



wwPDB EM Validation Summary Report ⓘ

Nov 13, 2022 – 06:28 PM EST

PDB ID : 6XE0
EMDB ID : EMD-22143
Title : Cryo-EM structure of NusG-CTD bound to 70S ribosome (30S: NusG-CTD fragment)
Authors : Washburn, R.; Zuber, P.; Sun, M.; Hashem, Y.; Shen, B.; Li, W.; Harvey, S.; Acosta-Reyes, F.J.; Knauer, S.H.; Frank, J.; Gottesman, M.E.
Deposited on : 2020-06-11
Resolution : 6.80 Å (reported)
Based on initial models : 2KVQ, 4GD2

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.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

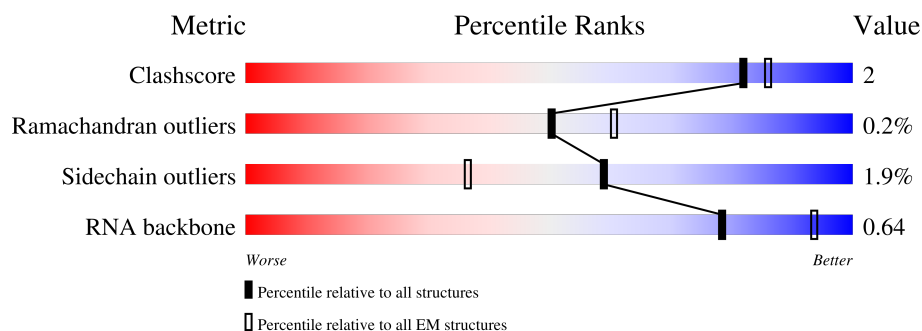
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.80 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	218	
2	B	206	
3	C	205	
4	D	150	
5	E	100	
6	F	151	
7	G	129	

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Mol	Chain	Length	Quality of chain
8	H	127	
9	I	98	
10	J	117	
11	K	123	
12	L	114	
13	M	100	
14	O	88	
15	P	82	
16	Q	80	
17	R	55	
18	S	79	
19	T	85	
20	U	51	
21	V	181	
22	W	1539	

2 Entry composition

There are 22 unique types of molecules in this entry. The entry contains 52034 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 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	218	Total	C	N	O	S	0	0
			1705	1081	305	312	7		

- Molecule 2 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	206	Total	C	N	O	S	0	0
			1625	1028	305	289	3		

- Molecule 3 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 4 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	150	Total	C	N	O	S	0	0
			1106	687	211	202	6		

- Molecule 5 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	100	Total	C	N	O	S	0	0
			818	515	148	149	6		

- Molecule 6 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	151	Total	C	N	O	S	0	0
			1182	735	227	216	4		

- Molecule 7 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 8 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 9 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	98	Total	C	N	O	S	0	0
			787	493	150	143	1		

- Molecule 10 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 11 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 12 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	114	Total	C	N	O	S	0	0
			884	546	178	157	3		

- Molecule 13 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	96	Total	C	N	O	S	0	0
			774	483	160	128	3		

- Molecule 14 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 15 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 16 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	80	Total	C	N	O	S	0	0
			649	411	121	114	3		

- Molecule 17 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	R	55	Total	C	N	O	0	0
			456	288	86	82		

- Molecule 18 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	79	Total	C	N	O	S	0	0
			638	408	120	108	2		

- Molecule 19 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 20 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	51	Total	C	N	O	S	0	0
			426	265	86	74	1		

- Molecule 21 is a protein called Transcription termination/antitermination protein NusG.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	59	Total	C	N	O	S	0	0
			468	297	78	92	1		

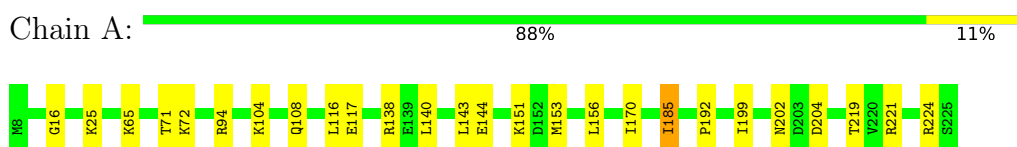
- Molecule 22 is a RNA chain called 16s rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

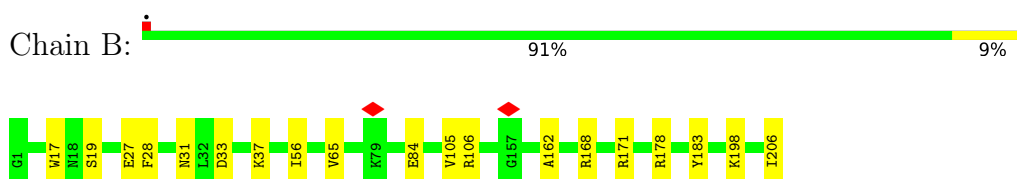
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

