



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 10:28 AM UTC

PDB ID : 8ABZ / pdb_00008abz
EMDB ID : EMD-15328
Title : RNA polymerase at U-rich pause bound to non-regulatory RNA - pause prone, closed clamp state
Authors : Dey, S.; Weixlbaumer, A.
Deposited on : 2022-07-05
Resolution : 3.40 Å(reported)
Based on initial model : 6ALH

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:

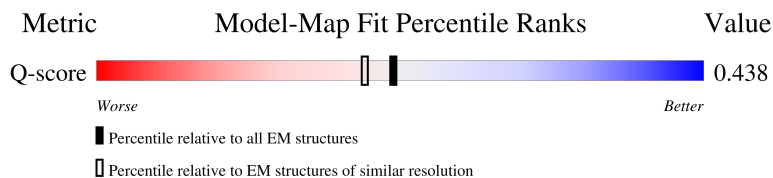
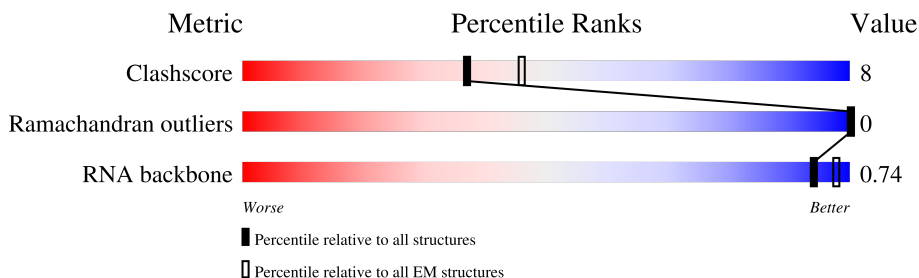
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
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 3.40 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	14717 (2.90 - 3.90)

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	A	329	
1	B	329	
2	C	1342	
3	D	1406	

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Mol	Chain	Length	Quality of chain
4	E	91	12% 64% 16% 20%
5	N	295	96%
6	R	122	5% 92%
7	T	295	5% 92%

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 25739 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 DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	221	Total	C	N	O	S	0	0
			1706	1068	300	332	6		
1	B	218	Total	C	N	O	S	0	0
			1683	1051	297	329	6		

- Molecule 2 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	1319	Total	C	N	O	S	0	0
			10407	6530	1814	2020	43		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	1335	Total	C	N	O	S	0	0
			10388	6526	1854	1958	50		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	73	Total	C	N	O	S	0	0
			582	355	111	115	1		

- Molecule 5 is a DNA chain called Non-template DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	N	13	Total	C	N	O	P	0	0
			265	127	44	81	13		

- Molecule 6 is a RNA chain called Non-regulatory RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	R	10	Total	C	N	O	P	0	0
			209	93	30	76	10		

- Molecule 7 is a DNA chain called Template DNA.

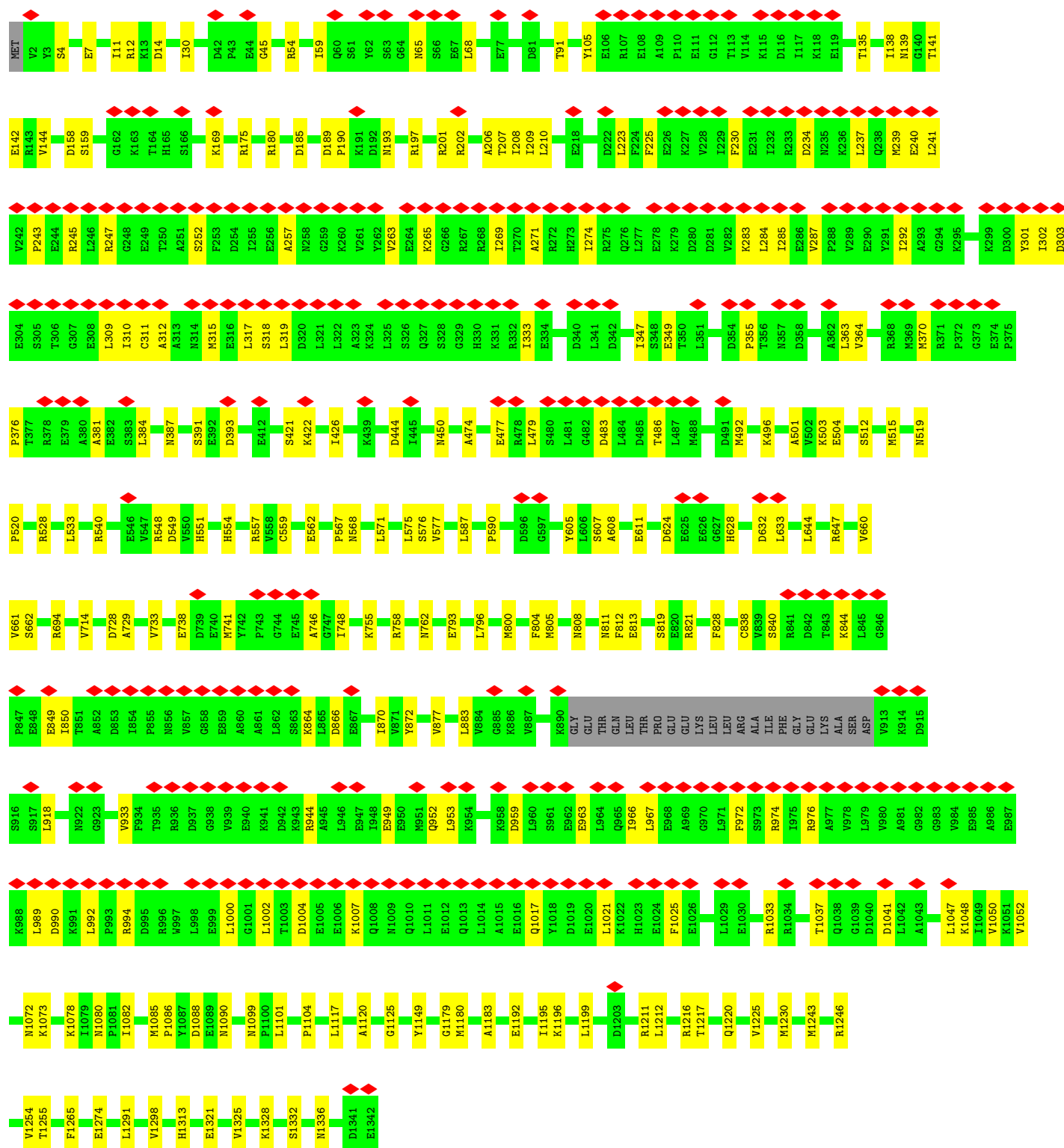
Mol	Chain	Residues	Atoms					AltConf	Trace
7	T	24	Total	C	N	O	P	0	0
			496	234	102	136	24		

- Molecule 8 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

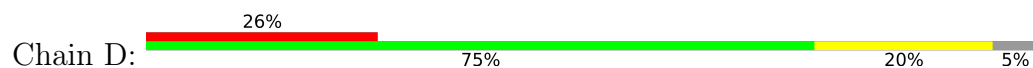
Mol	Chain	Residues	Atoms		AltConf
8	D	1	Total	Mg	0
			1	1	

- Molecule 9 is ZINC ION (CCD ID: ZN) (formula: Zn).

