



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 12:45 AM UTC

PDB ID : 8HIF / pdb_00008hif
EMDB ID : EMD-34815
Title : One asymmetric unit of Singapore grouper iridovirus capsid
Authors : Zhao, Z.N.; Liu, C.C.; Zhu, D.J.; Qi, J.X.; Zhang, X.Z.; Gao, G.F.
Deposited on : 2022-11-20
Resolution : 3.50 Å(reported)

This is a wwPDB EM Validation Summary 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

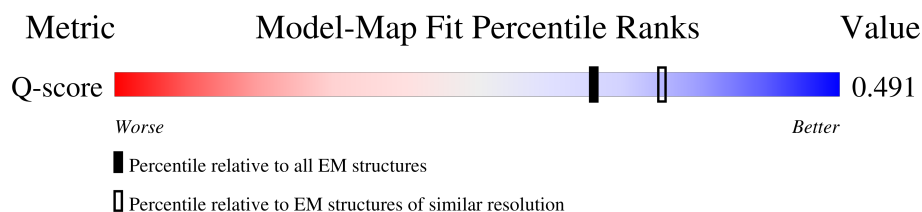
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 Å.

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	13950 (3.00 - 4.00)

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

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 450820 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 Major capsid protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A1	461	Total	C	N	O	S	0	0
			3516	2225	597	671	23		
1	A2	459	Total	C	N	O	S	0	0
			3504	2220	595	667	22		
1	A3	458	Total	C	N	O	S	0	0
			3497	2216	594	665	22		
1	B1	454	Total	C	N	O	S	0	0
			3480	2206	593	659	22		
1	B2	459	Total	C	N	O	S	0	0
			3510	2223	598	667	22		
1	B3	462	Total	C	N	O	S	0	0
			3524	2231	598	672	23		
1	C1	461	Total	C	N	O	S	0	0
			3523	2230	600	670	23		
1	C2	462	Total	C	N	O	S	0	0
			3521	2229	598	672	22		
1	C3	458	Total	C	N	O	S	0	0
			3503	2219	597	665	22		
1	D1	458	Total	C	N	O	S	0	0
			3497	2216	594	665	22		
1	D2	461	Total	C	N	O	S	0	0
			3517	2227	597	670	23		
1	D3	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	E1	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	E2	461	Total	C	N	O	S	0	0
			3523	2230	600	670	23		
1	E3	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	F1	461	Total	C	N	O	S	0	0
			3504	2220	594	668	22		
1	F2	455	Total	C	N	O	S	0	0
			3480	2205	591	662	22		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	F3	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	G1	461	Total	C	N	O	S	0	0
			3517	2227	597	670	23		
1	G2	461	Total	C	N	O	S	0	0
			3514	2226	596	669	23		
1	G3	462	Total	C	N	O	S	0	0
			3527	2233	600	671	23		
1	H1	457	Total	C	N	O	S	0	0
			3495	2213	596	664	22		
1	H2	461	Total	C	N	O	S	0	0
			3523	2230	600	670	23		
1	H3	461	Total	C	N	O	S	0	0
			3523	2230	600	670	23		
1	I1	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	I2	459	Total	C	N	O	S	0	0
			3510	2223	598	667	22		
1	I3	461	Total	C	N	O	S	0	0
			3523	2230	600	670	23		
1	J1	457	Total	C	N	O	S	0	0
			3489	2210	593	664	22		
1	J3	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	K1	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	K2	462	Total	C	N	O	S	0	0
			3528	2233	601	671	23		
1	K3	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	L1	458	Total	C	N	O	S	0	0
			3503	2219	597	665	22		
1	L2	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	L3	461	Total	C	N	O	S	0	0
			3523	2230	600	670	23		
1	M1	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	M2	461	Total	C	N	O	S	0	0
			3523	2230	600	670	23		
1	M3	455	Total	C	N	O	S	0	0
			3484	2209	591	662	22		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	N1	458	Total	C	N	O	S	0	0
			3503	2219	597	665	22		
1	N2	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	N3	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	O1	456	Total	C	N	O	S	0	0
			3491	2211	595	663	22		
1	O2	462	Total	C	N	O	S	0	0
			3526	2232	601	670	23		
1	O3	462	Total	C	N	O	S	0	0
			3520	2229	598	670	23		
1	P1	461	Total	C	N	O	S	0	0
			3523	2230	600	670	23		
1	P2	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	P3	462	Total	C	N	O	S	0	0
			3524	2231	598	672	23		
1	Q1	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	Q2	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	Q3	457	Total	C	N	O	S	0	0
			3495	2215	596	662	22		
1	R1	461	Total	C	N	O	S	0	0
			3523	2230	600	670	23		
1	R2	454	Total	C	N	O	S	0	0
			3482	2206	593	661	22		
1	R3	461	Total	C	N	O	S	0	0
			3523	2230	600	670	23		
1	S1	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	S2	457	Total	C	N	O	S	0	0
			3499	2217	596	664	22		
1	S3	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	T1	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	T2	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	T3	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	U1	460	Total	C	N	O	S	0	0
			3515	2224	599	669	23		
1	U2	461	Total	C	N	O	S	0	0
			3517	2227	597	670	23		
1	U3	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	V1	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	V2	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	V3	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	W1	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	W2	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	W3	461	Total	C	N	O	S	0	0
			3523	2230	600	670	23		
1	X1	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	X2	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	X3	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	Y1	461	Total	C	N	O	S	0	0
			3520	2229	600	668	23		
1	Y2	455	Total	C	N	O	S	0	0
			3490	2212	594	662	22		
1	Y3	461	Total	C	N	O	S	0	0
			3519	2228	600	668	23		
1	Z1	456	Total	C	N	O	S	0	0
			3494	2214	595	663	22		
1	Z2	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	Z3	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	a1	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	a2	462	Total	C	N	O	S	0	0
			3524	2231	598	672	23		
1	a3	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	b1	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	b2	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	b3	461	Total	C	N	O	S	0	0
			3523	2230	600	670	23		
1	d1	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	d2	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	d3	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	e1	456	Total	C	N	O	S	0	0
			3488	2211	592	663	22		
1	e2	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	e3	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	f1	456	Total	C	N	O	S	0	0
			3488	2211	592	663	22		
1	f2	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	f3	462	Total	C	N	O	S	0	0
			3520	2230	595	672	23		
1	g1	462	Total	C	N	O	S	0	0
			3524	2231	598	672	23		
1	g2	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	g3	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	h1	456	Total	C	N	O	S	0	0
			3464	2199	585	658	22		
1	h2	460	Total	C	N	O	S	0	0
			3517	2227	599	669	22		
1	h3	462	Total	C	N	O	S	0	0
			3524	2231	598	672	23		
1	j1	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	j2	461	Total	C	N	O	S	0	0
			3511	2224	594	670	23		
1	j3	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	k1	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	k2	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	k3	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	m1	462	Total	C	N	O	S	0	0
			3524	2231	598	672	23		
1	m2	462	Total	C	N	O	S	0	0
			3524	2231	598	672	23		
1	m3	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	n1	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	n2	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	n3	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	p1	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	p2	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	p3	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	r1	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	r2	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	r3	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	J2	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	c1	462	Total	C	N	O	S	0	0
			3520	2229	598	670	23		
1	c2	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	c3	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	q1	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		
1	q2	462	Total	C	N	O	S	0	0
			3530	2234	601	672	23		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	q3	462	Total	C	N	O	S	0	0
			3520	2229	598	670	23		

