



wwPDB EM Validation Summary Report ⓘ

Apr 6, 2026 – 11:23 PM UTC

PDB ID : 9XFK / pdb_00009xfk
EMDB ID : EMD-66639
Title : In situ structure of bacterial 50S ribosomes
Authors : Wu, F.; Naschberger, A.
Deposited on : 2025-10-29
Resolution : 2.98 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.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

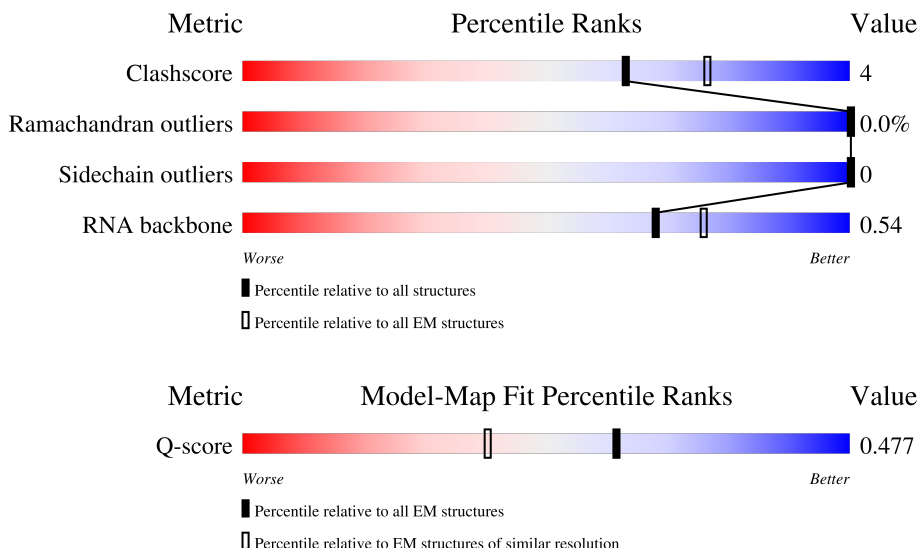
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.98 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	13236 (2.48 - 3.48)

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	I	2904	
2	J	118	
3	K	271	

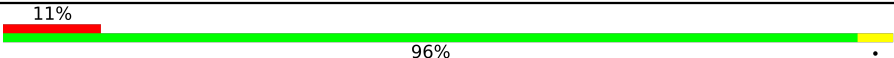


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Mol	Chain	Length	Quality of chain
4	L	209	<div>57%</div> <div>90%10%</div>
5	M	201	<div>75%</div> <div>90%10%</div>
6	N	177	<div>100%</div> <div>85%15%</div>
7	O	176	<div>100%</div> <div>85%15%</div>
8	P	149	<div>100%</div> <div>87%13%</div>
9	Q	134	<div>100%</div> <div>78%22%</div>
10	R	142	<div>54%</div> <div>91%9%</div>
11	S	122	<div>86%</div> <div>89%11%</div>
12	T	144	<div>69%</div> <div>88%12%</div>
13	U	136	<div>91%</div> <div>93%7%</div>
14	V	120	<div>40%</div> <div>90%10%</div>
15	W	116	<div>100%</div> <div>80%20%</div>
16	X	114	<div>87%</div> <div>91%9%</div>
17	Y	117	<div>44%</div> <div>95%5%</div>
18	Z	103	<div>83%</div> <div>87%13%</div>
19	a	110	<div>49%</div> <div>94%6%</div>
20	b	93	<div>96%</div> <div>90%10%</div>
21	c	102	<div>100%</div> <div>85%14%</div>
22	d	94	<div>100%</div> <div>80%20%</div>
23	e	75	<div>92%</div> <div>93%7%</div>
24	f	77	<div>81%</div> <div>94%6%</div>
25	g	62	<div>100%</div> <div>81%19%</div>
26	h	58	<div>78%</div> <div>90%10%</div>
27	i	56	<div>57%</div> <div>86%14%</div>
28	j	50	<div>100%</div> <div>80%20%</div>

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Mol	Chain	Length	Quality of chain
29	k	46	 11% 96%
30	l	64	 47% 83% 17%
31	m	38	 100% 82% 18%

2 Entry composition

There are 35 unique types of molecules in this entry. The entry contains 150936 atoms, of which 59918 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	I	2898	Total	C	H	N	O	P	0	0
			93464	27768	31235	11448	20115	2898		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
2	J	118	Total	C	H	N	O	P	0	0
			3810	1126	1281	464	821	118		

- Molecule 3 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	K	271	Total	C	H	N	O	S	0	0
			4235	1288	2152	423	365	7		

- Molecule 4 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	L	209	Total	C	H	N	O	S	0	0
			3182	979	1617	288	294	4		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
5	M	201	Total	C	H	N	O	S	0	0
			3170	974	1618	283	290	5		

- Molecule 6 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	N	177	Total	C	H	N	O	S	0	0
			2855	899	1444	249	257	6		

- Molecule 7 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	O	176	Total	C	H	N	O	S	0	0
			2694	832	1371	243	246	2		

- Molecule 8 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	P	149	Total	C	H	N	O	S	0	0
			2258	699	1148	197	213	1		

- Molecule 9 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	Q	134	Total	C	H	N	O	S	0	0
			2007	619	1028	169	185	6		

- Molecule 10 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	R	142	Total	C	H	N	O	S	0	0
			2291	714	1162	212	199	4		

- Molecule 11 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	S	122	Total	C	H	N	O	S	0	0
			1950	587	1012	180	165	6		

- Molecule 12 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	T	144	Total	C	H	N	O	S	0	0
			2182	654	1129	207	190	2		

- Molecule 13 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	U	136	Total	C	H	N	O	S	0	0
			2222	686	1147	205	178	6		

- Molecule 14 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	V	120	Total	C	H	N	O	S	
			1960	593	1000	196	166	5	
								0	0

- Molecule 15 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	W	116	Total	C	H	N	O		
			1815	552	923	178	162		
								0	0

- Molecule 16 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	X	114	Total	C	H	N	O	S	
			1879	574	962	179	163	1	
									0

- Molecule 17 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Y	117	Total	C	H	N	O		
			1967	604	1020	192	151		
								0	0

- Molecule 18 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Z	103	Total	C	H	N	O	S	
			1655	516	839	153	145	2	
									0

- Molecule 19 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	a	110	Total	C	H	N	O	S	
			1779	532	922	166	156	3	
									0

- Molecule 20 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	b	93	Total	C	H	N	O	S	
			1546	466	807	139	132	2	
									0

- Molecule 21 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	c	102	Total	C	H	N	O	0	0
			1611	492	831	146	142		

- Molecule 22 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	d	94	Total	C	H	N	O	S	0	0
			1533	479	780	137	134	3		

- Molecule 23 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	e	75	Total	C	H	N	O	S	0	0
			1167	356	592	116	102	1		

- Molecule 24 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	f	77	Total	C	H	N	O	S	0	0
			1277	388	652	129	106	2		

- Molecule 25 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace	
25	g	62	Total	C	H	N	O	S	0	0
			1032	308	531	98	94	1		

- Molecule 26 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	h	58	Total	C	H	N	O	S	0	0
			937	281	488	87	79	2		

- Molecule 27 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace	
27	i	56	Total	C	H	N	O	S	0	0
			902	269	458	94	80	1		

- Molecule 28 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	j	50	Total	C	H	N	O	0	0
			848	263	439	75	71		

- Molecule 29 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace	
29	k	46	Total	C	H	N	O	S	0	0
			795	228	418	90	57	2		

- Molecule 30 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	l	64	Total	C	H	N	O	S	0	0
			1076	323	572	105	74	2		

- Molecule 31 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace	
31	m	38	Total	C	H	N	O	S	0	0
			642	185	340	65	48	4		

- Molecule 32 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
32	I	161	Total	Mg	0
			161	161	
32	J	1	Total	Mg	0
			1	1	
32	K	2	Total	Mg	0
			2	2	
32	L	1	Total	Mg	0
			1	1	
32	k	1	Total	Mg	0
			1	1	

- Molecule 33 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		AltConf
33	K	1	Total	Na	0
			1	1	

- Molecule 34 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
34	m	1	Total 1	Zn 1	0

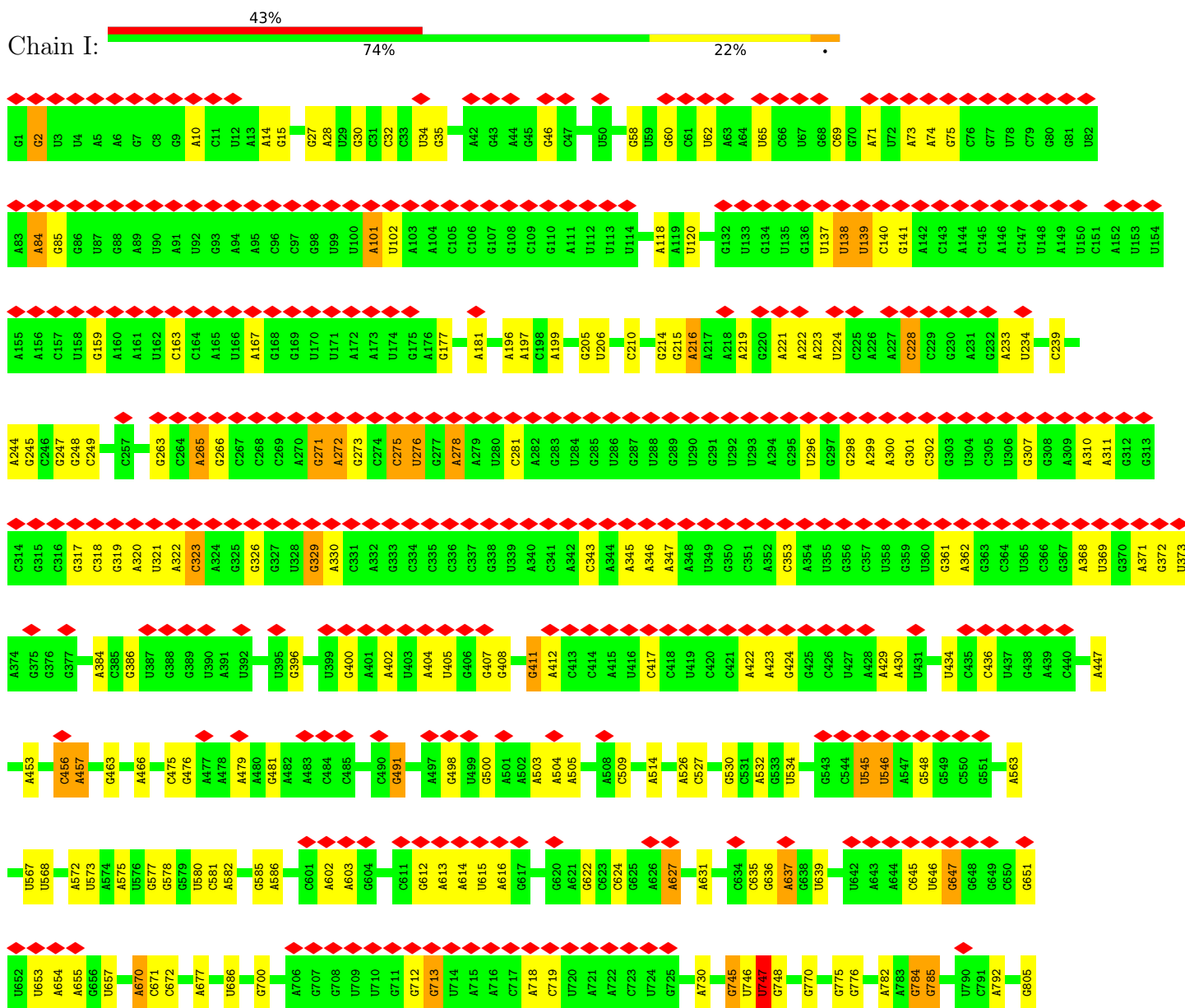
- Molecule 35 is water.

