



wwPDB EM Validation Summary Report ⓘ

Mar 7, 2026 – 03:20 AM UTC

PDB ID : 7DL2 / pdb_00007dl2
EMDB ID : EMD-30708
Title : Cryo-EM structure of human TSC complex
Authors : Yang, H.; Yu, Z.; Chen, X.; Li, J.; Li, N.; Cheng, J.; Gao, N.; Yuan, H.; Ye, D.; Guan, K.; Xu, Y.
Deposited on : 2020-11-25
Resolution : 4.40 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:

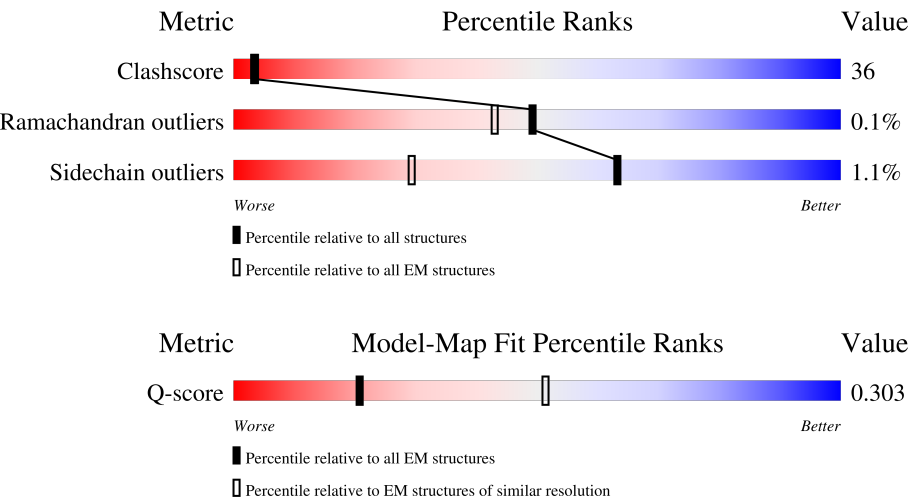
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 4.40 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.



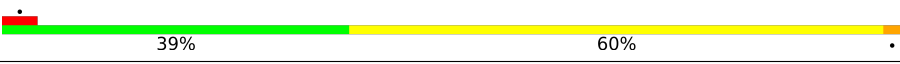
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	3132 (3.91 - 4.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	C	1164	
1	D	1164	
2	A	1692	
2	B	1692	

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Mol	Chain	Length	Quality of chain
3	E	267	 39% 60%
4	F	261	 60% 75% 22%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 23285 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 Hamartin.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	D	226	Total	C	N	O	S	0	0
			1575	973	294	305	3		
1	C	224	Total	C	N	O	S	0	0
			1558	962	291	302	3		

- Molecule 2 is a protein called Isoform 7 of Tuberin.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	1127	Total	C	N	O	S	0	0
			9016	5785	1544	1632	55		
2	B	1042	Total	C	N	O	S	0	0
			7952	5079	1379	1455	39		

- Molecule 3 is a protein called TBC1 domain family member 7.

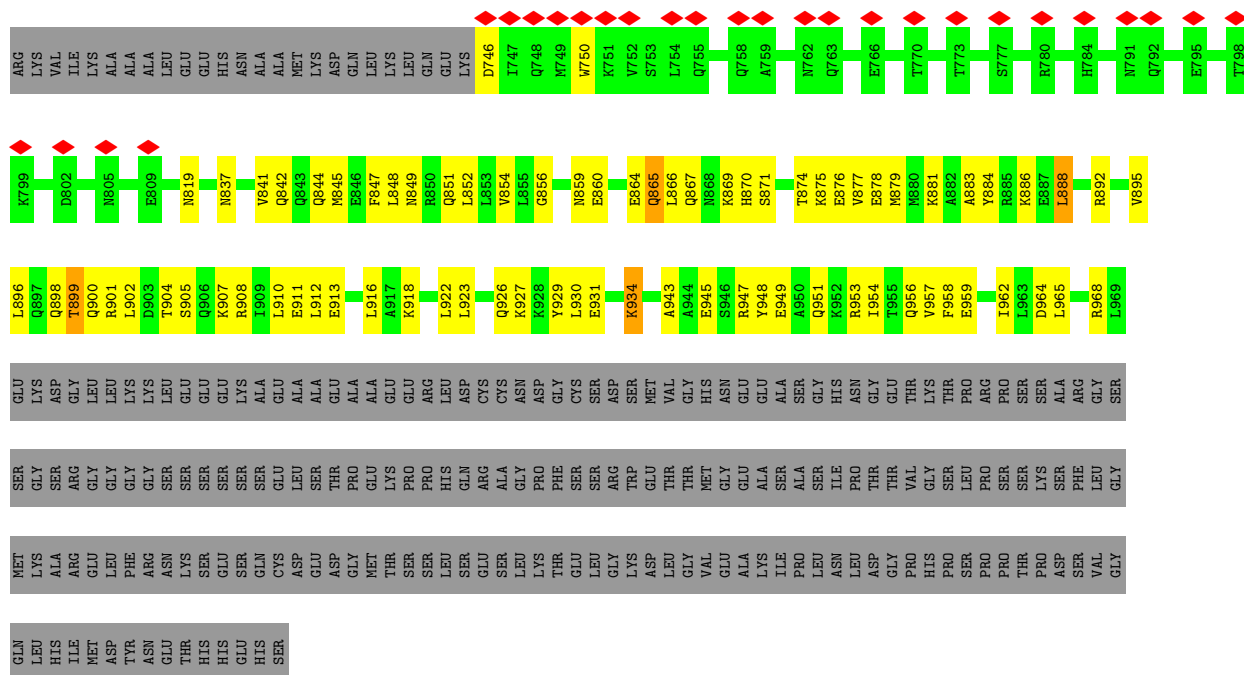
Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	267	Total	C	N	O	S	0	0
			2169	1403	364	387	15		

- Molecule 4 is a protein called unknown protein.

