



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 07:00 PM UTC

PDB ID : 8YIH / pdb_00008yih
EMDB ID : EMD-39319
Title : DmDcr-2/LoqsPD/slm1 in pre-dicing state
Authors : Cao, N.; Su, S.; Wang, J.; Ma, J.; Wang, H.-W.
Deposited on : 2024-02-29
Resolution : 4.08 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
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

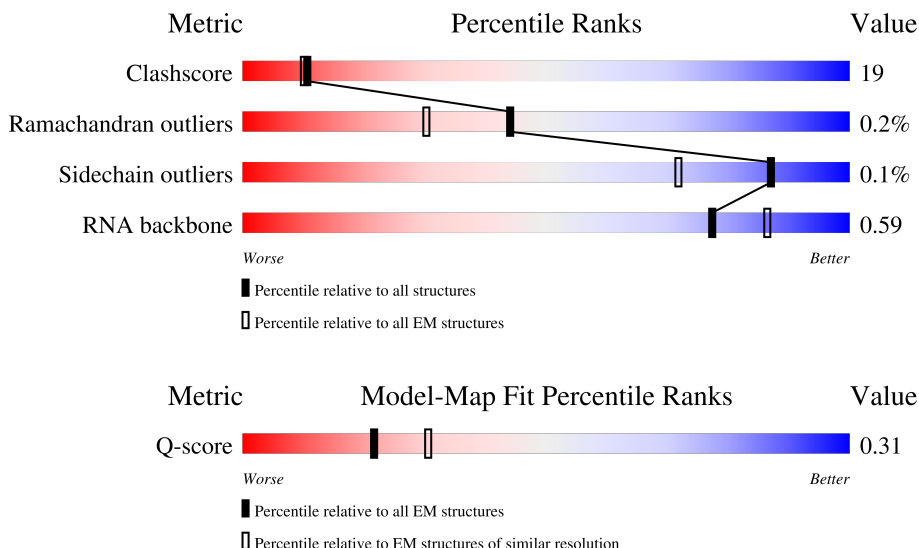
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

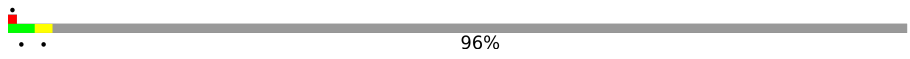
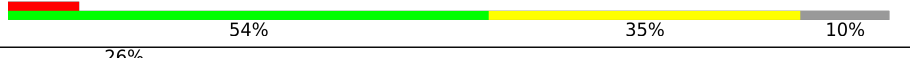
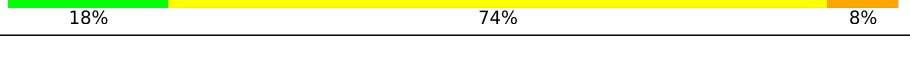
The reported resolution of this entry is 4.08 Å.

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	-
RNA backbone	8273	3508	-
Q-score	-	25397	6428 (3.58 - 4.58)

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	B	359	 96%
2	A	1721	 8% 54% 35% 10%
3	C	96	 26% 18% 74% 8%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 14692 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 Isoform PD of Protein Loquacious.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	B	16	Total	C	N	O	0	0
			144	94	22	28		

- Molecule 2 is a protein called Dicer-2, isoform A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	1544	Total	C	N	O	S	0	0
			12490	8004	2134	2284	68		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1217	ASN	ASP	conflict	UNP A1ZAW0
A	1476	ASN	ASP	conflict	UNP A1ZAW0

- Molecule 3 is a RNA chain called slm1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	96	Total	C	N	O	P	0	0
			2029	910	349	674	96		

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

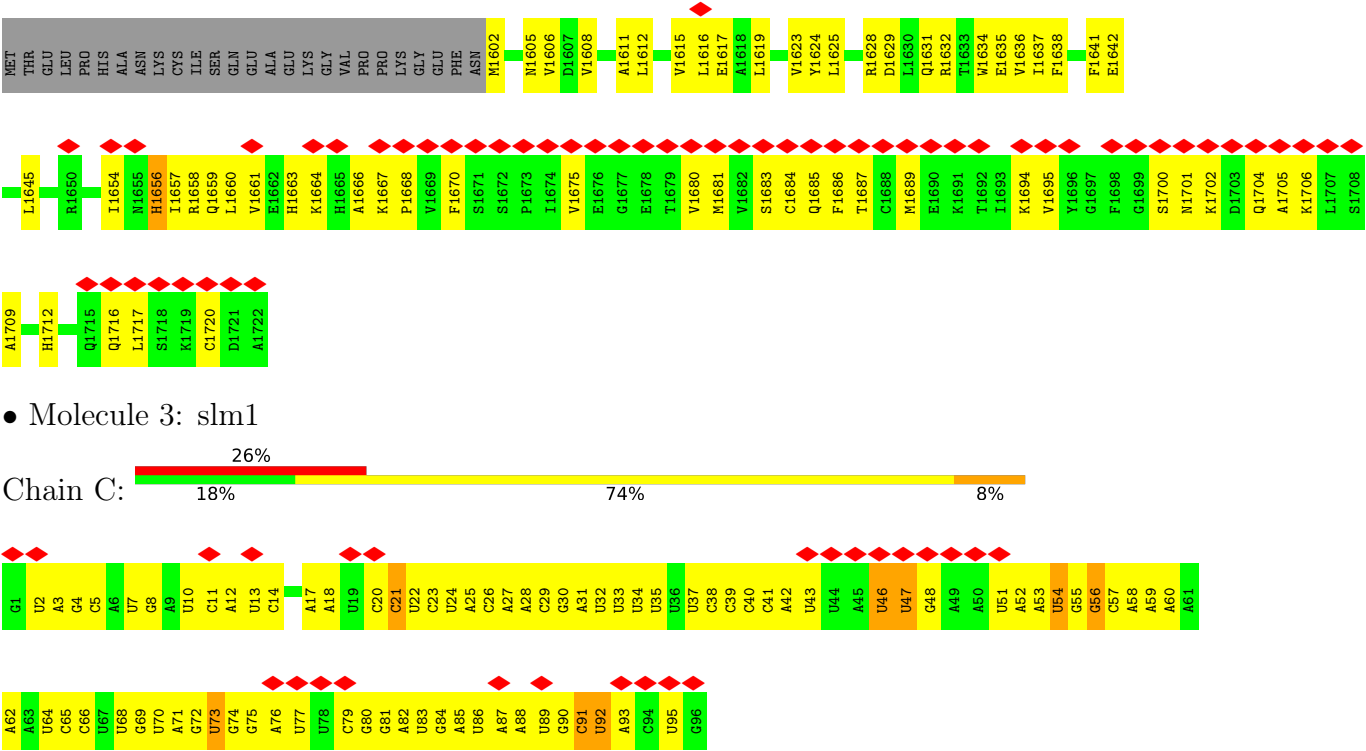
Mol	Chain	Residues	Atoms		AltConf
4	A	2	Total	Mg	0
			2	2	

- Molecule 5 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
5	A	1	27	10	5	10	2	0

