



wwPDB EM Validation Summary Report ⓘ

Jun 21, 2026 – 09:15 am BST

PDB ID : 7AC7 / pdb_00007ac7
EMDB ID : EMD-11713
Title : Structure of accomodated trans-translation complex on E. Coli stalled ribosome.
Authors : Guyomar, C.; D'Urso, G.; Chat, S.; Giudice, E.; Gillet, R.
Deposited on : 2020-09-10
Resolution : 3.08 Å(reported)
Based on initial model : 4YBB

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:

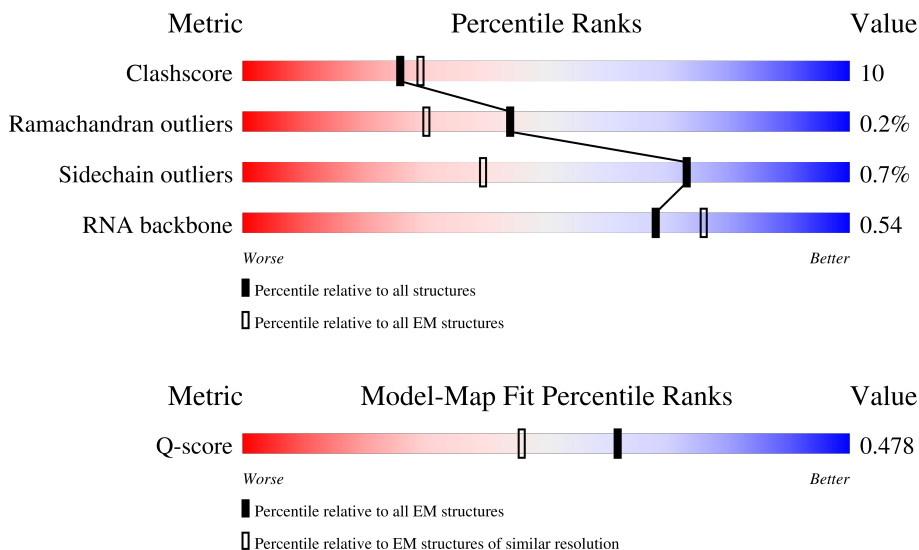
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal 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 3.08 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.



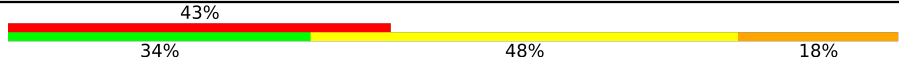
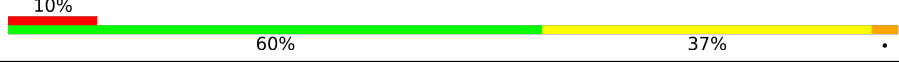
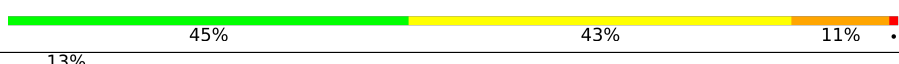
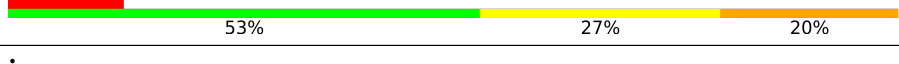

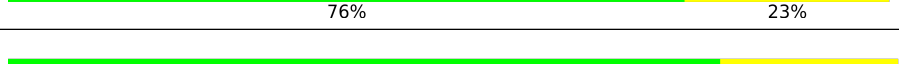
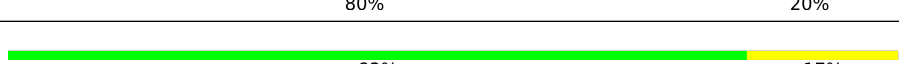
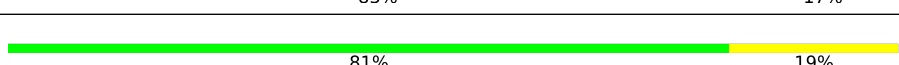
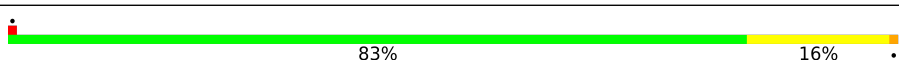

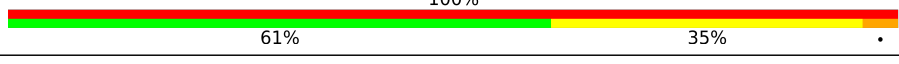
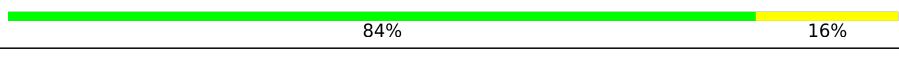
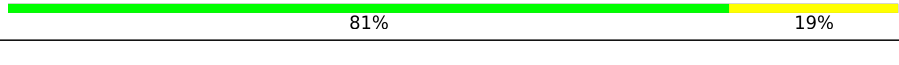

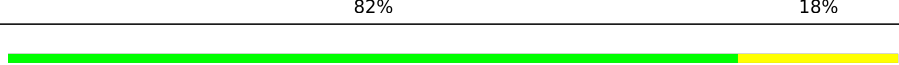


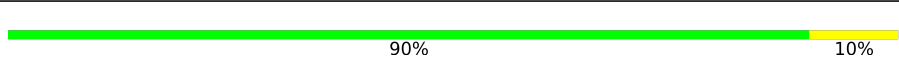



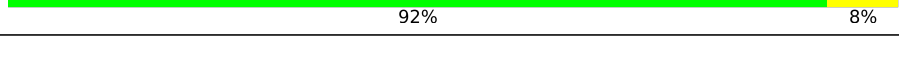



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14000 (2.58 - 3.58)

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	1	2903	
2	2	1540	
3	3	120	

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Mol	Chain	Length	Quality of chain
4	4	363	
5	5	147	
6	7	76	
7	8	15	
8	A	84	
9	B	271	
10	C	209	
11	D	201	
12	E	177	
13	F	175	
14	G	149	
15	H	130	
16	J	141	
17	K	123	
18	L	144	
19	M	136	
20	N	119	
21	O	115	
22	P	114	
23	Q	117	
24	R	103	
25	S	109	
26	T	94	
27	U	103	
28	V	94	






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Mol	Chain	Length	Quality of chain
29	W	2	100%
30	X	77	73% 27%
31	Y	58	72% 28%
32	Z	56	77% 23%
33	a	66	6% 79% 20%
34	b	54	85% 15%
35	c	52	75% 25%
36	d	46	93% 7%
37	e	64	75% 22%
38	f	37	78% 22%
39	g	225	85% 15%
40	h	208	83% 17%
41	i	205	80% 20%
42	j	156	78% 22%
43	k	104	80% 20%
44	l	151	85% 15%
45	m	129	88% 12%
46	n	126	71% 28%
47	o	99	68% 31%
48	p	117	79% 21%
49	q	123	76% 24%
50	r	115	78% 21%
51	s	100	87% 13%
52	t	87	90% 10%
53	u	81	85% 14%

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Mol	Chain	Length	Quality of chain
54	v	80	 90% 10%
55	w	65	 86% 14%
56	x	82	 71% 29%
57	y	85	 82% 18%
58	z	70	 10% 89% 11%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	3TD	1	1915	-	-	X	-

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 154883 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 ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	2903	62336	27816	11470	20147	2903	0	0

- Molecule 2 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	2	1540	33049	14747	6057	10705	1540	0	0

- Molecule 3 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	3	120	2569	1144	468	837	120	0	0

- Molecule 4 is a RNA chain called transfer-messenger RNA (tmRNA).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	4	363	7759	3466	1410	2520	363	0	0

- Molecule 5 is a protein called SsrA-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	5	147	1191	753	223	211	4	0	0

- Molecule 6 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	N	O	P	S		
6	7	76	1635	735	291	532	75	2	0	0

- Molecule 7 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
7	8	15	324	145	60	105	14	0	0

- Molecule 8 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	A	84	634	391	129	113	1	0	0

- Molecule 9 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	B	271	2083	1288	423	365	7	0	0

- Molecule 10 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	C	209	1565	979	288	294	4	0	0

- Molecule 11 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	D	201	1552	974	283	290	5	0	0

- Molecule 12 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	E	177	1411	899	249	257	6	0	0

- Molecule 13 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	F	175	1313	826	241	244	2	0	0

- Molecule 14 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	G	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 15 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	H	130	Total	C	N	O	S	0	0
			980	620	174	182	4		

- Molecule 16 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	J	141	Total	C	N	O	S	0	0
			1121	709	211	198	3		

- Molecule 17 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	K	123	Total	C	N	O	S	0	0
			946	593	181	166	6		

- Molecule 18 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	L	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 19 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	M	136	Total	C	N	O	S	0	0
			1075	686	205	178	6		

- Molecule 20 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	N	119	Total	C	N	O	S	0	0
			951	588	195	163	5		

- Molecule 21 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	O	115	Total	C	N	O	0	0
			884	548	177	159		

- Molecule 22 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	P	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 23 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	Q	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 24 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	R	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 25 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	S	109	Total	C	N	O	S	0	0
			849	527	165	155	2		

- Molecule 26 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	T	94	Total	C	N	O	S	0	0
			746	470	140	134	2		

- Molecule 27 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	U	103	Total	C	N	O	0	0
			788	498	148	142		

- Molecule 28 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	V	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 29 is a protein called Nascent peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	W	2	Total	C	N	O	0	0
			16	12	2	2		

- Molecule 30 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	X	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 31 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Y	58	Total	C	N	O	S	0	0
			477	294	93	89	1		

- Molecule 32 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Z	56	Total	C	N	O	S	0	0
			434	272	84	76	2		

- Molecule 33 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	a	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 34 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	b	54	Total	C	N	O	S	0	0
			429	260	91	77	1		

- Molecule 35 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	c	52	Total	C	N	O	0	0
			426	275	78	73		

- Molecule 36 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	d	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 37 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	e	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 38 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	f	37	Total	C	N	O	S	0	0
			297	183	64	46	4		

- Molecule 39 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	g	225	Total	C	N	O	S	0	0
			1760	1113	316	323	8		

- Molecule 40 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	h	208	Total	C	N	O	S	0	0
			1636	1036	307	290	3		

- Molecule 41 is a protein called 30S ribosomal protein S4.

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

- Molecule 42 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	j	156	1152	717	217	212	6	0	0

- Molecule 43 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	k	104	848	536	153	152	7	0	0

- Molecule 44 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	l	151	1181	735	227	215	4	0	0

- Molecule 45 is a protein called 30S ribosomal protein S8.

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

- Molecule 46 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	n	126	1010	628	202	177	3	0	0

- Molecule 47 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	o	99	790	495	151	143	1	0	0

- Molecule 48 is a protein called 30S ribosomal protein S11.

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

- Molecule 49 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	q	123	Total	C	N	O	S	0	0
			957	591	196	165	5		

- Molecule 50 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	r	115	Total	C	N	O	S	0	0
			891	552	179	157	3		

- Molecule 51 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	s	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 52 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	t	87	Total	C	N	O	S	0	0
			708	436	143	128	1		

- Molecule 53 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	u	81	Total	C	N	O	S	0	0
			643	403	127	112	1		

- Molecule 54 is a protein called 30S ribosomal protein S17.

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

- Molecule 55 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	w	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 56 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	x	82	658	421	125	110	2	0	0

- Molecule 57 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
57	y	85	664	411	137	113	3	0	0

- Molecule 58 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
58	z	70	589	366	125	97	1	0	0

- Molecule 59 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
59	1	303	Total 303	Mg 303	0
59	2	118	Total 118	Mg 118	0
59	3	9	Total 9	Mg 9	0
59	7	1	Total 1	Mg 1	0
59	B	2	Total 2	Mg 2	0
59	C	1	Total 1	Mg 1	0
59	D	1	Total 1	Mg 1	0
59	L	1	Total 1	Mg 1	0
59	Q	2	Total 2	Mg 2	0
59	Z	1	Total 1	Mg 1	0
59	b	2	Total 2	Mg 2	0

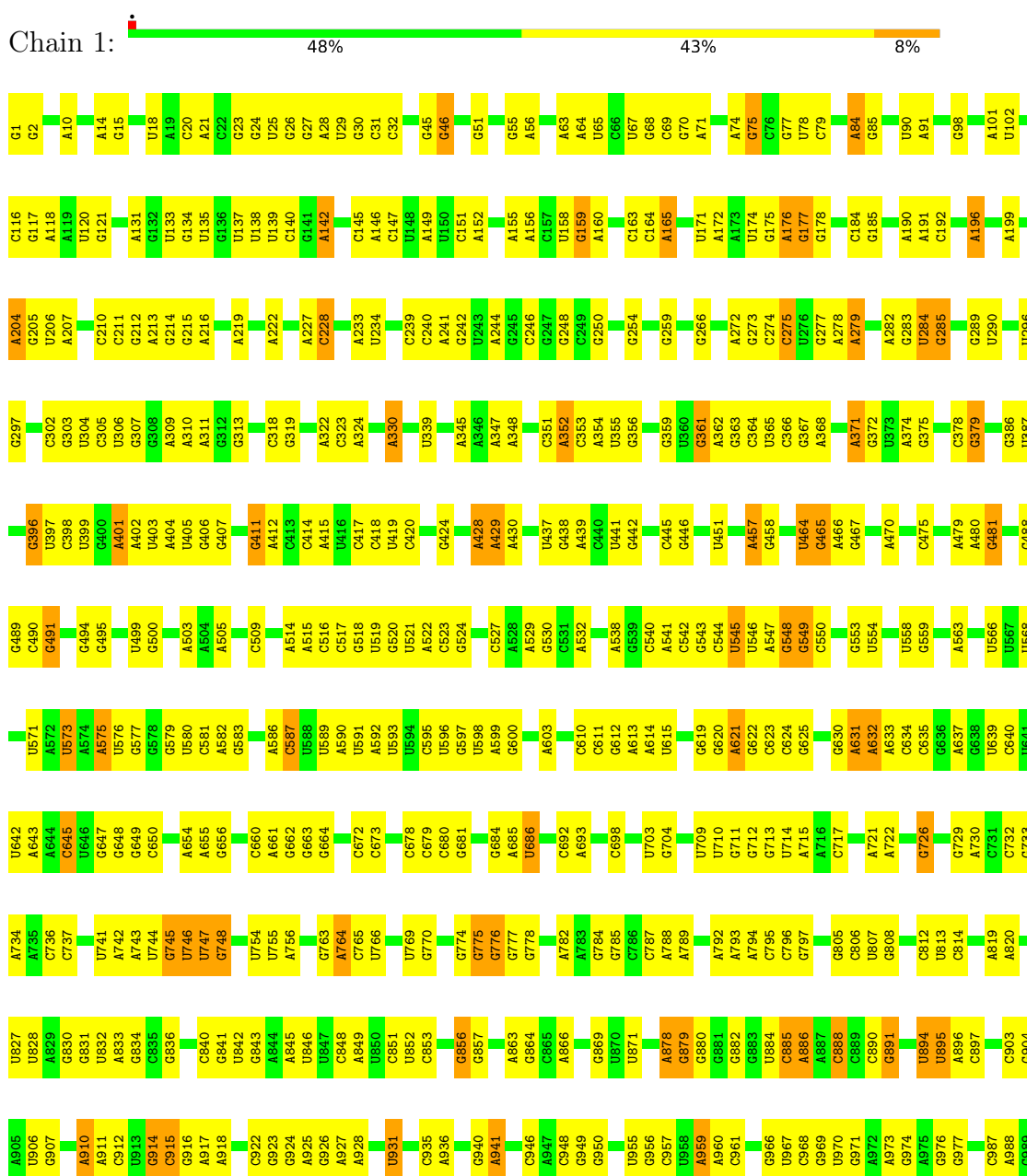
- Molecule 60 is ZINC ION (CCD ID: ZN) (formula: Zn).

