



wwPDB EM Validation Summary Report ⓘ

Nov 3, 2025 – 02:23 PM EST

PDB ID : 9P4I / pdb_00009p4i
EMDB ID : EMD-71268
Title : YsxC-GTP treated 44.5SYsxC particles. Class 5.
Authors : Ortega, J.; Seffouh, A.
Deposited on : 2025-06-16
Resolution : 2.80 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:

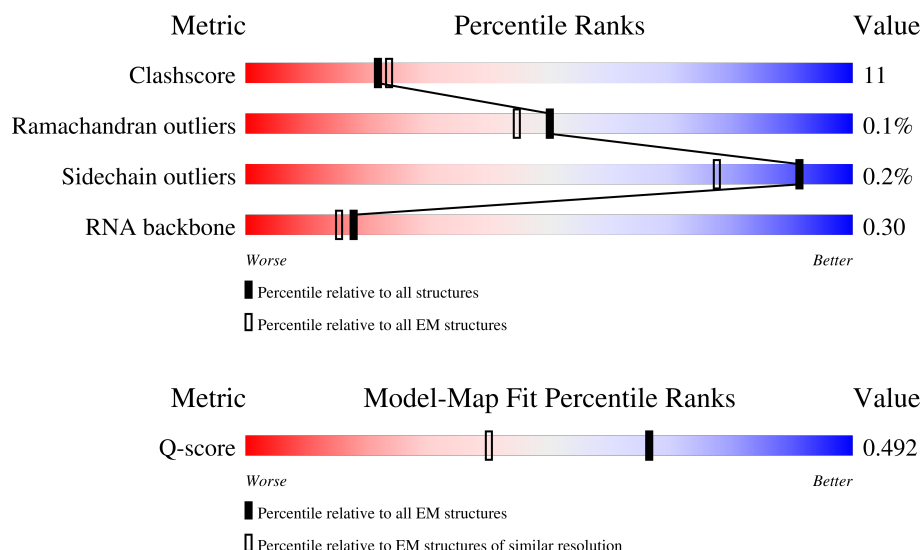
EMDB validation analysis : 0.0.1.dev129
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.46

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 2.80 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.













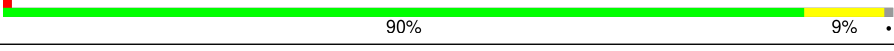

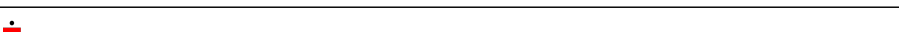


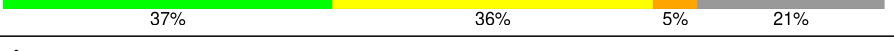



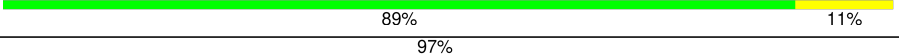
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
RNA backbone	6643	2191	-
Q-score	-	25397	11806 (2.30 - 3.30)

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	2927	
2	B	119	
3	C	277	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	D	209	
5	E	207	
6	G	179	
7	J	145	
8	K	122	
9	L	146	
10	N	120	
11	O	120	
12	P	115	
13	Q	118	
14	R	102	
15	S	113	
16	T	95	
17	U	103	
18	V	94	
19	Y	66	
20	Z	59	
21	b	59	
22	d	44	
23	f	37	

2 Entry composition

There are 23 unique types of molecules in this entry. The entry contains 82115 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 RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2818	Total	C	N	O	P	0	0
			60508	26994	11168	19528	2818		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	267	C	U	conflict	GB 2210155072
A	1558	C	G	conflict	GB 2210155072

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	112	Total	C	N	O	P	0	0
			2395	1068	435	780	112		

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	275	Total	C	N	O	S	0	0
			2111	1312	416	377	6		

- Molecule 4 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	207	Total	C	N	O	S	0	0
			1575	988	290	292	5		

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	205	Total	C	N	O	S	0	0
			1561	980	289	290	2		

- Molecule 6 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	175	Total	C	N	O	S	0	0
			1342	835	248	257	2		

- Molecule 7 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	J	142	Total	C	N	O	S	0	0
			1123	710	206	202	5		

- Molecule 8 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	K	122	Total	C	N	O	S	0	0
			920	571	173	172	4		

- Molecule 9 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L	146	Total	C	N	O	S	0	0
			1081	671	207	201	2		

- Molecule 10 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	N	119	Total	C	N	O	S	0	0
			953	583	186	180	4		

- Molecule 11 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	O	118	Total	C	N	O	S	0	0
			892	549	173	169	1		

- Molecule 12 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	P	114	Total	C	N	O	0	0
			936	595	184	157		

- Molecule 13 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Q	117	Total	C	N	O	S	0	0
			940	591	189	156	4		

- Molecule 14 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	R	101	Total	C	N	O		0	0
			786	501	139	146			

- Molecule 15 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	S	109	Total	C	N	O	S	0	0
			842	525	164	150	3		

- Molecule 16 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	T	93	Total	C	N	O	S	0	0
			752	472	137	139	4		

- Molecule 17 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	U	100	Total	C	N	O	S	0	0
			754	473	141	137	3		

- Molecule 18 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	V	74	Total	C	N	O		0	0
			578	359	113	106			

- Molecule 19 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Y	65	Total	C	N	O	S	0	0
			530	328	102	98	2		

- Molecule 20 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Z	58	Total	C	N	O	S	0	0
			455	281	89	84	1		

- Molecule 21 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	b	54	Total	C	N	O	S	0	0
			426	262	86	71	7		

- Molecule 22 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	d	44	Total	C	N	O	S	0	0
			367	222	89	54	2		

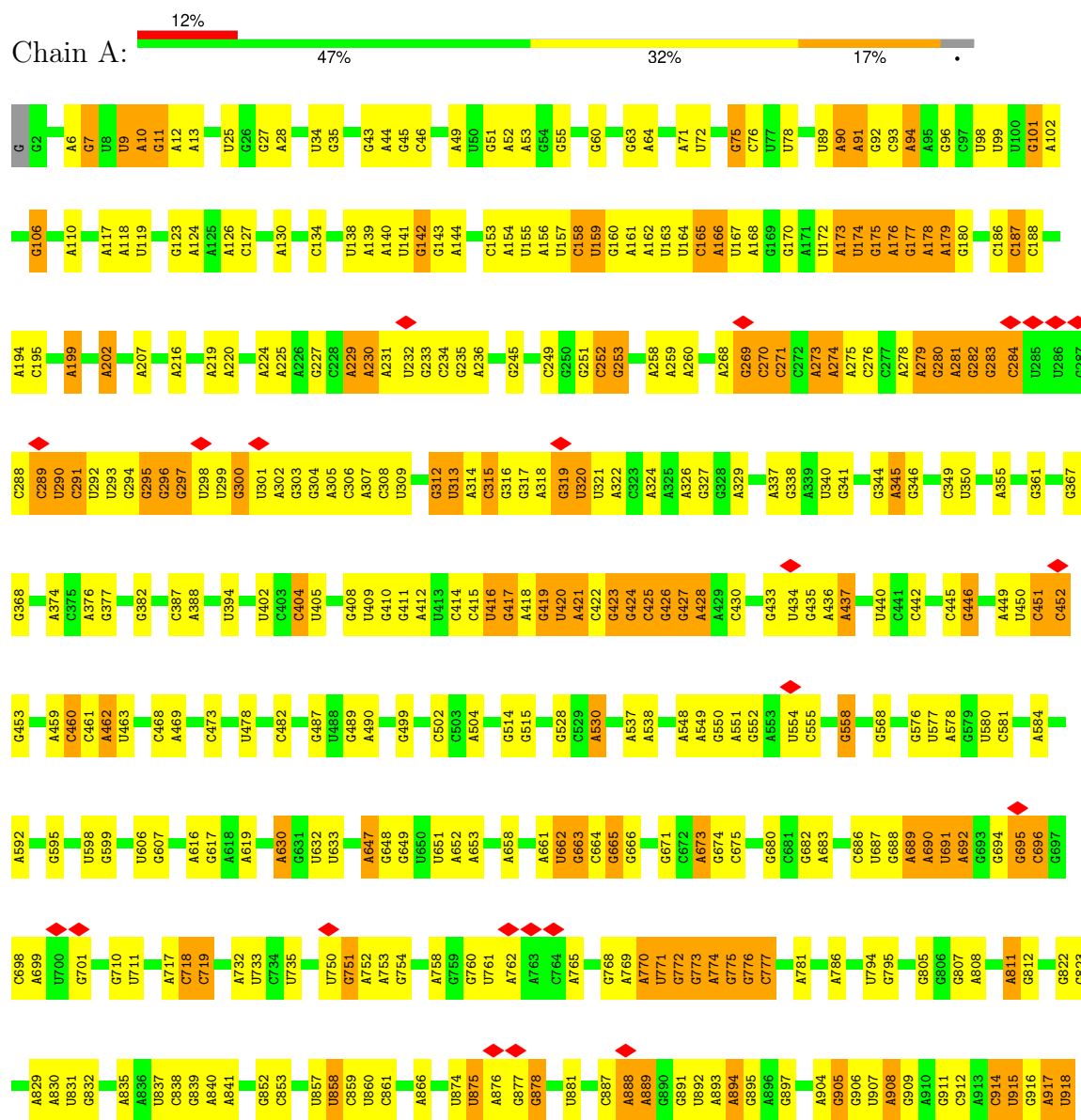
- Molecule 23 is a protein called Large ribosomal subunit protein bL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	f	36	Total	C	N	O	S	0	0
			288	181	59	44	4		