- Molecule 2 is a protein called VP38.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	s1	95	Total	C	N	O	S	0	0
			692	421	127	137	7		
2	s2	76	Total	C	N	O	S	0	0
			573	351	104	114	4		
2	s3	98	Total	C	N	O	S	0	0
			739	453	136	143	7		
2	s4	100	Total	C	N	O	S	0	0
			738	453	132	147	6		
2	s5	94	Total	C	N	O	S	0	0
			700	426	129	139	6		
2	s6	94	Total	C	N	O	S	0	0
			692	422	126	138	6		
2	t1	98	Total	C	N	O	S	0	0
			725	442	133	143	7		
2	t2	96	Total	C	N	O	S	0	0
			715	436	132	140	7		
2	t3	97	Total	C	N	O	S	0	0
			722	444	131	141	6		
2	t4	93	Total	C	N	O	S	0	0
			666	406	121	134	5		
2	t5	74	Total	C	N	O	S	0	0
			554	340	102	110	2		
2	t6	98	Total	C	N	O	S	0	0
			727	444	134	142	7		
2	t7	98	Total	C	N	O	S	0	0
			739	453	136	143	7		
2	y7	53	Total	C	N	O	S	0	0
			400	247	74	77	2		
2	y8	49	Total	C	N	O	S	0	0
			355	218	64	71	2		

- Molecule 3 is a protein called VP137.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	y2	379	Total	C	N	O	S	0	0
			2716	1690	500	511	15		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	y1	80	Total	C	N	O	S	0	0
			552	345	94	111	2		

- Molecule 4 is a protein called VP88.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	y4	312	Total	C	N	O	S	0	0
			2399	1516	404	472	7		

- Molecule 5 is a protein called VP59.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	y5	78	Total	C	N	O	S	0	0
			631	391	119	116	5		

- Molecule 6 is a protein called VP139.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	y6	92	Total	C	N	O	S	0	0
			694	441	127	118	8		

- Molecule 7 is a protein called Penton protein (VP14).

Mol	Chain	Residues	Atoms					AltConf	Trace
7	y3	139	Total	C	N	O	S	0	0
			1062	671	189	196	6		

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	37161	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1300	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.105	Depositor
Minimum map value	-0.071	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.01	Depositor
Map size ($\text{\AA}$)	1106.0, 1079.4, 796.6	wwPDB
Map dimensions	790, 771, 569	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.4, 1.4, 1.4	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.