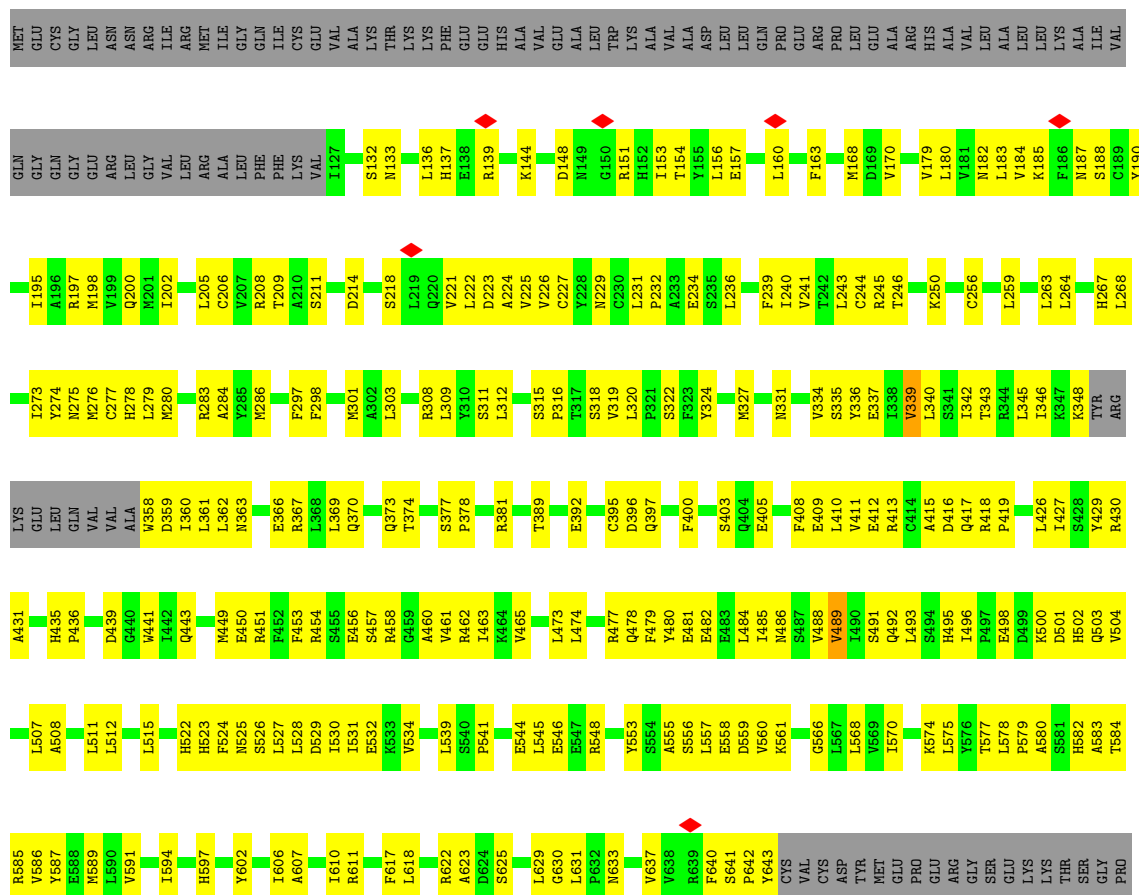
Mol	Chain	Residues	Atoms				AltConf	Trace
4	F	203	Total	C	N	O	0	0
			1015	609	203	203		

- Molecule 1: Hamartin





• Molecule 2: Isoform 7 of Tuberin





Chain B:



