



Full wwPDB EM Validation Report ⓘ

Apr 15, 2026 – 12:48 PM UTC

PDB ID : 9HCJ / pdb_00009hcj
EMDB ID : EMD-19137
Title : D. discoideum nuclear pore complex
Authors : Obarska-Kosinska, A.; Hoffmann, P.C.; Beck, M.
Deposited on : 2024-11-10
Resolution : 30.00 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

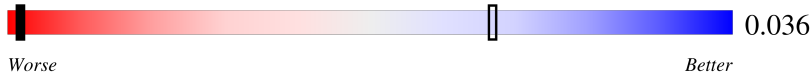
The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
MolProbity : **FAILED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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ELECTRON MICROSCOPY

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Q-score	25397	9 (30.00 - 30.30)

2 Entry composition

There are 25 unique types of molecules in this entry. The entry contains 579851 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called RanBP2-type zinc finger.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	00	780	Total	C	N	O	S	0	0
			6455	4104	1065	1269	17		
1	01	780	Total	C	N	O	S	0	0
			6455	4104	1065	1269	17		

- Molecule 2 is a protein called Nucleoporin 210.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	10	1788	Total	C	N	O	S	0	0
			13985	8854	2349	2747	35		
2	11	1788	Total	C	N	O	S	0	0
			13985	8854	2349	2747	35		
2	12	1788	Total	C	N	O	S	0	0
			13985	8854	2349	2747	35		
2	13	1788	Total	C	N	O	S	0	0
			13985	8854	2349	2747	35		
2	14	1788	Total	C	N	O	S	0	0
			13985	8854	2349	2747	35		
2	15	1788	Total	C	N	O	S	0	0
			13985	8854	2349	2747	35		
2	16	1788	Total	C	N	O	S	0	0
			13985	8854	2349	2747	35		
2	17	1788	Total	C	N	O	S	0	0
			13985	8854	2349	2747	35		

- Molecule 3 is a protein called WD40 repeat-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	40	471	Total	C	N	O	S	0	0
			3808	2437	630	726	15		
3	41	471	Total	C	N	O	S	0	0
			3808	2437	630	726	15		

- Molecule 4 is a protein called Nuclear pore protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A0	801	Total	C	N	O	S	0	0
			6619	4185	1119	1295	20		
4	A1	703	Total	C	N	O	S	0	0
			5782	3686	953	1126	17		
4	A2	703	Total	C	N	O	S	0	0
			5782	3686	953	1126	17		
4	A3	703	Total	C	N	O	S	0	0
			5782	3686	953	1126	17		
4	A4	703	Total	C	N	O	S	0	0
			5782	3686	953	1126	17		
4	A5	752	Total	C	N	O	S	0	0
			6200	3939	1040	1202	19		

- Molecule 5 is a protein called Nup188.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B0	1987	Total	C	N	O	S	0	0
			16130	10274	2663	3147	46		
5	B1	1987	Total	C	N	O	S	0	0
			16130	10274	2663	3147	46		

- Molecule 6 is a protein called Nup205.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C0	1399	Total	C	N	O	S	0	0
			11337	7257	1859	2166	55		
6	C1	1327	Total	C	N	O	S	0	0
			10779	6916	1760	2050	53		
6	C2	1327	Total	C	N	O	S	0	0
			10779	6916	1760	2050	53		
6	C3	1399	Total	C	N	O	S	0	0
			11337	7257	1859	2166	55		

- Molecule 7 is a protein called Nucleoporin 155.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D0	1283	Total	C	N	O	S	0	0
			10402	6662	1707	2006	27		
7	D1	1283	Total	C	N	O	S	0	0
			10402	6662	1707	2006	27		
7	D2	1283	Total	C	N	O	S	0	0
			10402	6662	1707	2006	27		

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Mol	Chain	Residues	Atoms					AltConf	Trace
7	D3	1283	Total	C	N	O	S	0	0
			10402	6662	1707	2006	27		

- Molecule 8 is a protein called NDC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E0	595	Total	C	N	O	S	0	0
			4959	3273	784	885	17		
8	E1	595	Total	C	N	O	S	0	0
			4959	3273	784	885	17		

- Molecule 9 is a protein called Nup35.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F0	95	Total	C	N	O	S	0	0
			783	506	124	149	4		
9	F1	95	Total	C	N	O	S	0	0
			783	506	124	149	4		
9	F2	95	Total	C	N	O	S	0	0
			783	506	124	149	4		
9	F3	95	Total	C	N	O	S	0	0
			783	506	124	149	4		

- Molecule 10 is a protein called Nuclear pore complex protein nup54.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	H0	245	Total	C	N	O	S	0	0
			2036	1295	343	388	10		
10	H1	245	Total	C	N	O	S	0	0
			2036	1295	343	388	10		
10	H2	245	Total	C	N	O	S	0	0
			2036	1295	343	388	10		
10	H3	245	Total	C	N	O	S	0	0
			2036	1295	343	388	10		

- Molecule 11 is a protein called Nup58.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	I0	197	Total	C	N	O	S	0	0
			1617	1031	271	310	5		
11	I1	197	Total	C	N	O	S	0	0
			1617	1031	271	310	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
11	I2	197	Total	C	N	O	S	0	0
			1617	1031	271	310	5		
11	I3	197	Total	C	N	O	S	0	0
			1617	1031	271	310	5		

- Molecule 12 is a protein called Nuclear pore protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	J0	189	Total	C	N	O	S	0	0
			1528	947	268	310	3		
12	J1	189	Total	C	N	O	S	0	0
			1528	947	268	310	3		
12	J2	184	Total	C	N	O	S	0	0
			1483	923	257	300	3		
12	J3	184	Total	C	N	O	S	0	0
			1483	923	257	300	3		
12	J4	184	Total	C	N	O	S	0	0
			1483	923	257	300	3		
12	J5	184	Total	C	N	O	S	0	0
			1483	923	257	300	3		