T1500	P1403	G1303	S1201	L905	L820	P718	D533	E538	S431	D347
R1503	L1404	P1304	S1202	S906	D821	I723	P634	K539	E436	D348
N1508	T1405	H1305	V1206	Y907	R822	C724	M635	T540	S435	D349
T1511	L1408	L1307	F1207	N908	Y829	Y727	N637	E541	V437	D350
L1512	N1409	R1308	D1208	Q913	V831	E732	V638	P542	L438	D351
L1513	N1410		E1209	D914	V832	P733	K639	E543	E439	N352
L1514	E1411		R1211	K915	P833	F734	T640	L544	R440	E356
C1516	L1412		I1214	Y916	L834	Q734	K642	I547	E443	E357
V1517	K1415		L1215	Y917		Y735	I643	K548	Q443	V358
R1518	M1416		E1216	Y918	G839	Y740	S644	G549	A446	I359
L1521	M1417		R1009	N922	E840		A645	H550	E446	M360
I1525	R1418		L1100	S923	G843	H743	F647	D554	M454	F362
E1528	A1419		L1020	K924	F844	M744	K648	P557	A455	R369
N1529	N1420		P1021	Y925	D845	Y745	L653	F558	M456	F370
A1530	V1421		F1022	G926	L848	L748	Y654	T559	L457	L371
K1531	N1422		F1023	N927	M849	Q749	G857	N560	M458	M372
L1532	N1423		T1026	R928		R752	E658	P568	I459	S373
E1425	T1424		D1027	T929	Q857	A755	L659	B577	L464	L374
E1425	E1424		Y1028	D931	G860	L757	N660	Y578	E465	F378
F1444	E1425		R1031	Y932	S861	L758	R662	T581	E466	
R1448	F1444		P1032	H934	N862	L762	F663	F587	H475	K381
K1538	R1449		L1033	F938	V863	L765	N664	G588	V476	D382
F1539	L1450		E1034	N939	Q864	L765	R665	F587	F477	P383
V1540	N1541		A1036	I940	Q865	L765	T667	G587	V482	I386
N1541	A1453		D1036	E941	R866	M768	E670	F587	M486	L389
F1542	L1454		K1040	Y942	Q868	P769	H679	G588	M487	L390
Q1543	T1455		ARG	N943		L770	F680	E601	A507	M407
H1548	H1456		ASN	D944	P872	F771	H679	R602	D508	Y408
N1552	P1457		PRO	L949	D876	G775	E681	D603	K509	I409
VAL	S1458		GLY	F951	F877	K776	H682	R604	E510	Q410
ILE	M1462		ASN	Y952	T881	N792	K885	H614	R511	S411
LEU	R1463		VAL	R956	V882	S793	D888	V615	R512	T412
GLU	I1464		TYR	G957	T883	E794	S689	I616	K513	P413
GLU	T1465		THR	K958	Q884	L799	V690	S617	Q517	E414
ALA	Q1469		THR	F959	W886	Q800	K885	M620	A524	L415
ASP	L1471		GLY	N960	Y886	H800	D888	P621	D527	R416
VAL	F1473		ASN	A961	N888	Q801	S689	D621	I528	M417
GLN	D1480		VAL	K962	Y889	H803	K885	C624	M625	V418
PRO	F1481		CYS	S963	D890	G804	A697	M625	Y531	L419
THR	L1482		GLY	K964	K891	M805	D890	D702	E531	T420
PRO	N1483		GLY	N966	P892	V806	D890	R702	K533	
LEU	S1484		LEU	K966	M893	F807	K698	R703	L536	R427
ASP	T1487		GLY	N967	L894	R808	K699	T704	K533	M428
ASP	T1492		PRO	1972	V895	I810	S700	Y705	V536	M429
GLU	K1493		ASP	1973	V898	W814	K701	D628	L537	
LEU	D1401		THR	E974	H899	V819	R703	T629		
ASP	M1494		GLY	L975	F901		Y705	I630		
	A1498		ASP	F981	L902		L717	Y631		
	L1499			D984				S632		



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	78861	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)	1000	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOCONTINUUM (6k x 4k)	Depositor
Maximum map value	1.141	Depositor
Minimum map value	-0.519	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.049	Depositor
Recommended contour level	0.3	Depositor
Map size (Å)	257.808, 257.808, 257.808	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0742, 1.0742, 1.0742	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ADP

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	B	0.11	0/146	0.26	0/192
2	A	0.15	0/12759	0.35	2/17259 (0.0%)
3	C	0.12	0/2266	0.26	0/3524
All	All	0.14	0/15171	0.34	2/20975 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	872	PRO	N-CD-CG	-8.98	89.73	103.20
2	A	872	PRO	CA-N-CD	-6.62	102.73	112.00

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	B	144	0	140	7	0
2	A	12490	0	12567	457	0
3	C	2029	0	1026	84	0
4	A	2	0	0	0	0
5	A	27	0	12	4	0
All	All	14692	0	13745	532	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 19.

The worst 5 of 532 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:A:1020:LEU:HG	2:A:1022:PRO:HD2	1.60	0.83
3:C:2:U:H3	3:C:93:A:H61	1.29	0.78
2:A:1641:PHE:HB3	2:A:1645:LEU:HD23	1.65	0.77
2:A:1032:PRO:HD2	2:A:1206:VAL:HG22	1.67	0.76
2:A:632:SER:HB3	2:A:645:ALA:HB2	1.69	0.75

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	B	14/359 (4%)	11 (79%)	3 (21%)	0	100	100
2	A	1538/1721 (89%)	1467 (95%)	68 (4%)	3 (0%)	43	75
All	All	1552/2080 (75%)	1478 (95%)	71 (5%)	3 (0%)	44	75

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	1036	ASP
2	A	1656	HIS
2	A	1657	ILE

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	B	16/289 (6%)	16 (100%)	0	100	100
2	A	1386/1548 (90%)	1385 (100%)	1 (0%)	88	89
All	All	1402/1837 (76%)	1401 (100%)	1 (0%)	87	89

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	341	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
2	A	1267	ASN
2	A	1659	GLN
2	A	1329	ASN
2	A	1685	GLN
2	A	1639	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	C	95/96 (98%)	11 (11%)	2 (2%)

5 of 11 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	C	21	C
3	C	47	U
3	C	48	G
3	C	54	U
3	C	56	G

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	C	46	U
3	C	91	C

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](#)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	ADP	A	1802	4	28,29,29	1.38	5 (17%)	43,45,45	1.82	11 (25%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	ADP	A	1802	4	-	5/16/32/32	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1802	ADP	C5-C4	4.56	1.47	1.39
5	A	1802	ADP	C5-C6	2.65	1.48	1.41
5	A	1802	ADP	C8-N7	2.37	1.36	1.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1802	ADP	C5-N7	-2.33	1.34	1.39
5	A	1802	ADP	C4-N9	-2.06	1.33	1.37

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1802	ADP	C5-C4-N3	-5.69	118.88	126.72
5	A	1802	ADP	N3-C4-N9	4.48	134.78	127.17
5	A	1802	ADP	C2-N3-C4	3.57	120.55	111.83
5	A	1802	ADP	C4-C5-N7	-3.39	106.70	110.58
5	A	1802	ADP	N3-C2-N1	-2.93	124.15	128.58

There are no chirality outliers.

