



Full wwPDB EM Validation Report ⓘ

Sep 8, 2025 – 02:20 pm BST

PDB ID : 9QZF / pdb_00009qzf
EMDB ID : EMD-53471
Title : Proximal A-C linker of Tetrahymena centriole, six repeating units
Authors : Cai, B.; Xu, J.W.; Luo, L.; Aarts, E.; Leitner, A.; Ishikawa, T.; Beltro, P.;
Pilhofer, M.; Wieczorek, M.
Deposited on : 2025-04-22
Resolution : 3.80 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.dev126
MolProbity : **FAILED**
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.45.1

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 Å.

There are no overall percentile quality scores available for this entry.

MolProbity failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 130144 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 WD repeat WRAP73-like protein, putative.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	429	Total	C	N	O	0	0
			2129	1271	429	429		
1	C	429	Total	C	N	O	0	0
			2129	1271	429	429		
1	i	429	Total	C	N	O	0	0
			2129	1271	429	429		
1	BD	429	Total	C	N	O	0	0
			2129	1271	429	429		
1	CP	429	Total	C	N	O	0	0
			2129	1271	429	429		
1	Ca	429	Total	C	N	O	0	0
			2129	1271	429	429		

- Molecule 2 is a protein called Centrosomal protein, putative.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	D	284	Total	C	N	O	0	0
			1415	847	284	284		
2	f	258	Total	C	N	O	0	0
			1288	772	258	258		
2	k	284	Total	C	N	O	0	0
			1415	847	284	284		
2	q	284	Total	C	N	O	0	0
			1415	847	284	284		
2	s	258	Total	C	N	O	0	0
			1288	772	258	258		
2	y	258	Total	C	N	O	0	0
			1288	772	258	258		
2	BK	284	Total	C	N	O	0	0
			1415	847	284	284		
2	BR	258	Total	C	N	O	0	0
			1288	772	258	258		
2	CW	284	Total	C	N	O	0	0
			1415	847	284	284		

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Mol	Chain	Residues	Atoms				AltConf	Trace
2	Cd	258	Total	C	N	O	0	0
			1288	772	258	258		
2	Ch	284	Total	C	N	O	0	0
			1415	847	284	284		
2	z	258	Total	C	N	O	0	0
			1288	772	258	258		

- Molecule 3 is a protein called Rab-GAP TBC domain-containing protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	E	724	Total	C	N	O	0	0
			3597	2149	724	724		
3	I	813	Total	C	N	O	0	0
			4040	2414	813	813		
3	n	665	Total	C	N	O	0	0
			3302	1972	665	665		
3	1	621	Total	C	N	O	0	0
			3082	1840	621	621		
3	7	813	Total	C	N	O	0	0
			4040	2414	813	813		
3	BY	773	Total	C	N	O	0	0
			3841	2295	773	773		

- Molecule 4 is a protein called Unknown Protein Chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	F	151	Total	C	N	O	0	0
			755	453	151	151		
4	d	151	Total	C	N	O	0	0
			755	453	151	151		
4	o	151	Total	C	N	O	0	0
			755	453	151	151		
4	BO	151	Total	C	N	O	0	0
			755	453	151	151		
4	BZ	151	Total	C	N	O	0	0
			755	453	151	151		
4	Bw	151	Total	C	N	O	0	0
			755	453	151	151		

- Molecule 5 is a protein called TBC1 domain family member 31.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	G	414	Total	C	N	O	0	0
			2064	1236	414	414		
5	L	518	Total	C	N	O	0	0
			2584	1548	518	518		
5	M	354	Total	C	N	O	0	0
			1752	1044	354	354		
5	R	354	Total	C	N	O	0	0
			1752	1044	354	354		
5	v	359	Total	C	N	O	0	0
			1790	1072	359	359		
5	9	303	Total	C	N	O	0	0
			1510	904	303	303		
5	AB	354	Total	C	N	O	0	0
			1752	1044	354	354		
5	AE	518	Total	C	N	O	0	0
			2584	1548	518	518		
5	AO	354	Total	C	N	O	0	0
			1752	1044	354	354		
5	AU	354	Total	C	N	O	0	0
			1752	1044	354	354		
5	Bf	468	Total	C	N	O	0	0
			2334	1398	468	468		
5	Bt	354	Total	C	N	O	0	0
			1752	1044	354	354		

- Molecule 6 is a protein called Unknown Protein Chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	H	164	Total	C	N	O	0	0
			820	492	164	164		
6	l	164	Total	C	N	O	0	0
			820	492	164	164		
6	w	164	Total	C	N	O	0	0
			820	492	164	164		
6	BV	164	Total	C	N	O	0	0
			820	492	164	164		
6	Bg	164	Total	C	N	O	0	0
			820	492	164	164		
6	B4	164	Total	C	N	O	0	0
			820	492	164	164		

- Molecule 7 is a protein called POC1 centriolar protein homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	J	365	Total	C	N	O	0	0
			1806	1076	365	365		
7	O	365	Total	C	N	O	0	0
			1806	1076	365	365		
7	4	365	Total	C	N	O	0	0
			1806	1076	365	365		
7	AG	365	Total	C	N	O	0	0
			1806	1076	365	365		
7	AM	365	Total	C	N	O	0	0
			1806	1076	365	365		
7	Bm	365	Total	C	N	O	0	0
			1806	1076	365	365		

- Molecule 8 is a protein called Unknown Protein Chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	K	167	Total	C	N	O	0	0
			835	501	167	167		
8	t	167	Total	C	N	O	0	0
			835	501	167	167		
8	5	167	Total	C	N	O	0	0
			835	501	167	167		
8	Bc	167	Total	C	N	O	0	0
			835	501	167	167		
8	Bn	167	Total	C	N	O	0	0
			835	501	167	167		
8	CA	167	Total	C	N	O	0	0
			835	501	167	167		

