



wwPDB EM Validation Summary Report ⓘ

Jun 22, 2026 – 11:03 PM EDT

PDB ID : 4V6V / pdb_00004v6v
EMDB ID : EMD-5562
Title : Tetracycline resistance protein Tet(O) bound to the ribosome
Authors : Li, W.; Atkinson, G.C.; Thakor, N.S.; Allas, U.; Lu, C.; Chan, K.Y.; Tenson, T.; Schulten, K.; Wilson, K.S.; Hauryliuk, V.; Frank, J.
Deposited on : 2013-02-25
Resolution : 9.80 Å(reported)
Based on initial models : 2I2U, 2I2V

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

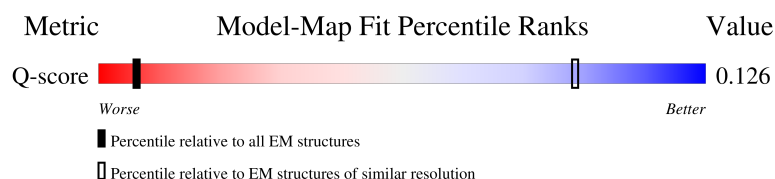
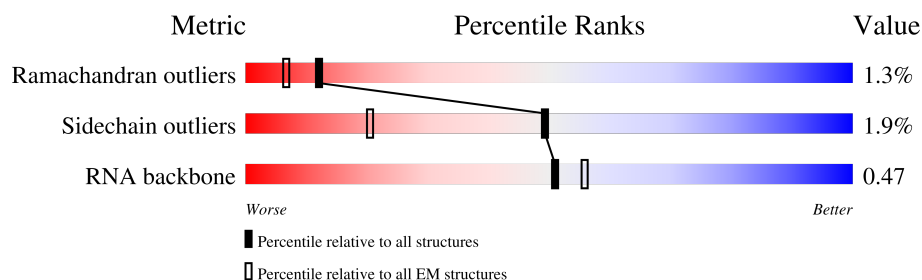
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 9.80 Å.

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



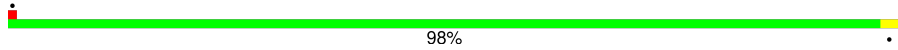
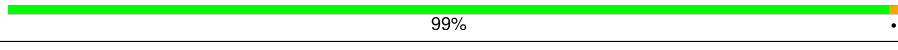
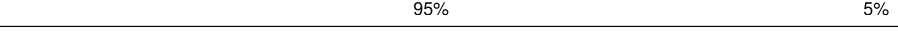
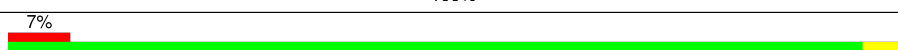
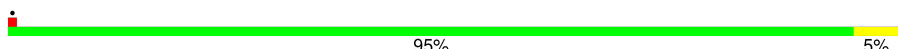
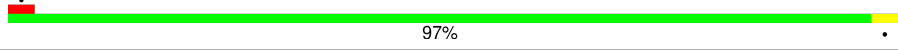
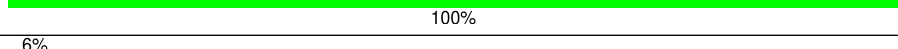
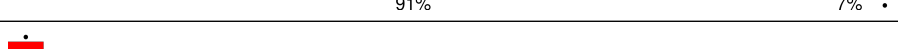
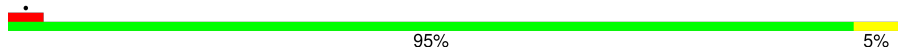
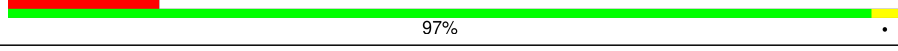
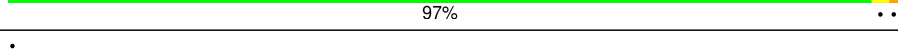
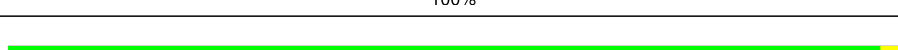
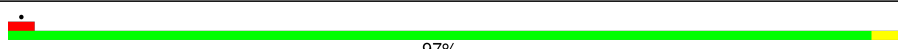
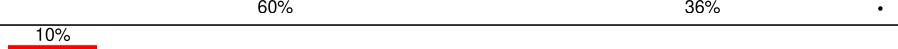
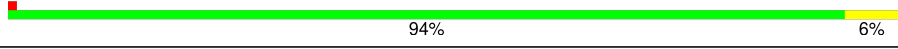
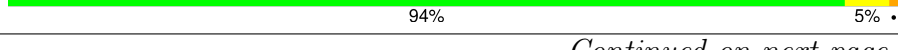
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	157 (9.30 - 10.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	AJ	103	
2	AK	128	
3	AL	123	
4	AM	117	