All (5) torsion outliers are listed below:

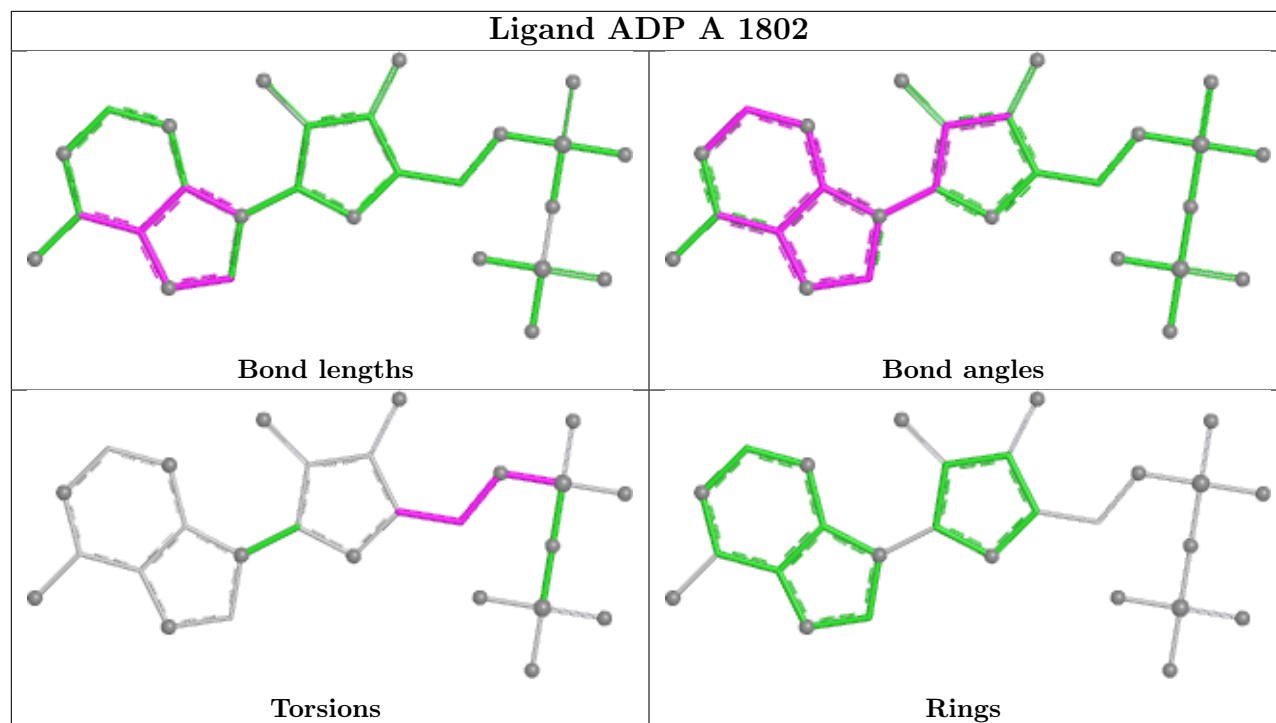
Mol	Chain	Res	Type	Atoms
5	A	1802	ADP	C5'-O5'-PA-O1A
5	A	1802	ADP	C5'-O5'-PA-O2A
5	A	1802	ADP	C5'-O5'-PA-O3A
5	A	1802	ADP	C4'-C5'-O5'-PA
5	A	1802	ADP	O4'-C4'-C5'-O5'

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1802	ADP	4	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

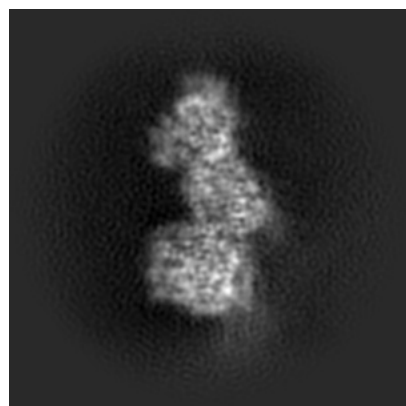
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-39319. These allow visual inspection of the internal detail of the map and identification of artifacts.

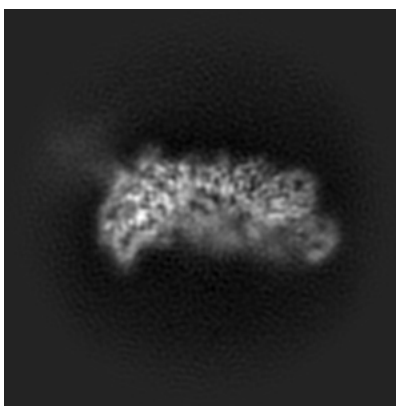
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

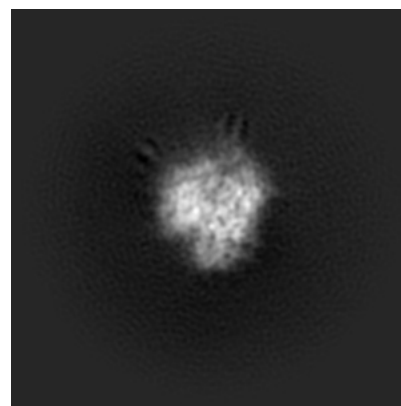
6.1.1 Primary map



X

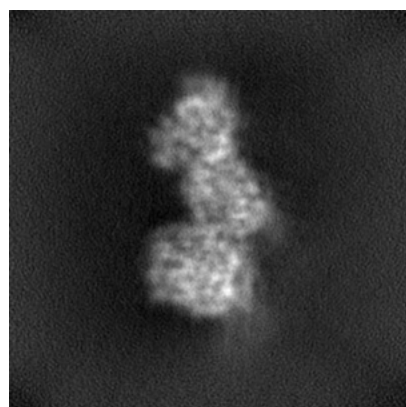


Y

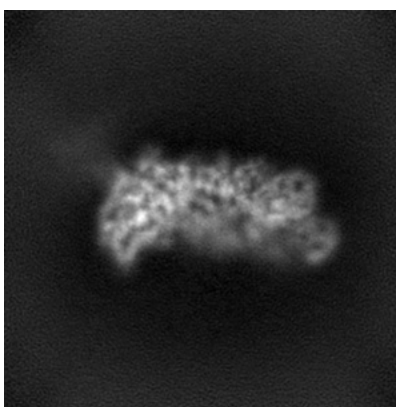


Z

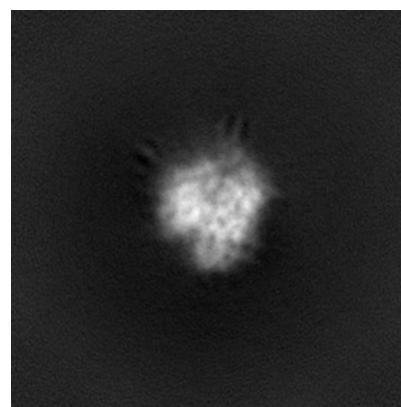
6.1.2 Raw map



X



Y

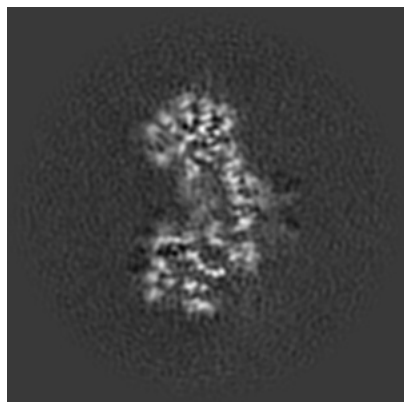


Z

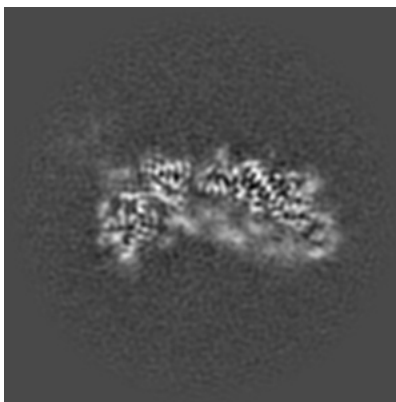
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