- Molecule 9 is a protein called Unknown Protein Chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	N	161	Total	C	N	O	0	0
			805	483	161	161		
9	2	161	Total	C	N	O	0	0
			805	483	161	161		
9	AC	161	Total	C	N	O	0	0
			805	483	161	161		
9	Bj	161	Total	C	N	O	0	0
			805	483	161	161		
9	Bu	161	Total	C	N	O	0	0
			805	483	161	161		
9	CH	161	Total	C	N	O	0	0
			805	483	161	161		

- Molecule 10 is a protein called Unknown Protein Chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	P	32	Total	C	N	O	0	0
			160	96	32	32		
10	U	32	Total	C	N	O	0	0
			160	96	32	32		
10	AJ	32	Total	C	N	O	0	0
			160	96	32	32		
10	AW	32	Total	C	N	O	0	0
			160	96	32	32		
10	Ac	32	Total	C	N	O	0	0
			160	96	32	32		
10	B1	32	Total	C	N	O	0	0
			160	96	32	32		

- Molecule 11 is a protein called Unknown Protein Chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	Q	105	Total	C	N	O	0	0
			525	315	105	105		
11	0	105	Total	C	N	O	0	0
			525	315	105	105		
11	AK	105	Total	C	N	O	0	0
			525	315	105	105		
11	Bq	105	Total	C	N	O	0	0
			525	315	105	105		
11	B2	105	Total	C	N	O	0	0
			525	315	105	105		
11	CO	105	Total	C	N	O	0	0
			525	315	105	105		

- Molecule 12 is a protein called Unknown Protein Chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	S	33	Total	C	N	O	0	0
			165	99	33	33		
12	X	33	Total	C	N	O	0	0
			165	99	33	33		
12	AR	33	Total	C	N	O	0	0
			165	99	33	33		
12	Ae	33	Total	C	N	O	0	0
			165	99	33	33		
12	Ak	33	Total	C	N	O	0	0
			165	99	33	33		

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Mol	Chain	Residues	Atoms				AltConf	Trace
12	B8	33	Total	C	N	O	0	0
			165	99	33	33		

- Molecule 13 is a protein called Unknown Protein Chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	T	127	Total	C	N	O	0	0
			635	381	127	127		
13	AH	127	Total	C	N	O	0	0
			635	381	127	127		
13	AS	127	Total	C	N	O	0	0
			635	381	127	127		
13	Bx	127	Total	C	N	O	0	0
			635	381	127	127		
13	B9	127	Total	C	N	O	0	0
			635	381	127	127		
13	CV	127	Total	C	N	O	0	0
			635	381	127	127		

- Molecule 14 is a protein called Unknown Protein Chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	V	153	Total	C	N	O	0	0
			765	459	153	153		
14	a	153	Total	C	N	O	0	0
			765	459	153	153		
14	AZ	153	Total	C	N	O	0	0
			765	459	153	153		
14	Am	153	Total	C	N	O	0	0
			765	459	153	153		
14	As	153	Total	C	N	O	0	0
			765	459	153	153		
14	CE	153	Total	C	N	O	0	0
			765	459	153	153		

- Molecule 15 is a protein called Unknown Protein Chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	W	102	Total	C	N	O	0	0
			510	306	102	102		
15	AP	102	Total	C	N	O	0	0
			510	306	102	102		

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Mol	Chain	Residues	Atoms				AltConf	Trace
15	Aa	102	Total	C	N	O	0	0
			510	306	102	102		
15	B5	102	Total	C	N	O	0	0
			510	306	102	102		
15	CF	102	Total	C	N	O	0	0
			510	306	102	102		
15	Cc	102	Total	C	N	O	0	0
			510	306	102	102		

- Molecule 16 is a protein called SWIM-type domain-containing protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	Z	151	Total	C	N	O	0	0
			748	446	151	151		
16	c	158	Total	C	N	O	0	0
			783	467	158	158		
16	Ai	151	Total	C	N	O	0	0
			748	446	151	151		
16	An	151	Total	C	N	O	0	0
			748	446	151	151		
16	Aq	158	Total	C	N	O	0	0
			783	467	158	158		
16	Av	158	Total	C	N	O	0	0
			783	467	158	158		
16	Az	151	Total	C	N	O	0	0
			748	446	151	151		
16	A7	158	Total	C	N	O	0	0
			783	467	158	158		
16	CB	151	Total	C	N	O	0	0
			748	446	151	151		
16	CI	158	Total	C	N	O	0	0
			783	467	158	158		
16	CM	151	Total	C	N	O	0	0
			748	446	151	151		
16	CT	158	Total	C	N	O	0	0
			783	467	158	158		

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

3 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	155485	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	13.599	Depositor
Minimum map value	0.000	Depositor
Average map value	0.223	Depositor
Map value standard deviation	1.035	Depositor
Recommended contour level	5	Depositor
Map size (Å)	631.2, 631.2, 631.2	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.315, 1.315, 1.315	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 ⓘ

There are no chain breaks in this entry.

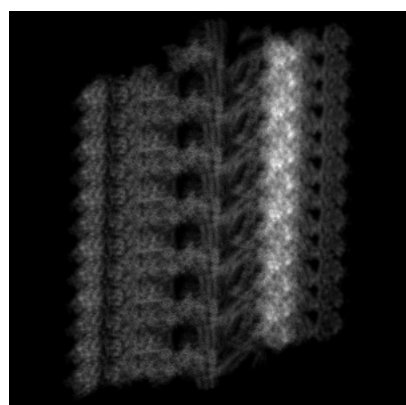
5 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-53471. These allow visual inspection of the internal detail of the map and identification of artifacts.