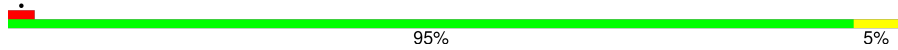
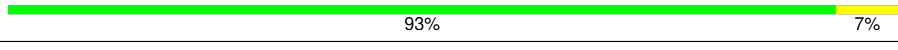
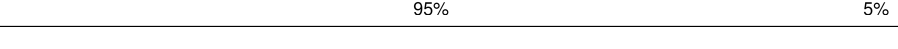
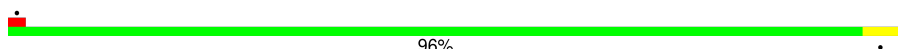
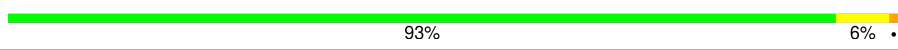
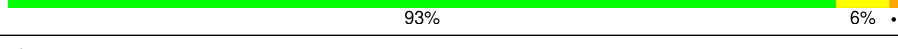
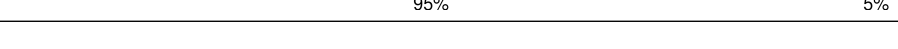
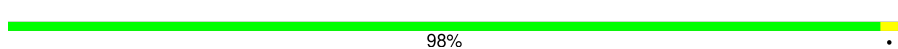
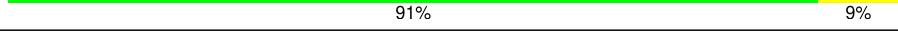
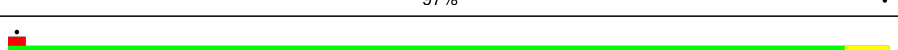
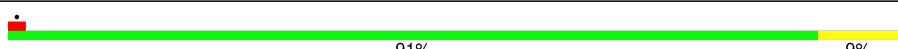
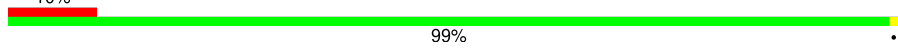
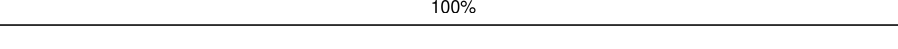
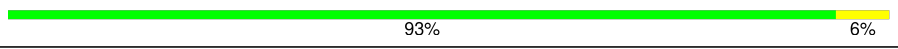
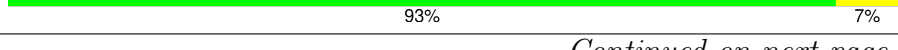
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Mol	Chain	Length	Quality of chain
5	AN	100	
6	AO	88	
7	AP	82	
8	AQ	83	
9	AR	74	
10	AS	91	
11	AB	240	
12	AT	86	
13	AU	70	
14	AC	232	
15	AD	205	
16	AE	166	
17	AF	135	
18	AG	178	
19	AH	129	
20	AI	129	
21	A1	639	
22	AA	1542	
23	A2	47	
24	A3	77	
25	BC	234	
26	BJ	164	
27	BK	141	
28	BN	142	
29	BO	123	

