wwPDB EM Validation Summary Report (i)

Nov 20, 2022 – 04:26 PM EST

PDB ID	:	7SA4
EMDB ID	:	EMD-24944
Title	:	Damaged 70S ribosome with PrfH bound
Authors	:	Tian, Y.; Zeng, F.; Raybarman, A.; Carruthers, A.; Li, Q.; Fatma, S.; Huang, R.H.
Deposited on	:	2021-09-22
Resolution	:	2.55 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 (i) 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 (i)) were used in the production of this report:

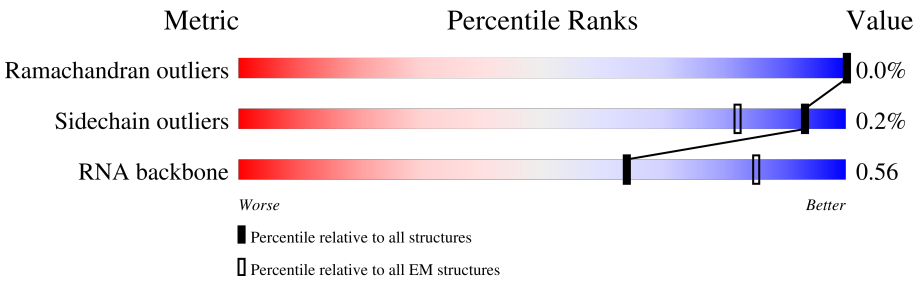
EMDB validation analysis	:	0.0.1.dev43
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.55 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)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	5% 82% 17%
2	2	1534	• 82% 17% •
3	4	120	• 88% 12%
4	5	77	• 83% 16% •
4	6	77	84% 79% 21%
5	7	25	28% 24% 28% 48%
6	8	204	13% 97% •
7	B	273	99% •

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
8	C	209	100%
9	D	201	100%
10	E	179	99%
11	F	177	98%
12	G	149	64% 99%
13	H	165	78% 78% 21%
14	I	142	94% 95% 5%
15	J	142	100%
16	K	123	100%
17	L	144	100%
18	M	136	100%
19	N	127	94% 6%
20	O	117	99%
21	P	115	99%
22	Q	118	98%
23	R	103	100%
24	S	110	99%
25	T	100	94% 6%
26	U	104	98%
27	V	94	100%
28	W	85	89% 11%
29	X	78	99%
30	Y	63	98%
31	Z	59	98%
32	a	70	11% 94% 6%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
33	b	57	98%
34	c	55	95% 5%
35	d	46	98%
36	e	65	95%
37	f	38	100%
38	g	241	10% 93% 7%
39	h	233	89% 11%
40	i	206	100%
41	j	167	93% 7%
42	k	135	76% 23%
43	l	179	13% 84% 16%
44	m	130	99%
45	n	130	97%
46	o	103	14% 96%
47	p	129	91% 9%
48	q	124	98%
49	r	118	98%
50	s	101	99%
51	t	89	99%
52	u	82	100%
53	v	84	6% 95% 5%
54	w	75	88% 12%
55	x	92	90% 10%
56	y	87	99%
57	z	71	20% 97%

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	G7M	1	2069	X	-	-	-

2 Entry composition (i)

There are 60 unique types of molecules in this entry. The entry contains 150065 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	1534	32930	14693	6041	10662	1534	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	4	120	2569	1144	468	837	120	0	0

- Molecule 4 is a RNA chain called P-tRNA, E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	5	77	1643	732	297	537	77	0	0
4	6	77	1640	732	297	535	76	0	0

- Molecule 5 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
5	7	13	275	124	49	89	13	0	0

- Molecule 6 is a protein called Peptide chain release factor H.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	8	203	1606	991	308	301	6	0	0

- Molecule 7 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	B	271	2082	1288	423	364	7	0	0

- Molecule 8 is a protein called 50S ribosomal protein L3.

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

- Molecule 9 is a protein called 50S ribosomal protein L4.

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

- Molecule 10 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	E	177	1410	899	249	256	6	0	0

- Molecule 11 is a protein called 50S ribosomal protein L6.

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

- Molecule 12 is a protein called 50S ribosomal protein L9.

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

- Molecule 13 is a protein called 50S ribosomal protein L10.

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

- Molecule 14 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	I	135	984	622	171	185	6	0	0

- Molecule 15 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	J	142	1129	714	212	199	4	0	0

- Molecule 16 is a protein called 50S ribosomal protein L14.

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

- Molecule 17 is a protein called 50S ribosomal protein L15.

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

- Molecule 18 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	M	136	1074	686	205	177	6	0	0

- Molecule 19 is a protein called 50S ribosomal protein L17.

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

- Molecule 20 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
20	O	116	892	552	178	162	0	0

- Molecule 21 is a protein called 50S ribosomal protein L19.

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

- Molecule 22 is a protein called 50S ribosomal protein L20.

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

- Molecule 23 is a protein called 50S ribosomal protein L21.

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

- Molecule 24 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	S	110	857	532	166	156	3	0	0

- Molecule 25 is a protein called 50S ribosomal protein L23.

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

- Molecule 26 is a protein called 50S ribosomal protein L24.

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

- Molecule 27 is a protein called 50S ribosomal protein L25.

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

- Molecule 28 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	W	76	582	360	117	104	1	0	0

- Molecule 29 is a protein called 50S ribosomal protein L28.

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

- Molecule 30 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	Y	62	501	308	98	94	1	0	0

- Molecule 31 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	Z	58	448	281	87	78	2	0	0

- Molecule 32 is a protein called 50S ribosomal protein L31.

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

- Molecule 33 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	b	56	444	269	94	80	1	0	0

- Molecule 34 is a protein called 50S ribosomal protein L33.

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

- Molecule 35 is a protein called 50S ribosomal protein L34.

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

- Molecule 36 is a protein called 50S ribosomal protein L35.

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

- Molecule 37 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	f	38	302	185	65	48	4	0	0

- Molecule 38 is a protein called 30S ribosomal protein S2.

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

- Molecule 39 is a protein called 30S ribosomal protein S3.

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

- Molecule 40 is a protein called 30S ribosomal protein S4.

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

- Molecule 41 is a protein called 30S ribosomal protein S5.

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

- Molecule 42 is a protein called 30S ribosomal protein S6.

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

- Molecule 43 is a protein called 30S ribosomal protein S7.

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

- Molecule 44 is a protein called 30S ribosomal protein S8.

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

- Molecule 45 is a protein called 30S ribosomal protein S9.

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

- Molecule 46 is a protein called 30S ribosomal protein S10.

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

- Molecule 47 is a protein called 30S ribosomal protein S11.

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

- Molecule 48 is a protein called 30S ribosomal protein S12.

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

- Molecule 49 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	r	116	900	558	181	158	3	0	0

- Molecule 50 is a protein called 30S ribosomal protein S14.

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

- Molecule 51 is a protein called 30S ribosomal protein S15.

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

- Molecule 52 is a protein called 30S ribosomal protein S16.

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

- Molecule 53 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	v	80	648	411	121	113	3	0	0

- Molecule 54 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	w	66	544	344	102	97	1	0	0

- Molecule 55 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	x	83	663	424	126	111	2	0	0

- Molecule 56 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	y	86	669	414	138	114	3	0	0

- Molecule 57 is a protein called 30S ribosomal protein S21.

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

- Molecule 58 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
58	1	292	292	292	0
58	2	127	127	127	0
58	4	8	8	8	0
58	5	6	6	6	0
58	B	1	1	1	0
58	C	1	1	1	0
58	Q	1	1	1	0
58	b	1	1	1	0
58	i	1	1	1	0
58	r	1	1	1	0

- Molecule 59 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

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

- Molecule 60 is water.

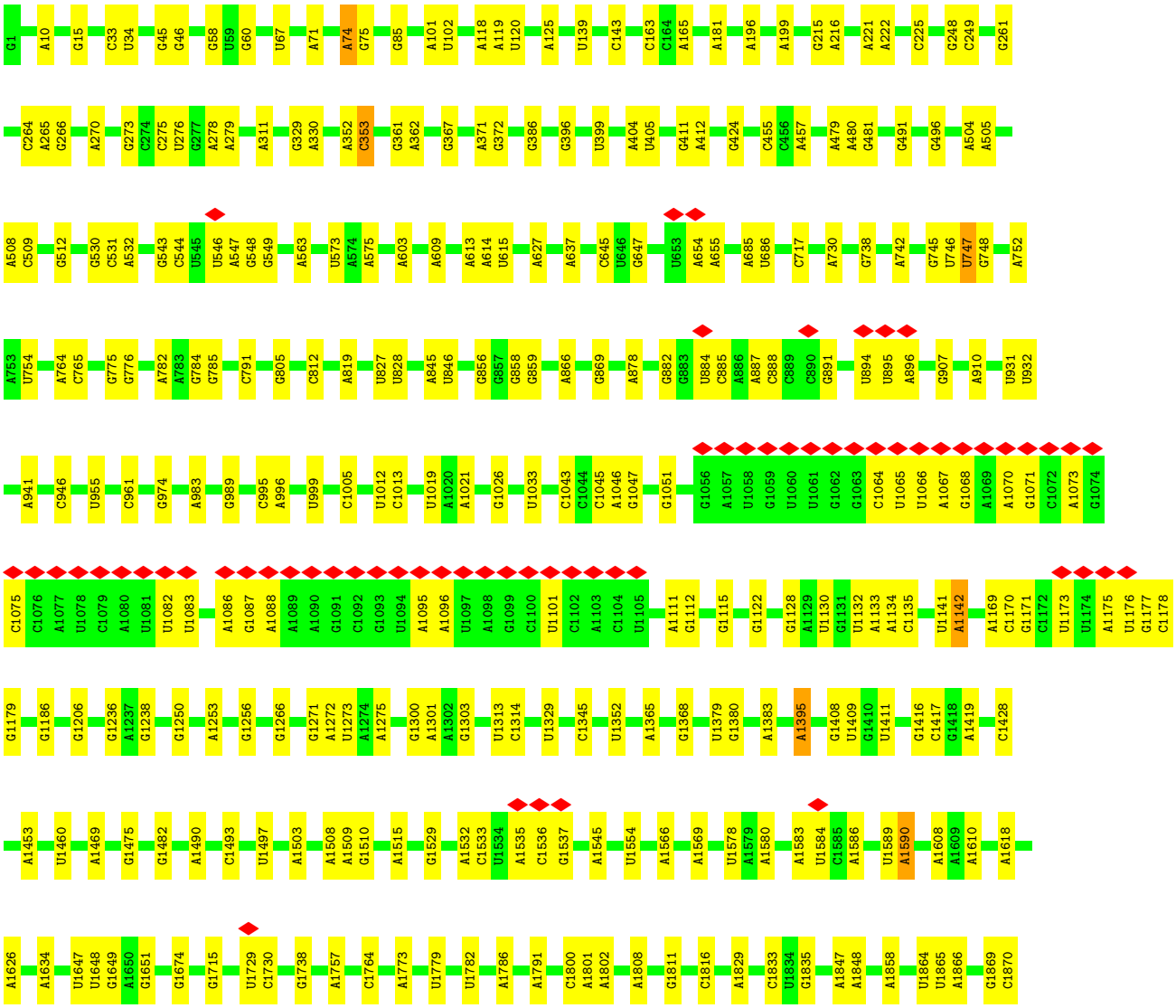
Mol	Chain	Residues	Atoms		AltConf
			Total	O	
60	B	2	2	2	0