- Molecule 13 is a protein called Nucleoporin 133.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	K0	717	Total	C	N	O	S	0	0
			5814	3721	962	1114	17		
13	K1	717	Total	C	N	O	S	0	0
			5814	3721	962	1114	17		
13	K2	717	Total	C	N	O	S	0	0
			5814	3721	962	1114	17		
13	K3	717	Total	C	N	O	S	0	0
			5814	3721	962	1114	17		

- Molecule 14 is a protein called Nuclear pore complex protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	L0	796	Total	C	N	O	S	0	0
			6582	4170	1113	1280	19		
14	L1	796	Total	C	N	O	S	0	0
			6582	4170	1113	1280	19		
14	L2	796	Total	C	N	O	S	0	0
			6582	4170	1113	1280	19		

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Mol	Chain	Residues	Atoms					AltConf	Trace
14	L3	791	Total	C	N	O	S	0	0
			6547	4150	1108	1270	19		

- Molecule 15 is a protein called Nuclear pore complex protein Nup98-Nup96.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	M0	687	Total	C	N	O	S	0	0
			5650	3617	953	1071	9		
15	M1	687	Total	C	N	O	S	0	0
			5650	3617	953	1071	9		
15	M2	687	Total	C	N	O	S	0	0
			5650	3617	953	1071	9		
15	M3	687	Total	C	N	O	S	0	0
			5650	3617	953	1071	9		

- Molecule 16 is a protein called Protein SEC13 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	N0	301	Total	C	N	O	S	0	0
			2375	1512	408	447	8		
16	N1	301	Total	C	N	O	S	0	0
			2375	1512	408	447	8		
16	N2	301	Total	C	N	O	S	0	0
			2375	1512	408	447	8		
16	N3	301	Total	C	N	O	S	0	0
			2375	1512	408	447	8		

- Molecule 17 is a protein called Seh1.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	O0	311	Total	C	N	O	S	0	0
			2537	1599	437	485	16		
17	O1	311	Total	C	N	O	S	0	0
			2537	1599	437	485	16		
17	O2	311	Total	C	N	O	S	0	0
			2537	1599	437	485	16		
17	O3	311	Total	C	N	O	S	0	0
			2537	1599	437	485	16		

- Molecule 18 is a protein called Nuclear pore complex protein nup85.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	P0	755	Total	C	N	O	S	0	0
			6121	3868	1034	1188	31		
18	P1	755	Total	C	N	O	S	0	0
			6121	3868	1034	1188	31		
18	P2	755	Total	C	N	O	S	0	0
			6121	3868	1034	1188	31		
18	P3	755	Total	C	N	O	S	0	0
			6121	3868	1034	1188	31		

- Molecule 19 is a protein called Nuclear pore complex protein nup43.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Q0	373	Total	C	N	O	S	0	0
			2962	1863	499	587	13		
19	Q1	373	Total	C	N	O	S	0	0
			2962	1863	499	587	13		
19	Q2	373	Total	C	N	O	S	0	0
			2962	1863	499	587	13		
19	Q3	373	Total	C	N	O	S	0	0
			2962	1863	499	587	13		

- Molecule 20 is a protein called Nup160.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	R0	1790	Total	C	N	O	S	0	0
			14662	9233	2493	2889	47		
20	R1	1790	Total	C	N	O	S	0	0
			14662	9233	2493	2889	47		
20	R2	1790	Total	C	N	O	S	0	0
			14662	9233	2493	2889	47		
20	R3	1790	Total	C	N	O	S	0	0
			14662	9233	2493	2889	47		

- Molecule 21 is a protein called ELYS-like domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	T0	1057	Total	C	N	O	S	0	0
			8600	5500	1420	1662	18		
21	T1	1168	Total	C	N	O	S	0	0
			9517	6057	1583	1859	18		
21	T2	1168	Total	C	N	O	S	0	0
			9517	6057	1583	1859	18		

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Mol	Chain	Residues	Atoms					AltConf	Trace
21	T3	1168	Total	C	N	O	S	0	0
			9517	6057	1583	1859	18		

- Molecule 22 is a protein called Nuclear pore complex protein Nup98-Nup96.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	U0	25	Total	C	N	O	0	0
			201	122	36	43		
22	U1	25	Total	C	N	O	0	0
			201	122	36	43		
22	U2	25	Total	C	N	O	0	0
			201	122	36	43		
22	U3	25	Total	C	N	O	0	0
			201	122	36	43		

- Molecule 23 is a protein called WD40-like domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V0	258	Total	C	N	O	S	0	0
			2120	1306	381	429	4		
23	V1	258	Total	C	N	O	S	0	0
			2120	1306	381	429	4		

- Molecule 24 is a protein called Nup88.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W0	890	Total	C	N	O	S	0	0
			7264	4570	1217	1458	19		
24	W1	890	Total	C	N	O	S	0	0
			7264	4570	1217	1458	19		

- Molecule 25 is a protein called Nup205.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	X0	405	Total	C	N	O	S	0	0
			3312	2101	554	646	11		
25	X1	405	Total	C	N	O	S	0	0
			3312	2101	554	646	11		
25	X2	405	Total	C	N	O	S	0	0
			3312	2101	554	646	11		
25	X3	405	Total	C	N	O	S	0	0
			3312	2101	554	646	11		

MolProbity failed to run properly - this section is therefore empty.