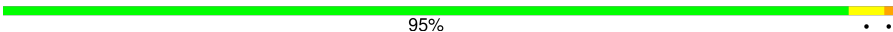
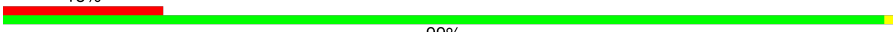
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Mol	Chain	Length	Quality of chain
30	BP	144	 95%5%
31	BQ	136	 93%7%
32	BR	127	 95%5%
33	BS	117	 99%.
34	BT	114	 95%5%
35	BD	272	 96%. .
36	BU	117	 93%6% .
37	BV	103	 93%6% .
38	BW	110	 95%5% .
39	BX	100	 94%6%
40	BY	103	 98% .
41	BZ	94	 98% .
42	B0	84	 7%87%11% .
43	B1	77	 91%9%
44	B2	63	 97% .
45	BE	209	 94%5%
46	B3	58	 91%9%
47	B4	70	 10%99% .
48	B5	56	 89%11%
49	B6	54	 100%
50	B7	46	 87%13%
51	B8	64	 95%5%
52	B9	38	 95%5%
53	BF	201	 93%6%
54	BG	178	93%7% .

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Mol	Chain	Length	Quality of chain
55	BH	176	 95% . .
56	BL	149	 18% 99% .
57	BA	2904	 63% 30% 6%
58	Ba	120	 77% 19% . .

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 154956 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 protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AJ	103	Total	C	N	O	S	0	0
			794	483	158	151	2		

- Molecule 2 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AK	128	Total	C	N	O	S	0	0
			923	553	196	171	3		

- Molecule 3 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AL	123	Total	C	N	O	S	0	0
			923	558	196	165	4		

- Molecule 4 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AM	117	Total	C	N	O	S	0	0
			876	530	183	160	3		

- Molecule 5 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AN	100	Total	C	N	O	S	0	0
			771	465	164	139	3		

- Molecule 6 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AO	88	Total	C	N	O	S	0	0
			690	414	146	129	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AO	79	ARG	GLN	conflict	UNP P0ADZ4

- Molecule 7 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AP	82	Total	C	N	O	S	0	0
			620	377	128	114	1		

- Molecule 8 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AQ	83	Total	C	N	O	S	0	0
			657	410	124	120	3		

- Molecule 9 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AR	74	Total	C	N	O	S	0	0
			603	372	123	107	1		

- Molecule 10 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AS	91	Total	C	N	O	S	0	0
			708	445	139	122	2		

- Molecule 11 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AB	240	Total	C	N	O	S	0	0
			1805	1113	332	352	8		

- Molecule 12 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AT	86	Total	C	N	O	S	0	0
			636	380	138	115	3		

- Molecule 13 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AU	70	Total	C	N	O	S	0	0
			564	340	125	98	1		

- Molecule 14 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AC	232	Total	C	N	O	S	0	0
			1761	1088	346	323	4		

- Molecule 15 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AD	205	Total	C	N	O	S	0	0
			1587	970	315	298	4		

- Molecule 16 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AE	166	Total	C	N	O	S	0	0
			1182	718	232	226	6		

- Molecule 17 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AF	135	Total	C	N	O	S	0	0
			1061	637	198	219	7		

- Molecule 18 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AG	178	Total	C	N	O	S	0	0
			1347	821	269	253	4		

- Molecule 19 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AH	129	Total	C	N	O	S	0	0
			948	585	173	184	6		

- Molecule 20 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AI	129	Total	C	N	O	S	0	0
			1000	606	208	183	3		

- Molecule 21 is a protein called Tetracycline resistance protein TetO.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	A1	639	Total	C	N	O	S	0	0
			4989	3146	850	966	27		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A1	227	ILE	THR	conflict	UNP P10952

- Molecule 22 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AA	1542	Total	C	N	O	P	0	0
			33089	14767	6064	10717	1541		

- Molecule 23 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	A2	47	Total	C	N	O	P	0	0
			993	445	167	335	46		

- Molecule 24 is a RNA chain called P-tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	A3	77	Total	C	N	O	P	S	0	0
			1640	734	297	533	75	1		

- Molecule 25 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BC	234	Total	C	N	O	S	0	0
			1733	1081	315	330	7		

- Molecule 26 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BJ	164	Total	C	N	O	S	0	0
			1233	776	220	231	6		

- Molecule 27 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	BK	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 28 is a protein called 50S ribosomal protein L13.