Mol	Chain	Residues	Atoms		AltConf
35	I	27	Total 27	O 27	0

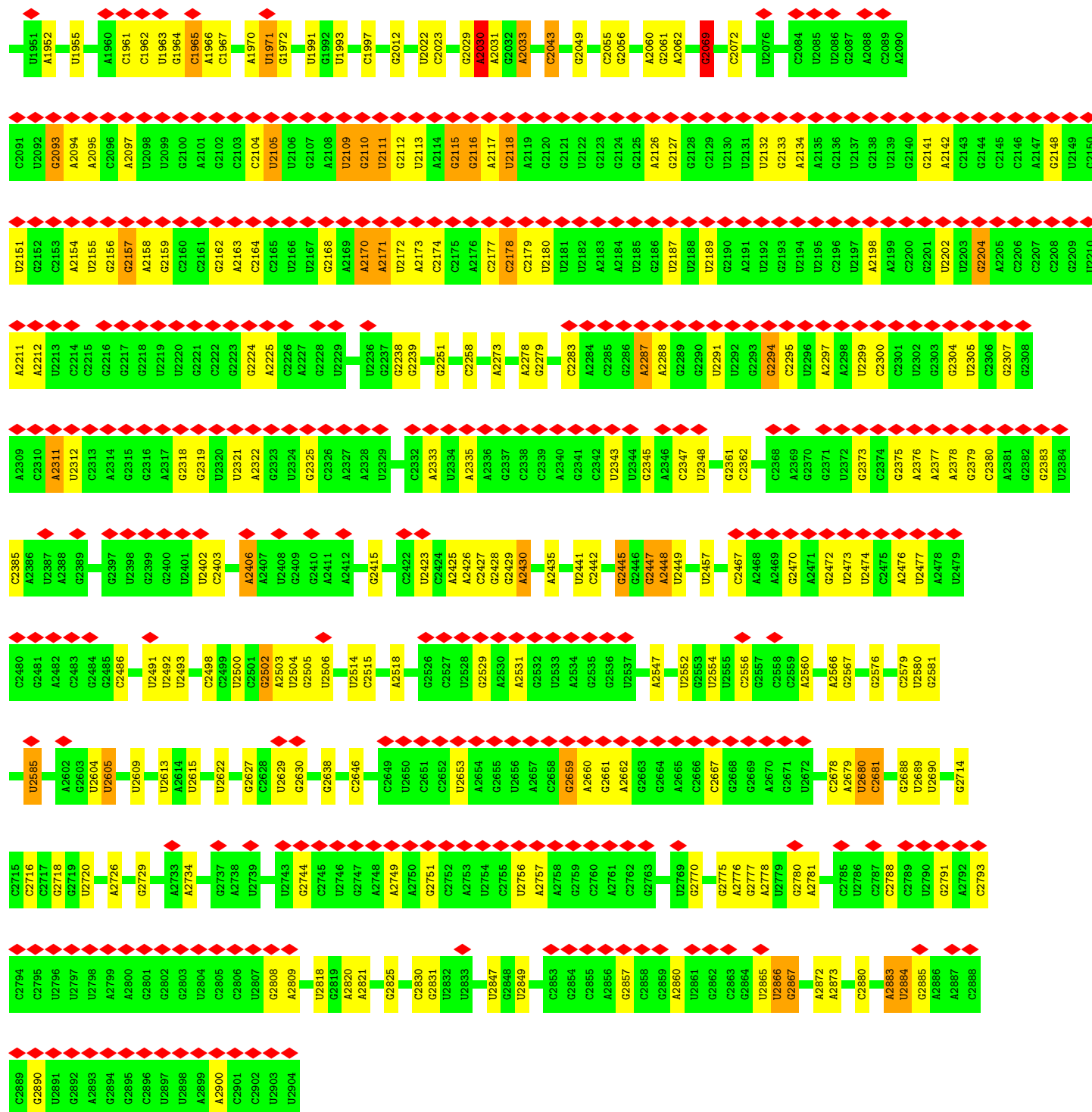
3 Residue-property plots

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.

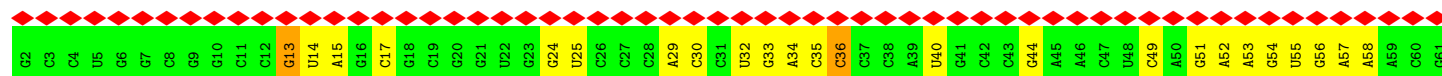
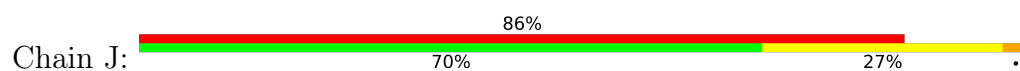
• Molecule 1: 23S rRNA

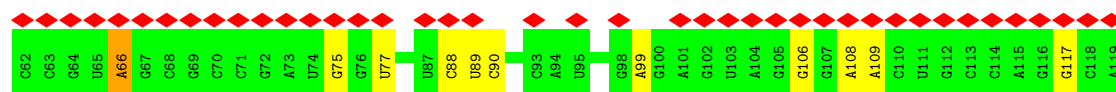




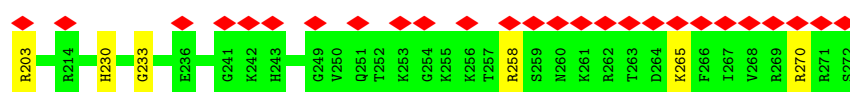
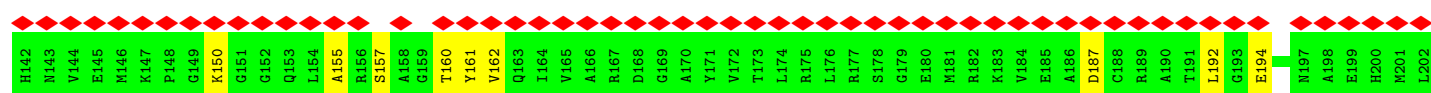
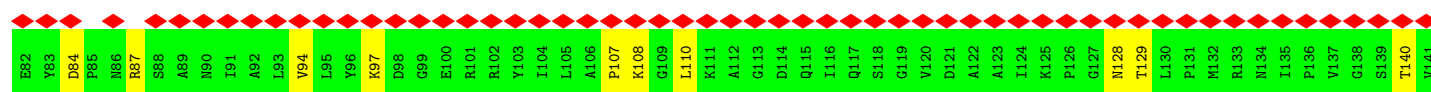
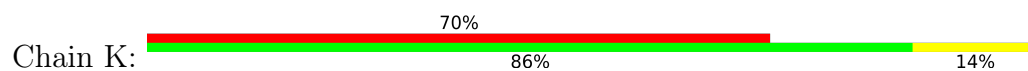


• Molecule 2: 5S rRNA

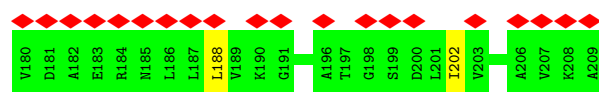
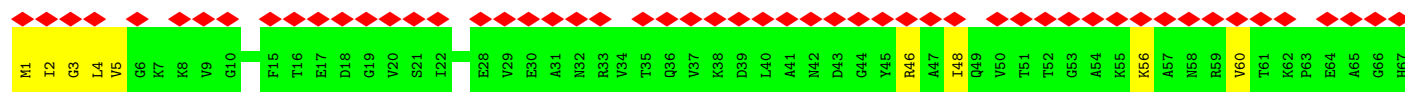
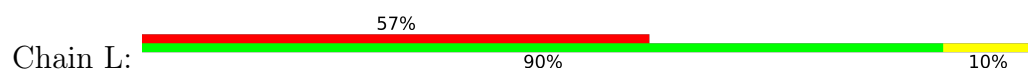




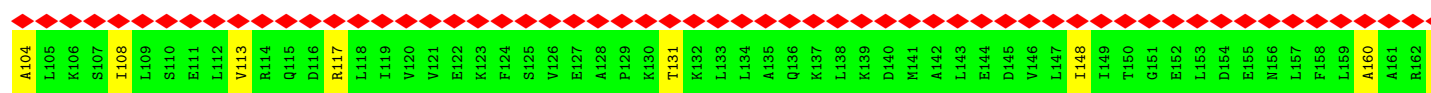
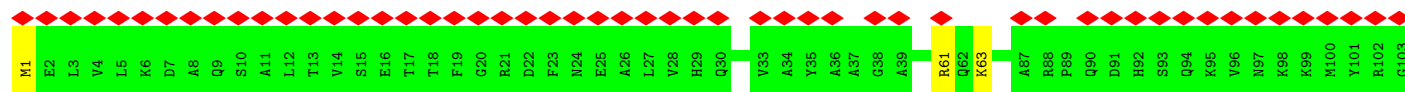
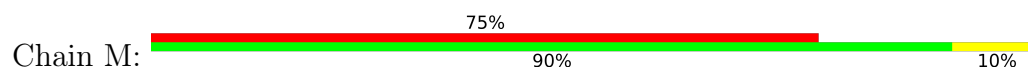
• Molecule 3: Large ribosomal subunit protein uL2

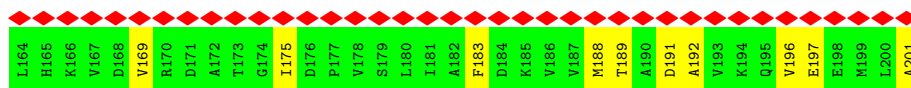


• Molecule 4: Large ribosomal subunit protein uL3

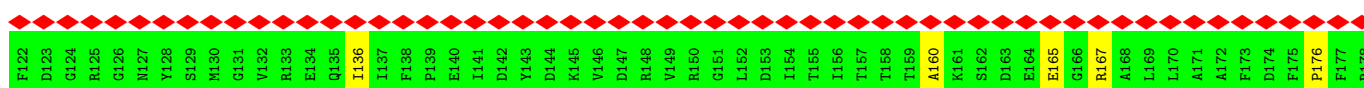
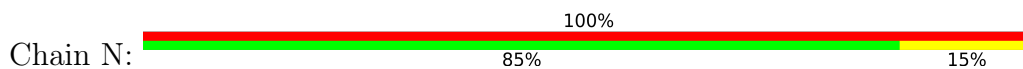


• Molecule 5: 50S ribosomal protein L4

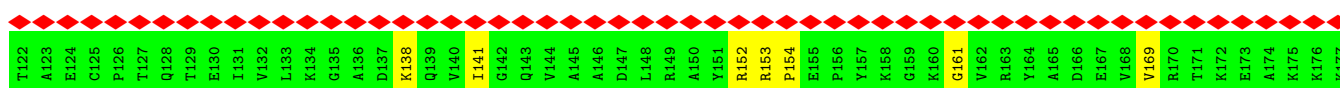
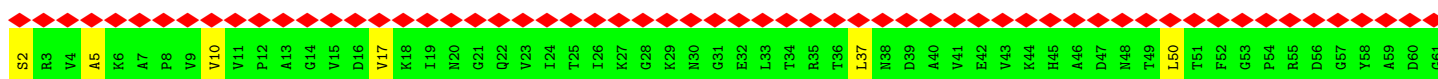
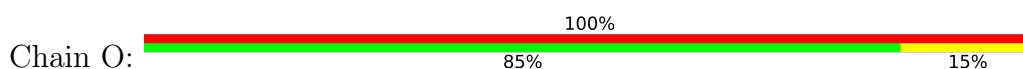




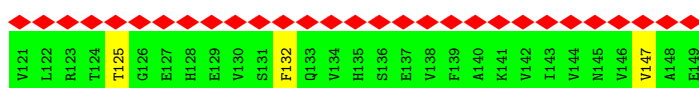
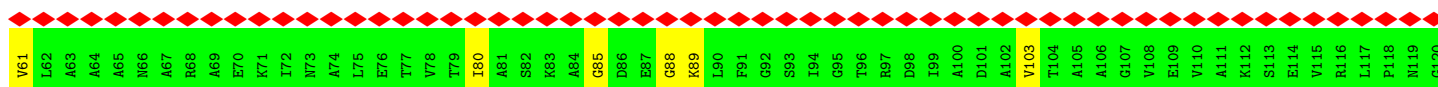
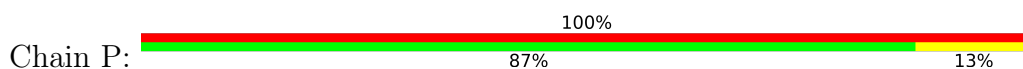
• Molecule 6: 50S ribosomal protein L5



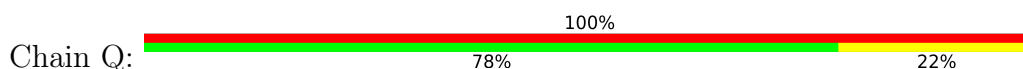
• Molecule 7: Large ribosomal subunit protein uL6

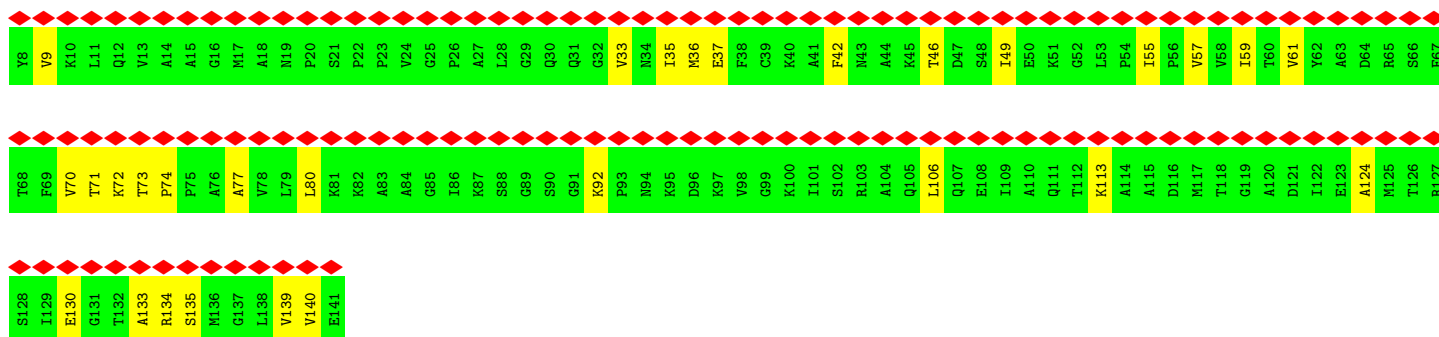


• Molecule 8: 50S ribosomal protein L9

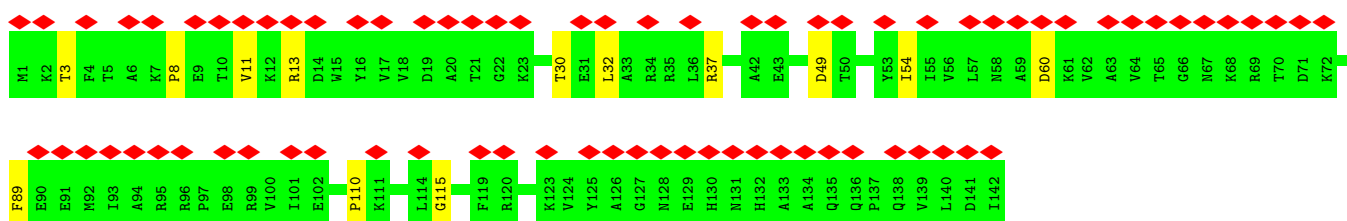
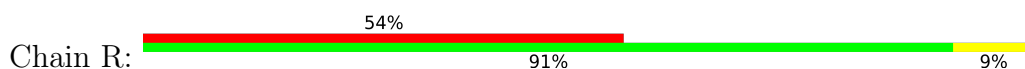