3 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C8	Depositor
Number of subtomograms used	4921	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	130	Depositor
Minimum defocus (nm)	2500	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	11.923	Depositor
Minimum map value	-7.925	Depositor
Average map value	0.080	Depositor
Map value standard deviation	0.606	Depositor
Recommended contour level	1	Depositor
Map size ($\text{\AA}$)	2088.9602, 2088.9602, 2088.9602	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	8.704, 8.704, 8.704	Depositor

4 Model quality [i](#)

4.1 Standard geometry [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

4.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

4.6 Ligand geometry [i](#)

There are no ligands in this entry.

4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
9	F2	1
9	F0	1
9	F3	1
9	F1	1
20	R3	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	F2	174:GLU	C	380:LYS	N	105.57
1	F0	174:GLU	C	380:LYS	N	100.31
1	F3	174:GLU	C	380:LYS	N	42.15
1	F1	174:GLU	C	380:LYS	N	41.08
1	R3	188:GLY	C	189:SER	N	2.36

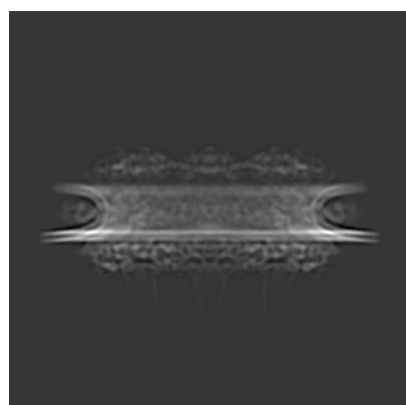
5 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-19137. These allow visual inspection of the internal detail of the map and identification of artifacts.

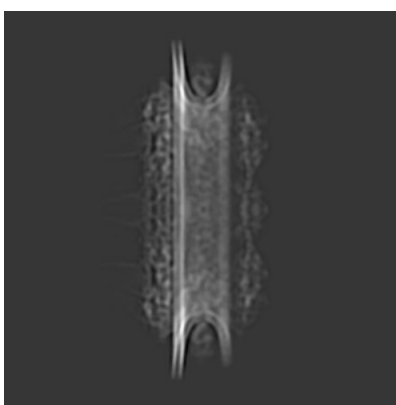
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

5.1 Orthogonal projections [i](#)

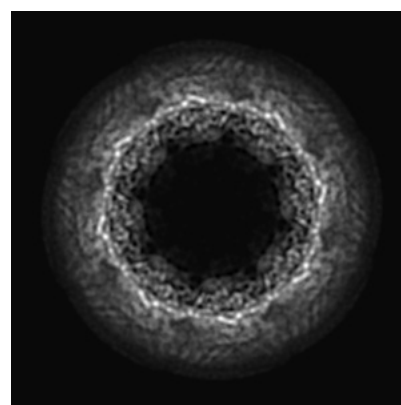
5.1.1 Primary map



X



Y



Z

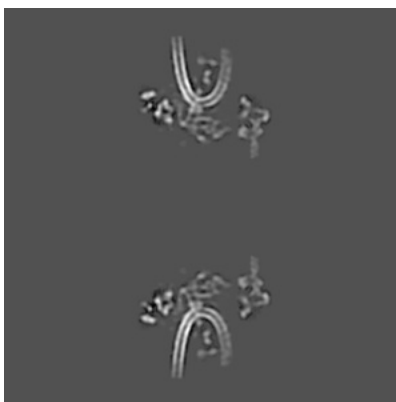
The images above show the map projected in three orthogonal directions.

5.2 Central slices [i](#)

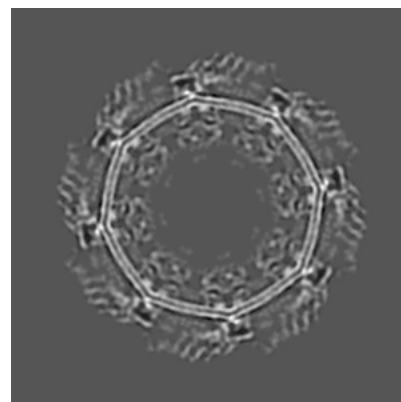
5.2.1 Primary map



X Index: 120



Y Index: 120



Z Index: 120

The images above show central slices of the map in three orthogonal directions.

5.3 Largest variance slices [i](#)

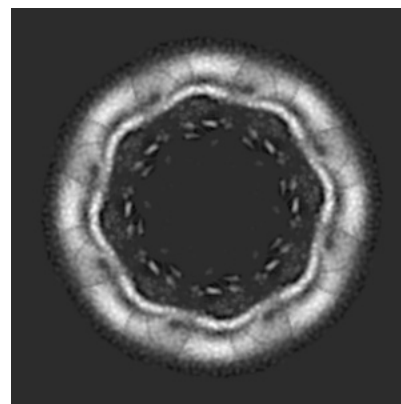
5.3.1 Primary map



X Index: 59



Y Index: 181



Z Index: 107

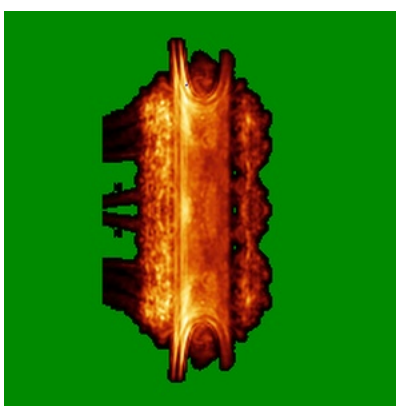
The images above show the largest variance slices of the map in three orthogonal directions.