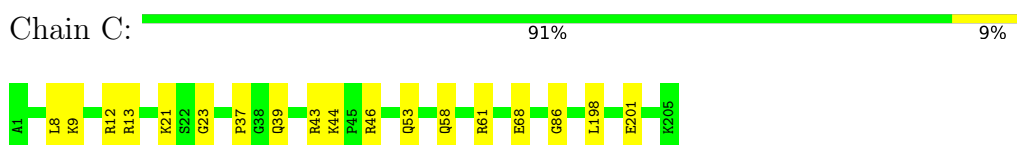
- Molecule 1: 30S ribosomal protein S2



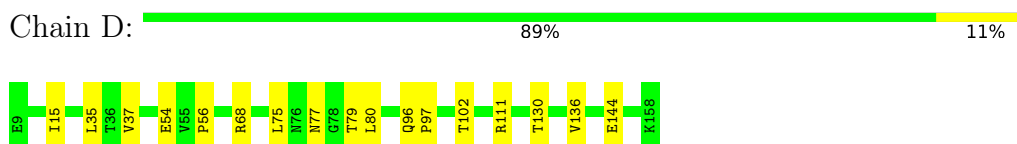
- Molecule 2: 30S ribosomal protein S3



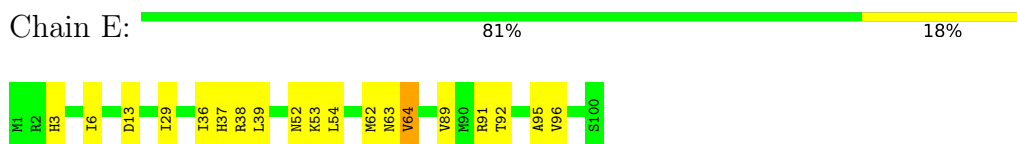
- Molecule 3: 30S ribosomal protein S4




- Molecule 4: 30S ribosomal protein S5



- Molecule 5: 30S ribosomal protein S6




- Molecule 6: 30S ribosomal protein S7

Chain F:  90% 10%



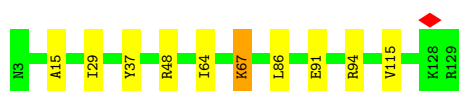
- Molecule 7: 30S ribosomal protein S8

Chain G:  86% 14%




- Molecule 8: 30S ribosomal protein S9

Chain H:  92% 7%




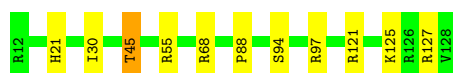
- Molecule 9: 30S ribosomal protein S10

Chain I:  81% 19%




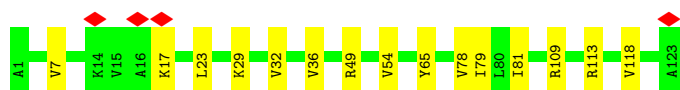
- Molecule 10: 30S ribosomal protein S11

Chain J:  91% 9%



- Molecule 11: 30S ribosomal protein S12

Chain K:  88% 12%




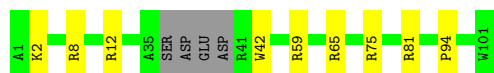
- Molecule 12: 30S ribosomal protein S13

Chain L:  96%



- Molecule 13: 30S ribosomal protein S14

Chain M:  87% 9% .




- Molecule 14: 30S ribosomal protein S15

Chain O:  95% 5%




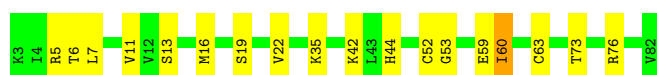
- Molecule 15: 30S ribosomal protein S16

Chain P:  87% 13%



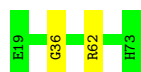
- Molecule 16: 30S ribosomal protein S17

Chain Q:  78% 21%



- Molecule 17: 30S ribosomal protein S18

Chain R:  96%



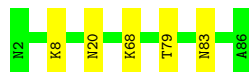
- Molecule 18: 30S ribosomal protein S19

Chain S:  94% 6%



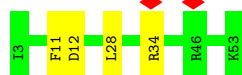
- Molecule 19: 30S ribosomal protein S20

Chain T:  94% 6%



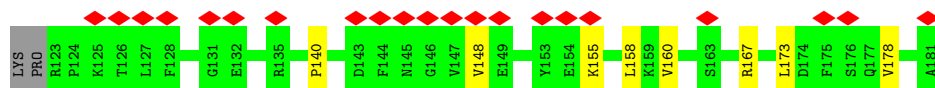
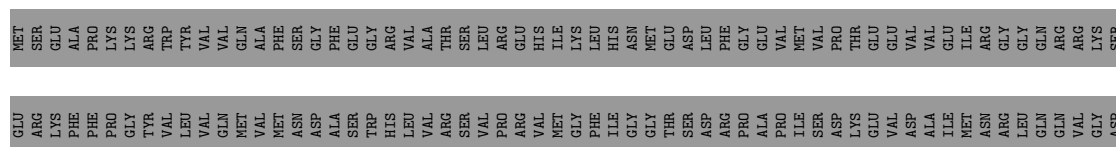
- Molecule 20: 30S ribosomal protein S21

Chain U:  92% 8%




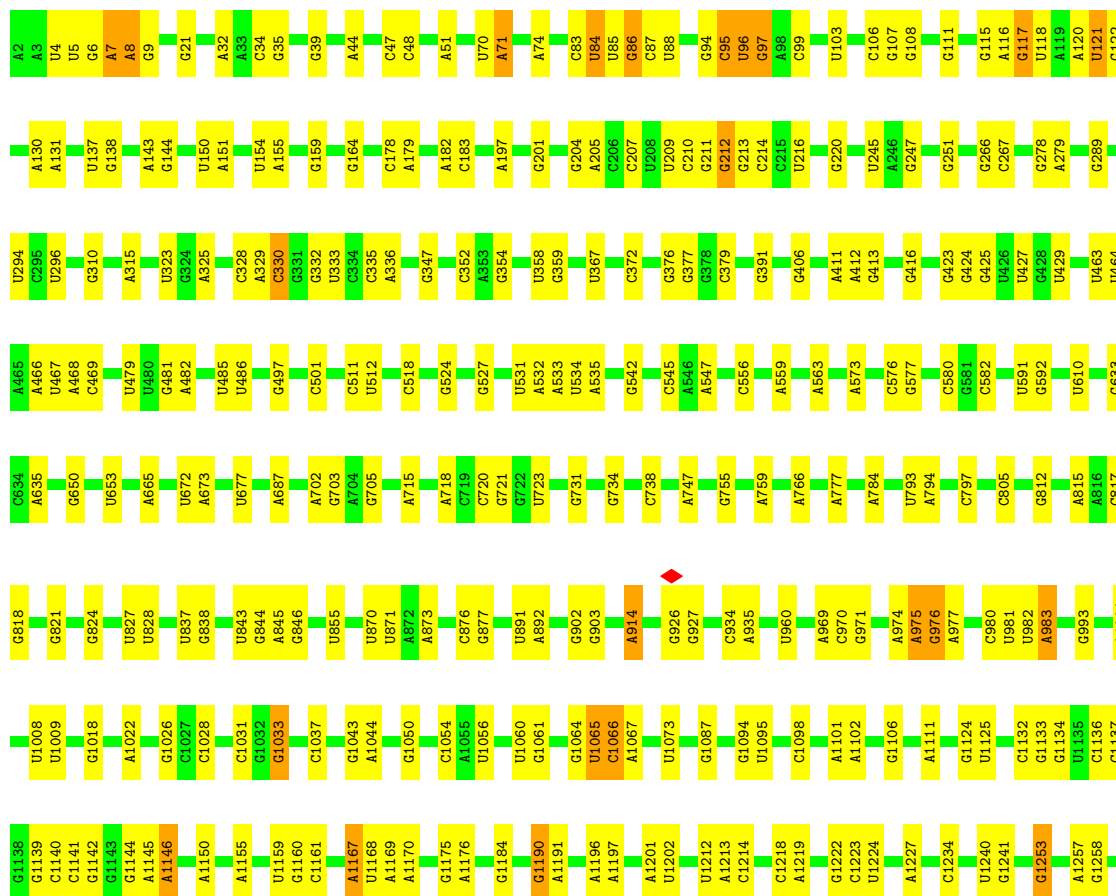
- Molecule 21: Transcription termination/antitermination protein NusG

