



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 03:33 PM UTC

PDB ID : 8G8Z / pdb_00008g8z
EMDB ID : EMD-29859
Title : Cryo-EM structure of 3DVA component 1 of Escherichia coli que-PEC (paused elongation complex) RNA Polymerase plus preQ1 ligand
Authors : Porta, J.C.; Ohi, M.D.; Walter, N.G.; Frank, A.T.; Deb, I.; Meze, K.
Deposited on : 2023-02-20
Resolution : 4.30 Å(reported)
Based on initial model : 6ASX

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:

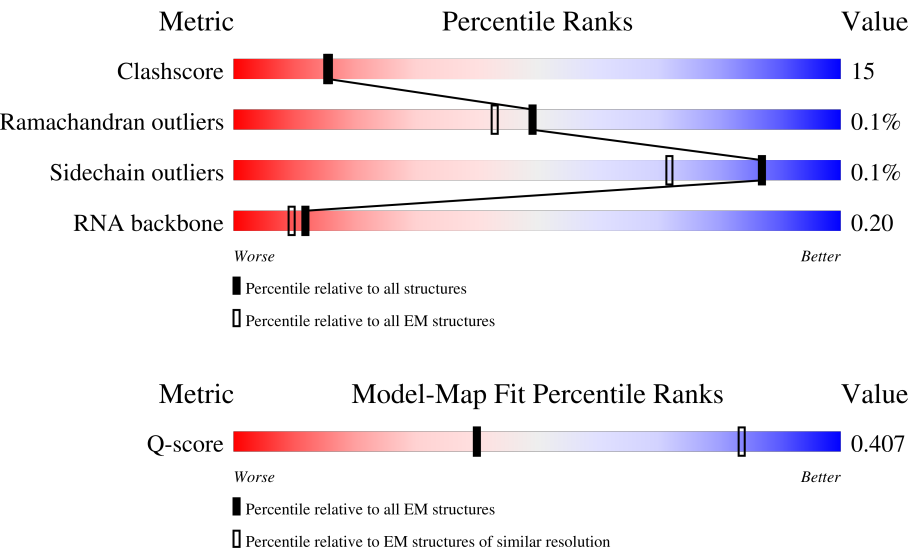
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 i

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

The reported resolution of this entry is 4.30 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	4585 (3.80 - 4.80)

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	A	39	
2	B	31	
3	G	235	

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Mol	Chain	Length	Quality of chain
3	H	235	
4	K	80	
5	R	48	
6	I	1340	
7	J	1358	

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 26822 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 DNA chain called DNA (39-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	18	Total	C	N	O	P	0	0
			369	177	75	101	16		

- Molecule 2 is a DNA chain called DNA (31-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	31	Total	C	N	O	P	0	0
			631	301	107	192	31		

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	219	Total	C	N	O	S	0	0
			1692	1057	301	328	6		
3	H	218	Total	C	N	O	S	0	0
			1685	1052	297	330	6		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	235	GLU	-	expression tag	UNP A0A5B9AW69
H	235	GLU	-	expression tag	UNP A0A5B9AW69

- Molecule 4 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	K	79	Total	C	N	O	S	0	0
			627	382	118	126	1		

- Molecule 5 is a RNA chain called RNA (48-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	R	48	Total	C	N	O	P	0	0
			1020	459	190	324	47		

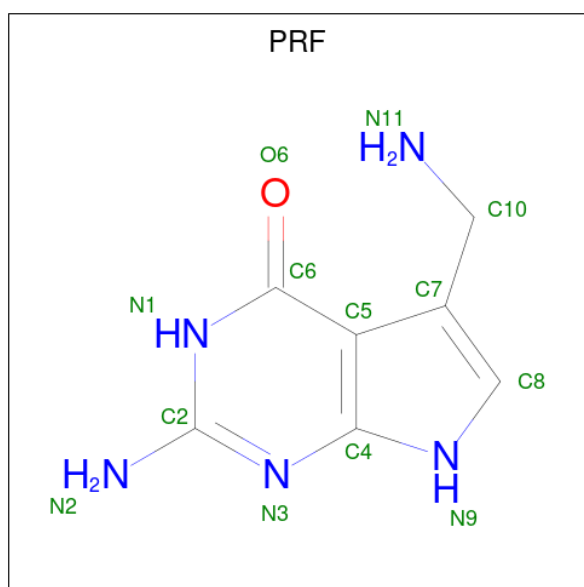
- Molecule 6 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	I	1316	Total	C	N	O	S	0	0
			10381	6514	1810	2014	43		

- Molecule 7 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	J	1337	Total	C	N	O	S	0	0
			10403	6536	1856	1961	50		

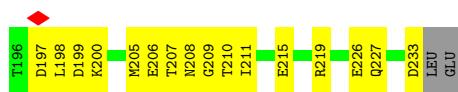
- Molecule 8 is 7-DEAZA-7-AMINOMETHYL-GUANINE (CCD ID: PRF) (formula: $C_7H_9N_5O$) (labeled as "Ligand of Interest" by depositor).



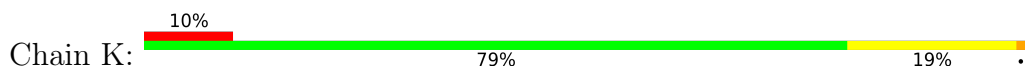
Mol	Chain	Residues	Atoms				AltConf
8	R	1	Total	C	N	O	0
			13	7	5	1	

- Molecule 9 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

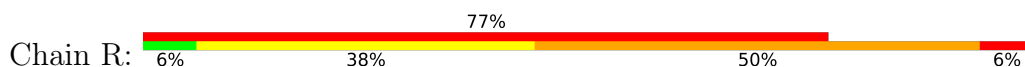
Mol	Chain	Residues	Atoms		AltConf
9	J	1	Total	Mg	0
			1	1	



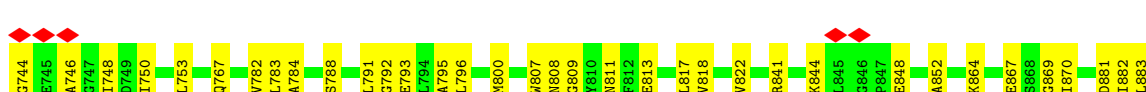
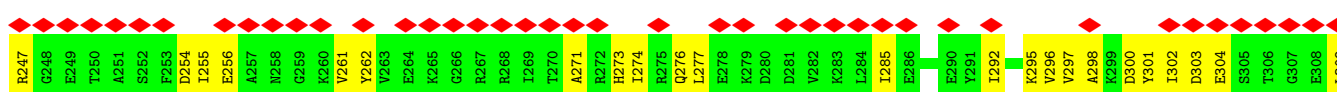
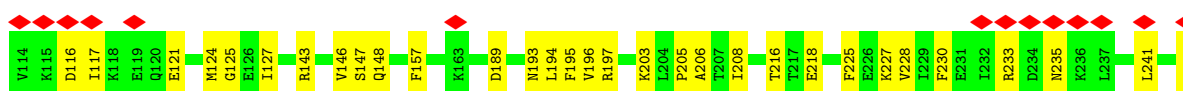
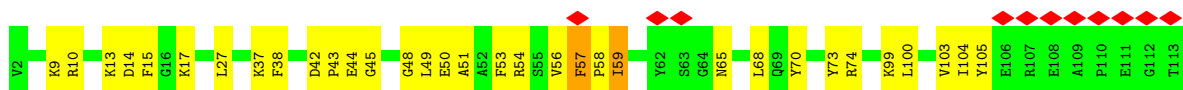
- Molecule 4: DNA-directed RNA polymerase subunit omega