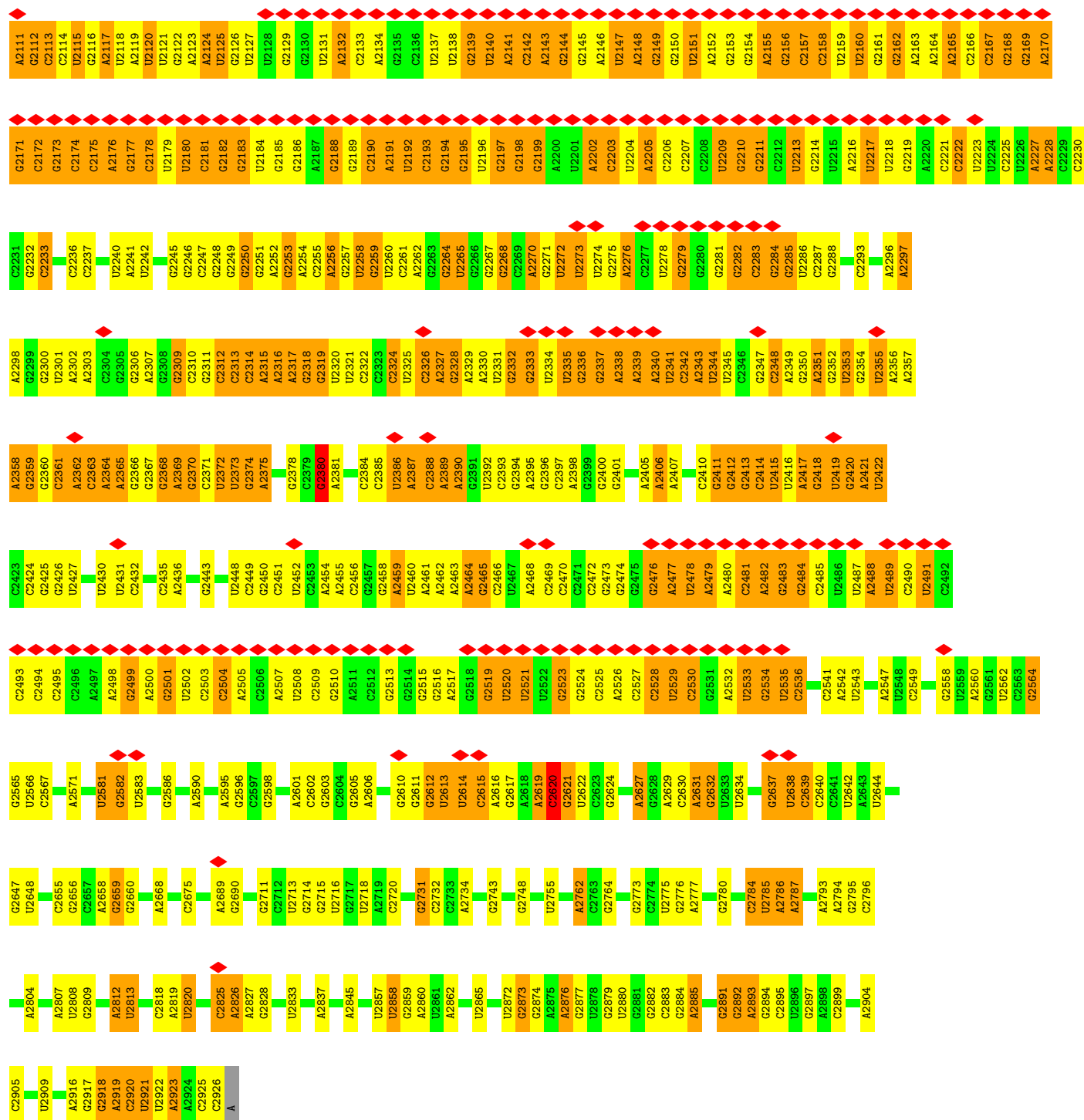
3 Residue-property plots

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.

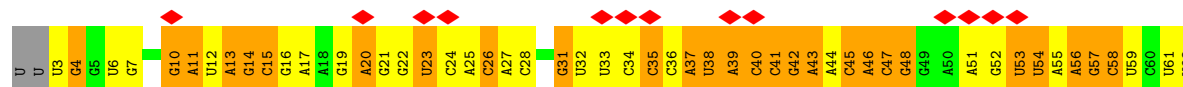
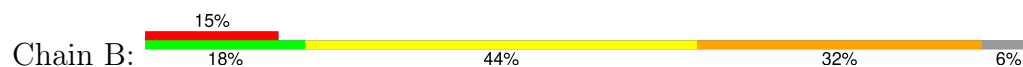
• Molecule 1: 23S rRNA

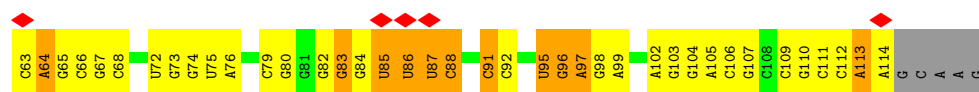




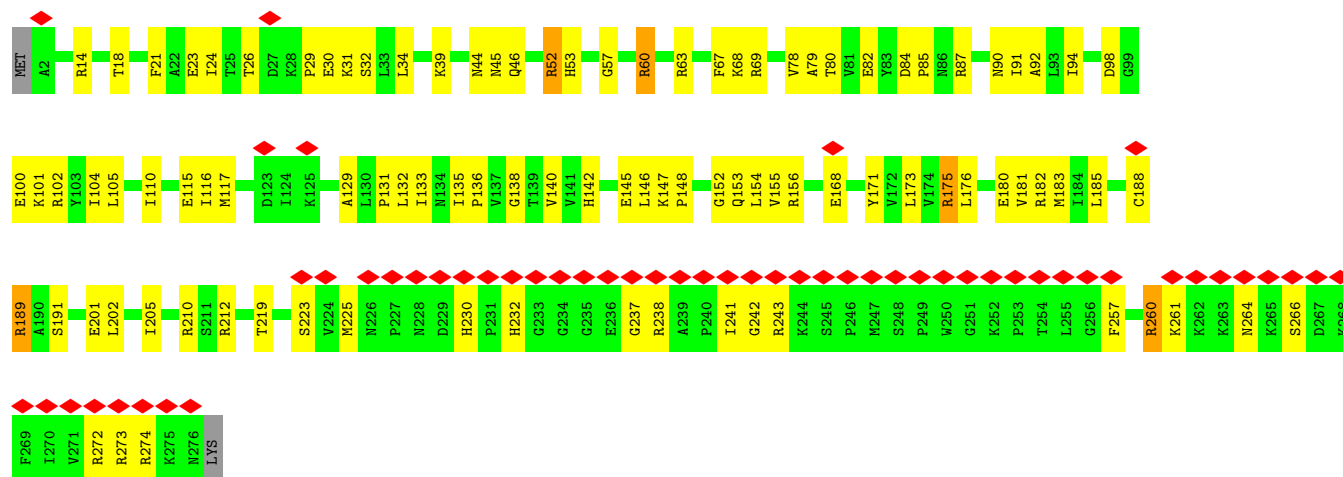


• Molecule 2: 5S rRNA

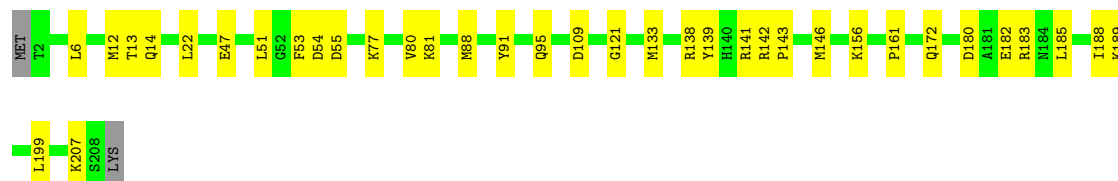
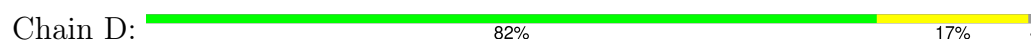




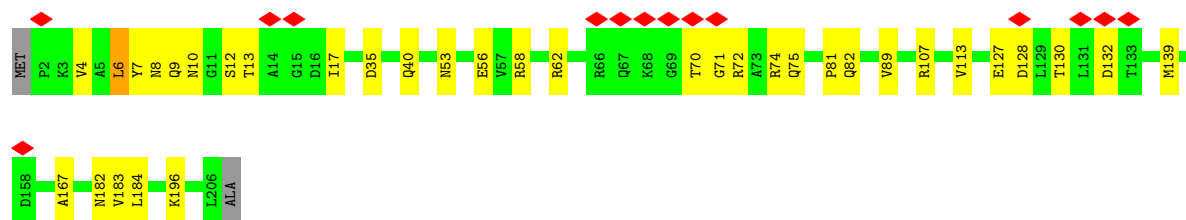
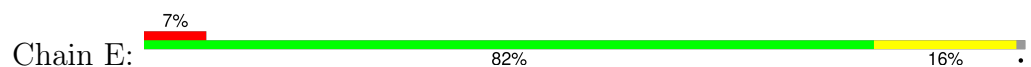
• Molecule 3: 50S ribosomal protein L2