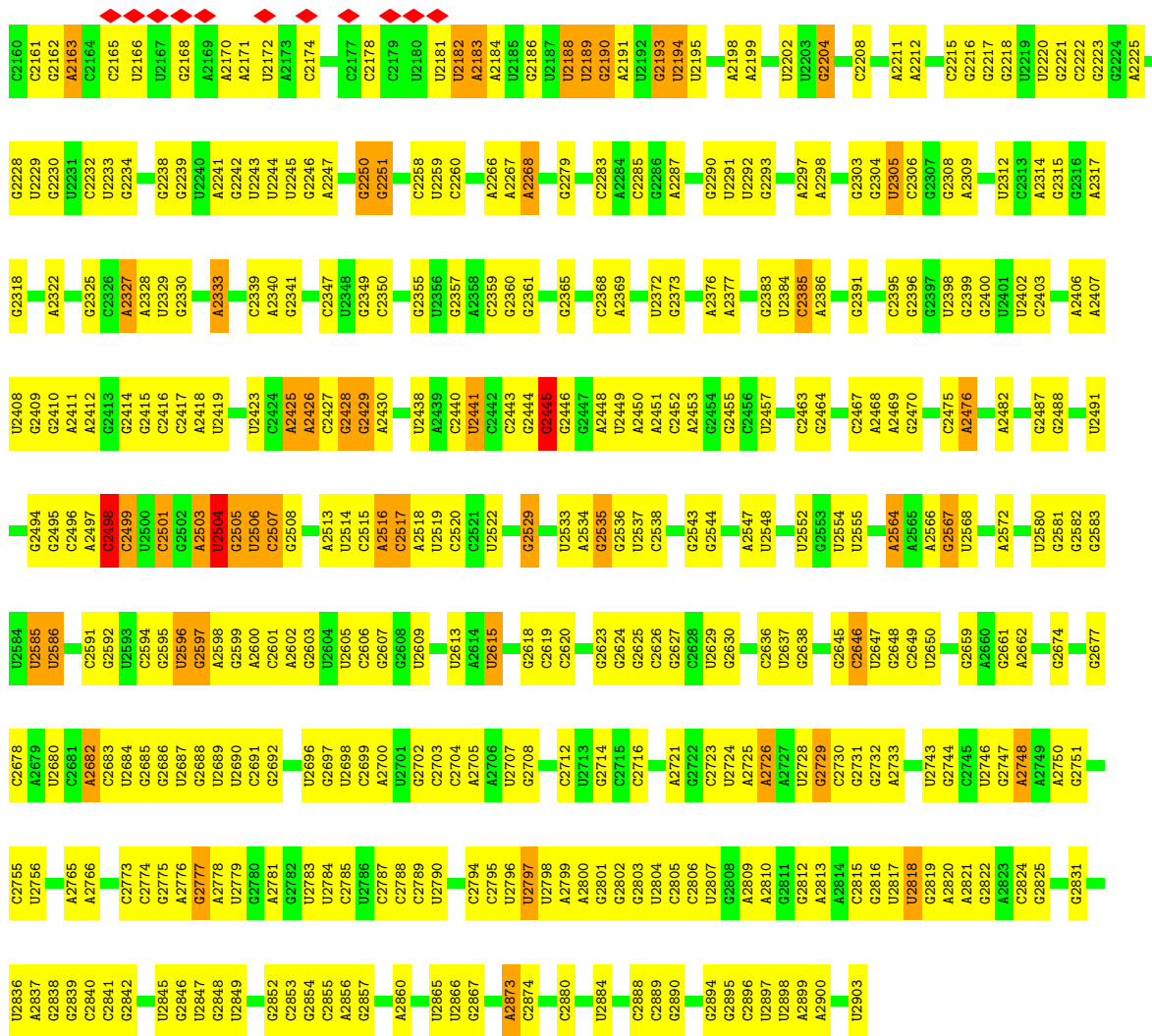
Mol	Chain	Residues	Atoms		AltConf
60	a	1	Total 1	Zn 1	0
60	f	1	Total 1	Zn 1	0

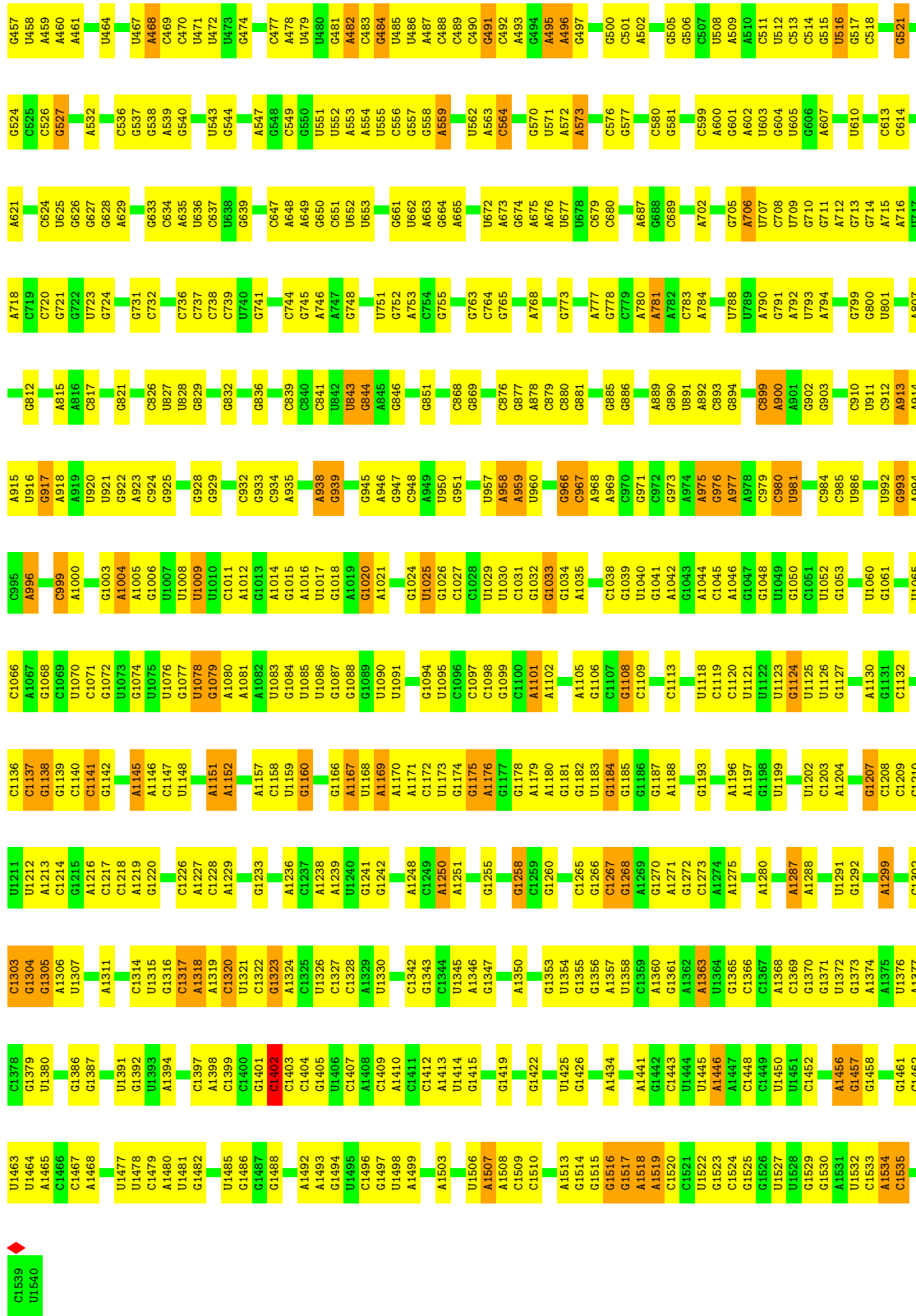
3 Residue-property plots

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 ribosomal RNA

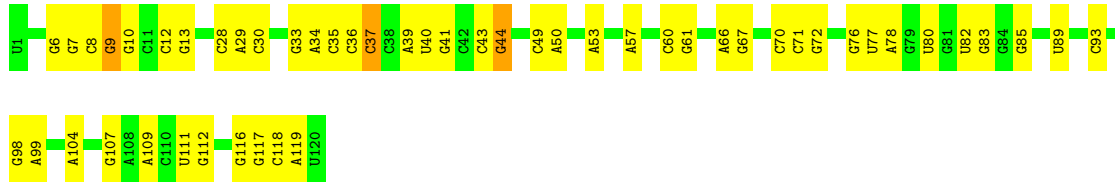




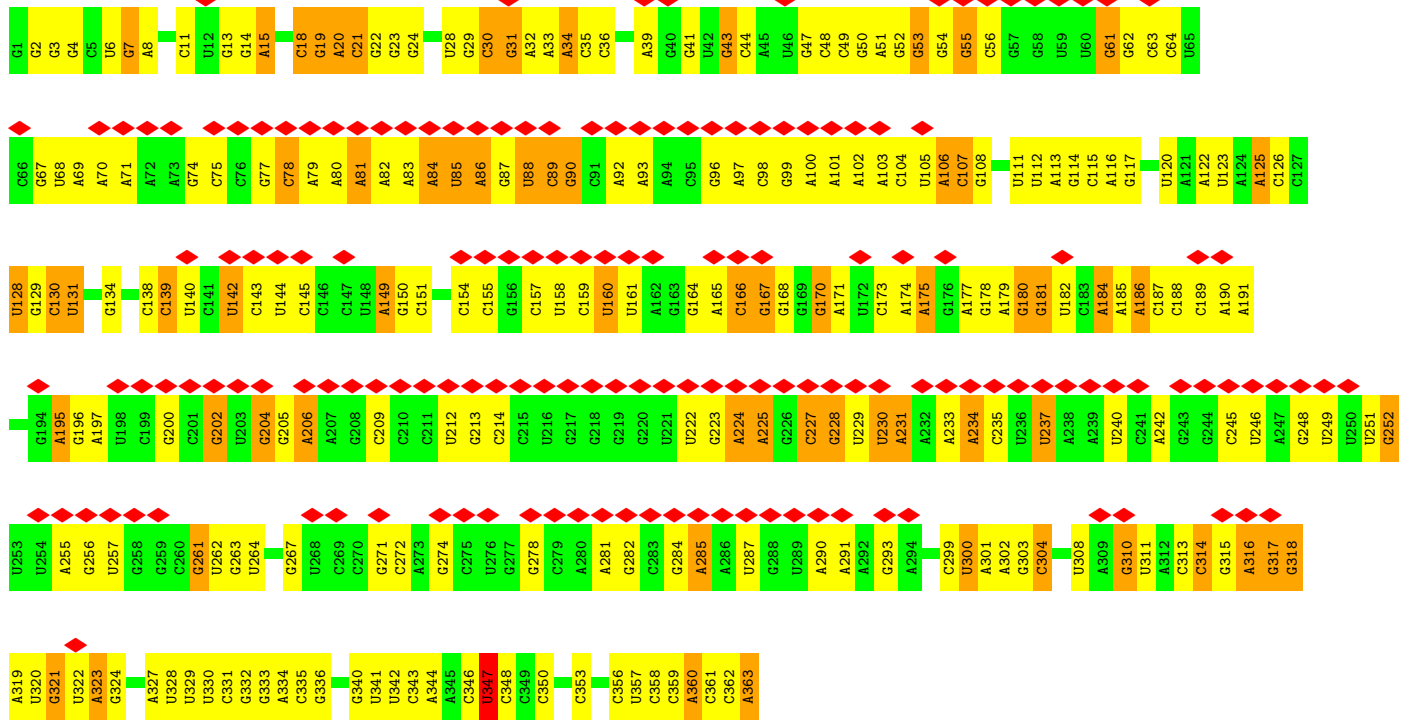


• Molecule 3: 5S ribosomal RNA

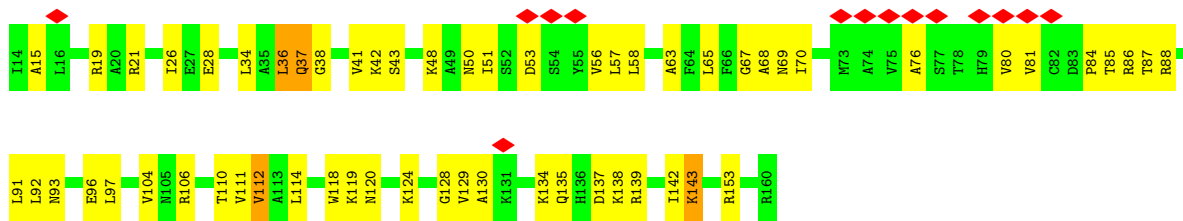




• Molecule 4: transfer-messenger RNA (tmRNA)