• Molecule 9: 50S ribosomal protein L11

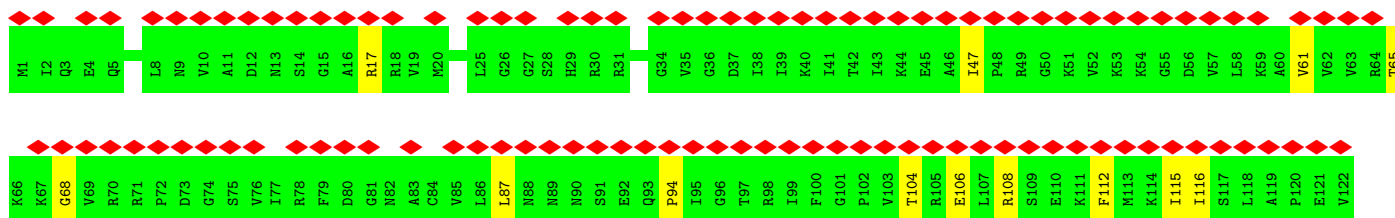
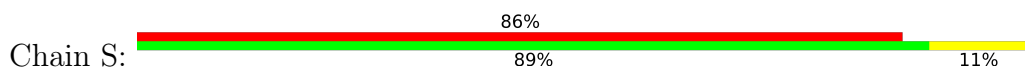




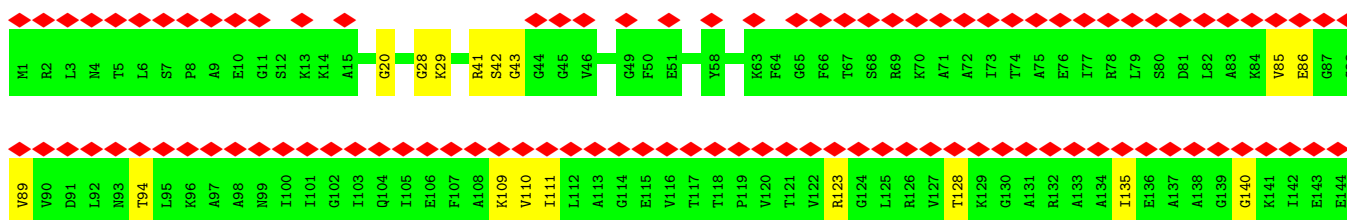
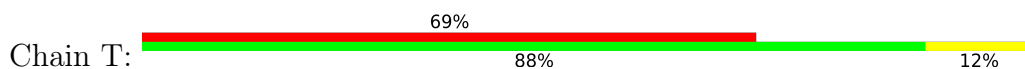
• Molecule 10: 50S ribosomal protein L13



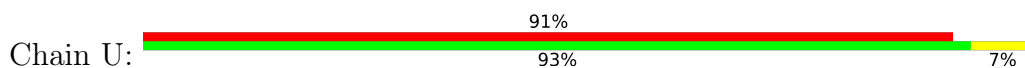
• Molecule 11: Large ribosomal subunit protein uL14



• Molecule 12: 50S ribosomal protein L15

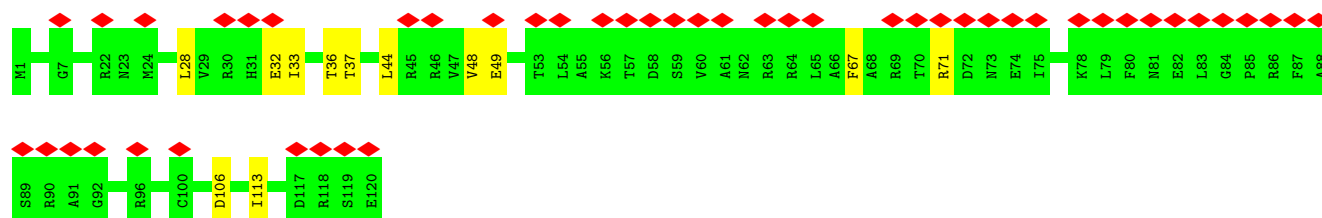
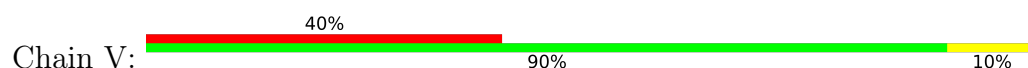


• Molecule 13: Large ribosomal subunit protein uL16

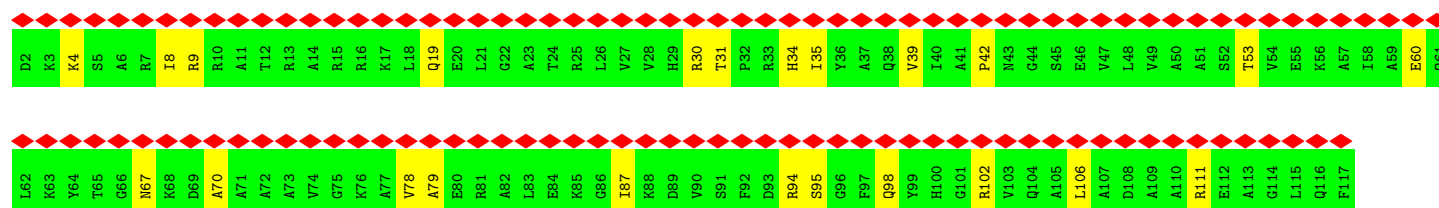
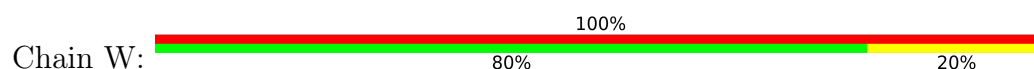




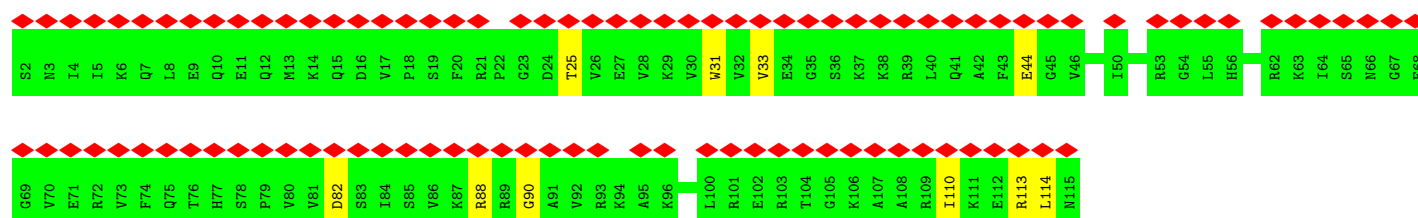
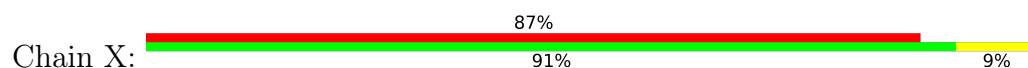
• Molecule 14: Large ribosomal subunit protein bL17



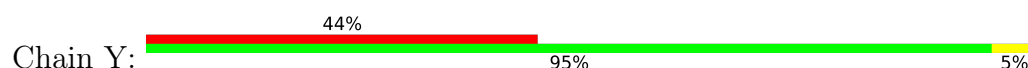
• Molecule 15: 50S ribosomal protein L18

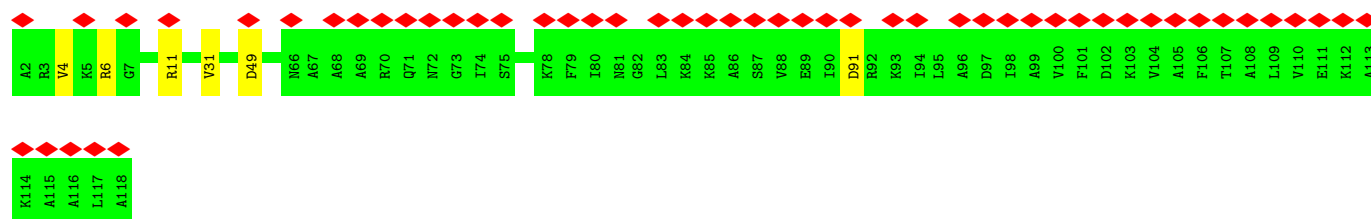


• Molecule 16: 50S ribosomal protein L19

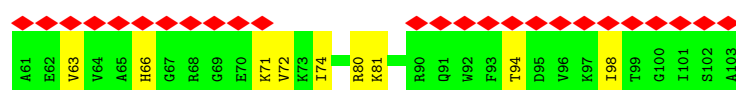
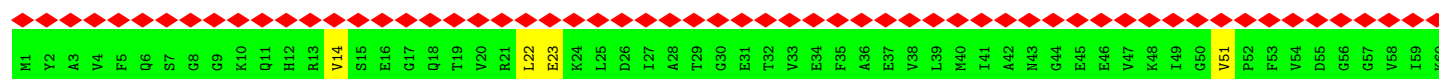
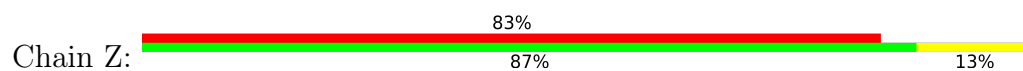


• Molecule 17: 50S ribosomal protein L20

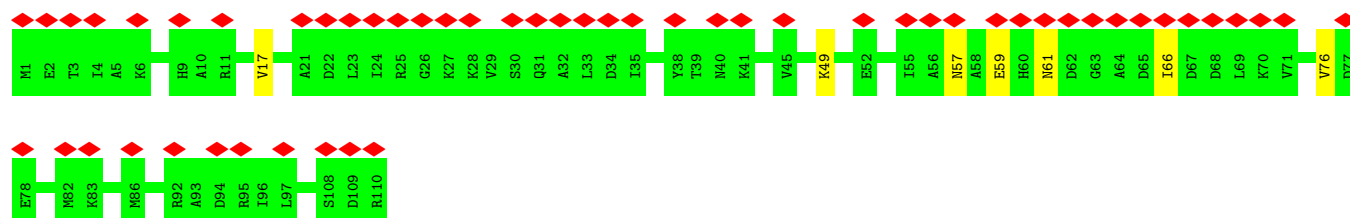
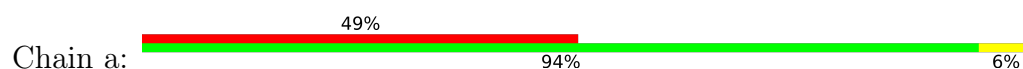




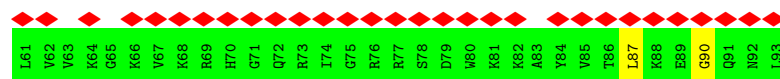
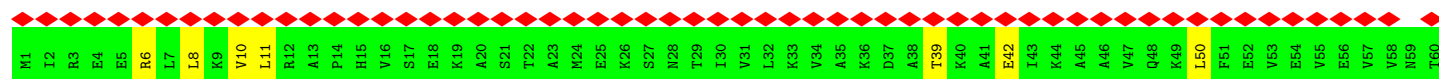
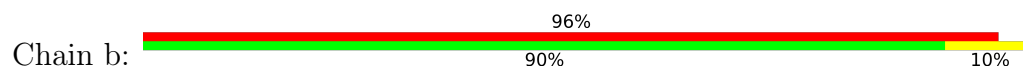
- Molecule 18: 50S ribosomal protein L21



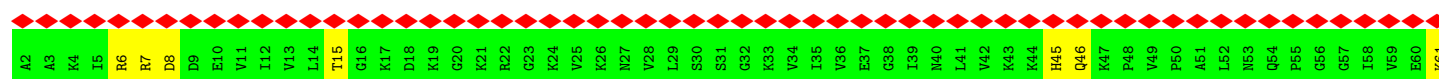
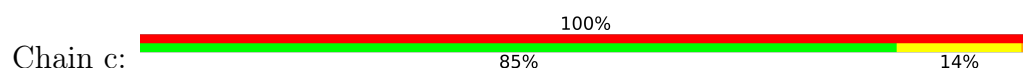
- Molecule 19: 50S ribosomal protein L22