5.4 Orthogonal standard-deviation projections (False-color) [i](#)

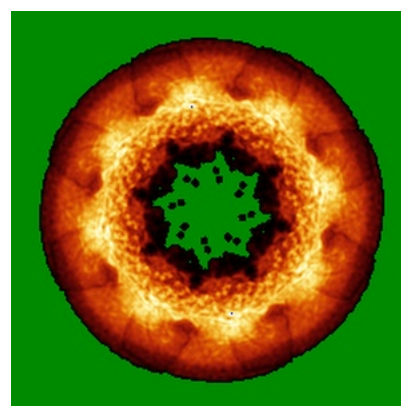
5.4.1 Primary map



X



Y

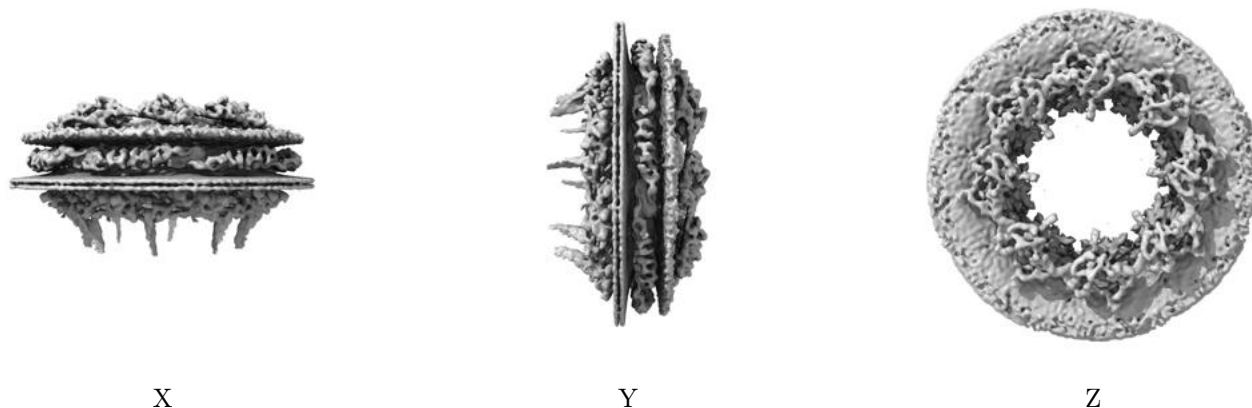


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

5.5 Orthogonal surface views [i](#)

5.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

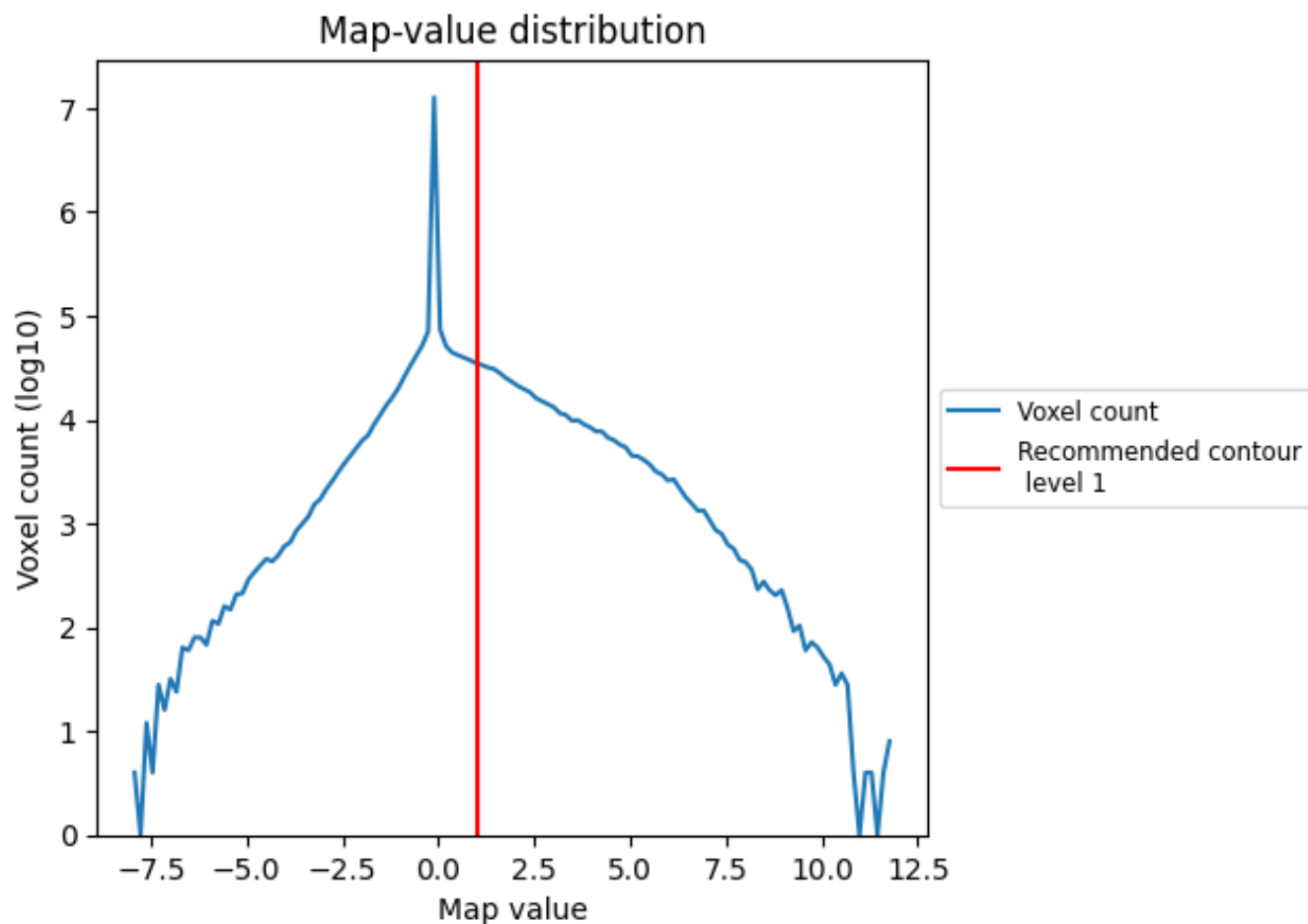
5.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