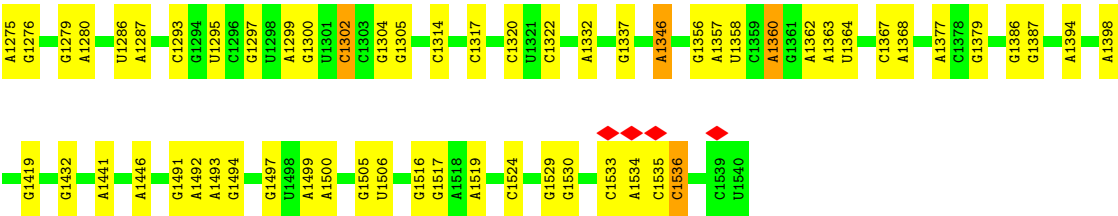
Chain V:  12% 28% 67%



- Molecule 22: 16s rRNA

Chain W:  77% 21%





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	17122	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	100	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	0.019	Depositor
Minimum map value	-0.009	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0028	Depositor
Map size (\AA)	378.47998, 378.47998, 378.47998	wwPDB
Map dimensions	228, 228, 228	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.66, 1.66, 1.66	Depositor

5 Model quality

5.1 Standard geometry

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	0.64	0/1736	0.81	0/2338
2	B	0.61	0/1652	0.74	0/2225
3	C	0.62	0/1665	0.75	0/2227
4	D	0.63	0/1119	0.79	0/1504
5	E	0.64	0/836	0.80	0/1128
6	F	0.60	0/1196	0.69	0/1602
7	G	0.59	0/989	0.68	0/1326
8	H	0.62	0/1034	0.80	0/1375
9	I	0.60	0/797	0.83	0/1077
10	J	0.60	0/893	0.73	0/1205
11	K	0.60	0/969	0.73	0/1300
12	L	0.62	0/893	0.70	0/1193
13	M	0.59	0/785	0.75	0/1043
14	O	0.62	0/722	0.68	0/964
15	P	0.62	0/659	0.77	0/884
16	Q	0.64	0/658	0.85	0/881
17	R	0.58	0/463	0.62	0/621
18	S	0.59	0/653	0.68	0/877
19	T	0.64	0/671	0.76	0/888
20	U	0.63	0/431	0.86	0/570
21	V	0.59	0/477	0.72	0/642
22	W	0.42	0/36963	0.87	0/57662
All	All	0.49	0/56261	0.84	0/83532

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 ⓘ

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	1705	0	1732	11	0
2	B	1625	0	1699	10	0
3	C	1643	0	1710	13	0
4	D	1106	0	1148	10	0
5	E	818	0	808	10	0
6	F	1182	0	1240	10	0
7	G	979	0	1034	11	0
8	H	1022	0	1070	4	0
9	I	787	0	828	12	0
10	J	877	0	887	7	0
11	K	955	0	1019	7	0
12	L	884	0	944	2	0
13	M	774	0	827	8	0
14	O	714	0	737	2	0
15	P	649	0	666	9	0
16	Q	649	0	691	10	0
17	R	456	0	478	1	0
18	S	638	0	665	4	0
19	T	665	0	714	4	0
20	U	426	0	449	3	0
21	V	468	0	458	7	0
22	W	33012	0	16618	101	0
All	All	52034	0	36422	200	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 2.

The worst 5 of 200 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)
7:G:25:THR:HG22	7:G:59:GLU:HG3	1.79	0.64
1:A:140:LEU:O	1:A:144:GLU:HB2	1.98	0.62
18:S:36:ARG:NH1	22:W:1320:C:N3	2.49	0.61
3:C:86:GLY:H	4:D:102:THR:HG21	1.66	0.60
10:J:30:ILE:HD11	22:W:705:G:H21	1.67	0.60

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	216/218 (99%)	195 (90%)	21 (10%)	0	100	100
2	B	204/206 (99%)	198 (97%)	6 (3%)	0	100	100
3	C	203/205 (99%)	192 (95%)	10 (5%)	1 (0%)	29	69
4	D	148/150 (99%)	137 (93%)	11 (7%)	0	100	100
5	E	98/100 (98%)	86 (88%)	10 (10%)	2 (2%)	7	38
6	F	149/151 (99%)	146 (98%)	3 (2%)	0	100	100
7	G	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
8	H	125/127 (98%)	114 (91%)	11 (9%)	0	100	100
9	I	96/98 (98%)	90 (94%)	5 (5%)	1 (1%)	15	54
10	J	115/117 (98%)	111 (96%)	4 (4%)	0	100	100
11	K	121/123 (98%)	118 (98%)	3 (2%)	0	100	100
12	L	112/114 (98%)	106 (95%)	6 (5%)	0	100	100
13	M	92/100 (92%)	90 (98%)	2 (2%)	0	100	100
14	O	86/88 (98%)	82 (95%)	4 (5%)	0	100	100
15	P	80/82 (98%)	75 (94%)	5 (6%)	0	100	100
16	Q	78/80 (98%)	70 (90%)	8 (10%)	0	100	100
17	R	53/55 (96%)	52 (98%)	1 (2%)	0	100	100
18	S	77/79 (98%)	75 (97%)	2 (3%)	0	100	100
19	T	83/85 (98%)	81 (98%)	2 (2%)	0	100	100
20	U	49/51 (96%)	45 (92%)	4 (8%)	0	100	100
21	V	57/181 (32%)	56 (98%)	1 (2%)	0	100	100
All	All	2369/2539 (93%)	2243 (95%)	122 (5%)	4 (0%)	50	81