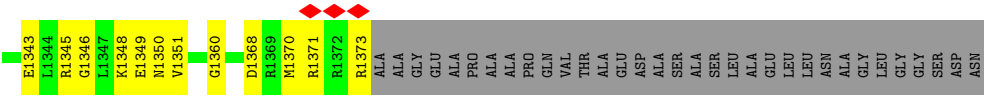
Mol	Chain	Residues	Atoms		AltConf
9	D	2	Total	Zn	0
			2	2	



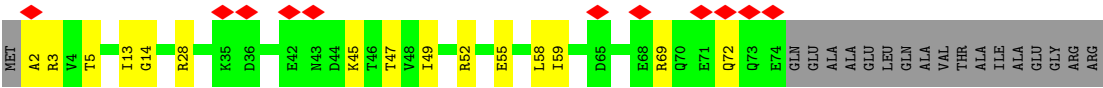
• Molecule 3: DNA-directed RNA polymerase subunit beta'



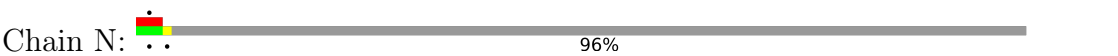
G1207	D1208	V1209	E1215	D1219	I1220	L1221	R1222	L1223	R1224	G1225	V1226	V1237	Q1238	D1239	R1242	L1243	Q1244	D1250	I1253	Q1259	M1260	L1261	I1266	A1269	G1270	S1271	S1272	D1273	F1274	L1275	E1276	G1277	E1278	V1285	E1291	L1292	E1293	A1294	M1295	G1296	K1297	V1298	R1304	D1305	F1325														
THR	G1136	D1143	R1149	P1150	K1151	E1152	L1156	E1158	I1159	S1160	G1161	I1162	V1163	S1164	F1165	G1166	K1167	E1168	T1169	K1170	G1171	K1172	R1173	R1174	I1177	T1178	P1179	V1180	G1182	S1183	D1184	P1185	Y1186	E1187	E1188	M1189	I1190	P1191	K1192	W1193	R1194	Q1195	L1196	N1197	V1198	F1199	E1200	G1201	E1202	R1203	V1204	E1205	R1206						
R1075	P1076	A1077	L1078	K1079	I1080	V1081	D1082	A1083	Q1084	G1085	N1086	D1087	V1088	L1089	I1090	P1091	G1092	T1093	D1094	M1095	P1096	A1097	Q1098	Y1099	F1100	L1101	P1102	G1103	K1104	A1105	I1106	V1107	Q1108	L1109	E1110	D1111	G1112	V1113	Q1114	I1115	S1116	S1117	G1118	D1119	T1120	L1121	A1122	R1123	I1124	P1125	Q1126	GLU	SER	GLY	GLY	THR	LYS	ASP	ILE
V952	K953	N954	K955	G956	S957	I958	K959	L960	S961	N962	V963	K964	S965	V966	V967	N968	S969	S970	G971	K972	L973	V974	I975	T976	S977	R978	N979	T980	E981	L982	K983	L984	I985	D986	E987	F988	G989	R990	T991	K992	E993	S994	Y995	K996	Y999	G1000	A1001	V1002	L1003	A1004	K1005	G1006	D1007	G1008	E1009	Q1010	V1011	A1012	
G1013	G1014	E1015	T1016	V1017	D1021	P1022	H1023	T1024	M1025	P1026	V1027	I1028	T1029	P1030	N1031	S1032	G1033	F1034	V1035	R1036	F1037	T1038	D1039	M1040	I1041	D1042	G1043	Q1044	T1045	I1046	T1047	R1048	Q1049	T1050	D1051	E1052	L1053	T1054	G1055	L1056	S1057	S1058	L1059	V1060	V1061	L1062	D1063	S1064	A1065	E1066	R1067	T1068	A1069	G1070	G1071	K1072	D1073	L1074	
K531	E532	A533	E534	R535	L536	V550	T553	D558	A559	N560	G561	T567	T573	W580	V583	G586	L596	I601	S602	R603	M604	Y609	L612	K615	P616	I624	M625	T626	T627	G628	F629	A633	G638	T640	M621	M622	T623	P647	W625	E627	G628	G629	D630	V631															
S670	G671	L672	V673	E677	R678	T685	Q702	T703	R709	S718	F719	N720	S721	I722	W723	M724	N725	A741	L746	P750	D751	G752	E756	T757	N762	K781	R799	D802	V803	A804	E818	G819	I820	M821	M822	T823	P824	W825	I826	G827	G828	G829	D830	V831															
L835	T844	D847	V848	K850	P851	G852	T853	A854	D855	V858	P859	R860	R861	L864	K868	C869	D870	L871	L872	E873	E874	D878	A879	T909	E912	G913	E925	P926	R933	THR	PHE	HIS	ILE	GLY	ALA	ALA	SER	ARG	ALA	ALA	GLU	S948	S949	I950	Q951														
V401	W409	L412	V415	I416	R417	H418	P420	N424	T428	H429	H430	R431	L432	F437	E438	P439	V440	L441	K445	Q448	L449	H450	D460	M466	L474	E475	I490	V501	Q504	D505	L508	G509	L510	T511	S512	M513	T514	R515	D516	L527	T528																		
T262	S263	D264	L265	D267	T273	R278	R281	D284	L285	A286	A287	P288	D289	I290	L291	V292	R293	N294	R311	R312	G313	R314	G318	S319	N320	K321	R322	D329	Y349	S353	G367	K370	K371	M372	P379	F380	I381	Y382	T393	K395	A396	A397	K398																
C88	E91	R101	P110	L114	L117	K118	S119	L120	P121	S122	I124	D129	M130	R133	D134	I135	E136	R137	V138	L139	Y140	F141	E142	S143	Y144	I147	E148	G149	G150	M151	T152	N153	L154	E155	R156	Q157	Q158	I159	L160	T161	E162	E163	Q164	V165	L166	D167	E168	L169	E170	E171									
F172	G173	D174	E175	F176	D177	A178	E183	A184	I185	M192	D193	L194	E195	Q196	Q200	L201	R202	E203	E204	L205	N206	E207	T208	N209	S210	E211	T212	K213	R214	K215	K216	K219	R220	I221	S230	G231	L242	P243	V244	L245	L249	R250	V253	P254	L255	D256	G257	R258	R259	F260	A261								
MET	LYS	ASP	LEU	LEU	LYS	PHE	LEU	ALA	GLN	THR	LYS	THR	GLU	E16	F17	D18	K21	M29	E37	V38	K39	E42	M45	Y46	R47	T48	F49	G55	C58	F62	E69	C70	C72	G73	K74	Y75	K76	R77	L78	K79	H80	R81	G82	V83	I84	C85	E86	K87											



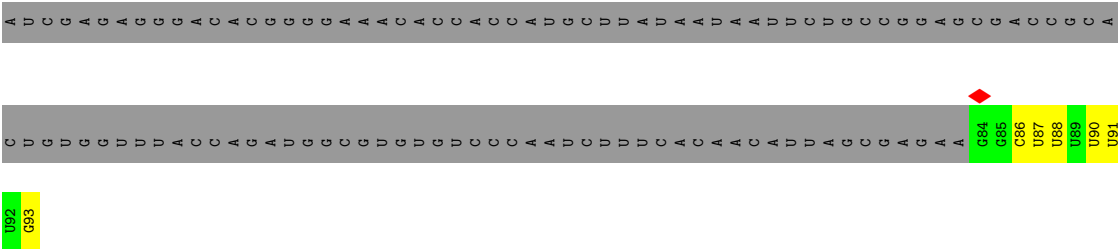
● Molecule 4: DNA-directed RNA polymerase subunit omega