S918	N919	V920	L921	F924	D925	D926	R934	R935	R936	S937	THR	LEU	ASN	GLU	ARG	PRO	LYS	SER	ILE	GLN	THR	SER	LEU	THR	SER	LEU	THR	SER	ALA	SER	LEU	ASP	ALA	ASP	GLU	ASN	SER	VAL	ALA	GLN	ALA	GLY	ALA	ASP	SER	L1015	H1019	L1022	C1026	L1027	D1028	M1029	M1030	A1031	R1032
Y1033	V1034	F1035	S1036	N1037	F1038	T1039	A1040	R1044	G1048	E1049	F1050	L1051	L1052	R1056	T1057	K1058	T1059	W1060	L1061	L1066	V1073	G1074	T1075	G1076	T1077	S1078	S1079	L1081	L1080	GLY	LEU	ASP	VAL	PRO	ALA	GLY	ASN	SER	GLU	GLN	PHE	LEU	GLY	ALA	ASP	THR	SER	PRO	GLY	ARG	THR	ALA	ALA	LYS	PRO
GLU	ALA	PRO	ALA	LEU	GLY	GLU	SER	GLN	GLN	VAL	VAL	SER	ARG	ALA	ARG	ASP	VAL	ARG	ARG	MET	SER	GLY	HIS	GLY	LEU	ARG	VAL	GLY	ALA	ASP	VAL	PRO	ALA	GLY	ASN	SER	GLU	GLN	PHE	LEU	GLY	ALA	ASP	THR	SER	PRO	GLY	ARG	THR	ALA	ALA	LYS	PRO		
GLU	LYS	ALA	SER	ALA	GLY	THR	ARG	VAL	VAL	GLU	K1180	T1181	L1182	L1183	A1184	A1185	Y1186	V1187	W1194	A1195	E1196	I1197	L1198	V1199	R1200	R1201	P1202	T1203	G1204	N1205	T1206	S1207	W1208	L1209	M1210	S1211	L1212	E1213	M1214	P1215	L1216	S1217	F1219	I1223	P1227	L1228	Q1229	E1230	L1231	S1232	L1235	M1236			
A1237	A1238	E1239	R1240	F1241	K1242	HIS	GLU	ASP	THR	ALA	LEU	TYR	SER	LEU	SER	VAL	PRO	ALA	ALA	THR	SER	LYS	ALA	LEU	PRO	LEU	PRO	ARG	VAL	GLY	ASN	THR	ASP	SER	ALA	VAL	ILE	PRO	GLU	VAL	SER	GLY	GLY	GLY	VAL	VAL	LEU	GLU	PRO	PHE	GLN	PRO	GLY	ASP	
VAL	GLU	ALA	LEU	GLY	MET	ASP	ARG	THR	THR	ALA	ALA	THR	SER	GLN	THR	VAL	GLY	GLN	GLY	GLU	GLY	LYS	ALA	VAL	GLU	GLU	GLU	PRO	LEU	VAL	GLY	ARG	ILE	PRO	ILE	GLN	GLY	THR	VAL	VAL	SER	GLY	GLY	GLY	ARG	PRO	SER	VAL	ASP	VAL	GLY	SER			
GLN	PRO	LEU	SER	LYS	SER	SER	SER	PRO	GLU	GLU	GLN	THR	THR	ILE	ASP	GLY	PRO	GLY	ASP	GLY	LYS	ALA	ASP	VAL	GLY	ARG	LEU	PRO	VAL	VAL	VAL	VAL	VAL	ARG	SER	GLN	GLY	THR	LEU	ASP	GLY	GLU	SER	ALA	ALA	TRP	SER	ALA	VAL	SER	GLY				
GLN	PRO	GLY	GLY	PRO	LEU	PRO	SER	ARG	PRO	SER	PRO	SER	GLY	ARG	PRO	ARG	GLY	TYR	THR	ILE	SER	ASP	SER	ALA	PRO	SER	ARG	GLY	LYS	VAL	ARG	GLY	ALA	ARG	ASP	ALA	GLN	GLY	THR	SER	ARG	ALA	VAL	SER	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY			
L1502	Q1503	L1504	Y1505	H1506	F1509	F1510	D1512	L1519	L1520	E1523	S1526	R1529	S1530	L1534	Q1535	I1537	F1538	Y1539	D1541	T1542	H1543	K1544	A1546	Y1549	V1550	G1551	E1552	G1553	Q1554	S1555	L1559	A1560	I1561	L1562	S1563	N1564	F1565	H1566	Y1571	T1572	L1575	L1578	I1582												
E1583	L1584	D1586	C1587	Q1588	P1589	D1590	K1591	Y1592	Y1593	L1594	G1595	V1599	CYS	GLY	GLU	ASP	GLY	Q1605	F1606	C1609	W1610	H1611	D1612	D1613	I1614	M1615	K1616	A1617	V1618	F1619	H1620	I1621	A1622	L1624	M1625	P1626	THR	LYS	ASP	VAL	ASP	LYS	HIS	ARG	CYS	D1636	K1637	K1638	F1639	H1640	N1643	D1644	F1645		
I1648	V1649	Y1650	N1651	D1652	S1653	K1654	E1655	D1656	F1657	K1658	T1661	I1662	Q1665	F1666	M1667	F1668	I1672	V1673	T1674	Y1678	E1679	V1683	C1687	R1688	K1689	D1690	M1691	E1692	D1696	T1697	K1701	I1702	V1703	S1704	D1705	R1706	M1707	L1708	P1709	F1710	V1711	Q1714	M1715	A1716	L1717	H1718	A1719	M1720	M1721	A1722					
S1723	Q1724	V1725	Y1736	P1737	S1738	K1739	W1740	I1741	A1742	R1743	H1746	I1747	L1750	R1753	I1754	C1755	GLU	GLU	ALA	ALA	TTR	SER	ASN	PRO	PRO	LEU	LEU	VAL	HIS	PRO	PRO	HIS	LYS	LYS	ALA	ALA	GLN	THR	PRO	ALA	GLU	PRO	THR	PRO	GLY	TYR	GLU	VAL	GLY	GLN	ARG	LYS			
ARG	LEU	ILE	SER	SER	VAL	ASP	PHE	THR	GLU	PHE	VAL																																												

• Molecule 3: TBC1 domain family member 7



G21	V22	E23	E24	K26	K28	S27	L28	E29	L30	K33	D34	D35	R36	L37	D38	T39	E40	K41	L42	C43	T44	F45	S46	Q47	L51	R56	A57	L58	V59	W60	V62	L63	I66	L67	P68	P69	H70	H71	E72	S73	H74	A75	K76	V77	M78	M79	Y80	R81	K82	E83	Q84	Y85	L86	D87
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	131022	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.065	Depositor
Minimum map value	-0.030	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.016	Depositor
Map size (Å)	705.12, 705.12, 705.12	wwPDB
Map dimensions	520, 520, 520	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.356, 1.356, 1.356	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	C	0.63	0/1568	0.94	1/2126 (0.0%)
1	D	0.61	0/1585	0.86	0/2148
2	A	0.32	0/9207	0.52	0/12489
2	B	0.32	0/8099	0.54	5/10996 (0.0%)
3	E	0.53	0/2221	0.74	0/3005
All	All	0.40	0/22680	0.62	6/30764 (0.0%)

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	B	232	PRO	N-CA-CB	6.80	110.48	103.00
2	B	131	PRO	N-CA-CB	6.45	110.35	103.39
2	B	1613	ASP	O-C-N	-6.17	115.67	122.09
2	B	290	PRO	N-CA-CB	6.15	110.03	103.39
2	B	237	PRO	N-CA-CB	6.02	110.18	103.44

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	1558	0	1313	189	0
1	D	1575	0	1329	183	0
2	A	9016	0	9119	633	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	7952	0	7731	553	0
3	E	2169	0	2210	256	0
4	F	1015	0	231	4	0
All	All	23285	0	21933	1612	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 36.