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	E	53	LYS
5	E	95	ALA
3	C	23	GLY
9	I	42	LEU

5.3.2 Protein sidechains ⓘ

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	A	180/180 (100%)	174 (97%)	6 (3%)	38	61
2	B	170/170 (100%)	166 (98%)	4 (2%)	49	69
3	C	172/172 (100%)	170 (99%)	2 (1%)	71	83
4	D	113/113 (100%)	110 (97%)	3 (3%)	44	65
5	E	87/87 (100%)	86 (99%)	1 (1%)	73	84
6	F	124/124 (100%)	124 (100%)	0	100	100
7	G	104/104 (100%)	104 (100%)	0	100	100
8	H	105/105 (100%)	101 (96%)	4 (4%)	33	57
9	I	86/86 (100%)	84 (98%)	2 (2%)	50	70
10	J	90/90 (100%)	87 (97%)	3 (3%)	38	61
11	K	103/103 (100%)	100 (97%)	3 (3%)	42	64
12	L	92/92 (100%)	90 (98%)	2 (2%)	52	71
13	M	79/83 (95%)	78 (99%)	1 (1%)	69	82
14	O	76/76 (100%)	75 (99%)	1 (1%)	69	82
15	P	65/65 (100%)	65 (100%)	0	100	100
16	Q	74/74 (100%)	71 (96%)	3 (4%)	30	55
17	R	48/48 (100%)	48 (100%)	0	100	100
18	S	70/70 (100%)	68 (97%)	2 (3%)	42	64
19	T	65/65 (100%)	65 (100%)	0	100	100
20	U	44/44 (100%)	43 (98%)	1 (2%)	50	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	V	52/158 (33%)	52 (100%)	0	100	100
All	All	1999/2109 (95%)	1961 (98%)	38 (2%)	59	75

5 of 38 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
12	L	24	VAL
18	S	11	ASP
12	L	64	VAL
16	Q	7	LEU
20	U	11	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
22	W	1538/1539 (99%)	237 (15%)	9 (0%)

5 of 237 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
22	W	4	U
22	W	5	U
22	W	6	G
22	W	7	A
22	W	8	A

5 of 9 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
22	W	1213	A
22	W	1493	A
22	W	115	G
22	W	1101	A
22	W	1145	A

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 monosaccharides 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.

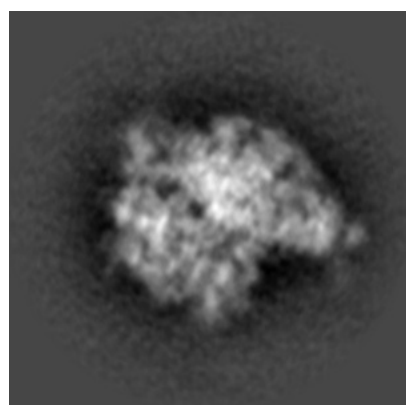
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22143. These allow visual inspection of the internal detail of the map and identification of artifacts.

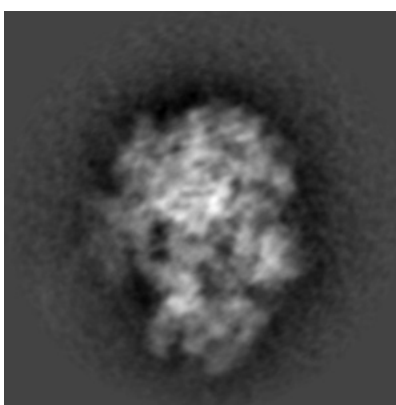
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

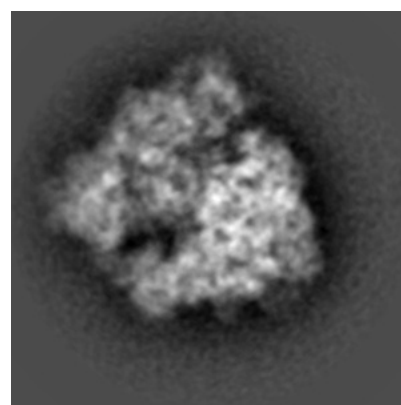
6.1.1 Primary map



X



Y

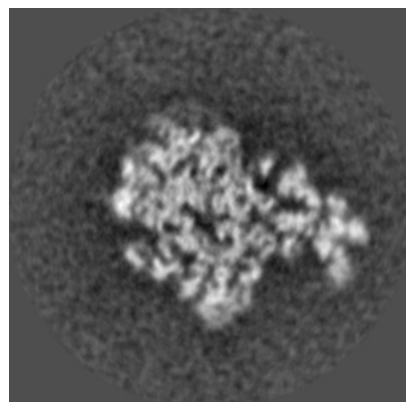


Z

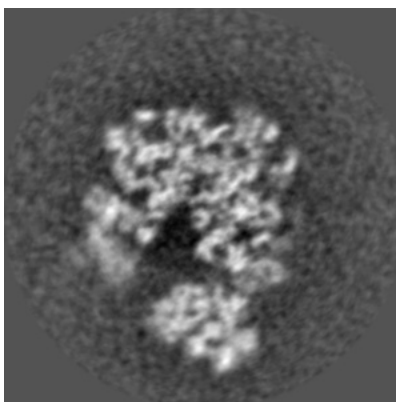
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