6 Map analysis [i](#)

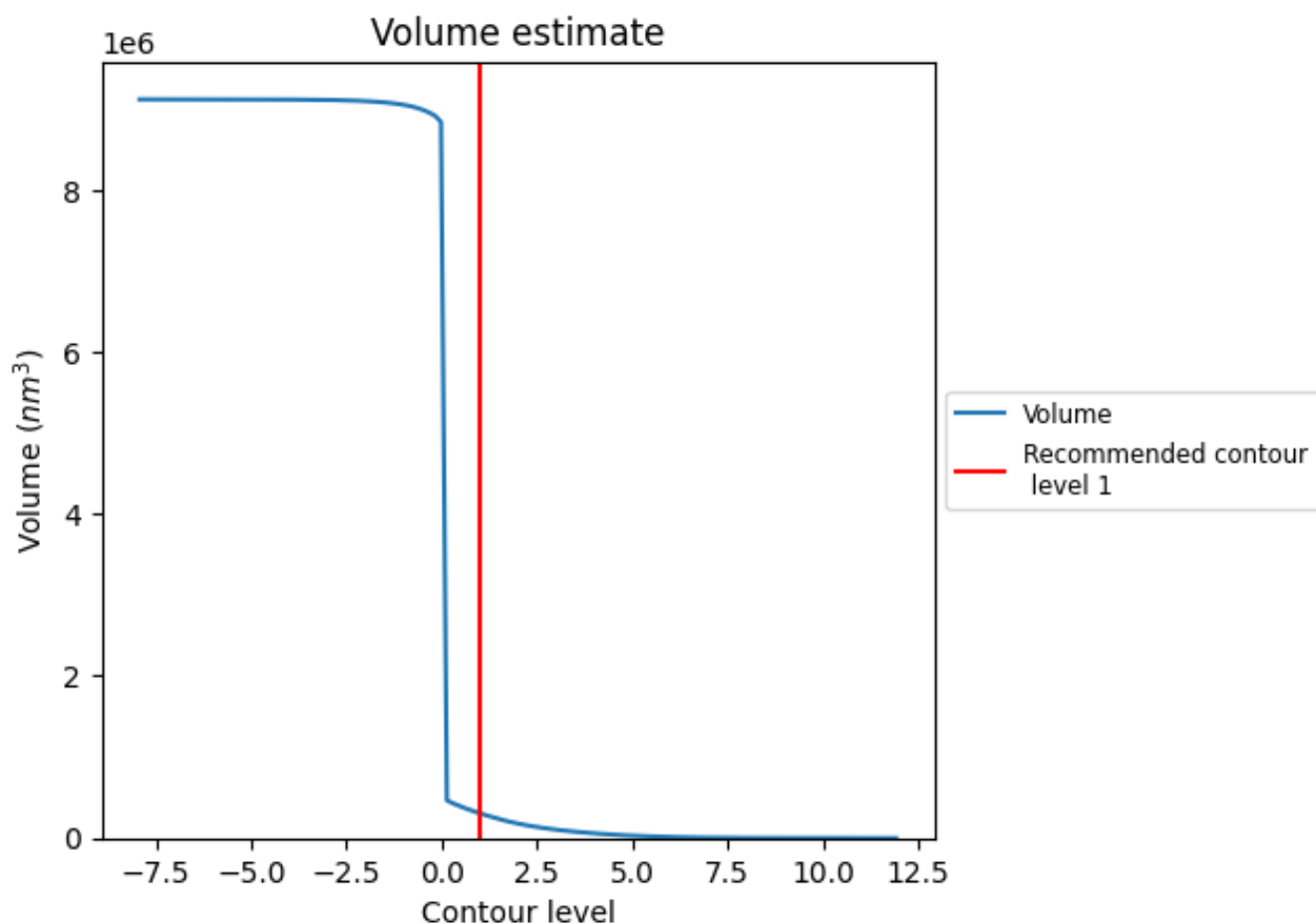
This section contains the results of statistical analysis of the map.