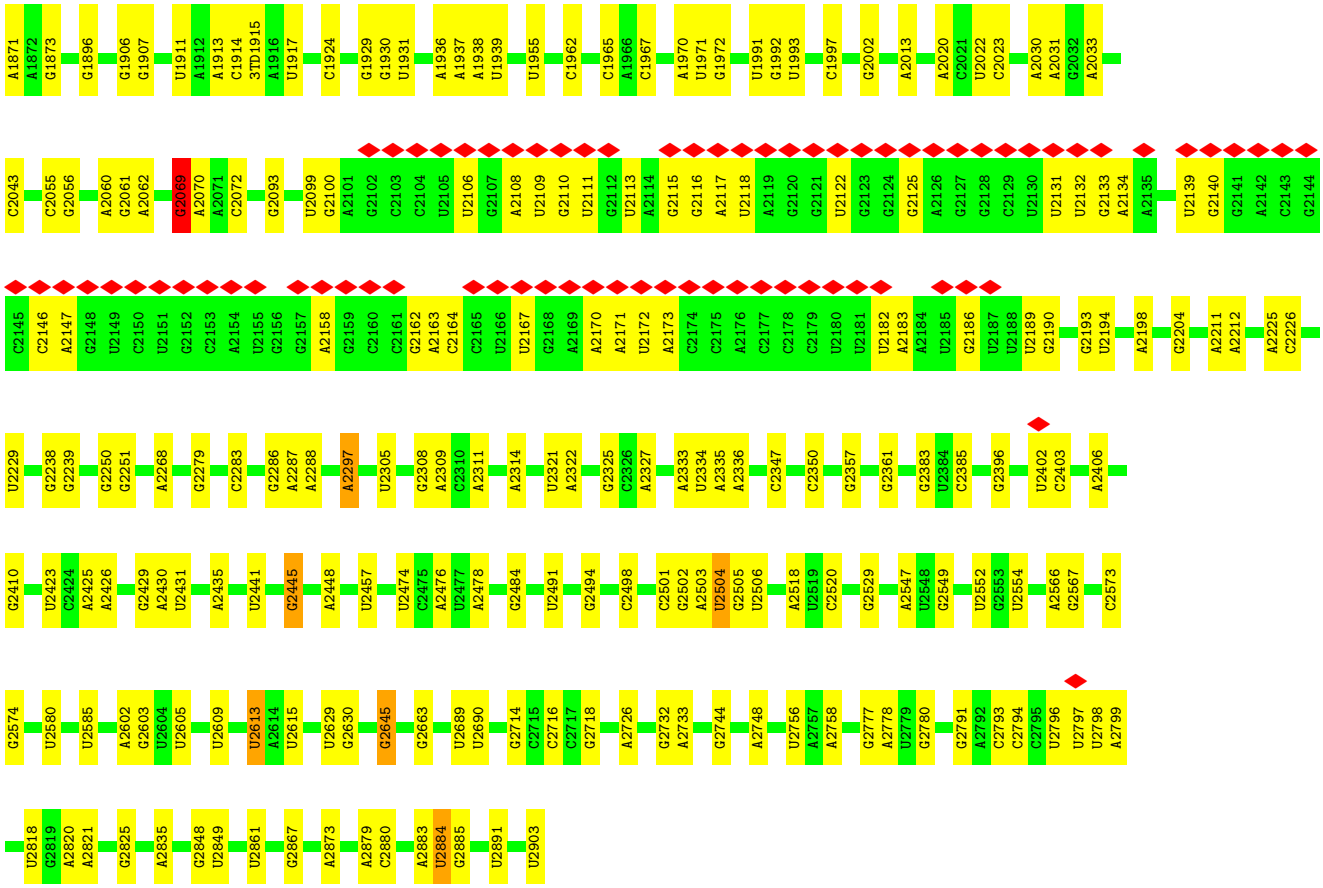
3 Residue-property plots (i)

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

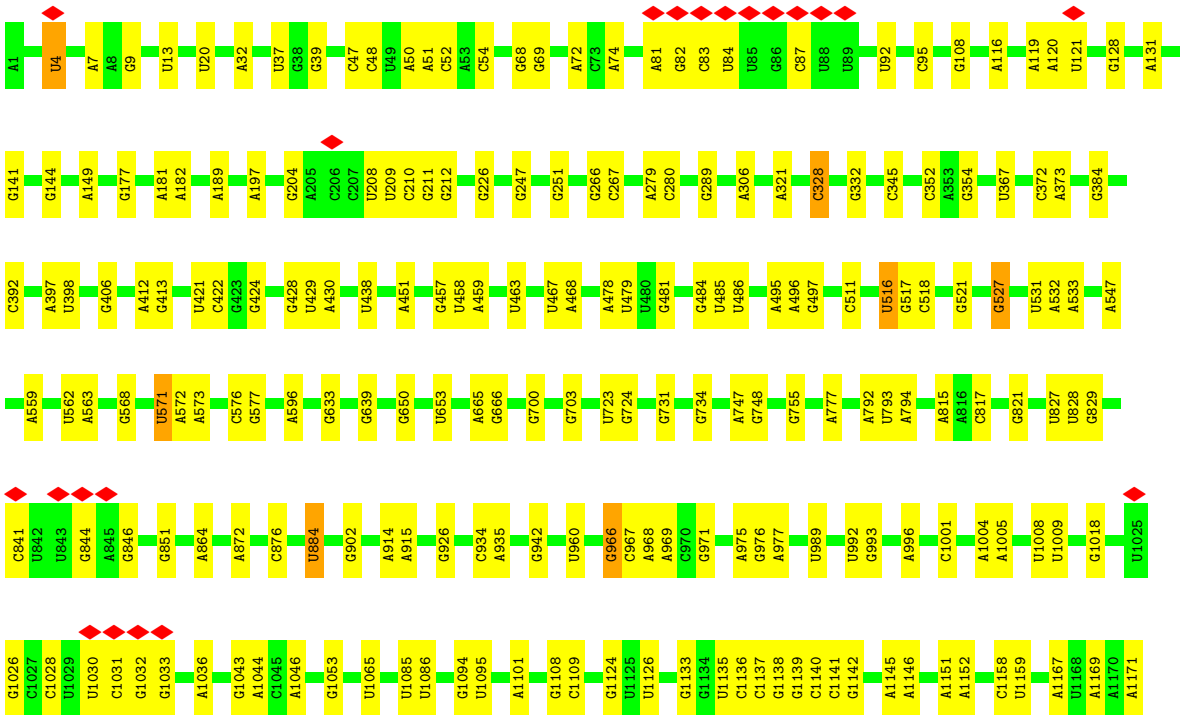
Chain 1: 5% 82% 17%

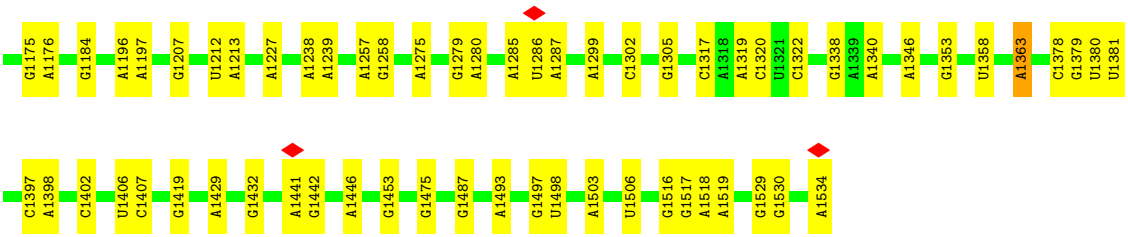




- Molecule 2: 16S ribosomal RNA

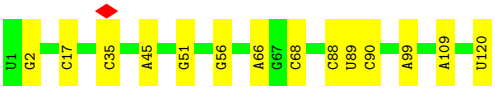
Chain 2:





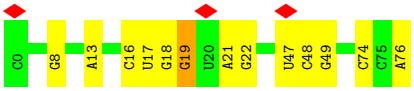
- Molecule 3: 5S ribosomal RNA

Chain 4:



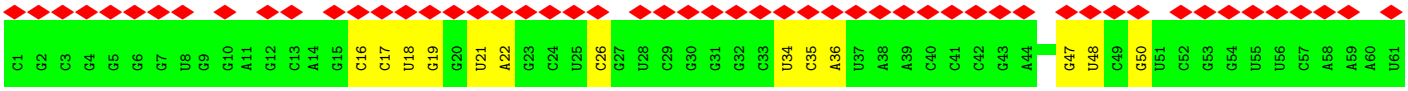
- Molecule 4: P-tRNA, E-tRNA

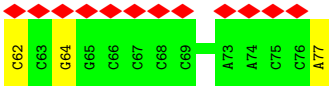
Chain 5:



- Molecule 4: P-tRNA, E-tRNA

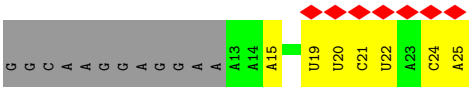
Chain 6:





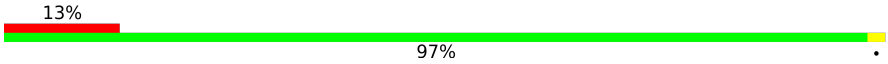
- Molecule 5: mRNA

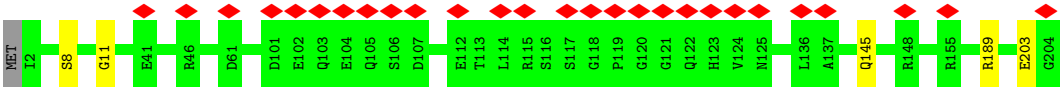
Chain 7:



- Molecule 6: Peptide chain release factor H

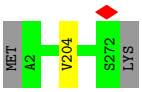
Chain 8:





- Molecule 7: 50S ribosomal protein L2

Chain B: 99%

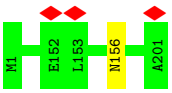


• Molecule 8: 50S ribosomal protein L3

Chain C: 100%

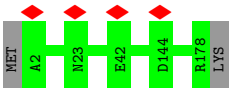
• Molecule 9: 50S ribosomal protein L4

Chain D: 100%



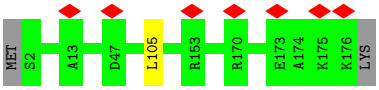
• Molecule 10: 50S ribosomal protein L5

Chain E: 99%



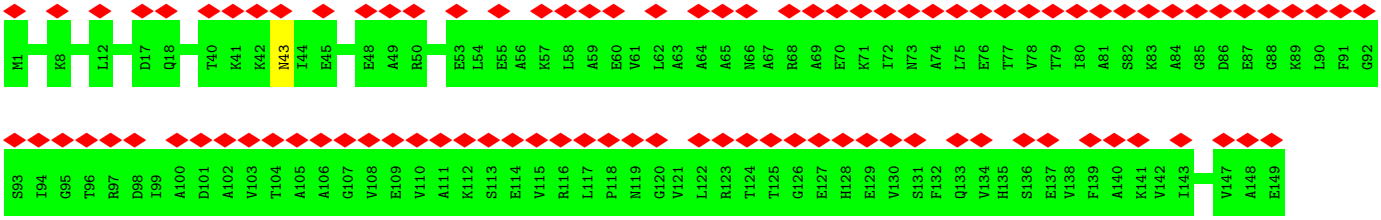
• Molecule 11: 50S ribosomal protein L6

Chain F: 98%



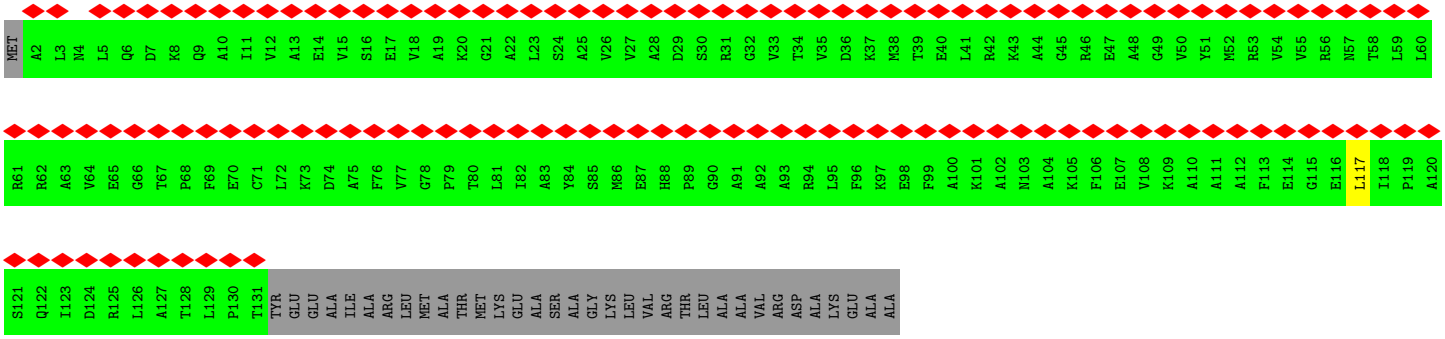
• Molecule 12: 50S ribosomal protein L9

Chain G: 64% 99%



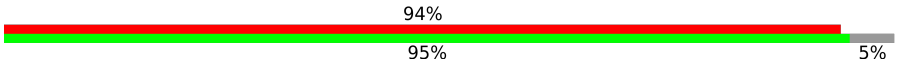
• Molecule 13: 50S ribosomal protein L10