The worst 5 of 1612 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1534:LEU:HB2	2:B:1746:HIS:CE1	1.41	1.52
3:E:249:LYS:HG2	3:E:262:PHE:CE1	1.50	1.46
1:D:854:VAL:CG2	2:B:1235:LEU:HD11	1.54	1.38
1:D:854:VAL:HG22	2:B:1235:LEU:CD1	1.57	1.34
3:E:249:LYS:HG2	3:E:262:PHE:CD1	1.64	1.32

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	222/1164 (19%)	215 (97%)	7 (3%)	0	100	100
1	D	224/1164 (19%)	216 (96%)	7 (3%)	1 (0%)	30	66
2	A	1107/1692 (65%)	960 (87%)	147 (13%)	0	100	100
2	B	1008/1692 (60%)	900 (89%)	106 (10%)	2 (0%)	43	77
3	E	265/267 (99%)	246 (93%)	18 (7%)	1 (0%)	30	66
All	All	2826/5979 (47%)	2537 (90%)	285 (10%)	4 (0%)	49	83

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	881	LYS
3	E	218	SER
2	B	1536	GLN
2	B	289	ALA

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	120/1033 (12%)	114 (95%)	6 (5%)	22	43
1	D	121/1033 (12%)	117 (97%)	4 (3%)	33	55
2	A	1017/1480 (69%)	1012 (100%)	5 (0%)	81	81
2	B	832/1480 (56%)	826 (99%)	6 (1%)	76	79
3	E	243/243 (100%)	238 (98%)	5 (2%)	47	65
All	All	2333/5269 (44%)	2307 (99%)	26 (1%)	63	74

5 of 26 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	1599	VAL
1	C	899	THR
3	E	109	LEU
1	C	888	LEU
1	C	931	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 49 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	600	HIS
2	B	1727	HIS
2	B	699	GLN
2	B	1554	GLN
1	C	844	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

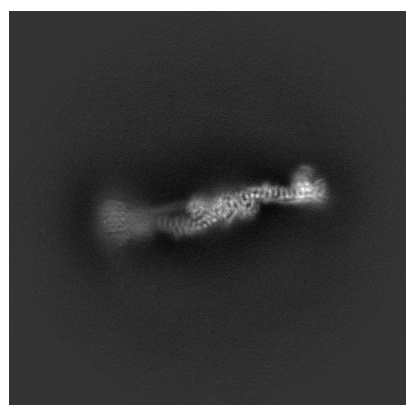
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30708. These allow visual inspection of the internal detail of the map and identification of artifacts.

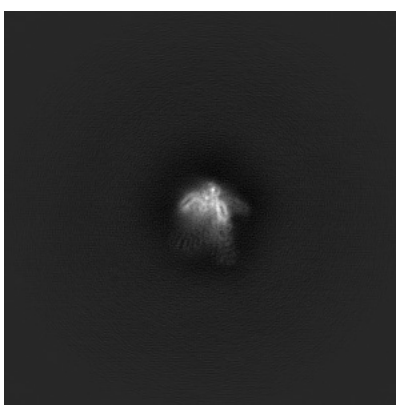
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

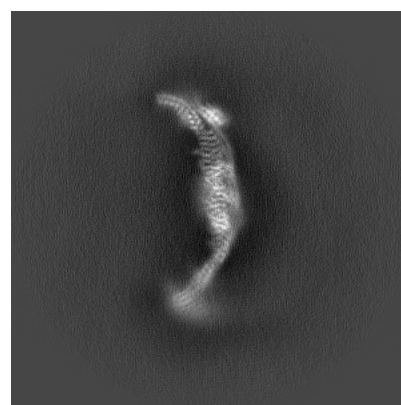
6.1.1 Primary map



X



Y



Z

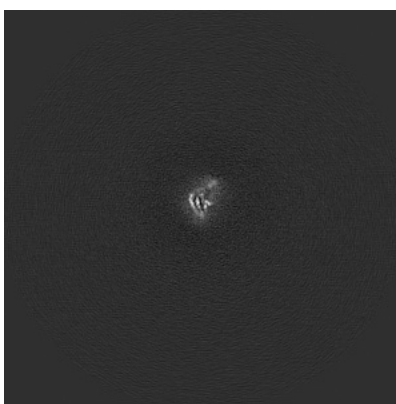
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 260



Y Index: 260

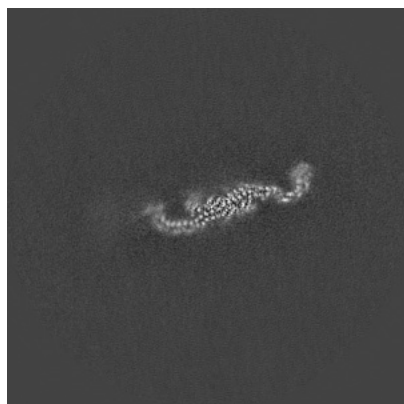


Z Index: 260

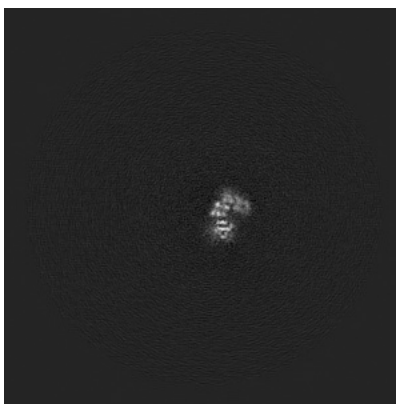
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