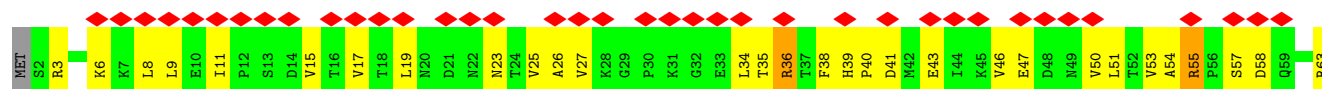
• Molecule 4: 50S ribosomal protein L3

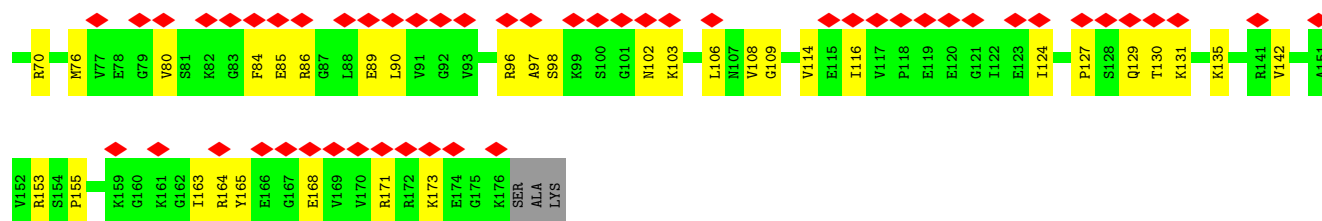


• Molecule 5: 50S ribosomal protein L4

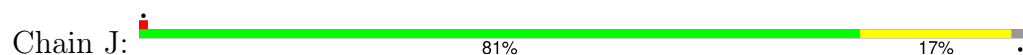


• Molecule 6: 50S ribosomal protein L6

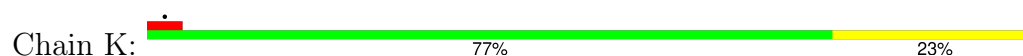




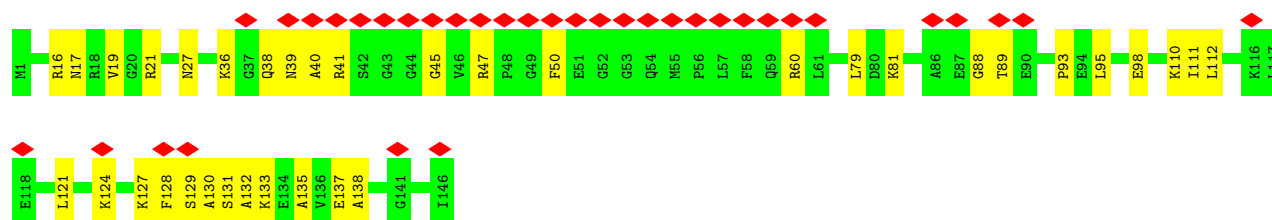
• Molecule 7: 50S ribosomal protein L13



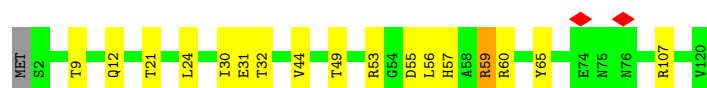
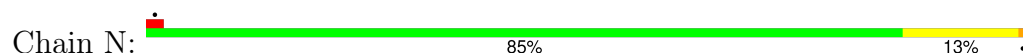
• Molecule 8: 50S ribosomal protein L14



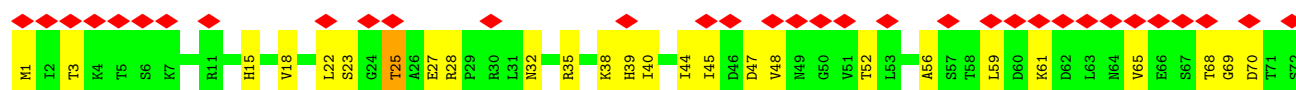
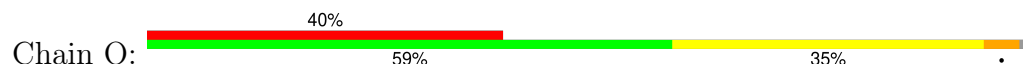
• Molecule 9: 50S ribosomal protein L15



• Molecule 10: 50S ribosomal protein L17

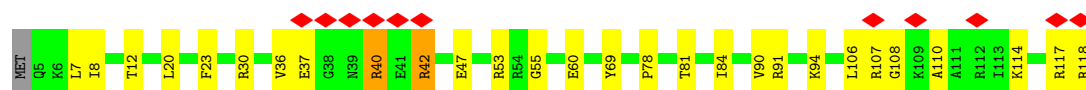
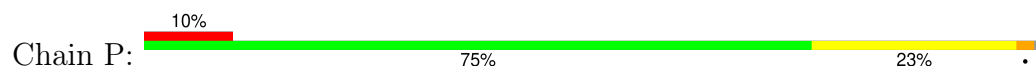


• Molecule 11: 50S ribosomal protein L18

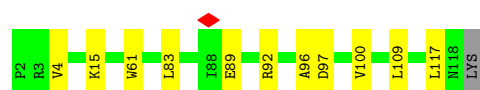
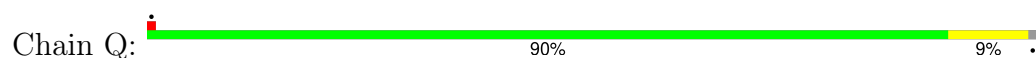




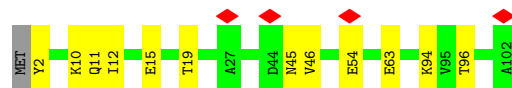
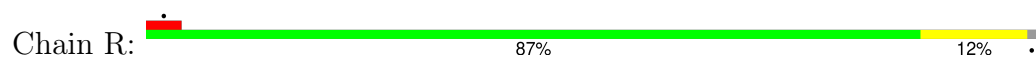
- Molecule 12: 50S ribosomal protein L19



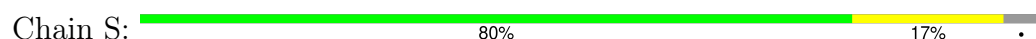
- Molecule 13: 50S ribosomal protein L20



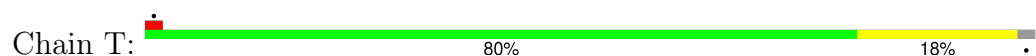
- Molecule 14: 50S ribosomal protein L21



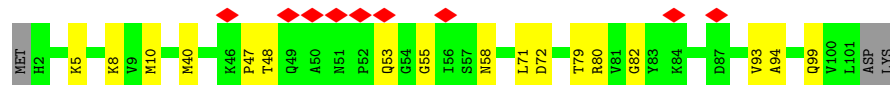
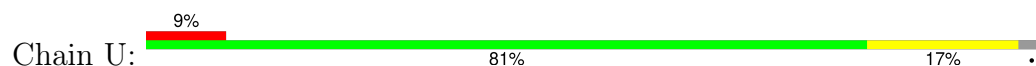
- Molecule 15: 50S ribosomal protein L22



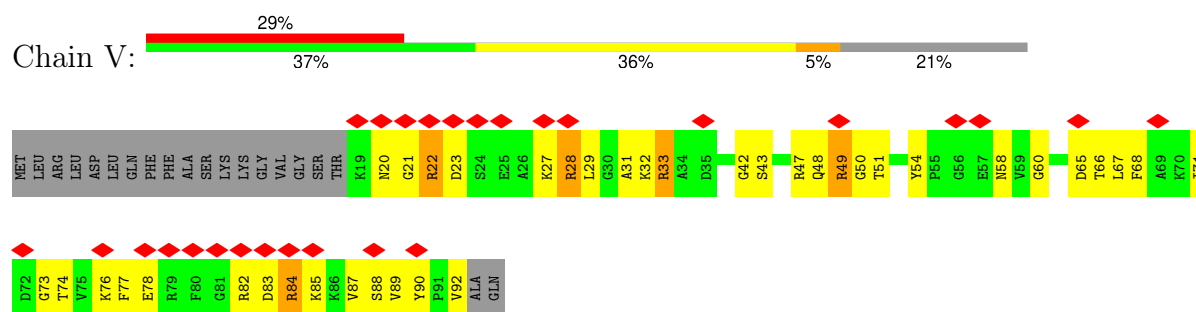
- Molecule 16: 50S ribosomal protein L23



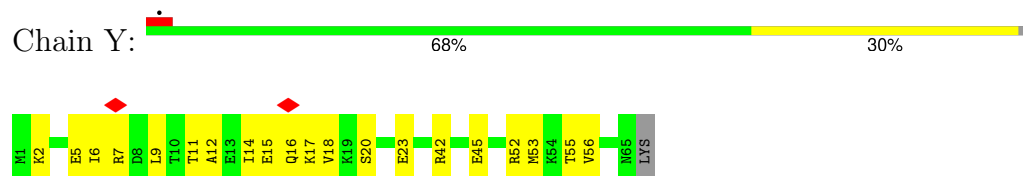
- Molecule 17: 50S ribosomal protein L24



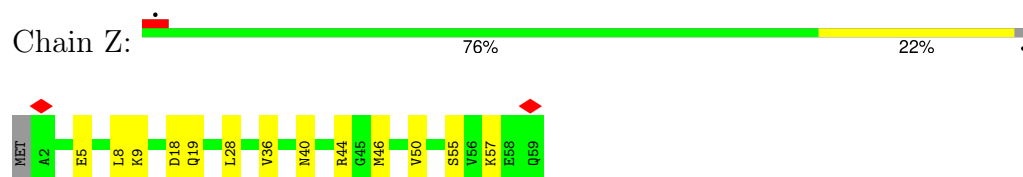
- Molecule 18: 50S ribosomal protein L27



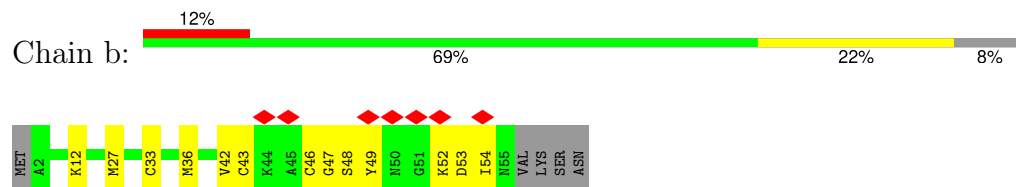
- Molecule 19: 50S ribosomal protein L29



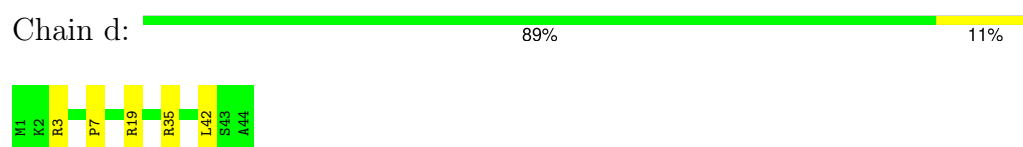
- Molecule 20: 50S ribosomal protein L30



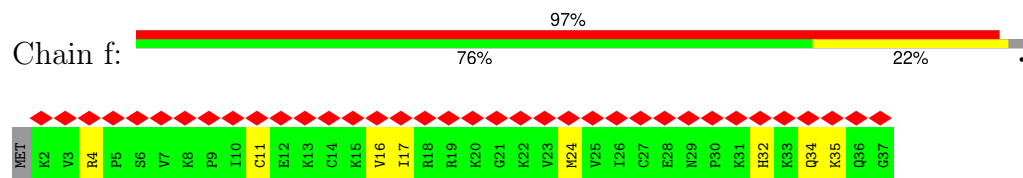
- Molecule 21: 50S ribosomal protein L32



