HADDOCK 2.4

@Bonvinlab

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HADDOCK server status for job "cford_TCR-csp-8"

Status: FINISHED

Your HADDOCK run has successfully completed. The complete run can be downloaded as a gzipped tar file **here**.
The file containing your docking parameters is **here**.

Please cite the following paper in your work:

G.C.P van Zundert, J.P.G.L.M. Rodrigues, M. Trellet, C. Schmitz, P.L. Kastritis, 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).

and add the following acknowledgment:

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How would you rate your experience with our portal?

Questions / feedback ? ask.bioexcel.eu

Do check up the HADDOCK best practice guide! There you can learn more about which settings are best used in which scenario and use HADDOCK in its full potential!

In the aim to improve our new web portal, we would really appreciate 2 min of your time to complete a short survey here! Thanks!

Post-processing: SUCCESS

Summary

HADDOCK clustered **183** structures in **8** cluster(s), which represents **91 %** 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.

You can also download all cluster files (best 4 of the top 10 cluster(s)).

Cluster 1

HADDOCK score	-125.5 +/- 2.5
Cluster size	76
RMSD from the overall lowest-energy structure	0.6 +/- 0.4
Van der Waals energy	-95.0 +/- 4.2
Electrostatic energy	-238.8 +/- 13.5
Desolvation energy	1.1 +/- 2.0
Restraints violation energy	161.6 +/- 64.9
Buried Surface Area	2252.7 +/- 62.9
Z-Score	-1.7

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Nr 3 best structure Download file
Nr 4 best structure Download file

Cluster 3

HADDOCK score	-122.4 +/- 3.7
Cluster size	22
RMSD from the overall lowest-energy structure	8.6 +/- 0.4
Van der Waals energy	-80.5 +/- 5.0
Electrostatic energy	-273.6 +/- 13.4
Desolvation energy	-1.5 +/- 3.3
Restraints violation energy	143.4 +/- 17.7
Buried Surface Area	2205.9 +/- 43.9
Z-Score	-1.5

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Cluster 4

HADDOCK score	-94.2 +/- 1.3
Cluster size	18
RMSD from the overall lowest-energy structure	19.3 +/- 0.7
Van der Waals energy	-74.4 +/- 5.8
Electrostatic energy	-191.0 +/- 34.5
Desolvation energy	-3.4 +/- 2.4
Restraints violation energy	217.6 +/- 53.1
Buried Surface Area	2165.6 +/- 82.8

Z-Score	0.0

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Cluster 5

HADDOCK score	-93.4 +/- 0.8
Cluster size	18
RMSD from the overall lowest-energy structure	3.7 +/- 0.3
Van der Waals energy	-70.6 +/- 1.8
Electrostatic energy	-218.2 +/- 18.0
Desolvation energy	-5.9 +/- 3.3
Restraints violation energy	266.9 +/- 24.8
Buried Surface Area	1888.7 +/- 59.9
Z-Score	0.1

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Cluster 6

HADDOCK score	-92.7 +/- 6.6
Cluster size	10
RMSD from the overall lowest-energy structure	15.0 +/- 0.1
Van der Waals energy	-55.8 +/- 4.6
Electrostatic energy	-270.7 +/- 8.7
Desolvation energy	-2.6 +/- 2.7
Restraints violation energy	197.9 +/- 38.4
Buried Surface Area	1705.8 +/- 36.0
Z-Score	0.1

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Cluster 8

HADDOCK score	-83.2 +/- 5.1

Cluster size	5
RMSD from the overall lowest-energy structure	14.6 +/- 0.3
Van der Waals energy	-66.8 +/- 5.8
Electrostatic energy	-173.0 +/- 46.3
Desolvation energy	-8.5 +/- 2.2
Restraints violation energy	266.9 +/- 28.7
Buried Surface Area	2005.4 +/- 78.5
Z-Score	0.6

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Cluster 7

HADDOCK score	-79.9 +/- 7.4
Cluster size	9
RMSD from the overall lowest-energy structure	9.9 +/- 0.4
Van der Waals energy	-64.5 +/- 6.1
Electrostatic energy	-226.2 +/- 21.7
Desolvation energy	2.0 +/- 4.6
Restraints violation energy	278.6 +/- 27.4
Buried Surface Area	2001.3 +/- 113.2
Z-Score	0.8