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

- Molecule 29 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	BO	123	Total	C	N	O	S	0	0
			947	593	181	167	6		

- Molecule 30 is a protein called 50S ribosomal protein L15.

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

- Molecule 31 is a protein called 50S ribosomal protein L16.

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

- Molecule 32 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	BR	127	Total	C	N	O	S	0	0
			1008	621	204	178	5		

- Molecule 33 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BS	117	Total	C	N	O	S	0	0
			900	557	179	163	1		

- Molecule 34 is a protein called 50S ribosomal protein L19.

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

- Molecule 35 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BD	272	Total	C	N	O	S	0	0
			2092	1294	425	366	7		

- Molecule 36 is a protein called 50S ribosomal protein L20.

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

- Molecule 37 is a protein called 50S ribosomal protein L21.

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

- Molecule 38 is a protein called 50S ribosomal protein L22.

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

- Molecule 39 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BX	100	Total	C	N	O	S	0	0
			787	496	146	143	2		

- Molecule 40 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	BY	103	Total	C	N	O		
			789	498	148	143	0	0

- Molecule 41 is a protein called 50S ribosomal protein L25.

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

- Molecule 42 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	B0	84	Total	C	N	O	S	
			634	391	129	113	1	0

- Molecule 43 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	B1	77	Total	C	N	O	S	
			625	388	129	106	2	0

- Molecule 44 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	B2	63	Total	C	N	O	S	
			509	313	99	95	2	0

- Molecule 45 is a protein called 50S ribosomal protein L3.

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

- Molecule 46 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	B3	58	Total	C	N	O	S	
			449	281	87	79	2	0

- Molecule 47 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	B4	70	Total	C	N	O	S	0	0
			549	339	104	100	6		

- Molecule 48 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	B5	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 49 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	B6	54	Total	C	N	O	S	0	0
			441	284	81	76			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	B7	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 51 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	B8	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 52 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	B9	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 53 is a protein called 50S ribosomal protein L4.

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

- Molecule 54 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	BG	178	Total	C	N	O	S	0	0
			1420	905	251	258	6		

- Molecule 55 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	BH	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 56 is a protein called 50S ribosomal protein L9.

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

- Molecule 57 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	BA	2904	Total	C	N	O	P	0	0
			62351	27824	11469	20155	2903		

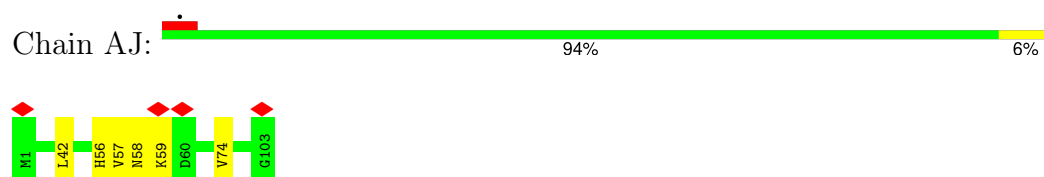
- Molecule 58 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Ba	120	Total	C	N	O	P	0	0
			2566	1144	468	835	119		

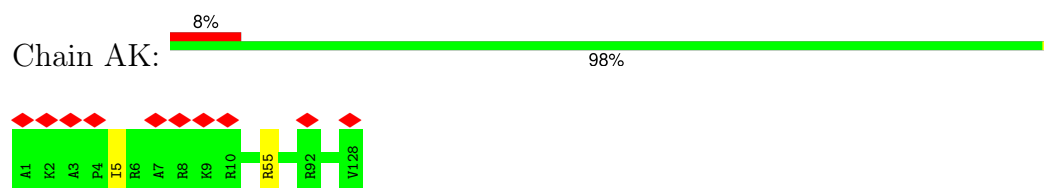
3 Residue-property plots [i](#)

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.