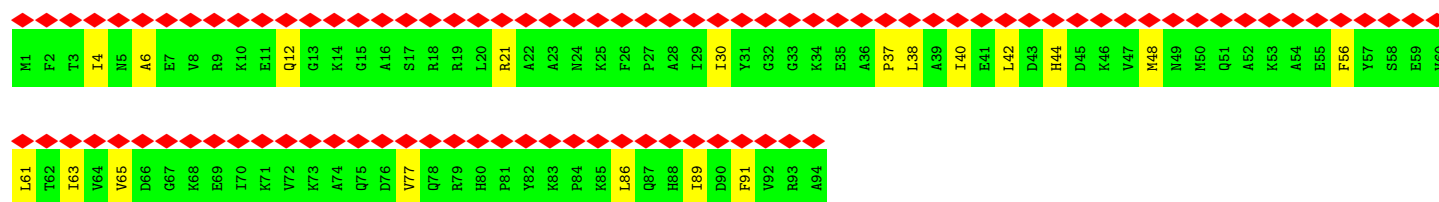
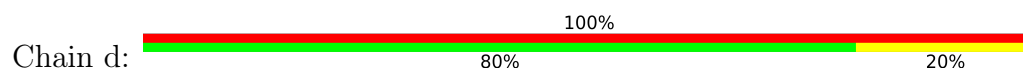
- Molecule 20: 50S ribosomal protein L23



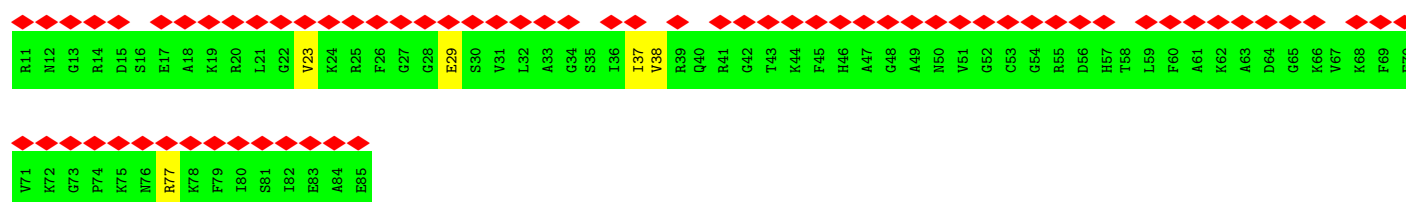
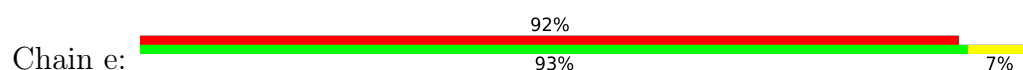
- Molecule 21: Large ribosomal subunit protein uL24



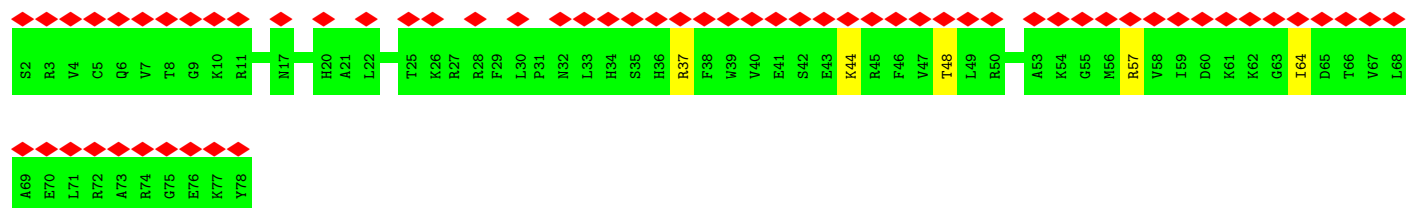
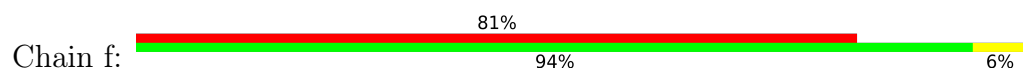
- Molecule 22: 50S ribosomal protein L25



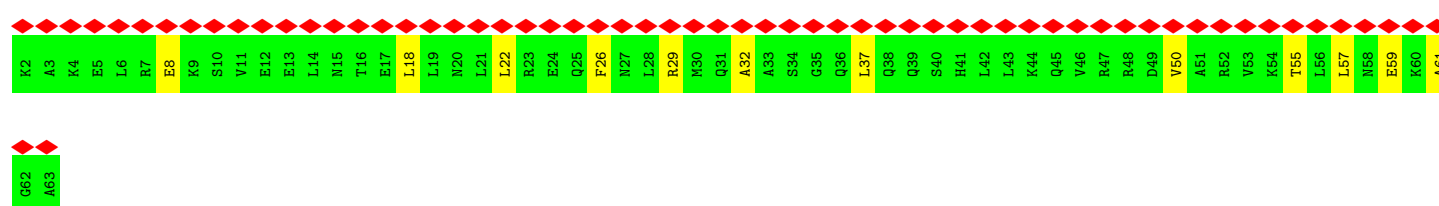
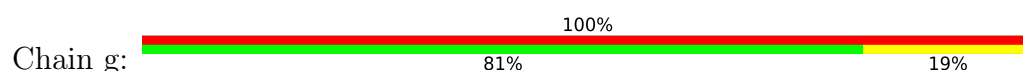
- Molecule 23: 50S ribosomal protein L27



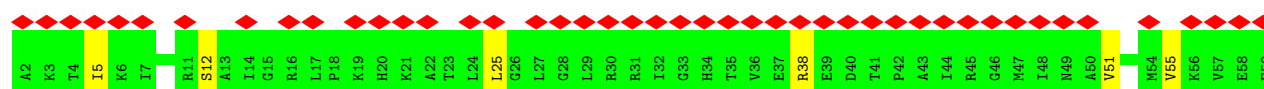
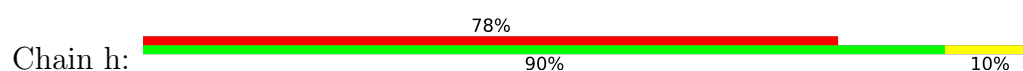
- Molecule 24: 50S ribosomal protein L28



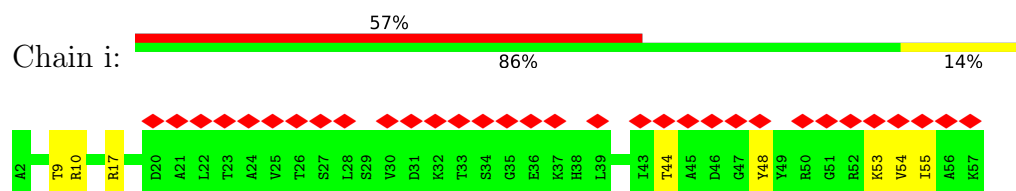
- Molecule 25: 50S ribosomal protein L29



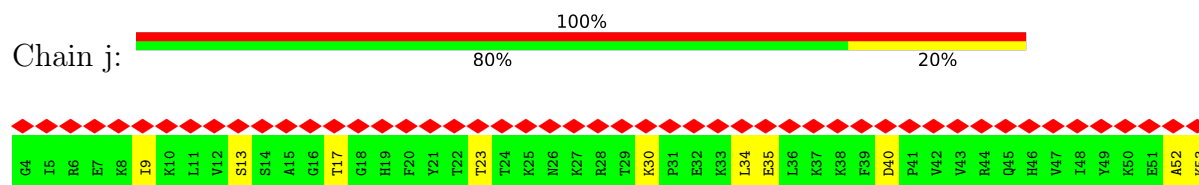
- Molecule 26: 50S ribosomal protein L30



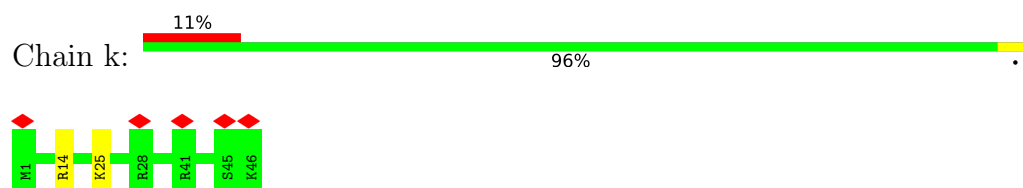
• Molecule 27: Large ribosomal subunit protein bL32



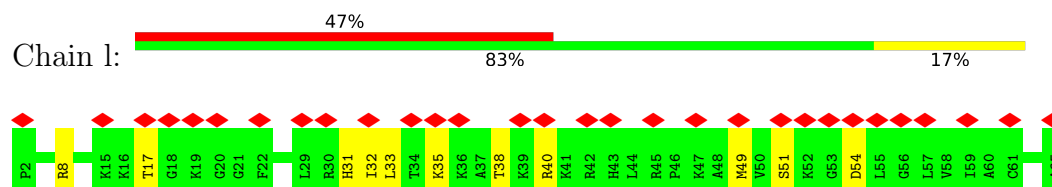
• Molecule 28: 50S ribosomal protein L33



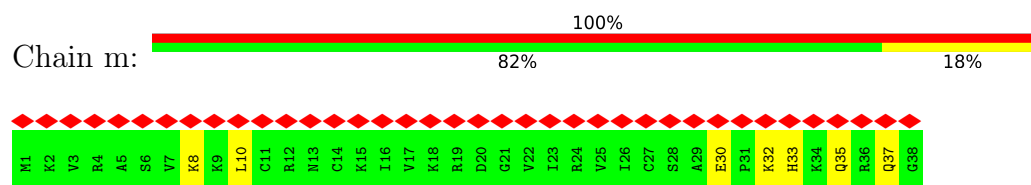
• Molecule 29: 50S ribosomal protein L34



• Molecule 30: 50S ribosomal protein L35



• Molecule 31: 50S ribosomal protein L36



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	48610	Depositor
Resolution determination method	FSC 0.33 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.017	Depositor
Minimum map value	-0.019	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.005	Depositor
Map size (\AA)	364.5, 364.5, 364.5	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.729, 0.729, 0.729	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: G7M, OMC, 2MG, H2U, NA, 4D4, ZN, 3TD, MG, 2MA, 5MU, OMU, 6MZ, OMG, 1MG, 5MC, PSU

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	I	0.12	0/69121	0.20	0/107828
2	J	0.09	0/2828	0.17	0/4410
3	K	0.10	0/2122	0.27	0/2852
4	L	0.12	0/1586	0.29	0/2134
5	M	0.10	0/1571	0.23	0/2113
6	N	0.09	0/1435	0.23	0/1926
7	O	0.09	0/1343	0.25	0/1816
8	P	0.08	0/1121	0.23	0/1515
9	Q	0.11	0/993	0.30	0/1341
10	R	0.10	0/1152	0.23	0/1551
11	S	0.09	0/947	0.26	0/1268
12	T	0.10	0/1062	0.25	0/1413
13	U	0.13	0/1081	0.26	0/1443
14	V	0.10	0/973	0.25	0/1301
15	W	0.08	0/902	0.24	0/1209
16	X	0.08	0/929	0.22	0/1242
17	Y	0.12	0/960	0.24	0/1278
18	Z	0.11	0/829	0.24	0/1107
19	a	0.11	0/864	0.26	0/1156
20	b	0.08	0/745	0.22	0/994
21	c	0.08	0/788	0.26	0/1051
22	d	0.10	0/766	0.24	0/1025
23	e	0.12	0/582	0.25	0/769
24	f	0.10	0/635	0.23	0/848
25	g	0.08	0/502	0.22	0/667
26	h	0.09	0/453	0.23	0/605
27	i	0.11	0/450	0.25	0/599
28	j	0.11	0/416	0.31	0/554
29	k	0.12	0/380	0.25	0/498
30	l	0.11	0/513	0.24	0/676
31	m	0.10	0/303	0.28	0/397

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.12	0/98352	0.21	0/147586

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	I	62229	31235	31316	290	0
2	J	2529	1281	1281	14	0
3	K	2083	2152	2154	25	0
4	L	1565	1617	1616	13	0
5	M	1552	1618	1618	13	0
6	N	1411	1444	1444	16	0
7	O	1323	1371	1371	15	0
8	P	1110	1148	1148	14	0
9	Q	979	1028	1028	20	0
10	R	1129	1162	1162	9	0
11	S	938	1012	1012	8	0
12	T	1053	1129	1129	14	0
13	U	1075	1147	1154	8	0
14	V	960	1000	1000	8	0
15	W	892	923	923	18	0
16	X	917	962	962	6	0
17	Y	947	1020	1019	6	0
18	Z	816	839	839	11	0
19	a	857	922	922	4	0
20	b	739	807	807	6	0
21	c	780	831	831	13	0
22	d	753	780	780	13	0
23	e	575	592	592	4	0
24	f	625	652	652	4	0
25	g	501	531	531	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	h	449	488	488	4	0
27	i	444	458	458	5	0
28	j	409	439	440	7	0
29	k	377	418	418	2	0
30	l	504	572	572	7	0
31	m	302	340	340	6	0
32	I	161	0	0	0	0
32	J	1	0	0	0	0
32	K	2	0	0	0	0
32	L	1	0	0	0	0
32	k	1	0	0	0	0
33	K	1	0	0	0	0
34	m	1	0	0	0	0
35	I	27	0	0	1	0
All	All	91018	59918	60007	525	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 4.