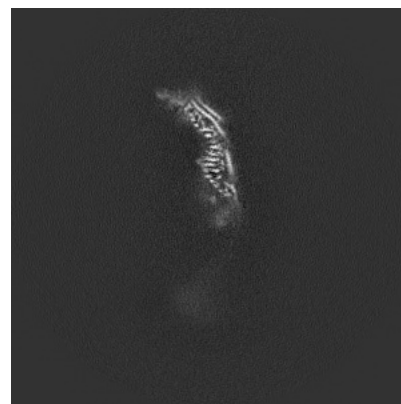
6.3.1 Primary map



X Index: 267



Y Index: 382

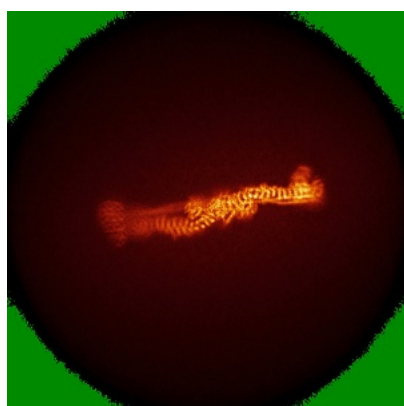


Z Index: 278

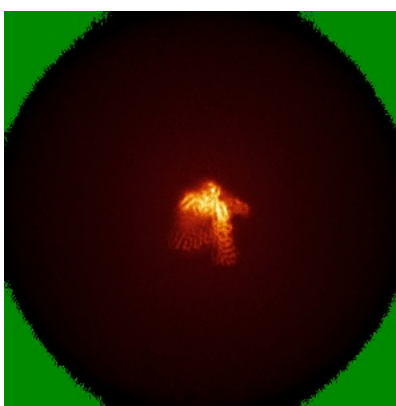
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 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.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.016. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

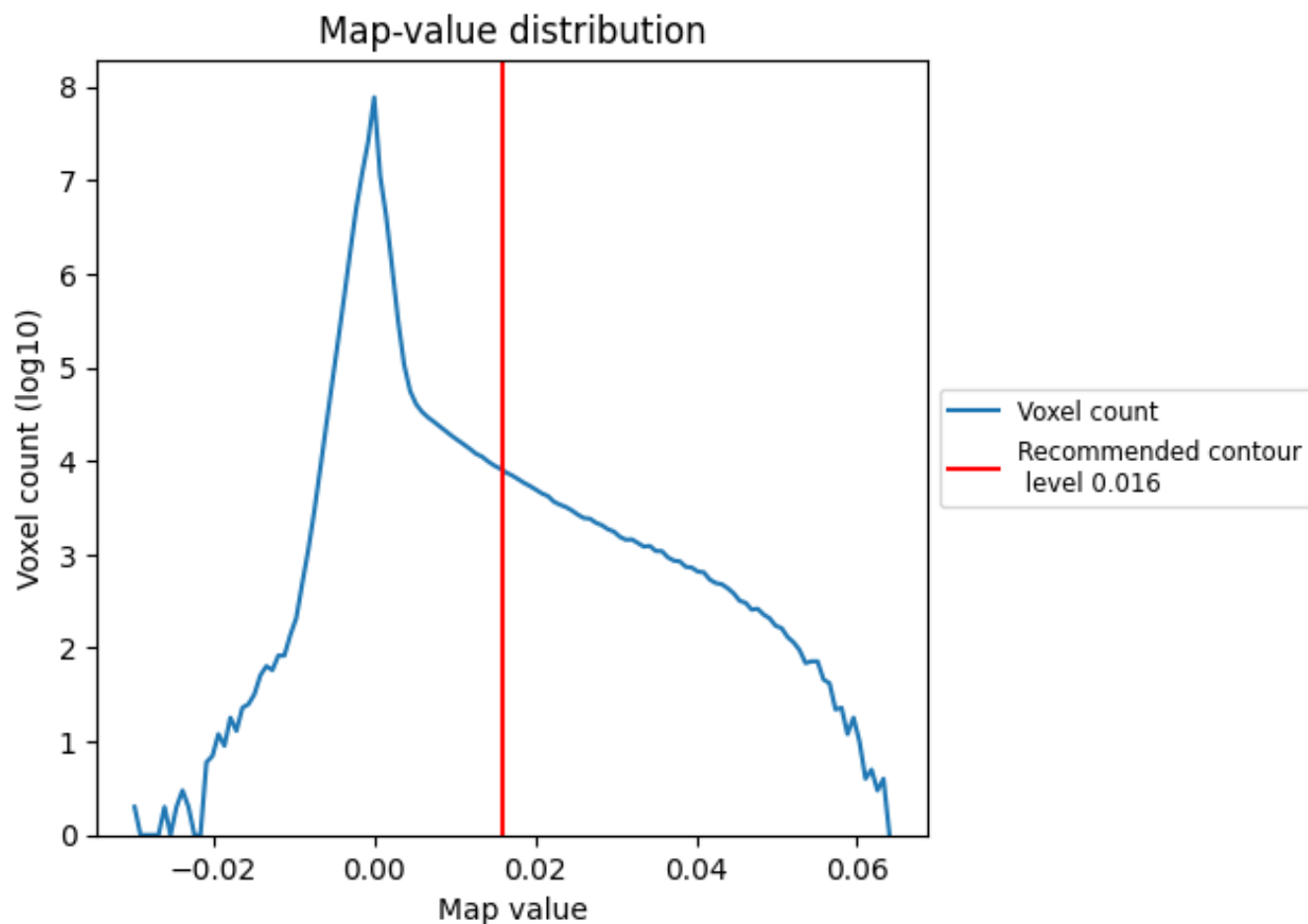
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