- Molecule 22: 50S ribosomal protein L34



- Molecule 23: Large ribosomal subunit protein bL36



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	113285	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.314	Depositor
Minimum map value	-0.104	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.066	Depositor
Map size (Å)	383.04, 383.04, 383.04	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.855, 0.855, 0.855	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.42	0/67774	0.57	6/105732 (0.0%)
2	B	0.72	0/2678	0.93	0/4174
3	C	0.96	0/2148	1.12	0/2881
4	D	0.40	0/1597	0.54	0/2140
5	E	0.52	0/1580	0.65	0/2132
6	G	0.48	0/1360	0.64	0/1832
7	J	0.30	0/1146	0.37	0/1542
8	K	0.39	0/927	0.56	0/1245
9	L	0.32	0/1093	0.60	0/1457
10	N	0.45	0/960	0.61	0/1284
11	O	0.64	0/900	0.91	1/1209 (0.1%)
12	P	0.38	0/949	0.54	0/1269
13	Q	0.34	0/952	0.47	0/1266
14	R	0.42	0/797	0.59	0/1070
15	S	0.35	0/851	0.51	0/1146
16	T	0.44	0/759	0.69	0/1011
17	U	0.31	0/764	0.57	0/1022
18	V	0.70	0/586	0.96	0/779
19	Y	0.39	0/531	0.71	0/707
20	Z	0.23	0/457	0.38	0/613
21	b	0.27	0/433	0.44	0/574
22	d	0.29	0/370	0.32	0/483
23	f	0.15	0/291	0.39	0/383
All	All	0.45	0/89903	0.61	7/135951 (0.0%)

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
3	C	0	13
4	D	0	3

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
5	E	0	2
6	G	0	2
7	J	0	1
10	N	0	3
11	O	0	3
12	P	0	2
15	S	0	1
18	V	0	7
All	All	0	37

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2380	G	C3'-C2'-C1'	-6.61	94.89	101.50
1	A	2620	C	O3'-P-O5'	6.09	113.14	104.00
1	A	1863	U	C1'-O4'-C4'	-5.85	103.85	109.70
1	A	2348	C	C2'-C3'-O3'	5.36	117.53	109.50
1	A	2621	G	C3'-C2'-C1'	-5.27	96.23	101.50

There are no chirality outliers.

5 of 37 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	14	ARG	Sidechain
3	C	52	ARG	Sidechain
3	C	60	ARG	Sidechain
3	C	63	ARG	Sidechain
3	C	87	ARG	Sidechain

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	60508	0	30450	854	0
2	B	2395	0	1212	61	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	2111	0	2200	122	0
4	D	1575	0	1642	31	0
5	E	1561	0	1647	42	0
6	G	1342	0	1388	72	0
7	J	1123	0	1162	17	0
8	K	920	0	977	38	0
9	L	1081	0	1132	35	0
10	N	953	0	983	14	0
11	O	892	0	925	93	0
12	P	936	0	1008	32	0
13	Q	940	0	1005	13	0
14	R	786	0	826	9	0
15	S	842	0	899	16	0
16	T	752	0	802	17	0
17	U	754	0	809	19	0
18	V	578	0	586	42	0
19	Y	530	0	568	29	0
20	Z	455	0	491	13	0
21	b	426	0	445	12	0
22	d	367	0	410	5	0
23	f	288	0	327	4	0
All	All	82115	0	51894	1496	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 11.

The worst 5 of 1496 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:G:46:VAL:CA	6:G:51:LEU:HD22	1.08	1.55
6:G:46:VAL:C	6:G:51:LEU:CD2	1.90	1.43
6:G:46:VAL:C	6:G:51:LEU:HD22	1.42	1.40
6:G:46:VAL:CA	6:G:51:LEU:CD2	2.00	1.36
6:G:47:GLU:N	6:G:51:LEU:CD2	1.89	1.35

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	C	273/277 (99%)	227 (83%)	45 (16%)	1 (0%)	30	61
4	D	205/209 (98%)	191 (93%)	14 (7%)	0	100	100
5	E	203/207 (98%)	179 (88%)	24 (12%)	0	100	100
6	G	173/179 (97%)	155 (90%)	18 (10%)	0	100	100
7	J	140/145 (97%)	128 (91%)	12 (9%)	0	100	100
8	K	120/122 (98%)	105 (88%)	15 (12%)	0	100	100
9	L	144/146 (99%)	119 (83%)	25 (17%)	0	100	100
10	N	117/120 (98%)	107 (92%)	10 (8%)	0	100	100
11	O	116/120 (97%)	92 (79%)	24 (21%)	0	100	100
12	P	112/115 (97%)	101 (90%)	11 (10%)	0	100	100
13	Q	115/118 (98%)	107 (93%)	8 (7%)	0	100	100
14	R	99/102 (97%)	86 (87%)	13 (13%)	0	100	100
15	S	107/113 (95%)	97 (91%)	10 (9%)	0	100	100
16	T	91/95 (96%)	87 (96%)	4 (4%)	0	100	100
17	U	98/103 (95%)	83 (85%)	15 (15%)	0	100	100
18	V	72/94 (77%)	54 (75%)	17 (24%)	1 (1%)	9	30
19	Y	63/66 (96%)	59 (94%)	4 (6%)	0	100	100
20	Z	56/59 (95%)	56 (100%)	0	0	100	100
21	b	52/59 (88%)	47 (90%)	5 (10%)	0	100	100
22	d	42/44 (96%)	39 (93%)	3 (7%)	0	100	100
23	f	34/37 (92%)	27 (79%)	7 (21%)	0	100	100
All	All	2432/2530 (96%)	2146 (88%)	284 (12%)	2 (0%)	50	77

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
18	V	31	ALA
3	C	155	VAL

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	
3	C	223/225 (99%)	222 (100%)	1 (0%)	89	96
4	D	168/170 (99%)	168 (100%)	0	100	100
5	E	169/170 (99%)	168 (99%)	1 (1%)	84	95
6	G	148/151 (98%)	147 (99%)	1 (1%)	81	94
7	J	120/123 (98%)	120 (100%)	0	100	100
8	K	101/101 (100%)	101 (100%)	0	100	100
9	L	110/110 (100%)	110 (100%)	0	100	100
10	N	99/100 (99%)	98 (99%)	1 (1%)	73	91
11	O	91/93 (98%)	90 (99%)	1 (1%)	70	90
12	P	99/100 (99%)	99 (100%)	0	100	100
13	Q	96/97 (99%)	96 (100%)	0	100	100
14	R	83/84 (99%)	83 (100%)	0	100	100
15	S	90/93 (97%)	90 (100%)	0	100	100
16	T	84/85 (99%)	84 (100%)	0	100	100
17	U	84/87 (97%)	84 (100%)	0	100	100
18	V	58/74 (78%)	58 (100%)	0	100	100
19	Y	56/57 (98%)	56 (100%)	0	100	100
20	Z	52/53 (98%)	52 (100%)	0	100	100
21	b	48/53 (91%)	48 (100%)	0	100	100
22	d	39/39 (100%)	39 (100%)	0	100	100
23	f	34/35 (97%)	34 (100%)	0	100	100
All	All	2052/2100 (98%)	2047 (100%)	5 (0%)	91	97

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	18	THR
5	E	6	LEU
6	G	84	PHE
10	N	57	HIS
11	O	102	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
11	O	32	ASN
12	P	15	GLN
11	O	43	GLN
15	S	95	GLN
4	D	140	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2816/2927 (96%)	1077 (38%)	82 (2%)
2	B	111/119 (93%)	64 (57%)	8 (7%)
All	All	2927/3046 (96%)	1141 (38%)	90 (3%)

5 of 1141 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	7	G
1	A	9	U
1	A	10	A
1	A	11	G
1	A	13	A

5 of 90 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	2116	G
1	A	2435	C
1	A	2143	A
1	A	2348	C
1	A	2581	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

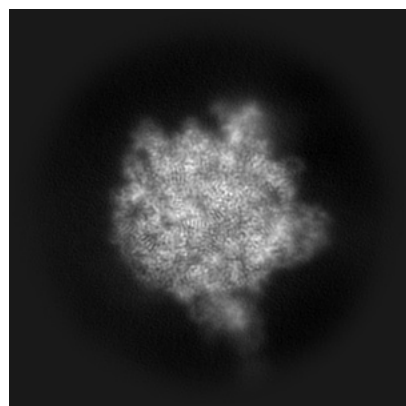
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-71268. These allow visual inspection of the internal detail of the map and identification of artifacts.