● Molecule 5: Non-template DNA



● Molecule 6: Non-regulatory RNA



● Molecule 7: Template DNA



[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	180841	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 ($e^-/\text{\AA}^2$)	52	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.028	Depositor
Minimum map value	-0.625	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.025	Depositor
Recommended contour level	0.155	Depositor
Map size ($\text{\AA}$)	310.32, 310.32, 310.32	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.86200005, 0.86200005, 0.86200005	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: ZN, IGU, MG

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	0.11	0/1726	0.28	0/2338
1	B	0.11	0/1702	0.28	0/2306
2	C	0.13	0/10573	0.29	0/14265
3	D	0.11	0/10545	0.27	0/14236
4	E	0.12	0/584	0.33	0/786
5	N	0.18	0/295	0.39	0/453
6	R	0.11	0/231	0.26	0/357
7	T	0.16	0/508	0.28	0/778
All	All	0.12	0/26164	0.29	0/35519

There are no bond length outliers.

There are no bond angle outliers.

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	A	1706	0	1746	30	0
1	B	1683	0	1719	32	0
2	C	10407	0	10420	160	0
3	D	10388	0	10610	178	0
4	E	582	0	593	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	N	265	0	149	2	0
6	R	209	0	104	4	0
7	T	496	0	267	6	0
8	D	1	0	0	0	0
9	D	2	0	0	0	0
All	All	25739	0	25608	390	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 8.

The worst 5 of 390 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)
3:D:196:GLN:HG2	3:D:200:GLN:HE22	1.43	0.83
2:C:1072:ASN:HD21	2:C:1230:MET:HE1	1.50	0.77
2:C:1336:ASN:ND2	3:D:29:MET:SD	2.58	0.76
2:C:193:ASN:ND2	2:C:349:GLU:OE1	2.18	0.76
2:C:185:ASP:HB2	2:C:197:ARG:HG3	1.70	0.73

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	A	217/329 (66%)	211 (97%)	6 (3%)	0	100	100
1	B	214/329 (65%)	212 (99%)	2 (1%)	0	100	100
2	C	1315/1342 (98%)	1266 (96%)	49 (4%)	0	100	100
3	D	1321/1406 (94%)	1283 (97%)	38 (3%)	0	100	100
4	E	71/91 (78%)	68 (96%)	3 (4%)	0	100	100
All	All	3138/3497 (90%)	3040 (97%)	98 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
6	R	9/122 (7%)	0	0

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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
7	IGU	T	14	7	21,24,25	1.33	3 (14%)	29,35,38	1.81	7 (24%)
7	IGU	T	13	5,7	21,24,25	1.19	3 (14%)	29,35,38	1.74	6 (20%)

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
7	IGU	T	14	7	-	1/7/21/22	0/3/3/3
7	IGU	T	13	5,7	-	0/7/21/22	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	T	14	IGU	C5-C6	3.51	1.47	1.40
7	T	13	IGU	C5-C6	2.80	1.46	1.40
7	T	13	IGU	C5-N7	-2.67	1.33	1.39
7	T	14	IGU	C5-N7	-2.49	1.34	1.39
7	T	14	IGU	O3'-C3'	2.28	1.48	1.43

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	T	14	IGU	C6-C5-N7	4.37	135.59	130.21
7	T	14	IGU	C5-C4-N3	-4.33	118.72	127.60
7	T	13	IGU	C5-C6-N6	-4.28	119.22	124.66
7	T	13	IGU	C5-C4-N3	-3.92	119.56	127.60
7	T	13	IGU	N9-C4-N3	3.50	135.03	127.05

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	T	14	IGU	C4'-C5'-O5'-P

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

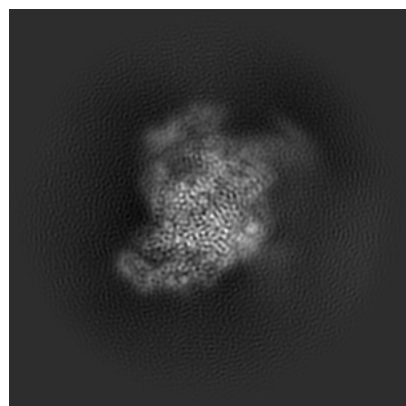
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-15328. These allow visual inspection of the internal detail of the map and identification of artifacts.

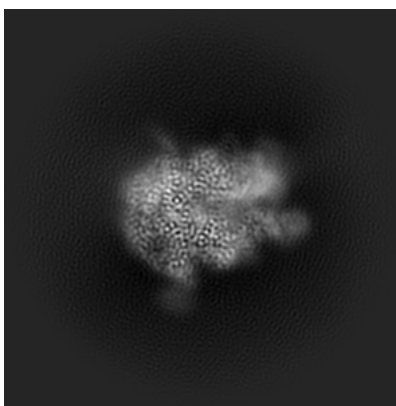
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

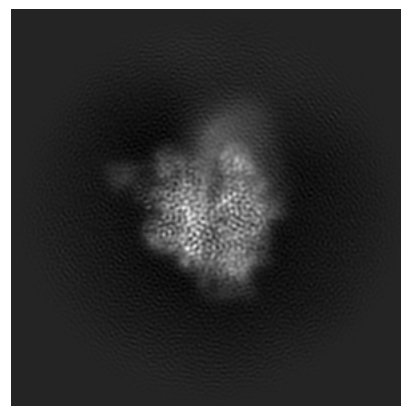
6.1.1 Primary map



X

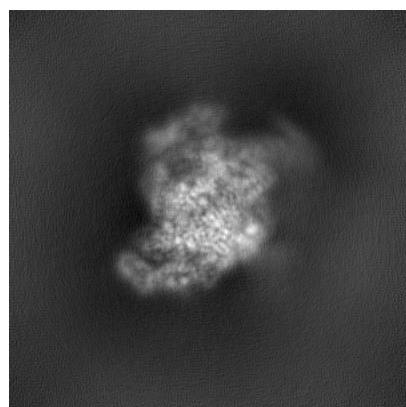


Y

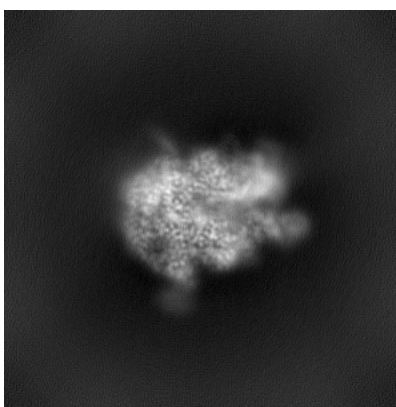


Z

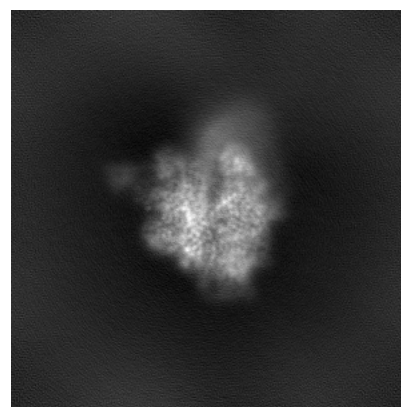
6.1.2 Raw map



X



Y

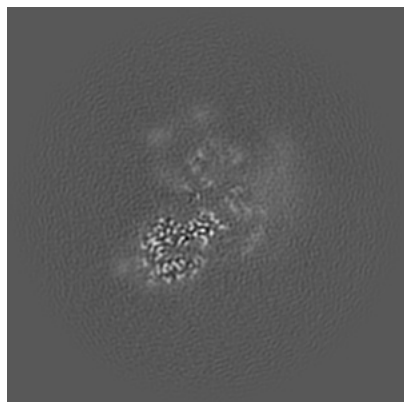


Z

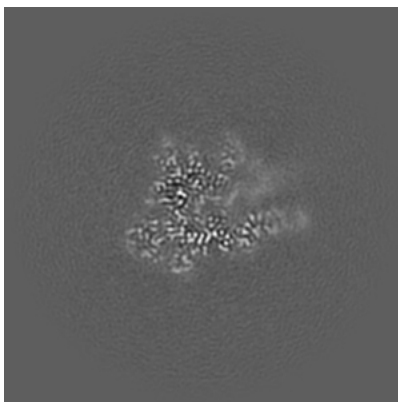
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