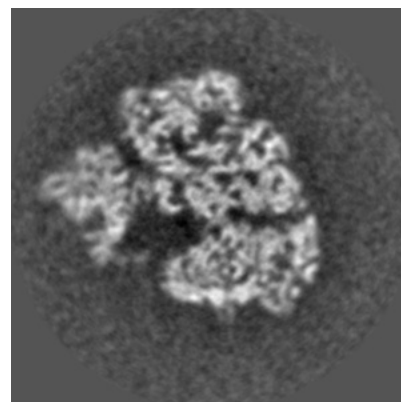
6.2.1 Primary map



X Index: 114



Y Index: 114

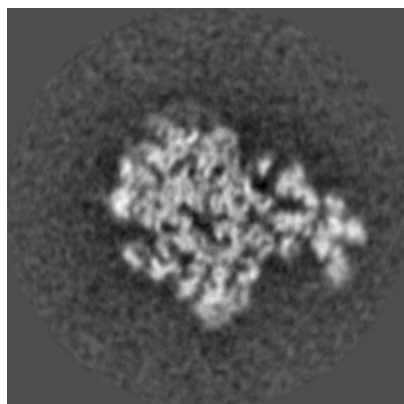


Z Index: 114

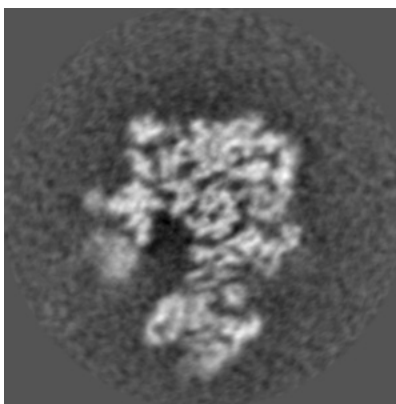
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

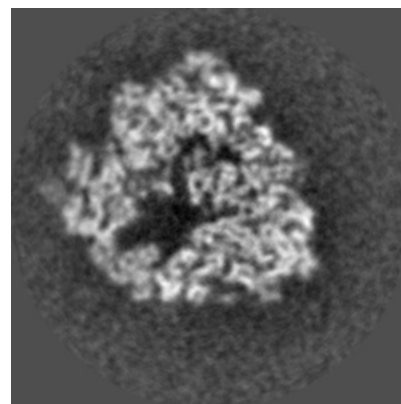
6.3.1 Primary map



X Index: 114



Y Index: 121

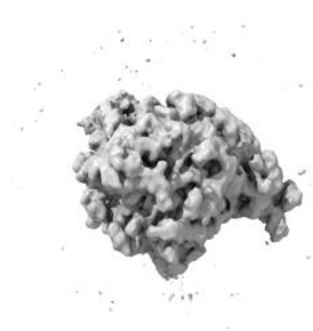


Z Index: 106

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

6.4 Orthogonal surface views [i](#)

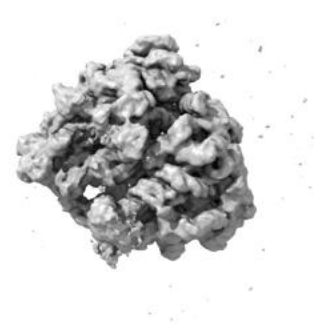
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0028. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

