



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 12:45 AM UTC

PDB ID : 6WU9 / pdb_00006wu9
EMDB ID : EMD-21907
Title : 50S subunit of 70S Ribosome Enterococcus faecalis MultiBody refinement
Authors : Jogl, G.; Khayat, R.
Deposited on : 2020-05-04
Resolution : 2.90 Å(reported)
Based on initial models : 4YBB, 5LI0

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:

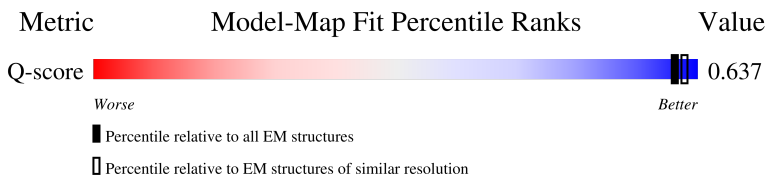
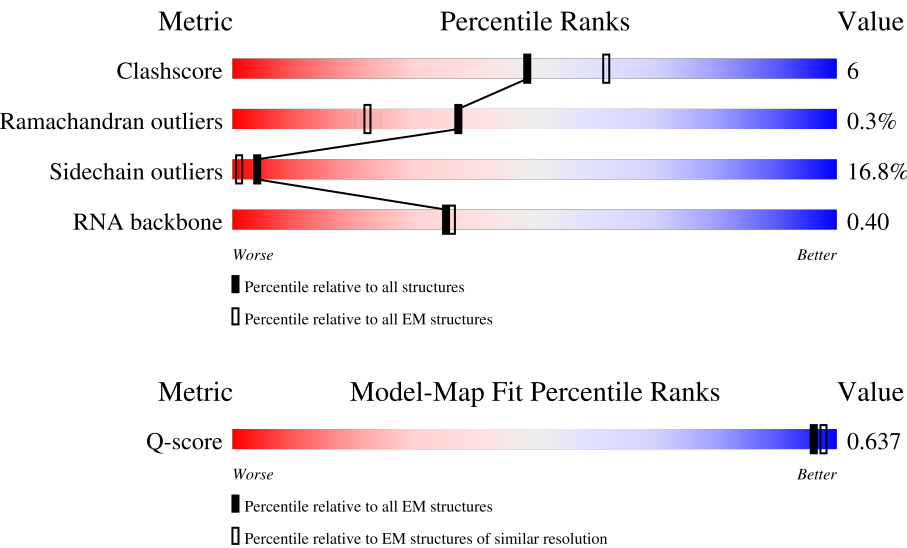
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



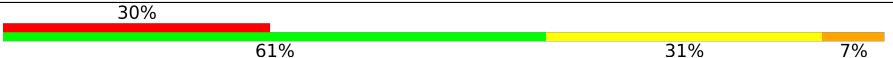
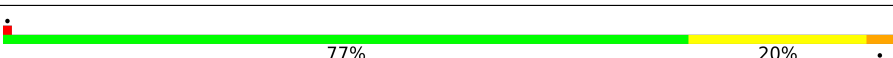
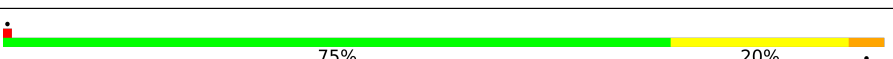
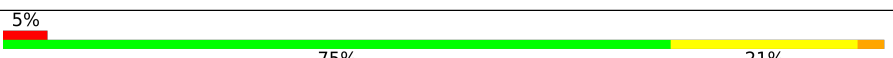
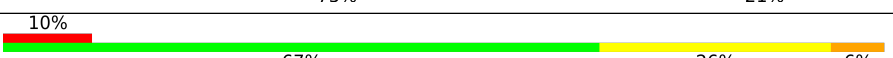
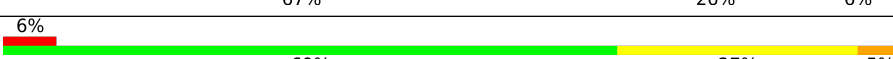
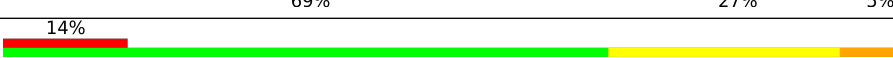
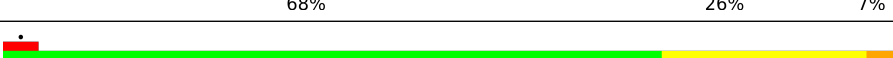
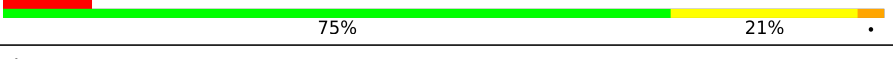
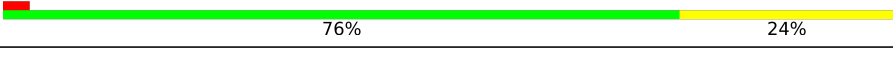
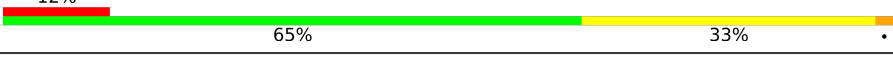
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13054 (2.40 - 3.40)

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	2908	
2	B	116	
3	D	207	

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Mol	Chain	Length	Quality of chain
4	E	206	
5	F	177	
6	G	176	
7	K	145	
8	L	122	
9	M	146	
10	N	141	
11	O	124	
12	P	117	
13	Q	114	
14	R	118	
15	S	102	
16	T	112	
17	U	89	
18	V	101	
19	X	76	
20	Y	54	
21	Z	61	
22	0	58	
23	2	56	
24	3	49	
25	4	44	
26	5	64	
27	6	38	

2 Entry composition

There are 28 unique types of molecules in this entry. The entry contains 82295 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	2739	Total	C	N	O	P	0	0
			58793	26244	10818	18992	2739		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	116	Total	C	N	O	P	0	0
			2480	1106	444	814	116		

- Molecule 3 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	207	Total	C	N	O	S	0	0
			1579	994	292	289	4		

- Molecule 4 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	206	Total	C	N	O	S	0	0
			1574	984	290	298	2		

- Molecule 5 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	177	Total	C	N	O	S	0	0
			1392	887	239	260	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	176	Total	C	N	O	S	0	0
			1345	842	244	255	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	K	145	Total	C	N	O	S	0	0
			1130	714	205	207	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L	122	Total	C	N	O	S	0	0
			922	574	176	170	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	M	146	Total	C	N	O	S	0	0
			1095	677	212	205	1		

- Molecule 10 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	N	141	Total	C	N	O	S	0	0
			1118	710	216	185	7		

- Molecule 11 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	O	124	Total	C	N	O	S	0	0
			991	612	191	185	3		

- Molecule 12 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	P	117	Total	C	N	O	S	0	0
			899	556	175	167	1		

- Molecule 13 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	Q	114	Total	C	N	O	0	0
			924	582	185	157		

- Molecule 14 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	R	118	Total	C	N	O	S	0	0
			950	602	184	160	4		

- Molecule 15 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	S	102	Total	C	N	O	S	0	0
			784	500	139	143	2		

- Molecule 16 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	T	112	Total	C	N	O	S	0	0
			849	532	156	159	2		

- Molecule 17 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	U	89	Total	C	N	O	S	0	0
			720	458	127	132	3		

- Molecule 18 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	V	101	Total	C	N	O	S	0	0
			763	486	135	140	2		

- Molecule 19 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	X	76	Total	C	N	O	0	0
			572	351	109	112		

- Molecule 20 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Y	54	Total	C	N	O	S	0	0
			425	265	86	72	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Y	51	ALA	THR	conflict	UNP A0A1B4XRZ8

- Molecule 21 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Z	61	Total	C	N	O	S	0	0
			504	314	94	95	1		

- Molecule 22 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	0	58	Total	C	N	O	S	0	0
			435	271	81	82	1		

- Molecule 23 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	2	56	Total	C	N	O	S	0	0
			429	262	88	73	6		

- Molecule 24 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	3	49	Total	C	N	O	S	0	0
			419	253	86	76	4		

- Molecule 25 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	4	44	Total	C	N	O	S	0	0
			374	227	91	54	2		

- Molecule 26 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	5	64	Total	C	N	O	S	0	0
			522	320	122	78	2		

- Molecule 27 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	6	38	Total	C	N	O	S	0	0
			304	188	66	44	6		