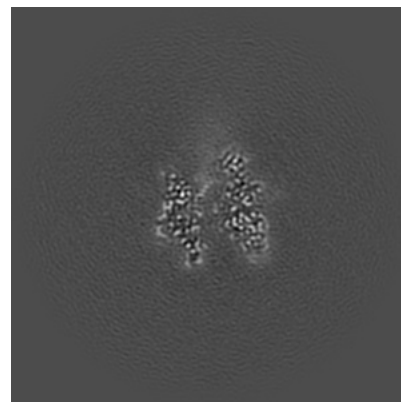
6.2.1 Primary map



X Index: 180

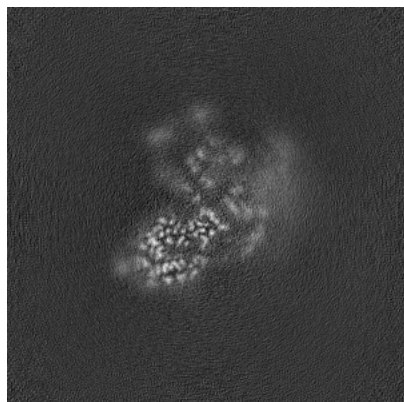


Y Index: 180

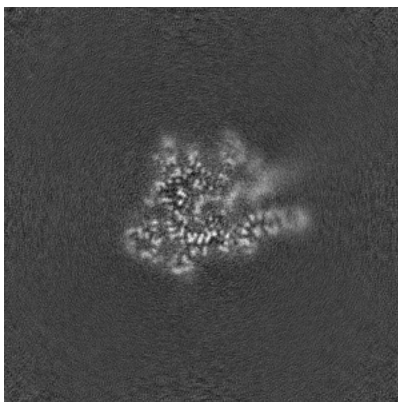


Z Index: 180

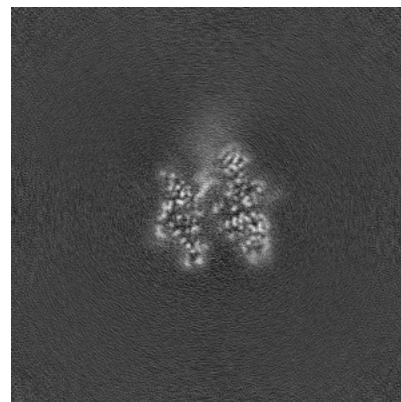
6.2.2 Raw map



X Index: 180



Y Index: 180

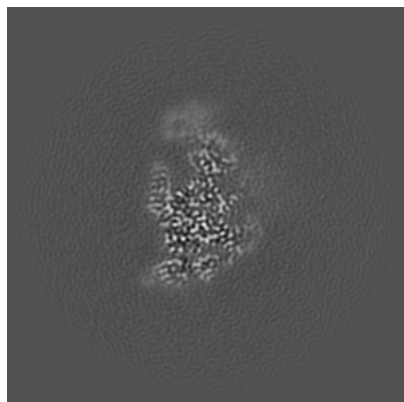


Z Index: 180

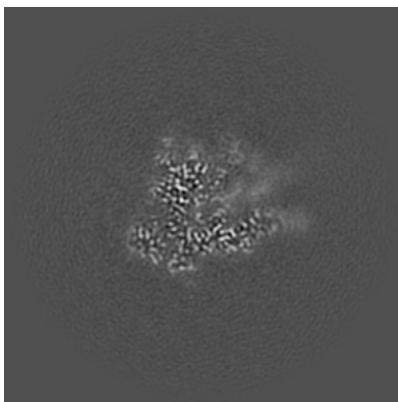
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

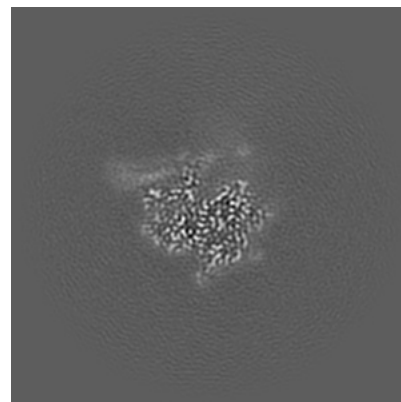
6.3.1 Primary map



X Index: 159

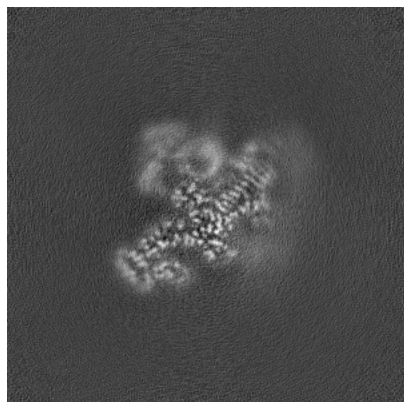


Y Index: 182

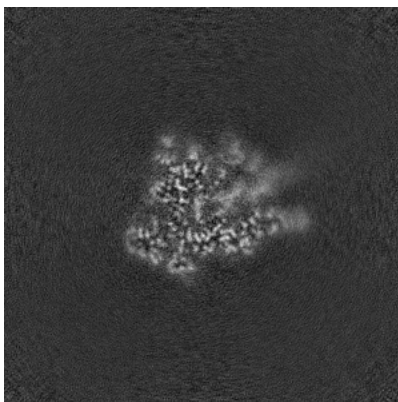


Z Index: 155

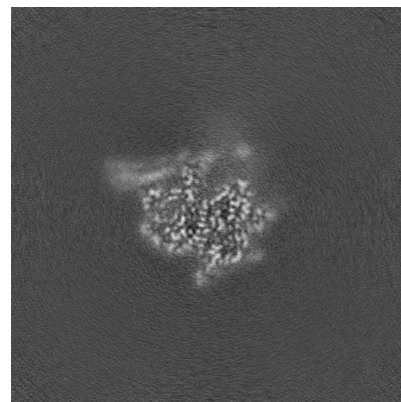
6.3.2 Raw map



X Index: 196



Y Index: 182

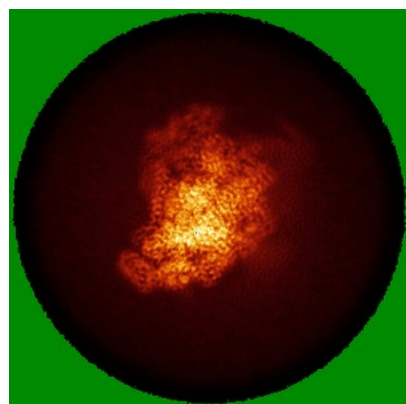


Z Index: 155

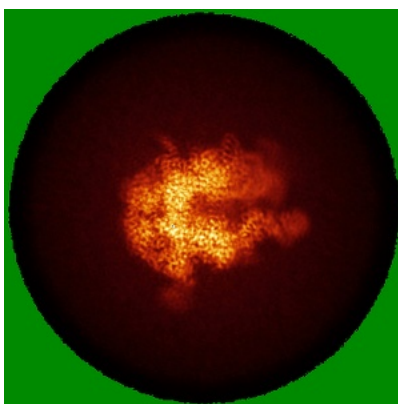
The images above show the largest variance slices of the map in three orthogonal directions.