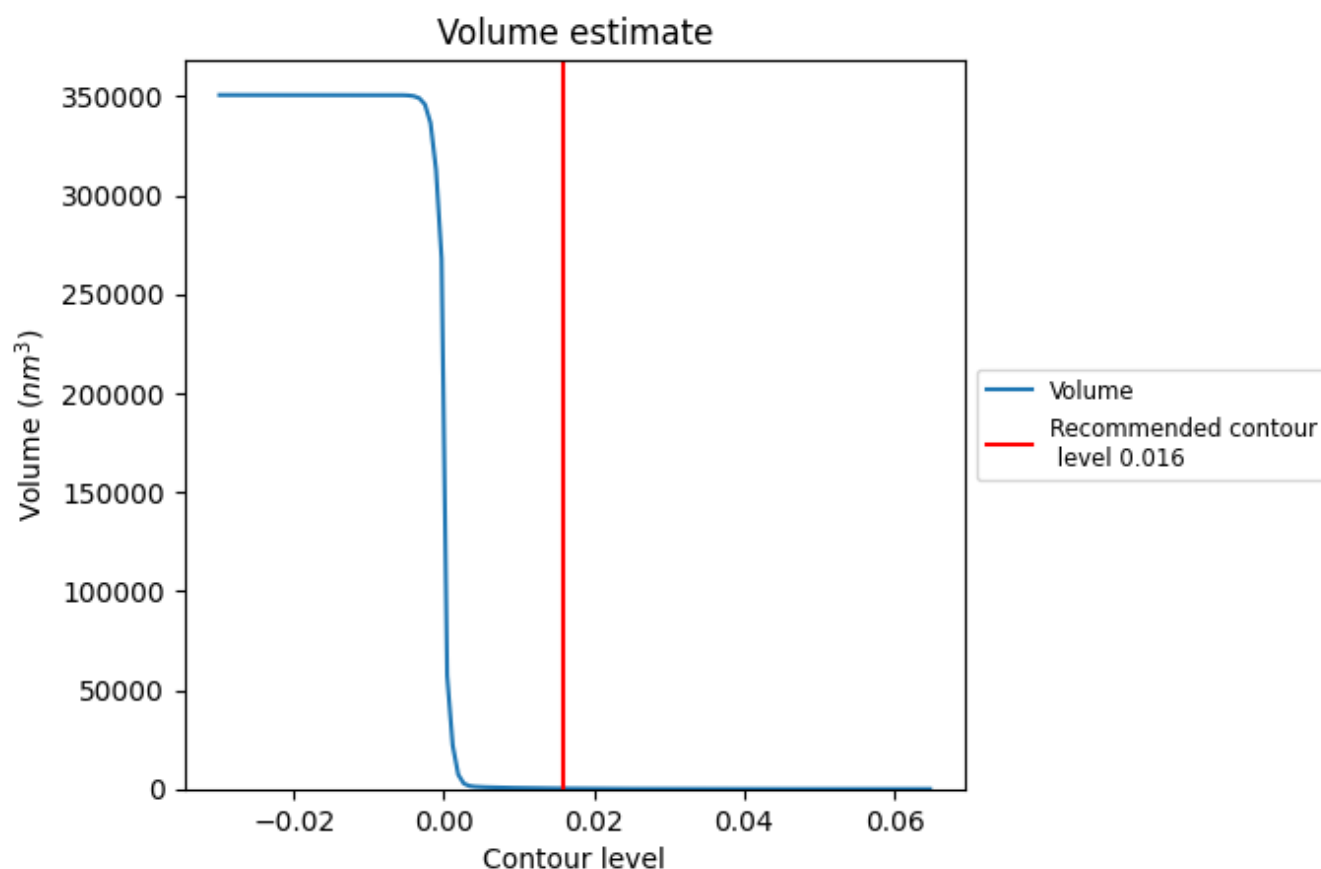
This section contains the results of statistical analysis of the map.

7.1 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.