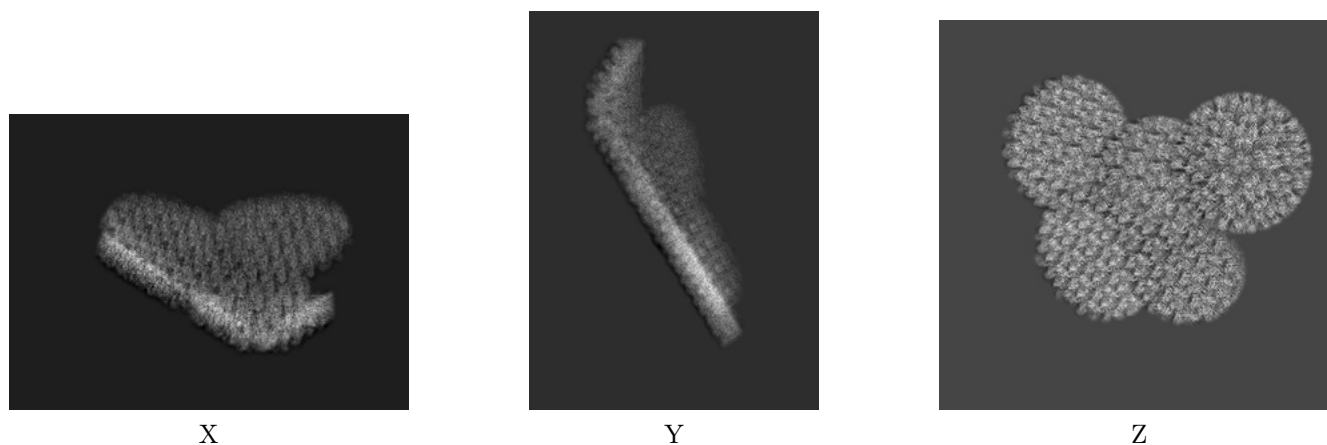
5 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-34815. 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](#)

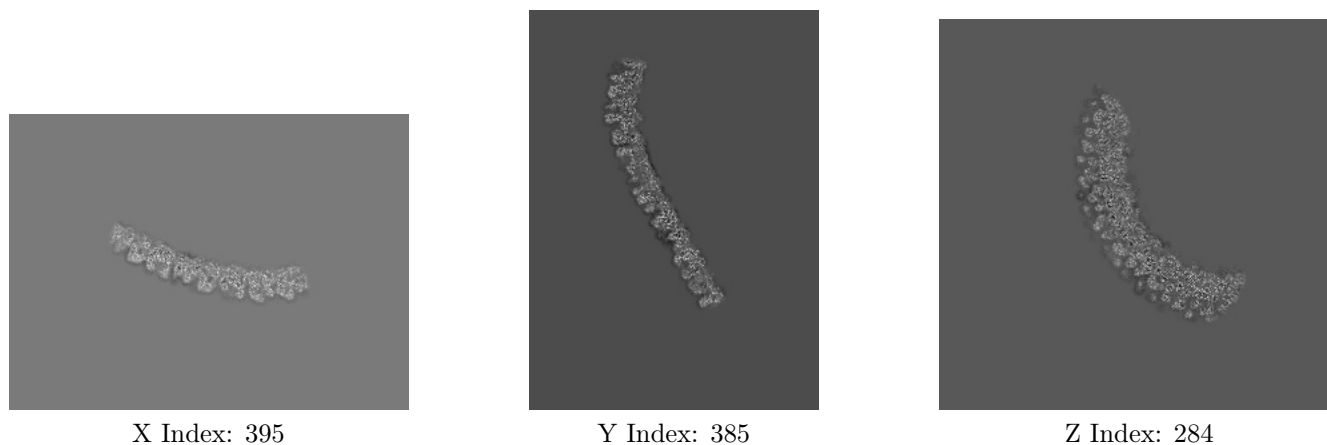
5.1.1 Primary map



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

5.2 Central slices [i](#)

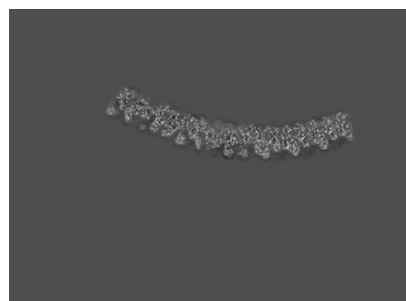
5.2.1 Primary map



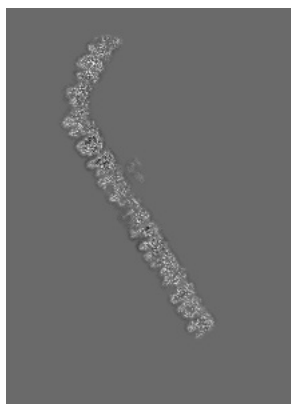
The images above show central slices of the map in three orthogonal directions.

5.3 Largest variance slices [i](#)

5.3.1 Primary map



X Index: 277



Y Index: 460

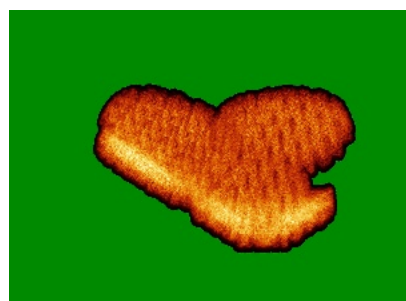


Z Index: 172

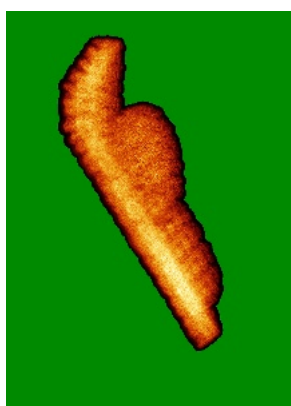
The images above show the largest variance slices of the map in three orthogonal directions.