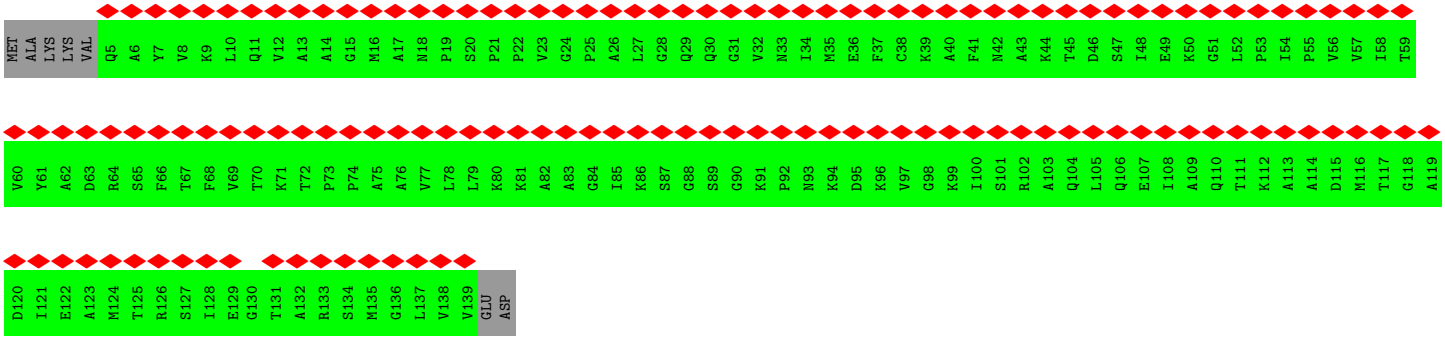
Chain H: 78% 78% 21%



- Molecule 14: 50S ribosomal protein L11

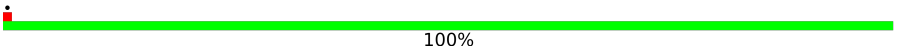
Chain I:





- Molecule 15: 50S ribosomal protein L13

Chain J:



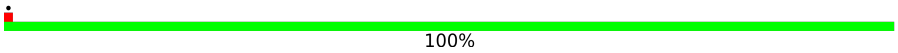
- Molecule 16: 50S ribosomal protein L14

Chain K:

There are no outlier residues recorded for this chain.

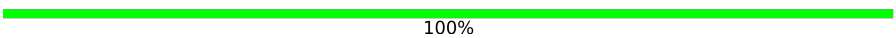
- Molecule 17: 50S ribosomal protein L15

Chain L:



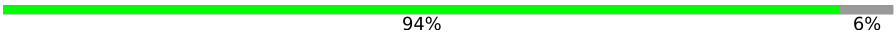
- Molecule 18: 50S ribosomal protein L16

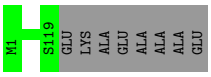
Chain M:



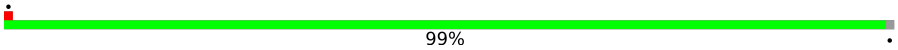
There are no outlier residues recorded for this chain.

• Molecule 19: 50S ribosomal protein L17

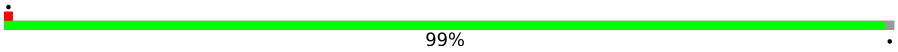
Chain N: 



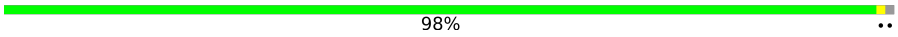
• Molecule 20: 50S ribosomal protein L18

Chain O: 

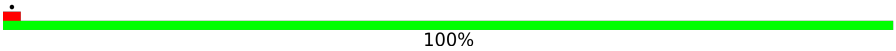
• Molecule 21: 50S ribosomal protein L19

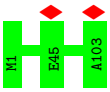
Chain P: 

• Molecule 22: 50S ribosomal protein L20

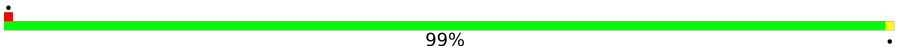
Chain Q: 

• Molecule 23: 50S ribosomal protein L21

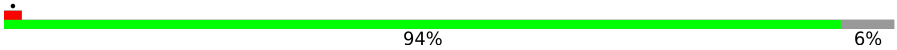
Chain R: 

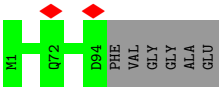


• Molecule 24: 50S ribosomal protein L22

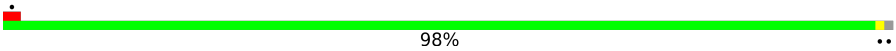
Chain S: 

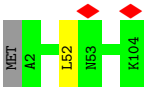
• Molecule 25: 50S ribosomal protein L23

Chain T: 

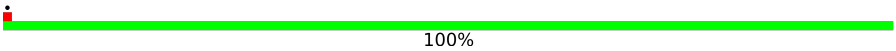


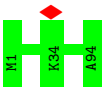
• Molecule 26: 50S ribosomal protein L24

Chain U: 



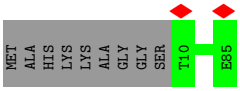
• Molecule 27: 50S ribosomal protein L25

Chain V: 

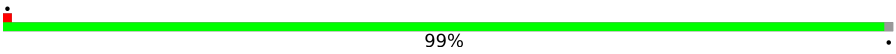


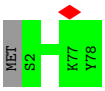
• Molecule 28: 50S ribosomal protein L27

Chain W:

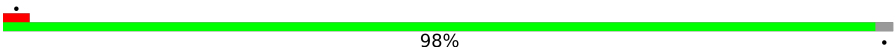


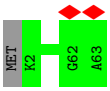
• Molecule 29: 50S ribosomal protein L28

Chain X: 

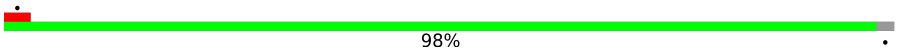


• Molecule 30: 50S ribosomal protein L29

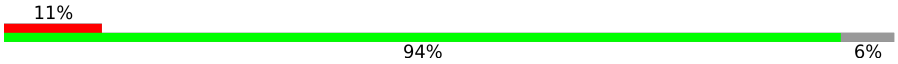
Chain Y: 

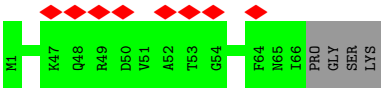


• Molecule 31: 50S ribosomal protein L30

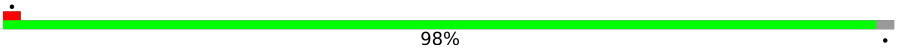
Chain Z: 

• Molecule 32: 50S ribosomal protein L31

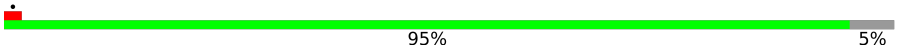
Chain a: 

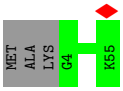


- Molecule 33: 50S ribosomal protein L32

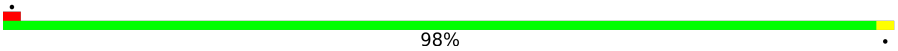
Chain b: 

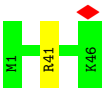
- Molecule 34: 50S ribosomal protein L33

Chain c: 

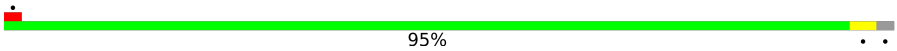


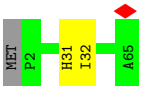
- Molecule 35: 50S ribosomal protein L34

Chain d: 

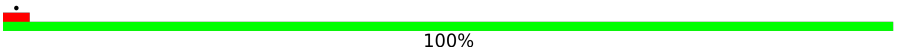


- Molecule 36: 50S ribosomal protein L35

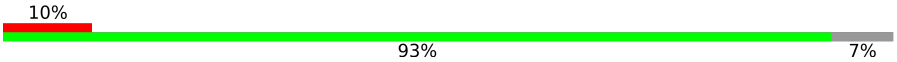
Chain e: 

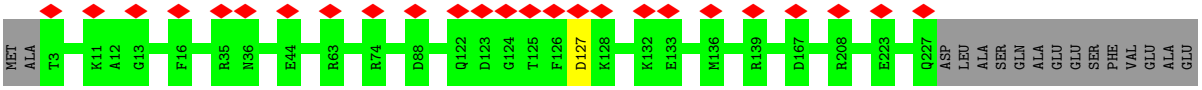


- Molecule 37: 50S ribosomal protein L36

Chain f: 

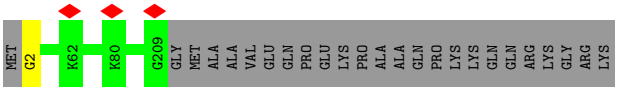
- Molecule 38: 30S ribosomal protein S2

Chain g: 



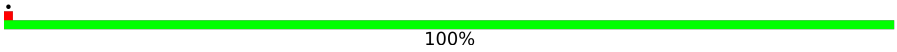
- Molecule 39: 30S ribosomal protein S3

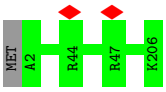
Chain h:



- Molecule 40: 30S ribosomal protein S4

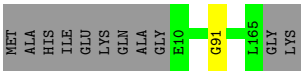
Chain i:





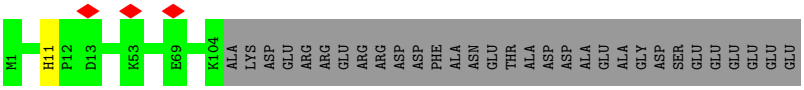
- Molecule 41: 30S ribosomal protein S5

Chain j:



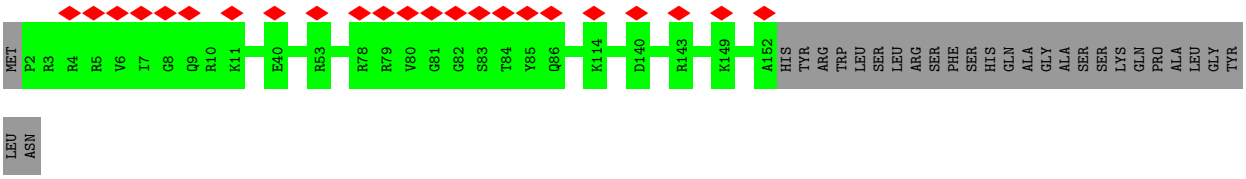
- Molecule 42: 30S ribosomal protein S6

Chain k:



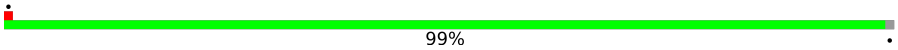
- Molecule 43: 30S ribosomal protein S7

Chain l:



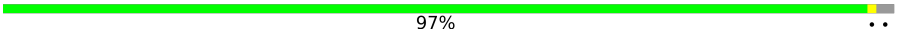
- Molecule 44: 30S ribosomal protein S8

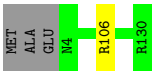
Chain m:



- Molecule 45: 30S ribosomal protein S9

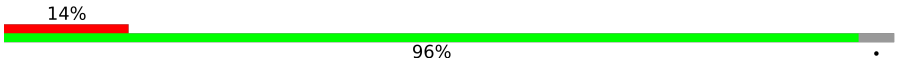
Chain n:

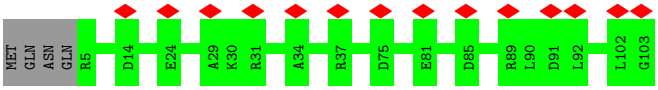




• Molecule 46: 30S ribosomal protein S10

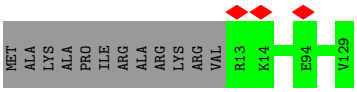
Chain o:





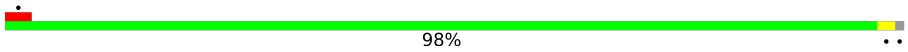
• Molecule 47: 30S ribosomal protein S11

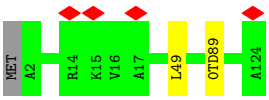
Chain p:



• Molecule 48: 30S ribosomal protein S12

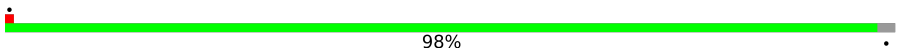
Chain q:

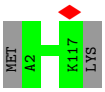




• Molecule 49: 30S ribosomal protein S13

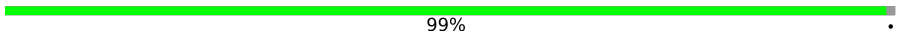
Chain r:





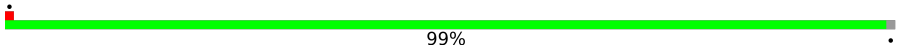
• Molecule 50: 30S ribosomal protein S14

Chain s:



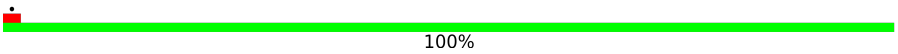
• Molecule 51: 30S ribosomal protein S15

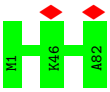
Chain t:



• Molecule 52: 30S ribosomal protein S16

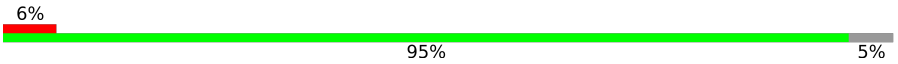
Chain u:

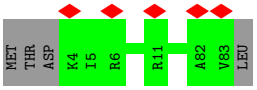




• Molecule 53: 30S ribosomal protein S17

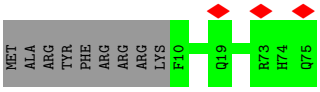
Chain v:





• Molecule 54: 30S ribosomal protein S18

Chain w:

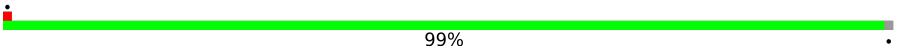


• Molecule 55: 30S ribosomal protein S19

Chain x:

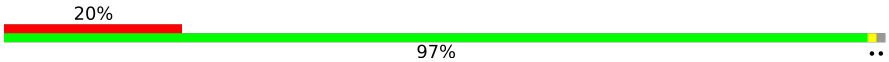
• Molecule 56: 30S ribosomal protein S20

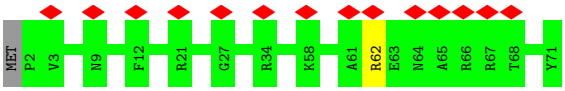
Chain y:



• Molecule 57: 30S ribosomal protein S21

Chain z:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	207600	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	30.0	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.139	Depositor
Minimum map value	-0.055	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	403.19998, 403.19998, 403.19998	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	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: MG, 5MU, 6MZ, ZN, 3TD, 2MG, OMU, A3P, OMC, PSU, MA6, OMG, UR3, 0TD, 5MC, G7M, 4OC, 2MA, 1MG

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	0.98	13/69285 (0.0%)	0.89	68/108083 (0.1%)
2	2	0.88	14/36558 (0.0%)	0.91	55/57015 (0.1%)
3	4	0.81	0/2872	0.81	0/4478
4	5	0.67	0/1835	0.85	1/2859 (0.0%)
4	6	0.31	0/1832	0.84	0/2855
5	7	0.61	0/307	0.88	0/475
6	8	0.45	1/1636 (0.1%)	0.60	0/2208
7	B	0.51	1/2121 (0.0%)	0.59	0/2852
8	C	0.48	0/1586	0.57	0/2134
9	D	0.43	0/1571	0.55	0/2113
10	E	0.38	0/1434	0.56	0/1926
11	F	0.36	0/1333	0.56	1/1805 (0.1%)
12	G	0.31	0/1122	0.54	0/1515
13	H	0.29	0/993	0.62	1/1340 (0.1%)
14	I	0.27	0/998	0.52	0/1348
15	J	0.48	0/1152	0.52	0/1551
16	K	0.46	0/955	0.55	0/1279
17	L	0.42	0/1062	0.58	0/1413
18	M	0.46	0/1093	0.56	0/1460
19	N	0.46	0/964	0.52	0/1289
20	O	0.40	0/902	0.53	0/1209
21	P	0.47	0/929	0.53	0/1242
22	Q	0.52	0/960	0.55	0/1278
23	R	0.48	0/829	0.58	0/1107
24	S	0.46	0/864	0.53	0/1156
25	T	0.39	0/752	0.49	0/1005
26	U	0.40	0/796	0.55	1/1062 (0.1%)
27	V	0.42	0/766	0.51	0/1025
28	W	0.48	0/589	0.59	0/779
29	X	0.45	0/635	0.54	0/848
30	Y	0.31	0/502	0.50	0/667

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
31	Z	0.41	0/452	0.59	0/605
32	a	0.35	0/531	0.51	0/709
33	b	0.46	0/450	0.57	0/599
34	c	0.43	0/433	0.53	0/576
35	d	0.44	0/380	0.51	0/498
36	e	0.47	0/513	0.60	0/676
37	f	0.46	0/303	0.54	0/397
38	g	0.34	0/1791	0.54	0/2413
39	h	0.41	0/1663	0.53	0/2241
40	i	0.41	0/1665	0.49	0/2227
41	j	0.48	0/1165	0.59	0/1568
42	k	0.37	0/867	0.52	0/1171
43	l	0.33	0/1195	0.51	0/1602
44	m	0.42	0/989	0.54	0/1326
45	n	0.39	0/1034	0.55	0/1375
46	o	0.39	0/800	0.60	0/1082
47	p	0.38	0/893	0.51	0/1205
48	q	0.45	0/960	0.62	1/1286 (0.1%)
49	r	0.38	0/909	0.55	0/1215
50	s	0.39	0/817	0.47	0/1088
51	t	0.38	0/722	0.47	0/964
52	u	0.41	0/659	0.53	0/884
53	v	0.40	0/657	0.56	0/881
54	w	0.43	0/553	0.53	0/743
55	x	0.37	0/680	0.50	0/915
56	y	0.37	0/675	0.51	0/895
57	z	0.33	0/597	0.49	0/792
All	All	0.81	29/161586 (0.0%)	0.81	128/241309 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	1	3	0
22	Q	0	1
36	e	0	1
38	g	0	1
39	h	0	1
All	All	3	4

The worst 5 of 29 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	8	11	GLY	C-N	8.55	1.50	1.34
1	1	74	A	C6-N1	-7.07	1.30	1.35
2	2	1363	A	C6-N1	-6.52	1.30	1.35
1	1	2013	A	C6-N1	-6.45	1.31	1.35
1	1	1142	A	C6-N1	-6.44	1.31	1.35

The worst 5 of 128 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	2	1358	U	C5-C4-O4	25.37	141.12	125.90
2	2	37	U	C5-C4-O4	25.30	141.08	125.90
1	1	2613	U	C5-C4-O4	24.51	140.61	125.90
1	1	1141	U	C5-C4-O4	24.49	140.59	125.90
2	2	37	U	N3-C4-O4	-24.23	102.44	119.40

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	1	2069	G7M	C4',C3',C2'

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
22	Q	5	LYS	Peptide
36	e	31	HIS	Peptide
38	g	127	ASP	Peptide
39	h	2	GLY	Peptide

5.2 Too-close contacts (i)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	
6	8	201/204 (98%)	184 (92%)	16 (8%)	1 (0%)	29	40
7	B	269/273 (98%)	263 (98%)	6 (2%)	0	100	100
8	C	207/209 (99%)	203 (98%)	4 (2%)	0	100	100
9	D	199/201 (99%)	194 (98%)	5 (2%)	0	100	100
10	E	175/179 (98%)	165 (94%)	10 (6%)	0	100	100
11	F	173/177 (98%)	164 (95%)	9 (5%)	0	100	100
12	G	147/149 (99%)	135 (92%)	12 (8%)	0	100	100
13	H	128/165 (78%)	114 (89%)	14 (11%)	0	100	100
14	I	133/142 (94%)	125 (94%)	8 (6%)	0	100	100
15	J	140/142 (99%)	139 (99%)	1 (1%)	0	100	100
16	K	121/123 (98%)	118 (98%)	3 (2%)	0	100	100
17	L	142/144 (99%)	140 (99%)	2 (1%)	0	100	100
18	M	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
19	N	117/127 (92%)	112 (96%)	5 (4%)	0	100	100
20	O	114/117 (97%)	112 (98%)	2 (2%)	0	100	100
21	P	112/115 (97%)	109 (97%)	3 (3%)	0	100	100
22	Q	115/118 (98%)	114 (99%)	1 (1%)	0	100	100
23	R	101/103 (98%)	95 (94%)	6 (6%)	0	100	100
24	S	108/110 (98%)	106 (98%)	2 (2%)	0	100	100
25	T	92/100 (92%)	91 (99%)	1 (1%)	0	100	100
26	U	101/104 (97%)	97 (96%)	4 (4%)	0	100	100
27	V	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
28	W	74/85 (87%)	74 (100%)	0	0	100	100
29	X	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
30	Y	60/63 (95%)	58 (97%)	2 (3%)	0	100	100
31	Z	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
32	a	64/70 (91%)	59 (92%)	5 (8%)	0	100	100
33	b	54/57 (95%)	51 (94%)	3 (6%)	0	100	100
34	c	50/55 (91%)	50 (100%)	0	0	100	100
35	d	44/46 (96%)	44 (100%)	0	0	100	100
36	e	62/65 (95%)	58 (94%)	3 (5%)	1 (2%)	9	12
37	f	36/38 (95%)	36 (100%)	0	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	g	223/241 (92%)	211 (95%)	12 (5%)	0	100	100
39	h	206/233 (88%)	197 (96%)	9 (4%)	0	100	100
40	i	203/206 (98%)	202 (100%)	1 (0%)	0	100	100
41	j	154/167 (92%)	144 (94%)	9 (6%)	1 (1%)	25	34
42	k	102/135 (76%)	100 (98%)	2 (2%)	0	100	100
43	l	149/179 (83%)	146 (98%)	3 (2%)	0	100	100
44	m	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
45	n	125/130 (96%)	115 (92%)	10 (8%)	0	100	100
46	o	97/103 (94%)	89 (92%)	8 (8%)	0	100	100
47	p	115/129 (89%)	112 (97%)	3 (3%)	0	100	100
48	q	120/124 (97%)	115 (96%)	5 (4%)	0	100	100
49	r	114/118 (97%)	108 (95%)	6 (5%)	0	100	100
50	s	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
51	t	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
52	u	80/82 (98%)	79 (99%)	1 (1%)	0	100	100
53	v	78/84 (93%)	74 (95%)	4 (5%)	0	100	100
54	w	64/75 (85%)	64 (100%)	0	0	100	100
55	x	81/92 (88%)	80 (99%)	1 (1%)	0	100	100
56	y	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
57	z	68/71 (96%)	68 (100%)	0	0	100	100
All	All	6070/6424 (94%)	5848 (96%)	219 (4%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	8	203	GLU
36	e	32	ILE
41	j	91	GLY