6.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

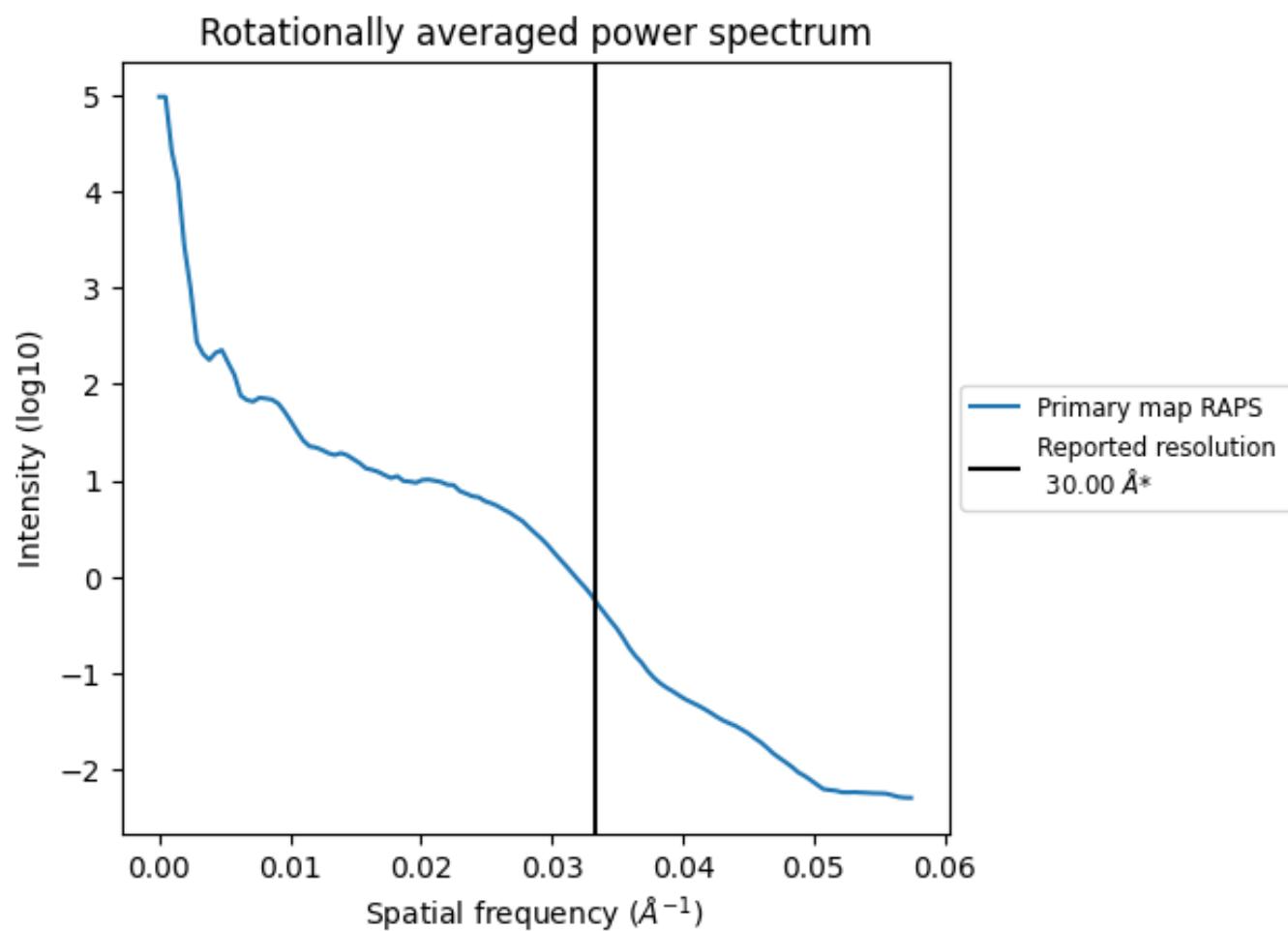
6.2 Volume estimate [i](#)



The volume at the recommended contour level is 306272 nm³; this corresponds to an approximate mass of 276664 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

6.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.033 Å⁻¹

7 Fourier-Shell correlation ⓘ

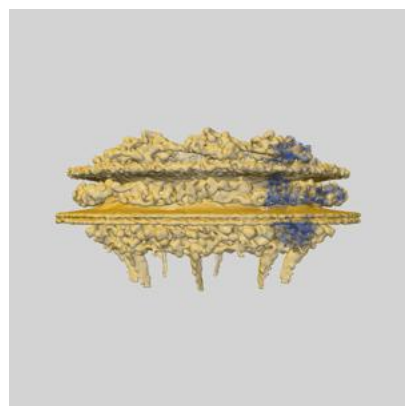
This section was not generated. No FSC curve or half-maps provided.

8 Map-model fit [i](#)

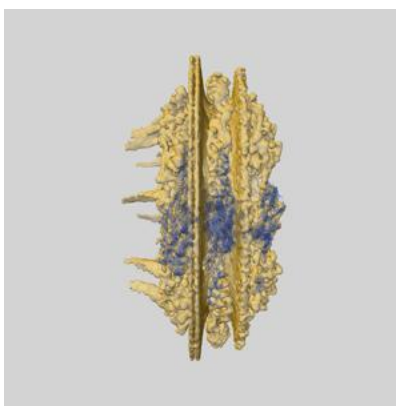
This section contains information regarding the fit between EMDB map EMD-19137 and PDB model 9HCJ. Per-residue inclusion information can be found in section ?? on page ??.

8.1 Map-model overlays

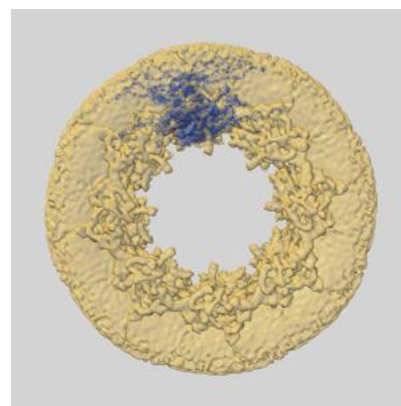
8.1.1 Map-model overlay [i](#)



X

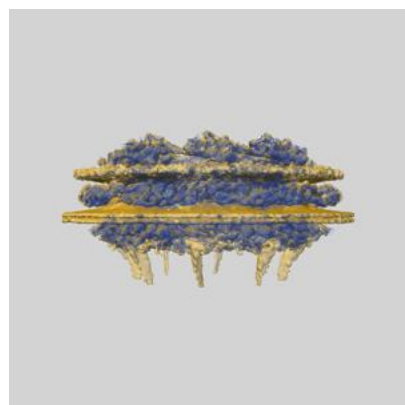


Y

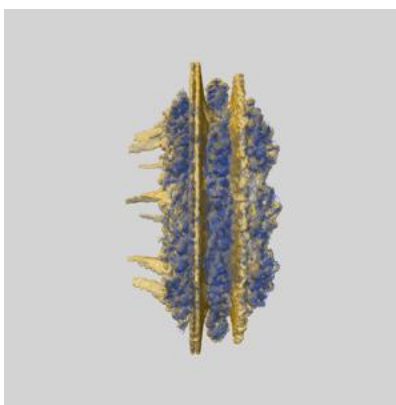


Z

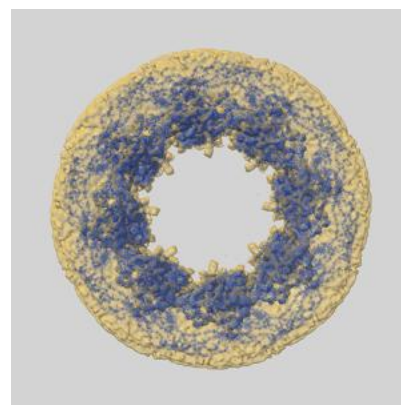
8.1.2 Map-model assembly overlay [i](#)