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

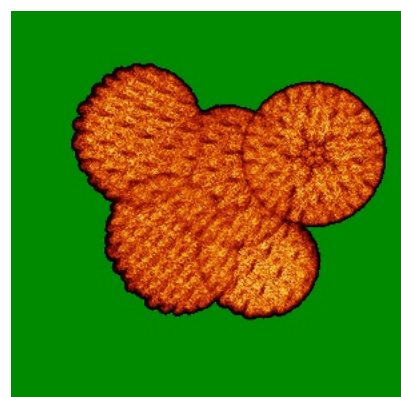
5.4.1 Primary map



X



Y

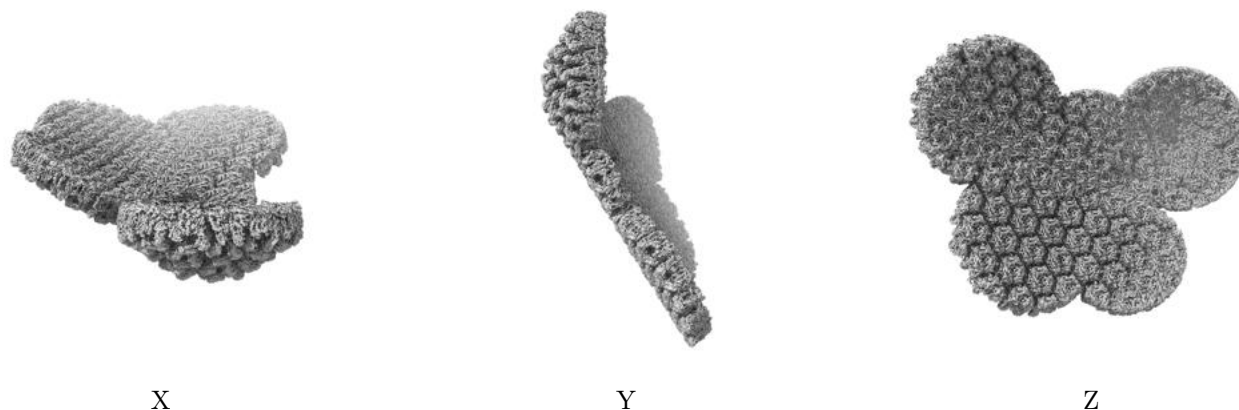


Z

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

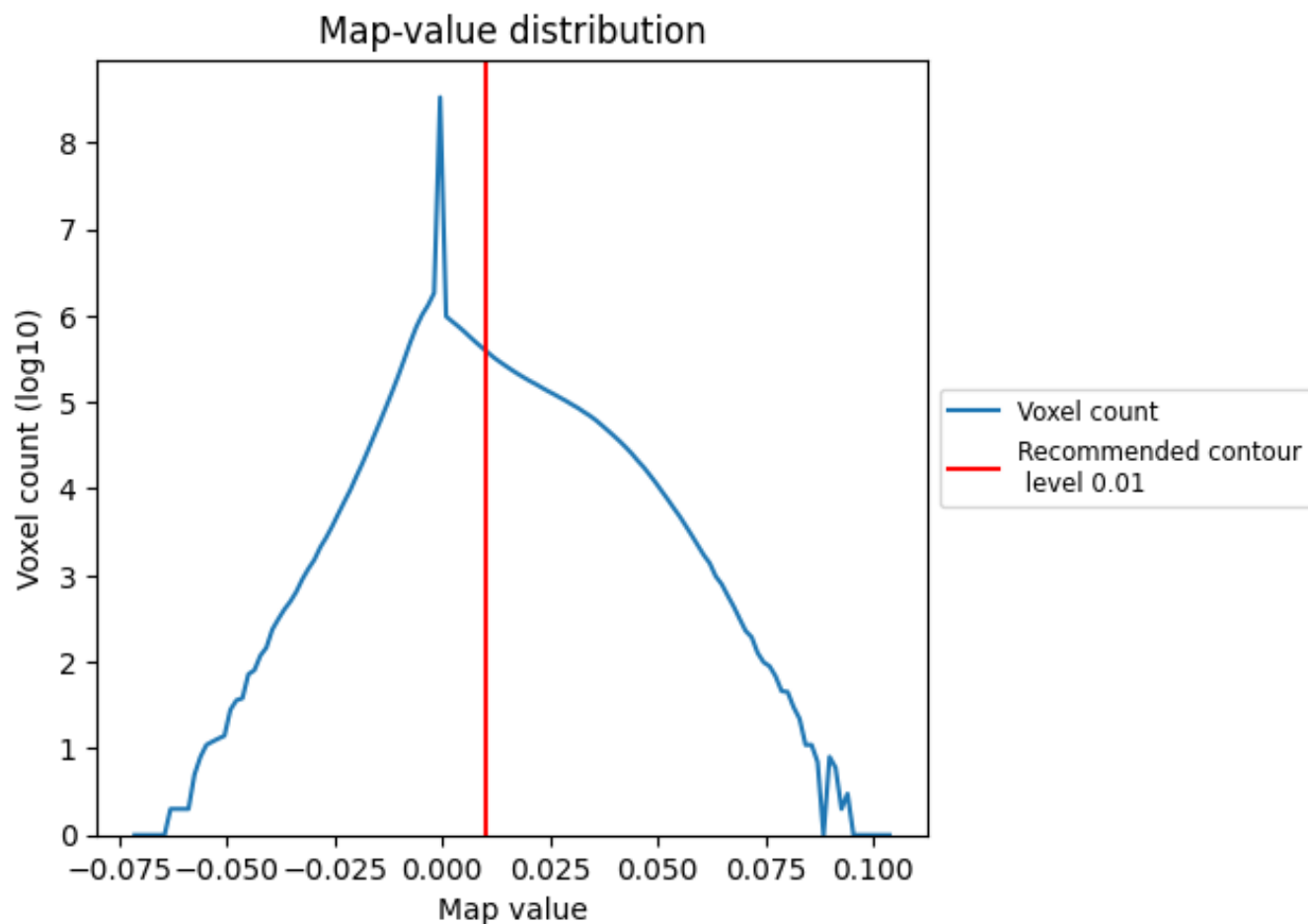
5.6 Mask visualisation [i](#)