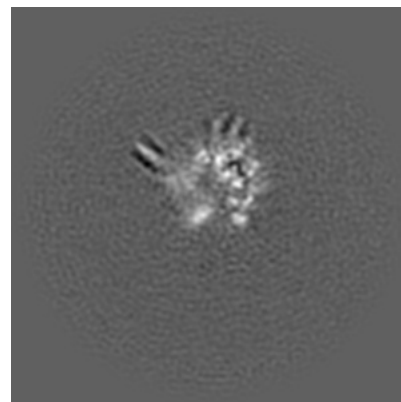
6.2.1 Primary map



X Index: 120

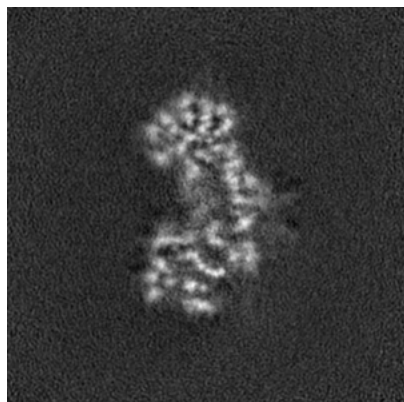


Y Index: 120

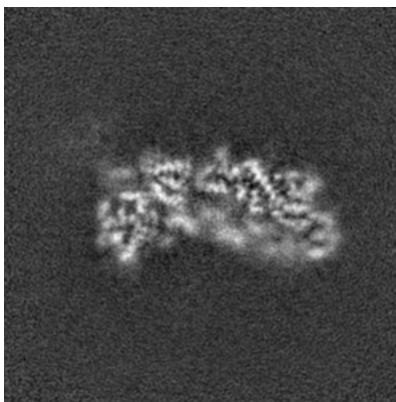


Z Index: 120

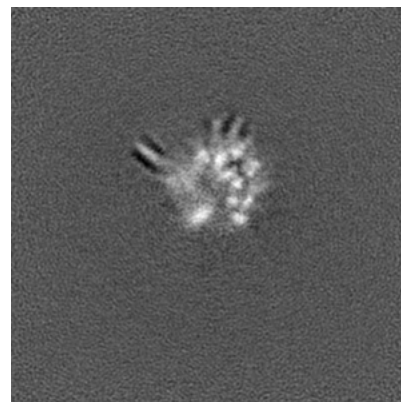
6.2.2 Raw map



X Index: 120



Y Index: 120

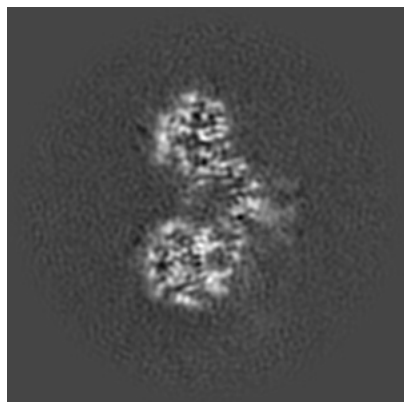


Z Index: 120

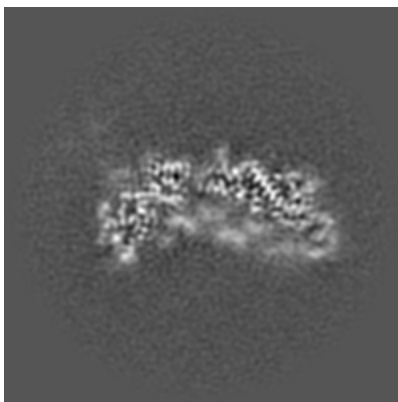
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

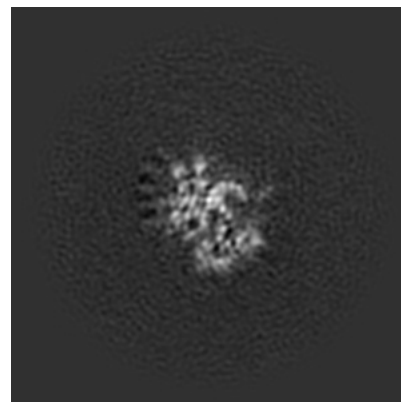
6.3.1 Primary map



X Index: 125

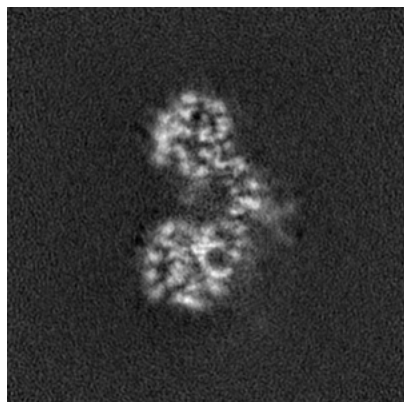


Y Index: 119

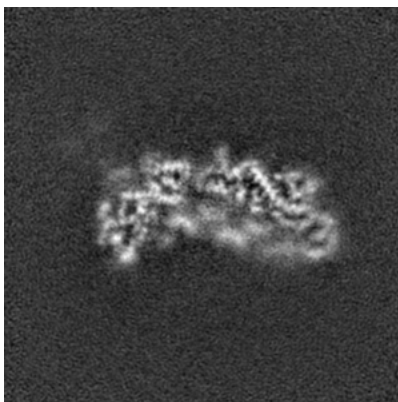


Z Index: 80

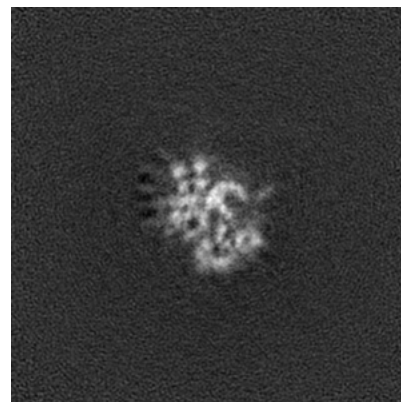
6.3.2 Raw map



X Index: 124



Y Index: 119

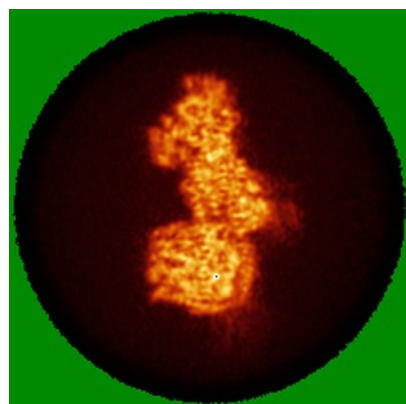


Z Index: 80

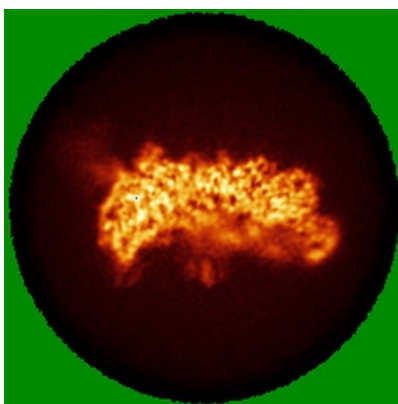
The images above show the largest variance slices of the map in three orthogonal directions.