• Molecule 5: SsrA-binding protein



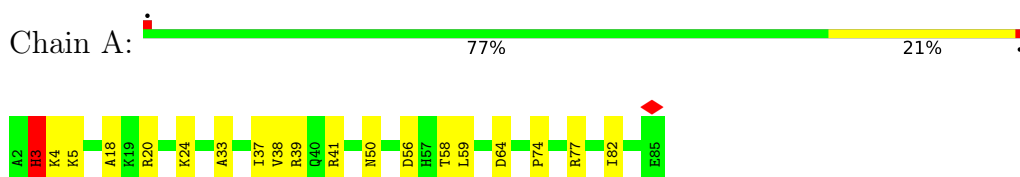
• Molecule 6: tRNA-Phe



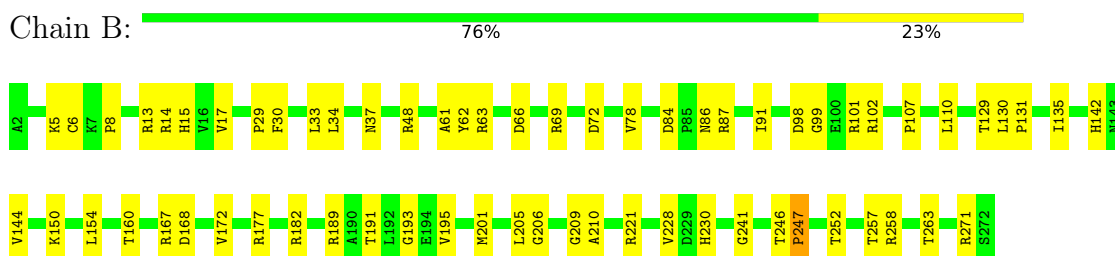
- Molecule 7: mRNA



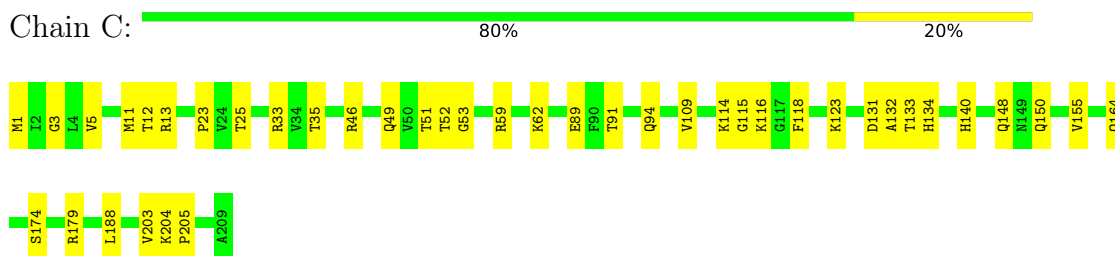
- Molecule 8: 50S ribosomal protein L27



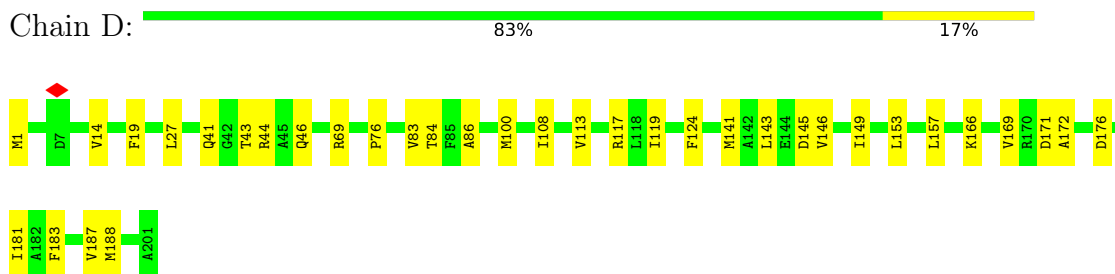
- Molecule 9: 50S ribosomal protein L2



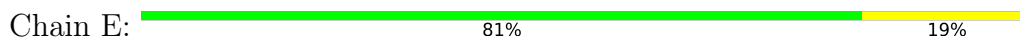
- Molecule 10: 50S ribosomal protein L3

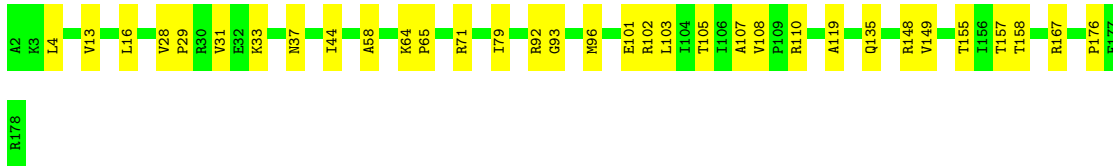


- Molecule 11: 50S ribosomal protein L4

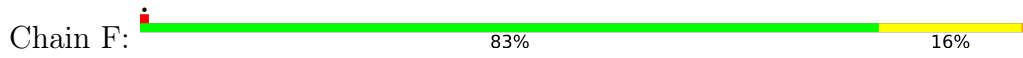


- Molecule 12: 50S ribosomal protein L5

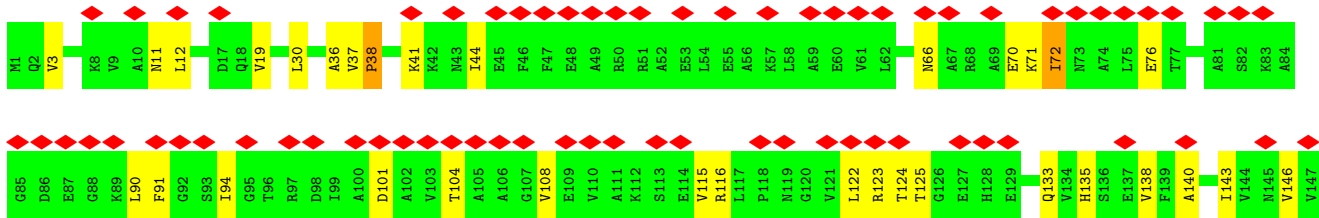
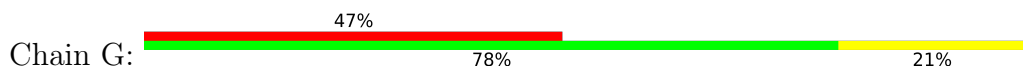




• Molecule 13: 50S ribosomal protein L6



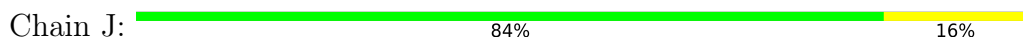
• Molecule 14: 50S ribosomal protein L9




• Molecule 15: 50S ribosomal protein L10



• Molecule 16: 50S ribosomal protein L13




- Molecule 17: 50S ribosomal protein L14

Chain K:  81% 19%




- Molecule 18: 50S ribosomal protein L15

Chain L:  85% 15%




- Molecule 19: 50S ribosomal protein L16

Chain M:  82% 18%




- Molecule 20: 50S ribosomal protein L17

Chain N:  82% 18%




- Molecule 21: 50S ribosomal protein L18

Chain O:  89% 11%




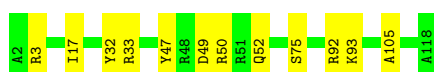
- Molecule 22: 50S ribosomal protein L19

Chain P:  85% 15%




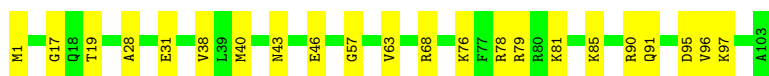
- Molecule 23: 50S ribosomal protein L20

Chain Q:  90% 10%



- Molecule 24: 50S ribosomal protein L21

Chain R:  79% 21%




- Molecule 25: 50S ribosomal protein L22

Chain S:  75% 25%



- Molecule 26: 50S ribosomal protein L23

Chain T:  82% 18%




- Molecule 27: 50S ribosomal protein L24

Chain U:  92% 8%



- Molecule 28: 50S ribosomal protein L25

Chain V:  84% 16%



- Molecule 29: Nascent peptide

Chain W:  100%



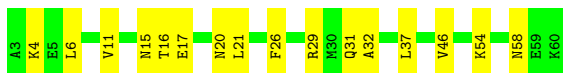
- Molecule 30: 50S ribosomal protein L28

Chain X:  73% 27%




- Molecule 31: 50S ribosomal protein L29

Chain Y:  72% 28%




- Molecule 32: 50S ribosomal protein L30

Chain Z:  77% 23%




- Molecule 33: 50S ribosomal protein L31

Chain a:  6% 79% 20%



- Molecule 34: 50S ribosomal protein L32

Chain b:  85% 15%



- Molecule 35: 50S ribosomal protein L33

Chain c:  75% 25%



- Molecule 36: 50S ribosomal protein L34

Chain d:  93% 7%




- Molecule 37: 50S ribosomal protein L35

Chain e:  75% 22%




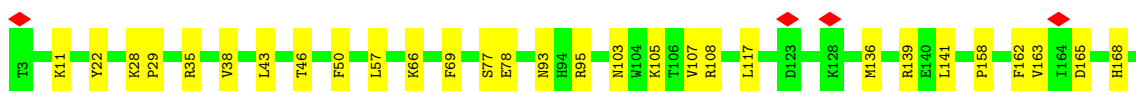
- Molecule 38: 50S ribosomal protein L36

Chain f:  78% 22%




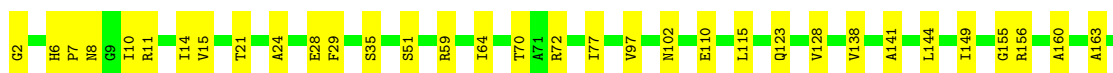
- Molecule 39: 30S ribosomal protein S2

Chain g:  85% 15%




- Molecule 40: 30S ribosomal protein S3

Chain h:  83% 17%




- Molecule 41: 30S ribosomal protein S4

Chain i:  80% 20%




- Molecule 42: 30S ribosomal protein S5

Chain j:  78% 22%

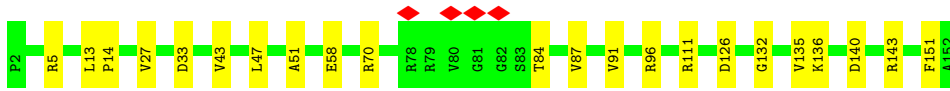
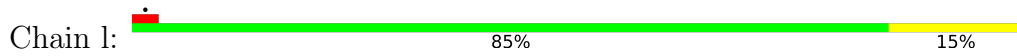


- Molecule 43: 30S ribosomal protein S6

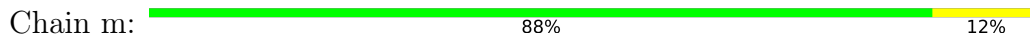
Chain k:  80% 20%



- Molecule 44: 30S ribosomal protein S7



- Molecule 45: 30S ribosomal protein S8



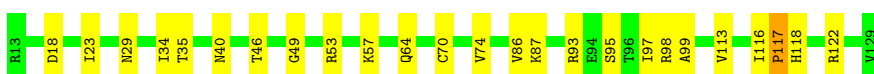
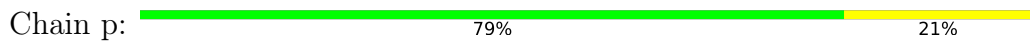
- Molecule 46: 30S ribosomal protein S9



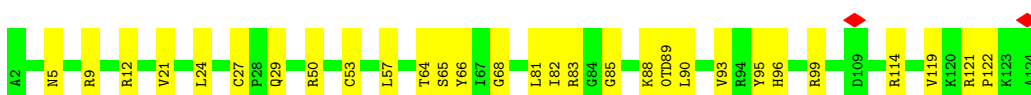
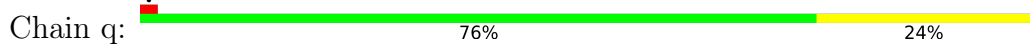
- Molecule 47: 30S ribosomal protein S10




- Molecule 48: 30S ribosomal protein S11

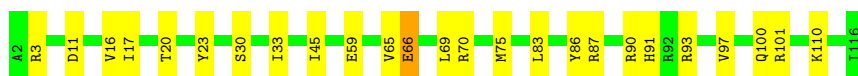


- Molecule 49: 30S ribosomal protein S12




- Molecule 50: 30S ribosomal protein S13

Chain r:  78% 21%




- Molecule 51: 30S ribosomal protein S14

Chain s:  87% 13%




- Molecule 52: 30S ribosomal protein S15

Chain t:  90% 10%




- Molecule 53: 30S ribosomal protein S16

Chain u:  85% 14%



- Molecule 54: 30S ribosomal protein S17

Chain v:  90% 10%



- Molecule 55: 30S ribosomal protein S18

Chain w:  86% 14%




- Molecule 56: 30S ribosomal protein S19

Chain x:  71% 29%




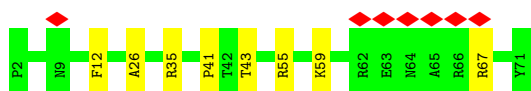
- Molecule 57: 30S ribosomal protein S20

Chain y:  82% 18%



- Molecule 58: 30S ribosomal protein S21

Chain z:  10% 89% 11%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	36069	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	29	Depositor
Minimum defocus (nm)	-700	Depositor
Maximum defocus (nm)	-2000	Depositor
Magnification	130000	Depositor
Image detector	GATAN K2 BASE (4k x 4k)	Depositor
Maximum map value	27.267	Depositor
Minimum map value	-12.720	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2.5	Depositor
Map size (\AA)	499.20026, 499.20026, 499.20026	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.0400006, 1.0400006, 1.0400006	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: 1MG, OMC, OMU, MG, 3AU, MIA, 6MZ, 0TD, 5MU, 4SU, G7M, H2U, MA6, PSU, 4OC, UR3, OMG, 3TD, 2MG, 4D4, 5MC, ZN, 2MA