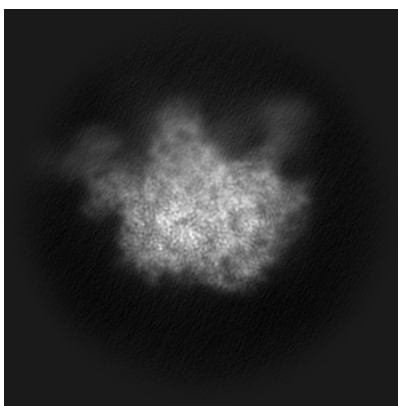
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

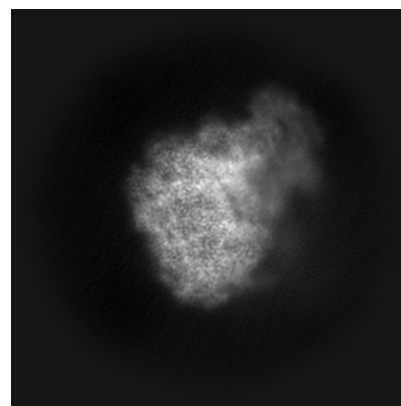
6.1.1 Primary map



X

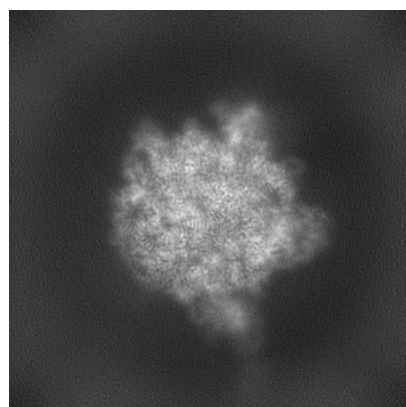


Y

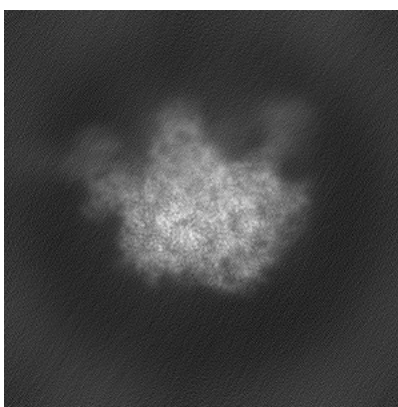


Z

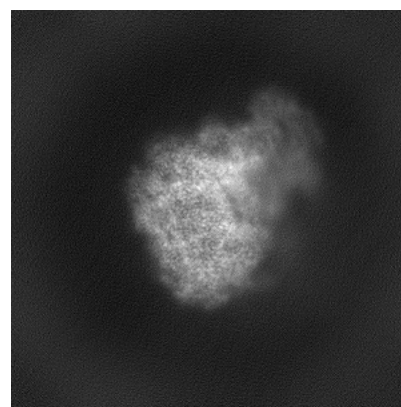
6.1.2 Raw map



X



Y

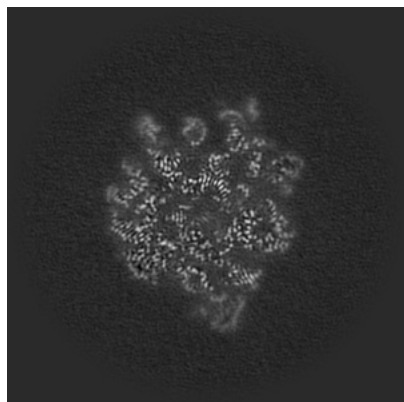


Z

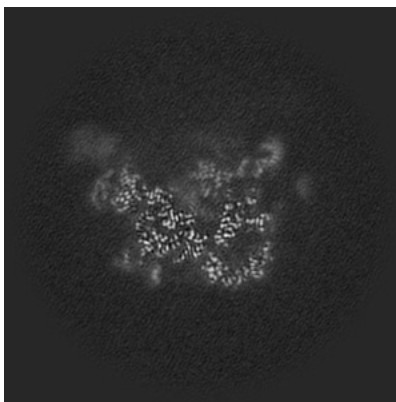
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

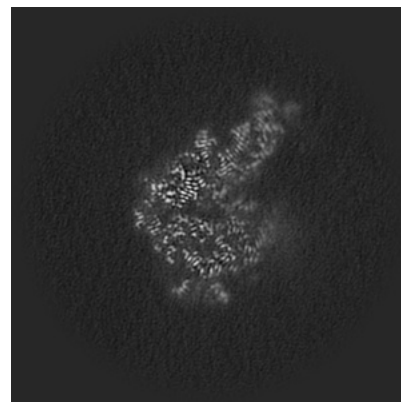
6.2.1 Primary map



X Index: 224

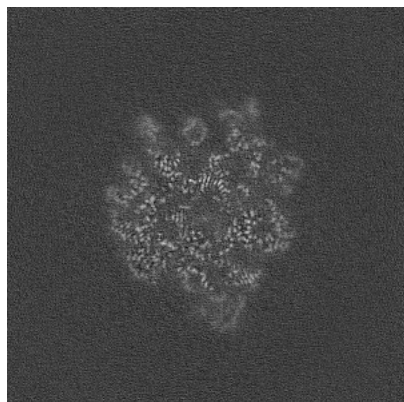


Y Index: 224

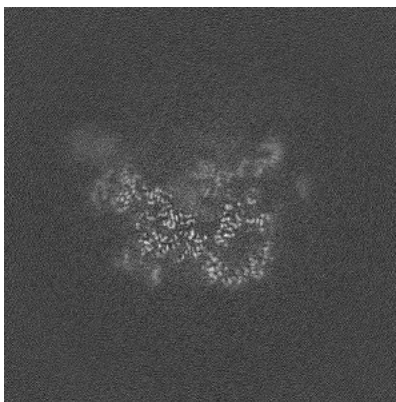


Z Index: 224

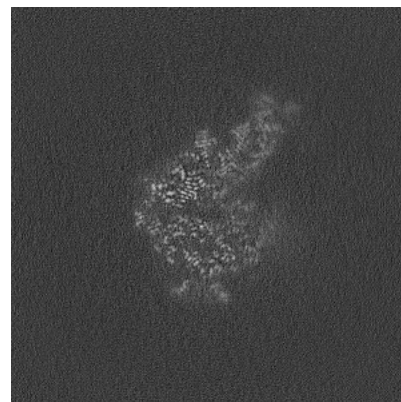
6.2.2 Raw map



X Index: 224



Y Index: 224

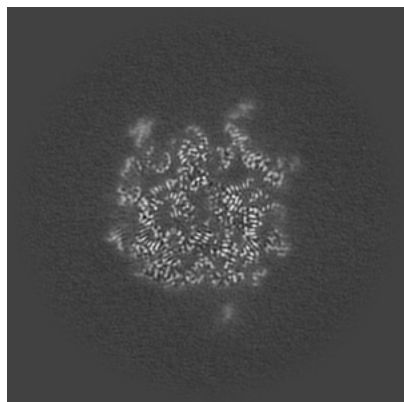


Z Index: 224

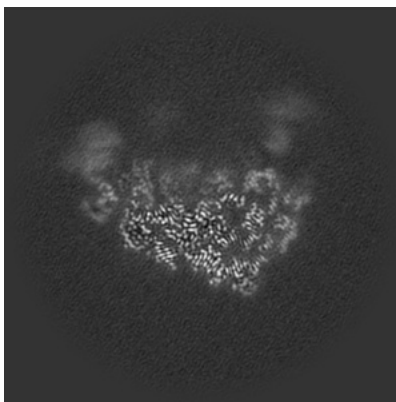
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

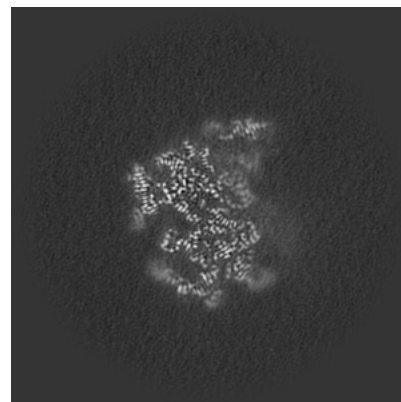
6.3.1 Primary map



X Index: 212

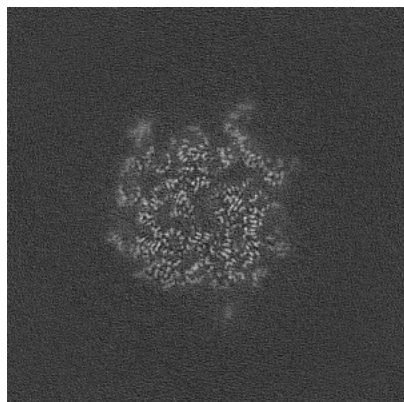


Y Index: 248

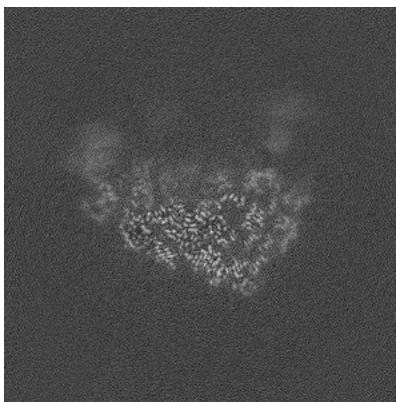


Z Index: 241

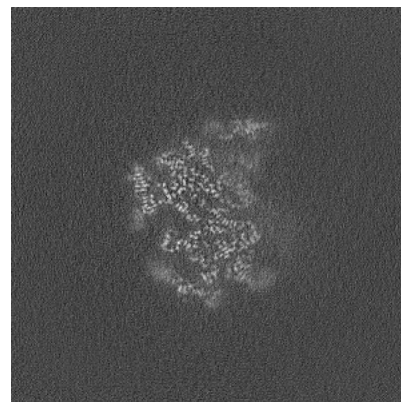
6.3.2 Raw map



X Index: 211



Y Index: 248

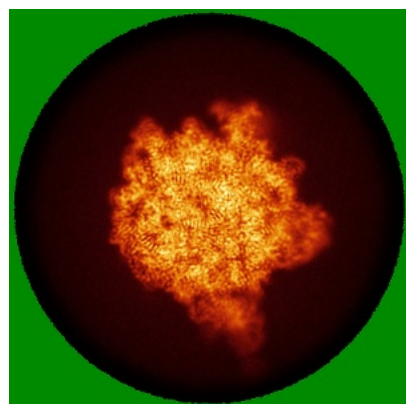


Z Index: 241

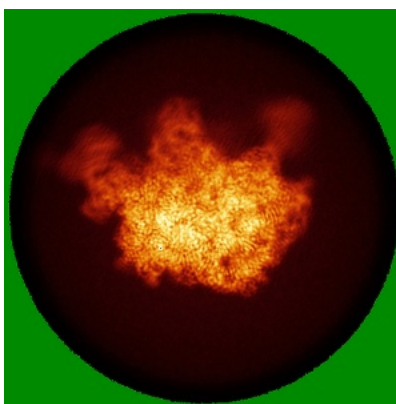
The images above show the largest variance slices of the map in three orthogonal directions.