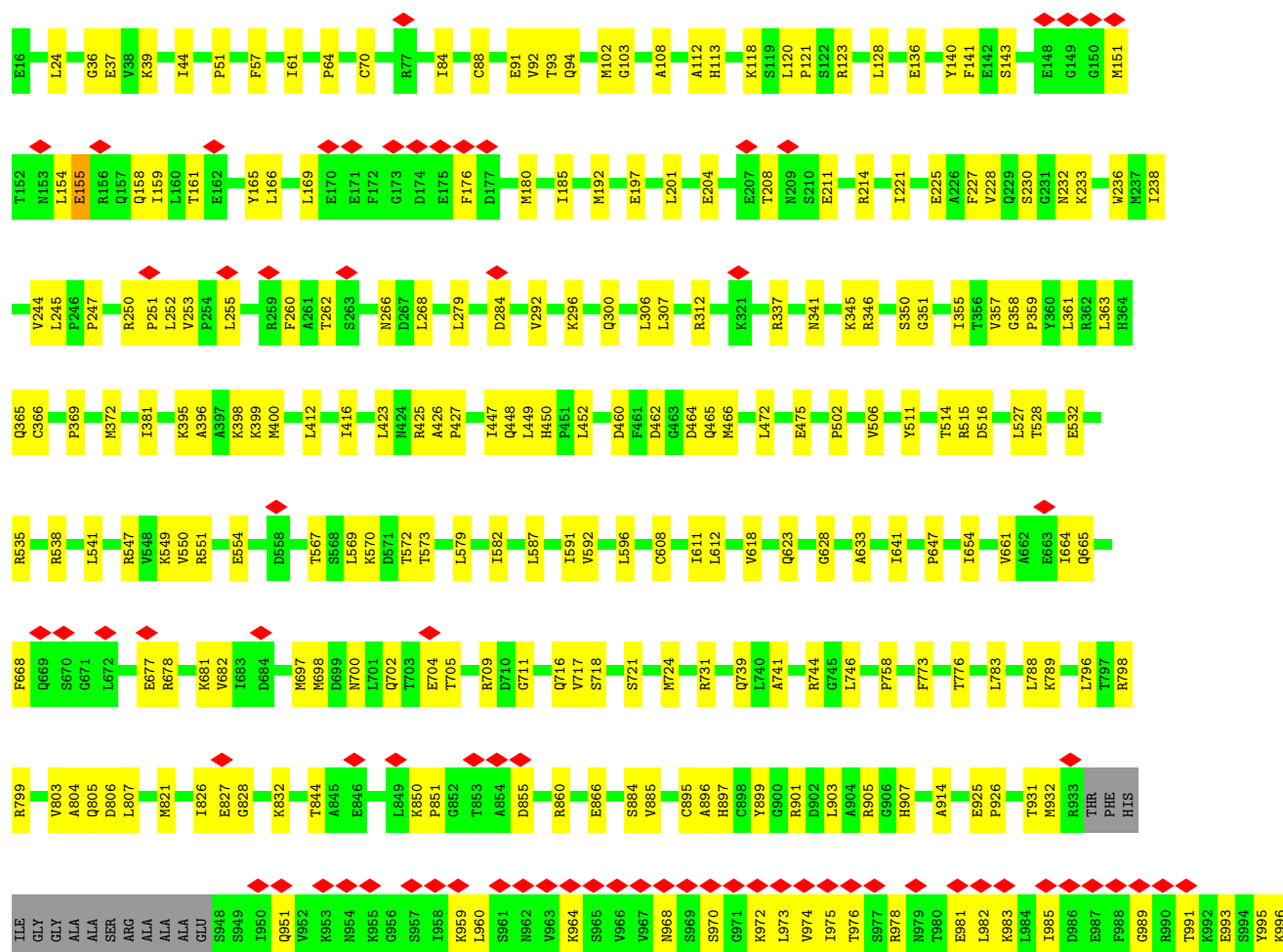
- Molecule 5: RNA (48-MER)



- Molecule 6: DNA-directed RNA polymerase subunit beta



- Molecule 7: DNA-directed RNA polymerase subunit beta'



Y1302	F1199	S1117	S1057	P997
L1306	E1200	G1118	S1058	P998
L1307	G1201	D1119	L1059	Y999
G1308	E1202	T1120	V1060	G1000
L1309	E1203	L1121	V1061	A1001
A1315	R1206	A1122	L1062	V1002
T1316	G1207	R1123	D1063	L1003
E1317	I1210	I1124	S1064	A1004
S1318	I1210	P1125	A1065	K1005
A1322	R1224	Q1126	E1066	G1006
V1337	R1231	GLU	R1067	D1007
R1341	E1236	SER	T1068	G1008
D1342	E1236	GLY	A1069	E1009
E1343	V1246	GLY	G1070	Q1010
L1344	K1247	THR	G1071	V1011
R1345	I1248	LYS	K1072	A1012
G1346	I1248	ASP	D1073	G1013
L1347	K1251	T1134	L1074	G1014
K1348	H1252	G1137	R1075	E1015
V1351	I1253	L1138	P1076	T1016
L1356	E1254	L1144	A1077	V1017
I1357	V1255	F1145	L1078	A1018
P1358	I1256	E1146	K1079	N1019
A1359	V1257	I1155	I1080	W1020
Y1363	R1258	S1160	V1081	D1021
H1366	Q1259	V1163	H1082	P1022
Q1367	L1261	S1164	A1083	H1023
D1368	R1262	F1165	Q1084	T1024
R1369	K1263	G1166	G1085	M1025
R1372	I1266	K1167	N1086	P1026
R1373	D1273	E1168	D1087	V1027
	F1274	T1169	V1088	I1028
	L1275	K1170	L1089	T1029
	E1278	G1171	I1090	E1030
	E1281	R1172	P1091	V1031
	R1284	L1173	G1033	S1032
V1285	V1285	R1174	G1092	G1033
K1286	K1286	L1175	T1093	F1034
N1289	N1289	I1177	D1094	V1035
L1292	L1292	T1178	M1095	R1036
N1295	N1295	P1179	P1096	F1037
G1296	G1296	V1180	A1097	T1038
K1297	K1297	D1181	Q1098	D1039
V1298	V1298	G1182	Y1099	M1040
G1299	G1299	S1183	F1100	I1041
		D1134	L1101	D1042
		P1185	P1102	G1043
		M1189	G1103	T1045
		T1190	K1104	I1046
		P1191	A1105	T1047
		K1192	I1106	R1048
		W1193	V1107	Q1049
		R1194	Q1108	T1050
			L1109	D1051
			E1110	E1052
			D1111	L1053
			G1112	T1054
			V1113	G1055
			Q1114	L1056
			I1115	
			S1116	

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	20469	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 ($e^-/\text{\AA}^2$)	62.00	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.265	Depositor
Minimum map value	-0.510	Depositor
Average map value	0.013	Depositor
Map value standard deviation	0.044	Depositor
Recommended contour level	0.25	Depositor
Map size ($\text{\AA}$)	300.0, 300.0, 300.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.0, 1.0, 1.0	Depositor

5 Model quality

5.1 Standard geometry

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

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	A	0.26	0/415	0.51	0/638
2	B	0.30	0/704	0.50	0/1084
3	G	0.17	0/1712	0.36	0/2319
3	H	0.31	0/1704	0.51	0/2309
4	K	0.24	1/629 (0.2%)	0.30	0/847
5	R	1.77	21/1142 (1.8%)	1.50	19/1777 (1.1%)
6	I	0.22	0/10547	0.36	1/14232 (0.0%)
7	J	0.18	0/10560	0.33	0/14257
All	All	0.42	22/27413 (0.1%)	0.49	20/37463 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
5	R	0	13

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	R	24	U	O3'-P	-7.26	1.50	1.61
5	R	27	A	P-O5'	-7.13	1.49	1.59
5	R	3	A	C5'-C4'	6.94	1.61	1.51
5	R	14	C	C5'-C4'	6.79	1.61	1.51
5	R	20	C	C3'-C2'	6.69	1.62	1.52

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	R	3	A	P-O5'-C5'	9.04	134.47	120.90
5	R	17	C	P-O5'-C5'	7.03	131.45	120.90
6	I	43	PRO	N-CA-C	-6.42	104.98	113.65
5	R	32	A	P-O5'-C5'	6.25	130.28	120.90
5	R	19	C	C5'-C4'-O4'	6.17	119.05	109.80

There are no chirality outliers.

5 of 13 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	R	1	G	Sidechain
5	R	10	C	Sidechain
5	R	4	G	Sidechain
5	R	7	G	Sidechain
5	R	9	U	Sidechain

5.2 Too-close contacts ⓘ

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	A	369	0	205	8	0
2	B	631	0	352	8	0
3	G	1692	0	1730	54	0
3	H	1685	0	1718	86	0
4	K	627	0	634	14	0
5	R	1020	0	522	9	0
6	I	10381	0	10392	314	0
7	J	10403	0	10634	315	0
8	R	13	0	9	0	0
9	J	1	0	0	0	0
All	All	26822	0	26196	758	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 15.