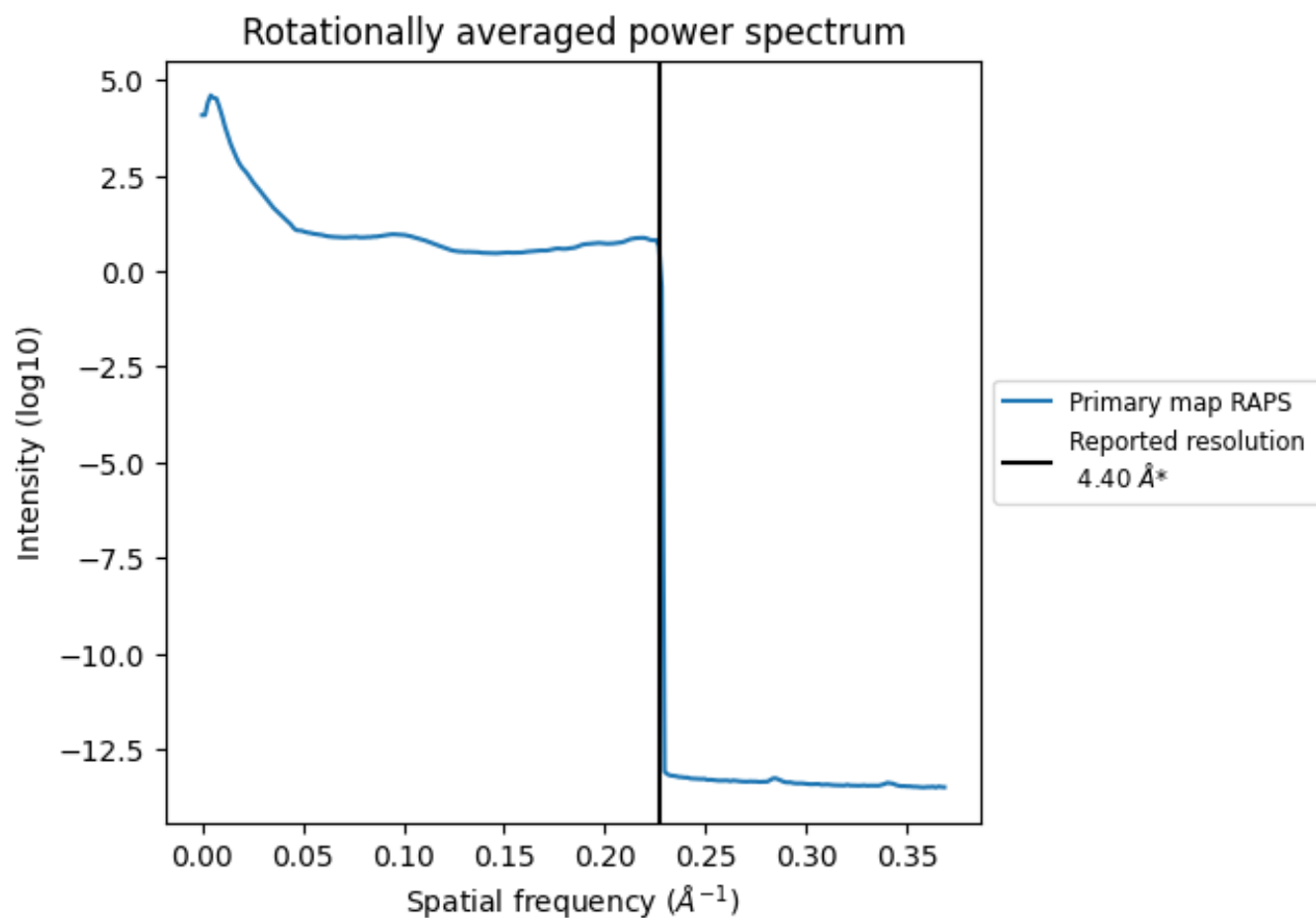
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 247 nm^3 ; this corresponds to an approximate mass of 223 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.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.227 Å⁻¹

8 Fourier-Shell correlation

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

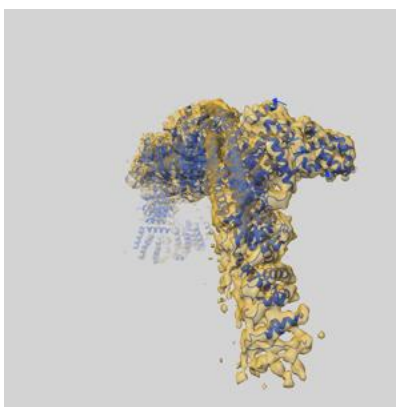
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-30708 and PDB model 7DL2. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



