOCK tutorials](#) [HADDOCK Support Center](#)

WELCOME TO THE UTRECHT BIOMOLECULAR INTERACTION WEB PORTAL >>

HADDOCK server status for docking run /5763854415/GSTTHETAMAPK8apo

Status: FINISHED

Your HADDOCK run has successfully completed. The complete run can be downloaded as a gzipped tar file [here](#) (Note that there might be a delay in the generation of this archive - in case of errors try again). The file containing your docking parameters is [here](#).

Please cite the following papers in your work:

- G.C.P van Zundert, J.P.G.L.M. Rodrigues, M. Trellet, C. Schmitz, P.L. Kastiris, E. Karaca, A.S.J. Melquiond, M. van Dijk, S.J. de Vries and A.M.J.J. Bonvin (2016). "The HADDOCK2.2 webserver: User-friendly integrative modeling of biomolecular complexes." *J. Mol. Biol.*, **428**, 720-725 (2015).
- Wassenaar et al., *WeNMR: Structural Biology on the Grid*. *J. Grid. Comp.*, **10**, 743-767 (2012).

And for the use of the WeNMR Grid resources please add the following acknowledgement:

"The FP7 WeNMR (project# 261572) and H2020 West-Life (project# 675858) European e-Infrastructure projects are acknowledged for the use of their web portals, which make use of the EGI infrastructure and the DIRAC4EGI service with the dedicated support of CESNET-MetaCloud, INFN-PADOVA, NCG-INGRID-PT, RAL-LCG2, TW-NCHC, IFCA-LCG2, SURFsara and NIKHEF, and the additional support of the national GRID Initiatives of Belgium, France, Italy, Germany, the Netherlands, Poland, Portugal, Spain, UK, South Africa, Malaysia, Taiwan and the US Open Science Grid."

Questions / feedback ? ask.bioexcel.eu

Please also consider giving us some feedback by filling our [online survey](#).

Summary

HADDOCK clustered **169** structures in **6** cluster(s), which represents **84.5 %** of the water-refined models HADDOCK generated. Note that currently the maximum number of models considered for clustering is 200.

The statistics of the top 10 clusters are shown below. The top cluster is the most reliable according to HADDOCK. Its Z-score indicates how many standard deviations from the average this cluster is located in terms of score (the more negative the better).

A [graphical representation](#) of the results is also provided at the bottom of the page.

C L U S T E R 2

HADDOCK score	-91.8 +/- 7.7
Cluster size	32
RMSD from the overall lowest-energy structure	1.0 +/- 0.8
Van der Waals energy	-96.5 +/- 11.6
Electrostatic energy	-516.7 +/- 40.9
Desolvation energy	10.8 +/- 4.1
Restraints violation energy	972.4 +/- 66.37
Buried Surface Area	2918.1 +/- 81.9
Z-Score	-1.2

Nr 1 best structure [Download structure](#)



Nr 2 best structure [Download structure](#)

Nr 3 best structure [Download structure](#)

Nr 4 best structure [Download structure](#)

C L U S T E R 3

HADDOCK score	-89.1 +/- 7.6
Cluster size	22
RMSD from the overall lowest-energy structure	6.2 +/- 0.2
Van der Waals energy	-91.8 +/- 5.9
Electrostatic energy	-531.0 +/- 58.1
Desolvation energy	27.5 +/- 11.2
Restraints violation energy	813.6 +/- 31.69
Buried Surface Area	3336.9 +/- 98.9
Z-Score	-1.1

Nr 1 best structure [Download structure](#)

Nr 2 best structure [Download structure](#)

Nr 3 best structure [Download structure](#)

Nr 4 best structure [Download structure](#)



C L U S T E R 1

HADDOCK score	-74.7 +/- 11.5
Cluster size	101
RMSD from the overall lowest-energy structure	21.4 +/- 0.7
Van der Waals energy	-80.9 +/- 9.4
Electrostatic energy	-330.2 +/- 71.2
Desolvation energy	-2.0 +/- 8.1
Restraints violation energy	741.9 +/- 165.15
Buried Surface Area	2869.6 +/- 201.9
Z-Score	-0.6

Nr 1 best structure [Download structure](#)

Nr 2 best structure [Download structure](#)

Nr 3 best structure [Download structure](#)

Nr 4 best structure [Download structure](#)



C L U S T E R 4

HADDOCK score	-33.3 +/- 16.4
Cluster size	5
RMSD from the overall lowest-energy structure	18.3 +/- 0.4
Van der Waals energy	-78.9 +/- 11.9
Electrostatic energy	-200.7 +/- 35.2
Desolvation energy	-2.0 +/- 9.7
Restraints violation energy	878.0 +/- 83.00
Buried Surface Area	2769.0 +/- 128.0
Z-Score	0.7