The worst 5 of 758 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)
6:I:53:PHE:CD1	6:I:57:PHE:CZ	1.81	1.65
7:J:337:ARG:CD	7:J:341:ASN:HD21	1.14	1.55
6:I:53:PHE:CD1	6:I:57:PHE:CE2	2.01	1.47
3:G:8:PHE:HZ	3:H:227:GLN:NE2	1.13	1.39
6:I:53:PHE:CG	6:I:57:PHE:CE2	2.08	1.39

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	
3	G	215/235 (92%)	204 (95%)	11 (5%)	0	100	100
3	H	214/235 (91%)	201 (94%)	11 (5%)	2 (1%)	14	49
4	K	77/80 (96%)	73 (95%)	4 (5%)	0	100	100
6	I	1312/1340 (98%)	1245 (95%)	65 (5%)	2 (0%)	43	77
7	J	1331/1358 (98%)	1273 (96%)	58 (4%)	0	100	100
All	All	3149/3248 (97%)	2996 (95%)	149 (5%)	4 (0%)	49	83

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	H	29	GLU
6	I	59	ILE
3	H	34	GLY
6	I	57	PHE

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	
3	G	187/202 (93%)	187 (100%)	0	100	100
3	H	187/202 (93%)	187 (100%)	0	100	100
4	K	67/68 (98%)	67 (100%)	0	100	100
6	I	1135/1155 (98%)	1134 (100%)	1 (0%)	88	88
7	J	1122/1134 (99%)	1119 (100%)	3 (0%)	86	84
All	All	2698/2761 (98%)	2694 (100%)	4 (0%)	87	88

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	I	864	LYS
7	J	155	GLU
7	J	255	LEU
7	J	465	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
6	I	1268	GLN
7	J	1126	GLN
7	J	450	HIS
7	J	921	GLN
7	J	158	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
5	R	48/48 (100%)	26 (54%)	3 (6%)

5 of 26 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	R	2	C
5	R	3	A
5	R	8	U
5	R	9	U

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Mol	Chain	Res	Type
5	R	10	C

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	R	1	G
5	R	15	U
5	R	38	G

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 2 ligands modelled in this entry, 1 is 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	$\# Z > 2$
8	PRF	R	101	-	14,14,14	1.60	3 (21%)	14,20,20	1.73	2 (14%)

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
8	PRF	R	101	-	-	0/0/2/2	0/2/2/2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	R	101	PRF	C2-N1	2.67	1.44	1.37
8	R	101	PRF	C2-N2	2.65	1.40	1.34
8	R	101	PRF	C4-N9	-2.18	1.32	1.36

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	R	101	PRF	C7-C5-C4	-5.14	106.79	112.68
8	R	101	PRF	N2-C2-N1	2.08	121.16	116.76

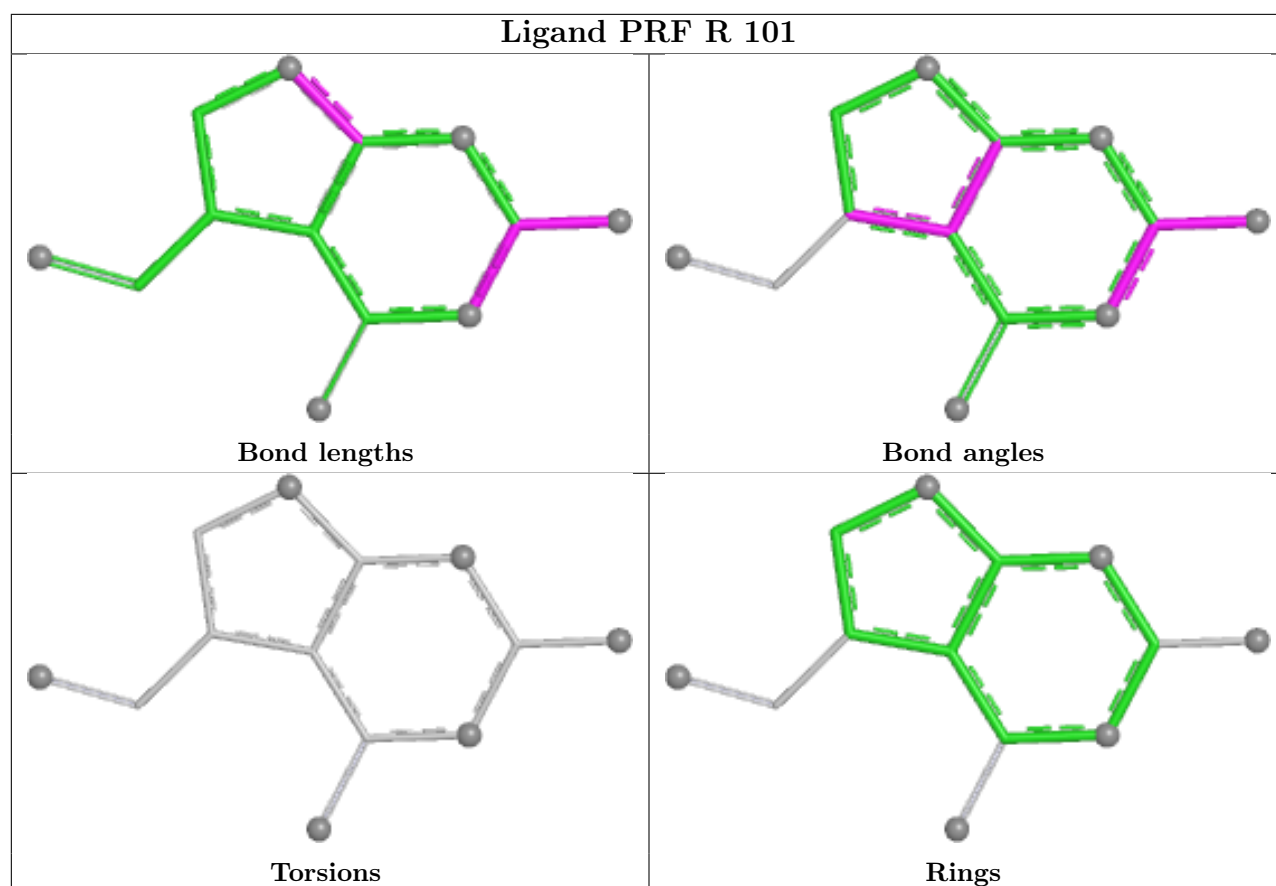
There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

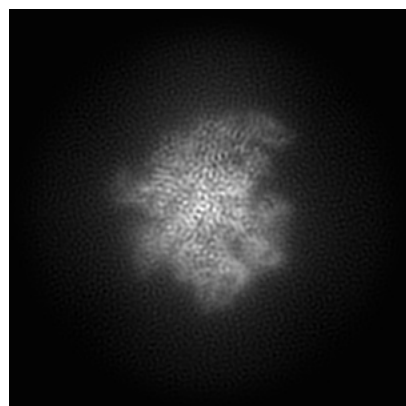
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-29859. These allow visual inspection of the internal detail of the map and identification of artifacts.