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

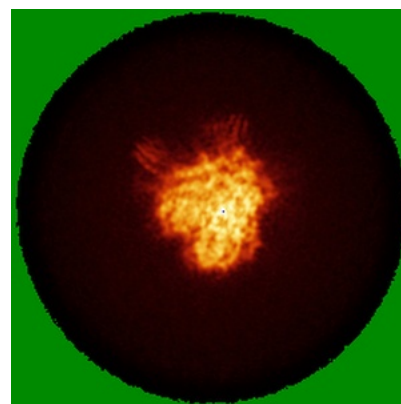
6.4.1 Primary map



X

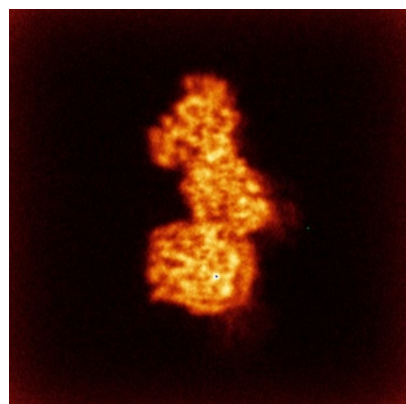


Y

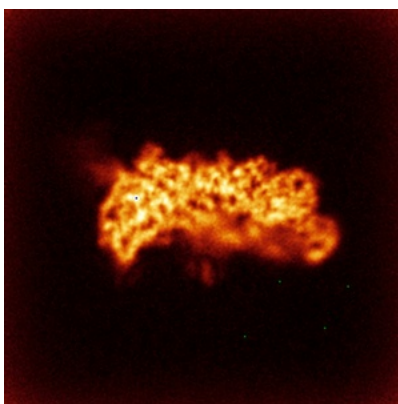


Z

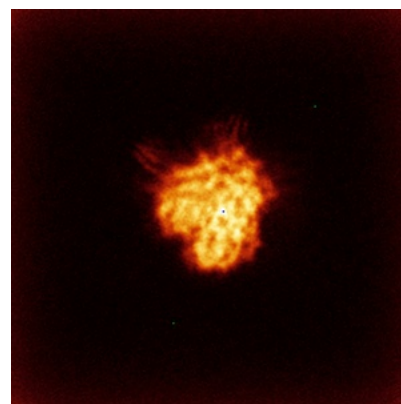
6.4.2 Raw map



X



Y

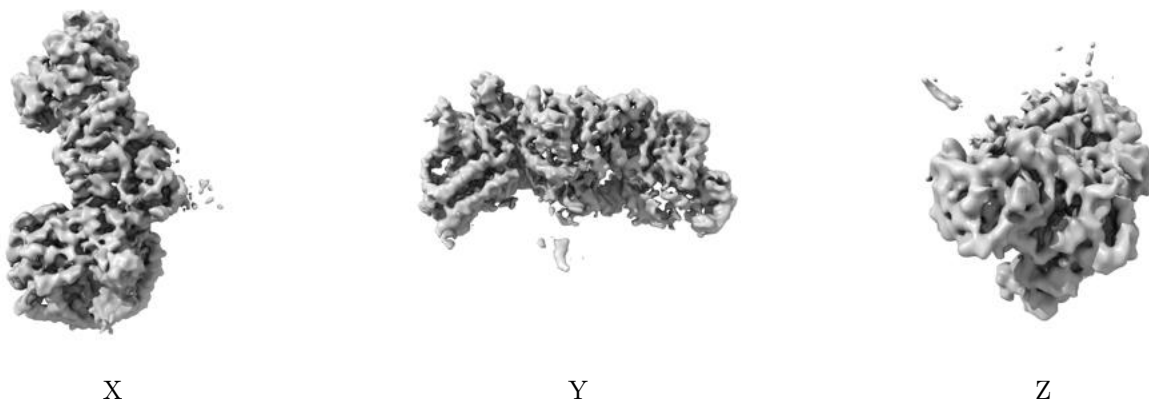


Z

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.

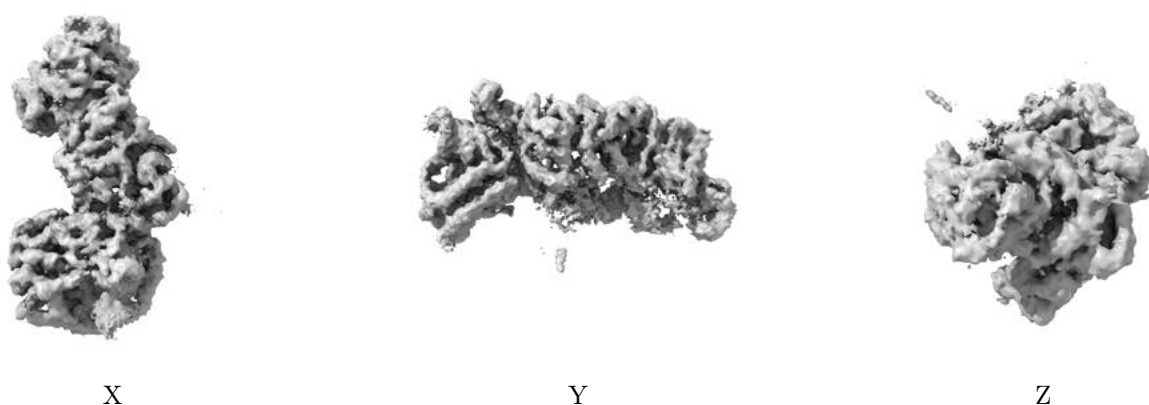
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

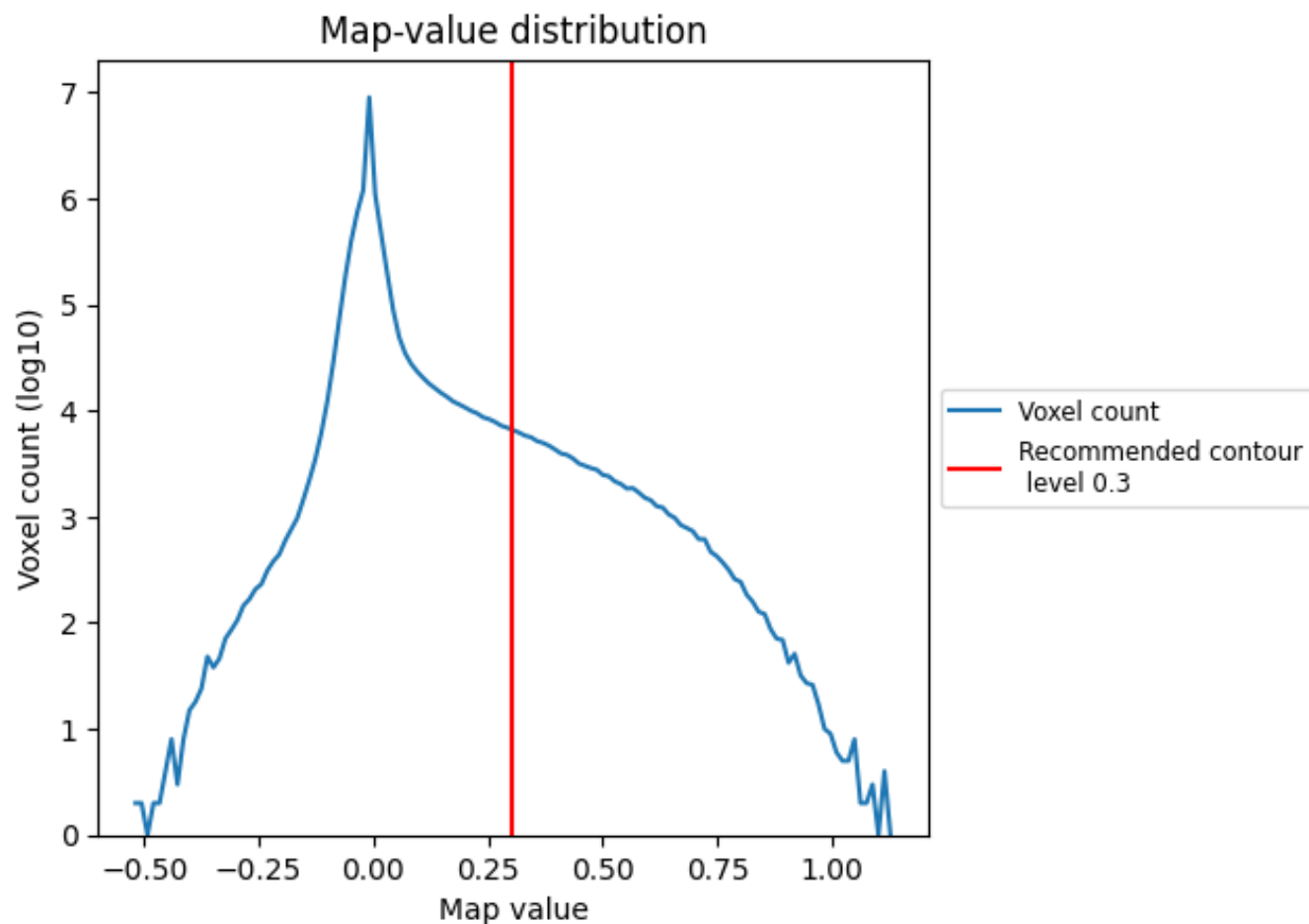
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