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Cluster 2

HADDOCK score	-69.5 +/- 2.9
Cluster size	25
RMSD from the overall lowest-energy structure	17.4 +/- 0.2
Van der Waals energy	-54.2 +/- 2.0
Electrostatic energy	-157.8 +/- 27.9
Desolvation energy	-5.0 +/- 2.3
Restraints violation energy	211.7 +/- 39.4
Buried Surface Area	1804.6 +/- 59.7
Z-Score	1.4

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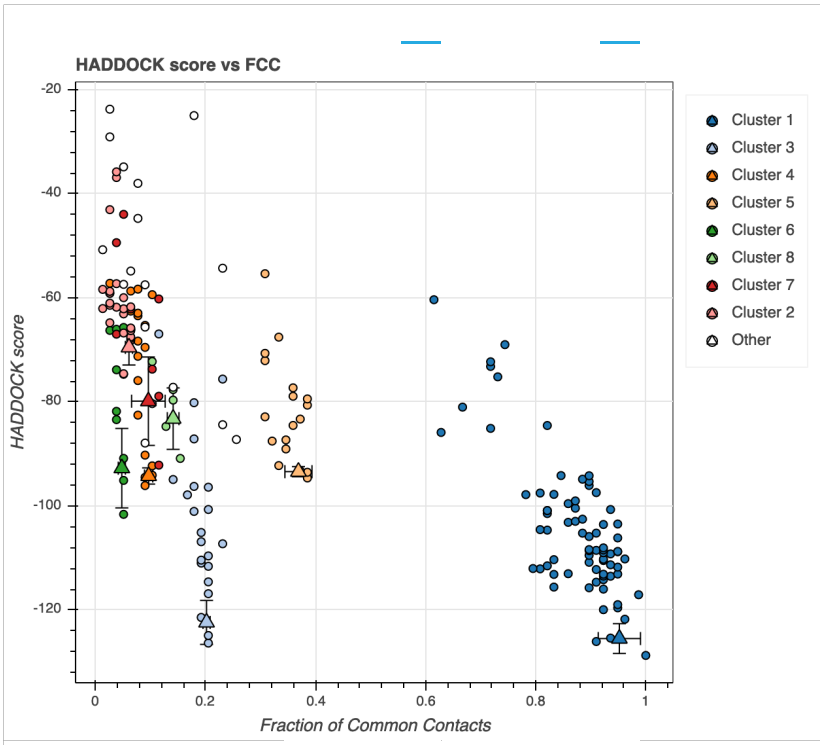
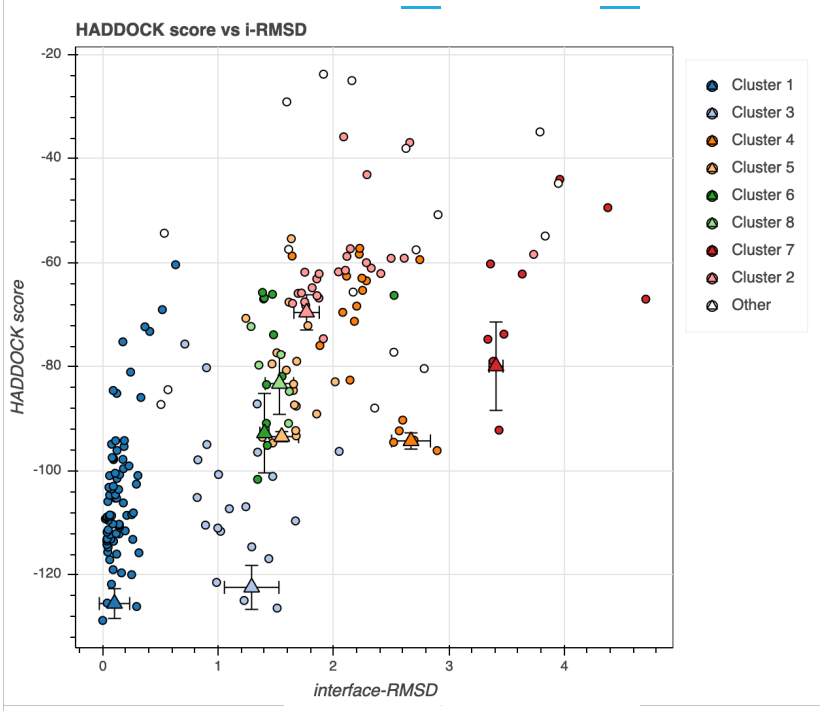
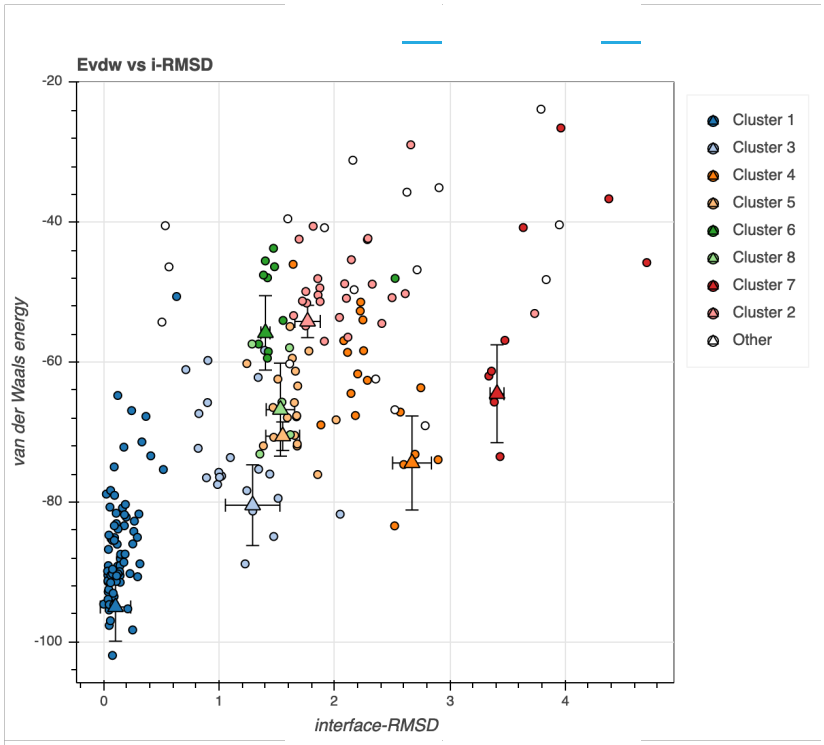
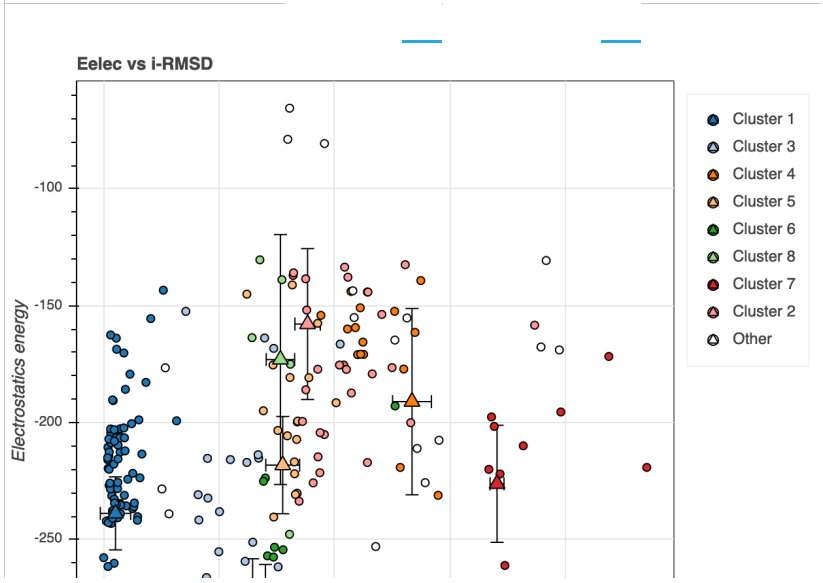
Model Analysis (Download all plots)