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	1	0.11	0/69286	0.23	1/108087 (0.0%)
2	2	0.10	0/36722	0.21	0/57278
3	3	0.07	0/2872	0.19	0/4478
4	4	0.18	1/8615 (0.0%)	0.38	4/13430 (0.0%)
5	5	0.40	0/1213	0.90	5/1630 (0.3%)
6	7	0.19	0/1580	0.27	0/2459
7	8	0.11	0/363	0.35	0/566
8	A	0.20	0/642	0.49	1/848 (0.1%)
9	B	0.18	1/2122 (0.0%)	0.37	0/2852
10	C	0.13	0/1586	0.36	0/2134
11	D	0.10	0/1571	0.32	0/2113
12	E	0.13	0/1435	0.40	1/1926 (0.1%)
13	F	0.28	1/1333 (0.1%)	0.48	2/1805 (0.1%)
14	G	0.28	1/1122 (0.1%)	0.54	4/1515 (0.3%)
15	H	0.38	0/993	0.80	0/1340
16	J	0.11	0/1144	0.33	0/1541
17	K	0.12	0/955	0.35	0/1279
18	L	0.11	0/1062	0.35	0/1413
19	M	0.13	0/1081	0.35	0/1443
20	N	0.13	0/964	0.36	0/1289
21	O	0.12	0/894	0.33	0/1198
22	P	0.13	0/929	0.40	0/1242
23	Q	0.12	0/960	0.36	0/1278
24	R	0.12	0/829	0.35	0/1107
25	S	0.12	0/856	0.40	0/1146
26	T	0.10	0/752	0.41	1/1005 (0.1%)
27	U	0.11	0/796	0.34	0/1062
28	V	0.11	0/766	0.34	0/1025
29	W	1.11	0/16	1.59	1/20 (5.0%)
30	X	0.16	0/635	0.59	3/848 (0.4%)
31	Y	0.10	0/478	0.33	0/637

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Z	0.12	0/438	0.34	0/587
33	a	0.13	0/531	0.49	2/709 (0.3%)
34	b	0.10	0/435	0.33	0/581
35	c	0.12	0/433	0.53	1/576 (0.2%)
36	d	0.14	0/380	0.47	0/498
37	e	0.34	1/513 (0.2%)	0.54	1/676 (0.1%)
38	f	0.12	0/298	0.41	0/392
39	g	0.12	0/1791	0.35	0/2413
40	h	0.15	0/1663	0.37	0/2241
41	i	0.11	0/1665	0.39	1/2227 (0.0%)
42	j	0.12	0/1165	0.40	0/1568
43	k	0.19	0/867	0.44	0/1171
44	l	0.11	0/1195	0.34	0/1602
45	m	0.12	0/989	0.39	0/1326
46	n	0.24	0/1022	0.55	1/1361 (0.1%)
47	o	0.14	0/800	0.42	0/1082
48	p	0.30	1/893 (0.1%)	0.41	1/1205 (0.1%)
49	q	0.13	0/960	0.42	0/1286
50	r	0.13	0/900	0.47	2/1204 (0.2%)
51	s	0.11	0/817	0.34	0/1088
52	t	0.10	0/716	0.35	0/956
53	u	0.13	0/653	0.46	1/877 (0.1%)
54	v	0.11	0/658	0.33	0/881
55	w	0.11	0/544	0.34	0/731
56	x	0.11	0/675	0.39	0/908
57	y	0.11	0/670	0.34	0/888
58	z	0.15	0/597	0.53	2/792 (0.3%)
All	All	0.13	6/166840 (0.0%)	0.30	35/249820 (0.0%)

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
48	p	117	PRO	N-CD	-8.03	1.36	1.47
14	G	38	PRO	N-CD	-7.95	1.36	1.47
37	e	33	LEU	CA-C	7.11	1.62	1.52
13	F	12	PRO	N-CD	-6.63	1.38	1.47
4	4	363	A	C3'-O3'	5.99	1.51	1.42

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	5	112	VAL	N-CA-CB	-10.85	98.71	110.53

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Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
30	X	67	VAL	N-CA-C	9.41	120.22	110.62
13	F	9	VAL	N-CA-C	7.84	119.19	107.51
58	z	43	THR	N-CA-C	7.82	119.81	111.28
4	4	316	A	C2'-C3'-O3'	7.75	121.12	109.50

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	1	62336	0	31369	1105	0
2	2	33049	0	16651	561	0
3	3	2569	0	1301	34	0
4	4	7759	0	3919	117	0
5	5	1191	0	1209	65	0
6	7	1635	0	848	26	0
7	8	324	0	162	5	0
8	A	634	0	653	12	0
9	B	2083	0	2154	62	0
10	C	1565	0	1616	31	0
11	D	1552	0	1619	22	0
12	E	1411	0	1444	22	0
13	F	1313	0	1358	25	0
14	G	1111	0	1148	38	0
15	H	980	0	1013	85	0
16	J	1121	0	1150	19	0
17	K	946	0	1023	18	0
18	L	1053	0	1129	17	0
19	M	1075	0	1154	18	0
20	N	951	0	994	15	0
21	O	884	0	919	11	0
22	P	917	0	962	16	0
23	Q	947	0	1019	12	0
24	R	816	0	839	15	0
25	S	849	0	910	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	T	746	0	811	11	0
27	U	788	0	844	8	0
28	V	753	0	780	12	0
29	W	16	0	16	13	0
30	X	625	0	652	13	0
31	Y	477	0	505	9	0
32	Z	434	0	470	8	0
33	a	522	0	520	27	0
34	b	429	0	440	10	0
35	c	426	0	464	8	0
36	d	377	0	418	3	0
37	e	504	0	572	19	0
38	f	297	0	338	5	0
39	g	1760	0	1787	20	0
40	h	1636	0	1710	27	0
41	i	1643	0	1707	32	0
42	j	1152	0	1196	22	0
43	k	848	0	846	28	0
44	l	1181	0	1238	13	0
45	m	979	0	1031	23	0
46	n	1010	0	1055	32	0
47	o	790	0	831	37	0
48	p	877	0	887	19	0
49	q	957	0	1017	27	0
50	r	891	0	952	31	0
51	s	805	0	844	9	0
52	t	708	0	729	6	0
53	u	643	0	661	9	0
54	v	649	0	691	5	0
55	w	535	0	552	6	0
56	x	658	0	683	36	0
57	y	664	0	714	14	0
58	z	589	0	629	8	0
59	1	303	0	0	0	0
59	2	118	0	0	0	0
59	3	9	0	0	0	0
59	7	1	0	0	0	0
59	B	2	0	0	0	0
59	C	1	0	0	0	0
59	D	1	0	0	0	0
59	L	1	0	0	0	0
59	Q	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	Z	1	0	0	0	0
59	b	2	0	0	0	0
60	a	1	0	0	0	0
60	f	1	0	0	0	0
All	All	154883	0	103153	2556	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 10.

The worst 5 of 2556 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)
50:r:23:TYR:CE1	50:r:69:LEU:HD22	1.20	1.68
50:r:23:TYR:HE1	50:r:69:LEU:CD2	1.08	1.60
5:5:50:ASN:HB3	5:5:69:ASN:CG	1.25	1.60
9:B:246:THR:HG23	9:B:252:THR:CG2	1.47	1.44
1:1:1084:A:OP1	15:H:54:VAL:CG1	1.73	1.34

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	
5	5	145/147 (99%)	114 (79%)	29 (20%)	2 (1%)	9	31
8	A	82/84 (98%)	80 (98%)	2 (2%)	0	100	100
9	B	269/271 (99%)	266 (99%)	3 (1%)	0	100	100
10	C	207/209 (99%)	204 (99%)	3 (1%)	0	100	100
11	D	199/201 (99%)	197 (99%)	2 (1%)	0	100	100
12	E	175/177 (99%)	168 (96%)	7 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	F	173/175 (99%)	165 (95%)	8 (5%)	0	100	100
14	G	147/149 (99%)	137 (93%)	10 (7%)	0	100	100
15	H	128/130 (98%)	98 (77%)	23 (18%)	7 (6%)	1	8
16	J	139/141 (99%)	138 (99%)	1 (1%)	0	100	100
17	K	121/123 (98%)	120 (99%)	1 (1%)	0	100	100
18	L	142/144 (99%)	137 (96%)	5 (4%)	0	100	100
19	M	133/136 (98%)	130 (98%)	3 (2%)	0	100	100
20	N	117/119 (98%)	113 (97%)	4 (3%)	0	100	100
21	O	113/115 (98%)	111 (98%)	2 (2%)	0	100	100
22	P	112/114 (98%)	112 (100%)	0	0	100	100
23	Q	115/117 (98%)	113 (98%)	2 (2%)	0	100	100
24	R	101/103 (98%)	98 (97%)	3 (3%)	0	100	100
25	S	107/109 (98%)	103 (96%)	4 (4%)	0	100	100
26	T	92/94 (98%)	92 (100%)	0	0	100	100
27	U	101/103 (98%)	100 (99%)	1 (1%)	0	100	100
28	V	92/94 (98%)	92 (100%)	0	0	100	100
30	X	75/77 (97%)	74 (99%)	1 (1%)	0	100	100
31	Y	56/58 (97%)	56 (100%)	0	0	100	100
32	Z	54/56 (96%)	53 (98%)	1 (2%)	0	100	100
33	a	64/66 (97%)	61 (95%)	3 (5%)	0	100	100
34	b	52/54 (96%)	52 (100%)	0	0	100	100
35	c	50/52 (96%)	49 (98%)	1 (2%)	0	100	100
36	d	44/46 (96%)	41 (93%)	3 (7%)	0	100	100
37	e	62/64 (97%)	57 (92%)	2 (3%)	3 (5%)	2	10
38	f	35/37 (95%)	35 (100%)	0	0	100	100
39	g	223/225 (99%)	219 (98%)	4 (2%)	0	100	100
40	h	206/208 (99%)	202 (98%)	4 (2%)	0	100	100
41	i	203/205 (99%)	198 (98%)	5 (2%)	0	100	100
42	j	154/156 (99%)	147 (96%)	7 (4%)	0	100	100
43	k	102/104 (98%)	102 (100%)	0	0	100	100
44	l	149/151 (99%)	147 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	m	127/129 (98%)	127 (100%)	0	0	100	100
46	n	124/126 (98%)	120 (97%)	4 (3%)	0	100	100
47	o	97/99 (98%)	92 (95%)	5 (5%)	0	100	100
48	p	115/117 (98%)	114 (99%)	1 (1%)	0	100	100
49	q	120/123 (98%)	114 (95%)	6 (5%)	0	100	100
50	r	113/115 (98%)	111 (98%)	2 (2%)	0	100	100
51	s	98/100 (98%)	98 (100%)	0	0	100	100
52	t	85/87 (98%)	83 (98%)	2 (2%)	0	100	100
53	u	79/81 (98%)	75 (95%)	4 (5%)	0	100	100
54	v	78/80 (98%)	72 (92%)	6 (8%)	0	100	100
55	w	63/65 (97%)	63 (100%)	0	0	100	100
56	x	80/82 (98%)	78 (98%)	2 (2%)	0	100	100
57	y	83/85 (98%)	82 (99%)	1 (1%)	0	100	100
58	z	68/70 (97%)	68 (100%)	0	0	100	100
All	All	5869/5973 (98%)	5678 (97%)	179 (3%)	12 (0%)	44	71

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
37	e	32	ILE
15	H	55	VAL
15	H	88	HIS
15	H	118	ILE
37	e	33	LEU

5.3.2 Protein sidechains [i](#)

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	
5	5	123/123 (100%)	113 (92%)	10 (8%)	11	34
8	A	62/62 (100%)	59 (95%)	3 (5%)	23	51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	B	216/216 (100%)	215 (100%)	1 (0%)	81	83
10	C	164/164 (100%)	164 (100%)	0	100	100
11	D	165/165 (100%)	165 (100%)	0	100	100
12	E	148/148 (100%)	148 (100%)	0	100	100
13	F	136/136 (100%)	133 (98%)	3 (2%)	45	68
14	G	114/114 (100%)	113 (99%)	1 (1%)	70	78
15	H	99/99 (100%)	96 (97%)	3 (3%)	36	62
16	J	115/115 (100%)	115 (100%)	0	100	100
17	K	104/104 (100%)	104 (100%)	0	100	100
18	L	103/103 (100%)	102 (99%)	1 (1%)	68	77
19	M	108/108 (100%)	107 (99%)	1 (1%)	70	78
20	N	99/99 (100%)	99 (100%)	0	100	100
21	O	85/85 (100%)	85 (100%)	0	100	100
22	P	99/99 (100%)	99 (100%)	0	100	100
23	Q	89/89 (100%)	89 (100%)	0	100	100
24	R	84/84 (100%)	84 (100%)	0	100	100
25	S	92/92 (100%)	92 (100%)	0	100	100
26	T	81/81 (100%)	81 (100%)	0	100	100
27	U	84/84 (100%)	84 (100%)	0	100	100
28	V	78/78 (100%)	78 (100%)	0	100	100
29	W	1/1 (100%)	0	1 (100%)	0	0
30	X	67/67 (100%)	66 (98%)	1 (2%)	57	73
31	Y	53/53 (100%)	53 (100%)	0	100	100
32	Z	47/47 (100%)	47 (100%)	0	100	100
33	a	59/59 (100%)	59 (100%)	0	100	100
34	b	46/46 (100%)	46 (100%)	0	100	100
35	c	47/47 (100%)	46 (98%)	1 (2%)	47	68
36	d	38/38 (100%)	38 (100%)	0	100	100
37	e	51/51 (100%)	51 (100%)	0	100	100
38	f	34/34 (100%)	34 (100%)	0	100	100
39	g	187/187 (100%)	187 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	h	171/171 (100%)	170 (99%)	1 (1%)	78	81
41	i	172/172 (100%)	171 (99%)	1 (1%)	78	81
42	j	119/119 (100%)	119 (100%)	0	100	100
43	k	91/91 (100%)	91 (100%)	0	100	100
44	l	124/124 (100%)	123 (99%)	1 (1%)	73	79
45	m	104/104 (100%)	104 (100%)	0	100	100
46	n	104/104 (100%)	102 (98%)	2 (2%)	50	70
47	o	86/86 (100%)	85 (99%)	1 (1%)	63	75
48	p	90/90 (100%)	90 (100%)	0	100	100
49	q	102/102 (100%)	102 (100%)	0	100	100
50	r	93/93 (100%)	93 (100%)	0	100	100
51	s	83/83 (100%)	83 (100%)	0	100	100
52	t	75/75 (100%)	75 (100%)	0	100	100
53	u	65/65 (100%)	65 (100%)	0	100	100
54	v	74/74 (100%)	74 (100%)	0	100	100
55	w	56/56 (100%)	56 (100%)	0	100	100
56	x	72/72 (100%)	72 (100%)	0	100	100
57	y	65/65 (100%)	65 (100%)	0	100	100
58	z	60/60 (100%)	60 (100%)	0	100	100
All	All	4884/4884 (100%)	4852 (99%)	32 (1%)	73	80

5 of 32 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
44	l	135	VAL
46	n	43	THR
8	A	5	LYS
8	A	4	LYS
46	n	107	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 37 such sidechains are listed below:

Mol	Chain	Res	Type
48	p	29	ASN

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Mol	Chain	Res	Type
57	y	55	GLN
48	p	38	GLN
53	u	59	HIS
28	V	49	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2902/2903 (99%)	540 (18%)	25 (0%)
2	2	1538/1540 (99%)	247 (16%)	13 (0%)
3	3	119/120 (99%)	13 (10%)	0
4	4	362/363 (99%)	164 (45%)	14 (3%)
6	7	75/76 (98%)	14 (18%)	2 (2%)
7	8	14/15 (93%)	4 (28%)	2 (14%)
All	All	5010/5017 (99%)	982 (19%)	56 (1%)

5 of 982 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	10	A
1	1	14	A
1	1	15	G
1	1	27	G
1	1	28	A

5 of 56 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	2	938	A
7	8	9	A
2	2	1303	C
7	8	7	U
4	4	314	C

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

48 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
6	PSU	7	39	6	18,21,22	1.08	1 (5%)	22,30,33	1.70	4 (18%)
1	2MG	1	1835	1	23,26,27	3.01	7 (30%)	32,38,41	2.17	9 (28%)
19	4D4	M	81	19	9,11,12	2.05	2 (22%)	8,13,15	1.84	3 (37%)
2	2MG	2	1207	2	23,26,27	3.01	7 (30%)	32,38,41	2.11	9 (28%)
6	5MU	7	54	6	19,22,23	4.88	7 (36%)	28,32,35	3.56	9 (32%)
6	H2U	7	20	6	18,21,22	1.10	2 (11%)	21,30,33	2.54	2 (9%)
1	G7M	1	2069	1	23,26,27	2.53	9 (39%)	35,39,42	2.16	10 (28%)
49	0TD	q	89	49	7,9,10	1.43	0	6,11,13	1.98	2 (33%)
2	2MG	2	1516	2	23,26,27	3.01	7 (30%)	32,38,41	2.13	10 (31%)
2	5MC	2	967	2	18,22,23	3.60	7 (38%)	26,32,35	0.98	1 (3%)
1	PSU	1	2457	1	18,21,22	1.04	1 (5%)	22,30,33	1.71	3 (13%)
1	1MG	1	745	1	22,26,27	2.69	6 (27%)	33,39,42	1.68	6 (18%)
1	PSU	1	1911	1	18,21,22	1.10	1 (5%)	22,30,33	1.76	4 (18%)
1	PSU	1	2504	1	18,21,22	1.08	1 (5%)	22,30,33	1.76	4 (18%)
2	UR3	2	1498	2	19,22,23	2.99	6 (31%)	26,32,35	1.31	1 (3%)
2	PSU	2	516	2	18,21,22	1.07	1 (5%)	22,30,33	1.69	5 (22%)
6	MIA	7	37	6	28,31,32	2.62	6 (21%)	40,44,47	3.14	17 (42%)
1	PSU	1	2580	1	18,21,22	1.07	1 (5%)	22,30,33	1.65	4 (18%)
6	PSU	7	32	6	18,21,22	1.07	1 (5%)	22,30,33	1.74	4 (18%)
1	6MZ	1	2030	1	22,25,26	2.81	2 (9%)	30,36,39	2.37	10 (33%)
1	5MU	1	1939	1	19,22,23	4.87	7 (36%)	28,32,35	3.63	9 (32%)
1	2MG	1	2445	1	23,26,27	2.99	7 (30%)	32,38,41	2.11	9 (28%)
2	MA6	2	1519	2	23,26,27	1.23	3 (13%)	34,38,41	4.03	14 (41%)
4	PSU	4	342	4	18,21,22	1.11	1 (5%)	22,30,33	1.74	4 (18%)
6	PSU	7	55	6	18,21,22	1.10	1 (5%)	22,30,33	1.73	4 (18%)
1	OMG	1	2251	6,1	23,26,27	2.47	8 (34%)	33,38,41	2.69	10 (30%)
4	5MU	4	341	4	19,22,23	4.89	7 (36%)	28,32,35	3.56	9 (32%)
2	MA6	2	1518	2	23,26,27	1.22	3 (13%)	34,38,41	4.02	15 (44%)
2	4OC	2	1402	2	20,23,24	3.28	9 (45%)	26,32,35	0.91	1 (3%)
2	G7M	2	527	2	23,26,27	2.55	8 (34%)	35,39,42	2.20	10 (28%)
1	PSU	1	1917	1	18,21,22	1.11	1 (5%)	22,30,33	1.77	4 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	PSU	4	347	4	18,21,22	1.12	1 (5%)	22,30,33	1.75	4 (18%)
1	OMU	1	2552	1	19,22,23	3.21	7 (36%)	26,31,34	1.67	5 (19%)
6	3AU	7	47	6	24,28,29	3.03	9 (37%)	33,40,43	1.30	3 (9%)
1	PSU	1	955	1	18,21,22	1.07	1 (5%)	22,30,33	1.75	4 (18%)
1	OMC	1	2498	1,59	19,22,23	3.05	8 (42%)	26,31,34	0.77	0
1	PSU	1	746	1,59	18,21,22	1.10	1 (5%)	22,30,33	1.79	5 (22%)
2	2MG	2	966	2	23,26,27	3.02	7 (30%)	32,38,41	2.13	9 (28%)
6	H2U	7	16	6	18,21,22	1.22	3 (16%)	21,30,33	1.79	3 (14%)
1	2MA	1	2503	1,59	22,25,26	3.68	7 (31%)	33,37,40	2.00	9 (27%)
1	3TD	1	1915	1	18,22,23	4.33	7 (38%)	22,32,35	1.60	3 (13%)
2	5MC	2	1407	2	18,22,23	3.62	7 (38%)	26,32,35	1.00	2 (7%)
1	5MC	1	1962	1	18,22,23	3.61	7 (38%)	26,32,35	1.04	2 (7%)
1	PSU	1	2605	1	18,21,22	1.10	1 (5%)	22,30,33	1.76	4 (18%)
1	6MZ	1	1618	1	22,25,26	2.86	2 (9%)	30,36,39	2.32	10 (33%)
1	5MU	1	747	1	19,22,23	4.90	7 (36%)	28,32,35	3.62	8 (28%)
6	G7M	7	46	6	23,26,27	3.68	12 (52%)	35,39,42	1.66	6 (17%)
6	4SU	7	8	6	18,21,22	3.74	8 (44%)	26,30,33	2.20	4 (15%)

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
6	PSU	7	39	6	-	0/7/25/26	0/2/2/2
1	2MG	1	1835	1	-	2/9/27/28	0/3/3/3
19	4D4	M	81	19	-	5/11/12/14	-
2	2MG	2	1207	2	-	0/9/27/28	0/3/3/3
6	5MU	7	54	6	-	2/7/25/26	0/2/2/2
6	H2U	7	20	6	-	6/7/38/39	0/2/2/2
1	G7M	1	2069	1	-	2/7/25/26	0/3/3/3
49	0TD	q	89	49	-	4/7/12/14	-
2	2MG	2	1516	2	-	0/9/27/28	0/3/3/3
2	5MC	2	967	2	-	0/7/25/26	0/2/2/2
1	PSU	1	2457	1	-	0/7/25/26	0/2/2/2
1	1MG	1	745	1	-	0/7/25/26	0/3/3/3
1	PSU	1	1911	1	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	1	2504	1	-	2/7/25/26	0/2/2/2
2	UR3	2	1498	2	-	2/7/25/26	0/2/2/2
2	PSU	2	516	2	-	2/7/25/26	0/2/2/2
6	MIA	7	37	6	-	5/15/33/34	0/3/3/3
1	PSU	1	2580	1	-	3/7/25/26	0/2/2/2
6	PSU	7	32	6	-	0/7/25/26	0/2/2/2
1	6MZ	1	2030	1	-	2/9/27/28	0/3/3/3
1	5MU	1	1939	1	-	0/7/25/26	0/2/2/2
1	2MG	1	2445	1	-	2/9/27/28	0/3/3/3
2	MA6	2	1519	2	-	2/11/29/30	0/3/3/3
4	PSU	4	342	4	-	1/7/25/26	0/2/2/2
6	PSU	7	55	6	-	0/7/25/26	0/2/2/2
1	OMG	1	2251	6,1	-	0/9/27/28	0/3/3/3
4	5MU	4	341	4	-	0/7/25/26	0/2/2/2
2	MA6	2	1518	2	-	0/11/29/30	0/3/3/3
2	4OC	2	1402	2	-	2/9/29/30	0/2/2/2
2	G7M	2	527	2	-	3/7/25/26	0/3/3/3
1	PSU	1	1917	1	-	2/7/25/26	0/2/2/2
4	PSU	4	347	4	-	2/7/25/26	0/2/2/2
1	OMU	1	2552	1	-	1/9/27/28	0/2/2/2
6	3AU	7	47	6	-	2/16/34/35	0/2/2/2
1	PSU	1	955	1	-	0/7/25/26	0/2/2/2
1	OMC	1	2498	1,59	-	2/9/27/28	0/2/2/2
1	PSU	1	746	1,59	-	0/7/25/26	0/2/2/2
2	2MG	2	966	2	-	0/9/27/28	0/3/3/3
6	H2U	7	16	6	-	1/7/38/39	0/2/2/2
1	2MA	1	2503	1,59	-	2/7/25/26	0/3/3/3
1	3TD	1	1915	1	-	2/7/25/26	0/2/2/2
2	5MC	2	1407	2	-	0/7/25/26	0/2/2/2
1	5MC	1	1962	1	-	0/7/25/26	0/2/2/2
1	PSU	1	2605	1	-	0/7/25/26	0/2/2/2
1	6MZ	1	1618	1	-	3/9/27/28	0/3/3/3
1	5MU	1	747	1	-	0/7/25/26	0/2/2/2
6	G7M	7	46	6	-	3/7/25/26	0/3/3/3
6	4SU	7	8	6	-	0/7/25/26	0/2/2/2

The worst 5 of 225 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	1915	3TD	C6-C5	12.55	1.49	1.35
1	1	1618	6MZ	C6-N6	12.49	1.47	1.34
1	1	2030	6MZ	C6-N6	12.23	1.47	1.34
1	1	2503	2MA	C4-N3	11.55	1.48	1.34
1	1	747	5MU	C2-N1	11.45	1.56	1.38

The worst 5 of 287 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	1939	5MU	C5-C4-N3	12.03	125.58	115.31
1	1	747	5MU	C5-C4-N3	11.95	125.52	115.31
6	7	54	5MU	C5-C4-N3	11.93	125.50	115.31
4	4	341	5MU	C5-C4-N3	11.82	125.40	115.31
2	2	1518	MA6	C1'-N9-C8	-11.70	100.71	127.14

There are no chirality outliers.

5 of 67 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
19	M	81	4D4	C-CA-CB-OB
19	M	81	4D4	C-CA-CB-CG
19	M	81	4D4	N-CA-CB-OB
19	M	81	4D4	N-CA-CB-CG
49	q	89	0TD	SB-CB-CG-OD2

There are no ring outliers.

17 monomers are involved in 35 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	2	1207	2MG	1	0
2	2	1516	2MG	1	0
2	2	967	5MC	2	0
1	1	745	1MG	1	0
1	1	2504	PSU	1	0
6	7	37	MIA	2	0
1	1	2030	6MZ	3	0
1	1	2445	2MG	4	0
1	1	2251	OMG	1	0
2	2	1518	MA6	4	0
2	2	1402	4OC	2	0
4	4	347	PSU	1	0
1	1	2498	OMC	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	1	746	PSU	1	0
2	2	966	2MG	2	0
6	7	16	H2U	1	0
1	1	1915	3TD	8	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 443 ligands modelled in this entry, 443 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

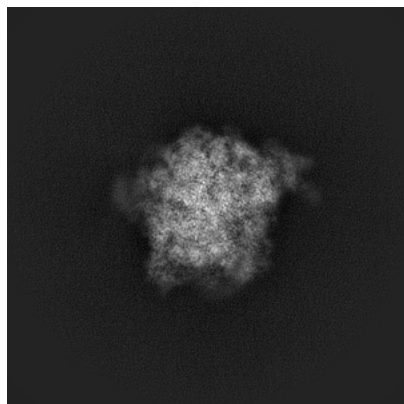
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11713. These allow visual inspection of the internal detail of the map and identification of artifacts.

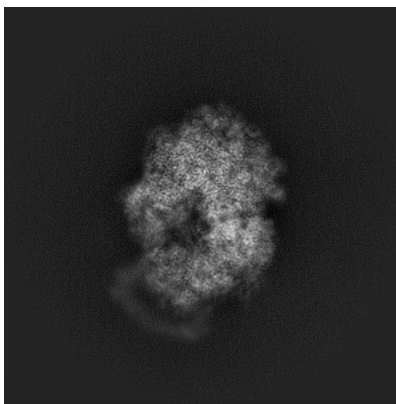
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

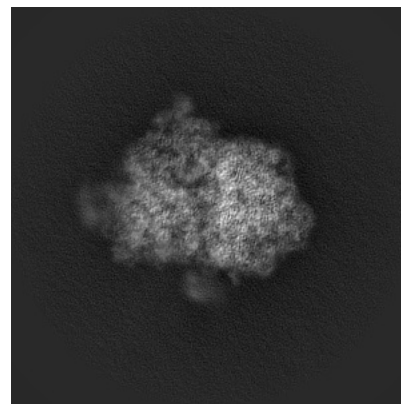
6.1.1 Primary map



X

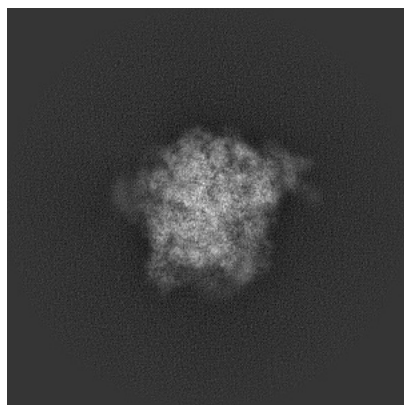


Y

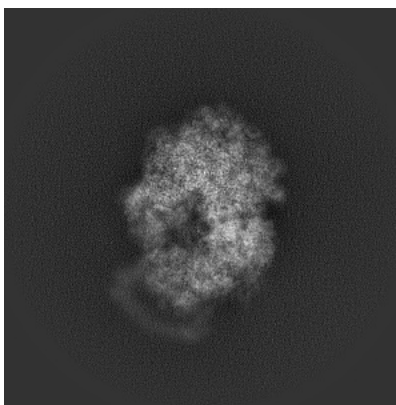


Z

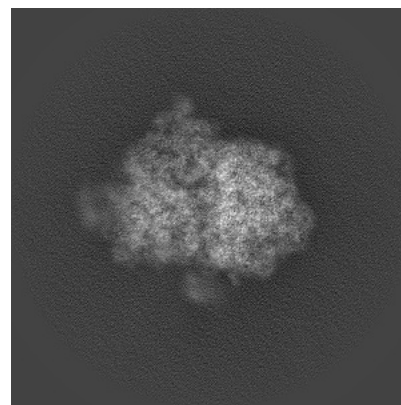
6.1.2 Raw map



X



Y

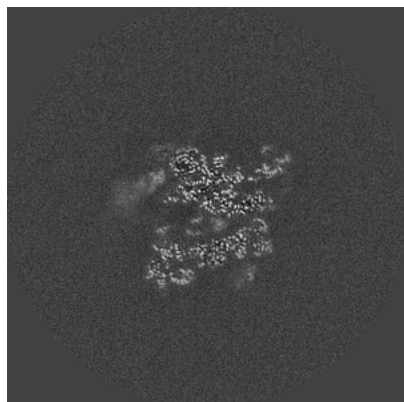


Z

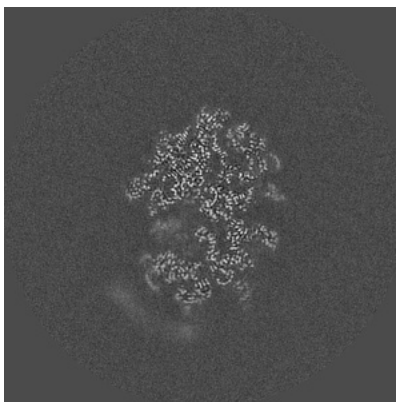
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