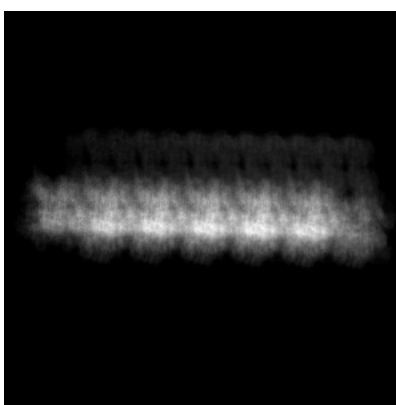
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

5.1 Orthogonal projections [i](#)

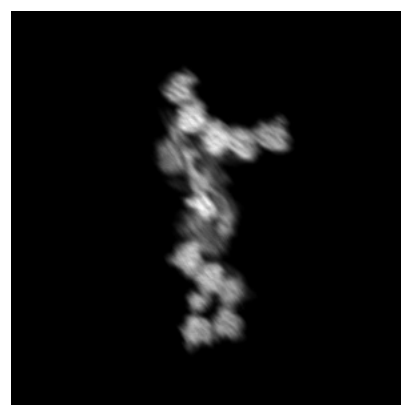
5.1.1 Primary map



X



Y

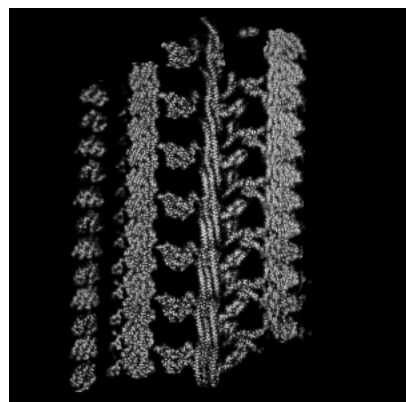


Z

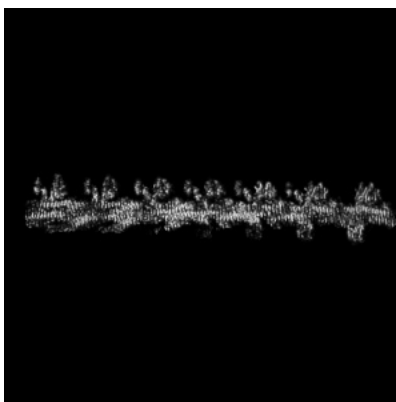
The images above show the map projected in three orthogonal directions.

5.2 Central slices [i](#)

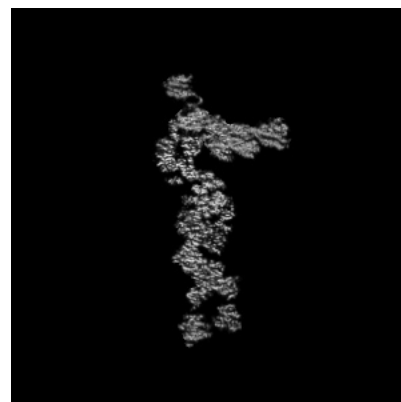
5.2.1 Primary map



X Index: 240



Y Index: 240

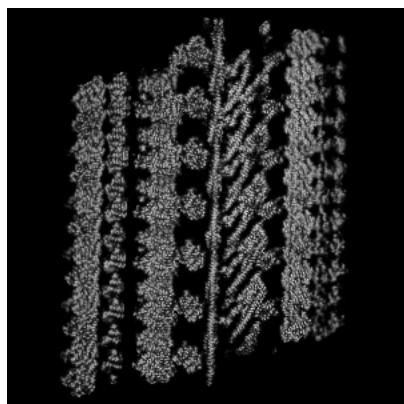


Z Index: 240

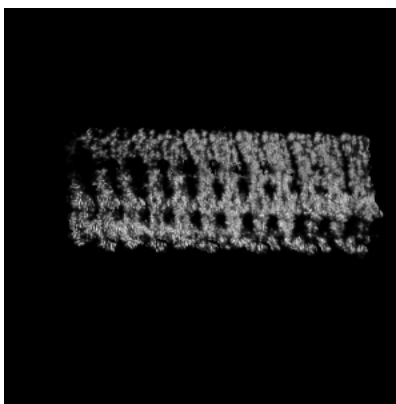
The images above show central slices of the map in three orthogonal directions.

5.3 Largest variance slices [i](#)

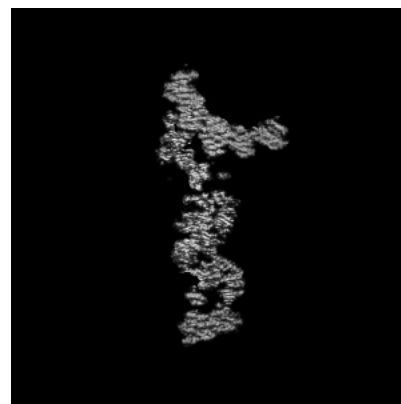
5.3.1 Primary map



X Index: 218



Y Index: 335

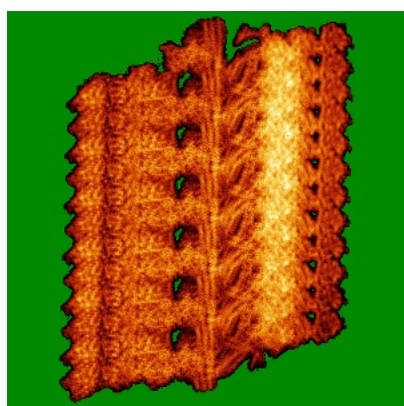


Z Index: 311

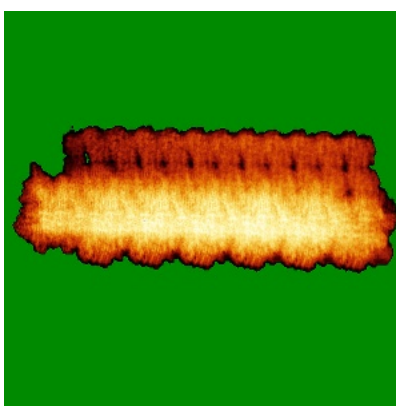
The images above show the largest variance slices of the map in three orthogonal directions.