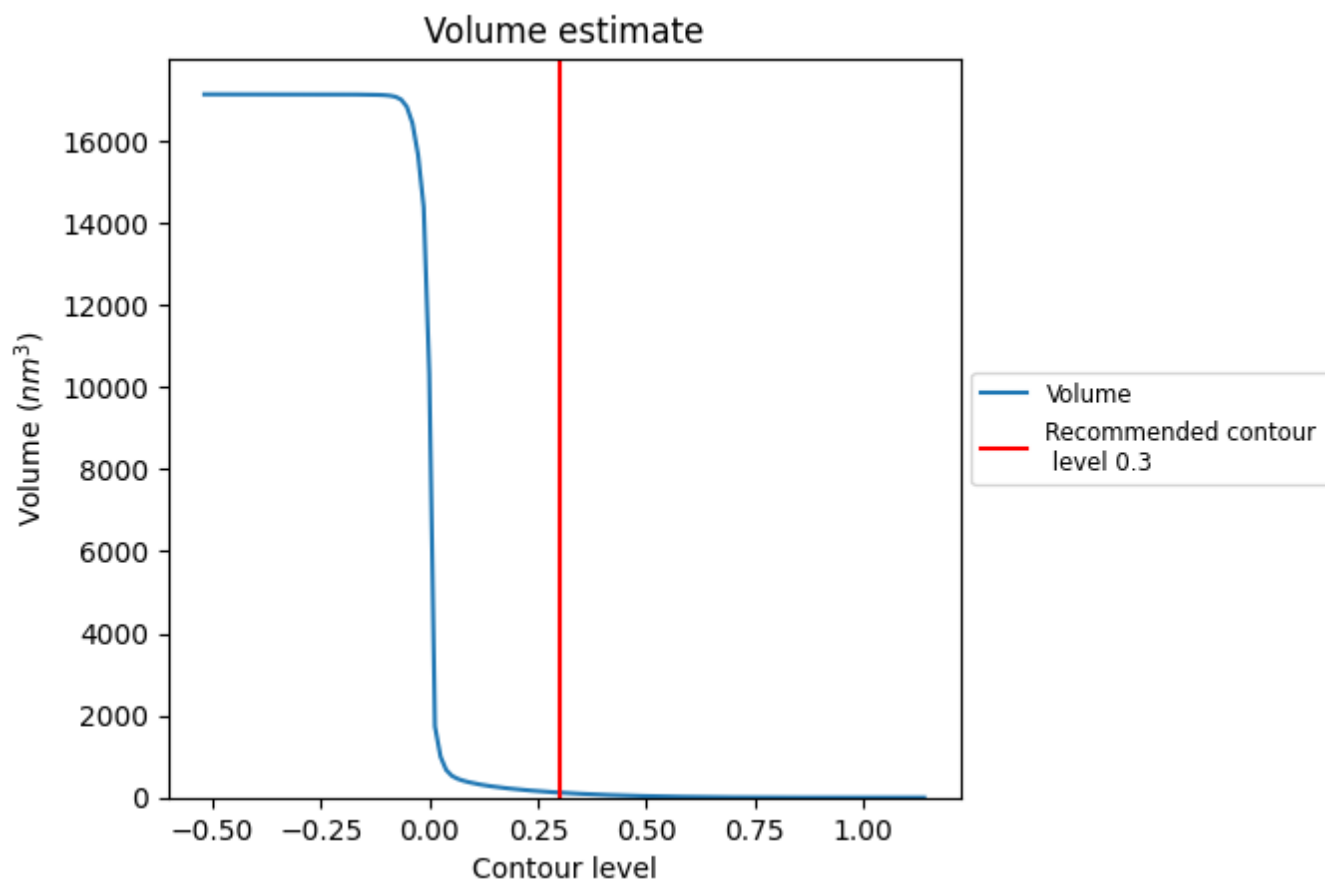
This section contains the results of statistical analysis of the map.

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.

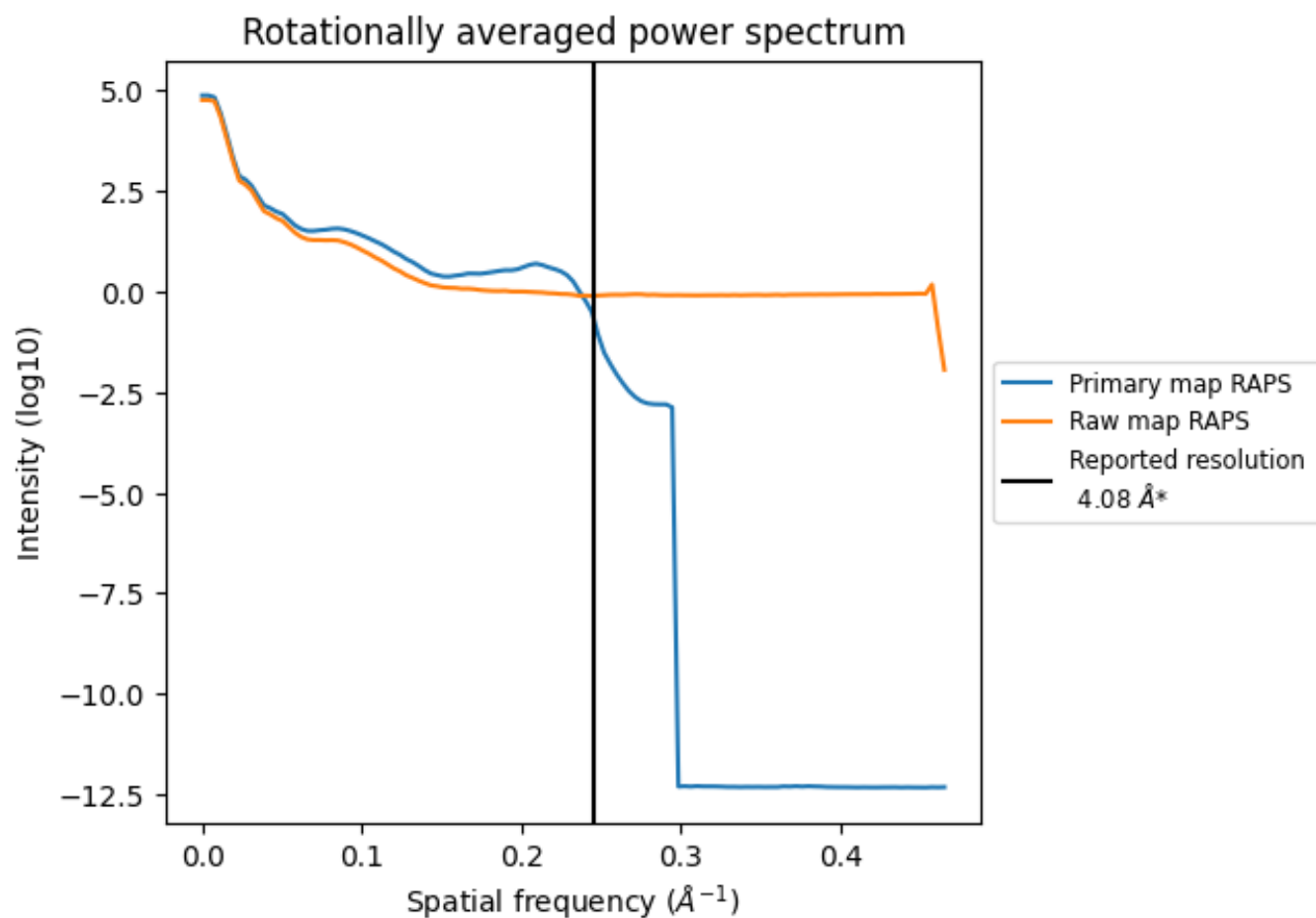
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 121 nm³; this corresponds to an approximate mass of 109 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 ⓘ