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

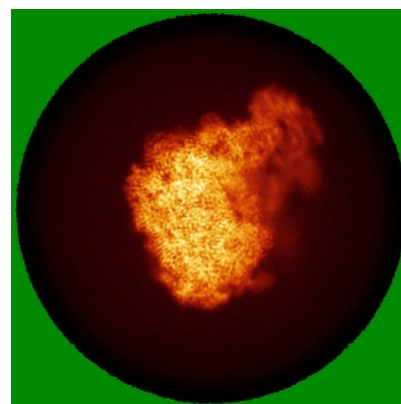
6.4.1 Primary map



X

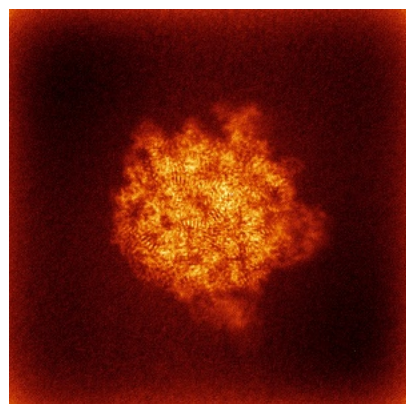


Y

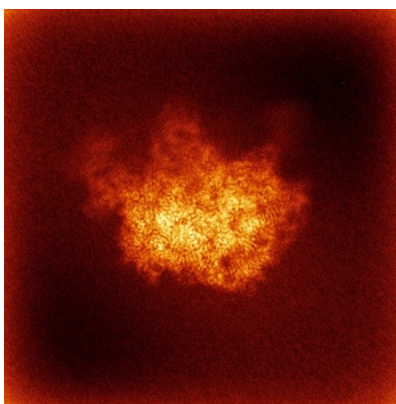


Z

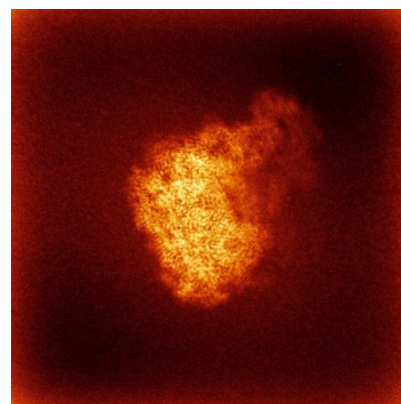
6.4.2 Raw map



X



Y

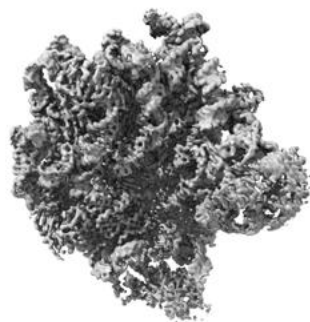


Z

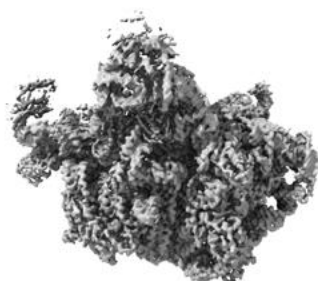
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

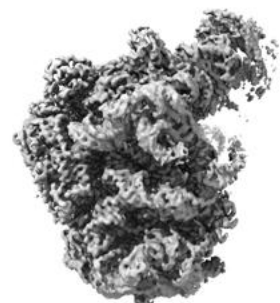
6.5.1 Primary map



X



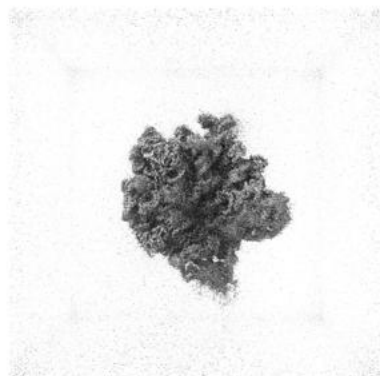
Y



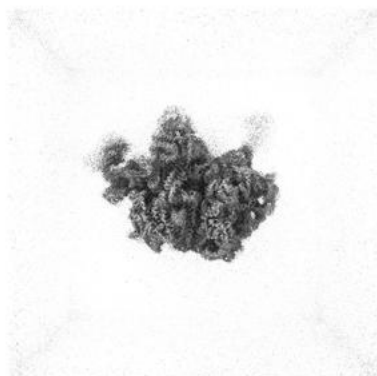
Z

The images above show the 3D surface view of the map at the recommended contour level 0.066. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

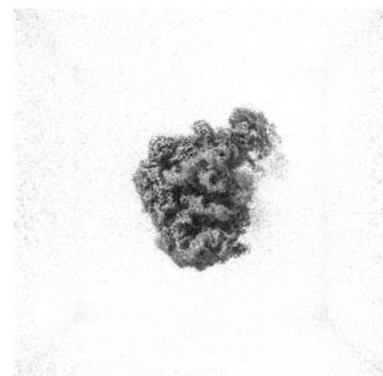
6.5.2 Raw map



X



Y



Z

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.

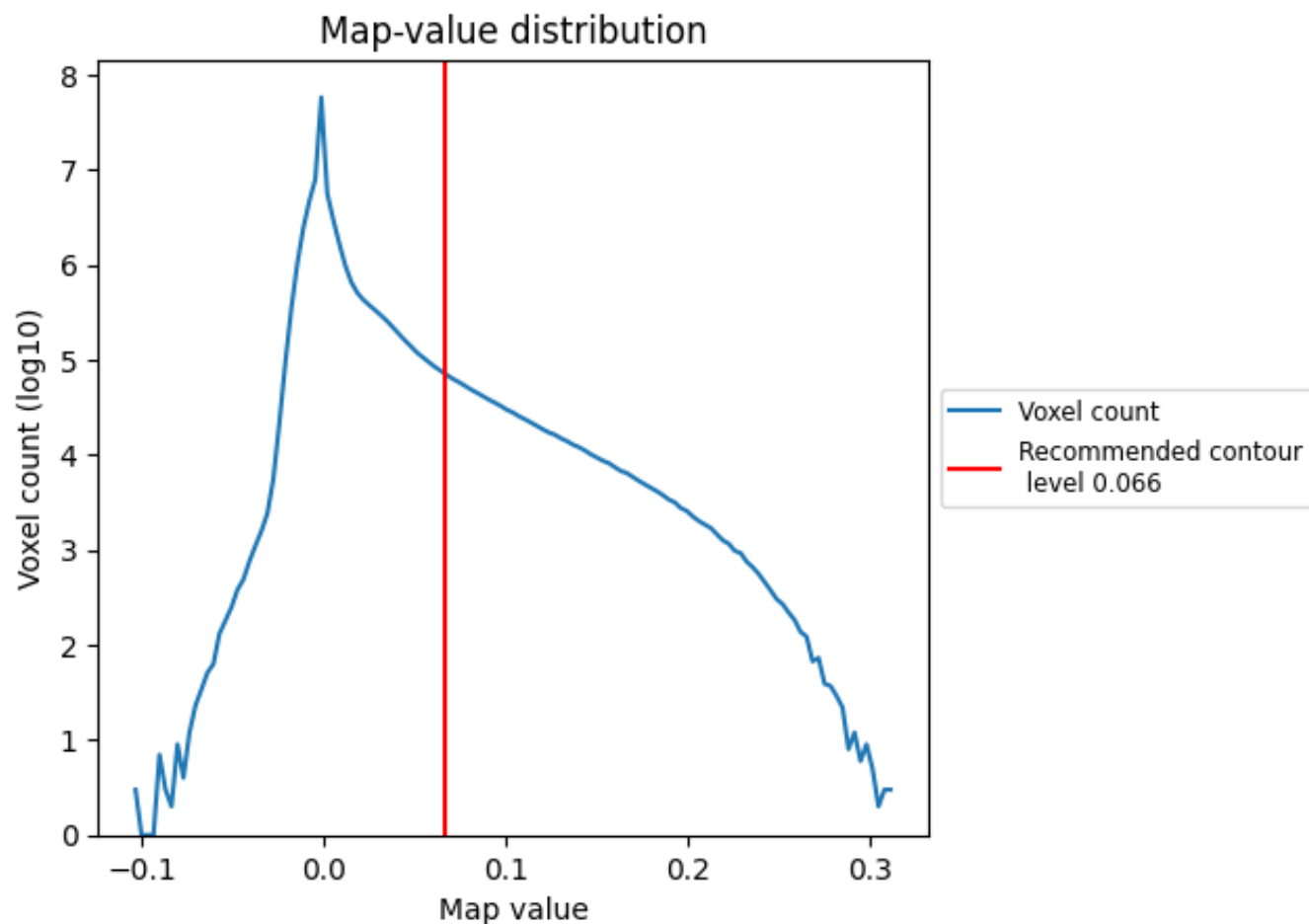
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