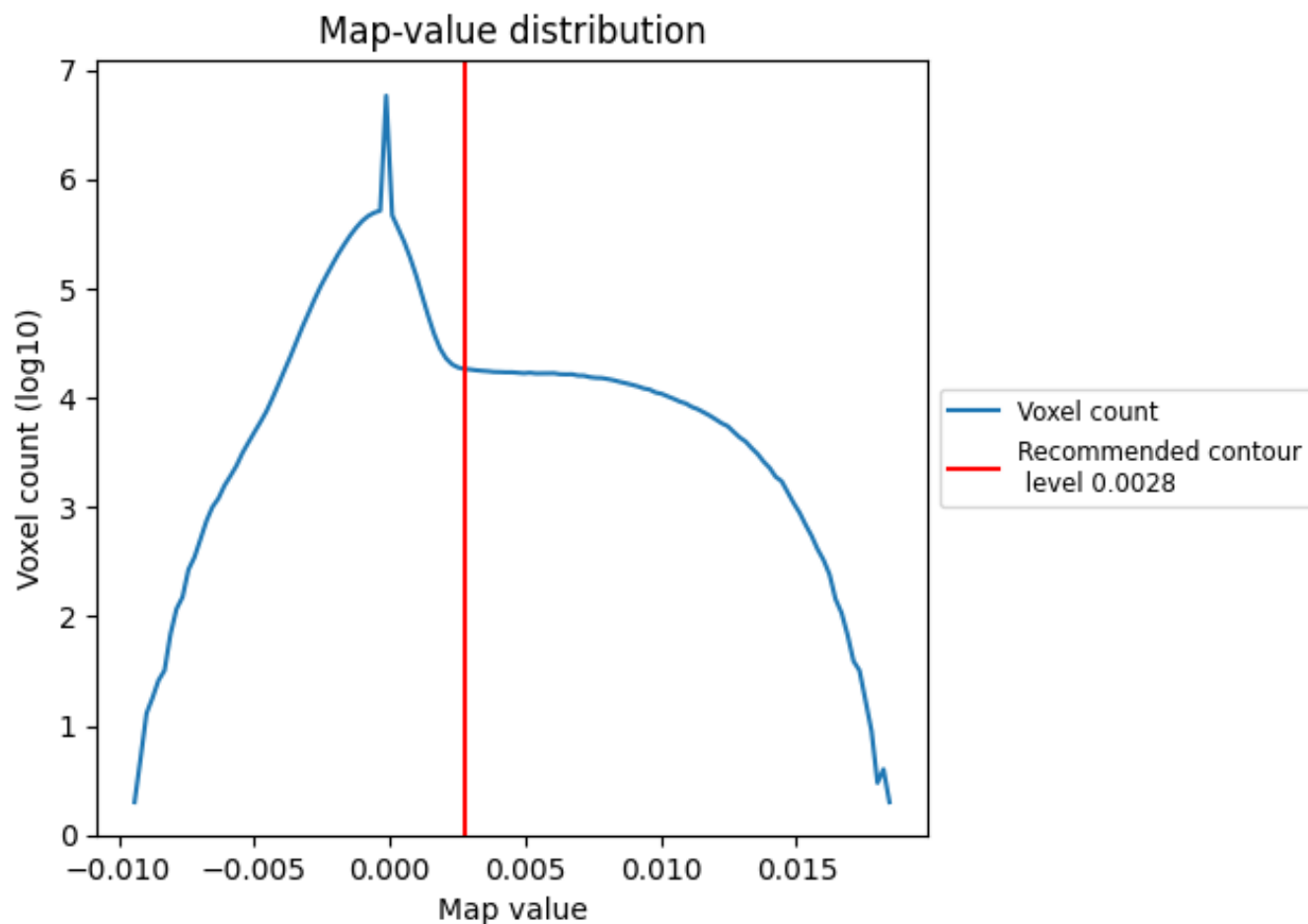
6.5 Mask visualisation

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

7 Map analysis [i](#)

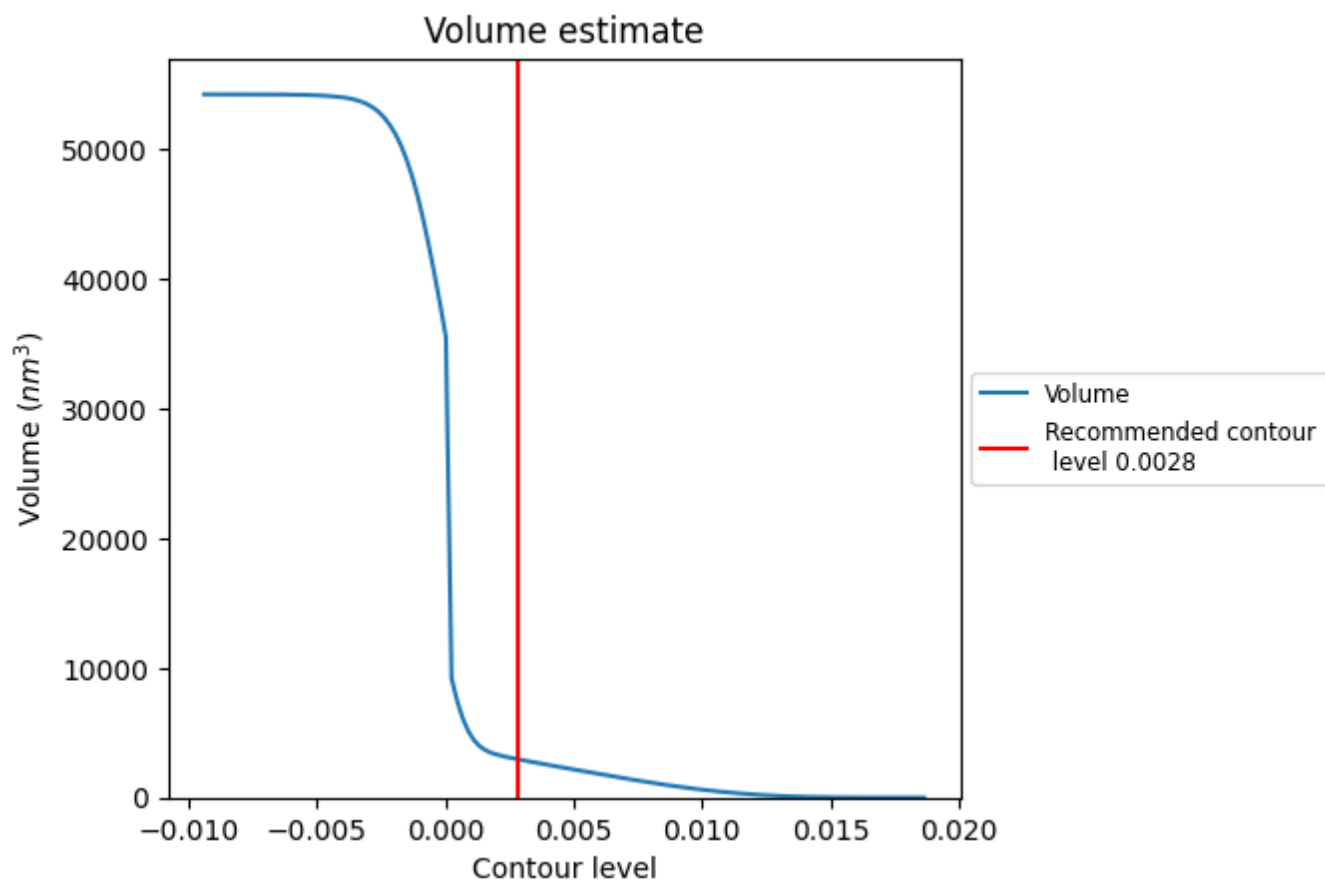
This section contains the results of statistical analysis of the map.

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.