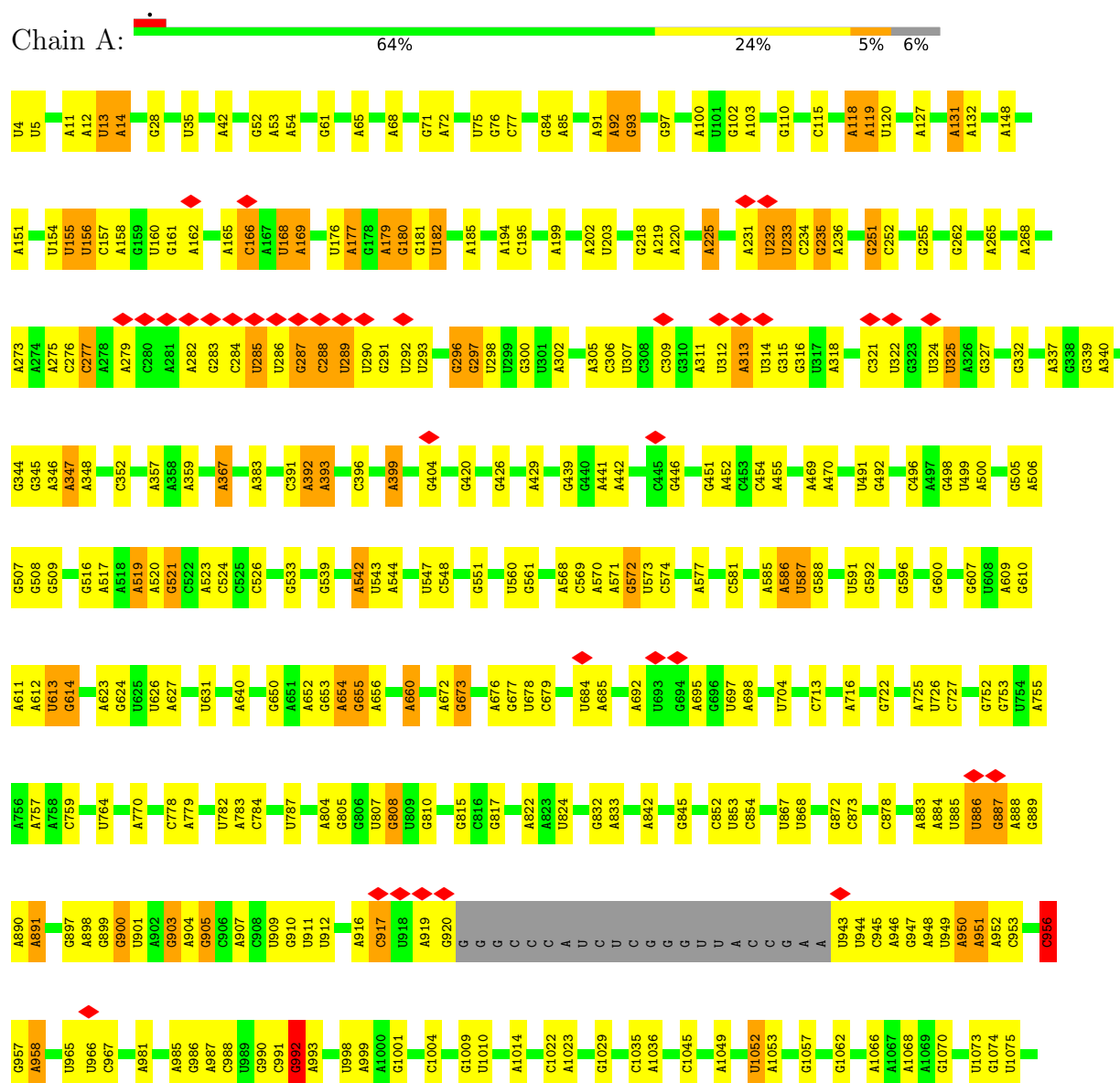
- Molecule 28 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

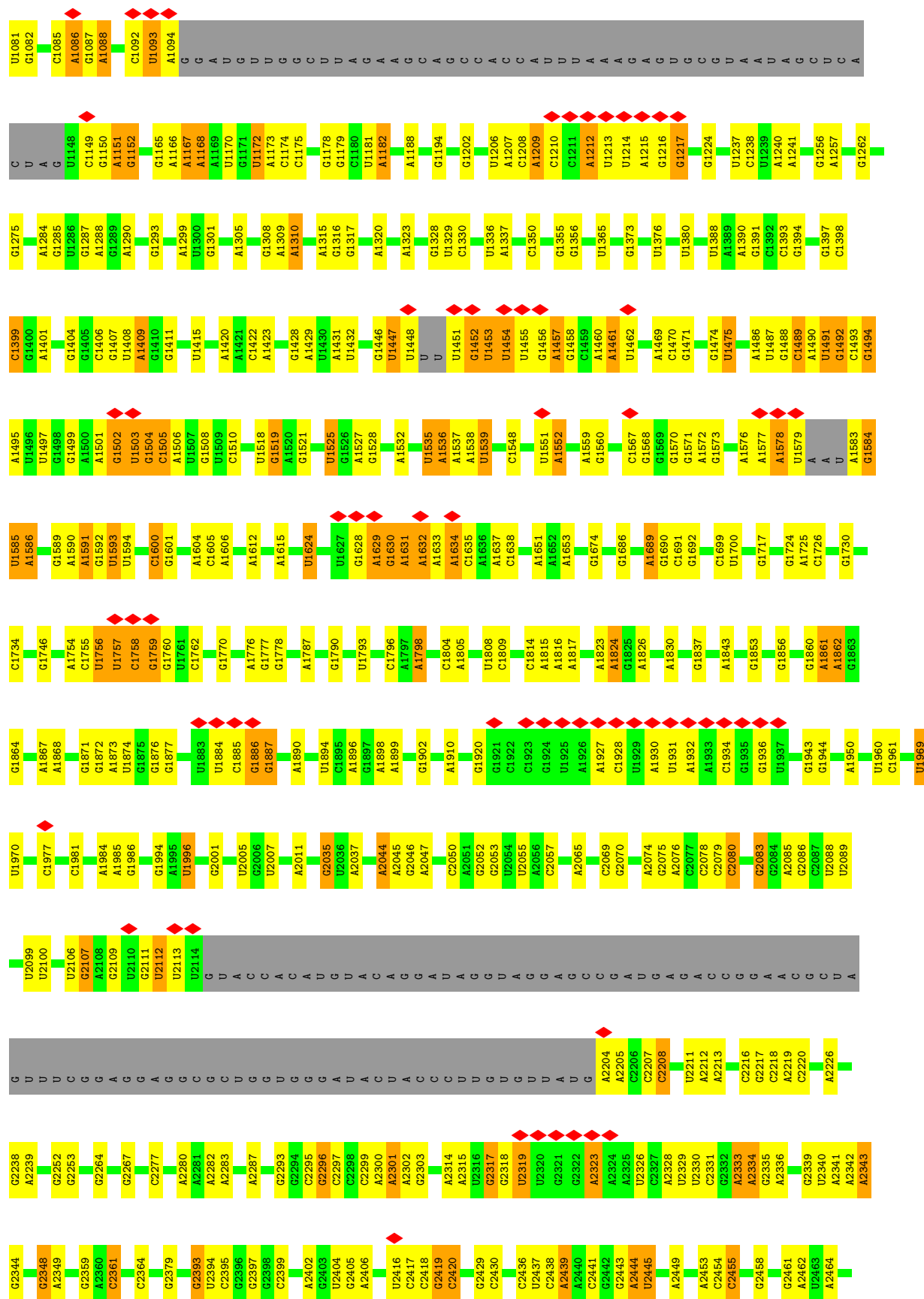
Mol	Chain	Residues	Atoms		AltConf
28	2	1	Total	Zn	0
			1	1	
28	3	1	Total	Zn	0
			1	1	
28	6	1	Total	Zn	0
			1	1	

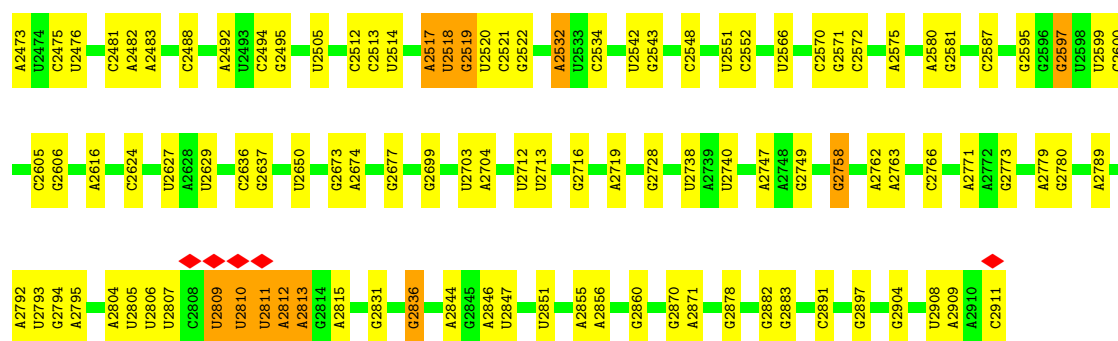
3 Residue-property plots

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.