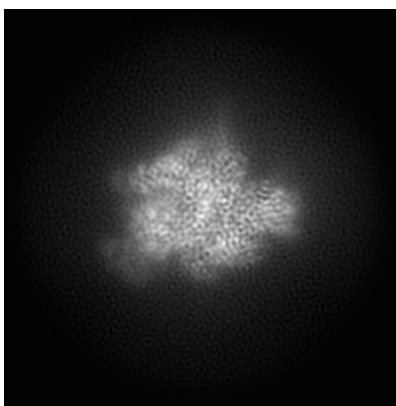
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

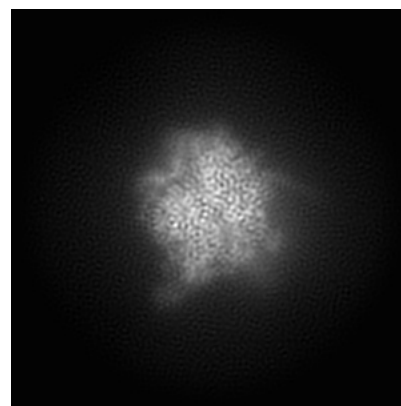
6.1.1 Primary map



X

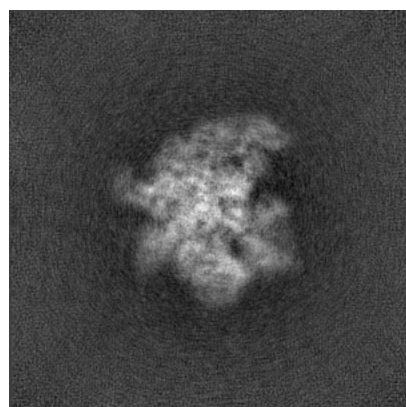


Y

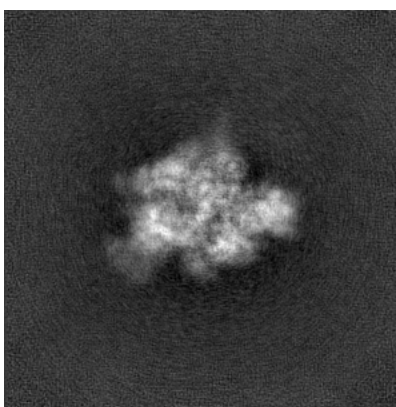


Z

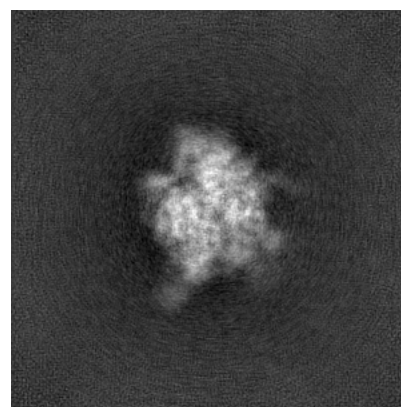
6.1.2 Raw map



X



Y

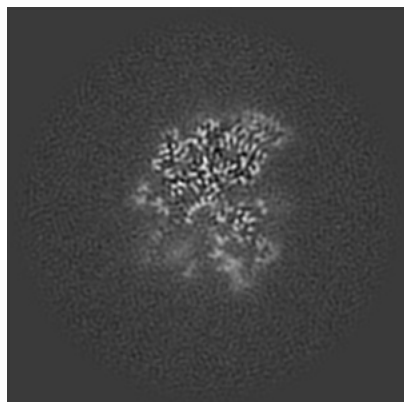


Z

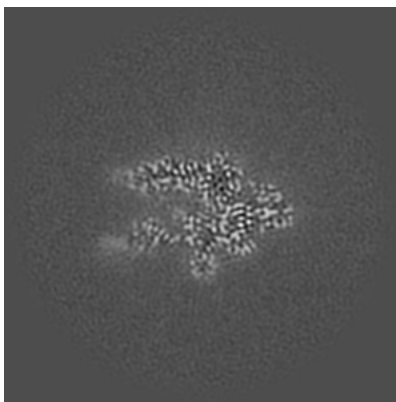
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

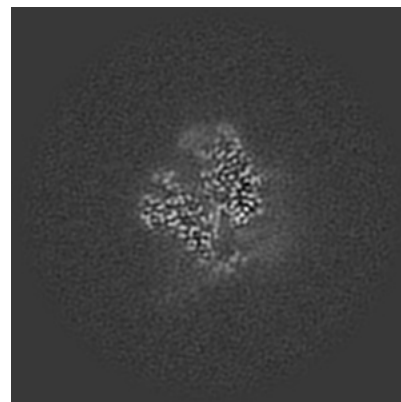
6.2.1 Primary map



X Index: 150

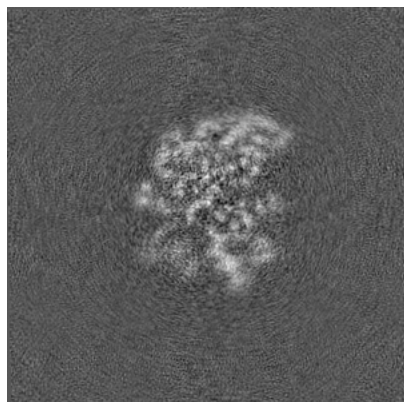


Y Index: 150

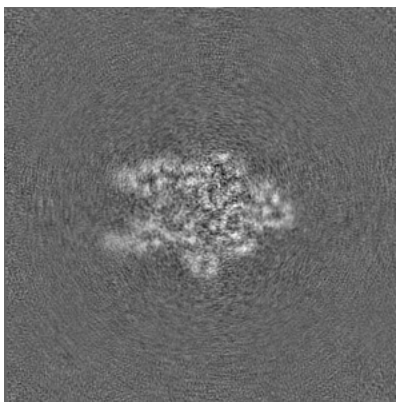


Z Index: 150

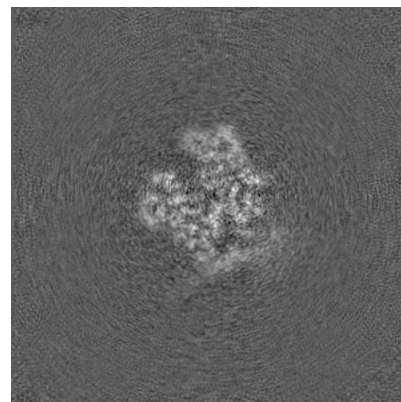
6.2.2 Raw map



X Index: 150



Y Index: 150

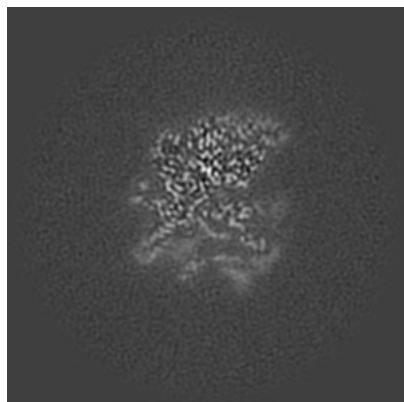


Z Index: 150

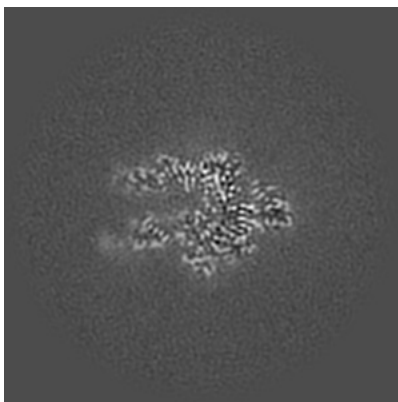
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