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

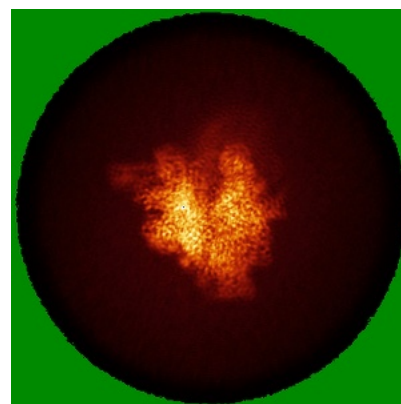
6.4.1 Primary map



X

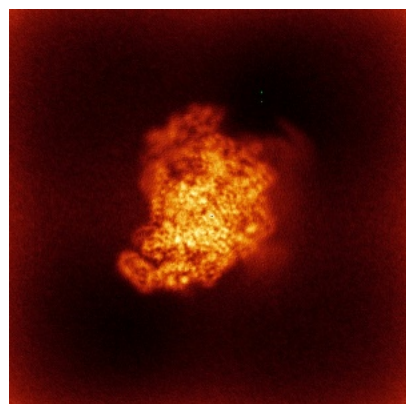


Y

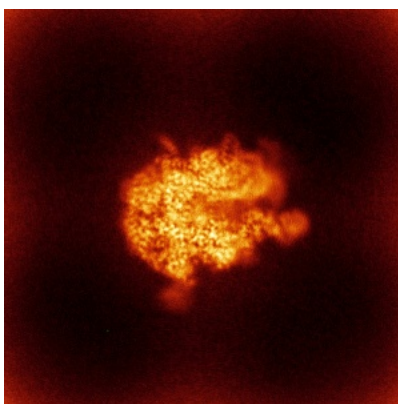


Z

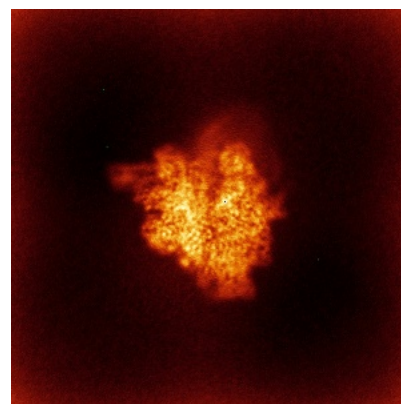
6.4.2 Raw map



X



Y

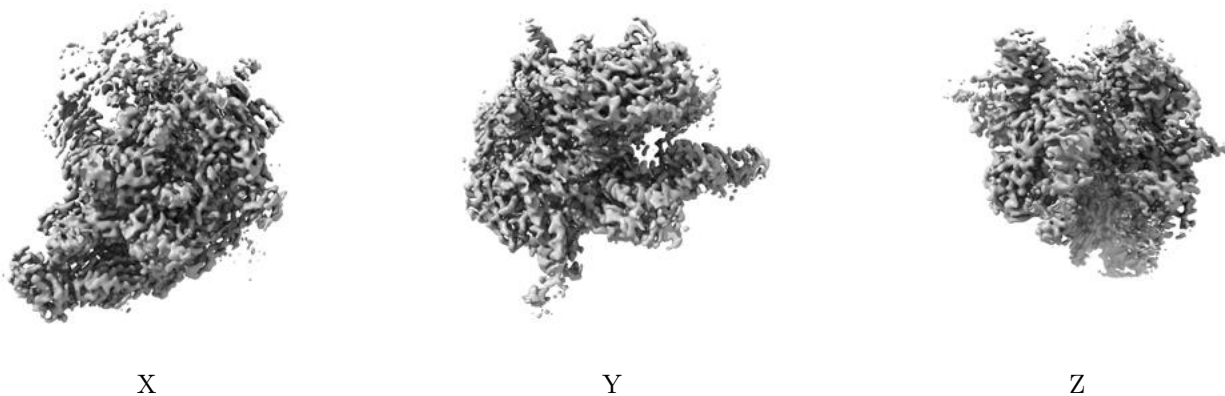


Z

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.

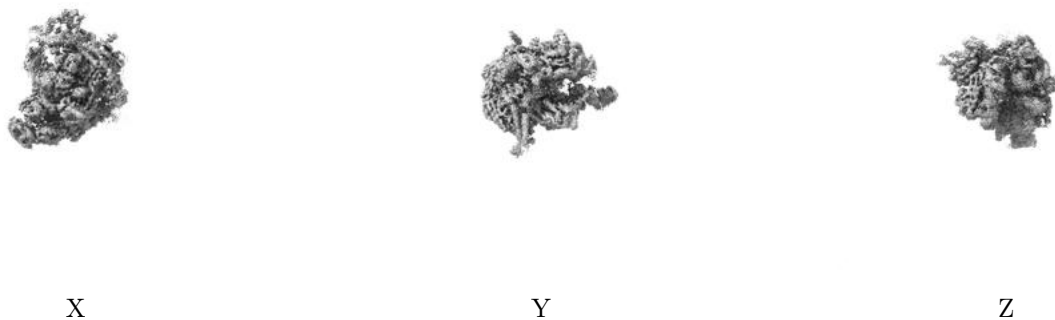
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.155. 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.