X



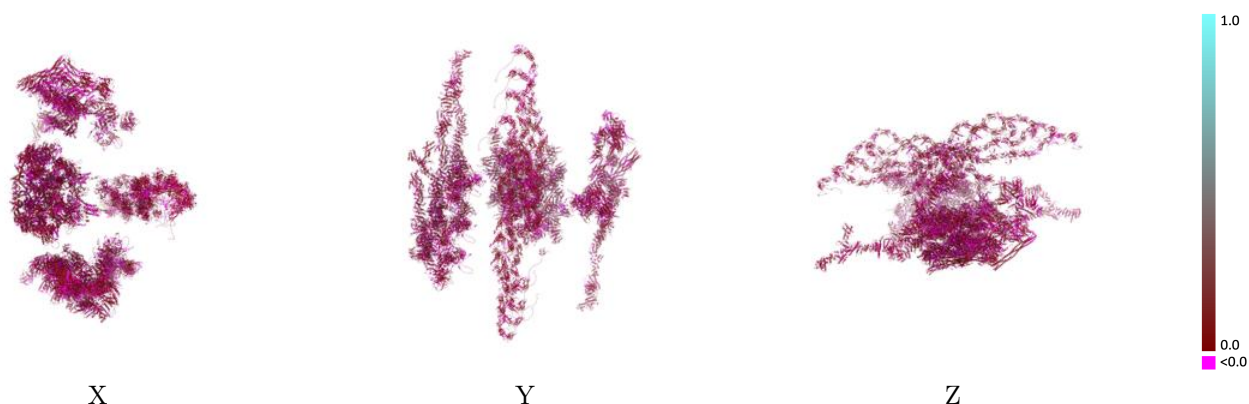
Y



Z

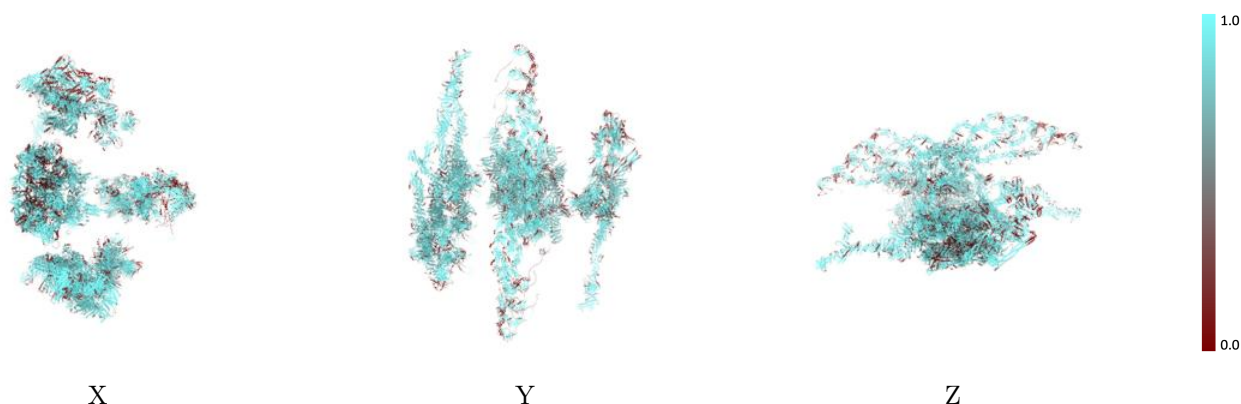
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