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

6 Map analysis [i](#)

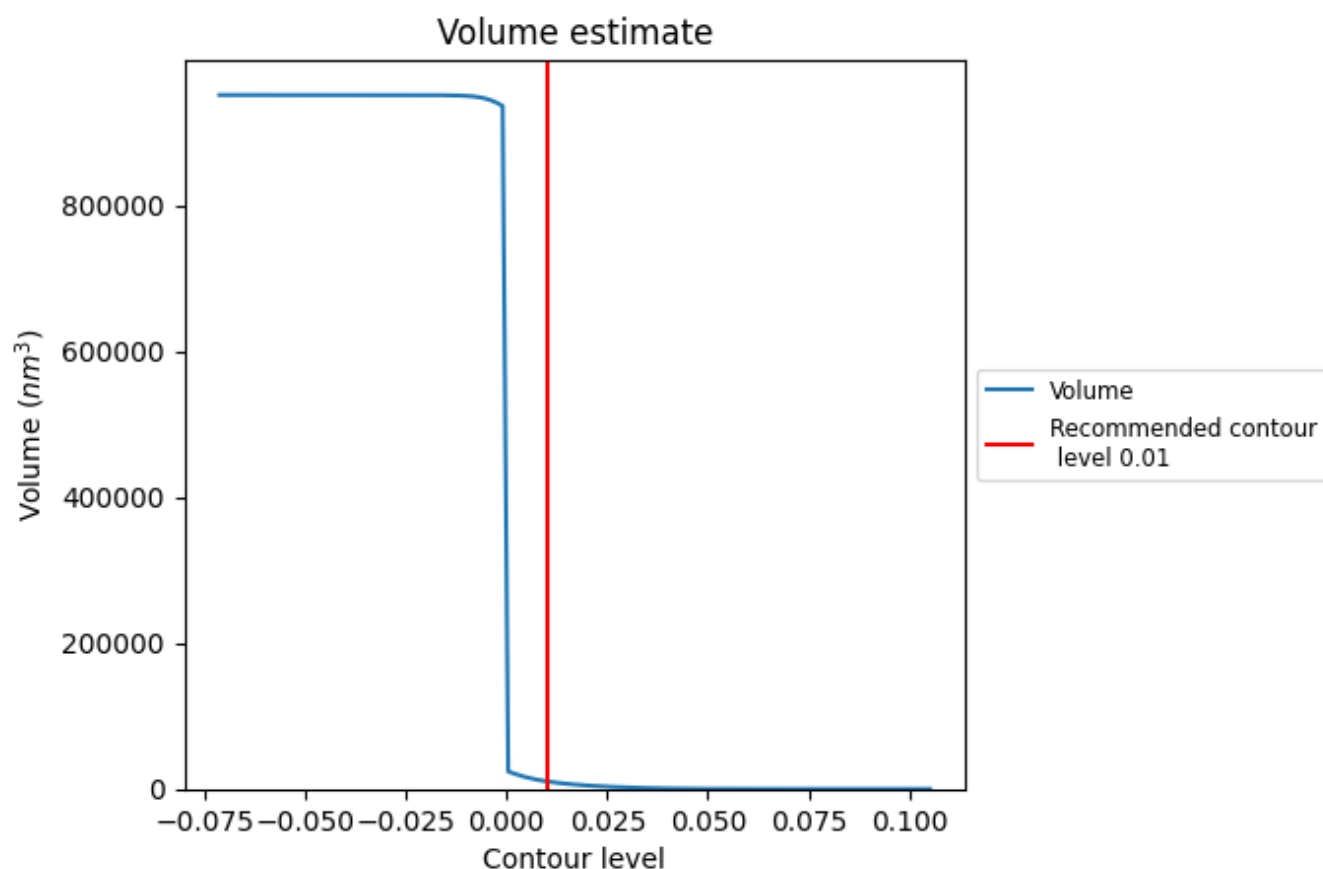
This section contains the results of statistical analysis of the map.