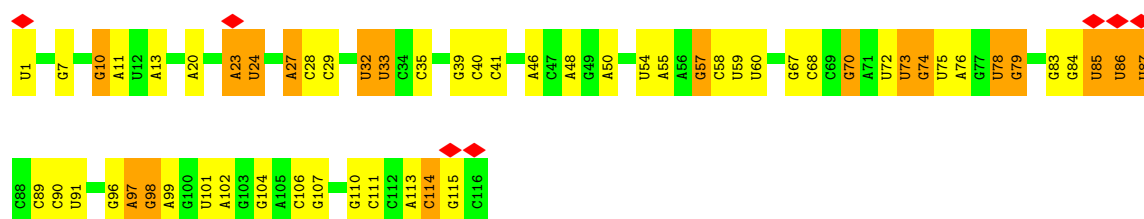
• Molecule 1: 23S rRNA



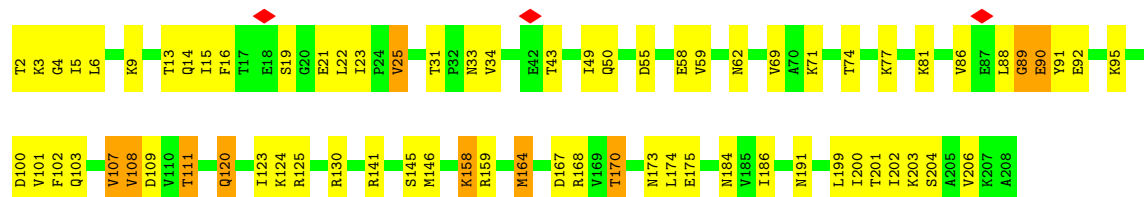




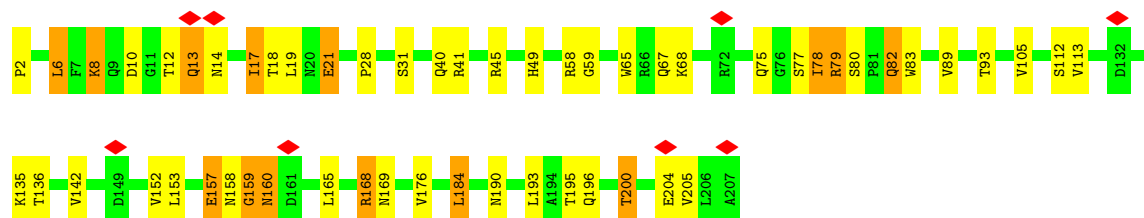
• Molecule 2: 5S rRNA



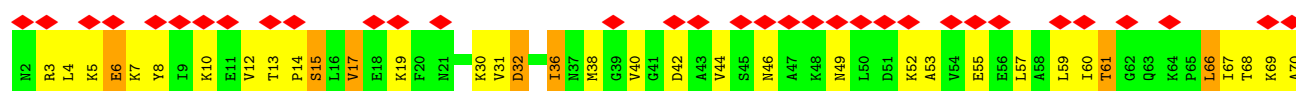
• Molecule 3: 50S ribosomal protein L3

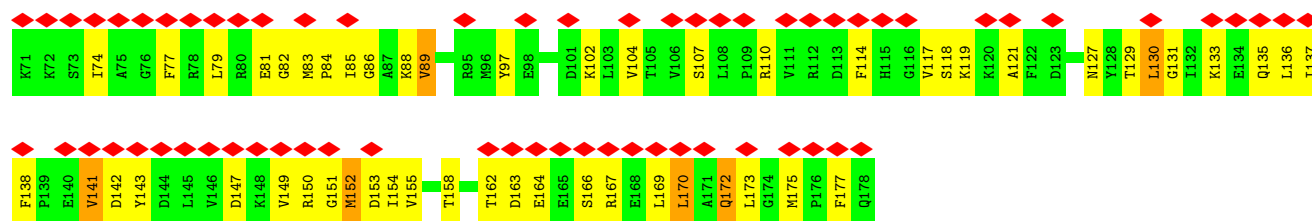


• Molecule 4: 50S ribosomal protein L4

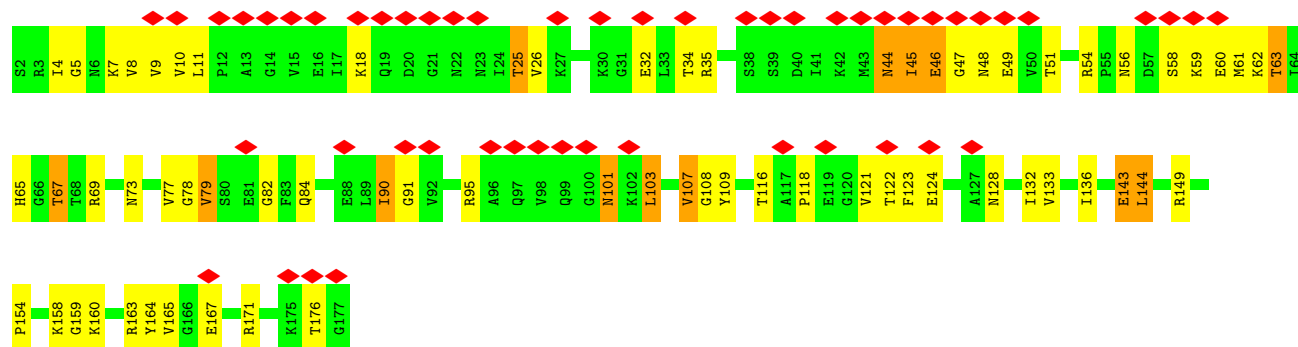


• Molecule 5: 50S ribosomal protein L5

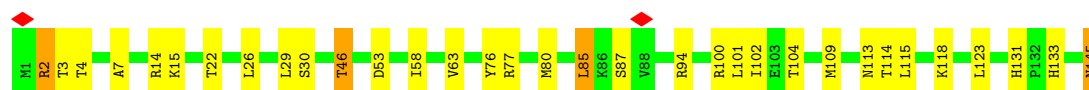
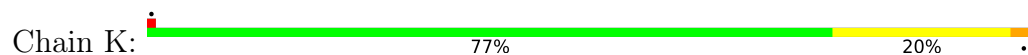




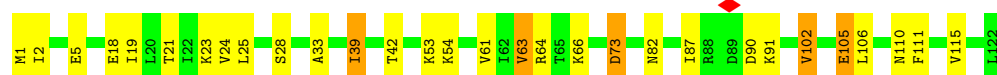
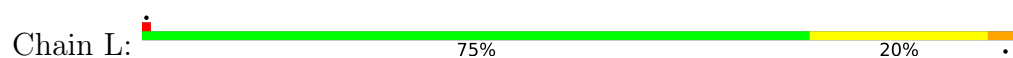
• Molecule 6: 50S ribosomal protein L6



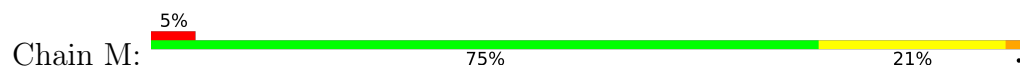
• Molecule 7: 50S ribosomal protein L13



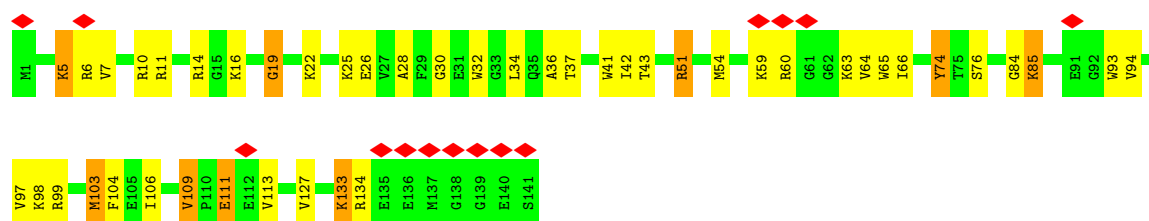
• Molecule 8: 50S ribosomal protein L14



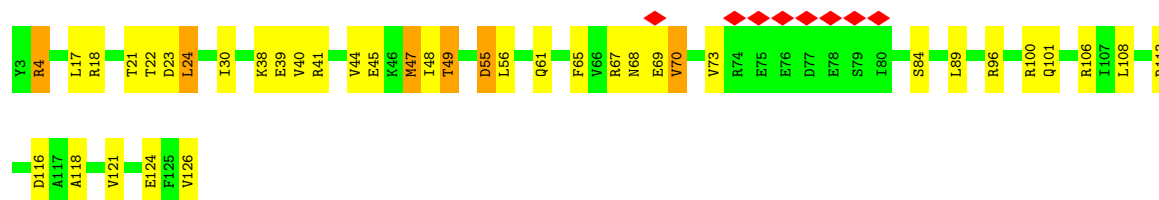
• Molecule 9: 50S ribosomal protein L15



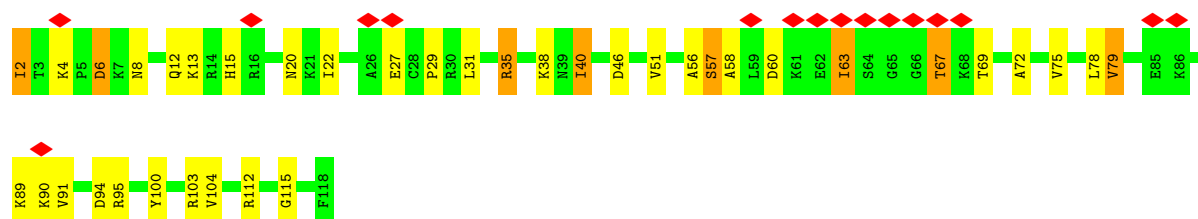
• Molecule 10: 50S ribosomal protein L16