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

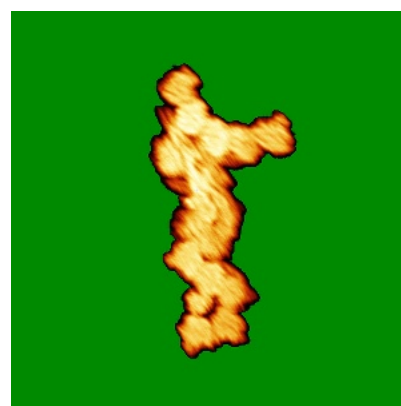
5.4.1 Primary map



X



Y

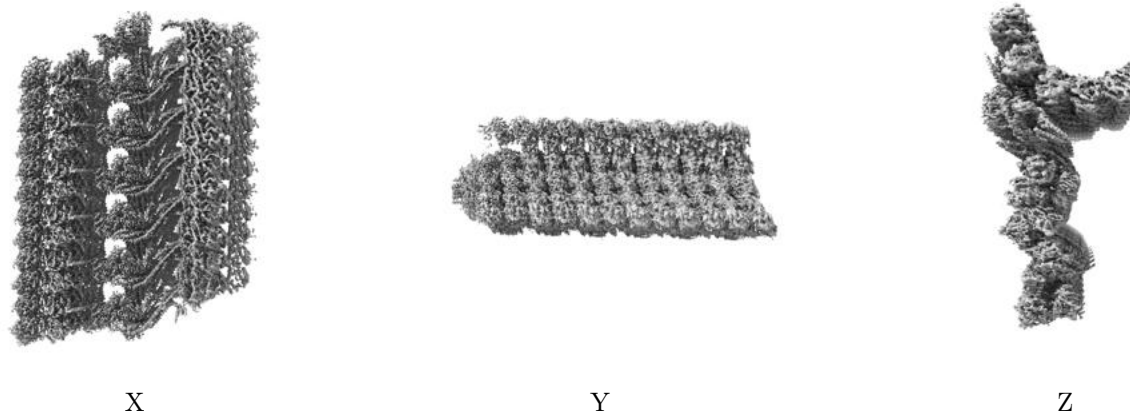


Z

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 5.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

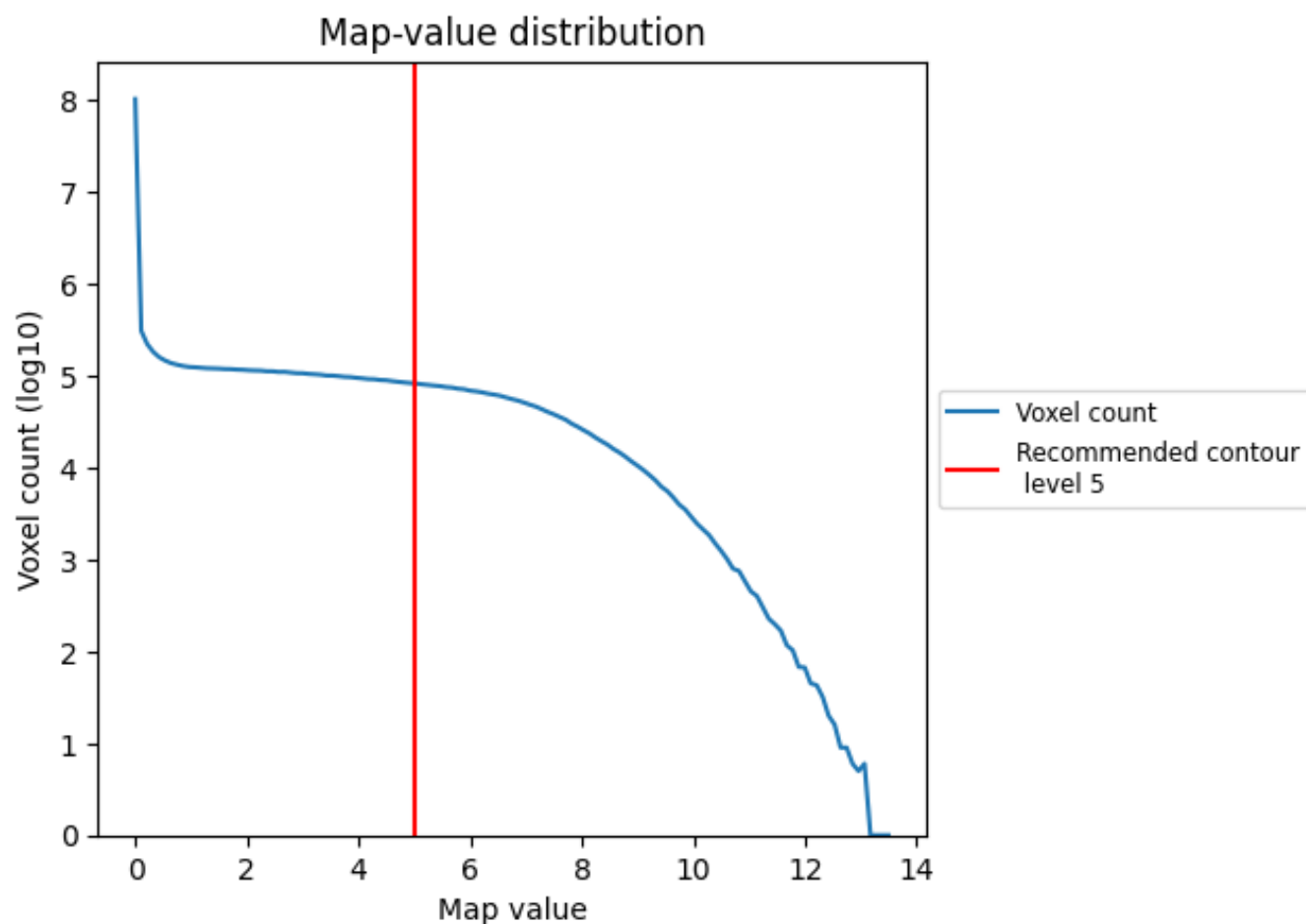
5.6 Mask visualisation [i](#)