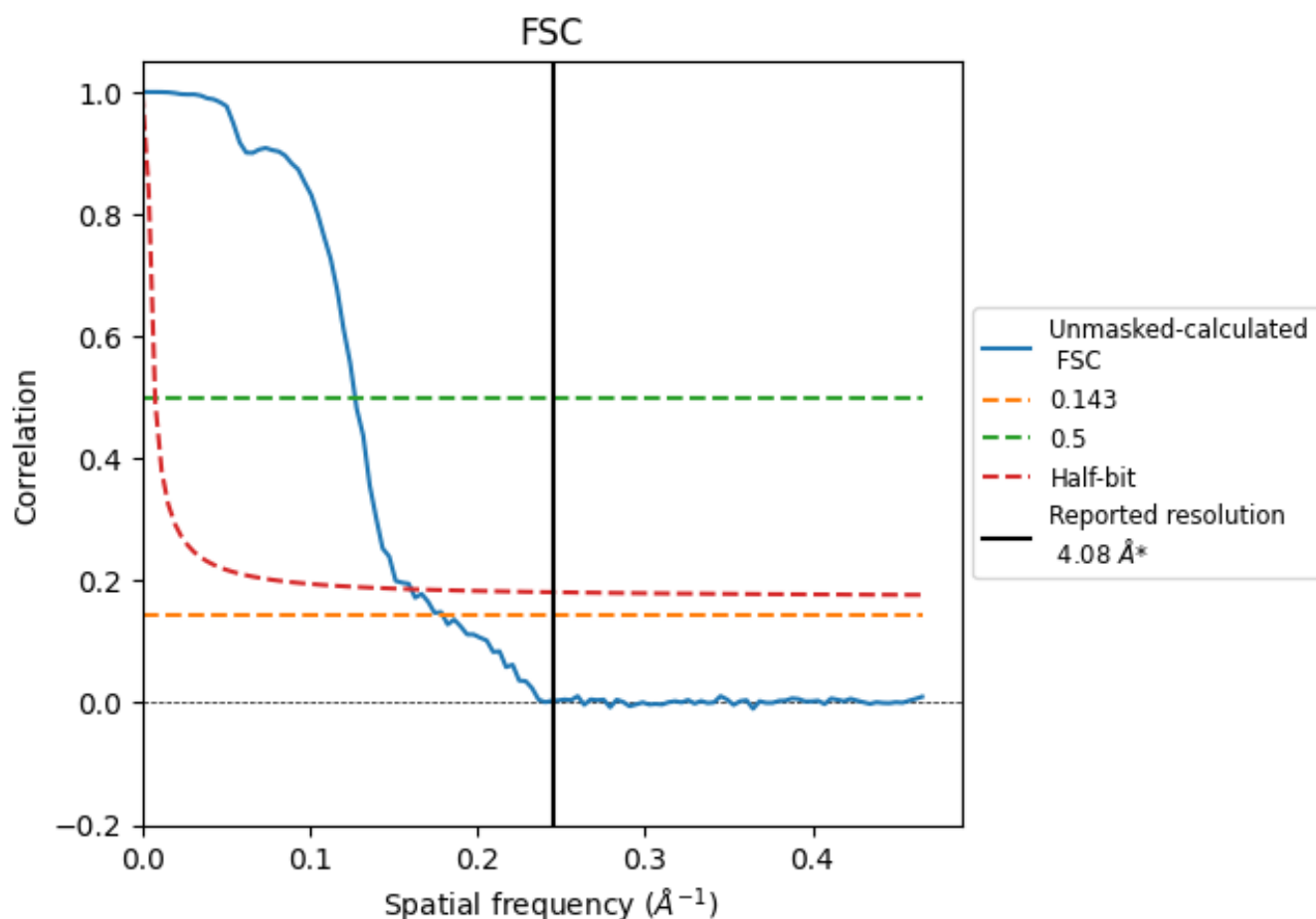


*Reported resolution corresponds to spatial frequency of 0.245 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.245 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

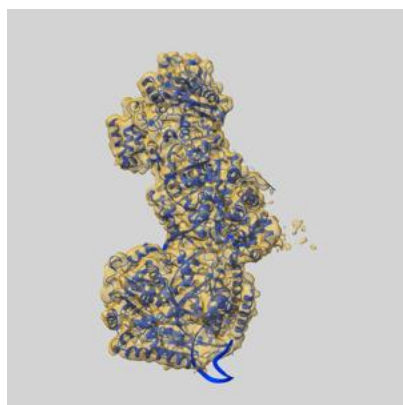
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.08	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	5.57	7.87	6.23

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.57 differs from the reported value 4.08 by more than 10 %

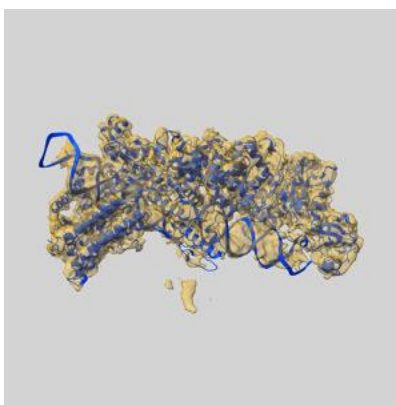
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-39319 and PDB model 8YIH. Per-residue inclusion information can be found in section [3](#) on page [5](#).