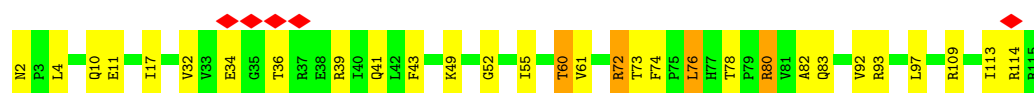
- Molecule 11: 50S ribosomal protein L17



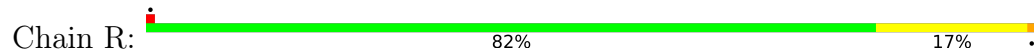
- Molecule 12: 50S ribosomal protein L18



- Molecule 13: 50S ribosomal protein L19

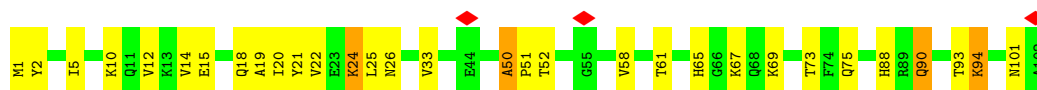


- Molecule 14: 50S ribosomal protein L20

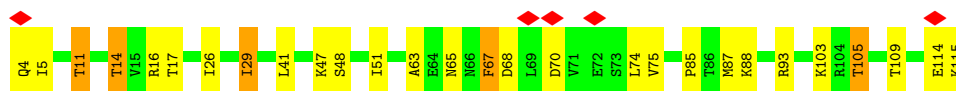
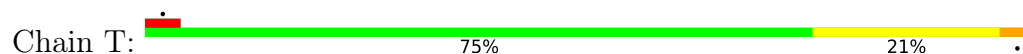


- Molecule 15: 50S ribosomal protein L21

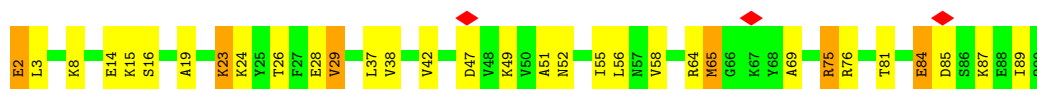




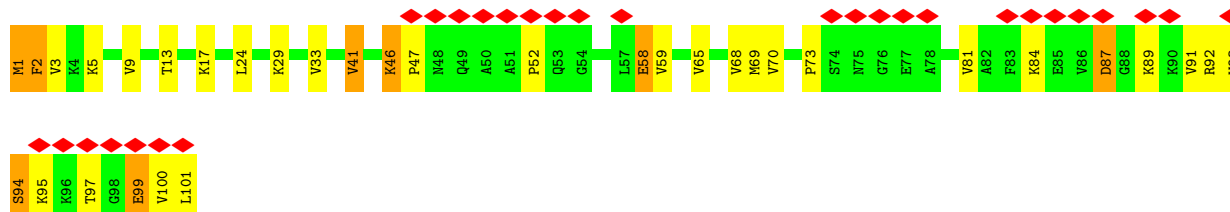
- Molecule 16: 50S ribosomal protein L22



- Molecule 17: 50S ribosomal protein L23



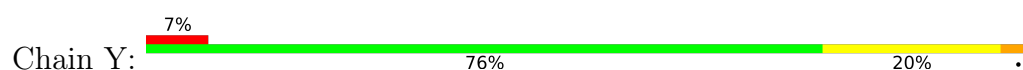
- Molecule 18: 50S ribosomal protein L24



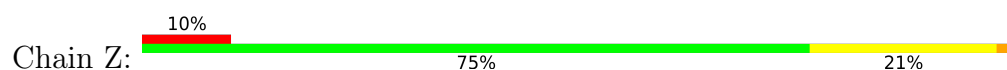
- Molecule 19: 50S ribosomal protein L27



- Molecule 20: 50S ribosomal protein L28

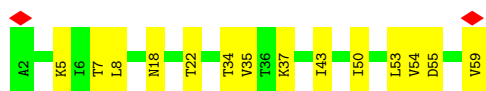
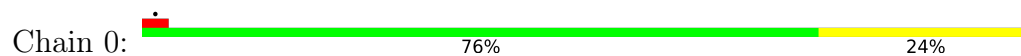


- Molecule 21: 50S ribosomal protein L29

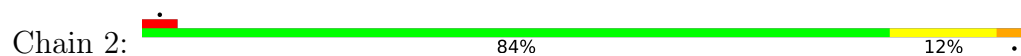




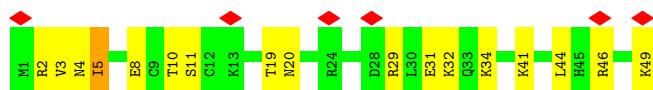
- Molecule 22: 50S ribosomal protein L30



- Molecule 23: 50S ribosomal protein L32



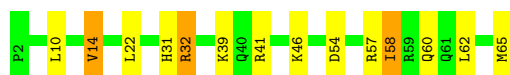
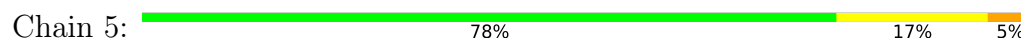
- Molecule 24: 50S ribosomal protein L33



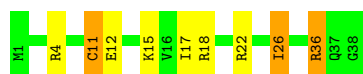
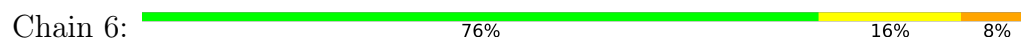
- Molecule 25: 50S ribosomal protein L34



- Molecule 26: 50S ribosomal protein L35



- Molecule 27: 50S ribosomal protein L36



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	335675	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 ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.226	Depositor
Minimum map value	-0.085	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.035	Depositor
Map size (Å)	482.68, 482.68, 482.68	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.097, 1.097, 1.097	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

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	0.56	0/65858	0.56	3/102721 (0.0%)
2	B	0.44	0/2773	0.55	0/4320
3	D	0.50	0/1601	0.66	0/2150
4	E	0.47	0/1596	0.61	0/2159
5	F	0.29	0/1411	0.50	0/1897
6	G	0.33	0/1365	0.58	0/1839
7	K	0.48	0/1151	0.63	0/1554
8	L	0.48	0/929	0.61	0/1247
9	M	0.45	0/1105	0.66	0/1474
10	N	0.44	0/1141	0.63	0/1519
11	O	0.51	0/1000	0.74	0/1341
12	P	0.40	0/908	0.62	0/1216
13	Q	0.48	0/938	0.60	1/1262 (0.1%)
14	R	0.52	0/963	0.57	0/1280
15	S	0.46	0/796	0.61	0/1068
16	T	0.46	0/858	0.59	0/1157
17	U	0.45	0/727	0.66	0/972
18	V	0.40	0/772	0.65	0/1035
19	X	0.48	0/578	0.58	0/773
20	Y	0.41	0/431	0.62	0/574
21	Z	0.39	0/505	0.54	0/672
22	0	0.46	0/437	0.57	0/589
23	2	0.49	0/436	0.57	0/578
24	3	0.39	0/423	0.58	0/563
25	4	0.47	0/377	0.59	0/491
26	5	0.43	0/528	0.61	0/689
27	6	0.44	0/309	0.67	0/409
All	All	0.53	0/89916	0.57	4/135549 (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	D	0	1
10	N	0	2
11	O	0	2
15	S	0	1
16	T	0	1
18	V	0	1
All	All	0	8

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	956	C	N3-C4-N4	-7.21	96.38	118.00
13	Q	52	GLY	N-CA-C	6.62	121.30	110.77
1	A	956	C	C5-C4-N4	5.94	138.03	120.20
1	A	992	G	N9-C1'-C2'	-5.15	106.27	114.00

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	D	89	GLY	Peptide
10	N	16	LYS	Peptide
10	N	19	GLY	Peptide
11	O	4	ARG	Peptide
11	O	73	VAL	Peptide

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	58793	0	29547	406	0
2	B	2480	0	1249	41	0
3	D	1579	0	1661	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	E	1574	0	1621	29	0
5	F	1392	0	1454	52	0
6	G	1345	0	1375	36	0
7	K	1130	0	1169	15	0
8	L	922	0	985	14	0
9	M	1095	0	1149	16	0
10	N	1118	0	1180	27	0
11	O	991	0	1028	23	0
12	P	899	0	932	27	0
13	Q	924	0	979	10	0
14	R	950	0	1009	11	0
15	S	784	0	826	12	0
16	T	849	0	906	13	0
17	U	720	0	772	14	0
18	V	763	0	824	16	0
19	X	572	0	580	9	0
20	Y	425	0	460	4	0
21	Z	504	0	538	5	0
22	0	435	0	472	7	0
23	2	429	0	444	3	0
24	3	419	0	435	9	0
25	4	374	0	424	8	0
26	5	522	0	576	5	0
27	6	304	0	337	6	0
28	2	1	0	0	0	0
28	3	1	0	0	0	0
28	6	1	0	0	0	0
All	All	82295	0	52932	770	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 6.