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

6 Map analysis [i](#)

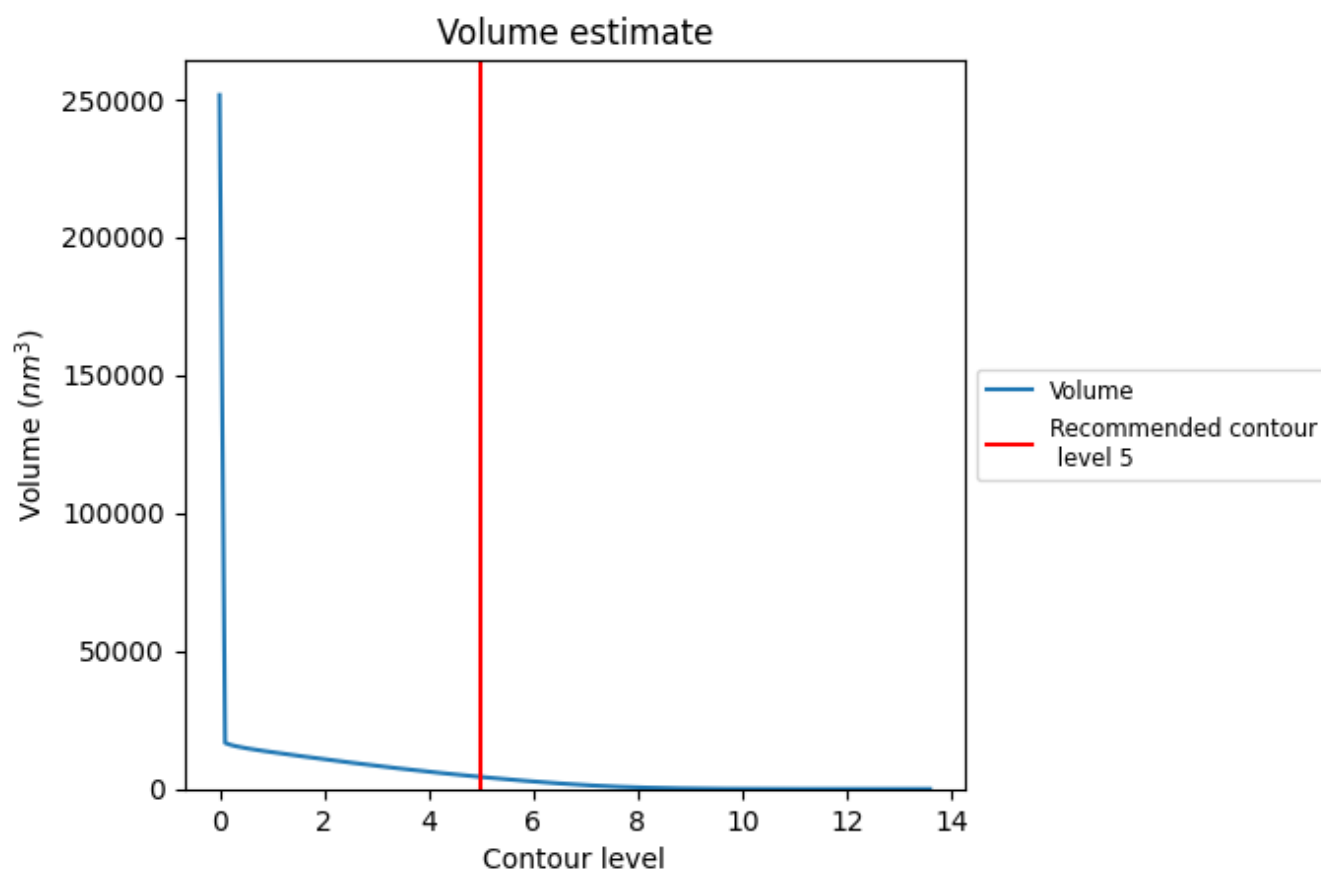
This section contains the results of statistical analysis of the map.

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.