The worst 5 of 525 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:I:1939:5MU:C4	1:I:1939:5MU:C5	1.79	1.70
1:I:747:5MU:C5	1:I:747:5MU:C4	1.79	1.62
1:I:2069:G7M:N2	1:I:2442:C:O2	2.06	0.88
1:I:1582:C:O2'	1:I:1585:C:N4	2.14	0.80
1:I:2134:A:N6	1:I:2157:G:O2'	2.15	0.80

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	K	269/271 (99%)	262 (97%)	7 (3%)	0	100	100
4	L	207/209 (99%)	200 (97%)	7 (3%)	0	100	100
5	M	199/201 (99%)	197 (99%)	2 (1%)	0	100	100
6	N	175/177 (99%)	170 (97%)	5 (3%)	0	100	100
7	O	174/176 (99%)	165 (95%)	9 (5%)	0	100	100
8	P	147/149 (99%)	144 (98%)	3 (2%)	0	100	100
9	Q	132/134 (98%)	126 (96%)	6 (4%)	0	100	100
10	R	140/142 (99%)	138 (99%)	2 (1%)	0	100	100
11	S	120/122 (98%)	118 (98%)	2 (2%)	0	100	100
12	T	142/144 (99%)	140 (99%)	2 (1%)	0	100	100
13	U	133/136 (98%)	133 (100%)	0	0	100	100
14	V	118/120 (98%)	117 (99%)	1 (1%)	0	100	100
15	W	114/116 (98%)	114 (100%)	0	0	100	100
16	X	112/114 (98%)	111 (99%)	1 (1%)	0	100	100
17	Y	115/117 (98%)	114 (99%)	1 (1%)	0	100	100
18	Z	101/103 (98%)	100 (99%)	1 (1%)	0	100	100
19	a	108/110 (98%)	107 (99%)	1 (1%)	0	100	100
20	b	91/93 (98%)	88 (97%)	3 (3%)	0	100	100
21	c	100/102 (98%)	96 (96%)	3 (3%)	1 (1%)	12	42
22	d	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
23	e	73/75 (97%)	71 (97%)	2 (3%)	0	100	100
24	f	75/77 (97%)	71 (95%)	4 (5%)	0	100	100
25	g	60/62 (97%)	59 (98%)	1 (2%)	0	100	100
26	h	56/58 (97%)	56 (100%)	0	0	100	100
27	i	54/56 (96%)	54 (100%)	0	0	100	100
28	j	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
29	k	44/46 (96%)	44 (100%)	0	0	100	100
30	l	62/64 (97%)	61 (98%)	1 (2%)	0	100	100
31	m	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
All	All	3297/3356 (98%)	3227 (98%)	69 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
21	c	89	ASP

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	K	216/216 (100%)	216 (100%)	0	100	100
4	L	164/164 (100%)	164 (100%)	0	100	100
5	M	165/165 (100%)	165 (100%)	0	100	100
6	N	148/148 (100%)	148 (100%)	0	100	100
7	O	137/137 (100%)	137 (100%)	0	100	100
8	P	114/114 (100%)	114 (100%)	0	100	100
9	Q	104/104 (100%)	104 (100%)	0	100	100
10	R	116/116 (100%)	116 (100%)	0	100	100
11	S	103/103 (100%)	103 (100%)	0	100	100
12	T	103/103 (100%)	103 (100%)	0	100	100
13	U	108/108 (100%)	108 (100%)	0	100	100
14	V	100/100 (100%)	100 (100%)	0	100	100
15	W	86/86 (100%)	86 (100%)	0	100	100
16	X	99/99 (100%)	99 (100%)	0	100	100
17	Y	89/89 (100%)	89 (100%)	0	100	100
18	Z	84/84 (100%)	84 (100%)	0	100	100
19	a	93/93 (100%)	93 (100%)	0	100	100
20	b	80/80 (100%)	80 (100%)	0	100	100
21	c	83/83 (100%)	83 (100%)	0	100	100
22	d	78/78 (100%)	78 (100%)	0	100	100
23	e	57/57 (100%)	57 (100%)	0	100	100
24	f	67/67 (100%)	67 (100%)	0	100	100
25	g	54/54 (100%)	54 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
26	h	48/48 (100%)	48 (100%)	0	100	100
27	i	47/47 (100%)	47 (100%)	0	100	100
28	j	45/45 (100%)	45 (100%)	0	100	100
29	k	38/38 (100%)	38 (100%)	0	100	100
30	l	51/51 (100%)	51 (100%)	0	100	100
31	m	34/34 (100%)	34 (100%)	0	100	100
All	All	2711/2711 (100%)	2711 (100%)	0	100	100

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

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

Mol	Chain	Res	Type
15	W	29	HIS
26	h	20	HIS
16	X	66	ASN
25	g	15	ASN
16	X	56	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	I	2896/2904 (99%)	385 (13%)	17 (0%)
2	J	117/118 (99%)	14 (11%)	0
All	All	3013/3022 (99%)	399 (13%)	17 (0%)

5 of 399 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	I	2	G
1	I	10	A
1	I	14	A
1	I	15	G
1	I	34	U

5 of 17 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	I	2447	G
1	I	2866	U
1	I	1358	G
1	I	1543	G
1	I	1730	C

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

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

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	1MG	I	745	1	23,26,27	2.92	8 (34%)	33,39,42	2.73	8 (24%)
1	OMC	I	2498	32,1	19,22,23	3.21	8 (42%)	25,31,34	0.72	0
1	PSU	I	746	1	18,21,22	4.29	6 (33%)	21,30,33	1.79	5 (23%)
13	4D4	U	81	13	9,11,12	2.56	2 (22%)	7,13,15	0.80	0
1	2MA	I	2503	32,1	22,25,26	3.80	8 (36%)	32,37,40	2.34	8 (25%)
1	PSU	I	955	1	18,21,22	4.24	6 (33%)	21,30,33	2.04	6 (28%)
1	2MG	I	2445	1	23,26,27	2.86	8 (34%)	33,38,41	2.32	12 (36%)
1	OMU	I	2552	1	19,22,23	3.28	8 (42%)	25,31,34	1.85	5 (20%)
1	5MC	I	1962	1	19,22,23	4.05	9 (47%)	26,32,35	1.02	1 (3%)
1	PSU	I	1917	1	18,21,22	0.94	1 (5%)	21,30,33	0.58	0
1	OMG	I	2251	1	23,26,27	2.99	8 (34%)	32,38,41	2.17	10 (31%)
1	PSU	I	1911	1	18,21,22	4.35	6 (33%)	21,30,33	2.04	6 (28%)
1	PSU	I	2604	1	18,21,22	4.26	7 (38%)	21,30,33	2.03	6 (28%)
1	PSU	I	2605	1	18,21,22	4.26	7 (38%)	21,30,33	2.01	6 (28%)
1	6MZ	I	1618	1	22,25,26	3.21	4 (18%)	29,36,39	2.30	11 (37%)
1	5MU	I	1939	1	19,22,23	7.34	8 (42%)	27,32,35	3.39	10 (37%)
1	PSU	I	2457	1	18,21,22	4.21	6 (33%)	21,30,33	2.07	6 (28%)
1	2MG	I	1835	1	23,26,27	2.95	7 (30%)	33,38,41	2.28	12 (36%)
1	H2U	I	2449	1	18,21,22	3.08	5 (27%)	19,30,33	1.48	4 (21%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	6MZ	I	2030	1	22,25,26	3.19	4 (18%)	29,36,39	2.35	13 (44%)
1	5MU	I	747	1	19,22,23	7.31	8 (42%)	27,32,35	3.47	10 (37%)
1	G7M	I	2069	1	23,26,27	2.96	8 (34%)	34,39,42	2.75	10 (29%)
1	PSU	I	2504	32,1	18,21,22	4.28	6 (33%)	21,30,33	2.03	5 (23%)
1	PSU	I	2580	1	18,21,22	4.23	7 (38%)	21,30,33	2.08	6 (28%)
1	3TD	I	1915	1	19,22,23	4.29	7 (36%)	23,32,35	1.65	2 (8%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	1MG	I	745	1	-	0/7/25/26	0/3/3/3
1	OMC	I	2498	32,1	-	0/9/27/28	0/2/2/2
1	PSU	I	746	1	-	0/7/25/26	0/2/2/2
13	4D4	U	81	13	-	2/11/12/14	-
1	2MA	I	2503	32,1	-	2/7/25/26	0/3/3/3
1	PSU	I	955	1	-	0/7/25/26	0/2/2/2
1	2MG	I	2445	1	-	2/9/27/28	0/3/3/3
1	OMU	I	2552	1	-	1/9/27/28	0/2/2/2
1	5MC	I	1962	1	-	0/7/25/26	0/2/2/2
1	PSU	I	1917	1	-	0/7/25/26	0/2/2/2
1	OMG	I	2251	1	-	0/9/27/28	0/3/3/3
1	PSU	I	1911	1	-	2/7/25/26	0/2/2/2
1	PSU	I	2604	1	-	0/7/25/26	0/2/2/2
1	PSU	I	2605	1	-	2/7/25/26	0/2/2/2
1	6MZ	I	1618	1	-	1/9/27/28	0/3/3/3
1	5MU	I	1939	1	-	0/7/25/26	0/2/2/2
1	PSU	I	2457	1	-	0/7/25/26	0/2/2/2
1	2MG	I	1835	1	-	0/9/27/28	0/3/3/3
1	H2U	I	2449	1	-	0/7/38/39	0/2/2/2
1	6MZ	I	2030	1	-	2/9/27/28	0/3/3/3
1	5MU	I	747	1	-	0/7/25/26	0/2/2/2
1	G7M	I	2069	1	-	2/7/25/26	0/3/3/3
1	PSU	I	2504	32,1	-	2/7/25/26	0/2/2/2
1	PSU	I	2580	1	-	0/7/25/26	0/2/2/2
1	3TD	I	1915	1	-	3/7/25/26	0/2/2/2

The worst 5 of 162 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	I	1939	5MU	C4-C5	21.49	1.79	1.44
1	I	747	5MU	C4-C5	21.46	1.79	1.44
1	I	1939	5MU	C6-N1	15.60	1.64	1.38
1	I	747	5MU	C6-N1	15.48	1.64	1.38
1	I	1618	6MZ	C6-N6	13.26	1.49	1.34

The worst 5 of 162 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	1939	5MU	C5-C4-N3	10.12	124.12	115.32
1	I	747	5MU	C5-C4-N3	10.10	124.10	115.32
1	I	745	1MG	C1'-N9-C8	-9.29	100.35	126.73
1	I	747	5MU	C5-C6-N1	-8.38	114.21	123.31
1	I	1939	5MU	C5-C6-N1	-8.23	114.37	123.31

There are no chirality outliers.

5 of 21 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	I	1915	3TD	O4'-C4'-C5'-O5'
1	I	1915	3TD	C3'-C4'-C5'-O5'
1	I	2030	6MZ	O4'-C4'-C5'-O5'
1	I	2030	6MZ	C3'-C4'-C5'-O5'
1	I	2445	2MG	C3'-C4'-C5'-O5'

There are no ring outliers.

7 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	I	745	1MG	1	0
1	I	1917	PSU	2	0
1	I	1911	PSU	1	0
1	I	1939	5MU	1	0
1	I	2030	6MZ	1	0
1	I	747	5MU	1	0
1	I	2069	G7M	1	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 168 ligands modelled in this entry, 168 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

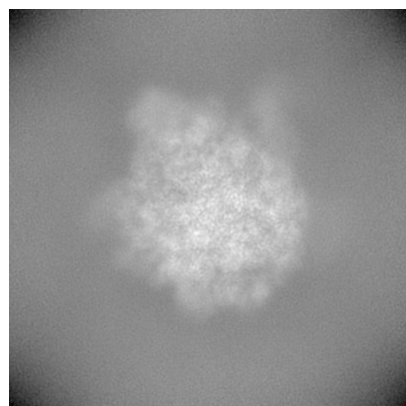
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-66639. These allow visual inspection of the internal detail of the map and identification of artifacts.

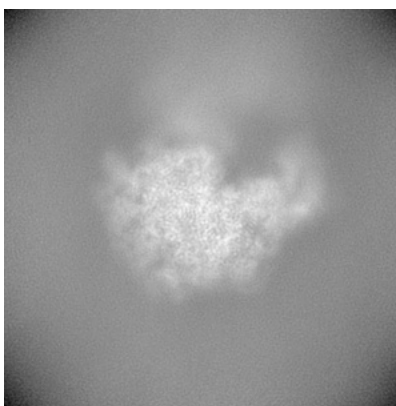
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