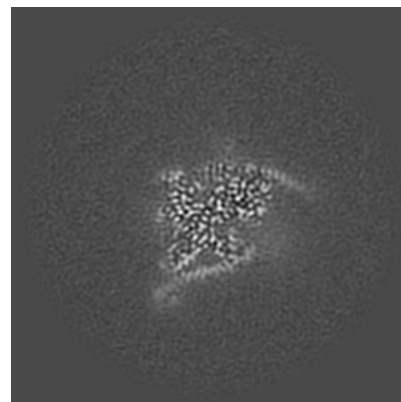
6.3.1 Primary map



X Index: 146

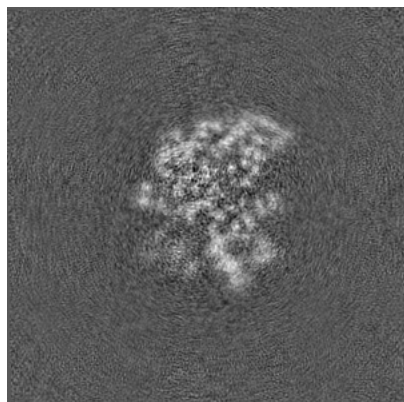


Y Index: 148

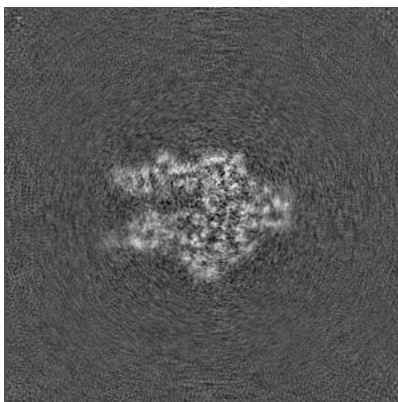


Z Index: 165

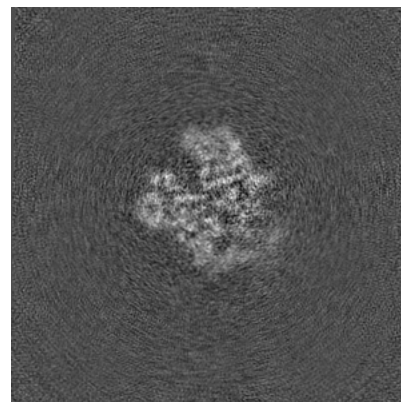
6.3.2 Raw map



X Index: 151



Y Index: 147

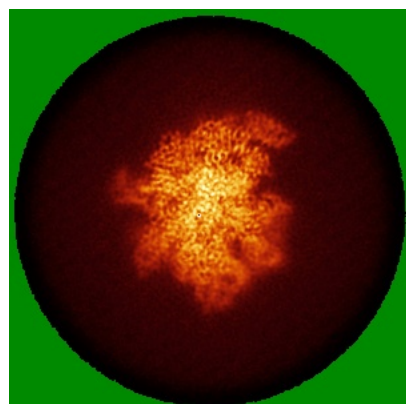


Z Index: 148

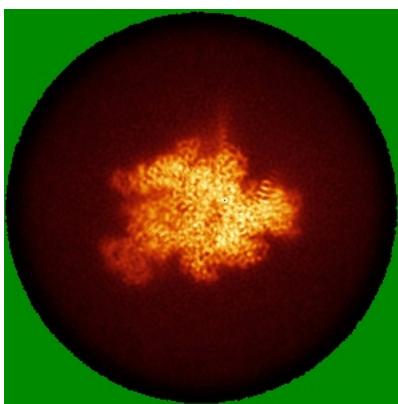
The images above show the largest variance slices of the map in three orthogonal directions.

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

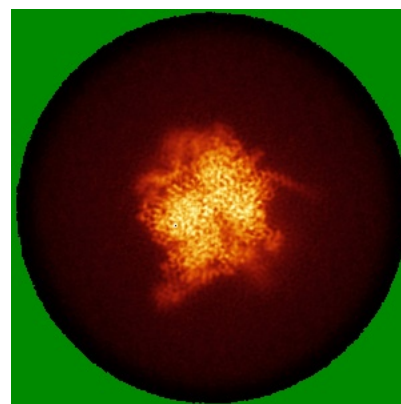
6.4.1 Primary map



X

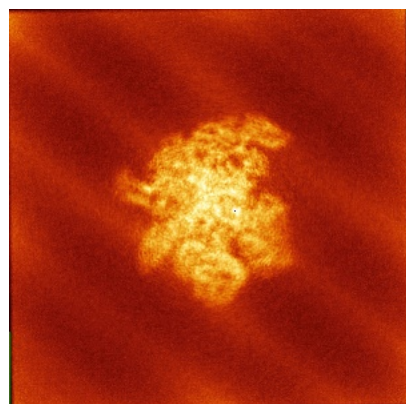


Y

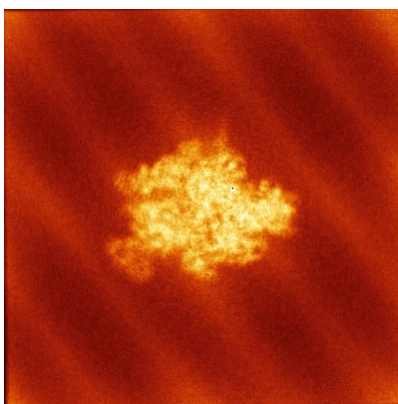


Z

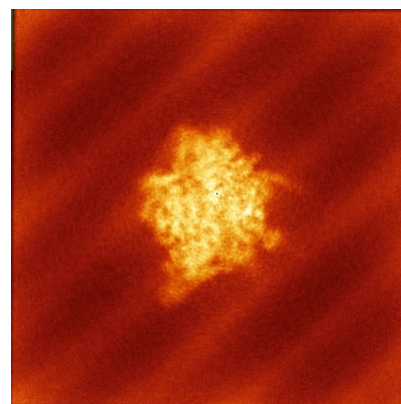
6.4.2 Raw map



X



Y

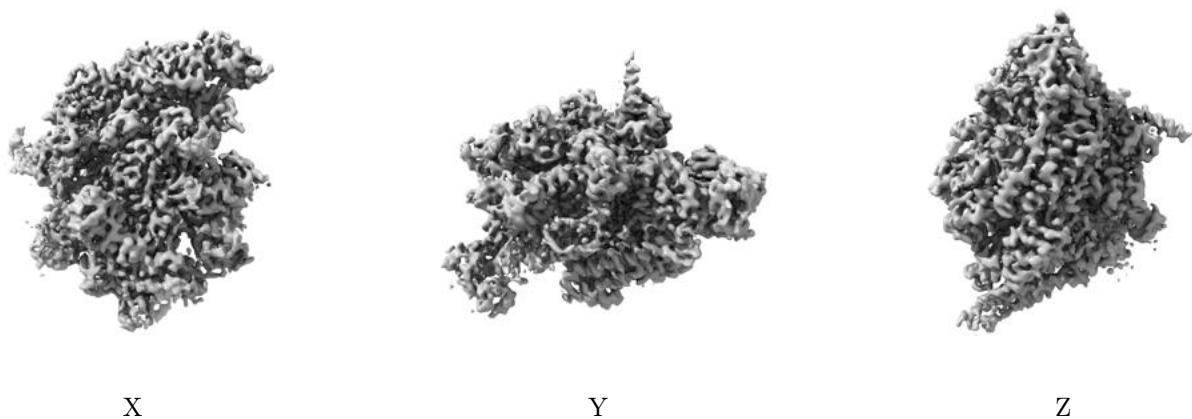


Z

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.

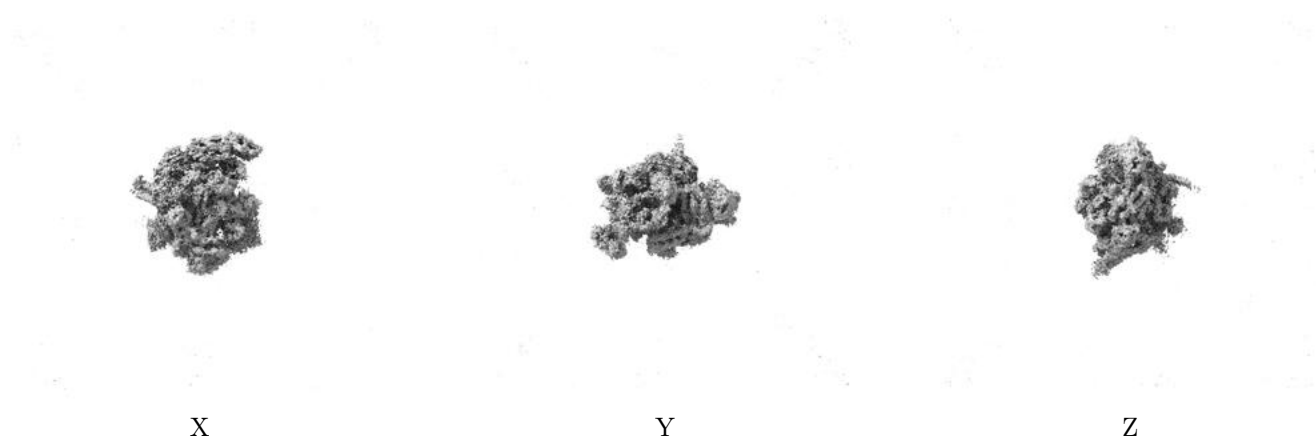
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.25. 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.