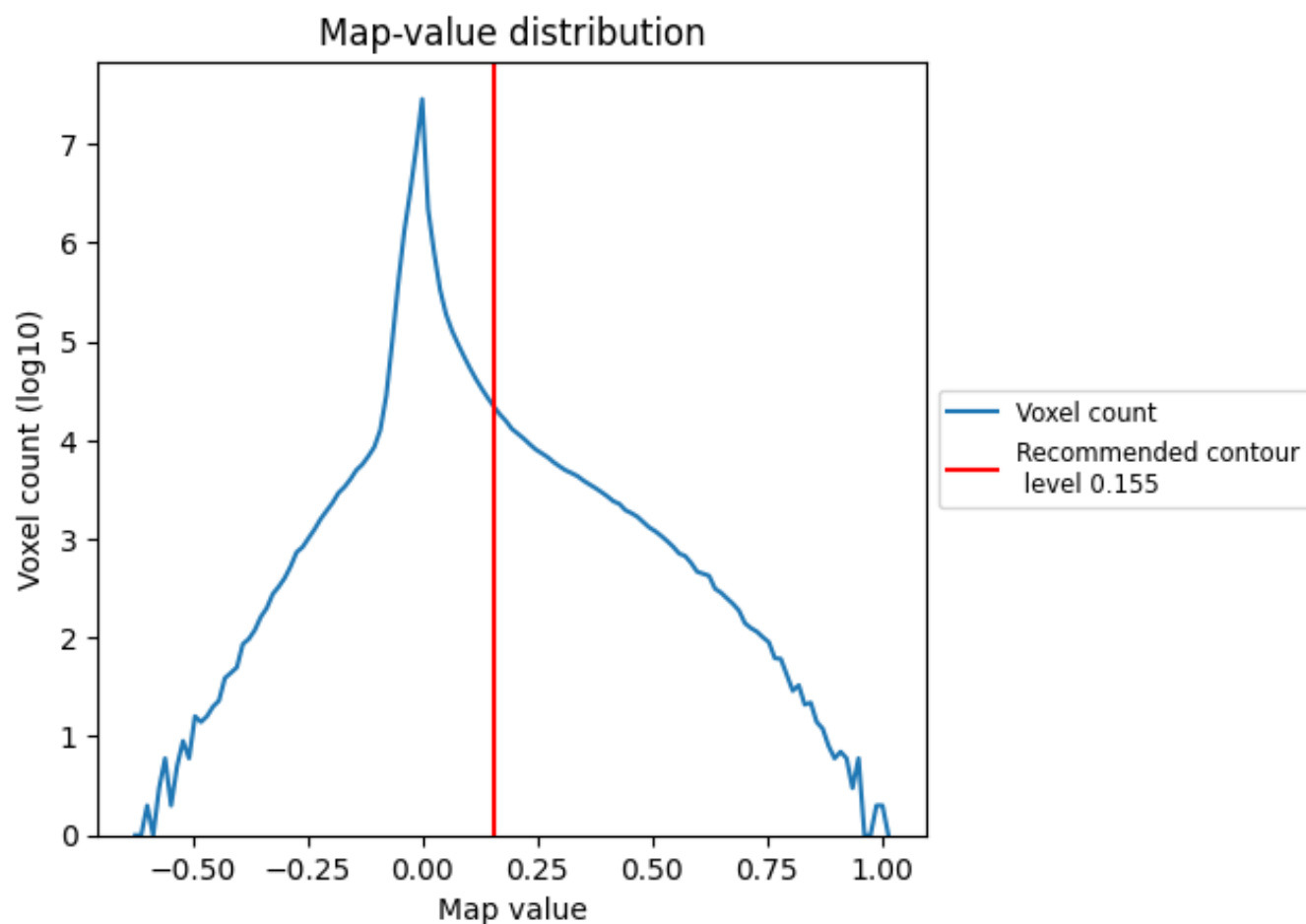
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

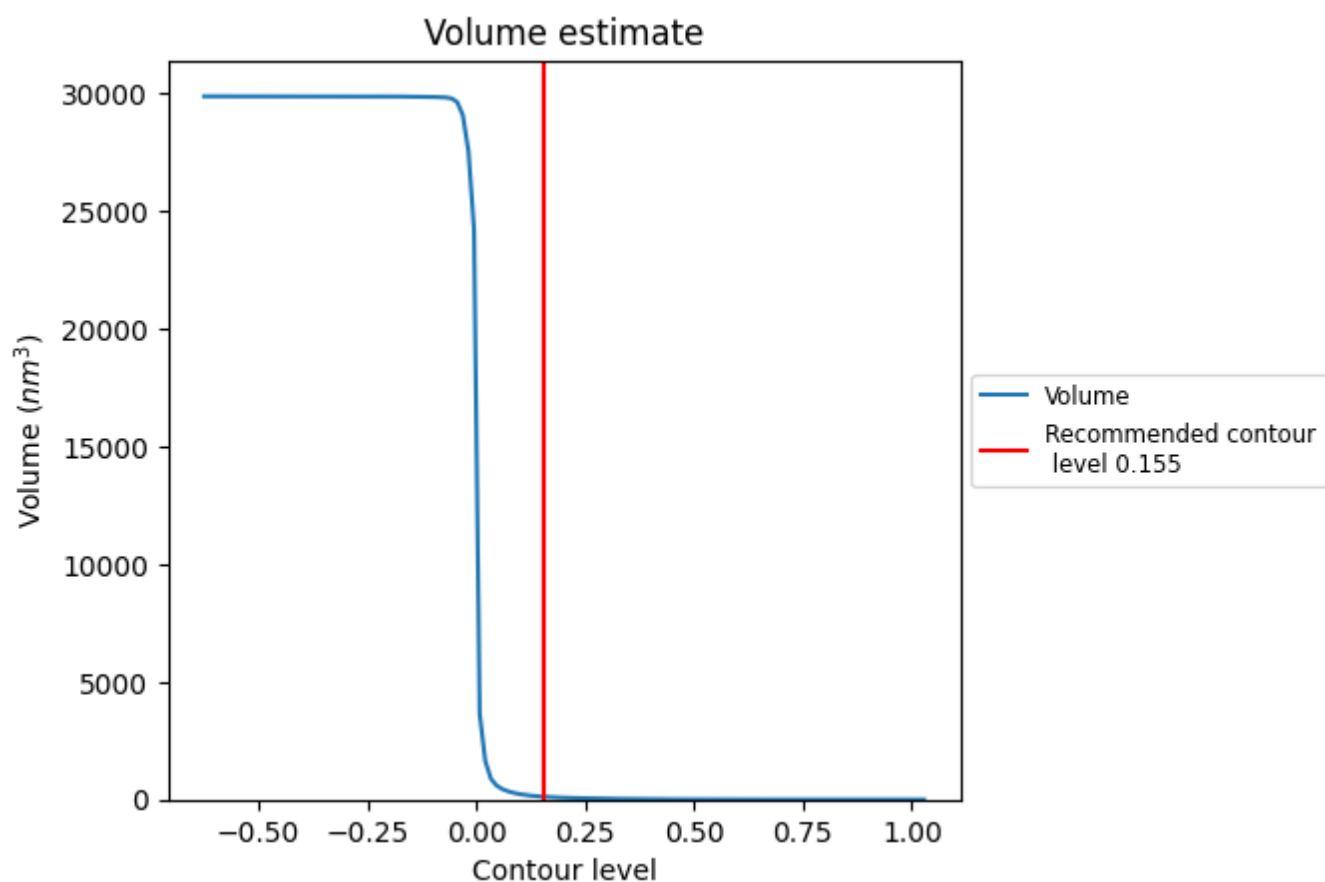
This section contains the results of statistical analysis of the map.

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.