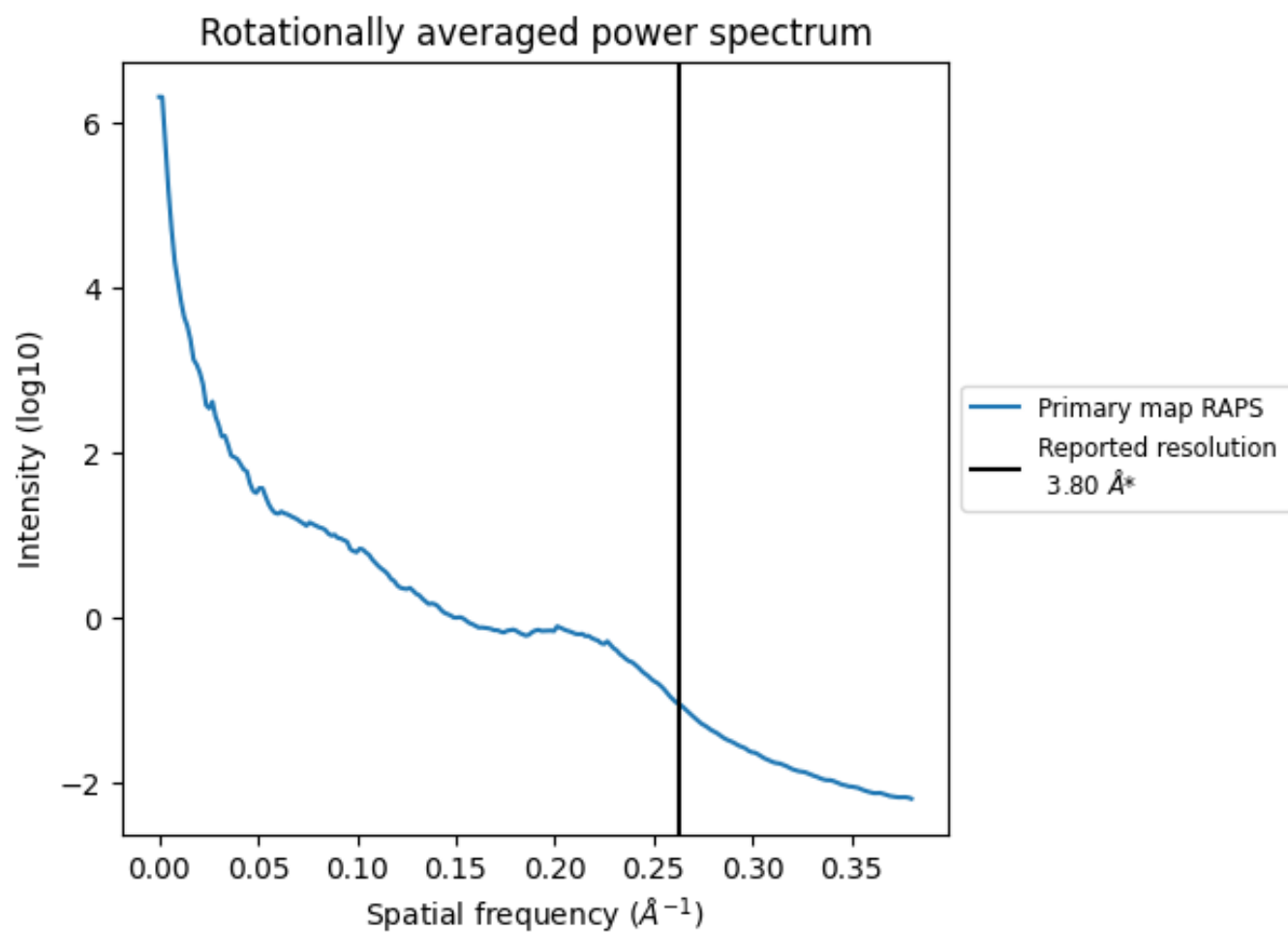
6.2 Volume estimate [i](#)



The volume at the recommended contour level is 4355 nm^3 ; this corresponds to an approximate mass of 3934 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 0.263 Å⁻¹