8.2 Q-score mapped to coordinate model [i](#)



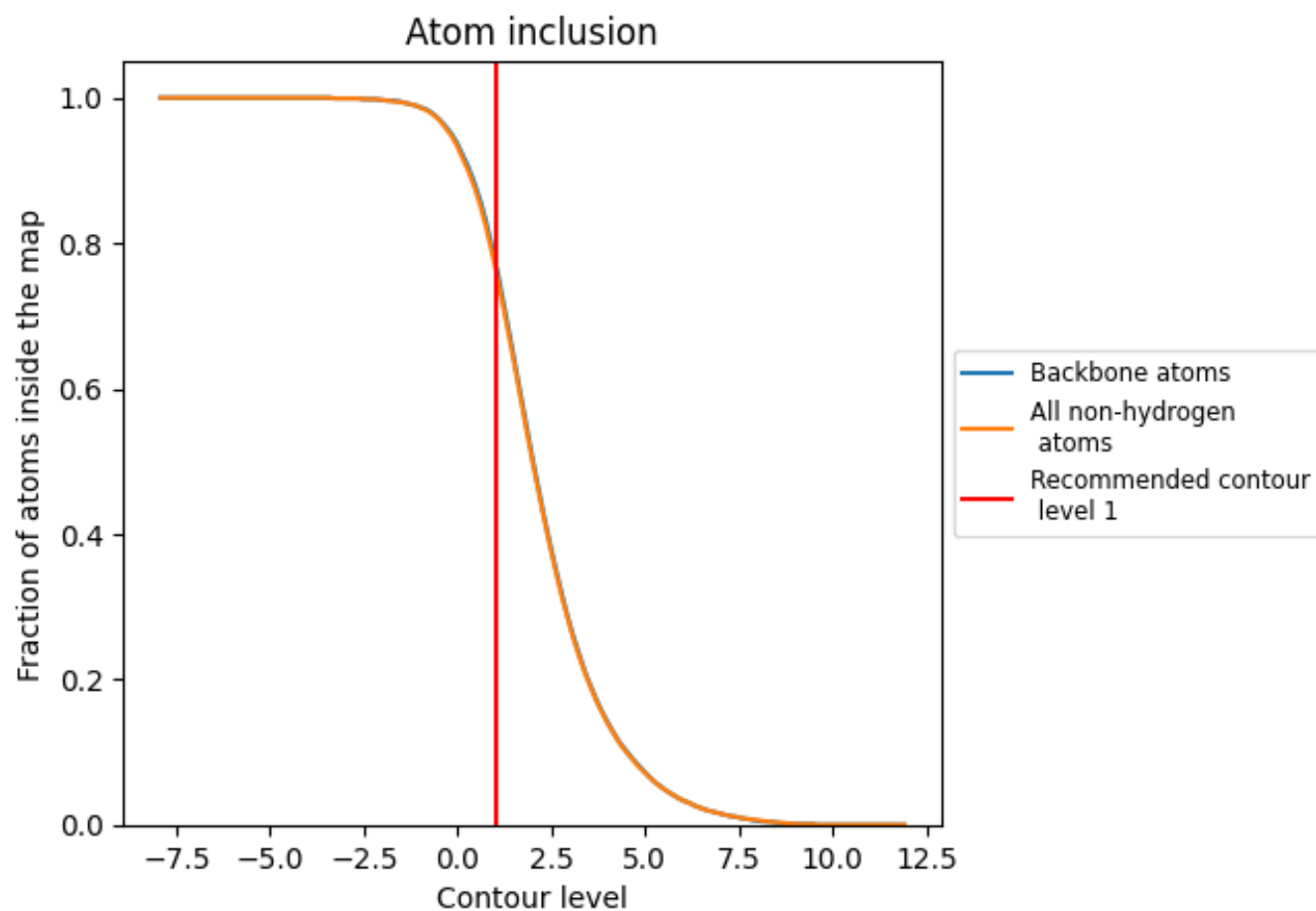
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

8.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (1).

8.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 77% of all non-hydrogen atoms, are inside the map.

8.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7680	 0.0360
00	 0.6780	 0.0380
01	 0.6090	 0.0190
10	 0.6520	 0.0370
11	 0.7700	 0.0400
12	 0.7790	 0.0390
13	 0.7610	 0.0410
14	 0.7200	 0.0440
15	 0.7400	 0.0420
16	 0.7840	 0.0470
17	 0.7490	 0.0440
40	 0.9400	 0.0270
41	 0.8650	 0.0250
A0	 0.7710	 0.0380
A1	 0.8070	 0.0440
A2	 0.6840	 0.0390
A3	 0.8660	 0.0480
A4	 0.7220	 0.0380
A5	 0.8570	 0.0390
B0	 0.6480	 0.0350
B1	 0.6940	 0.0380
C0	 0.7230	 0.0300
C1	 0.6330	 0.0300
C2	 0.6320	 0.0330
C3	 0.8030	 0.0320
D0	 0.7360	 0.0390
D1	 0.7930	 0.0370
D2	 0.7420	 0.0400
D3	 0.8230	 0.0390
E0	 0.9640	 0.0210
E1	 0.9500	 0.0240
F0	 0.4410	 0.0500
F1	 0.3390	 0.0320
F2	 0.6040	 0.0660
F3	 0.7740	 0.0540



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Chain	Atom inclusion	Q-score
H0	 0.8130	 0.0500
H1	 0.6180	 0.0330
H2	 0.5600	 0.0340
H3	 0.7960	 0.0460
I0	 0.6270	 0.0370
I1	 0.7170	 0.0440
I2	 0.6620	 0.0440
I3	 0.6780	 0.0350
J0	 0.6460	 0.0180
J1	 0.6590	 0.0370
J2	 0.7160	 0.0300
J3	 0.6730	 0.0420
J4	 0.5930	 0.0280
J5	 0.7530	 0.0500
K0	 0.8910	 0.0480
K1	 0.7930	 0.0330
K2	 0.8890	 0.0510
K3	 0.9070	 0.0570
L0	 0.8280	 0.0370
L1	 0.9430	 0.0530
L2	 0.9120	 0.0430
L3	 0.9130	 0.0460
M0	 0.9330	 0.0570
M1	 0.9350	 0.0530
M2	 0.8130	 0.0410
M3	 0.9000	 0.0450
N0	 0.7990	 0.0290
N1	 0.8060	 0.0120
N2	 0.7800	 0.0230
N3	 0.7870	 0.0300
O0	 0.8110	 0.0190
O1	 0.8190	 0.0150
O2	 0.9000	 0.0360
O3	 0.7940	 0.0190
P0	 0.7480	 0.0320
P1	 0.8160	 0.0250
P2	 0.7700	 0.0280
P3	 0.7910	 0.0270
Q0	 0.8710	 0.0400
Q1	 0.9220	 0.0340
Q2	 0.8370	 0.0260
Q3	 0.8320	 0.0410

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Chain	Atom inclusion	Q-score
R0	 0.6700	 0.0140
R1	 0.8030	 0.0250
R2	 0.7840	 0.0250
R3	 0.7530	 0.0160
T0	 0.7680	 0.0410
T1	 0.8360	 0.0330
T2	 0.7650	 0.0260
T3	 0.7870	 0.0390
U0	 0.2510	 0.0030
U1	 0.8540	 0.0450
U2	 0.3670	 -0.0300
U3	 0.9550	 0.0510
V0	 0.7420	 0.0500
V1	 0.5880	 0.0240
W0	 0.6320	 0.0200
W1	 0.6970	 0.0250
X0	 0.8470	 0.0390
X1	 0.8110	 0.0550
X2	 0.8650	 0.0530
X3	 0.8060	 0.0470