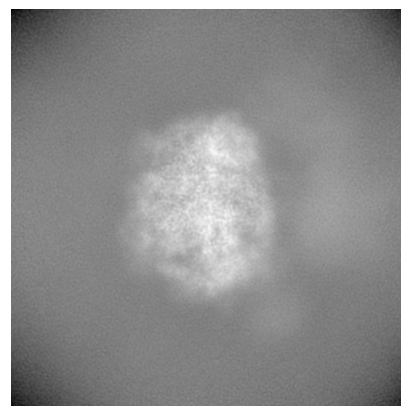
6.1.1 Primary map



X

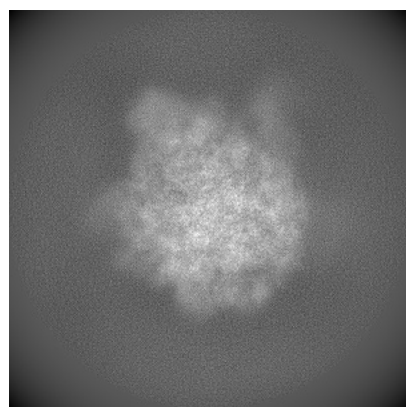


Y

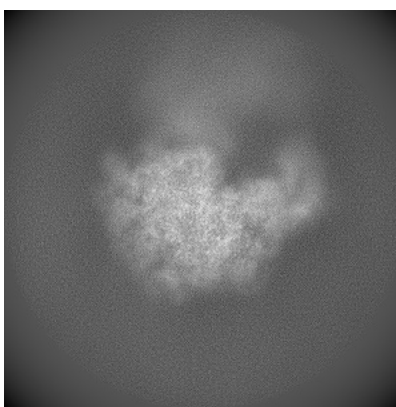


Z

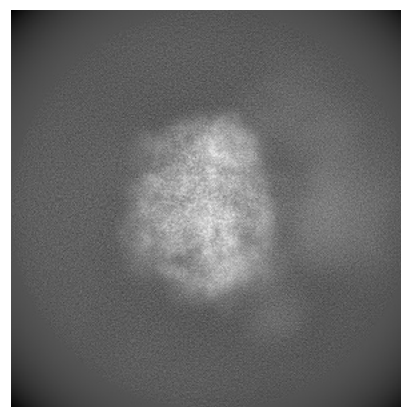
6.1.2 Raw map



X



Y

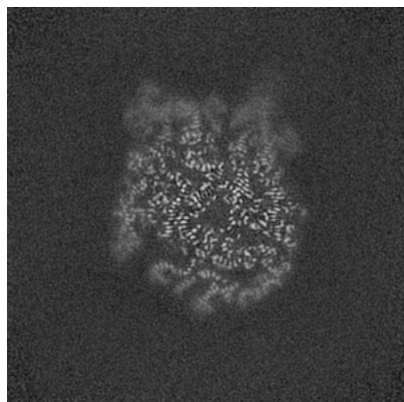


Z

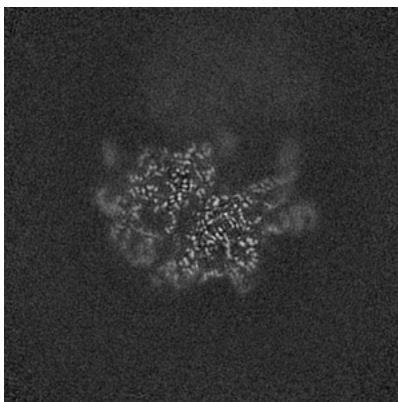
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

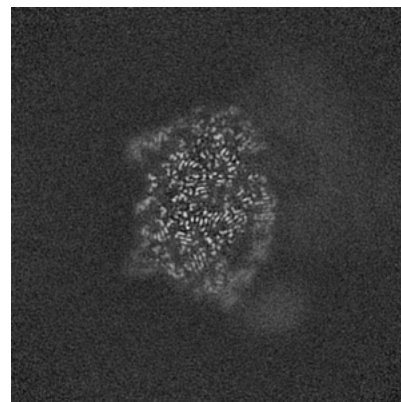
6.2.1 Primary map



X Index: 250

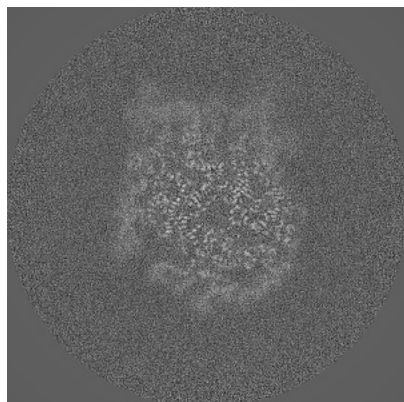


Y Index: 250

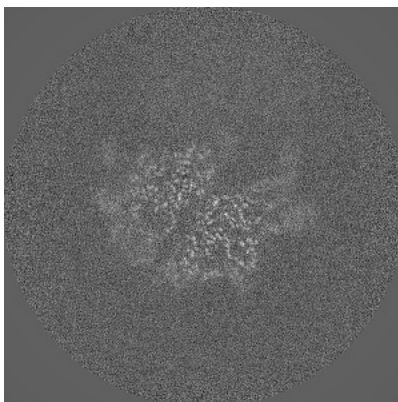


Z Index: 250

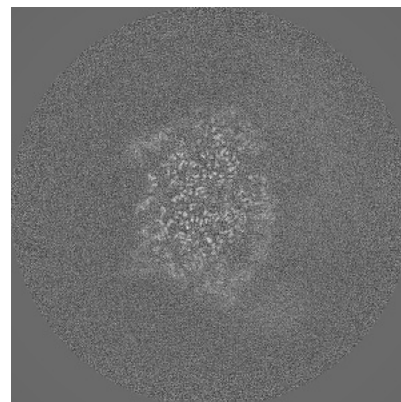
6.2.2 Raw map



X Index: 250



Y Index: 250

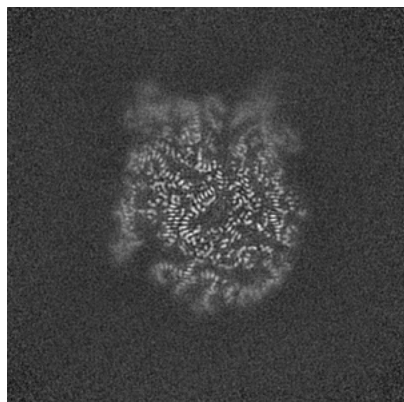


Z Index: 250

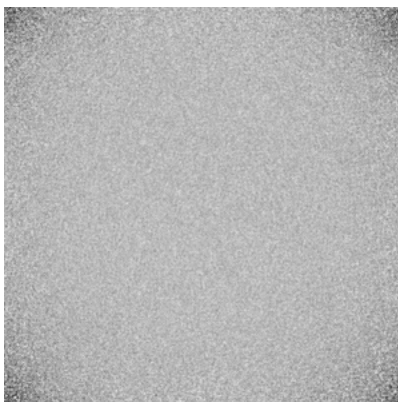
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

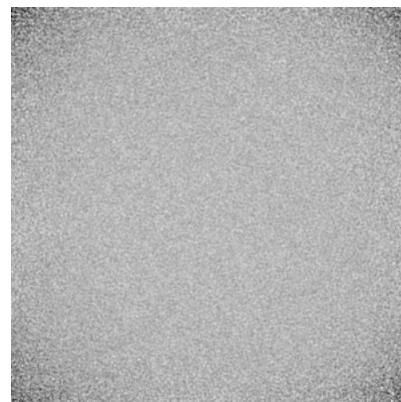
6.3.1 Primary map



X Index: 248

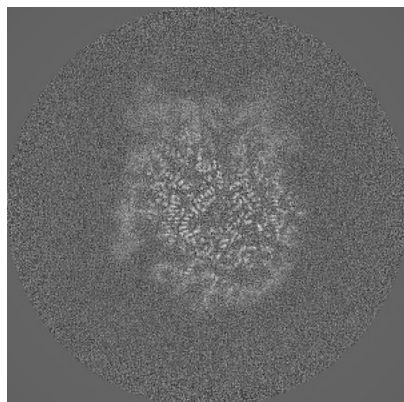


Y Index: 0

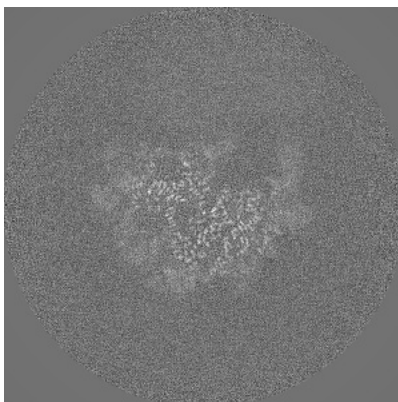


Z Index: 0

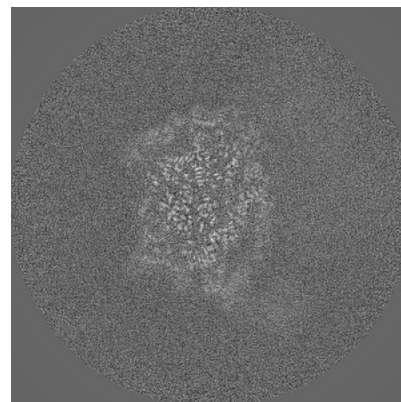
6.3.2 Raw map



X Index: 248



Y Index: 243

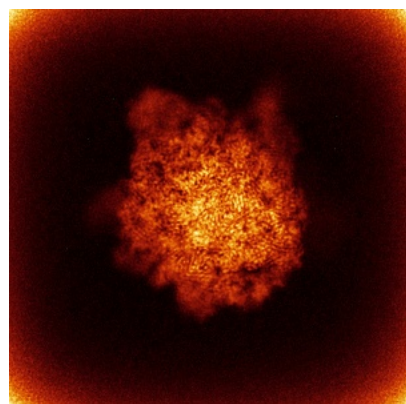


Z Index: 254

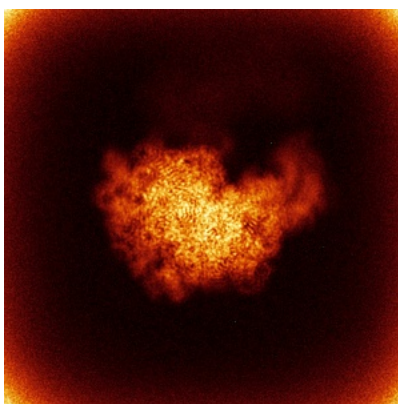
The images above show the largest variance slices of the map in three orthogonal directions.

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

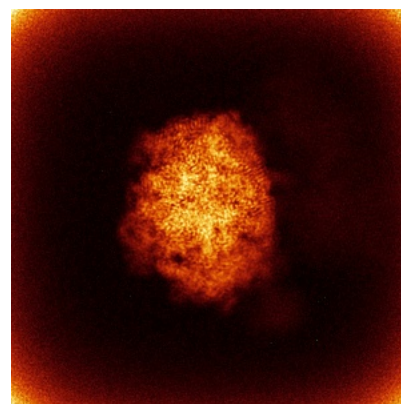
6.4.1 Primary map



X

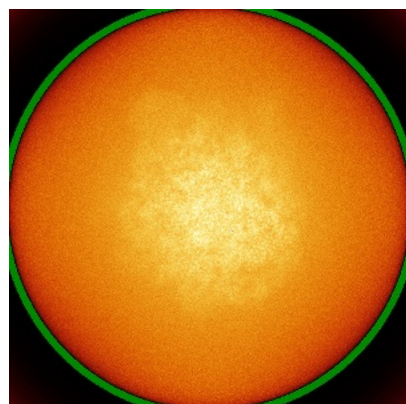


Y

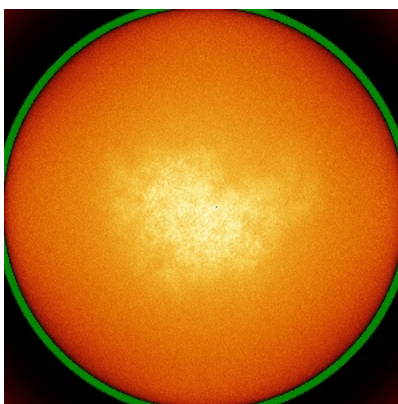


Z

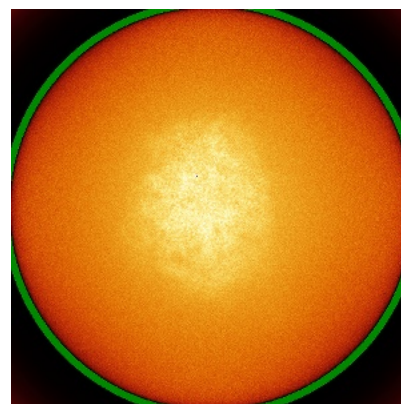
6.4.2 Raw map



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



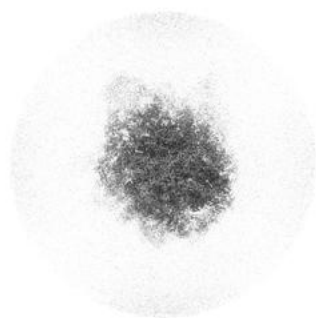
Y



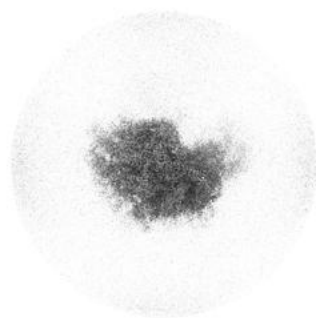
Z

The images above show the 3D surface view of the map at the recommended contour level 0.005. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

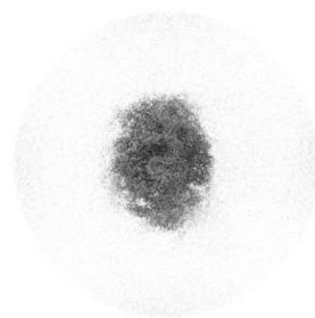
6.5.2 Raw map



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.