Nr 1 best structure [Download structure](#)

Nr 2 best structure [Download structure](#)

Nr 3 best structure [Download structure](#)

Nr 4 best structure [Download structure](#)



C L U S T E R 6

HADDOCK score	-22.2 +/- 28.6
Cluster size	4
RMSD from the overall lowest-energy structure	13.5 +/- 0.7
Van der Waals energy	-73.3 +/- 9.8
Electrostatic energy	-283.5 +/- 89.2

Desolvation energy	4.2 +/- 9.6
Restraints violation energy	1036.2 +/- 75.75
Buried Surface Area	2582.3 +/- 239.4
Z-Score	1.1

Nr 1 best structure [Download structure](#) 

Nr 2 best structure [Download structure](#)

Nr 3 best structure [Download structure](#)

Nr 4 best structure [Download structure](#)

C L U S T E R 5

HADDOCK score	-20.4 +/- 7.4
Cluster size	5
RMSD from the overall lowest-energy structure	17.3 +/- 0.3
Van der Waals energy	-72.2 +/- 4.9
Electrostatic energy	-300.4 +/- 16.2
Desolvation energy	9.9 +/- 7.2
Restraints violation energy	1019.9 +/- 114.06
Buried Surface Area	2768.5 +/- 136.1
Z-Score	1.1

Nr 1 best structure [Download structure](#) 

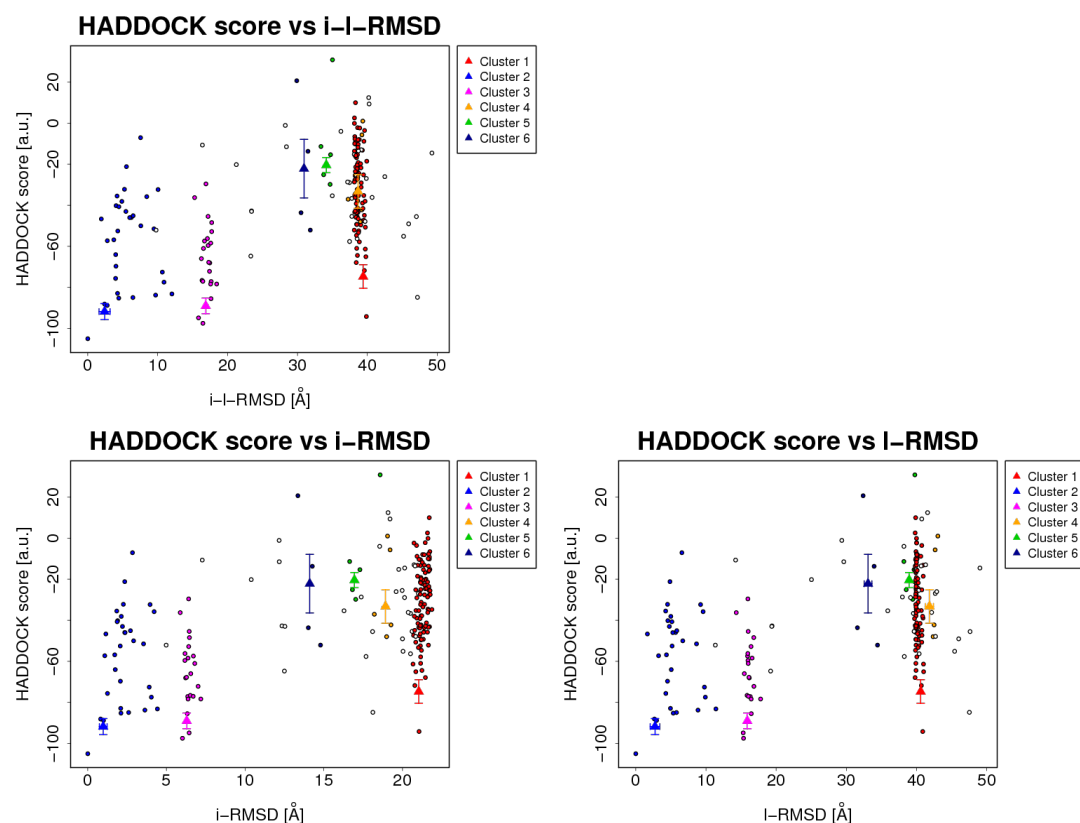
Nr 2 best structure [Download structure](#)