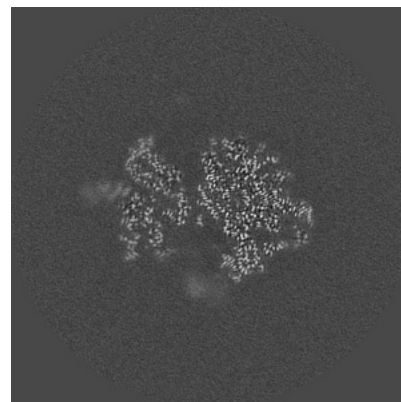
6.2.1 Primary map



X Index: 240

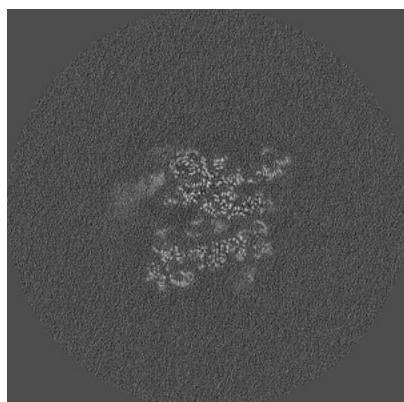


Y Index: 240

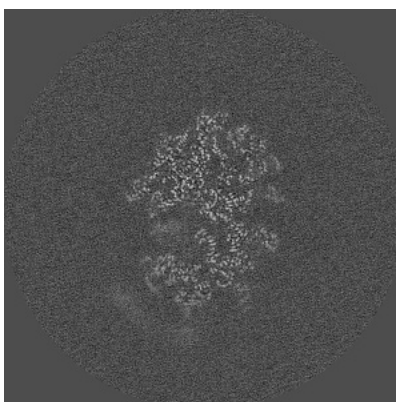


Z Index: 240

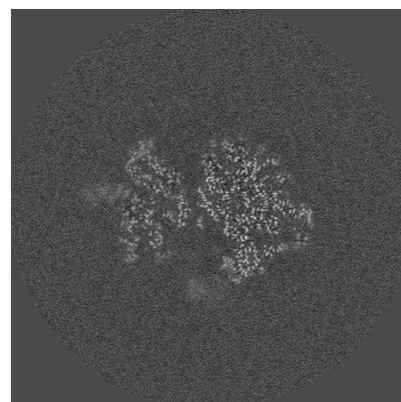
6.2.2 Raw map



X Index: 240



Y Index: 240

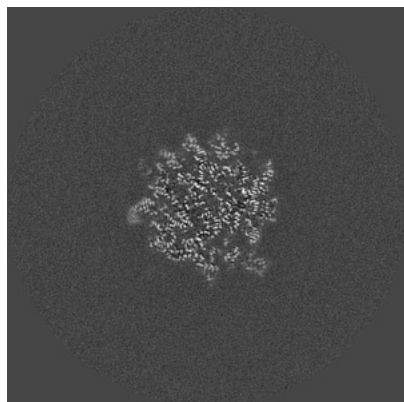


Z Index: 240

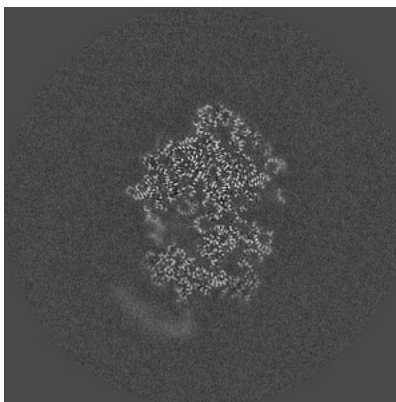
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

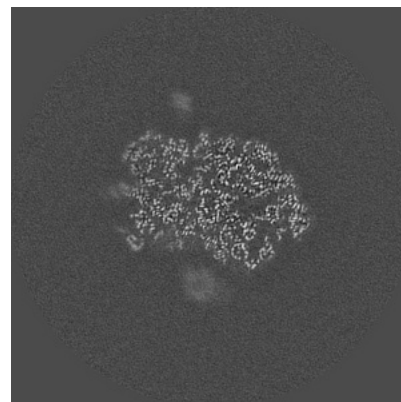
6.3.1 Primary map



X Index: 269

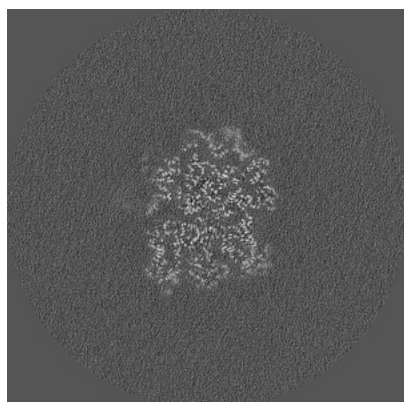


Y Index: 231

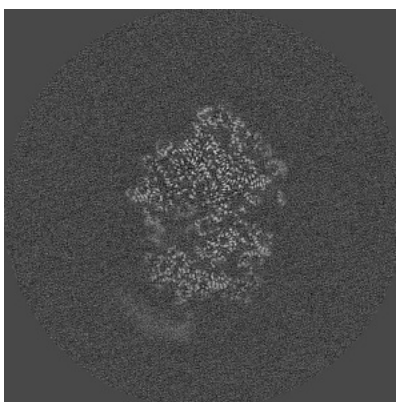


Z Index: 252

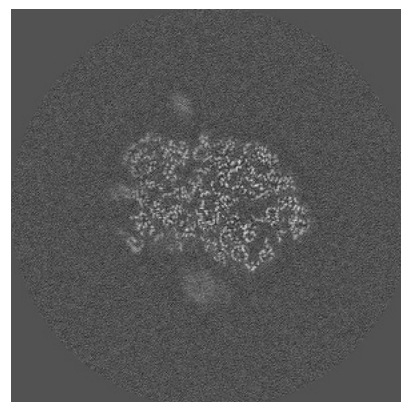
6.3.2 Raw map



X Index: 258



Y Index: 230

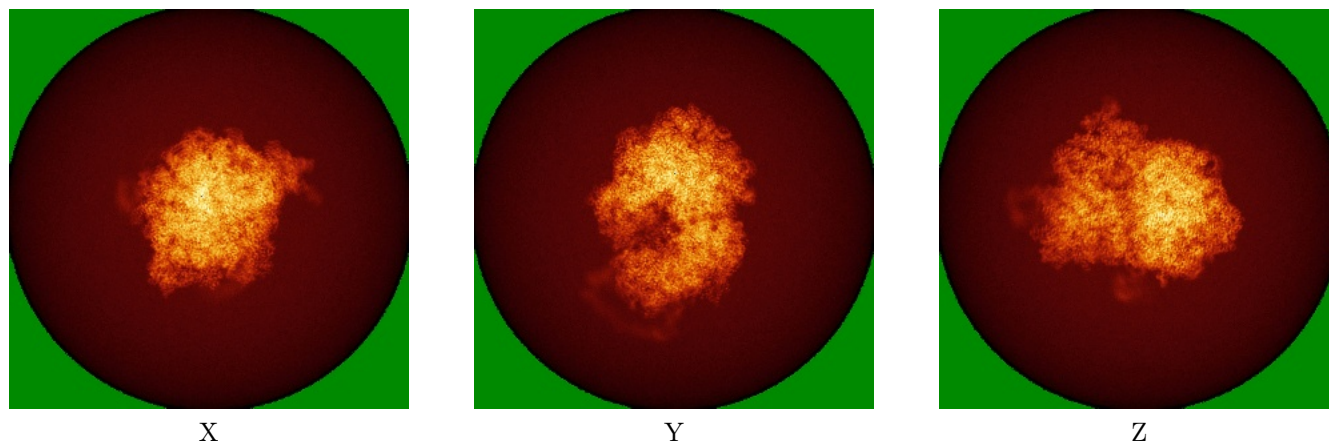


Z Index: 252

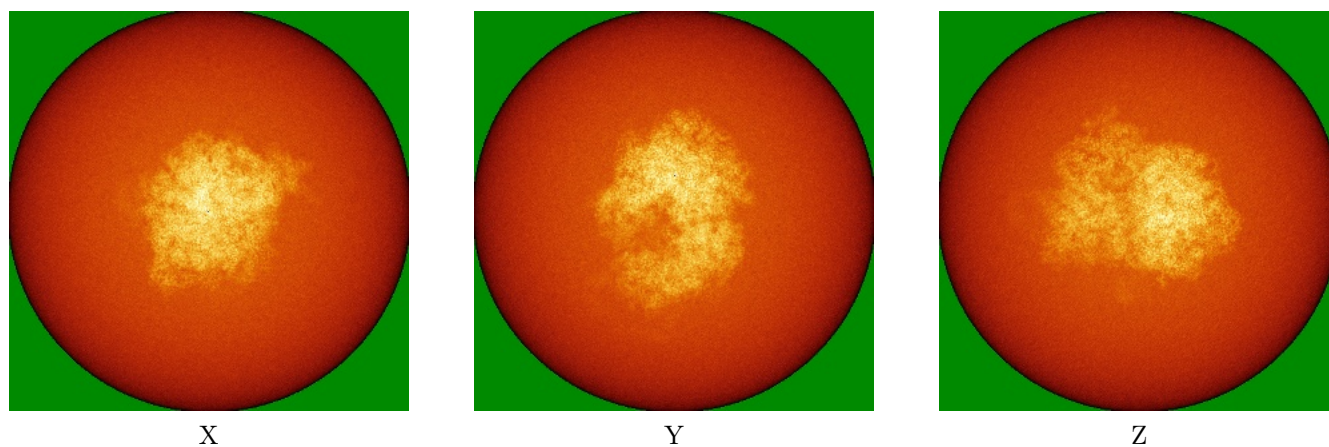
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



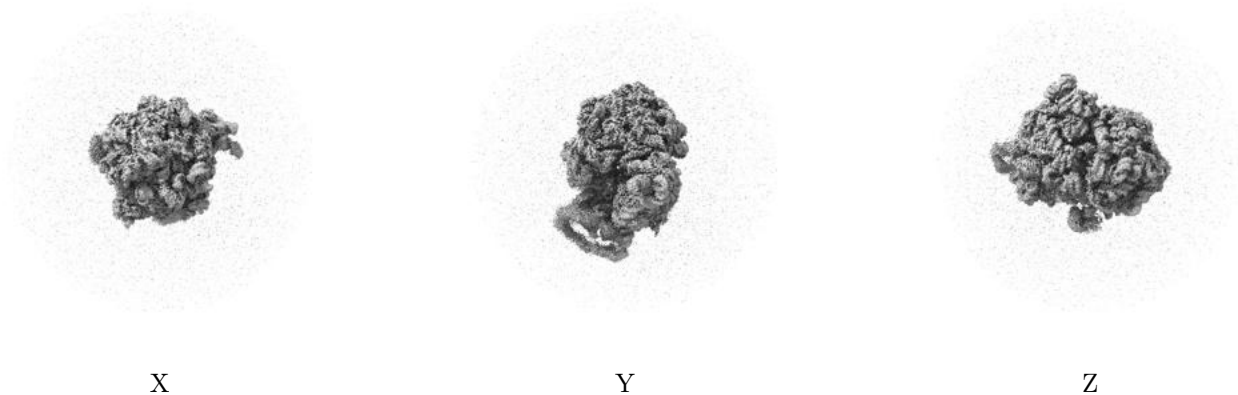
6.4.2 Raw map



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.