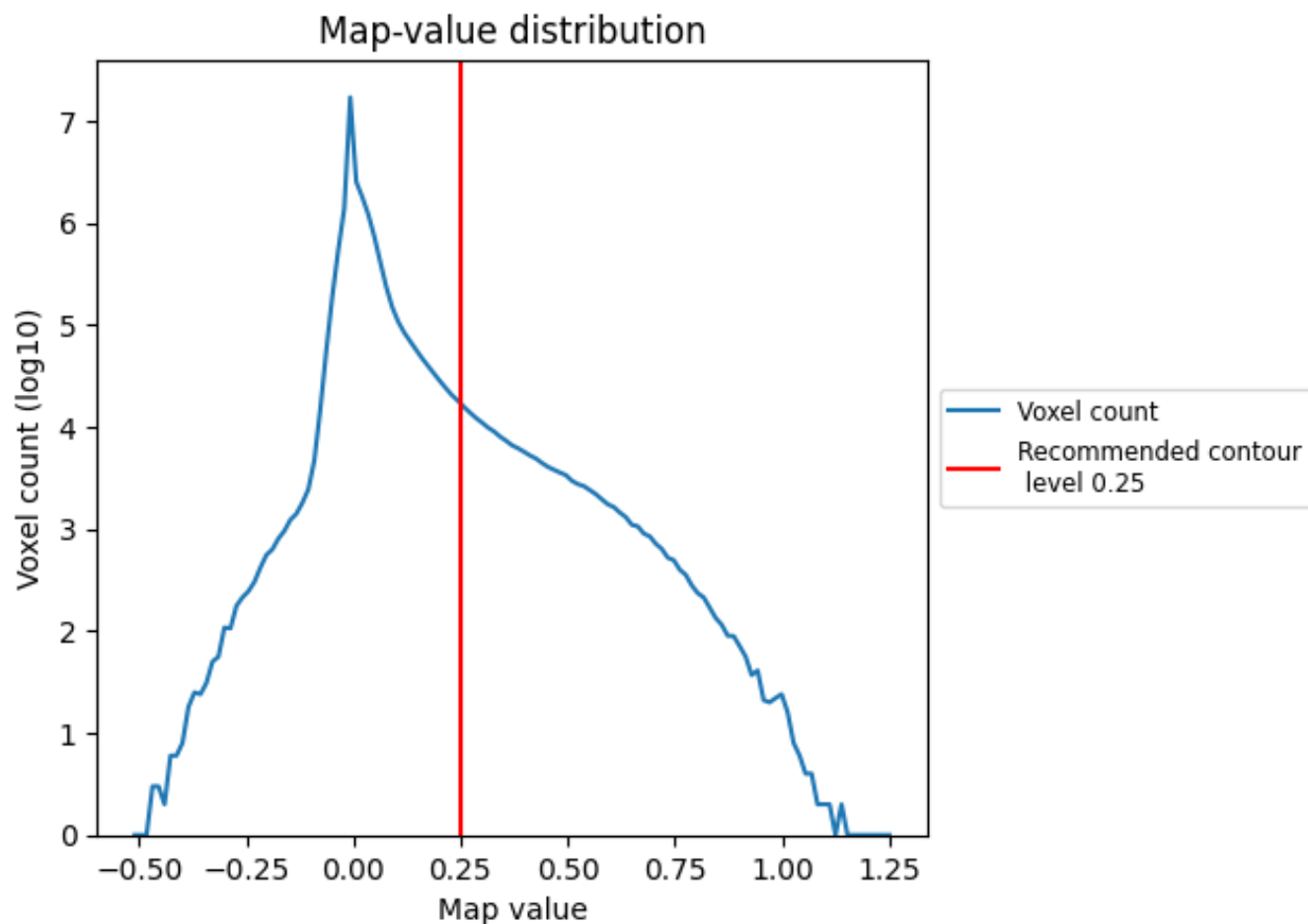
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

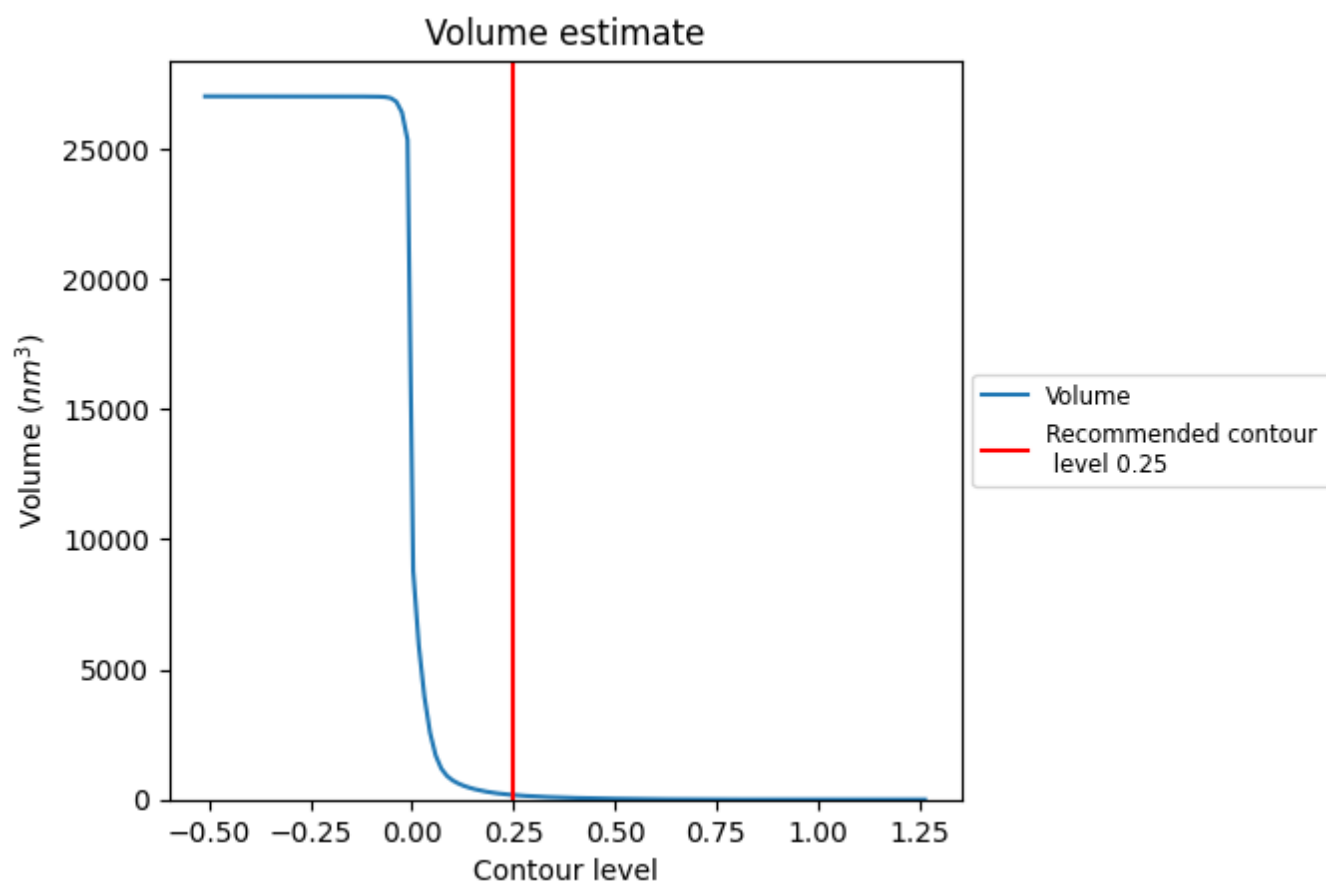
This section contains the results of statistical analysis of the map.

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.