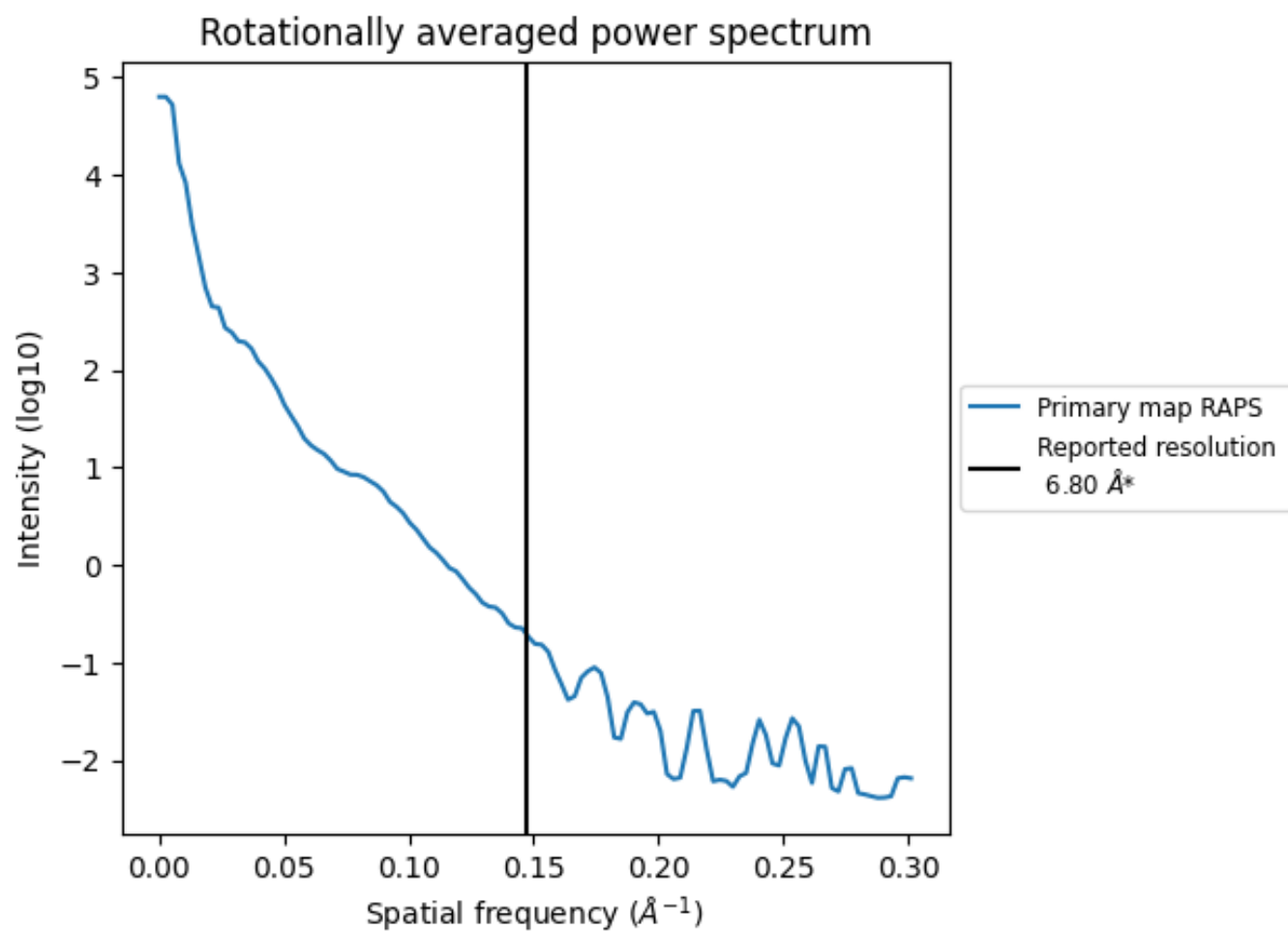
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2961 nm³; this corresponds to an approximate mass of 2675 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 0.147 Å⁻¹

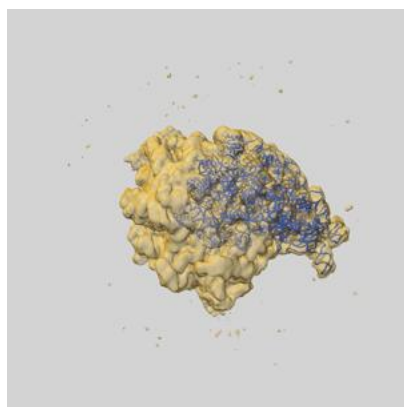
8 Fourier-Shell correlation

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

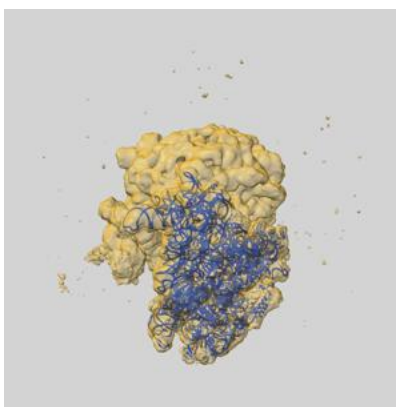
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-22143 and PDB model 6XE0. Per-residue inclusion information can be found in section [3](#) on page [8](#).

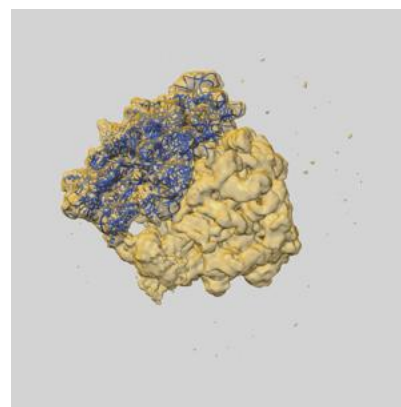
9.1 Map-model overlay [i](#)