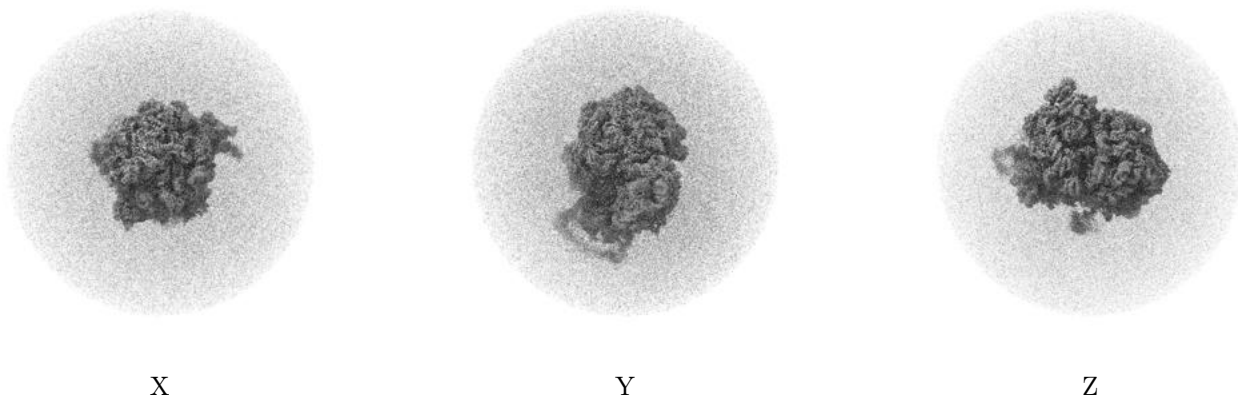
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

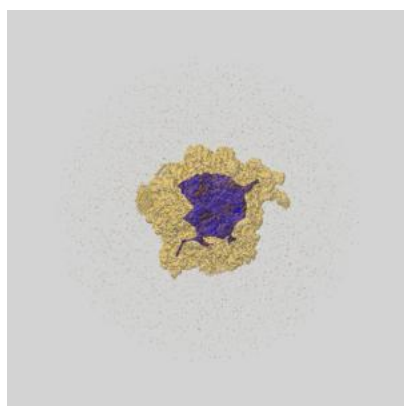
6.6 Mask visualisation [i](#)

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

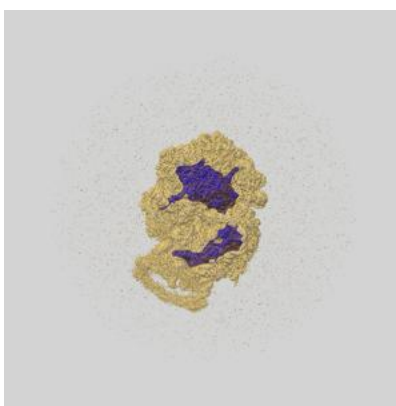
A mask typically either:

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

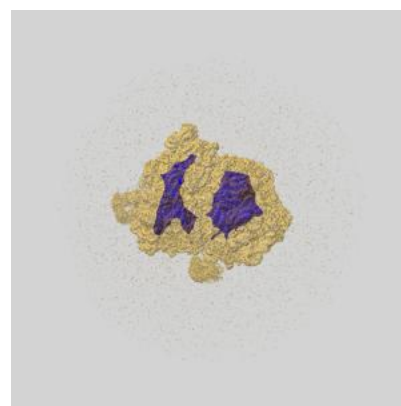
6.6.1 emd_11713_msk_1.map [i](#)



X



Y

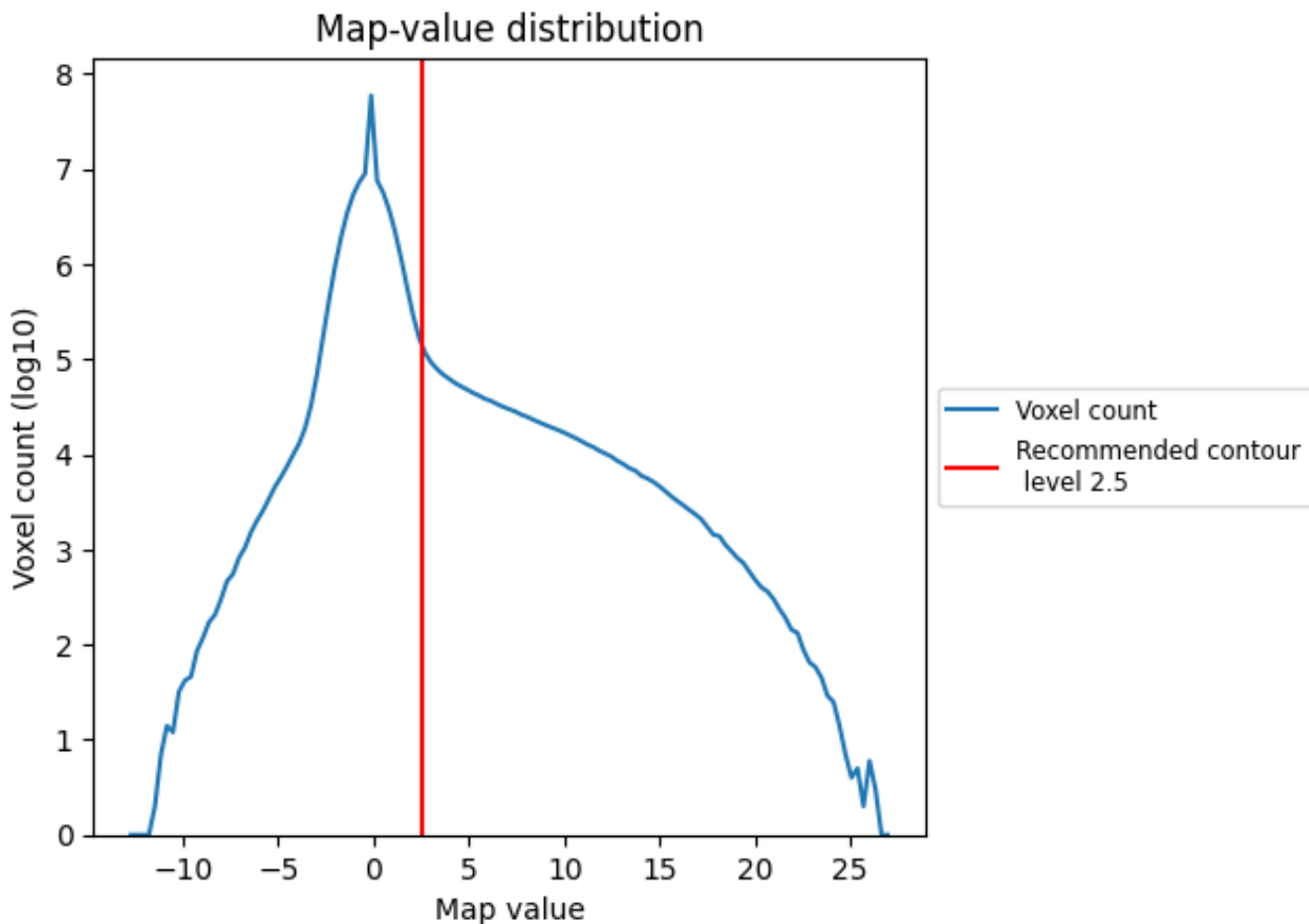


Z

7 Map analysis [i](#)

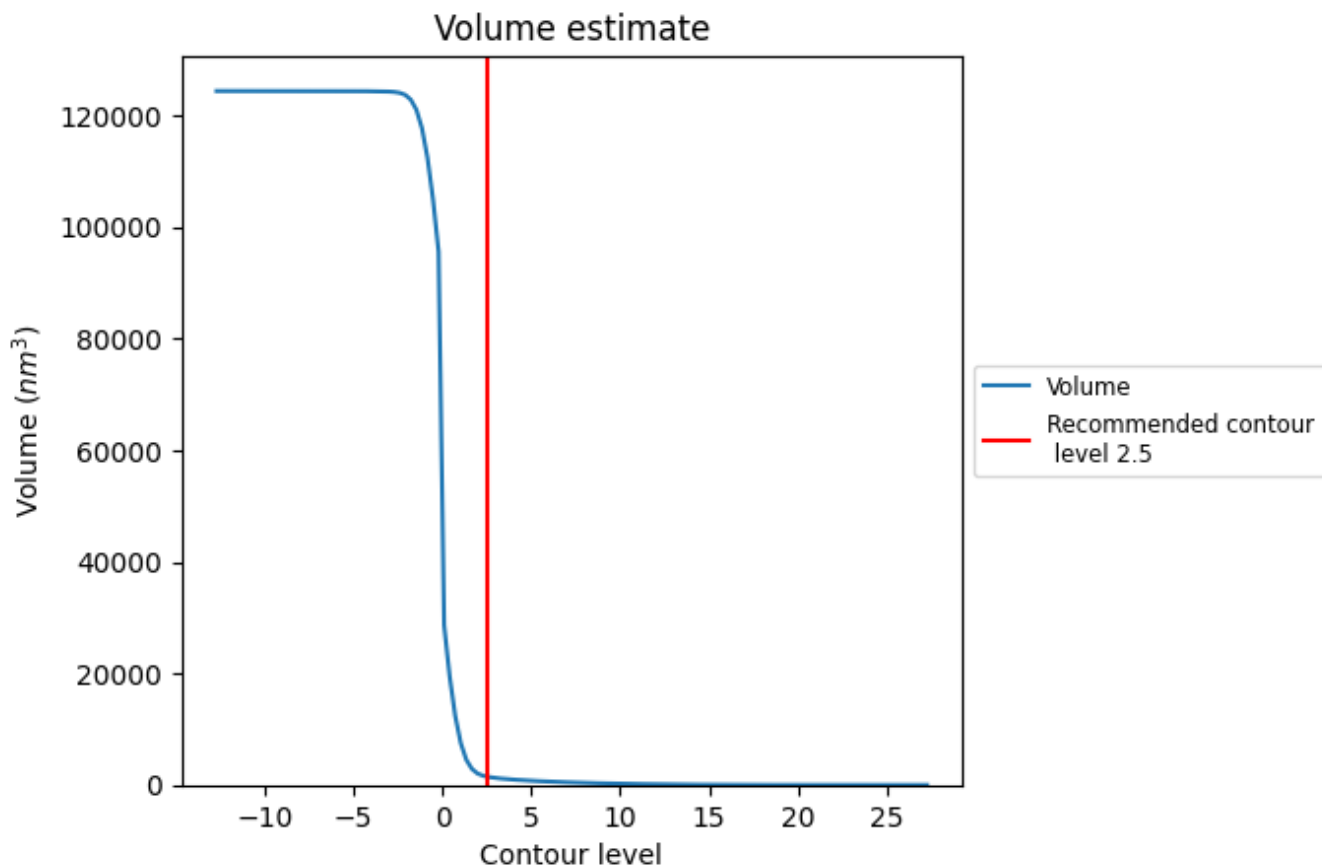
This section contains the results of statistical analysis of the map.

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.

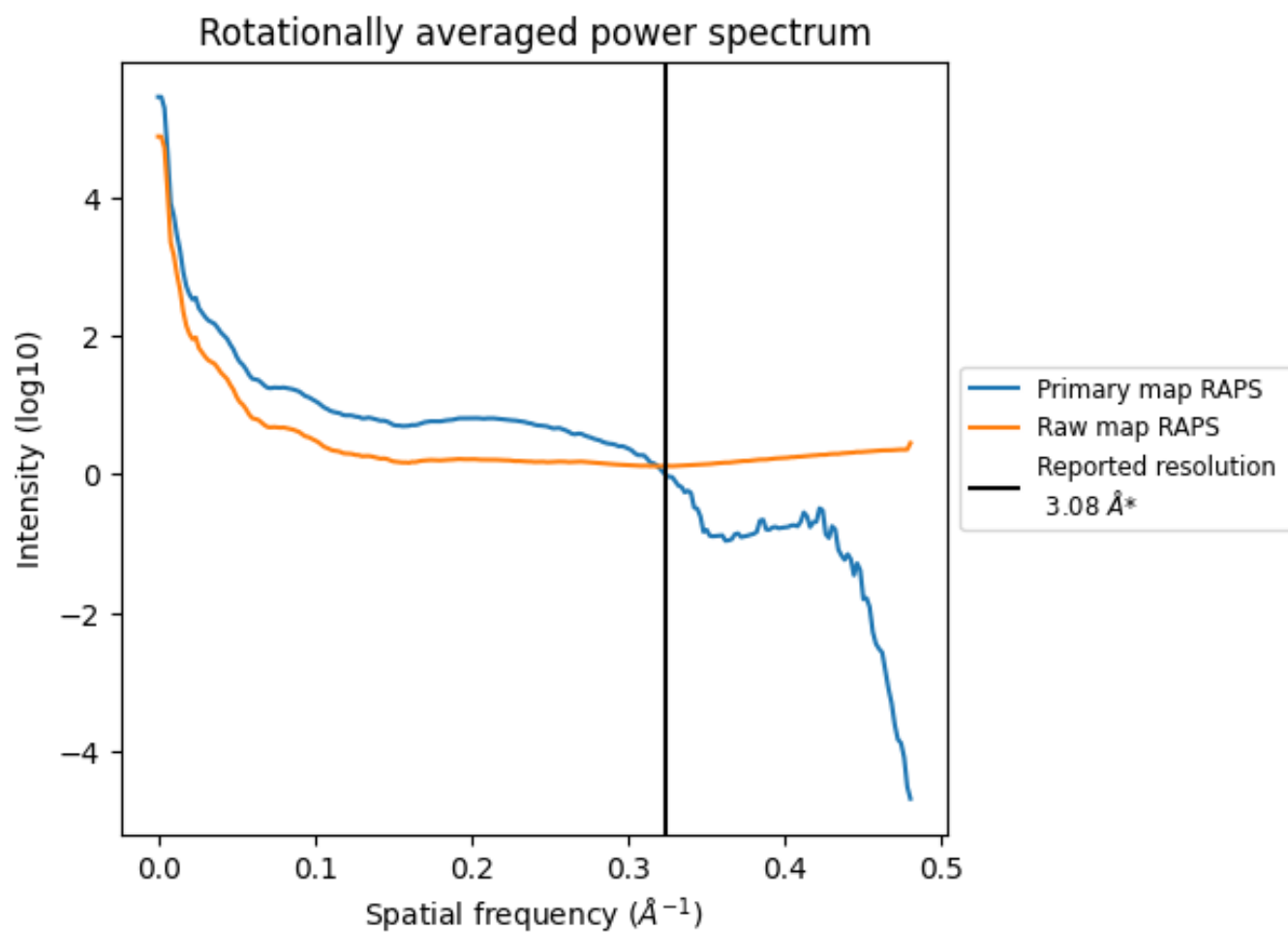
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 1491 nm^3 ; this corresponds to an approximate mass of 1347 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 [i](#)