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	
6	8	170/171 (99%)	167 (98%)	3 (2%)	59	74
7	B	216/218 (99%)	216 (100%)	0	100	100
8	C	164/164 (100%)	164 (100%)	0	100	100
9	D	165/165 (100%)	164 (99%)	1 (1%)	86	92
10	E	148/150 (99%)	148 (100%)	0	100	100
11	F	136/138 (99%)	136 (100%)	0	100	100
12	G	114/114 (100%)	113 (99%)	1 (1%)	78	86
13	H	99/123 (80%)	99 (100%)	0	100	100
14	I	104/110 (94%)	104 (100%)	0	100	100
15	J	116/116 (100%)	116 (100%)	0	100	100
16	K	104/104 (100%)	104 (100%)	0	100	100
17	L	103/103 (100%)	103 (100%)	0	100	100
18	M	109/109 (100%)	109 (100%)	0	100	100
19	N	99/103 (96%)	99 (100%)	0	100	100
20	O	86/87 (99%)	86 (100%)	0	100	100
21	P	99/100 (99%)	99 (100%)	0	100	100
22	Q	89/90 (99%)	89 (100%)	0	100	100
23	R	84/84 (100%)	84 (100%)	0	100	100
24	S	93/93 (100%)	92 (99%)	1 (1%)	73	83
25	T	81/84 (96%)	81 (100%)	0	100	100
26	U	84/85 (99%)	84 (100%)	0	100	100
27	V	78/78 (100%)	78 (100%)	0	100	100
28	W	58/63 (92%)	58 (100%)	0	100	100
29	X	67/68 (98%)	67 (100%)	0	100	100
30	Y	54/55 (98%)	54 (100%)	0	100	100
31	Z	48/49 (98%)	48 (100%)	0	100	100
32	a	59/62 (95%)	59 (100%)	0	100	100
33	b	47/48 (98%)	47 (100%)	0	100	100
34	c	47/49 (96%)	47 (100%)	0	100	100
35	d	38/38 (100%)	37 (97%)	1 (3%)	46	61

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	e	51/52 (98%)	51 (100%)	0	100	100
37	f	34/34 (100%)	34 (100%)	0	100	100
38	g	187/199 (94%)	187 (100%)	0	100	100
39	h	171/190 (90%)	171 (100%)	0	100	100
40	i	172/173 (99%)	172 (100%)	0	100	100
41	j	119/126 (94%)	119 (100%)	0	100	100
42	k	91/116 (78%)	90 (99%)	1 (1%)	73	83
43	l	124/147 (84%)	124 (100%)	0	100	100
44	m	104/105 (99%)	104 (100%)	0	100	100
45	n	105/107 (98%)	104 (99%)	1 (1%)	76	84
46	o	86/90 (96%)	86 (100%)	0	100	100
47	p	90/99 (91%)	90 (100%)	0	100	100
48	q	102/103 (99%)	102 (100%)	0	100	100
49	r	94/96 (98%)	94 (100%)	0	100	100
50	s	83/84 (99%)	83 (100%)	0	100	100
51	t	76/77 (99%)	76 (100%)	0	100	100
52	u	65/65 (100%)	65 (100%)	0	100	100
53	v	74/78 (95%)	74 (100%)	0	100	100
54	w	57/65 (88%)	57 (100%)	0	100	100
55	x	72/79 (91%)	72 (100%)	0	100	100
56	y	65/66 (98%)	65 (100%)	0	100	100
57	z	60/61 (98%)	59 (98%)	1 (2%)	60	75
All	All	5041/5233 (96%)	5031 (100%)	10 (0%)	93	97

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
42	k	11	HIS
45	n	106	ARG
57	z	62	ARG
9	D	156	ASN
12	G	43	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
38	g	93	ASN
48	q	5	ASN
42	k	58	HIS
50	s	60	GLN
14	I	104	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2897/2903 (99%)	473 (16%)	12 (0%)
2	2	1524/1534 (99%)	250 (16%)	8 (0%)
3	4	119/120 (99%)	14 (11%)	0
4	5	76/77 (98%)	13 (17%)	2 (2%)
4	6	76/77 (98%)	16 (21%)	1 (1%)
5	7	12/25 (48%)	7 (58%)	0
All	All	4704/4736 (99%)	773 (16%)	23 (0%)

5 of 773 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	10	A
1	1	15	G
1	1	33	C
1	1	34	U
1	1	45	G

5 of 23 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	2	484	G
2	2	1004	A
2	2	516	PSU
2	2	1109	C
1	1	2146	C

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

35 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	$\#\|Z\| > 2$
2	4OC	2	1402	2	20,23,24	0.77	0	26,32,35	1.02	2 (7%)
2	A3P	2	1493	2	23,28,29	0.97	0	23,42,45	1.36	3 (13%)
1	2MA	1	2503	1,58	17,25,26	0.96	1 (5%)	17,37,40	1.07	2 (11%)
1	PSU	1	746	1,58	18,21,22	1.47	5 (27%)	22,30,33	1.86	3 (13%)
1	6MZ	1	2030	1	18,25,26	0.86	0	16,36,39	2.66	4 (25%)
1	6MZ	1	1618	1	18,25,26	0.83	0	16,36,39	2.21	4 (25%)
1	3TD	1	1915	1	18,22,23	0.65	0	22,32,35	1.35	4 (18%)
1	PSU	1	2504	1	18,21,22	1.56	4 (22%)	22,30,33	1.97	4 (18%)
2	5MC	2	967	2	18,22,23	0.93	2 (11%)	26,32,35	1.15	2 (7%)
2	2MG	2	1516	2	18,26,27	1.09	1 (5%)	16,38,41	1.16	3 (18%)
1	PSU	1	2605	1	18,21,22	1.47	4 (22%)	22,30,33	1.91	4 (18%)
1	1MG	1	745	1	18,26,27	0.62	0	19,39,42	1.15	3 (15%)
1	OMU	1	2552	1	19,22,23	1.32	4 (21%)	26,31,34	1.87	5 (19%)
2	PSU	2	516	2,58	18,21,22	1.45	4 (22%)	22,30,33	2.07	4 (18%)
1	2MG	1	2445	1	18,26,27	1.15	1 (5%)	16,38,41	1.14	3 (18%)
2	2MG	2	966	2	18,26,27	1.04	1 (5%)	16,38,41	1.21	3 (18%)
1	OMG	1	2251	1,4	18,26,27	1.03	1 (5%)	19,38,41	1.12	3 (15%)
2	5MC	2	1407	2	18,22,23	0.98	2 (11%)	26,32,35	1.19	3 (11%)
1	5MU	1	1939	1	19,22,23	1.49	4 (21%)	28,32,35	2.28	6 (21%)
1	G7M	1	2069	1	20,26,27	1.26	2 (10%)	17,39,42	1.06	1 (5%)
1	5MU	1	747	1	19,22,23	1.43	4 (21%)	28,32,35	2.06	5 (17%)
1	PSU	1	1917	1	18,21,22	1.42	4 (22%)	22,30,33	1.98	3 (13%)
1	PSU	1	2457	1	18,21,22	1.54	5 (27%)	22,30,33	2.09	5 (22%)
1	2MG	1	1835	1	18,26,27	0.97	1 (5%)	16,38,41	1.23	4 (25%)
2	MA6	2	1518	2	19,26,27	0.85	0	18,38,41	1.79	5 (27%)
1	5MC	1	1962	1	18,22,23	0.95	2 (11%)	26,32,35	1.18	3 (11%)
48	0TD	q	89	48	7,9,10	1.41	1 (14%)	6,11,13	1.00	0
2	UR3	2	1498	2	19,22,23	0.90	1 (5%)	26,32,35	1.46	1 (3%)
2	MA6	2	1519	2	19,26,27	0.86	1 (5%)	18,38,41	1.80	6 (33%)
2	2MG	2	1207	2	18,26,27	1.04	1 (5%)	16,38,41	1.16	3 (18%)
1	PSU	1	2580	1	18,21,22	1.50	5 (27%)	22,30,33	2.07	5 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
1	OMC	1	2498	1,58	19,22,23	0.91	1 (5%)	26,31,34	0.93	1 (3%)
1	PSU	1	955	1	18,21,22	1.52	4 (22%)	22,30,33	2.04	4 (18%)
2	G7M	2	527	2	20,26,27	2.53	4 (20%)	17,39,42	0.91	1 (5%)
1	PSU	1	1911	1	18,21,22	1.42	4 (22%)	22,30,33	1.97	4 (18%)

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
2	4OC	2	1402	2	-	2/9/29/30	0/2/2/2
2	A3P	2	1493	2	-	2/8/30/31	0/3/3/3
1	2MA	1	2503	1,58	-	2/3/25/26	0/3/3/3
1	PSU	1	746	1,58	-	4/7/25/26	0/2/2/2
1	6MZ	1	2030	1	-	2/5/27/28	0/3/3/3
1	6MZ	1	1618	1	-	2/5/27/28	0/3/3/3
1	3TD	1	1915	1	-	4/7/25/26	0/2/2/2
1	PSU	1	2504	1	-	2/7/25/26	0/2/2/2
2	5MC	2	967	2	-	0/7/25/26	0/2/2/2
2	2MG	2	1516	2	-	0/5/27/28	0/3/3/3
1	PSU	1	2605	1	-	0/7/25/26	0/2/2/2
1	1MG	1	745	1	-	0/3/25/26	0/3/3/3
1	OMU	1	2552	1	-	0/9/27/28	0/2/2/2
2	PSU	2	516	2,58	-	2/7/25/26	0/2/2/2
1	2MG	1	2445	1	-	2/5/27/28	0/3/3/3
2	2MG	2	966	2	-	2/5/27/28	0/3/3/3
1	OMG	1	2251	1,4	-	0/5/27/28	0/3/3/3
2	5MC	2	1407	2	-	0/7/25/26	0/2/2/2
1	5MU	1	1939	1	-	0/7/25/26	0/2/2/2
1	G7M	1	2069	1	3/3/5/5	2/3/25/26	0/3/3/3
1	5MU	1	747	1	-	0/7/25/26	0/2/2/2
1	PSU	1	1917	1	-	0/7/25/26	0/2/2/2
1	PSU	1	2457	1	-	0/7/25/26	0/2/2/2
1	2MG	1	1835	1	-	0/5/27/28	0/3/3/3
2	MA6	2	1518	2	-	1/7/29/30	0/3/3/3
1	5MC	1	1962	1	-	2/7/25/26	0/2/2/2
48	0TD	q	89	48	-	5/7/12/14	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	UR3	2	1498	2	-	0/7/25/26	0/2/2/2
2	MA6	2	1519	2	-	4/7/29/30	0/3/3/3
2	2MG	2	1207	2	-	0/5/27/28	0/3/3/3
1	PSU	1	2580	1	-	0/7/25/26	0/2/2/2
1	OMC	1	2498	1,58	-	0/9/27/28	0/2/2/2
1	PSU	1	955	1	-	0/7/25/26	0/2/2/2
2	G7M	2	527	2	-	2/3/25/26	0/3/3/3
1	PSU	1	1911	1	-	0/7/25/26	0/2/2/2