X



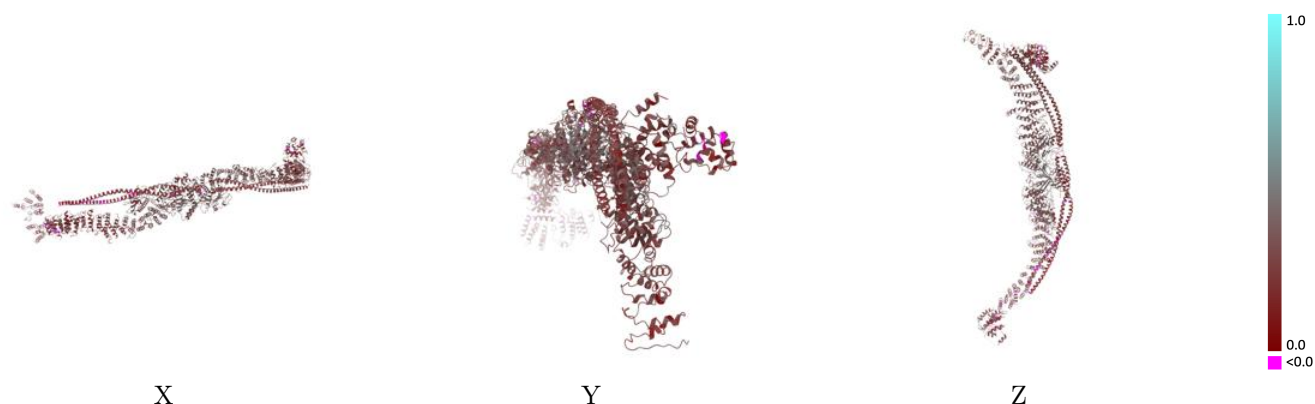
Y



Z

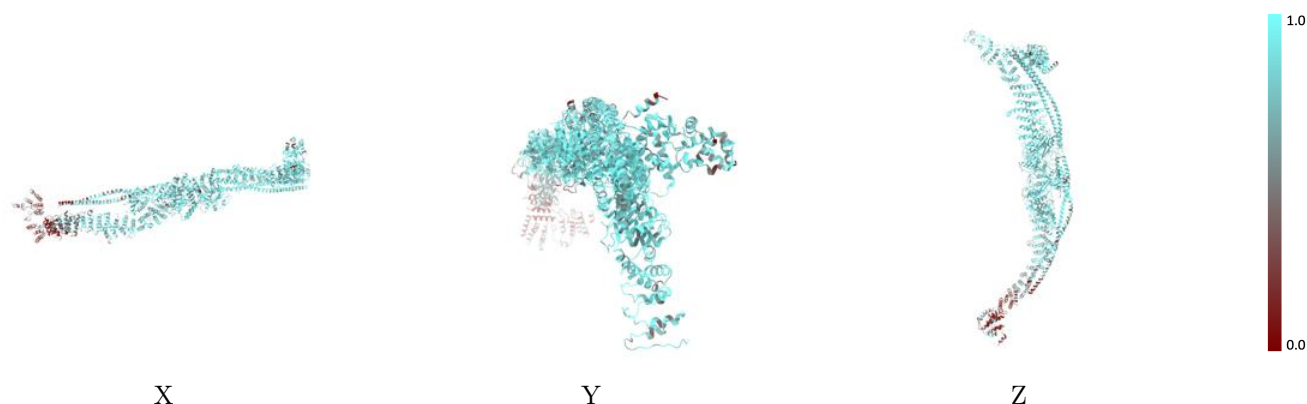
The images above show the 3D surface view of the map at the recommended contour level 0.016 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



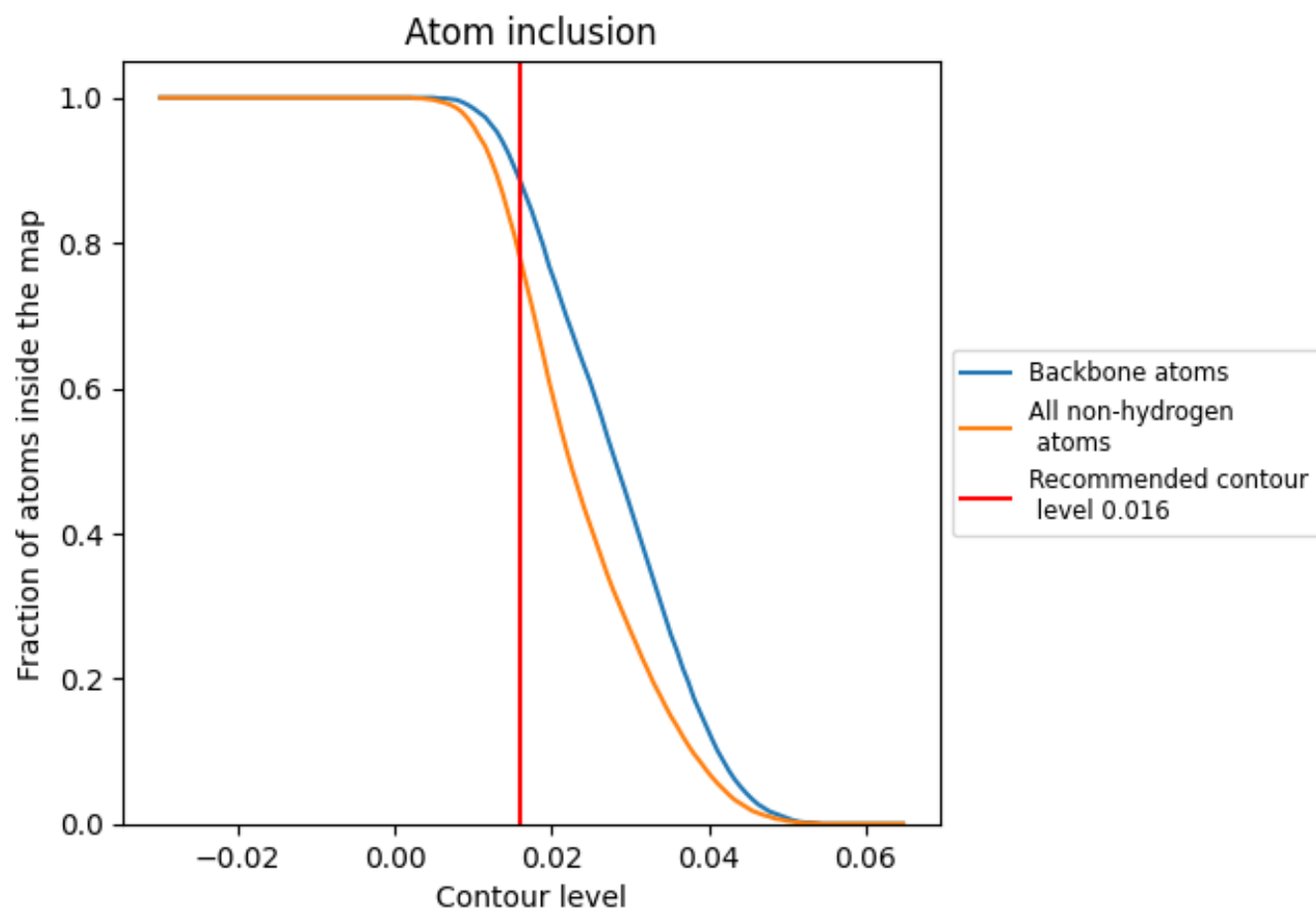
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 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 (0.016).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 78% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.016) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7780	0.3030
A	0.8560	0.3380
B	0.7500	0.3040
C	0.7780	0.2320
D	0.7650	0.2370
E	0.8080	0.2620
F	0.2780	0.2850

1.0

0.0

<0.0