The worst 5 of 770 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)
1:A:1571:G:N2	1:A:1591:A:H62	1.58	1.01
1:A:275:A:H62	1:A:296:G:N2	1.67	0.93
1:A:1571:G:H22	1:A:1591:A:H62	0.94	0.92
1:A:1871:G:N2	1:A:1899:A:H62	1.69	0.91
1:A:1871:G:H21	1:A:1899:A:H62	0.92	0.90

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	D	205/207 (99%)	188 (92%)	16 (8%)	1 (0%)	24	54
4	E	204/206 (99%)	181 (89%)	21 (10%)	2 (1%)	12	39
5	F	175/177 (99%)	148 (85%)	27 (15%)	0	100	100
6	G	174/176 (99%)	145 (83%)	27 (16%)	2 (1%)	11	36
7	K	143/145 (99%)	133 (93%)	10 (7%)	0	100	100
8	L	120/122 (98%)	104 (87%)	15 (12%)	1 (1%)	16	44
9	M	144/146 (99%)	118 (82%)	25 (17%)	1 (1%)	18	48
10	N	139/141 (99%)	119 (86%)	20 (14%)	0	100	100
11	O	122/124 (98%)	102 (84%)	20 (16%)	0	100	100
12	P	115/117 (98%)	105 (91%)	10 (9%)	0	100	100
13	Q	112/114 (98%)	104 (93%)	8 (7%)	0	100	100
14	R	116/118 (98%)	113 (97%)	3 (3%)	0	100	100
15	S	100/102 (98%)	91 (91%)	8 (8%)	1 (1%)	12	39
16	T	110/112 (98%)	103 (94%)	7 (6%)	0	100	100
17	U	87/89 (98%)	73 (84%)	14 (16%)	0	100	100
18	V	99/101 (98%)	81 (82%)	18 (18%)	0	100	100
19	X	74/76 (97%)	70 (95%)	4 (5%)	0	100	100
20	Y	52/54 (96%)	43 (83%)	8 (15%)	1 (2%)	6	23
21	Z	59/61 (97%)	57 (97%)	2 (3%)	0	100	100
22	0	56/58 (97%)	54 (96%)	2 (4%)	0	100	100
23	2	54/56 (96%)	46 (85%)	8 (15%)	0	100	100
24	3	47/49 (96%)	43 (92%)	4 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	4	42/44 (96%)	42 (100%)	0	0	100	100
26	5	62/64 (97%)	59 (95%)	3 (5%)	0	100	100
27	6	36/38 (95%)	32 (89%)	4 (11%)	0	100	100
All	All	2647/2697 (98%)	2354 (89%)	284 (11%)	9 (0%)	37	65

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	D	90	GLU
9	M	16	ARG
4	E	13	GLN
8	L	25	LEU
20	Y	20	HIS

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	D	170/170 (100%)	140 (82%)	30 (18%)	2	6
4	E	172/172 (100%)	139 (81%)	33 (19%)	1	5
5	F	154/154 (100%)	122 (79%)	32 (21%)	1	4
6	G	146/146 (100%)	121 (83%)	25 (17%)	2	7
7	K	122/122 (100%)	103 (84%)	19 (16%)	2	9
8	L	98/98 (100%)	81 (83%)	17 (17%)	2	7
9	M	112/112 (100%)	95 (85%)	17 (15%)	3	9
10	N	112/112 (100%)	96 (86%)	16 (14%)	3	11
11	O	106/106 (100%)	91 (86%)	15 (14%)	3	11
12	P	91/91 (100%)	76 (84%)	15 (16%)	2	8
13	Q	97/97 (100%)	82 (84%)	15 (16%)	2	9
14	R	94/94 (100%)	86 (92%)	8 (8%)	10	31
15	S	83/83 (100%)	67 (81%)	16 (19%)	1	5

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	T	95/95 (100%)	83 (87%)	12 (13%)	4	14
17	U	80/80 (100%)	60 (75%)	20 (25%)	0	2
18	V	85/85 (100%)	67 (79%)	18 (21%)	1	4
19	X	61/61 (100%)	46 (75%)	15 (25%)	1	2
20	Y	47/47 (100%)	39 (83%)	8 (17%)	2	7
21	Z	55/55 (100%)	44 (80%)	11 (20%)	1	4
22	0	49/49 (100%)	44 (90%)	5 (10%)	7	23
23	2	46/46 (100%)	40 (87%)	6 (13%)	4	13
24	3	49/49 (100%)	44 (90%)	5 (10%)	7	23
25	4	39/39 (100%)	33 (85%)	6 (15%)	2	9
26	5	51/51 (100%)	42 (82%)	9 (18%)	2	6
27	6	35/35 (100%)	30 (86%)	5 (14%)	3	11
All	All	2249/2249 (100%)	1871 (83%)	378 (17%)	4	7

5 of 378 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	Q	109	ARG
17	U	76	ARG
14	R	60	LEU
16	T	14	THR
18	V	46	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
15	S	86	GLN
20	Y	32	ASN
15	S	88	HIS
16	T	65	ASN
21	Z	36	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2733/2908 (93%)	536 (19%)	24 (0%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	115/116 (99%)	32 (27%)	3 (2%)
All	All	2848/3024 (94%)	568 (19%)	27 (0%)

5 of 568 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	13	U
1	A	14	A
1	A	28	G
1	A	35	U
1	A	42	A

5 of 27 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1590	A
1	A	1605	C
2	B	32	U
1	A	1604	A
1	A	1861	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 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
9	M	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	M	60:ARG	C	61:LEU	N	1.18

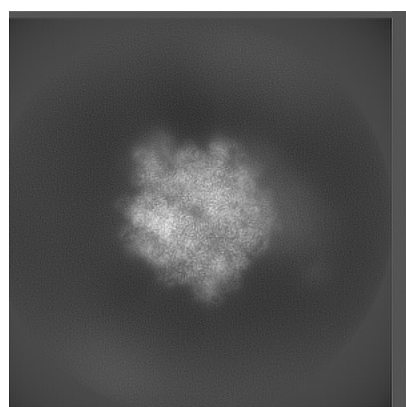
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21907. These allow visual inspection of the internal detail of the map and identification of artifacts.

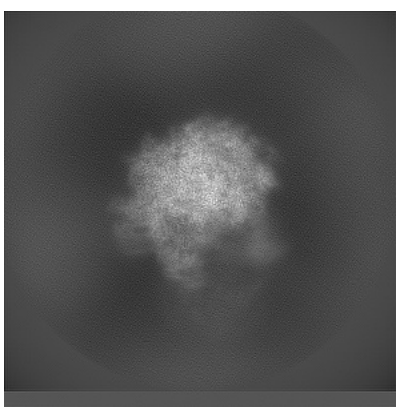
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

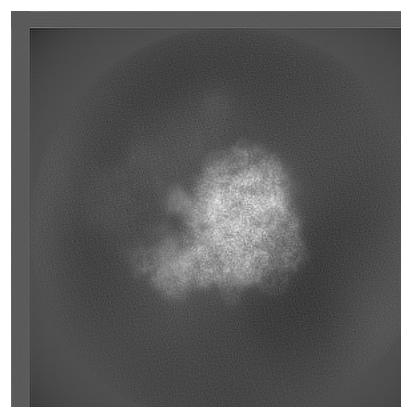
6.1.1 Primary map



X



Y

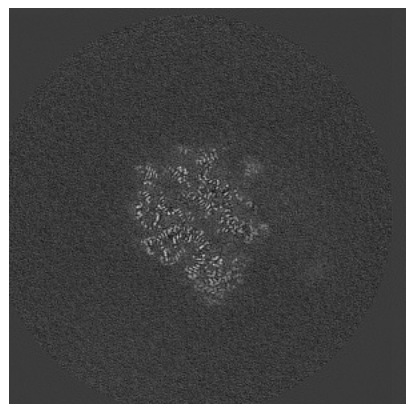


Z

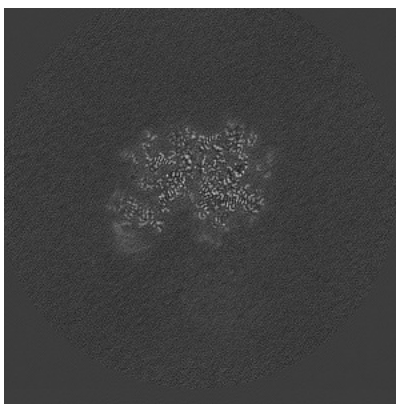
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