The worst 5 of 74 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	527	G7M	C8-N9	7.13	1.46	1.33
2	2	527	G7M	C8-N7	6.78	1.45	1.33
2	2	527	G7M	C5-C4	3.81	1.46	1.39
1	1	2504	PSU	C4-N3	-3.53	1.32	1.38
1	1	2445	2MG	C6-N1	-3.43	1.32	1.37

The worst 5 of 116 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1	2030	6MZ	C9-N6-C6	-6.82	117.00	122.87
1	1	2457	PSU	N1-C2-N3	6.51	122.50	115.13
1	1	2504	PSU	N1-C2-N3	6.47	122.46	115.13
1	1	955	PSU	N1-C2-N3	6.37	122.34	115.13
1	1	2580	PSU	N1-C2-N3	6.33	122.30	115.13

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	1	2069	G7M	C4'
1	1	2069	G7M	C3'
1	1	2069	G7M	C2'

5 of 42 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	2	516	PSU	O4'-C1'-C5-C4
2	2	516	PSU	O4'-C1'-C5-C6
2	2	527	G7M	C3'-C4'-C5'-O5'
2	2	966	2MG	C3'-C4'-C5'-O5'

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
2	2	1519	MA6	C5-C6-N6-C9

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 441 ligands modelled in this entry, 441 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	2	3
1	1	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	1	2314:A	O3'	2315:G	P	3.01
1	2	1276:G	O3'	1277:C	P	2.96

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	2	1383:C	O3'	1384:C	P	2.91
1	2	147:G	O3'	148:G	P	2.90

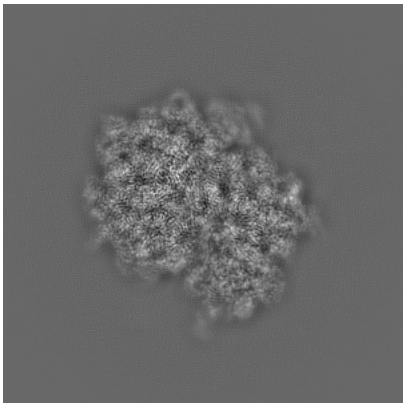
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-24944. These allow visual inspection of the internal detail of the map and identification of artifacts.

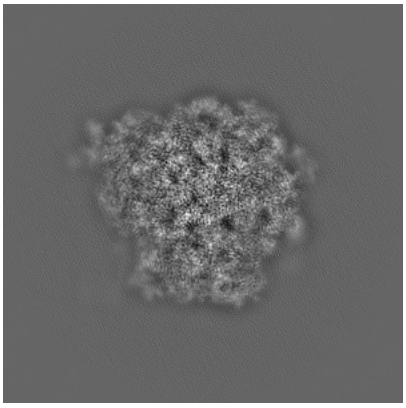
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

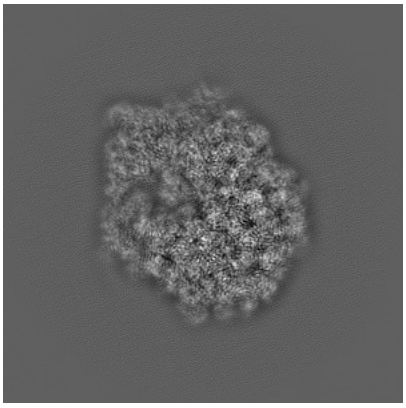
6.1.1 Primary map



X



Y

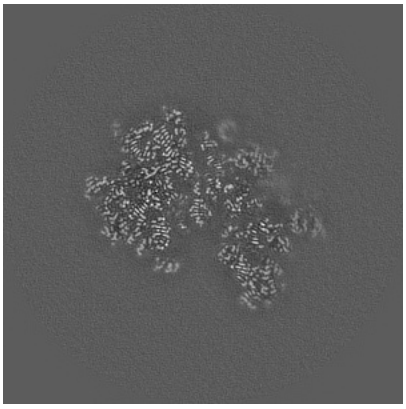


Z

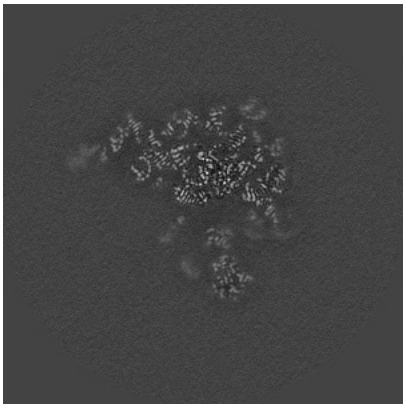
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

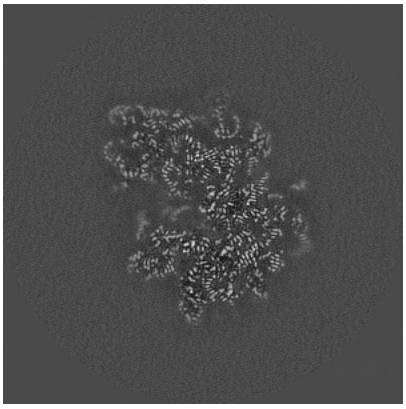
6.2.1 Primary map



X Index: 192



Y Index: 192

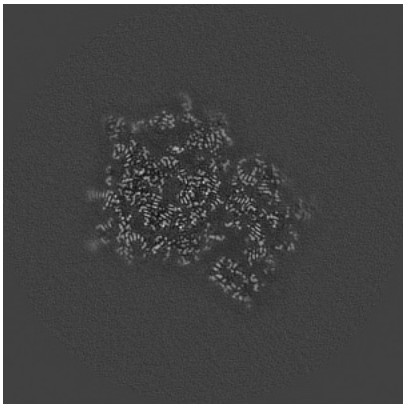


Z Index: 192

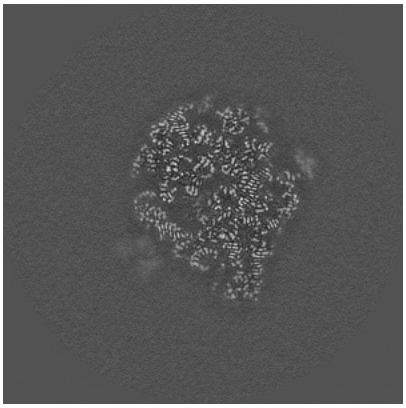
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

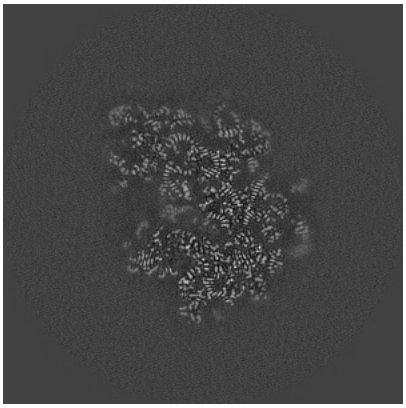
6.3.1 Primary map



X Index: 212



Y Index: 163



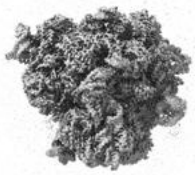
Z Index: 194

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

6.4 Orthogonal surface views (i)

6.4.1 Primary map

X



Y

Z

The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

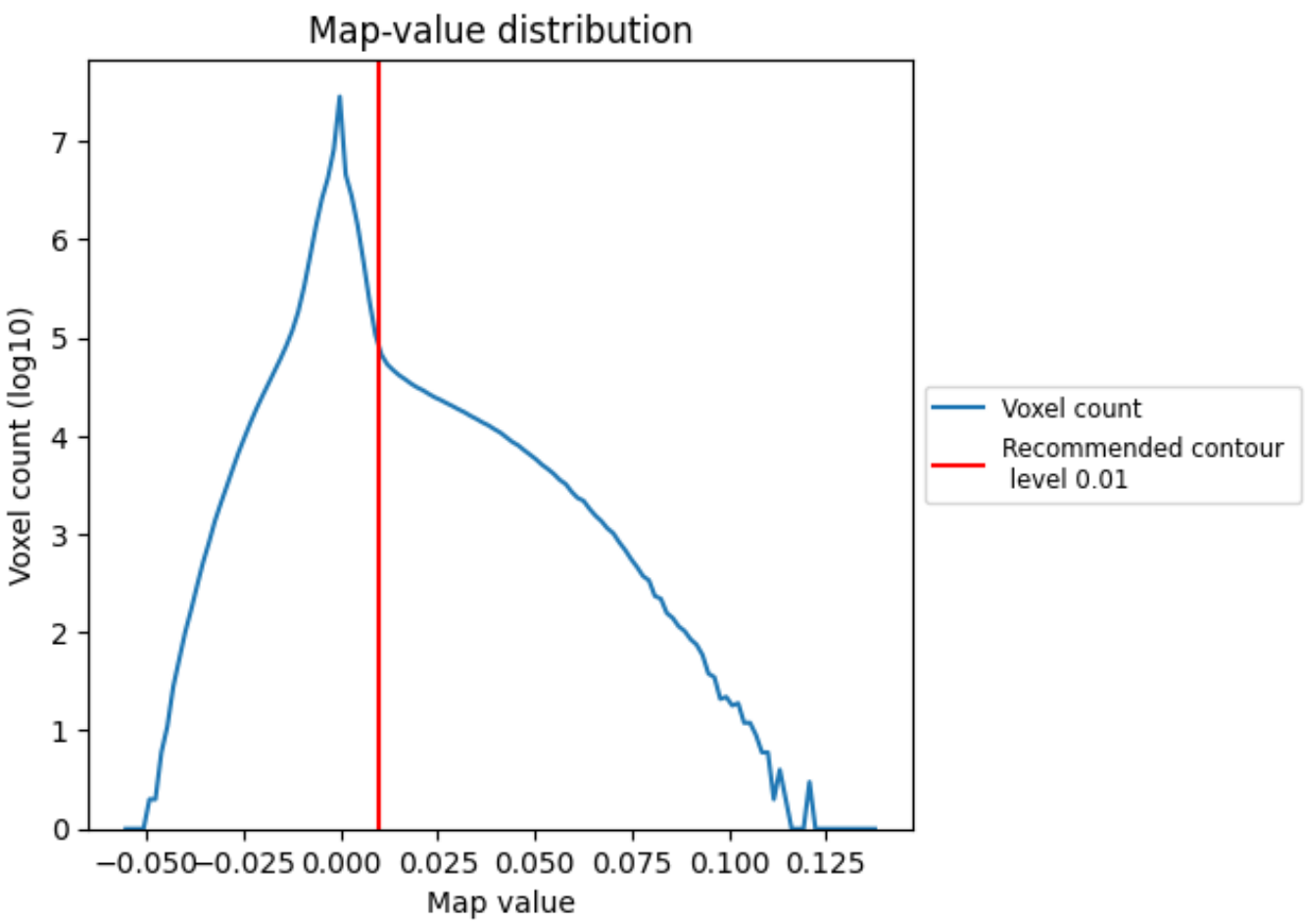
6.5 Mask visualisation (i)