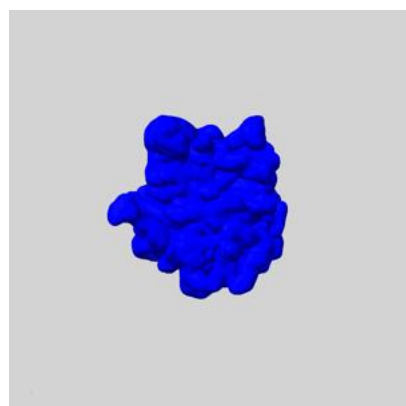
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

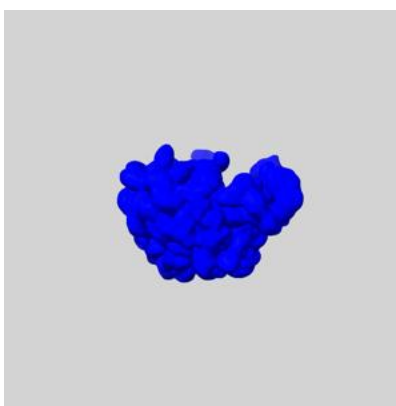
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

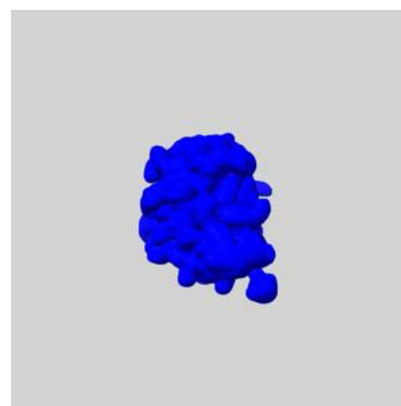
6.6.1 emd_66639_msk_1.map [i](#)



X



Y

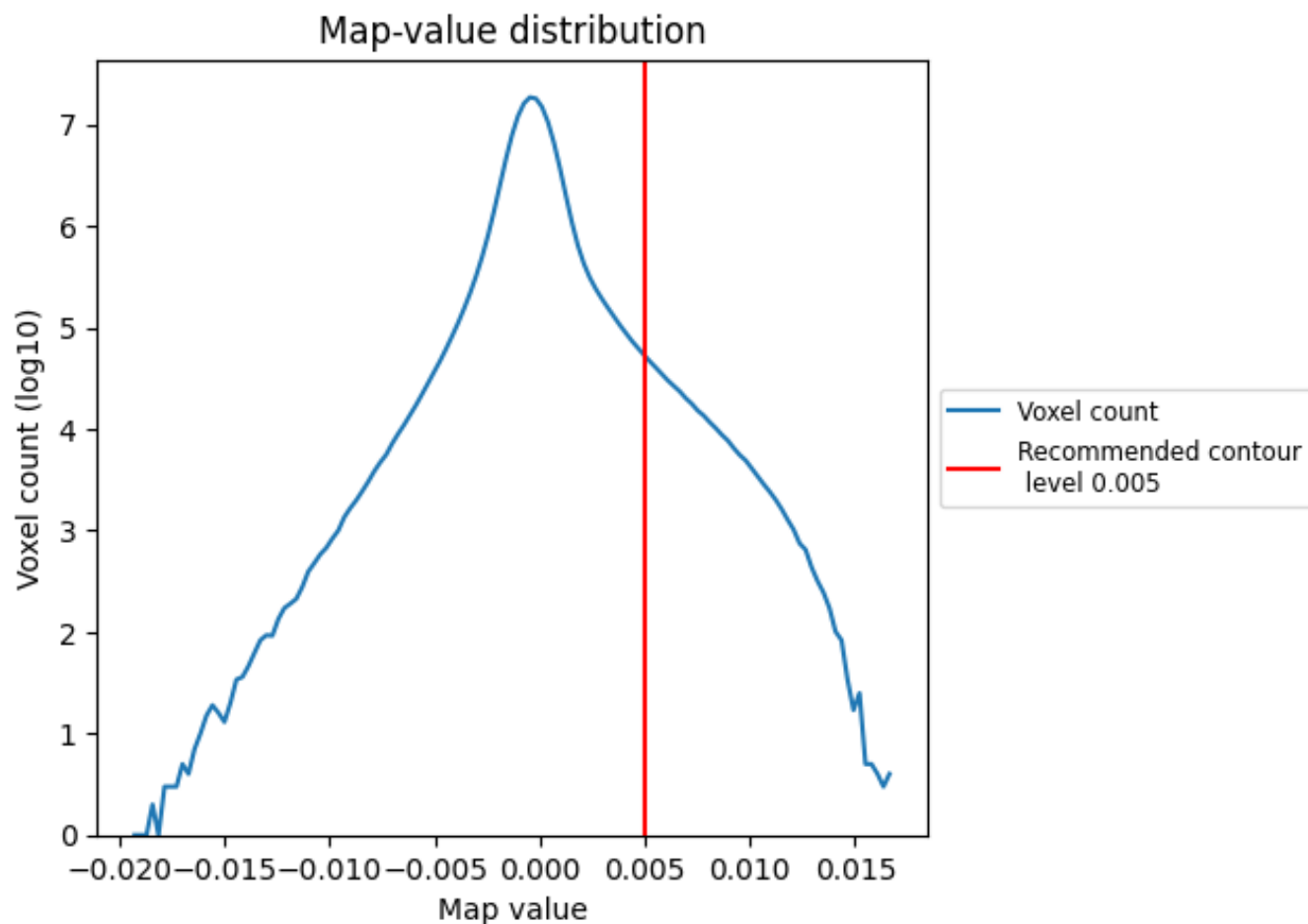


Z

7 Map analysis [i](#)

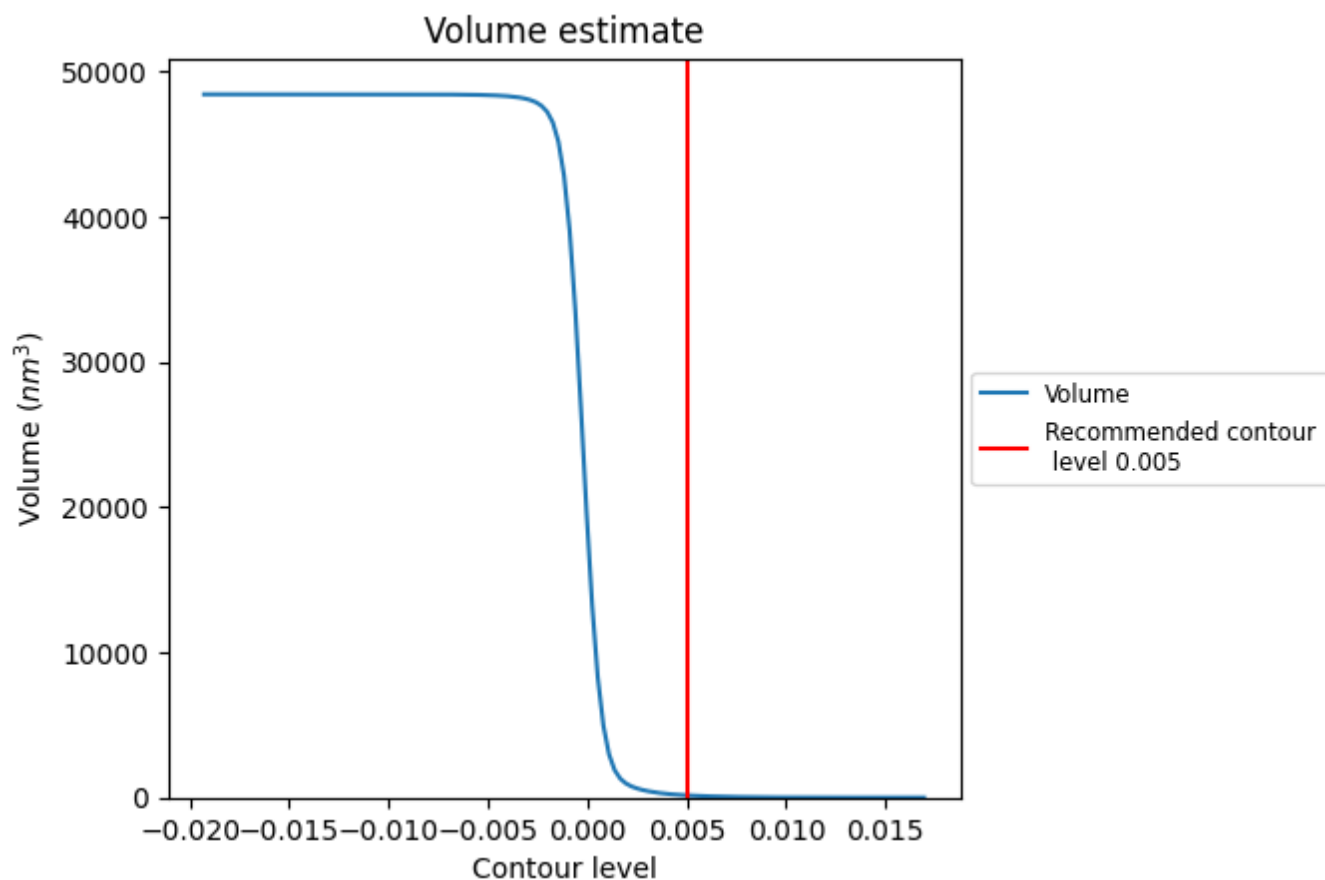
This section contains the results of statistical analysis of the map.

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.

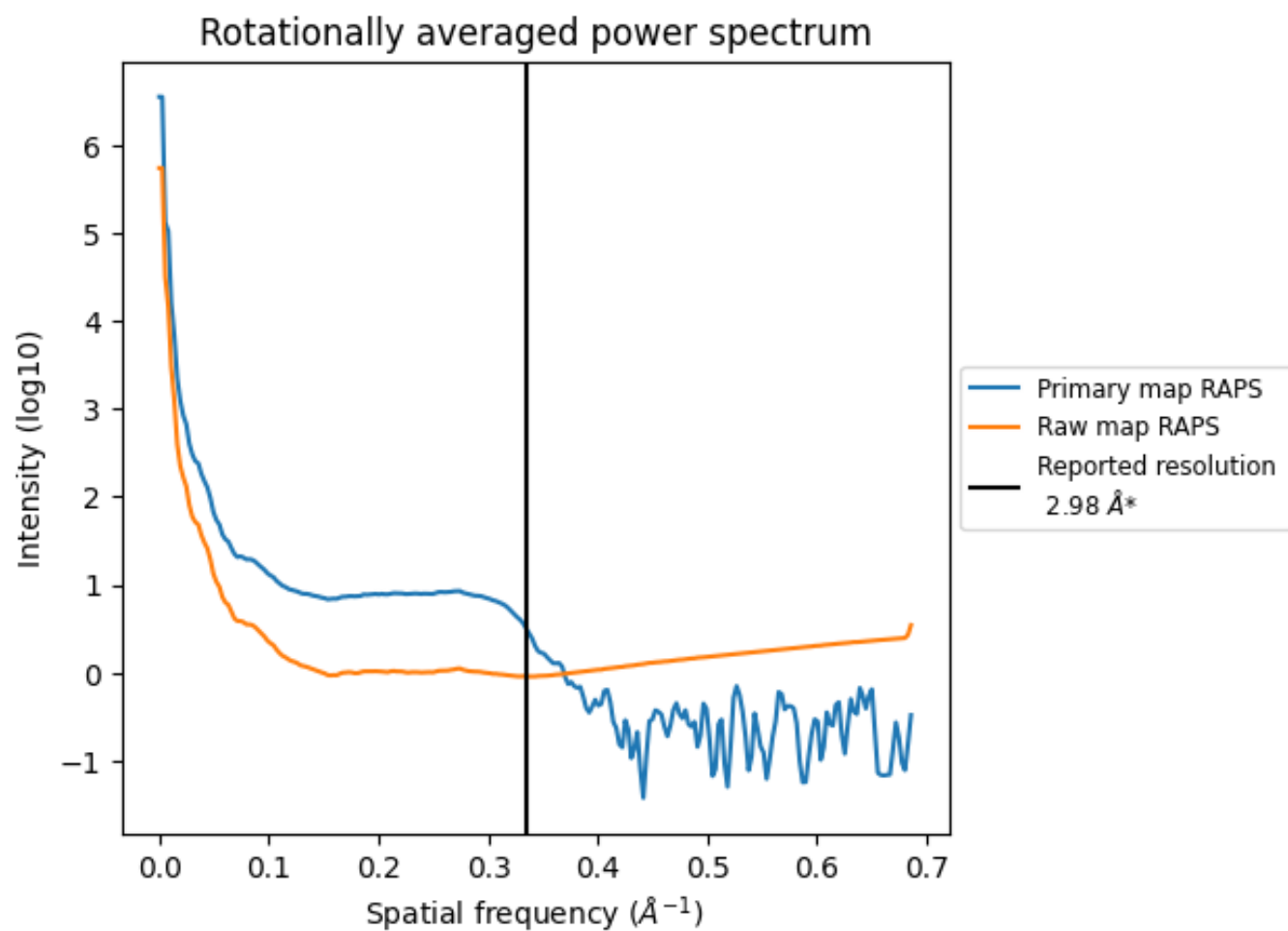
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 151 nm³; this corresponds to an approximate mass of 137 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 ⓘ