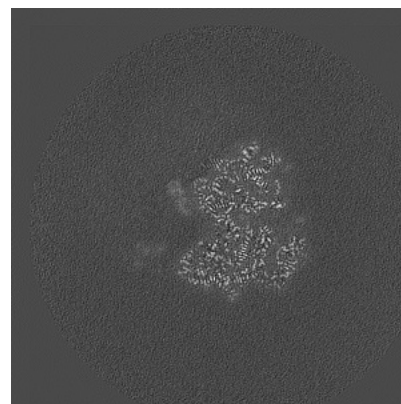
6.2.1 Primary map



X Index: 220



Y Index: 220

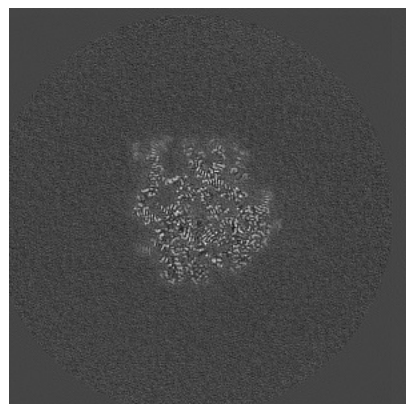


Z Index: 220

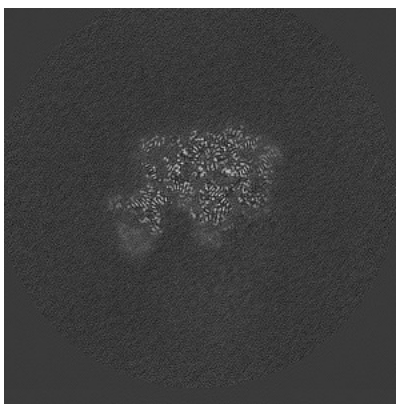
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

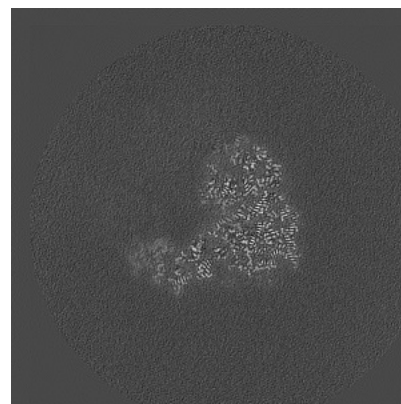
6.3.1 Primary map



X Index: 258



Y Index: 228

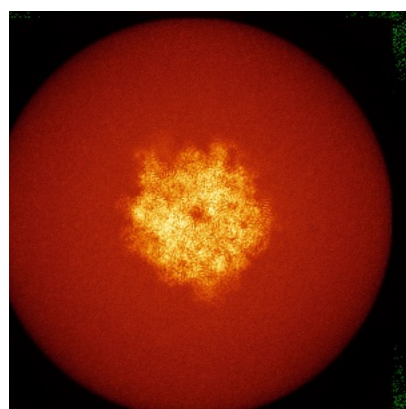


Z Index: 204

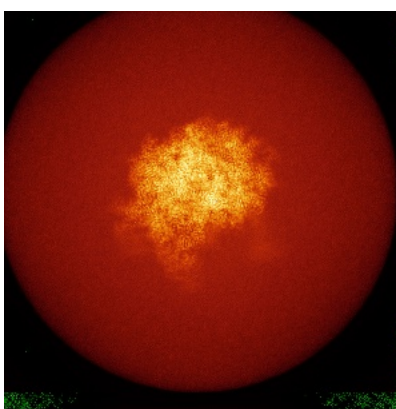
The images above show the largest variance slices of the map in three orthogonal directions.

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

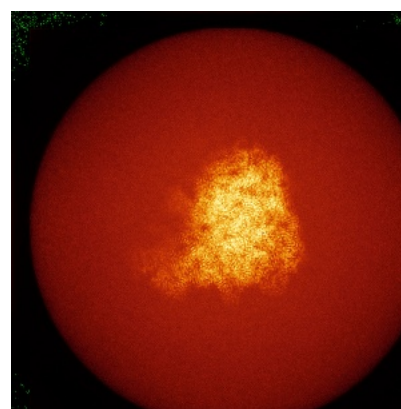
6.4.1 Primary map



X



Y

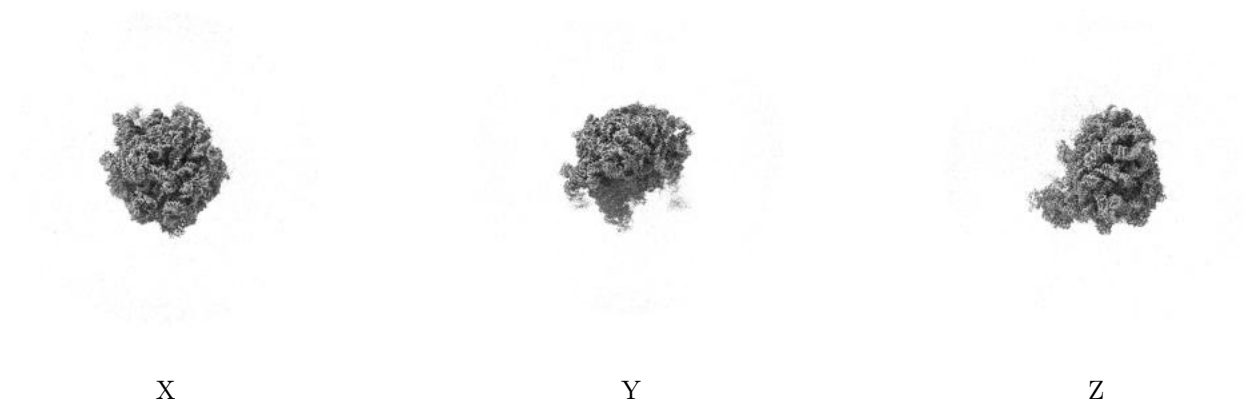


Z

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 0.035. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

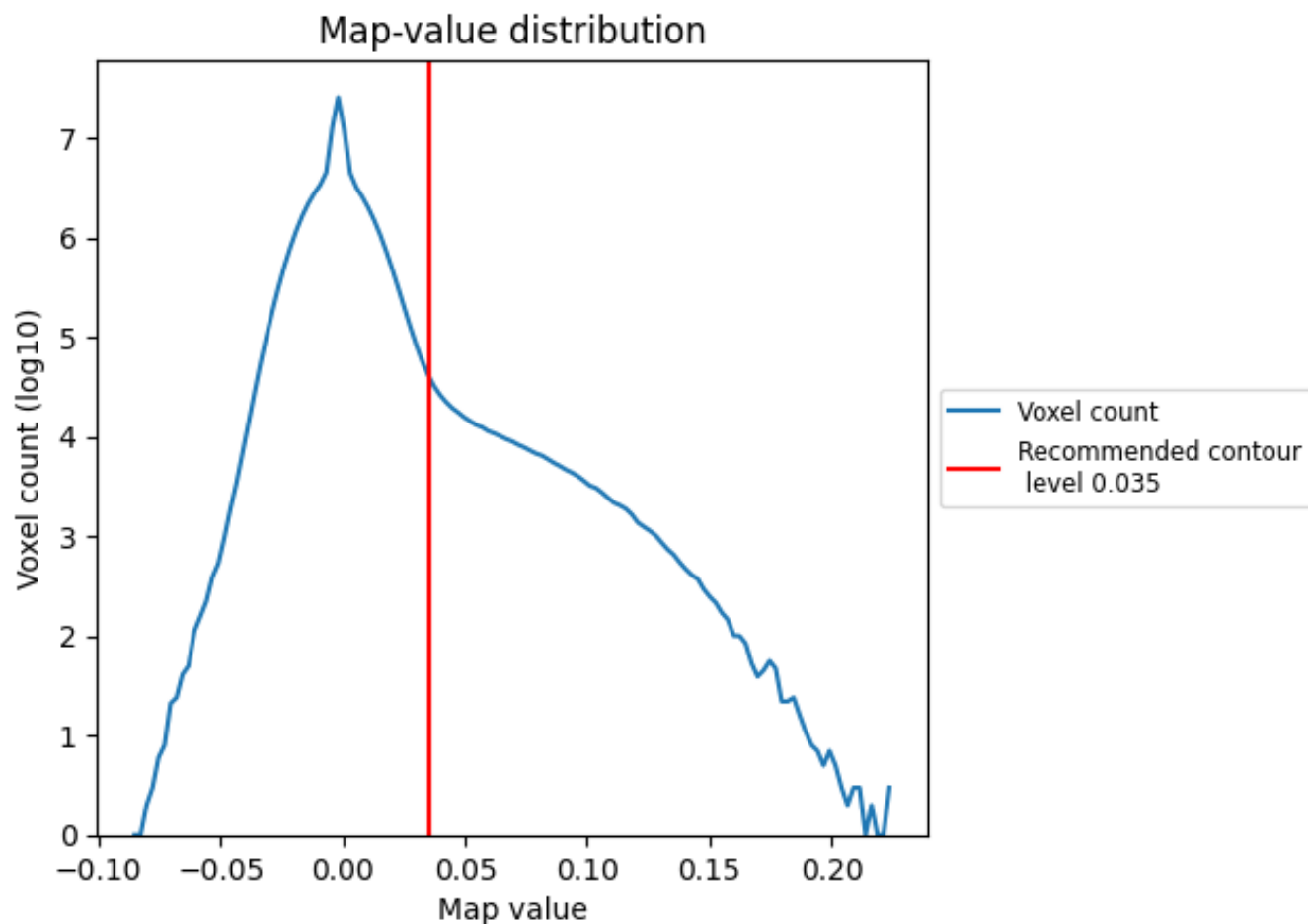
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