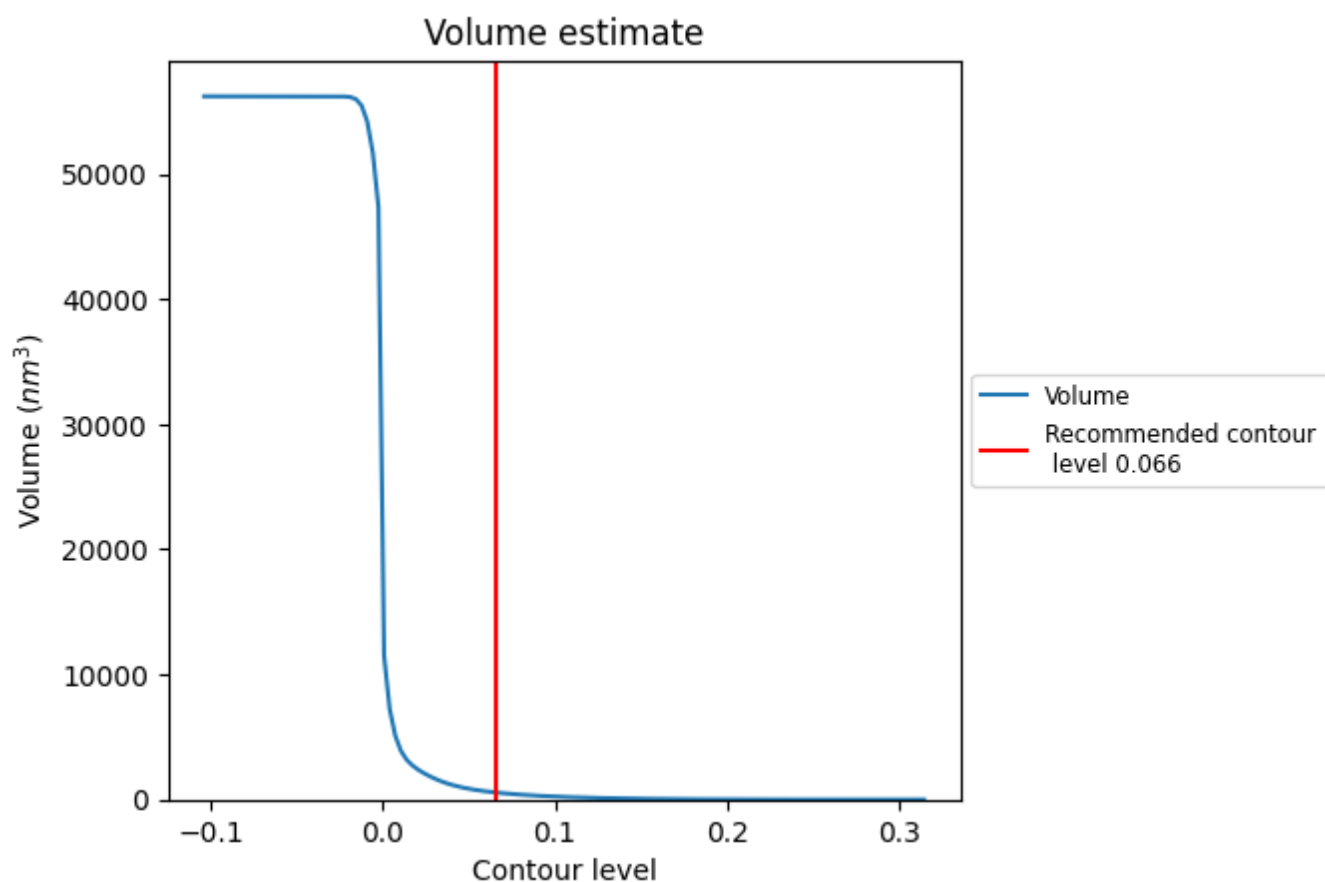
This section contains the results of statistical analysis of the map.

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.

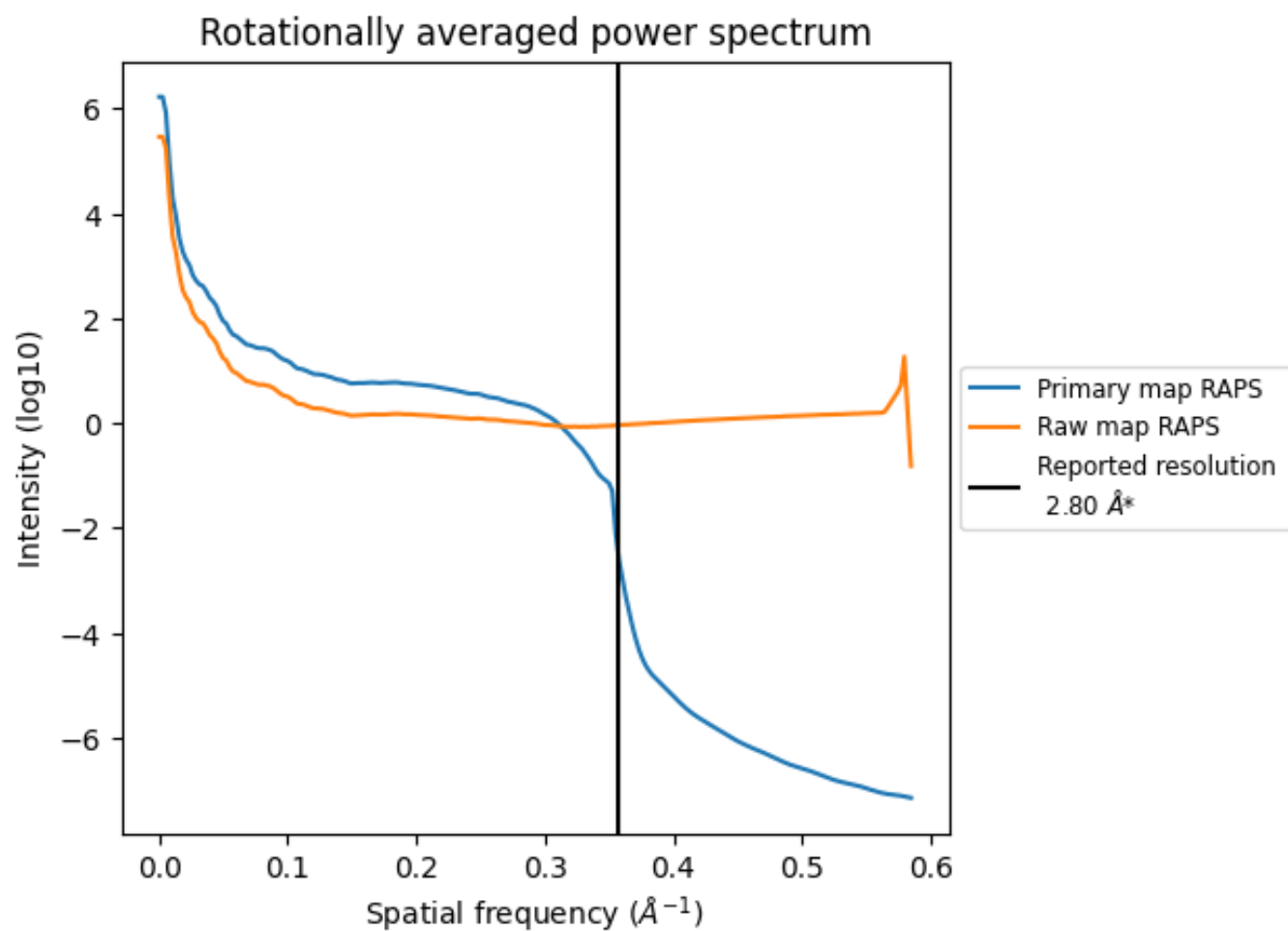
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 558 nm³; this corresponds to an approximate mass of 504 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 ⓘ