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

7 Map analysis (i)

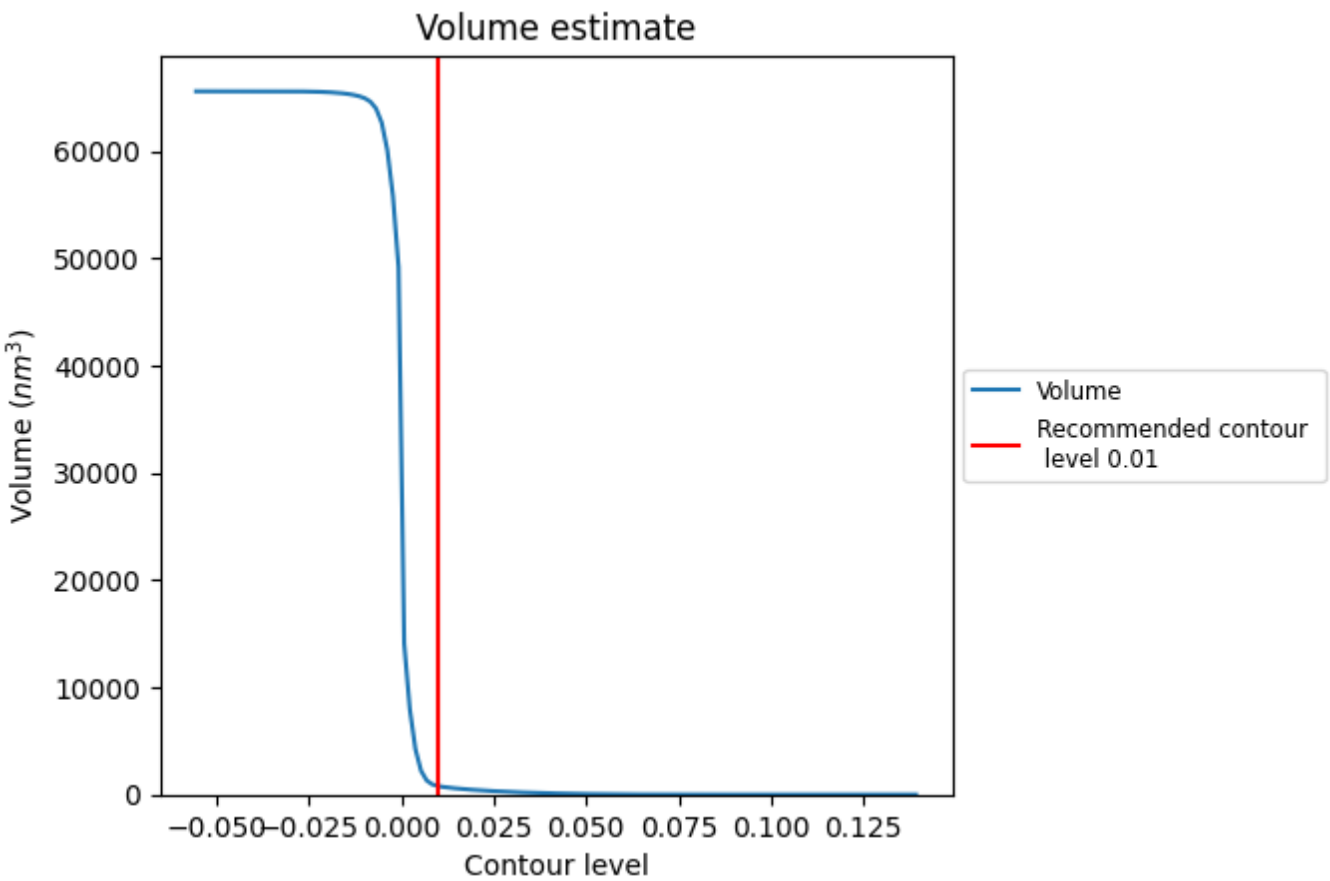
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

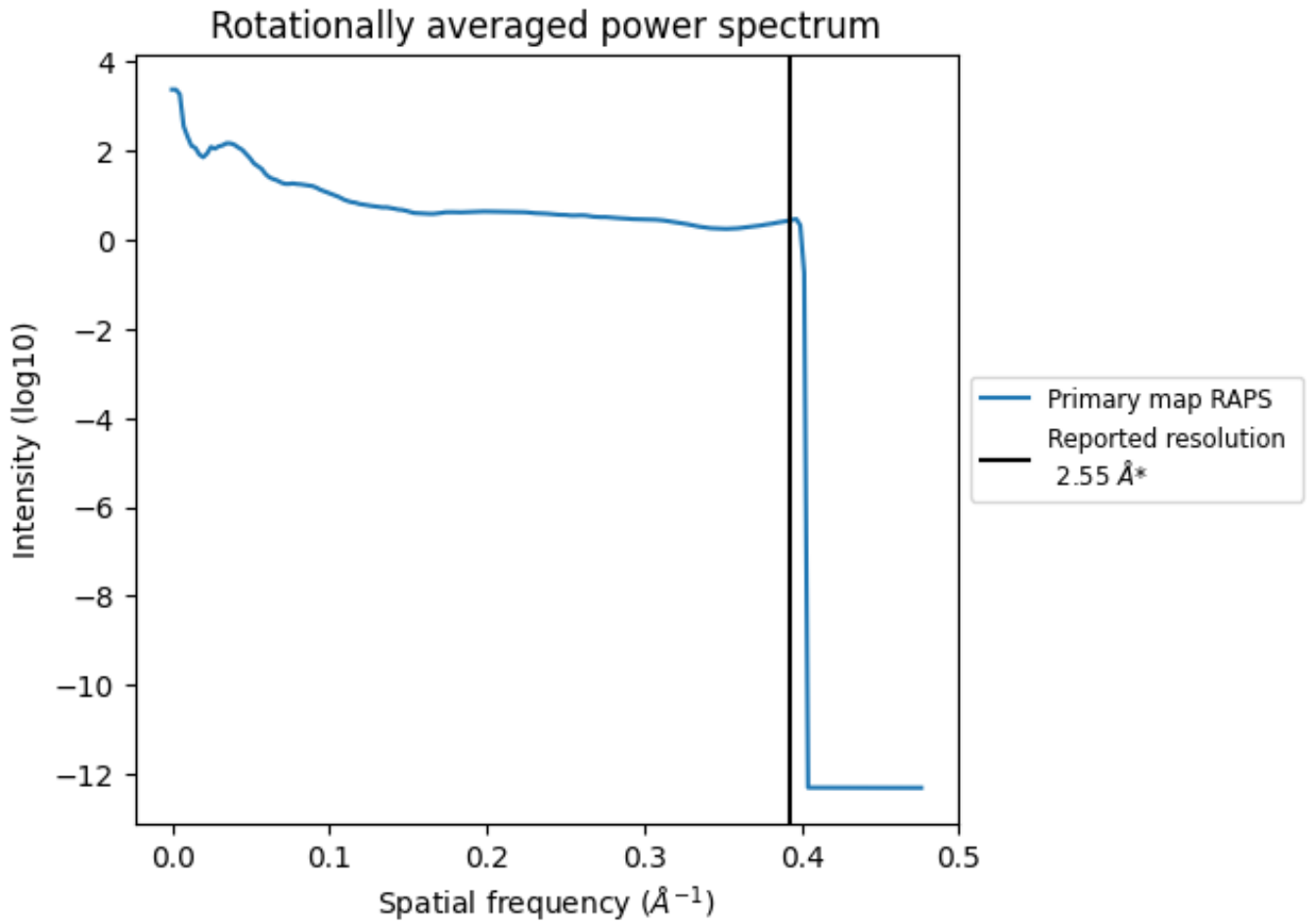
7.2 Volume estimate (i)



The volume at the recommended contour level is 790 nm^3; this corresponds to an approximate mass of 714 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)

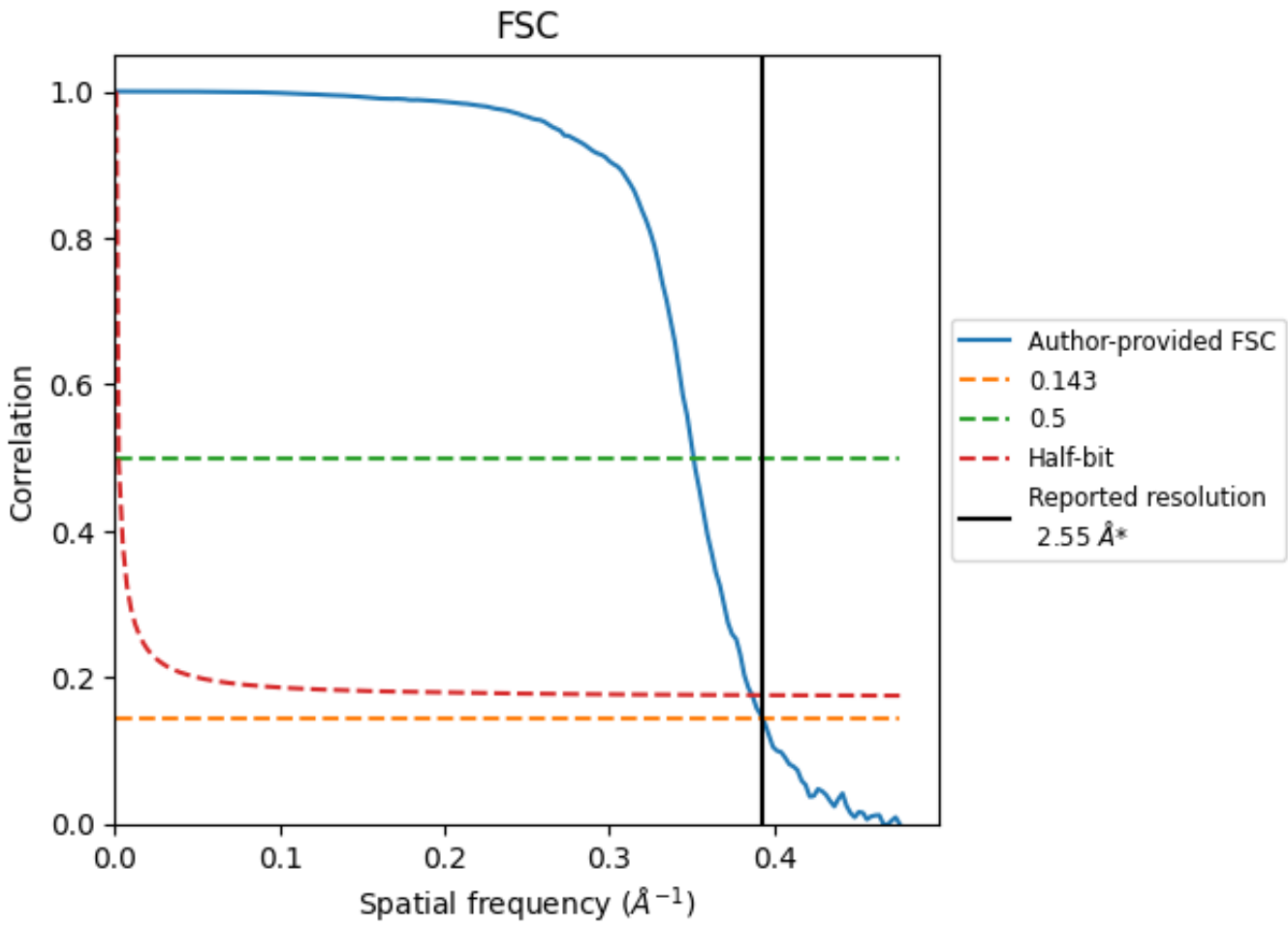


*Reported resolution corresponds to spatial frequency of 0.392 Å^{-1}

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 0.392 Å^{-1}

8.2 Resolution estimates (i)

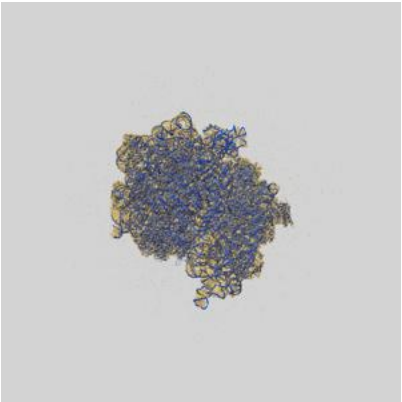
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.55	-	-
Author-provided FSC curve	2.54	2.85	2.59
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