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 10363 nm³; this corresponds to an approximate mass of 9361 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 [i](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

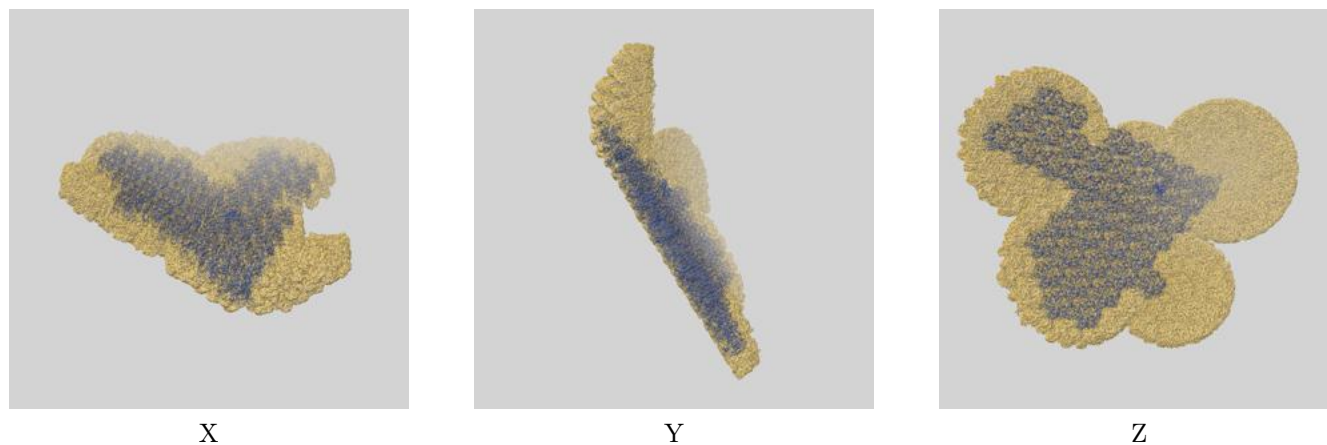
7 Fourier-Shell correlation ⓘ

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

8 Map-model fit [i](#)

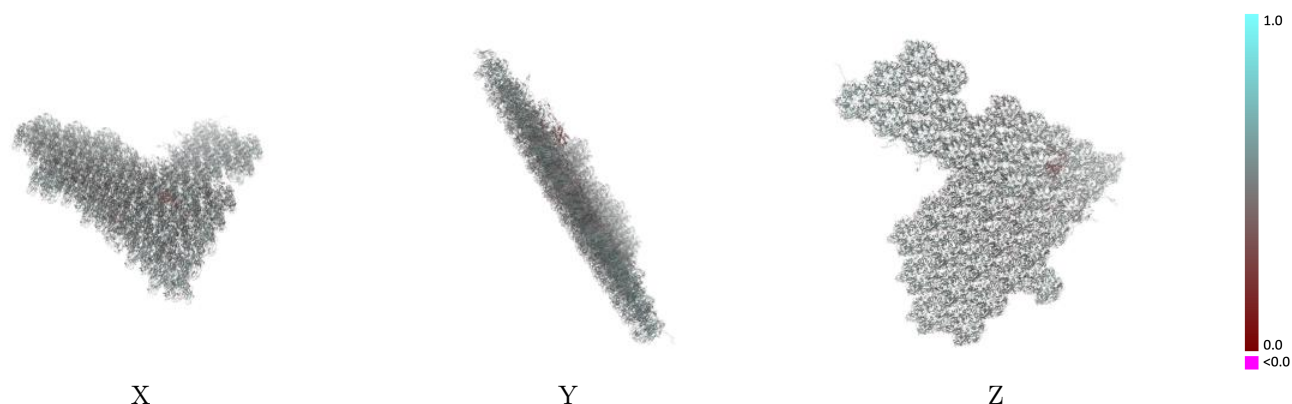
This section contains information regarding the fit between EMDB map EMD-34815 and PDB model 8HIF. Per-residue inclusion information can be found in section ?? on page ??.

8.1 Map-model overlay [i](#)



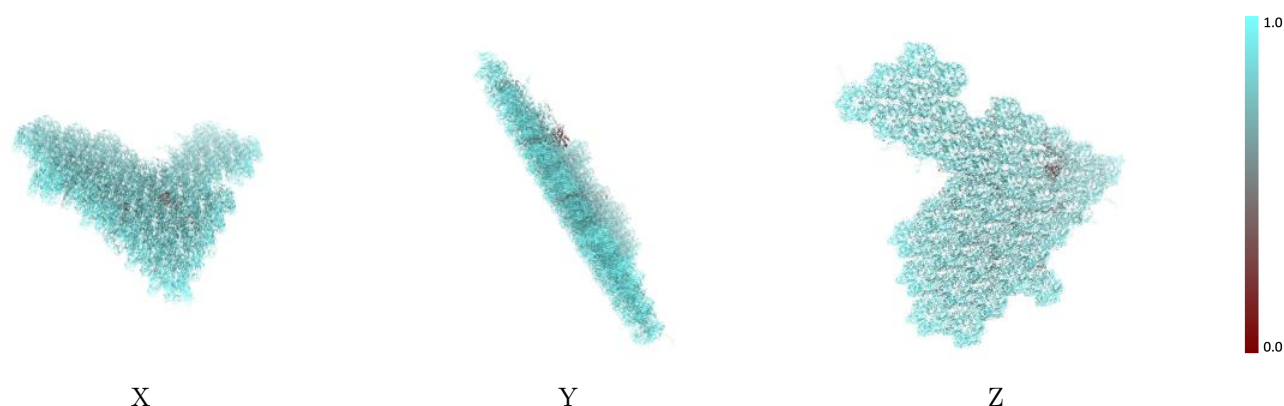
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