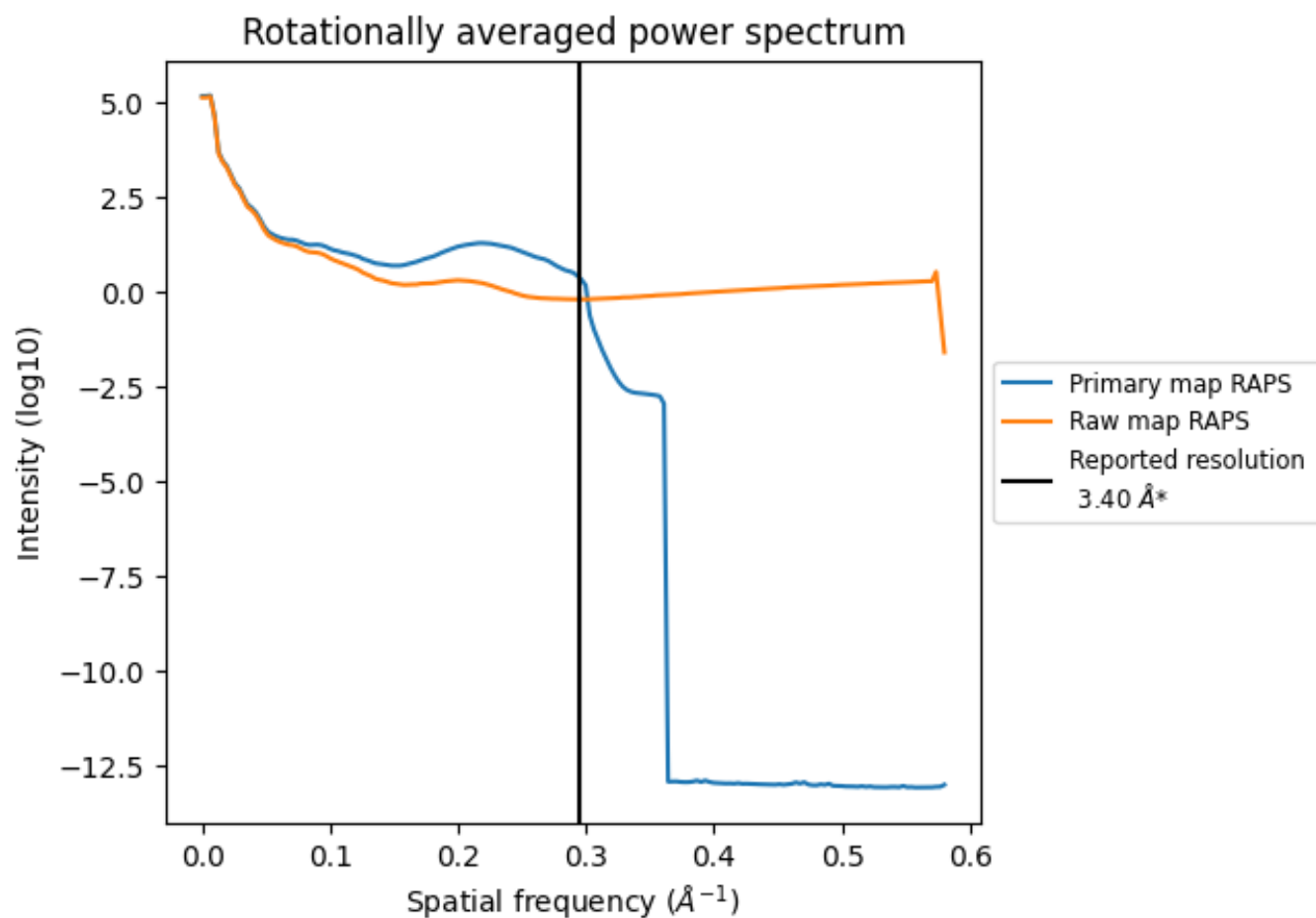
7.2 Volume estimate [i](#)



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 ⓘ

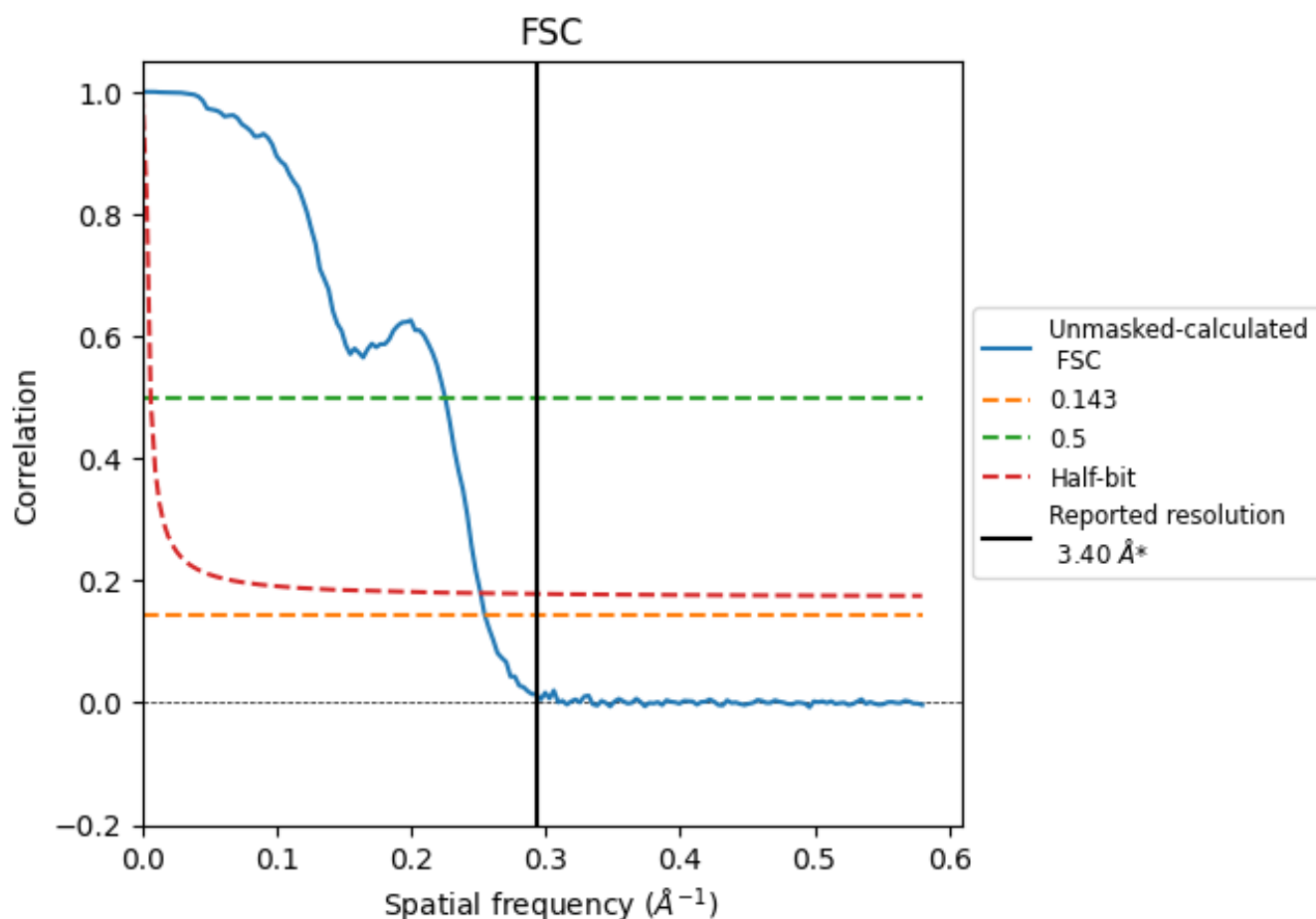


*Reported resolution corresponds to spatial frequency of 0.294 $\text{\AA}^{-1}$

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 0.294 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.92	4.44	3.97

*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 3.92 differs from the reported value 3.4 by more than 10 %