X



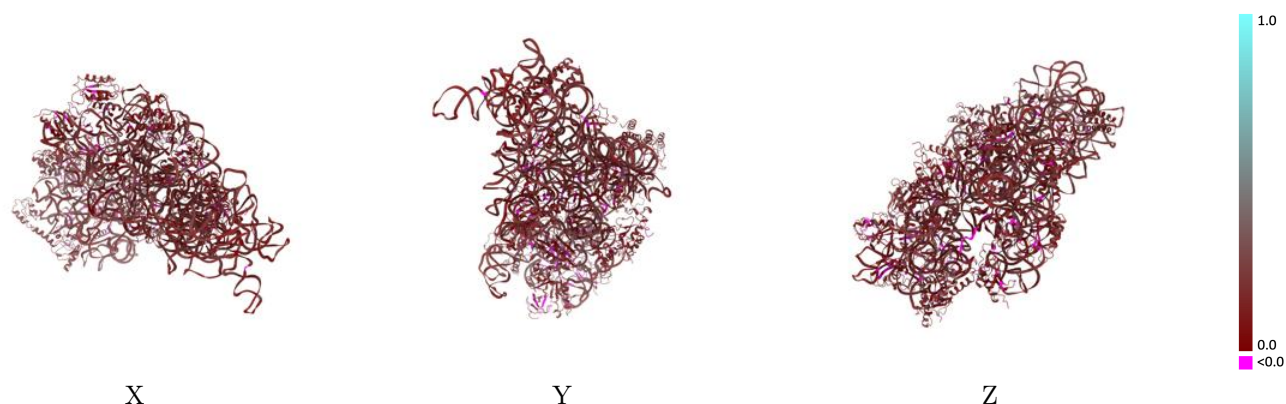
Y



Z

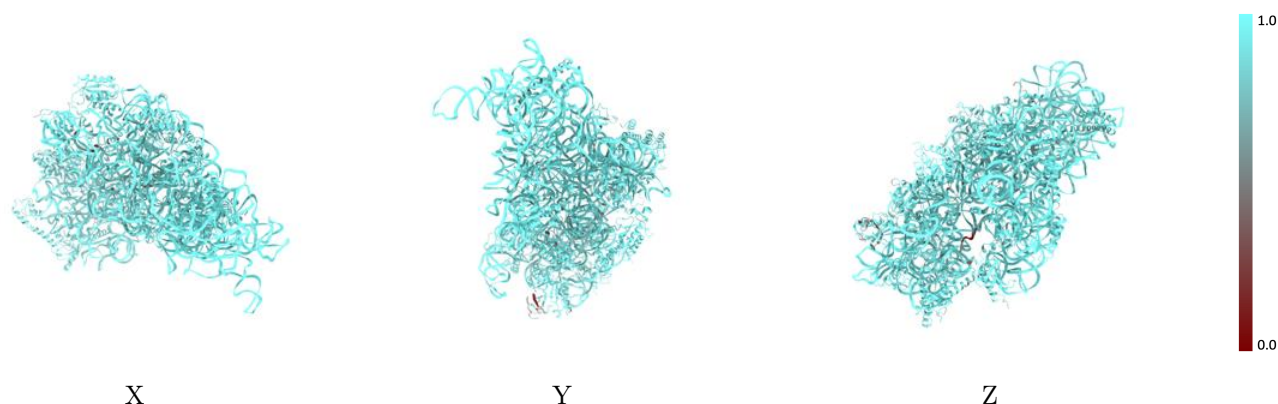
The images above show the 3D surface view of the map at the recommended contour level 0.0028 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



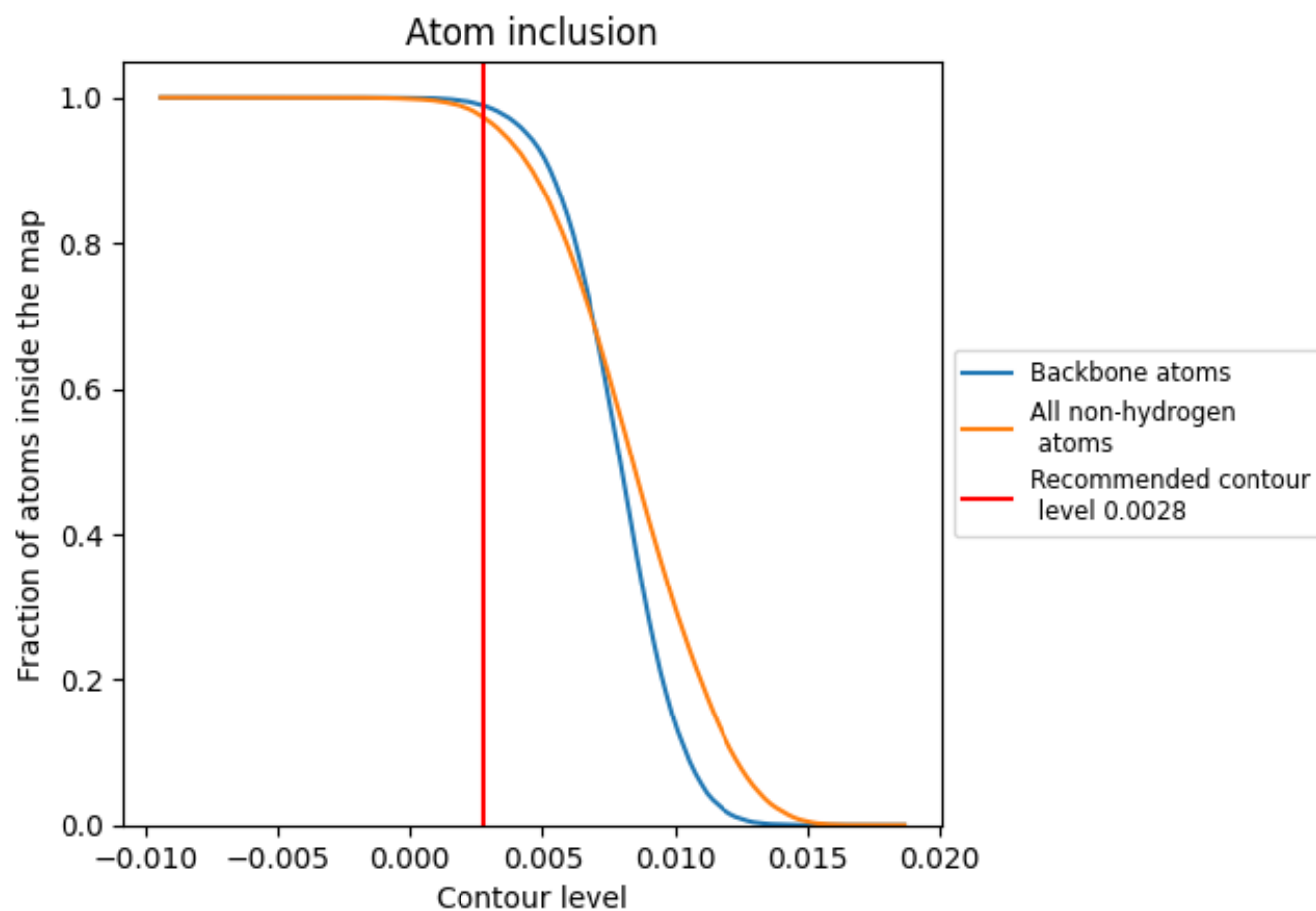
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0028).















































9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 97% 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 (0.0028) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9724	 0.1630
A	 0.9666	 0.1480
B	 0.9658	 0.1400
C	 0.9604	 0.1290
D	 0.9354	 0.1360
E	 0.9498	 0.1400
F	 0.9467	 0.1320
G	 0.9604	 0.1440
H	 0.9775	 0.0990
I	 0.9659	 0.0990
J	 0.9461	 0.1370
K	 0.8979	 0.1420
L	 0.9589	 0.1360
M	 0.9838	 0.1130
O	 0.9551	 0.1340
P	 0.9569	 0.1160
Q	 0.9352	 0.1270
R	 0.9931	 0.1410
S	 0.9662	 0.1180
T	 0.9523	 0.1380
U	 0.8673	 0.1350
V	 0.5534	 0.0710
W	 0.9882	 0.1820