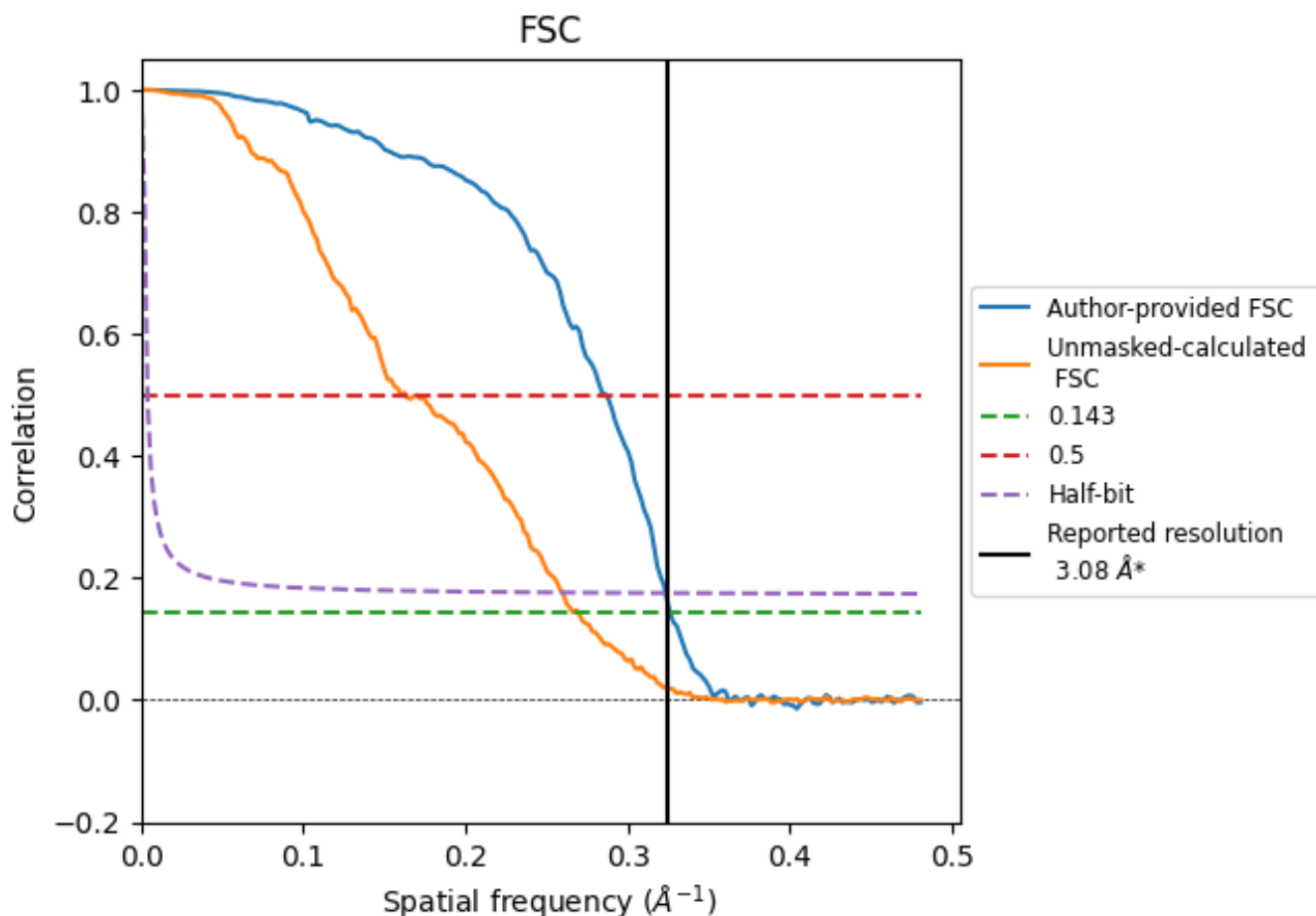


*Reported resolution corresponds to spatial frequency of 0.325 Å⁻¹

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 0.325 Å⁻¹

8.2 Resolution estimates [i](#)

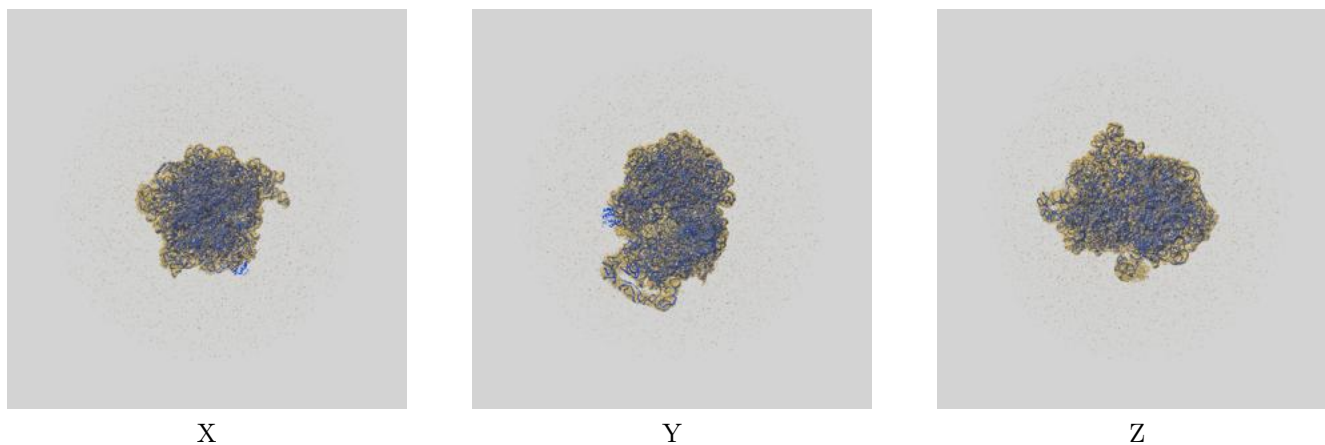
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.08	-	-
Author-provided FSC curve	3.06	3.49	3.09
Unmasked-calculated*	3.71	6.13	3.85

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.71 differs from the reported value 3.08 by more than 10 %

9 Map-model fit [i](#)

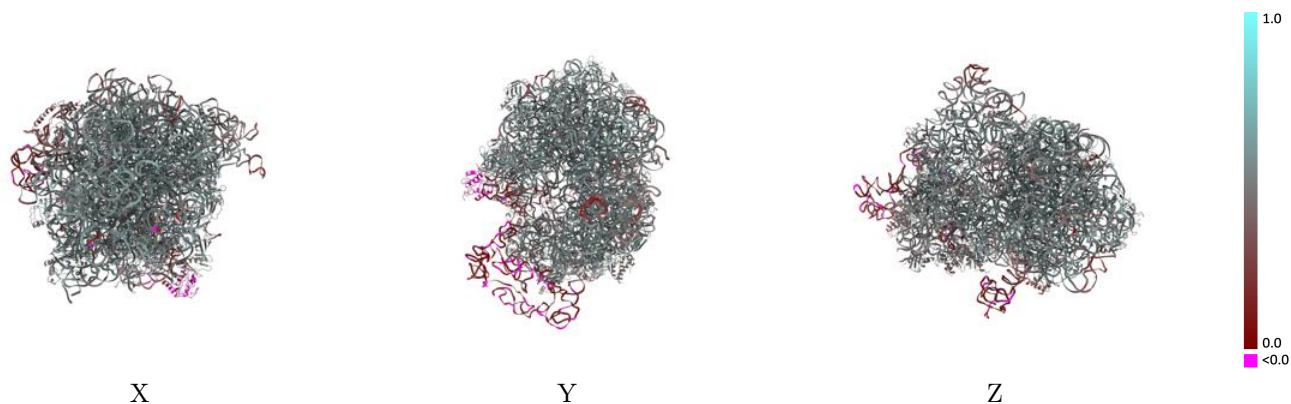
This section contains information regarding the fit between EMDB map EMD-11713 and PDB model 7AC7. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)



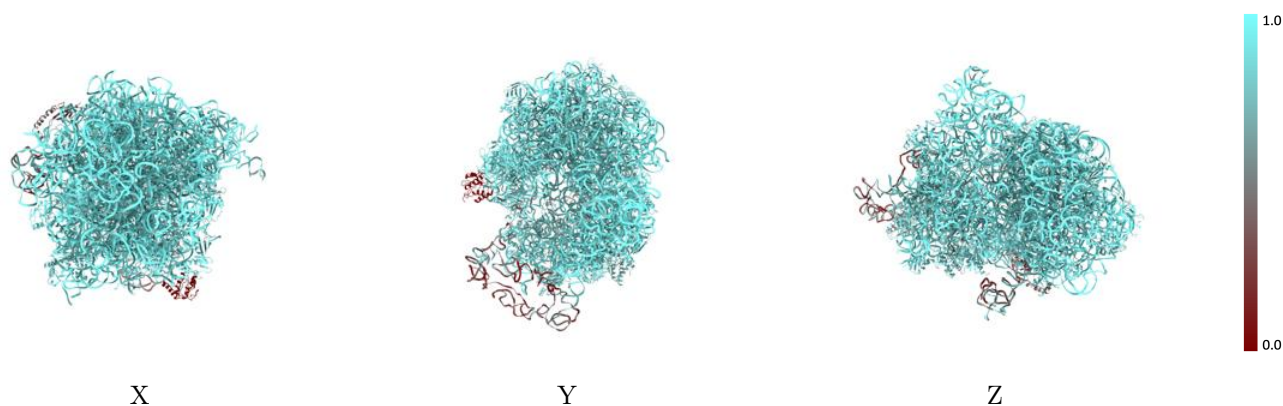
The images above show the 3D surface view of the map at the recommended contour level 2.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



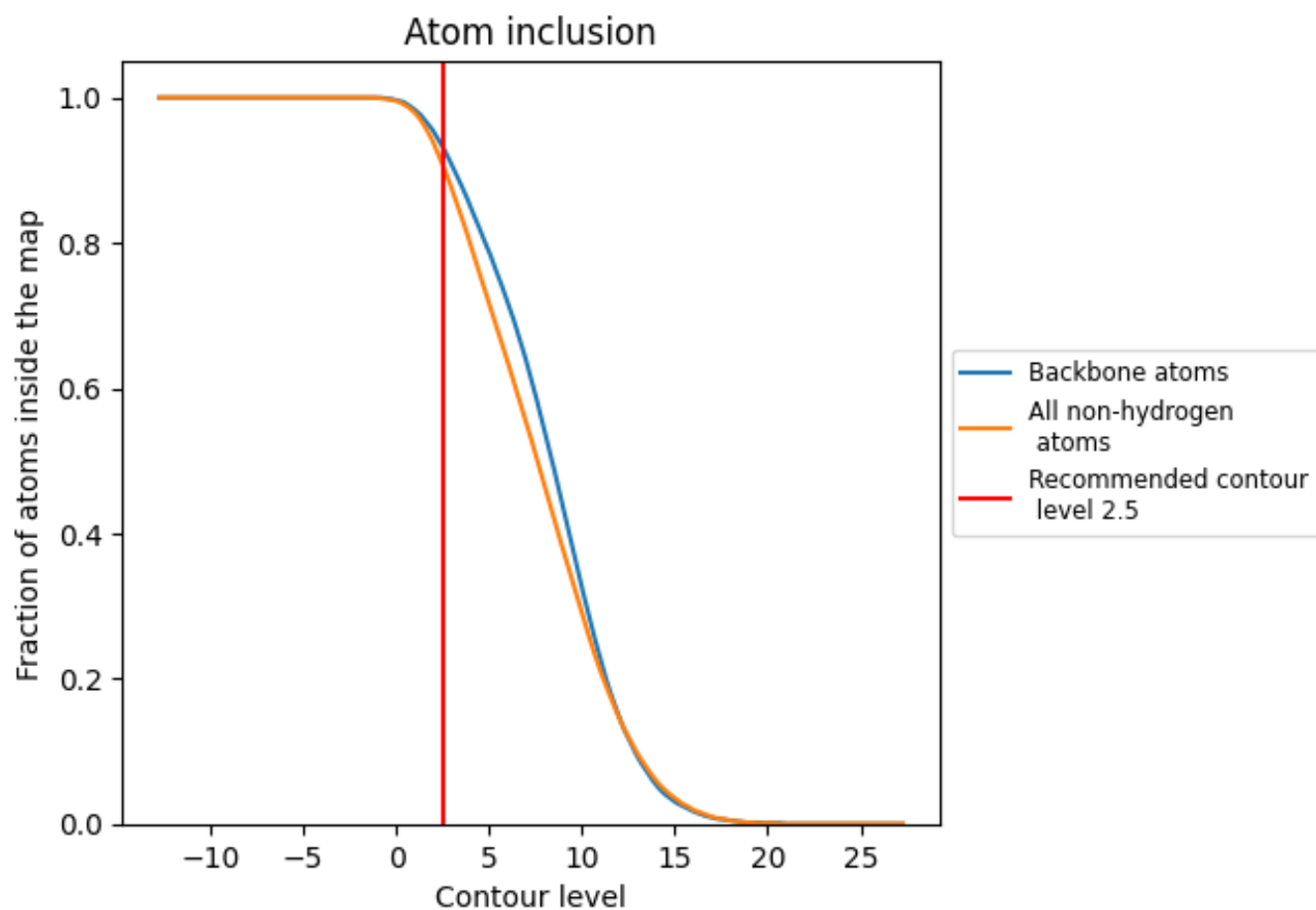
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.5).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 91% 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 (2.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9090	 0.4780
1	 0.9590	 0.5010
2	 0.9710	 0.4960
3	 0.9790	 0.5140
4	 0.5090	 0.1570
5	 0.7440	 0.3550
7	 0.9390	 0.5020
8	 0.6850	 0.2610
A	 0.9130	 0.5380
B	 0.9250	 0.5440
C	 0.9140	 0.5270
D	 0.9050	 0.5150
E	 0.8920	 0.4880
F	 0.8810	 0.4740
G	 0.4570	 0.3420
H	 0.0090	 0.0260
J	 0.9070	 0.5240
K	 0.9110	 0.5380
L	 0.9110	 0.5180
M	 0.9150	 0.5370
N	 0.9240	 0.5370
O	 0.9160	 0.5040
P	 0.9140	 0.5300
Q	 0.9190	 0.5300
R	 0.9160	 0.5250
S	 0.8860	 0.5090
T	 0.8860	 0.5110
U	 0.9100	 0.5100
V	 0.9160	 0.5240
W	 0.6880	 0.4110
X	 0.9130	 0.5340
Y	 0.9140	 0.4810
Z	 0.9240	 0.5240
a	 0.8460	 0.4550
b	 0.9200	 0.5280



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Chain	Atom inclusion	Q-score
c	 0.8920	 0.5180
d	 0.9240	 0.5260
e	 0.9040	 0.5340
f	 0.9620	 0.5560
g	 0.7650	 0.4510
h	 0.8900	 0.4950
i	 0.8870	 0.4930
j	 0.9070	 0.5140
k	 0.8790	 0.4710
l	 0.7970	 0.4310
m	 0.9210	 0.5290
n	 0.9080	 0.4780
o	 0.8630	 0.4600
p	 0.8990	 0.4910
q	 0.8890	 0.5090
r	 0.8910	 0.4660
s	 0.9070	 0.4980
t	 0.9080	 0.5030
u	 0.9070	 0.5020
v	 0.8830	 0.4990
w	 0.8790	 0.4890
x	 0.8970	 0.4770
y	 0.8870	 0.4890
z	 0.6830	 0.4030