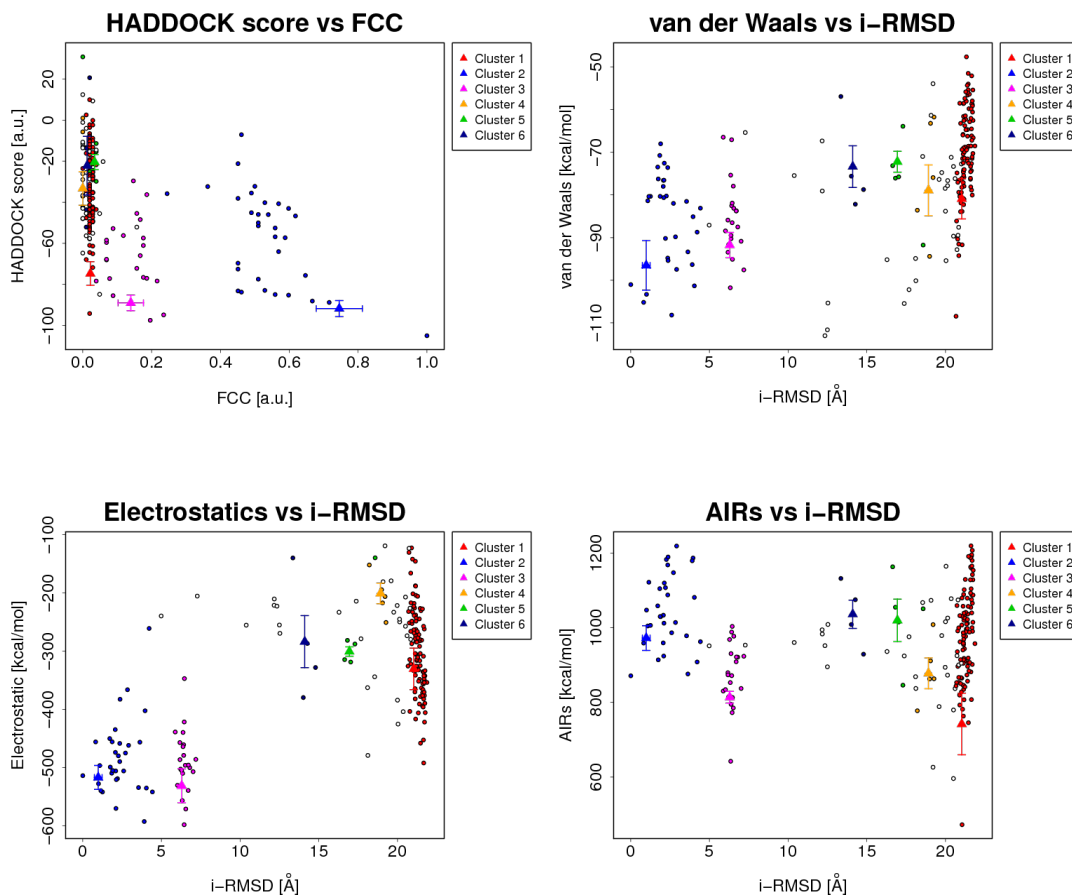
Nr 3 best structure [Download structure](#)

Nr 4 best structure [Download structure](#)

R E S U L T S A N A L Y S I S

The results and graphics presented below are based on water-refined models generated by HADDOCK. The clusters (indicated in color in the graphs) are calculated based on the interface-ligand RMSDs calculated by HADDOCK, with the interface defined automatically based on all observed contacts. The various structural analysis ([FCC](#), [i-RMSD](#) and [I-RMSD](#)) are made with respect to the best HADDOCK model (the one with the lowest HADDOCK score).





S U P P L E M E N T A R Y I N F O R M

i-RMSD -> interface-RMSD calculated on the backbone (CA,C,N,O,P) atoms of all residues involved in intermolecular contact using a 10Å cutoff

I-RMSD -> ligand-RMSD calculated on the backbone atoms (CA,C,N,O,P) of all (N>1) molecules after fitting on the backbone atoms of the first (N=1) molecule

FCC -> Fraction of common contacts. The intermolecular contacts are defined based on the best HADDOCK model using a 5Å cutoff (see [Rodrigues et al, Proteins 2012](#))

a.u. -> Arbitrary Units

The cluster averages and standard deviations are indicated by colored dots with associated error bars. The average values are calculated on the best 4 structures of each clusters (based on the HADDOCK score).

Note that HADDOCK results are deleted after one week.

[WeNMR home](#) [West-Life home](#) [West-Life services](#) [HADDOCK2.2](#) [HADDOCK tutorials](#)
[HADDOCK Support Center](#)

2008-2017 © Computational Structural Biology group. All rights reserved. Original webdesign by Marc van Dijk
 XHTML | CSS