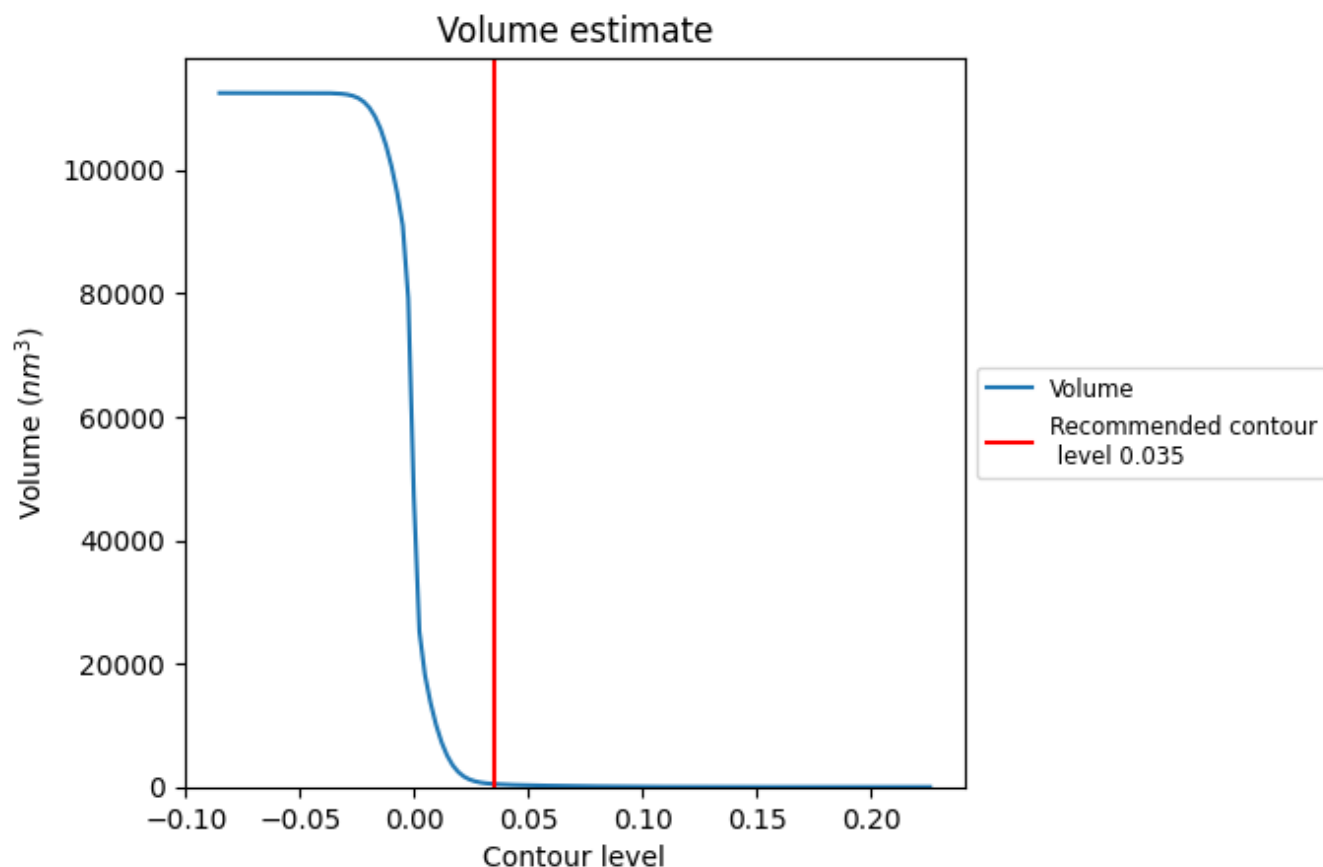
This section contains the results of statistical analysis of the map.

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.

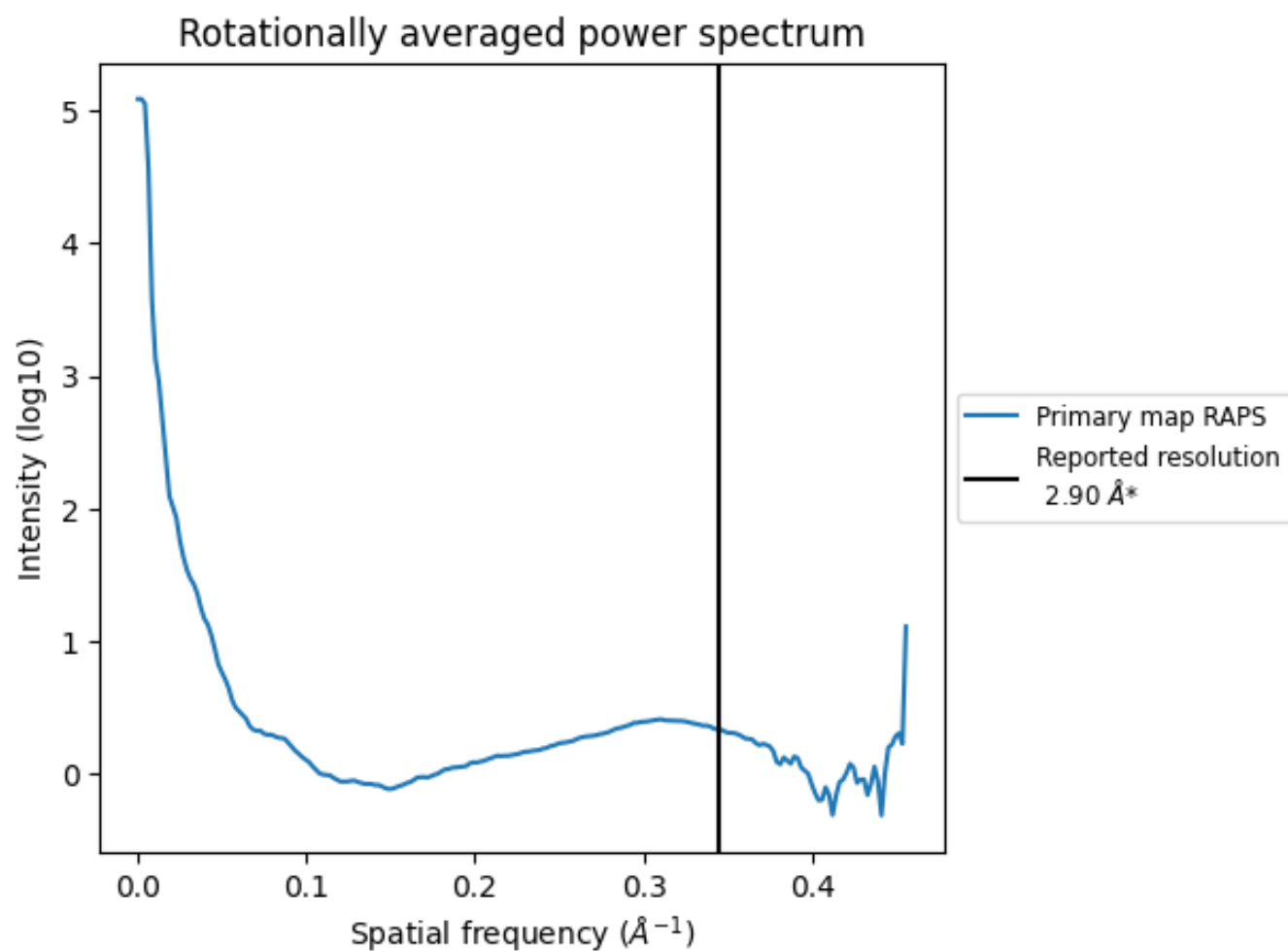
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 483 nm^3 ; this corresponds to an approximate mass of 437 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 0.345 Å⁻¹

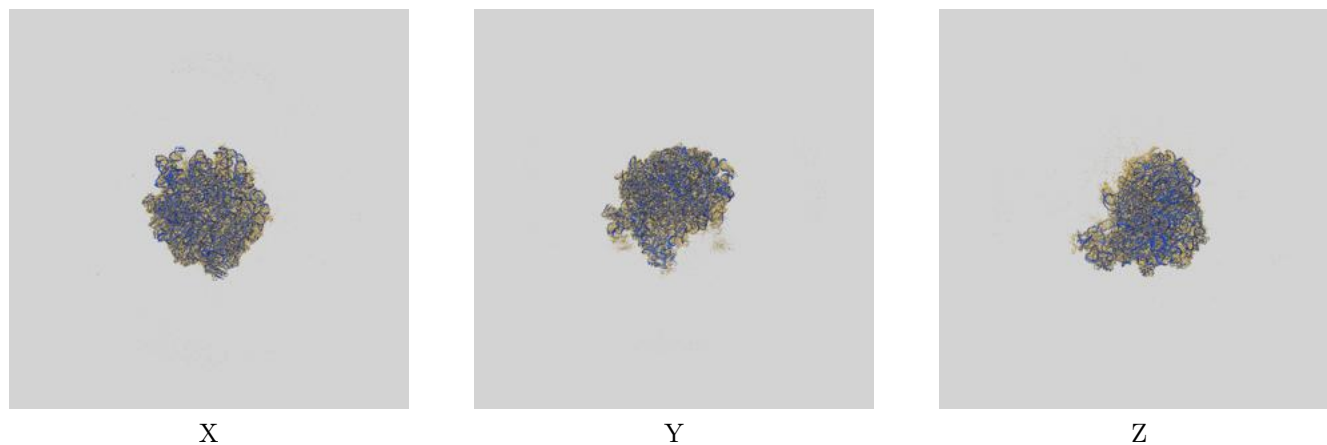
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