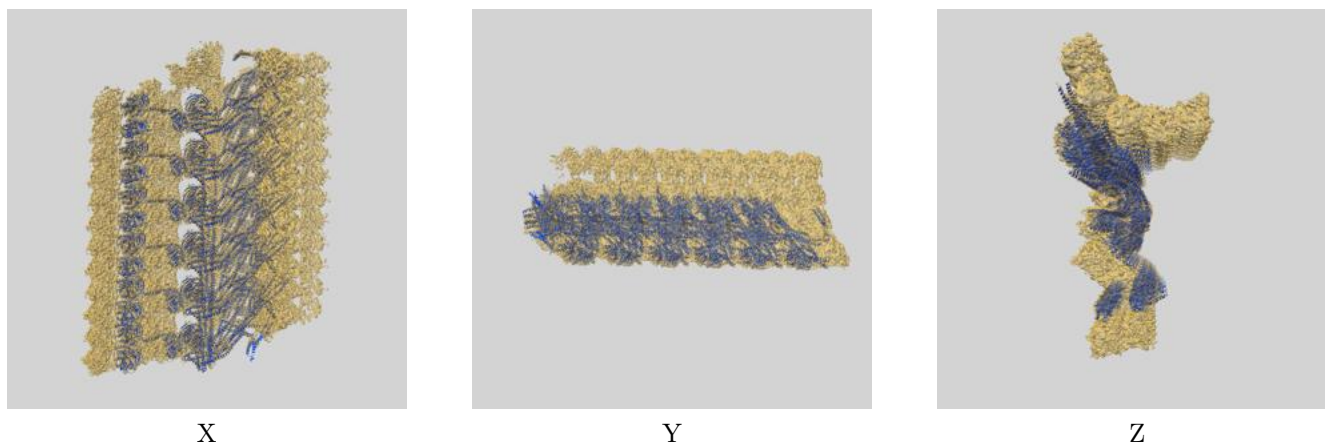
7 Fourier-Shell correlation ⓘ

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

8 Map-model fit [i](#)

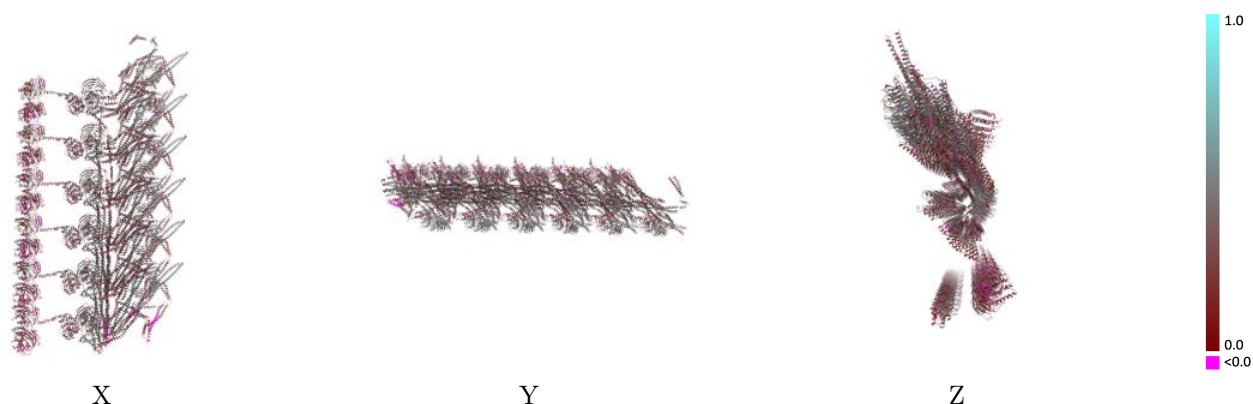
This section contains information regarding the fit between EMDB map EMD-53471 and PDB model 9QZF. Per-residue inclusion information can be found in section ?? on page ??.

8.1 Map-model overlay [i](#)



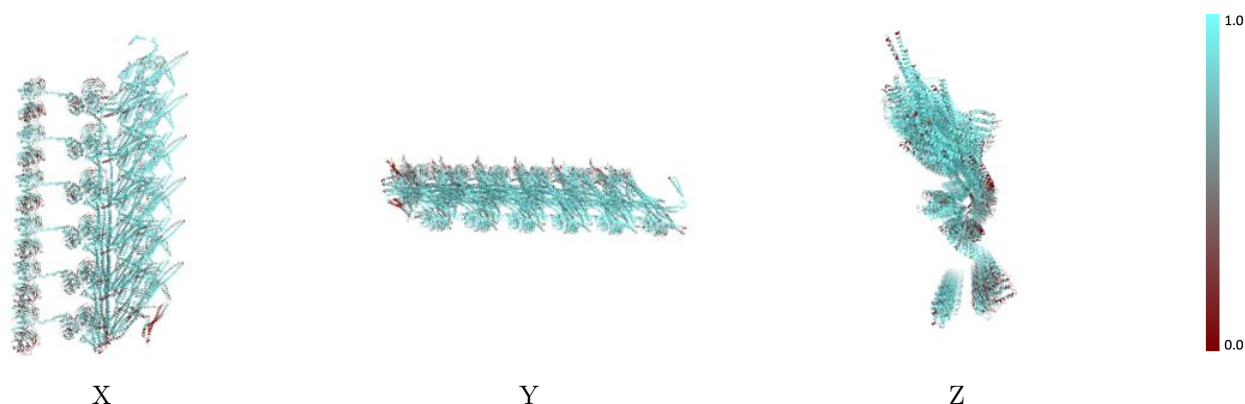
The images above show the 3D surface view of the map at the recommended contour level 5.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



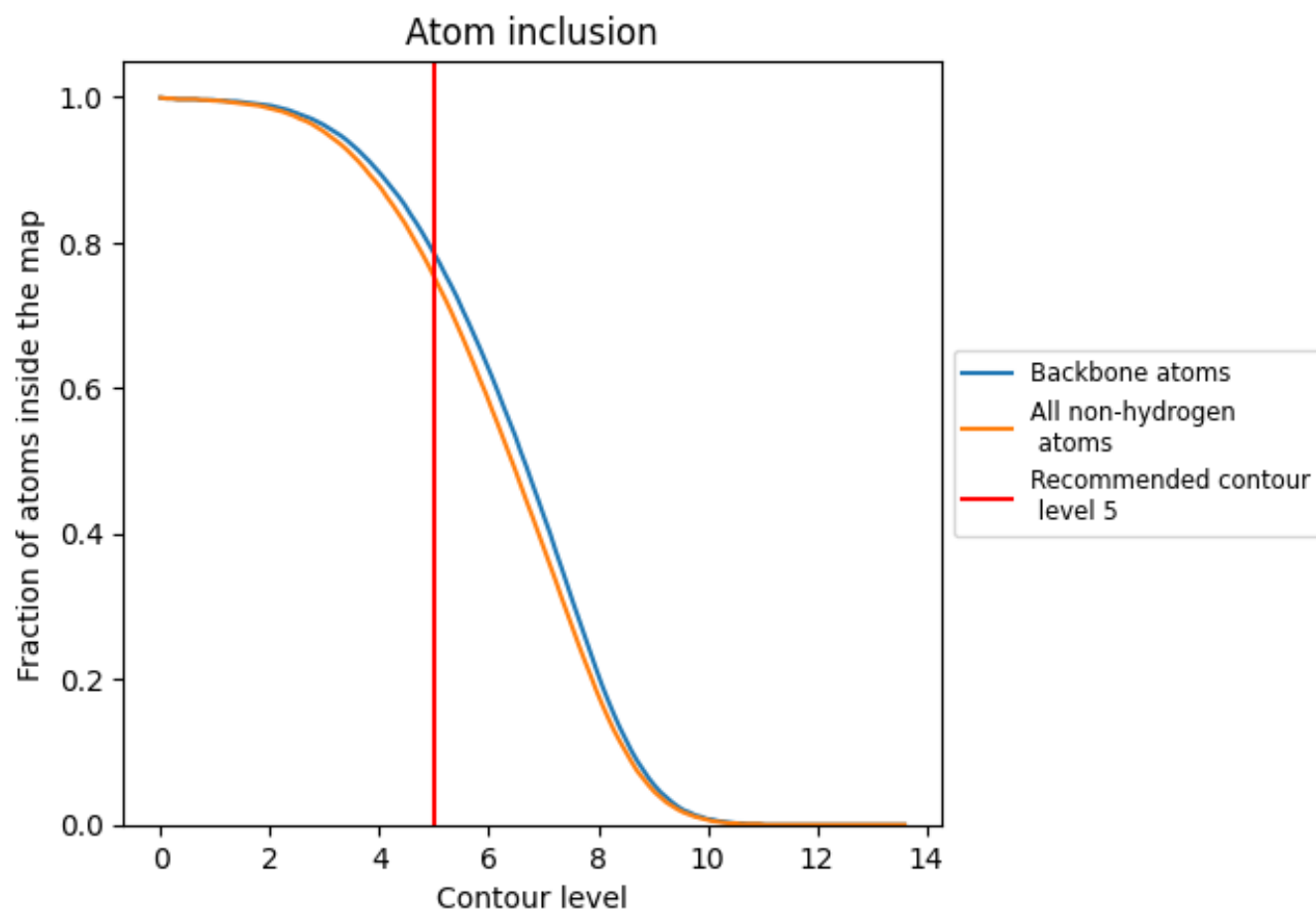
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (5).







































