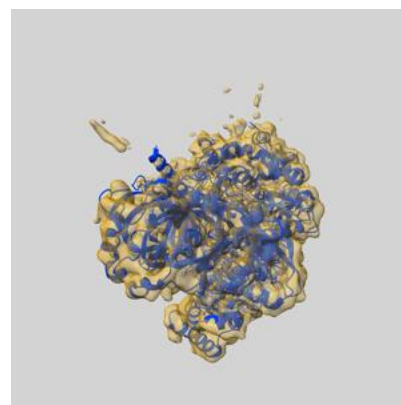
9.1 Map-model overlay [i](#)



X



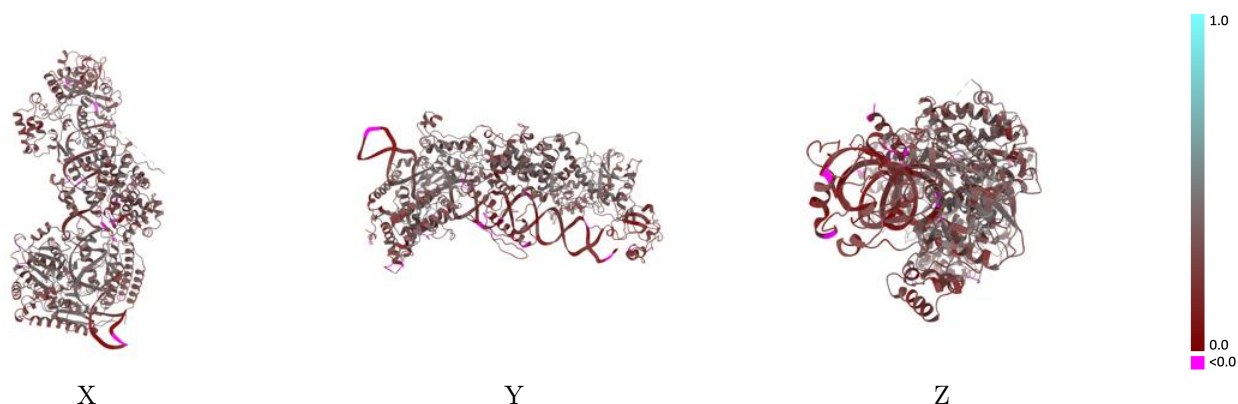
Y



Z

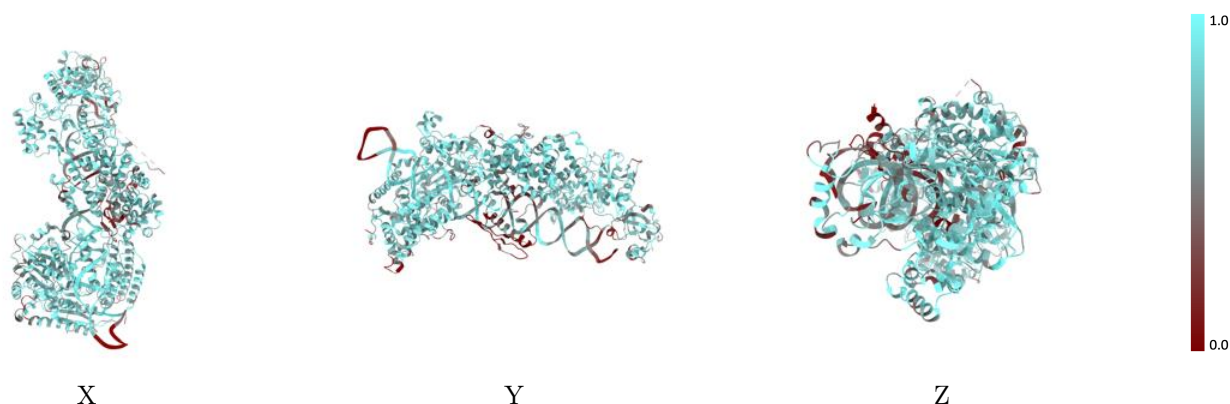
The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



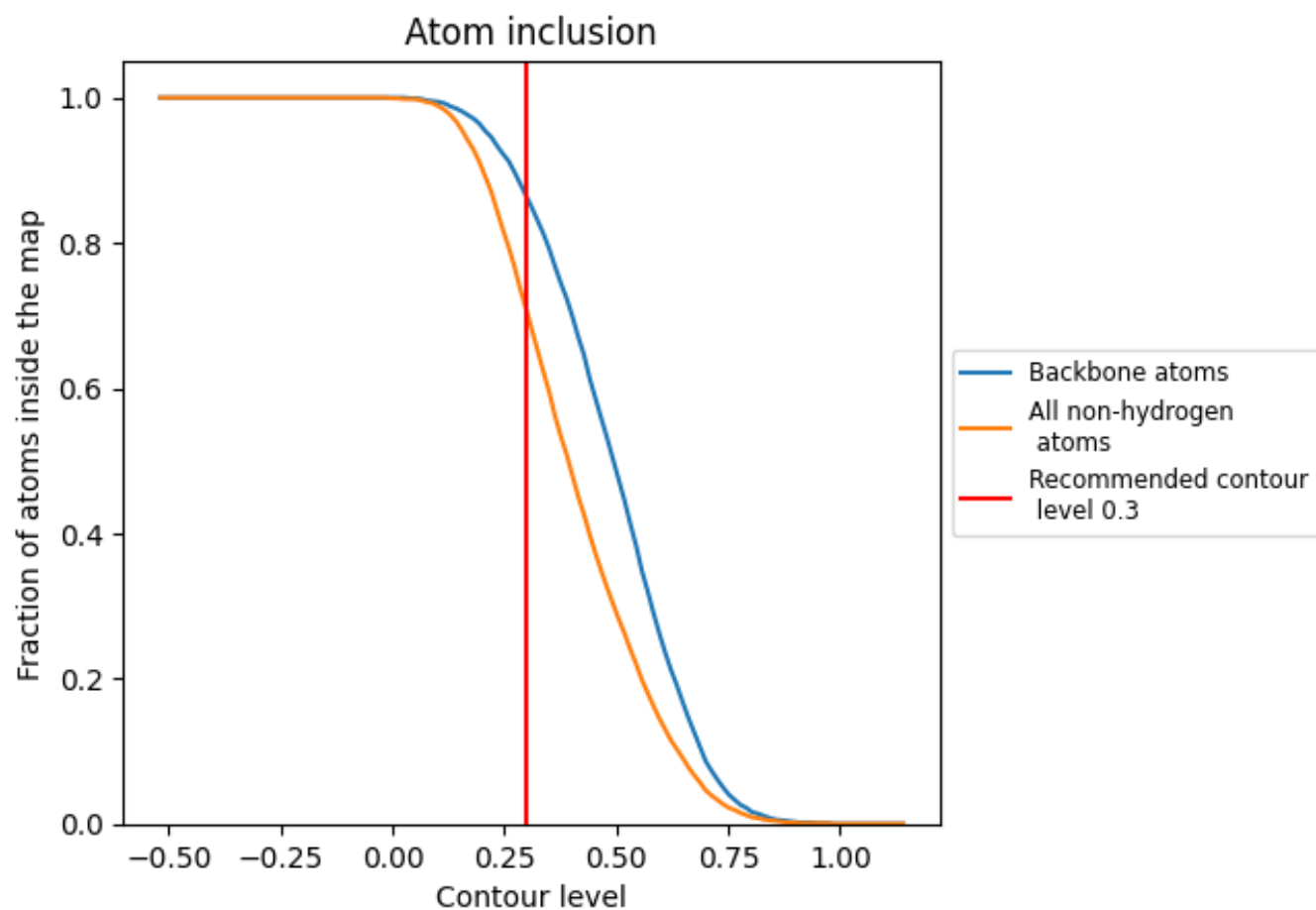
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 71% 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 (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7060	0.3100
A	0.7200	0.3260
B	0.5390	0.2530
C	0.6280	0.2130