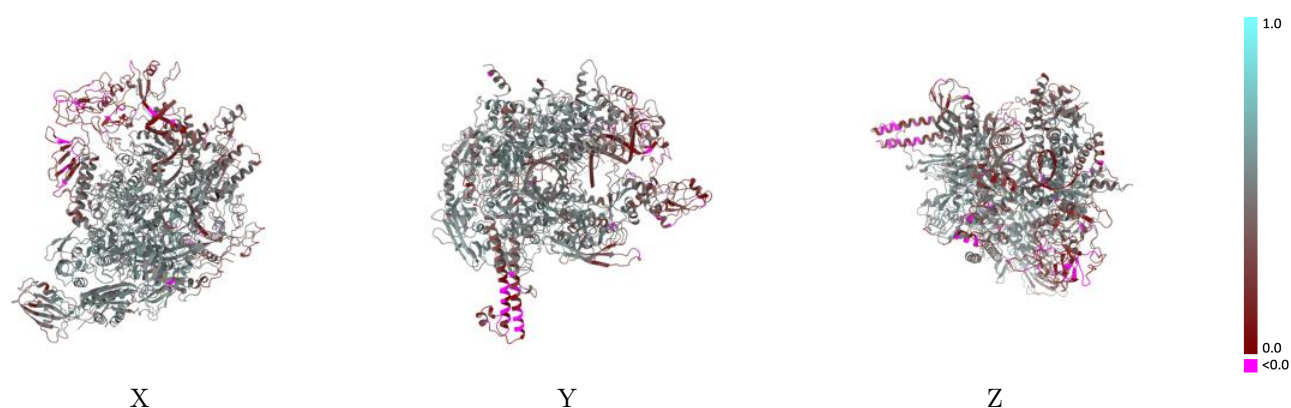
9 Map-model fit [i](#)

This section contains information regarding the fit between EMD map EMD-15328 and PDB model 8ABZ. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)

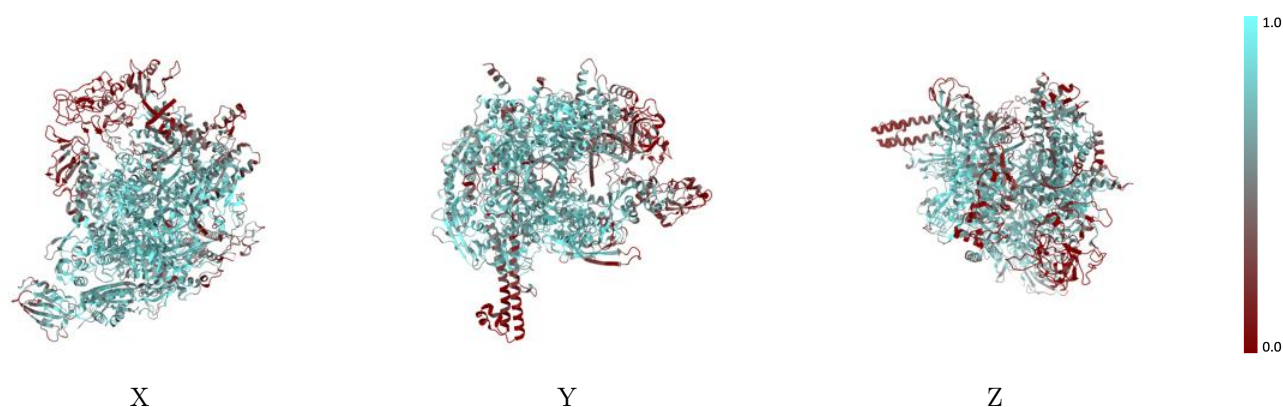
This section was not generated.

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



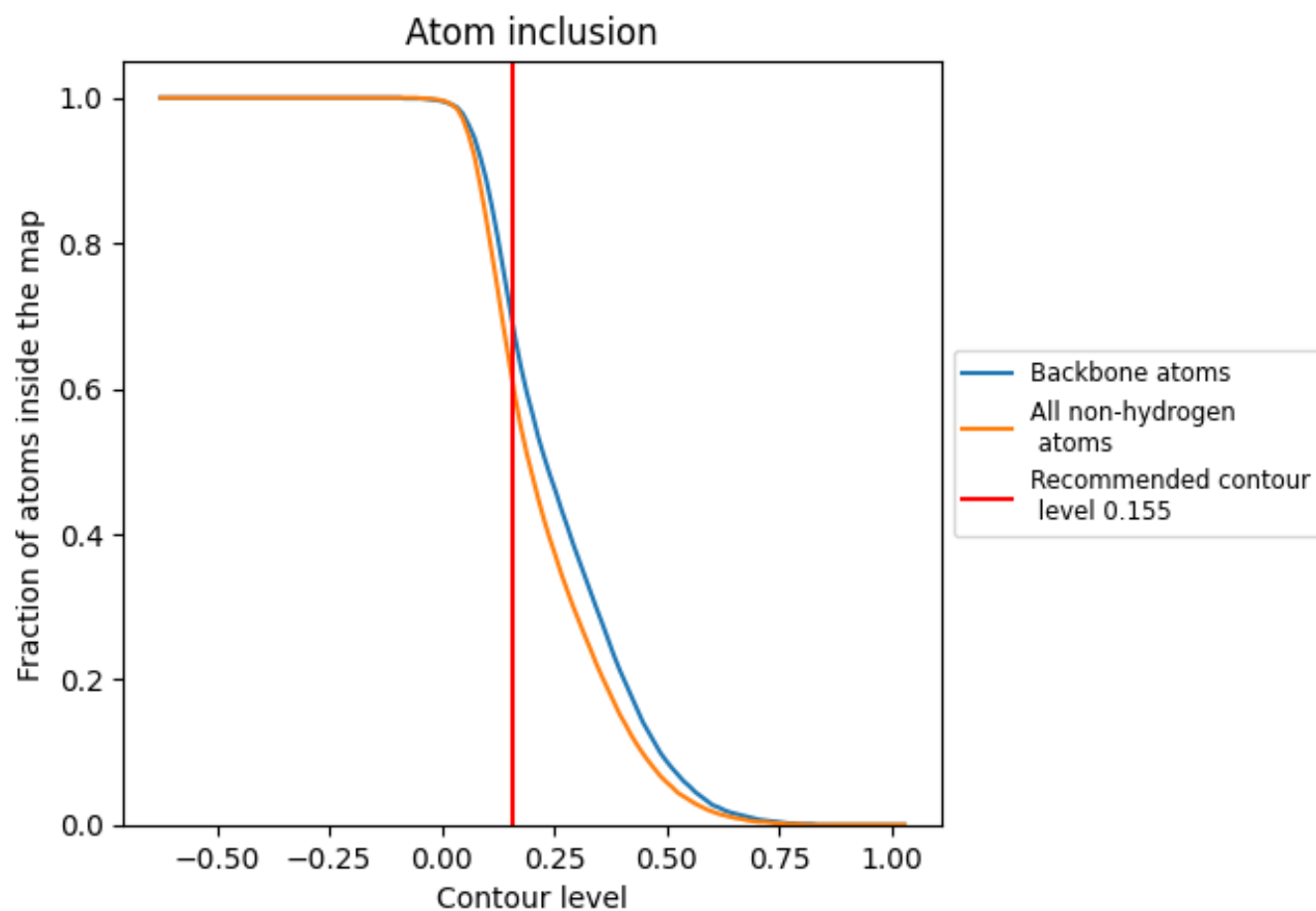
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.155).

9.4 Atom inclusion [i](#)



At the recommended contour level, 70% of all backbone atoms, 62% 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 (0.155) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6170	0.4380
A	0.7250	0.5060
B	0.6470	0.4670
C	0.6350	0.4410
D	0.5820	0.4300
E	0.6500	0.4770
N	0.3210	0.1450
R	0.7030	0.4100
T	0.5770	0.3490

1.0

0.0

<0.0