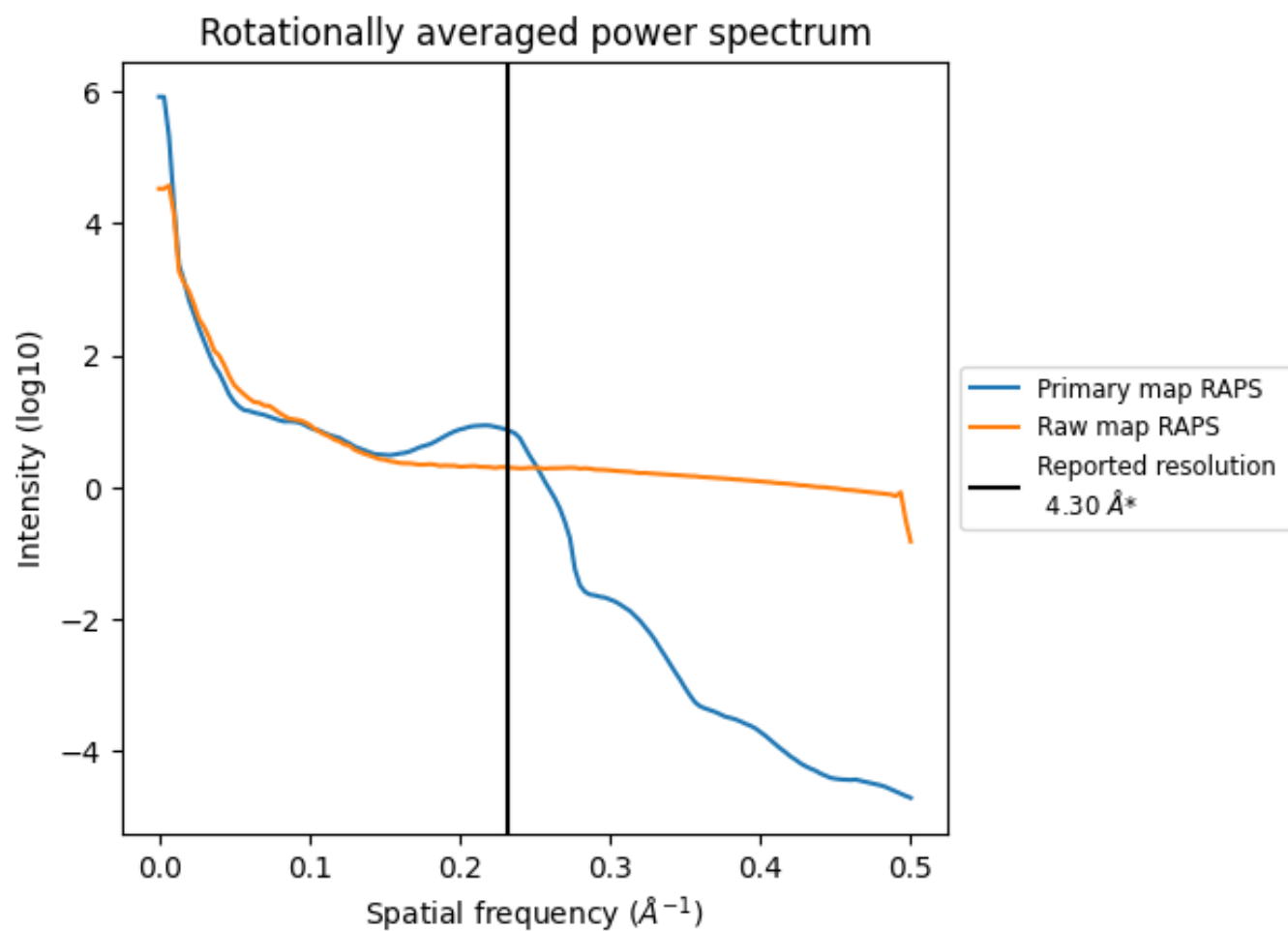
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 175 nm^3 ; this corresponds to an approximate mass of 158 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 ⓘ

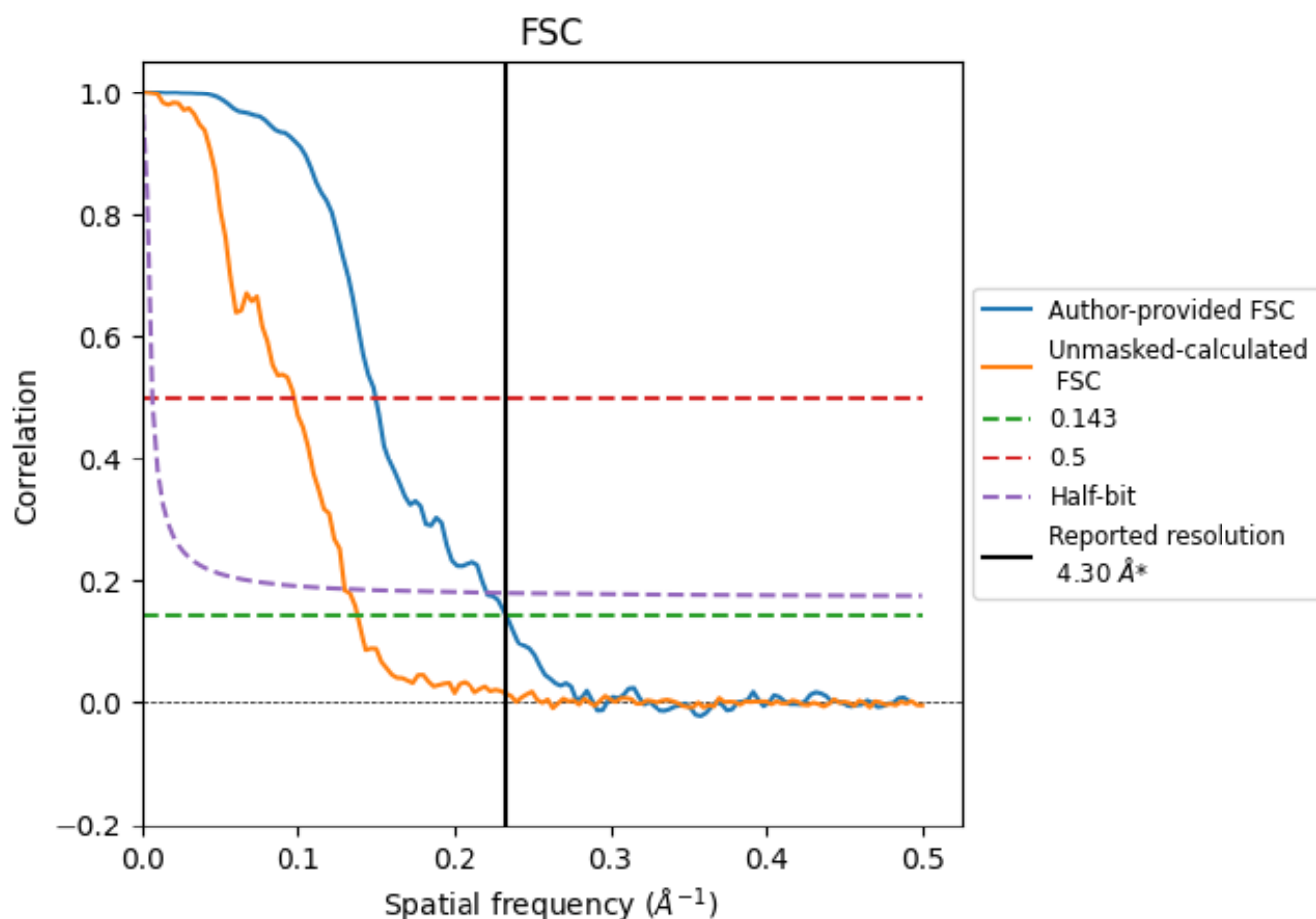


*Reported resolution corresponds to spatial frequency of 0.233 $\text{\AA}^{-1}$

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 $0.233 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

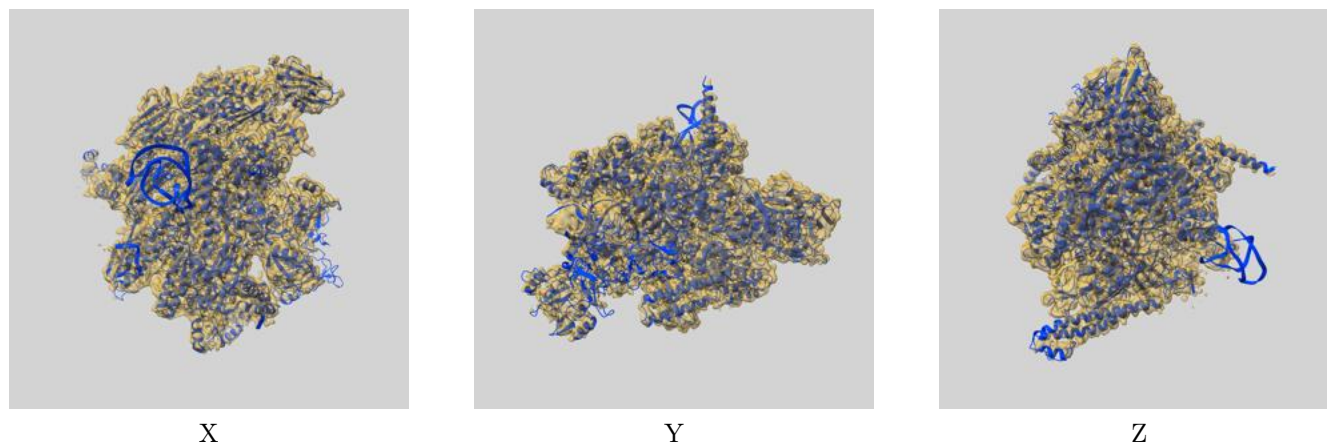
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.30	-	-
Author-provided FSC curve	4.28	6.68	4.52
Unmasked-calculated*	7.24	10.25	7.70