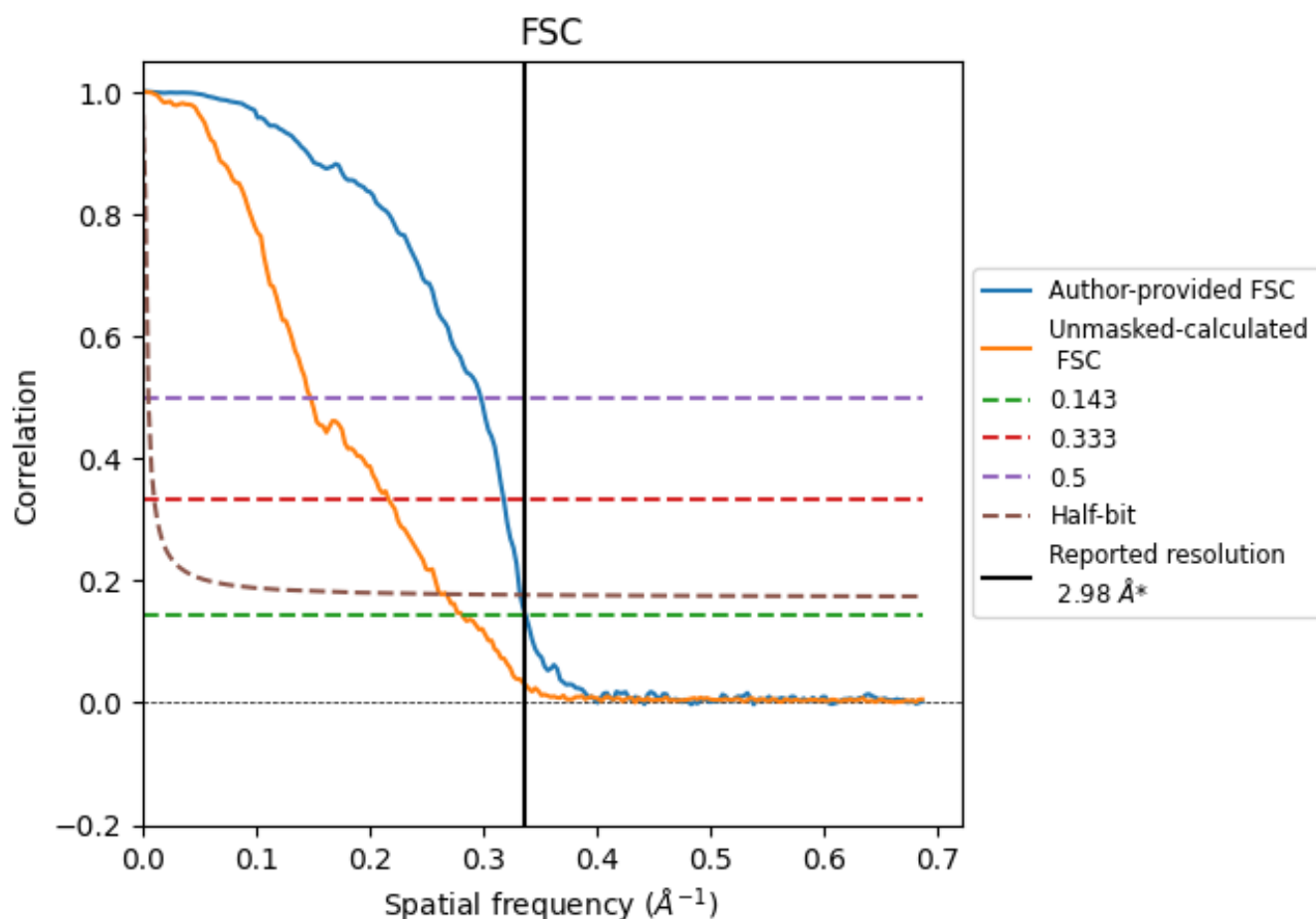


*Reported resolution corresponds to spatial frequency of 0.336 Å⁻¹

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 0.336 Å⁻¹

8.2 Resolution estimates [i](#)

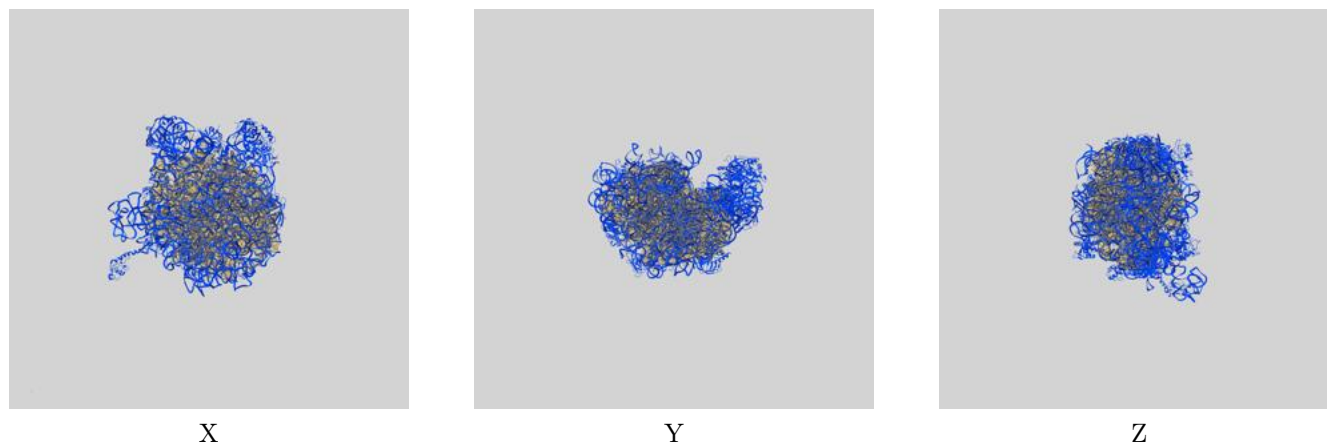
Resolution estimate (Å)	Estimation criterion (FSC cut-off)			
	0.143	0.5	Half-bit	0.333
Reported by author	-	-	-	2.98
Author-provided FSC curve	2.96	3.36	3.01	3.14
Unmasked-calculated*	3.55	6.76	3.81	4.62

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.33 CUT-OFF 4.62 differs from the reported value 2.98 by more than 10 %

9 Map-model fit [i](#)

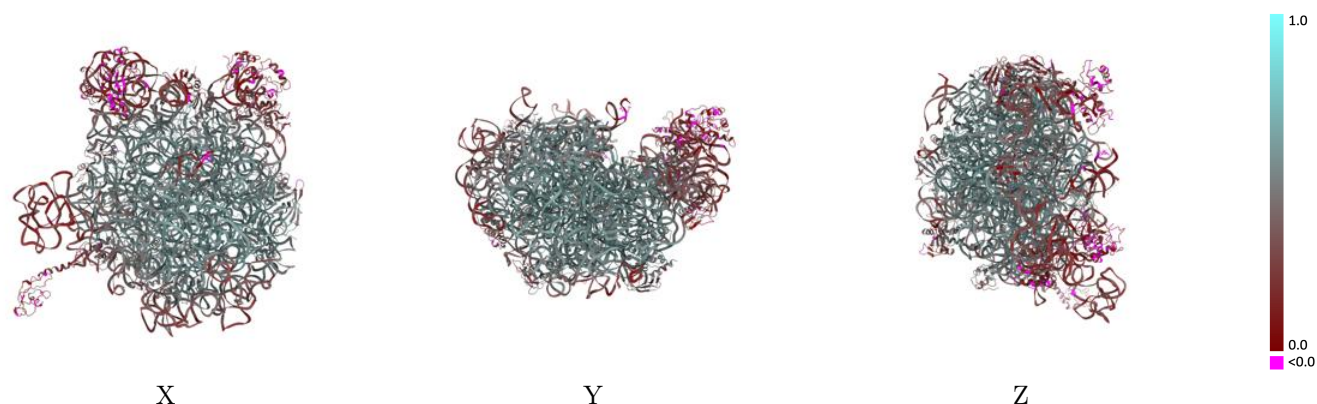
This section contains information regarding the fit between EMDB map EMD-66639 and PDB model 9XFK. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)



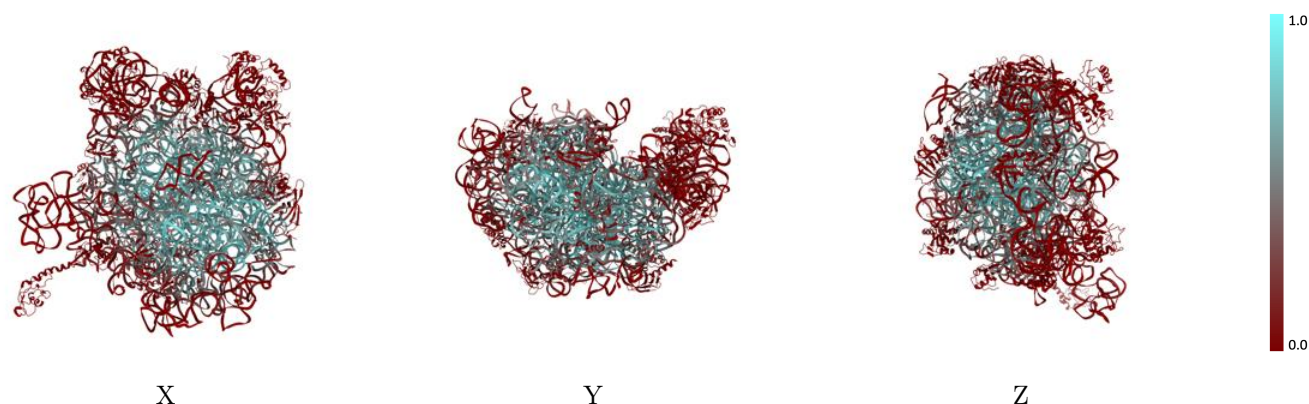
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



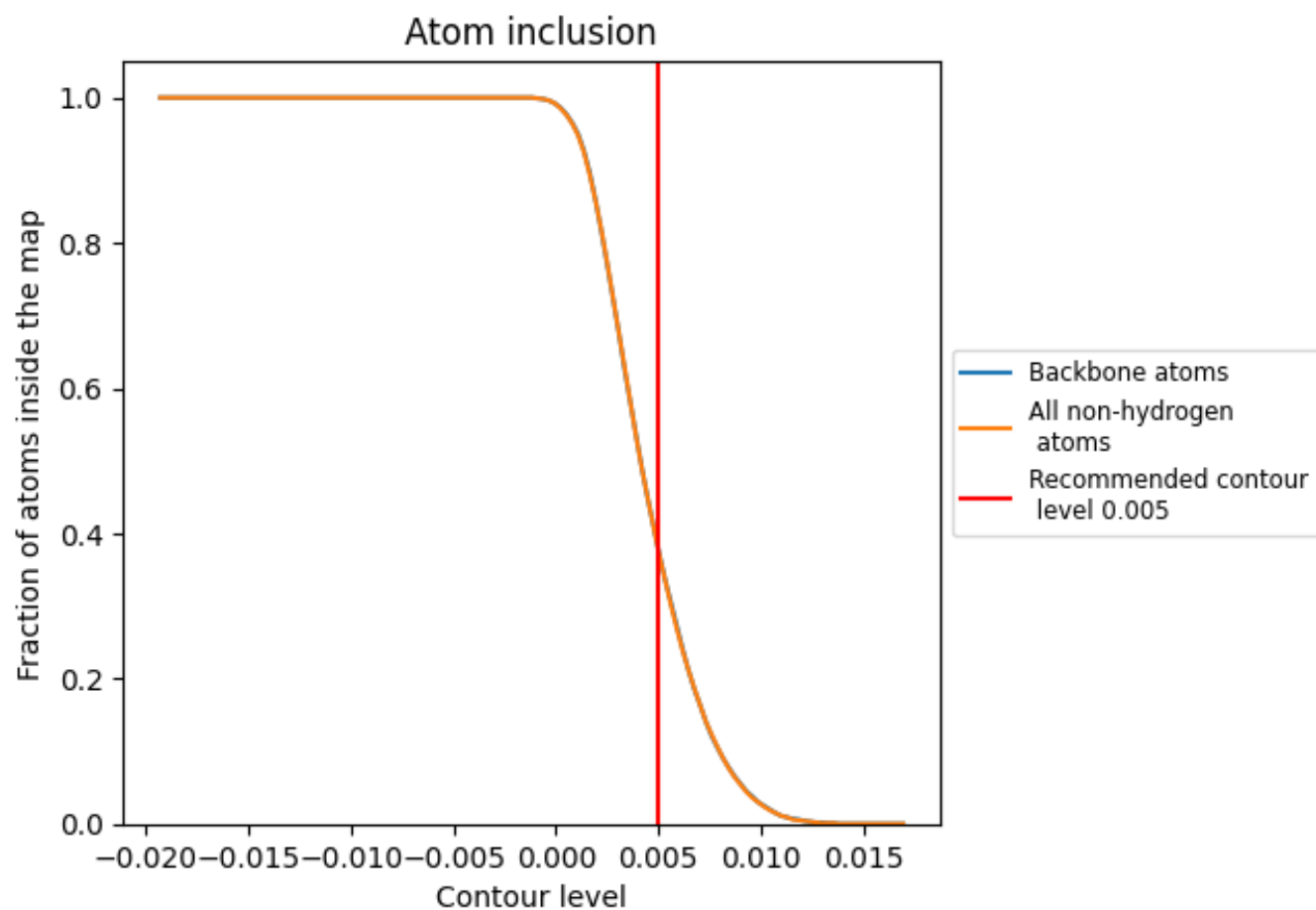
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.005).

































































9.4 Atom inclusion [i](#)



At the recommended contour level, 38% of all backbone atoms, 38% 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 (0.005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3770	 0.4770
I	 0.4700	 0.5060
J	 0.1170	 0.3080
K	 0.2470	 0.5240
L	 0.3380	 0.5490
M	 0.1900	 0.4340
N	 0.0000	 0.1250
O	 0.0000	 0.2470
P	 0.0000	 0.1850
Q	 0.0000	 0.1430
R	 0.3660	 0.5570
S	 0.1580	 0.5020
T	 0.2490	 0.5190
U	 0.1460	 0.4630
V	 0.4650	 0.5690
W	 0.0000	 0.2030
X	 0.1540	 0.4850
Y	 0.4630	 0.5650
Z	 0.1660	 0.4770
a	 0.3960	 0.5650
b	 0.1190	 0.4820
c	 0.0000	 0.3480
d	 0.0010	 0.2990
e	 0.1730	 0.4930
f	 0.1580	 0.4970
g	 0.0040	 0.3450
h	 0.2720	 0.5240
i	 0.3550	 0.5560
j	 0.0220	 0.3650
k	 0.6120	 0.6080
l	 0.4300	 0.5730
m	 0.0170	 0.4350