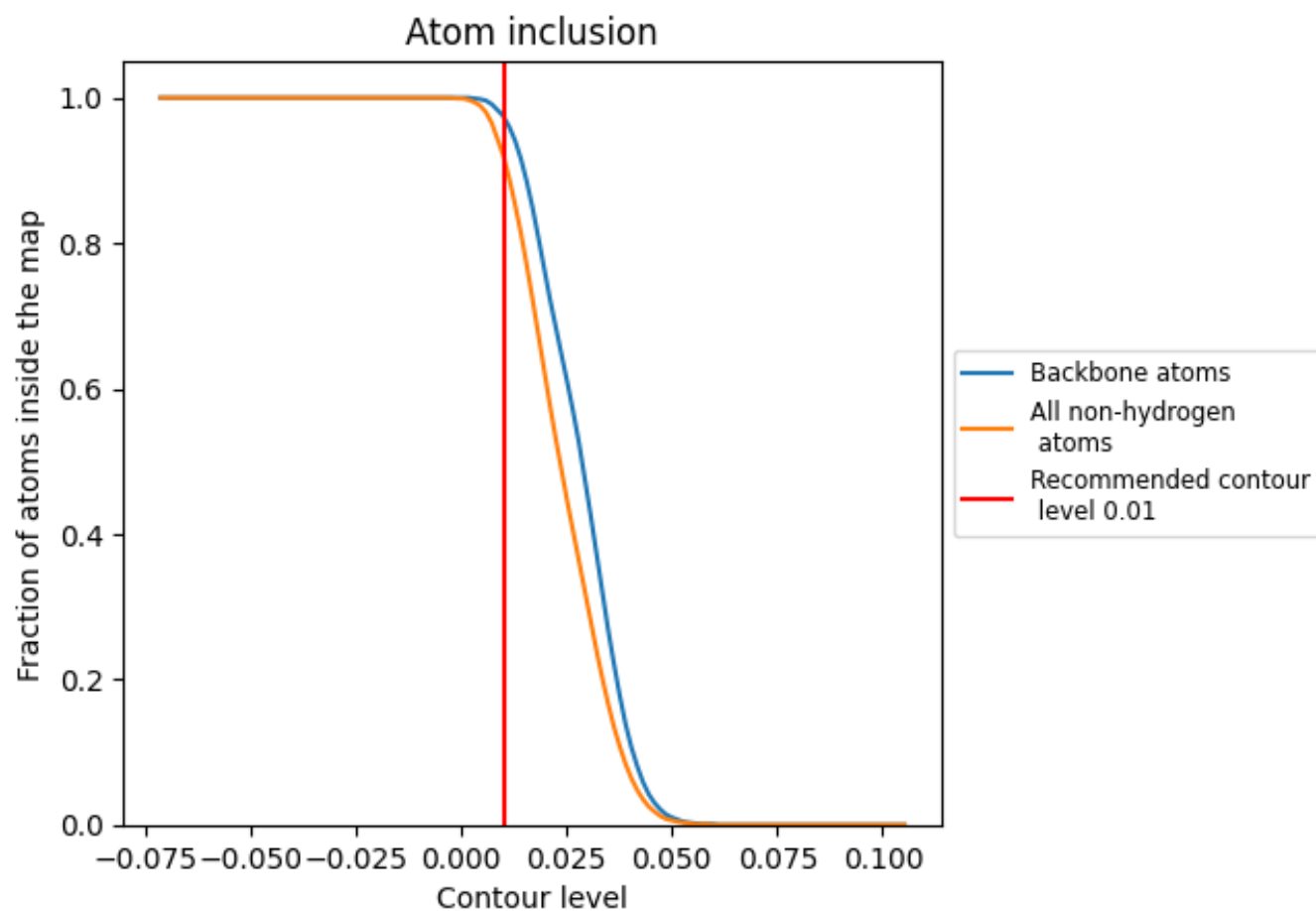
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).