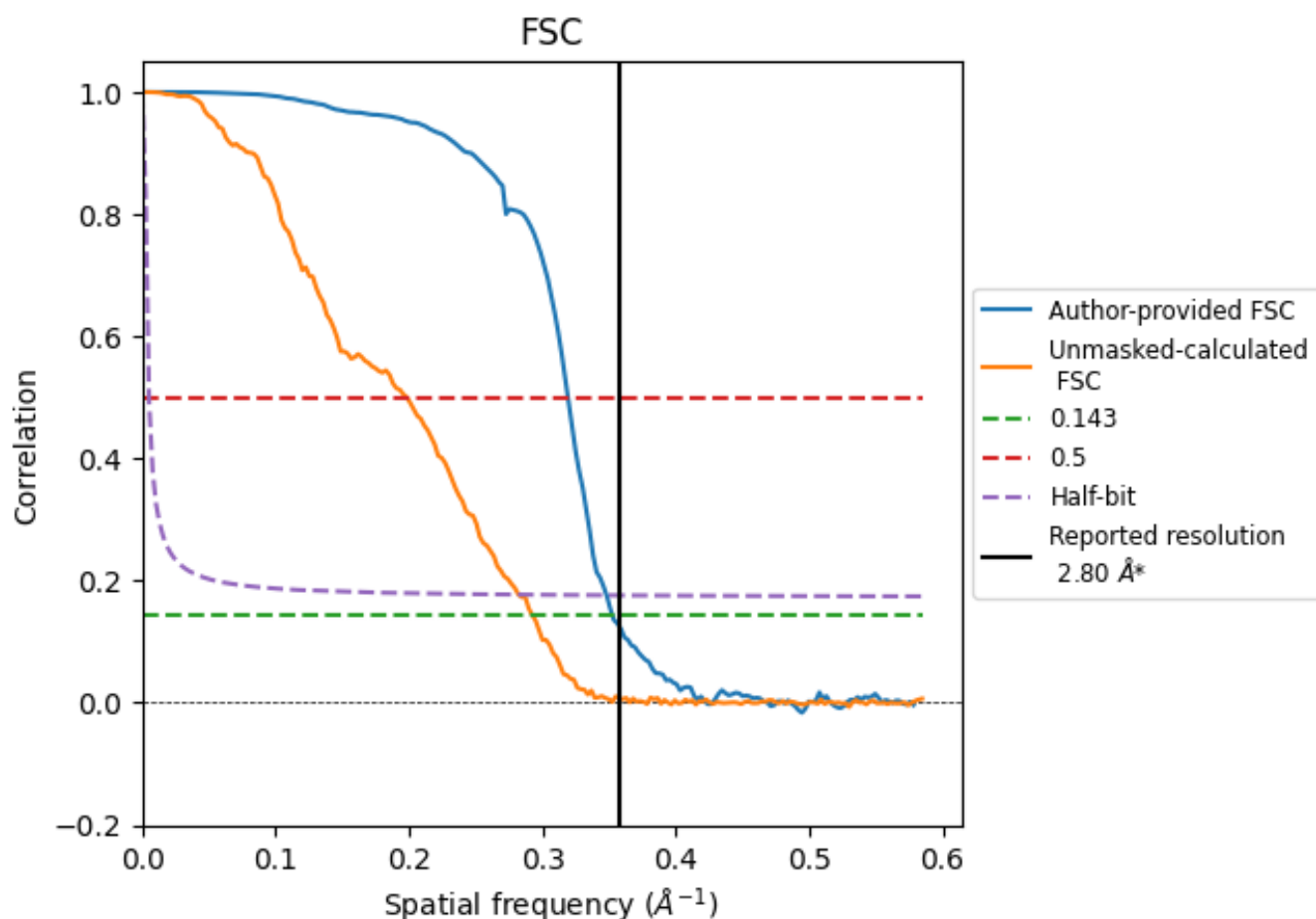


*Reported resolution corresponds to spatial frequency of 0.357 Å⁻¹

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 0.357 Å⁻¹

8.2 Resolution estimates [i](#)

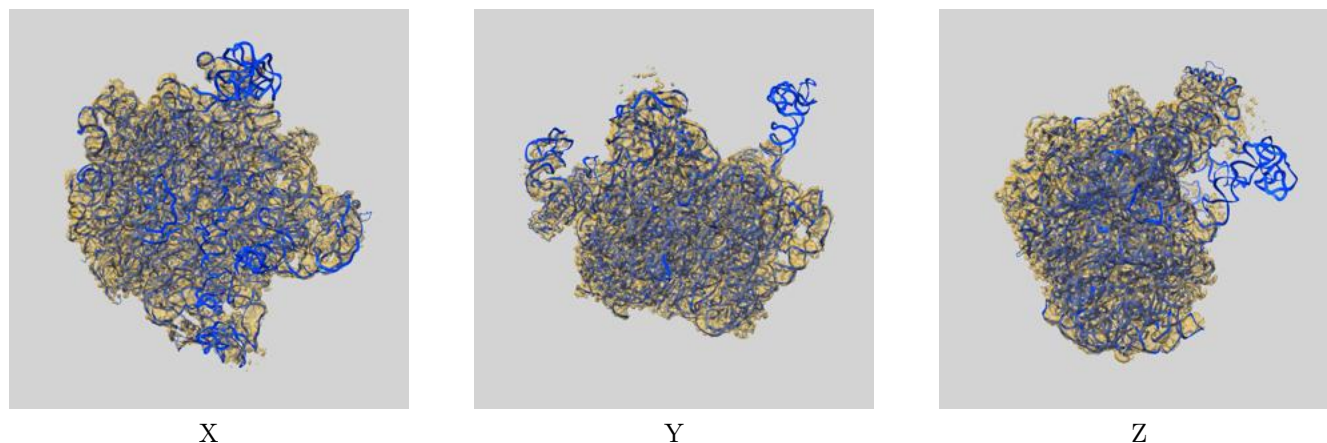
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	2.84	3.13	2.87
Unmasked-calculated*	3.42	5.04	3.54

*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 3.42 differs from the reported value 2.8 by more than 10 %

9 Map-model fit [i](#)

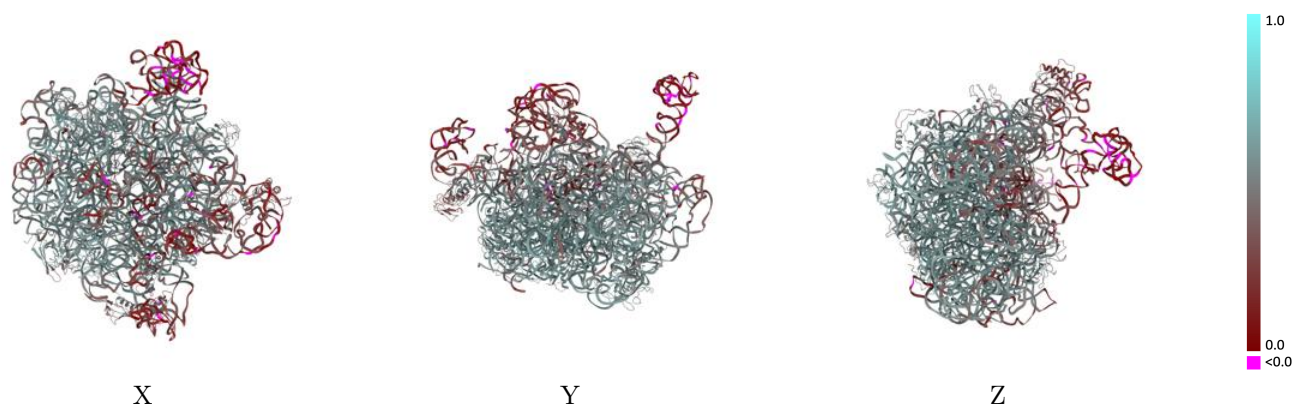
This section contains information regarding the fit between EMDB map EMD-71268 and PDB model 9P4I. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



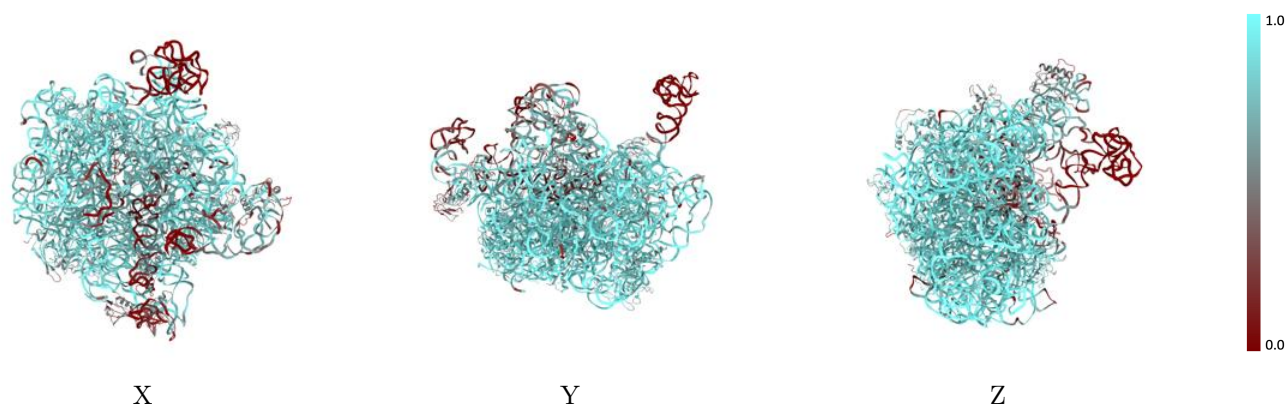
The images above show the 3D surface view of the map at the recommended contour level 0.066 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



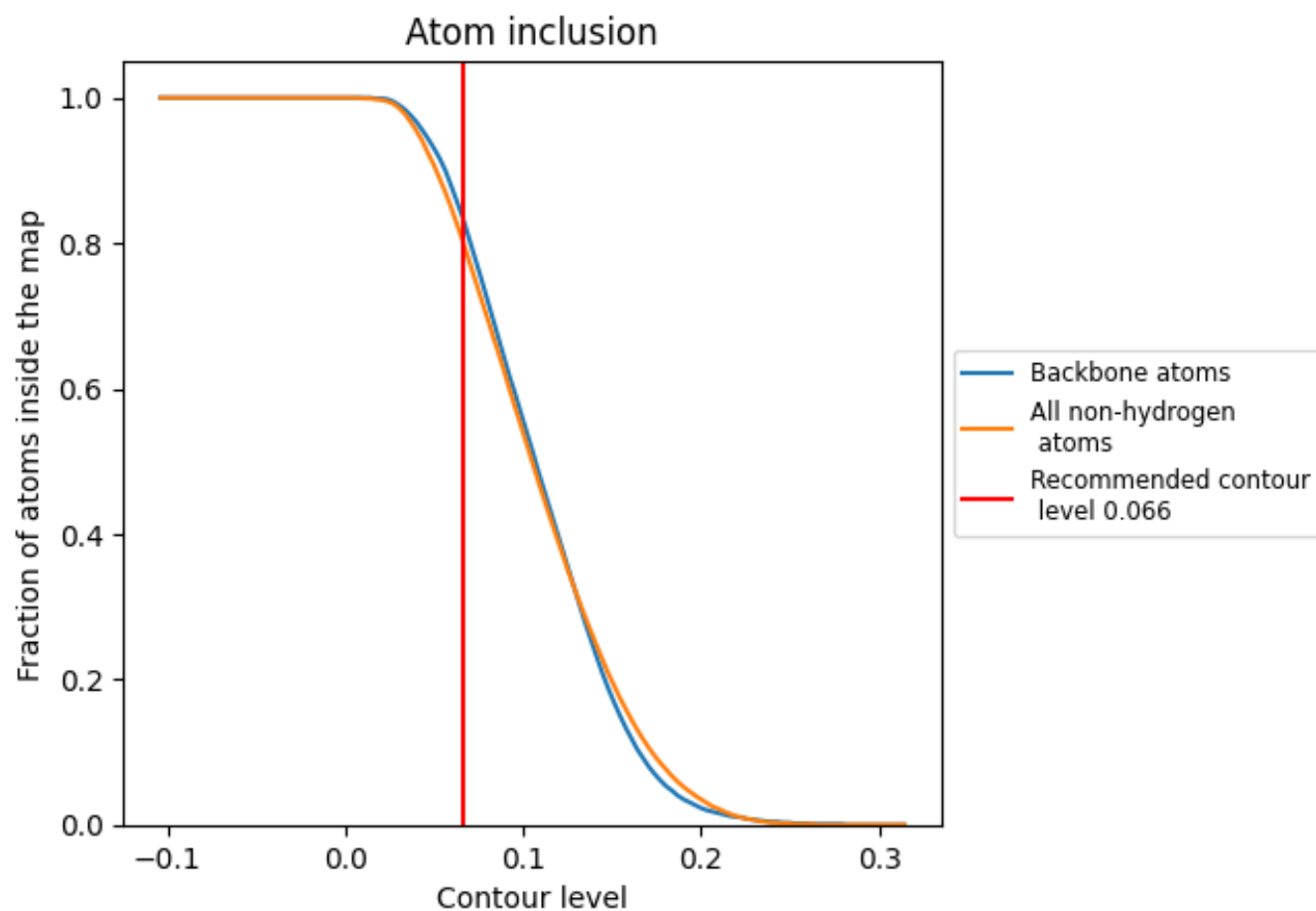
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.066).

















































9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 80% 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 (0.066) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8030	 0.4920
A	 0.8320	 0.4920
B	 0.6550	 0.2850
C	 0.6520	 0.4910
D	 0.8600	 0.5710
E	 0.7890	 0.5330
G	 0.3900	 0.3820
J	 0.8990	 0.5770
K	 0.7450	 0.5270
L	 0.6200	 0.4730
N	 0.8750	 0.5670
O	 0.4290	 0.3540
P	 0.7460	 0.5300
Q	 0.8970	 0.5720
R	 0.8470	 0.5710
S	 0.9020	 0.5880
T	 0.8450	 0.5640
U	 0.7540	 0.5310
V	 0.4540	 0.4620
Y	 0.7840	 0.5110
Z	 0.8290	 0.5570
b	 0.7940	 0.5180
d	 0.9330	 0.6170
f	 0.0960	 0.4660