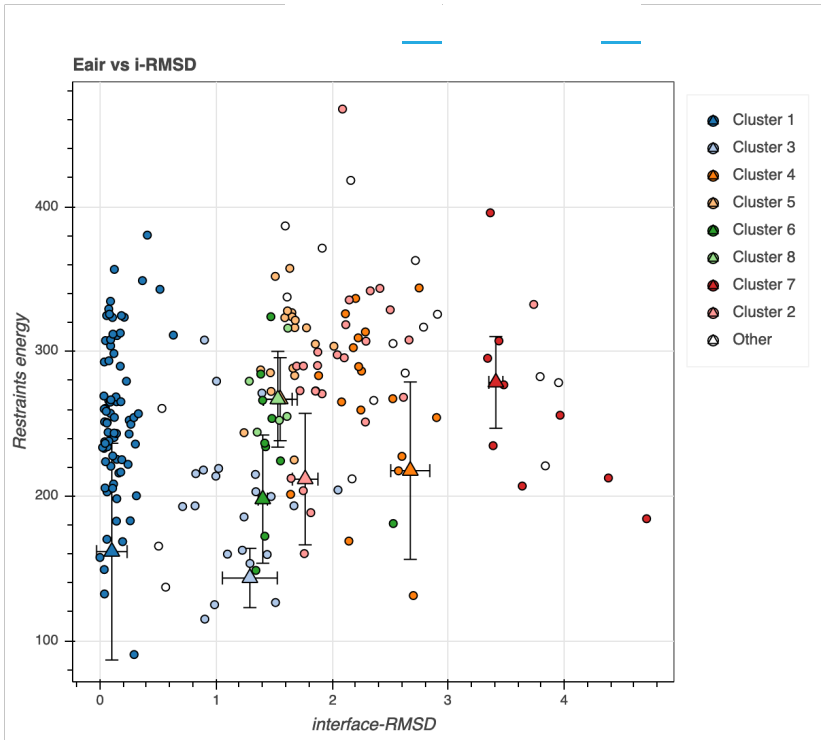
All | None | Cluster 1 | Cluster 3 | Cluster 4 | Cluster 5 | Cluster 6 | Cluster 8 | Cluster 7 | Cluster 2 | Oth