8.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 92% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9200	 0.4910
A1	 0.9510	 0.4990
A2	 0.9330	 0.5050
A3	 0.9030	 0.5040
B1	 0.9420	 0.4980
B2	 0.9380	 0.5030
B3	 0.9400	 0.4980
C1	 0.9310	 0.5010
C2	 0.9270	 0.4930
C3	 0.9320	 0.4940
D1	 0.8910	 0.4810
D2	 0.8670	 0.4710
D3	 0.8900	 0.4750
E1	 0.8960	 0.4880
E2	 0.9310	 0.4960
E3	 0.9000	 0.4840
F1	 0.8830	 0.4800
F2	 0.9310	 0.4920
F3	 0.9110	 0.4870
G1	 0.9320	 0.4910
G2	 0.9330	 0.4870
G3	 0.9150	 0.4870
H1	 0.9310	 0.5050
H2	 0.9340	 0.4960
H3	 0.9010	 0.4990
I1	 0.9270	 0.4990
I2	 0.9290	 0.4950
I3	 0.9350	 0.4970
J1	 0.9580	 0.4950
J2	 0.9500	 0.4830
J3	 0.9520	 0.4880
K1	 0.8760	 0.4790
K2	 0.9500	 0.4790
K3	 0.9300	 0.4830
L1	 0.9250	 0.4770



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Chain	Atom inclusion	Q-score
L2	 0.8980	 0.4830
L3	 0.9050	 0.4910
M1	 0.9420	 0.5040
M2	 0.9330	 0.5080
M3	 0.9460	 0.5120
N1	 0.9430	 0.5050
N2	 0.9430	 0.5080
N3	 0.9410	 0.4980
O1	 0.9210	 0.4790
O2	 0.8770	 0.4690
O3	 0.8880	 0.4540
P1	 0.8690	 0.4800
P2	 0.9280	 0.4870
P3	 0.9250	 0.4780
Q1	 0.9270	 0.5090
Q2	 0.8490	 0.4900
Q3	 0.9020	 0.4950
R1	 0.9050	 0.4900
R2	 0.9470	 0.4880
R3	 0.9460	 0.4920
S1	 0.9160	 0.4770
S2	 0.9050	 0.4660
S3	 0.9200	 0.4800
T1	 0.9300	 0.4850
T2	 0.9450	 0.4860
T3	 0.9400	 0.4820
U1	 0.9420	 0.5110
U2	 0.9320	 0.5050
U3	 0.9280	 0.4920
V1	 0.9100	 0.4790
V2	 0.9150	 0.4800
V3	 0.9460	 0.4970
W1	 0.8860	 0.4860
W2	 0.9070	 0.4920
W3	 0.9260	 0.4960
X1	 0.9420	 0.4890
X2	 0.8850	 0.4830
X3	 0.9150	 0.4850
Y1	 0.8950	 0.4810
Y2	 0.9270	 0.4830
Y3	 0.8950	 0.4730
Z1	 0.9060	 0.4930

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Chain	Atom inclusion	Q-score
Z2	 0.9290	 0.4940
Z3	 0.8860	 0.4930
a1	 0.9380	 0.5030
a2	 0.8850	 0.4930
a3	 0.9460	 0.5020
b1	 0.9430	 0.4900
b2	 0.9420	 0.4940
b3	 0.9440	 0.4980
c1	 0.9480	 0.4990
c2	 0.9520	 0.5010
c3	 0.9490	 0.5030
d1	 0.9460	 0.5110
d2	 0.9480	 0.5110
d3	 0.9450	 0.5090
e1	 0.9480	 0.5050
e2	 0.9440	 0.5080
e3	 0.9440	 0.5090
f1	 0.9440	 0.5140
f2	 0.9460	 0.5130
f3	 0.9470	 0.5110
g1	 0.9500	 0.5120
g2	 0.9510	 0.5150
g3	 0.9500	 0.5140
h1	 0.9500	 0.5140
h2	 0.9510	 0.5110
h3	 0.9500	 0.5080
j1	 0.9090	 0.4750
j2	 0.9130	 0.4800
j3	 0.9610	 0.4890
k1	 0.9400	 0.4980
k2	 0.9440	 0.4970
k3	 0.9370	 0.4980
m1	 0.9530	 0.4880
m2	 0.9580	 0.4910
m3	 0.9500	 0.4950
n1	 0.9400	 0.4990
n2	 0.9380	 0.4980
n3	 0.9370	 0.4950
p1	 0.9280	 0.4950
p2	 0.9350	 0.4970
p3	 0.9390	 0.4940
q1	 0.9340	 0.4910

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Chain	Atom inclusion	Q-score
q2	 0.9460	 0.4880
q3	 0.9460	 0.4800
r1	 0.9380	 0.4940
r2	 0.9380	 0.4960
r3	 0.9340	 0.4890
s1	 0.8940	 0.4920
s2	 0.7290	 0.4320
s3	 0.8660	 0.4740
s4	 0.8320	 0.4630
s5	 0.7850	 0.4510
s6	 0.7830	 0.4420
t1	 0.8060	 0.4590
t2	 0.8350	 0.4890
t3	 0.8930	 0.4900
t4	 0.8240	 0.4540
t5	 0.7400	 0.4380
t6	 0.8500	 0.4820
t7	 0.8110	 0.4550
y1	 0.5060	 0.3730
y2	 0.7730	 0.4460
y3	 0.9580	 0.4640
y4	 0.3770	 0.3480
y5	 0.8430	 0.4920
y6	 0.7190	 0.4310
y7	 0.6520	 0.4470
y8	 0.5400	 0.4210