*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 7.24 differs from the reported value 4.3 by more than 10 %

9 Map-model fit [i](#)

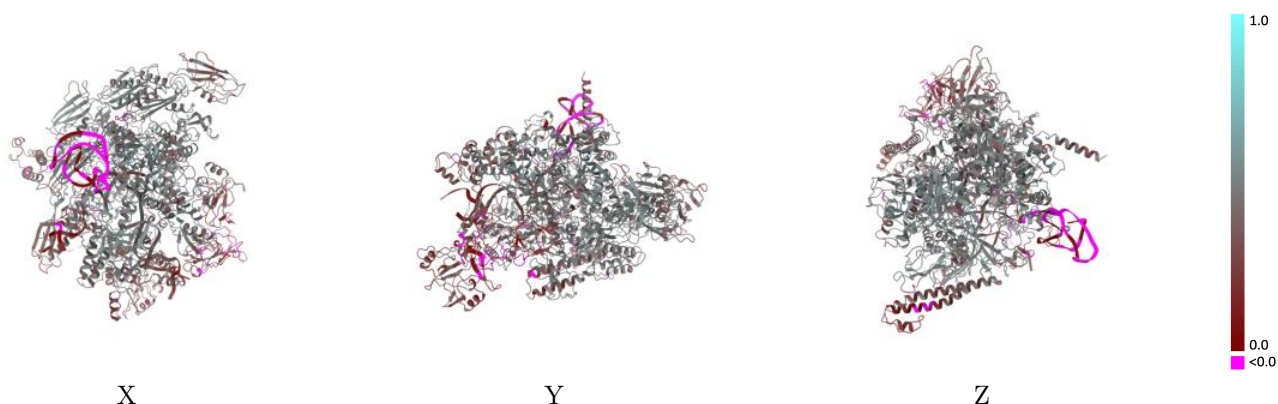
This section contains information regarding the fit between EMDB map EMD-29859 and PDB model 8G8Z. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



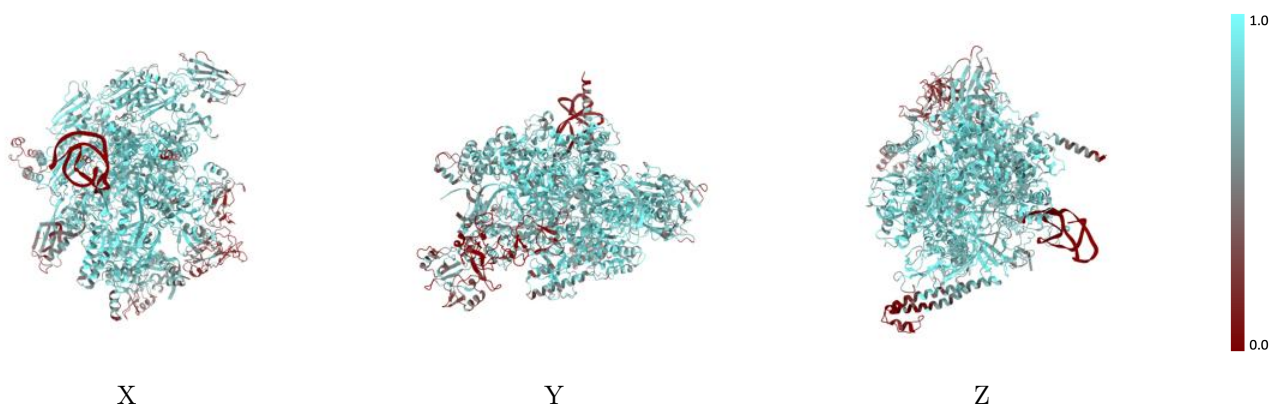
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



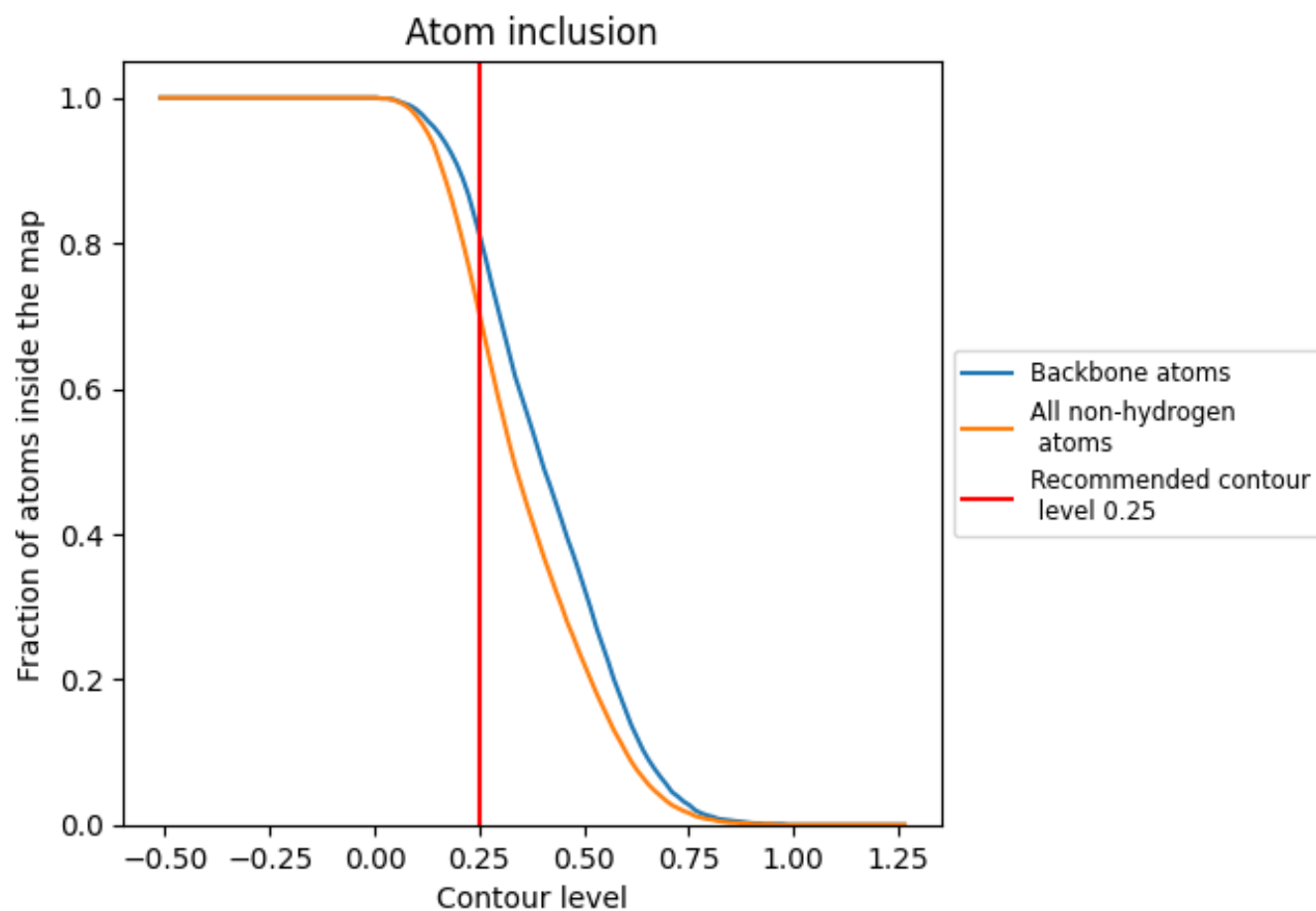
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.25).

9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 70% 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 (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7040	0.4070
A	0.7240	0.2550
B	0.7460	0.3140
G	0.7960	0.4790
H	0.6840	0.4110
I	0.7480	0.4360
J	0.6970	0.4080
K	0.7050	0.4530
R	0.1970	0.0680

1.0

0.0

<0.0