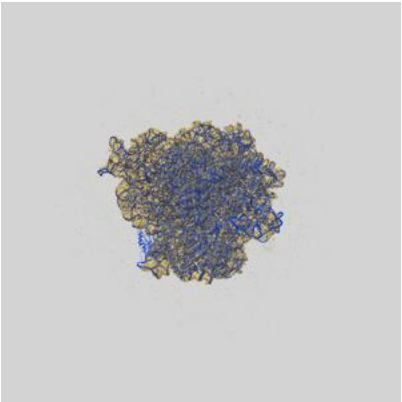
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-24944 and PDB model 7SA4. Per-residue inclusion information can be found in section 3 on page 16.

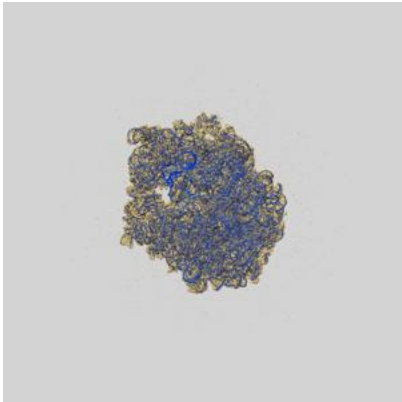
9.1 Map-model overlay (i)



X



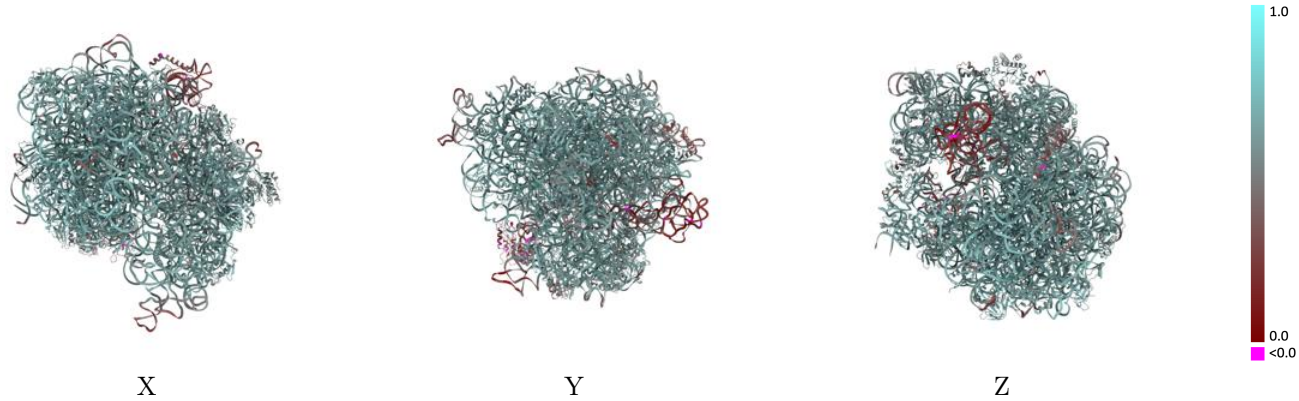
Y



Z

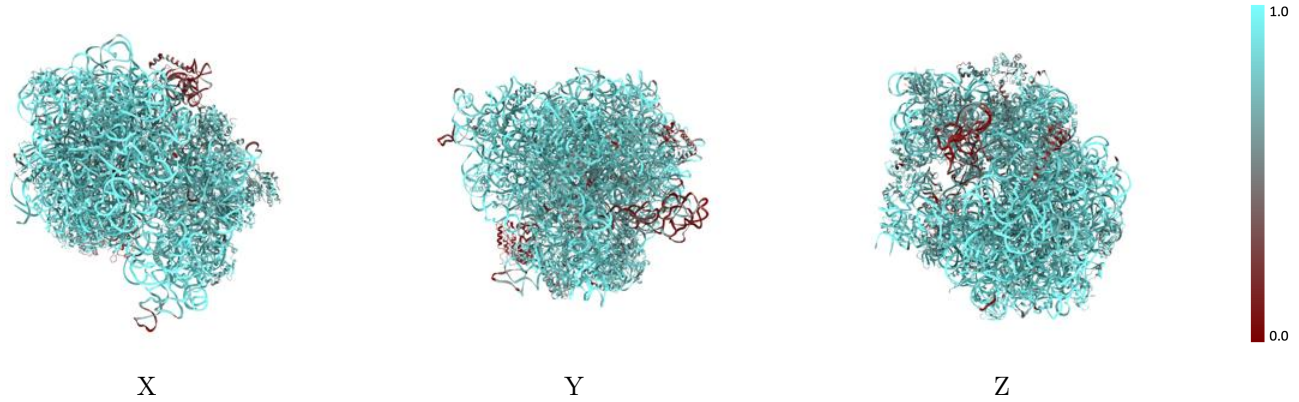
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



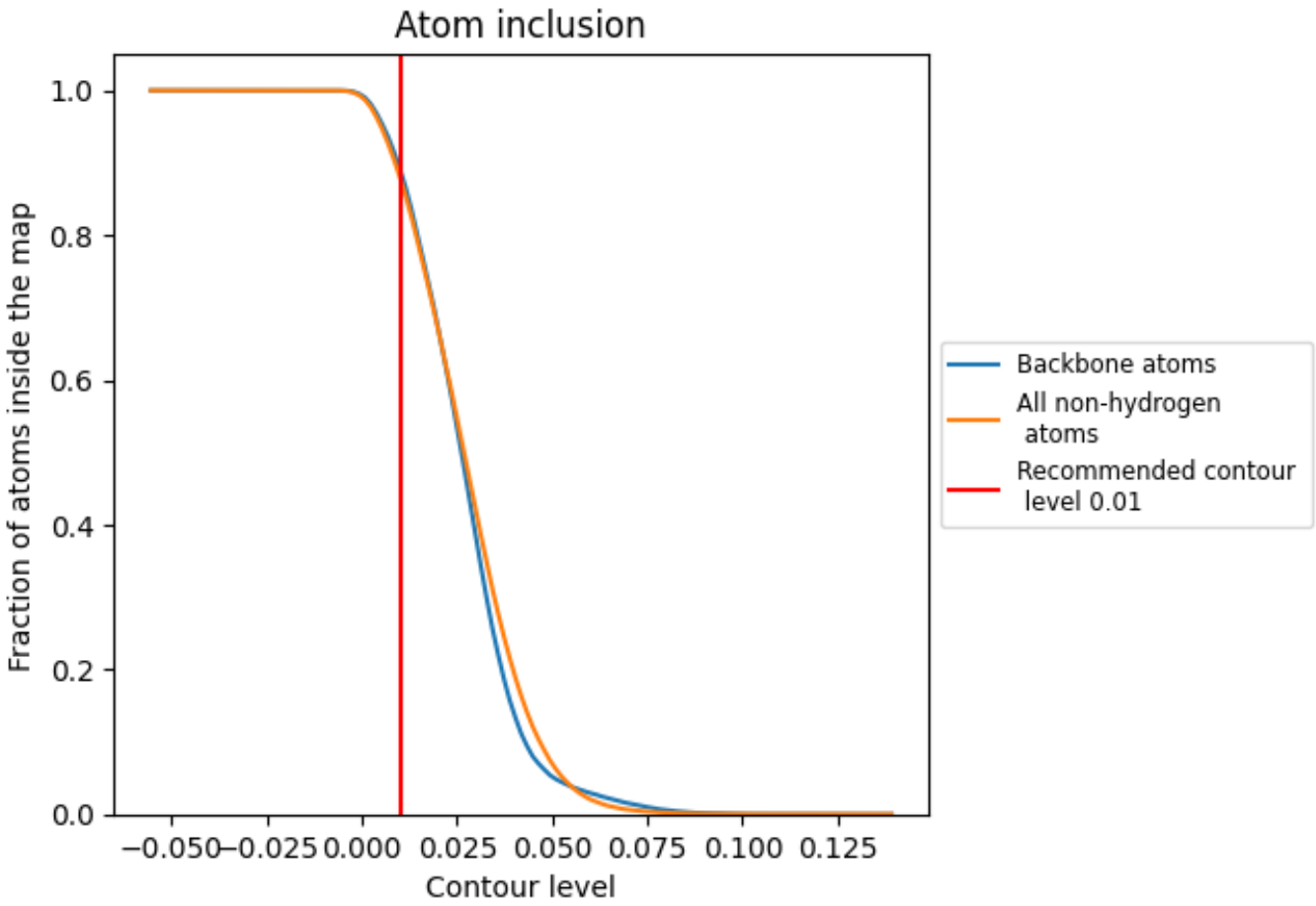
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model (i)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.01).

9.4 Atom inclusion (i)



At the recommended contour level, 89% of all backbone atoms, 88% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8795	0.6100
1	0.9306	0.6240
2	0.9472	0.6240
4	0.9523	0.6260
5	0.8666	0.5890
6	0.2817	0.2690
7	0.4545	0.4750
8	0.6878	0.5530
B	0.9207	0.6660
C	0.9214	0.6580
D	0.8612	0.6190
E	0.7800	0.5770
F	0.7964	0.5690
G	0.3084	0.3960
H	0.0167	0.1960
I	0.0051	0.1790
J	0.9155	0.6570
K	0.9153	0.6560
L	0.8926	0.6470
M	0.8992	0.6470
N	0.9452	0.6670
O	0.8667	0.6190
P	0.9167	0.6530
Q	0.9384	0.6690
R	0.9021	0.6370
S	0.8971	0.6520
T	0.8274	0.6330
U	0.8299	0.6040
V	0.8767	0.6230
W	0.8975	0.6490
X	0.9002	0.6550
Y	0.8057	0.5910
Z	0.9060	0.6360
a	0.6836	0.5080
b	0.8998	0.6510

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
c	0.8589	0.6290
d	0.9352	0.6740
e	0.9369	0.6740
f	0.8908	0.6480
g	0.6703	0.5390
h	0.8447	0.6020
i	0.8586	0.6260
j	0.8894	0.6340
k	0.7884	0.5720
l	0.6259	0.5460
m	0.8844	0.6310
n	0.8039	0.5880
o	0.7124	0.5490
p	0.8066	0.5870
q	0.8830	0.6470
r	0.8400	0.6070
s	0.8643	0.6240
t	0.8739	0.6160
u	0.8756	0.6260
v	0.8022	0.5950
w	0.7954	0.5930
x	0.8393	0.6080
y	0.8410	0.6210
z	0.5546	0.5170