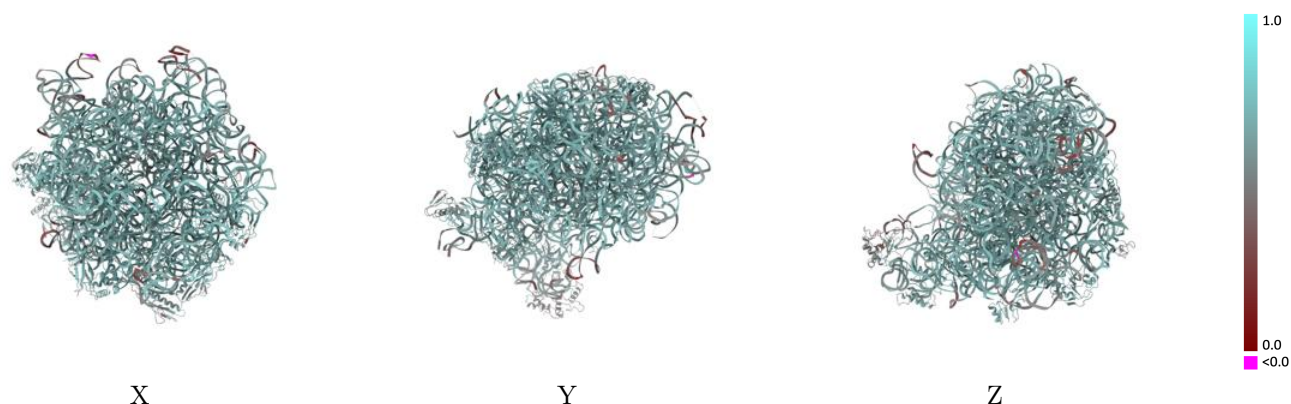
This section contains information regarding the fit between EMDB map EMD-21907 and PDB model 6WU9. Per-residue inclusion information can be found in [section 3](#) on [page 9](#).

9.1 Map-model overlay [i](#)



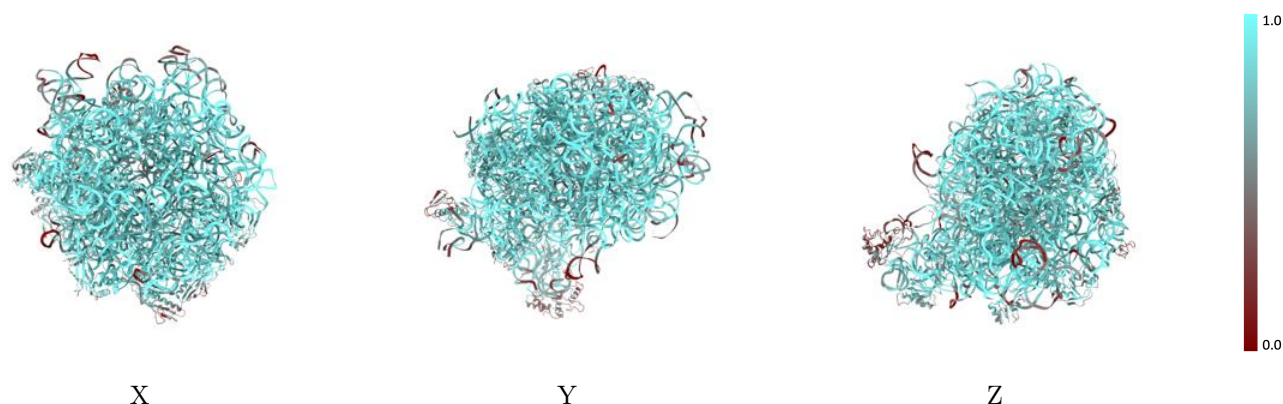
The images above show the 3D surface view of the map at the recommended contour level 0.035 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



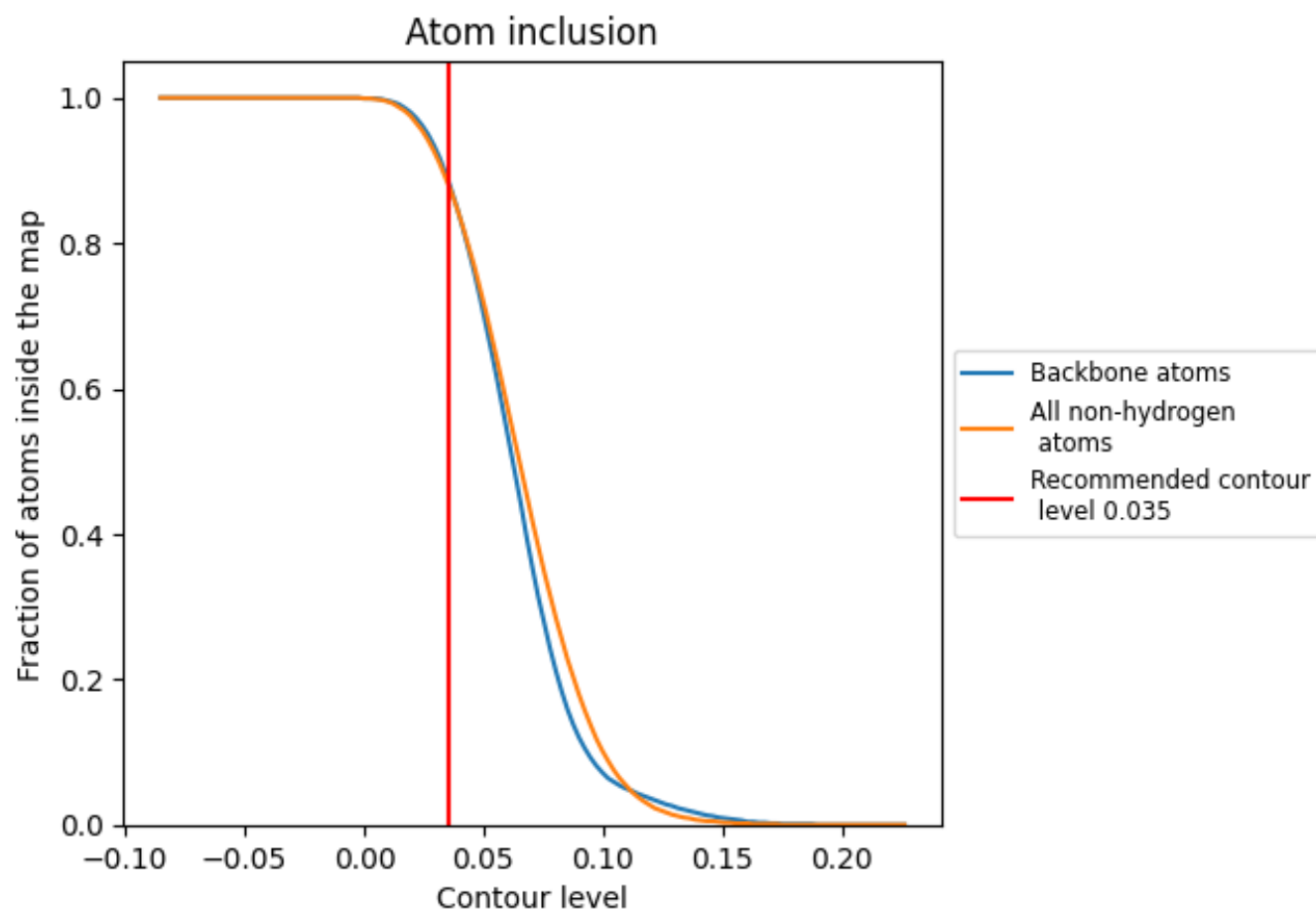
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.035).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 88% 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 (0.035) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8830	 0.6370
0	 0.8280	 0.6310
2	 0.8900	 0.6670
3	 0.7400	 0.6430
4	 0.9540	 0.6850
5	 0.9360	 0.6810
6	 0.9220	 0.6540
A	 0.9200	 0.6420
B	 0.8020	 0.5860
D	 0.8990	 0.6690
E	 0.8420	 0.6430
F	 0.3580	 0.4920
G	 0.5620	 0.5590
K	 0.9020	 0.6560
L	 0.8730	 0.6520
M	 0.8030	 0.6400
N	 0.7880	 0.6200
O	 0.8650	 0.6380
P	 0.7160	 0.6030
Q	 0.8590	 0.6450
R	 0.9220	 0.6720
S	 0.8120	 0.6380
T	 0.8750	 0.6550
U	 0.8240	 0.6310
V	 0.6190	 0.5810
X	 0.9080	 0.6680
Y	 0.7650	 0.6270
Z	 0.7070	 0.6050