8.4 Atom inclusion ⓘ



At the recommended contour level, 78% of all backbone atoms, 75% 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 (5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7530	 0.3370
0	 0.8930	 0.3640
1	 0.5950	 0.3520
2	 0.9020	 0.3790
4	 0.6570	 0.2890
5	 0.7290	 0.4000
7	 0.7440	 0.3410
9	 0.7150	 0.3350
A	 0.7590	 0.3960
A7	 0.7940	 0.3400
AB	 0.4420	 0.2140
AC	 0.8560	 0.4000
AE	 0.8500	 0.3580
AG	 0.6470	 0.2890
AH	 0.8900	 0.3500
AJ	 0.7690	 0.4220
AK	 0.8020	 0.3780
AM	 0.7320	 0.2870
AO	 0.4300	 0.2210
AP	 0.8800	 0.3710
AR	 0.8490	 0.3760
AS	 0.6830	 0.3720
AU	 0.5010	 0.2150
AW	 0.7810	 0.4480
AZ	 0.8180	 0.3400
Aa	 0.7060	 0.3870
Ac	 0.8440	 0.4140
Ae	 0.7880	 0.3640
Ai	 0.7740	 0.3300
Ak	 0.7880	 0.3420
Am	 0.5520	 0.2930
An	 0.7430	 0.3270
Aq	 0.7230	 0.3400
As	 0.8990	 0.3380
Av	 0.6900	 0.3360















































































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Chain	Atom inclusion	Q-score
Az	 0.7940	 0.3240
B1	 0.8500	 0.4240
B2	 0.9330	 0.3680
B4	 0.8520	 0.3670
B5	 0.9250	 0.3690
B8	 0.8730	 0.3710
B9	 0.9180	 0.3590
BD	 0.8410	 0.3990
BK	 0.8620	 0.3480
BO	 0.9420	 0.3710
BR	 0.8200	 0.3130
BV	 0.8540	 0.3530
BY	 0.7140	 0.3540
BZ	 0.9010	 0.3710
Bc	 0.8380	 0.3660
Bf	 0.8210	 0.3570
Bg	 0.8460	 0.3710
Bj	 0.9580	 0.3760
Bm	 0.6990	 0.2870
Bn	 0.8480	 0.3750
Bq	 0.9390	 0.3630
Bt	 0.4650	 0.1940
Bu	 0.9490	 0.3970
Bw	 0.9430	 0.3710
Bx	 0.9290	 0.3460
C	 0.7660	 0.4030
CA	 0.8520	 0.3760
CB	 0.8010	 0.3260
CE	 0.8850	 0.3430
CF	 0.9120	 0.3650
CH	 0.9430	 0.3910
CI	 0.7480	 0.3350
CM	 0.8050	 0.3230
CO	 0.9330	 0.3750
CP	 0.8500	 0.3950
CT	 0.8050	 0.3370
CV	 0.9200	 0.3590
CW	 0.8710	 0.3560
Ca	 0.7740	 0.3950
Cc	 0.9250	 0.3730
Cd	 0.8200	 0.3150
Ch	 0.8010	 0.3510

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Chain	Atom inclusion	Q-score
D	 0.8070	 0.3360
E	 0.7170	 0.3540
F	 0.8720	 0.3760
G	 0.8170	 0.3510
H	 0.7910	 0.3620
I	 0.6590	 0.3400
J	 0.7180	 0.2830
K	 0.7750	 0.3750
L	 0.8080	 0.3430
M	 0.5110	 0.2000
N	 0.9200	 0.3900
O	 0.6220	 0.2700
P	 0.8250	 0.4210
Q	 0.8910	 0.3580
R	 0.4080	 0.2080
S	 0.8610	 0.3590
T	 0.8740	 0.3600
U	 0.7810	 0.4140
V	 0.8690	 0.3470
W	 0.8760	 0.3700
X	 0.7390	 0.3470
Z	 0.8210	 0.3170
a	 0.8520	 0.3460
c	 0.7330	 0.3350
d	 0.8910	 0.3640
f	 0.7520	 0.3050
i	 0.8760	 0.3990
k	 0.7040	 0.3330
l	 0.7910	 0.3620
n	 0.5920	 0.3350
o	 0.4950	 0.2440
q	 0.8820	 0.3490
s	 0.6480	 0.2900
t	 0.7750	 0.3690
v	 0.7590	 0.3600
w	 0.7290	 0.3830
y	 0.8370	 0.3210
z	 0.7550	 0.3040