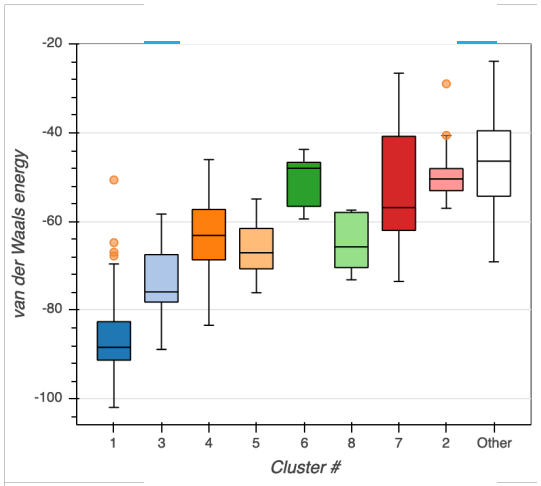

Evdw vs i-RMSD
van der Waals energy
interface-RMSD
-20
-40
-60
-80
-100
0
1
2
3
4
Cluster 1
Cluster 3
Cluster 4
Cluster 5
Cluster 6
Cluster 8
Cluster 7
Cluster 2
Other

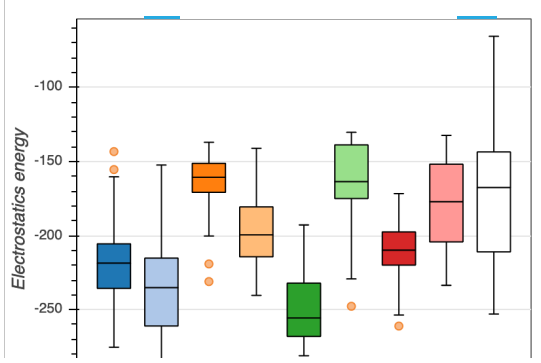

Eelec vs i-RMSD
Electrostatics energy
-100
-150
-200
-250
Cluster 1
Cluster 3
Cluster 4
Cluster 5
Cluster 6
Cluster 8
Cluster 7
Cluster 2
Other

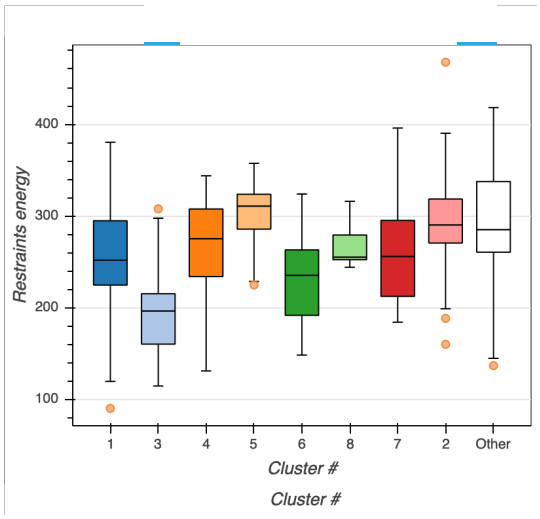


Cluster Analysis

All	None	Cluster 1	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 8	Cluster 7	Cluster 2	Oth






Restraints energy
400
300
200
100
1
3
4
5
6
8
7
2
Other
Cluster #
Cluster #