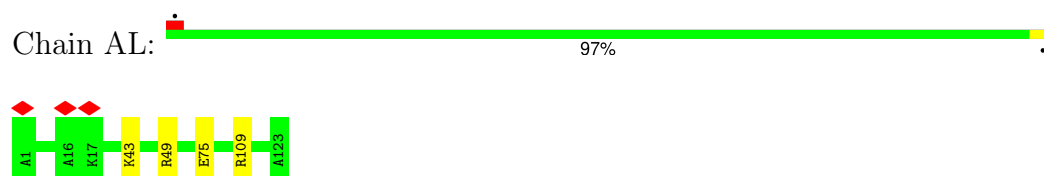
- Molecule 1: 30S ribosomal protein S10



- Molecule 2: 30S ribosomal protein S11



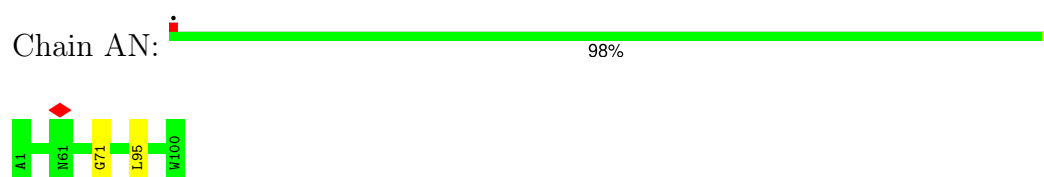
- Molecule 3: 30S ribosomal protein S12



- Molecule 4: 30S ribosomal protein S13



- Molecule 5: 30S ribosomal protein S14

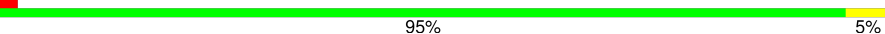


- Molecule 6: 30S ribosomal protein S15

Chain AO:  99%



- Molecule 7: 30S ribosomal protein S16

Chain AP:  95%

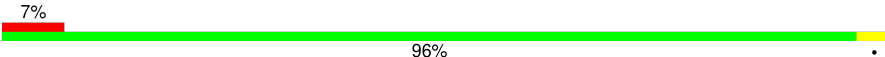


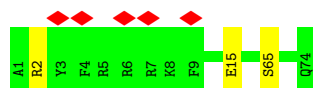
- Molecule 8: 30S ribosomal protein S17

Chain AQ:  100%

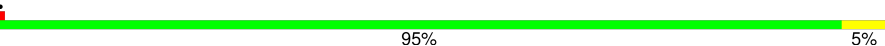
There are no outlier residues recorded for this chain.

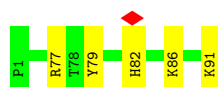
- Molecule 9: 30S ribosomal protein S18

Chain AR:  96%



- Molecule 10: 30S ribosomal protein S19

Chain AS:  95%

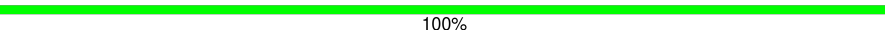


- Molecule 11: 30S ribosomal protein S2

Chain AB:  97%

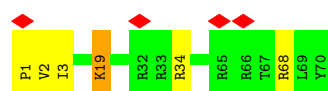


- Molecule 12: 30S ribosomal protein S20

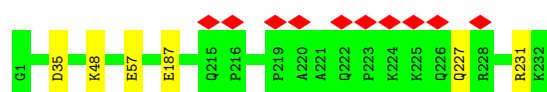
Chain AT:  100%

There are no outlier residues recorded for this chain.

- Molecule 13: 30S ribosomal protein S21



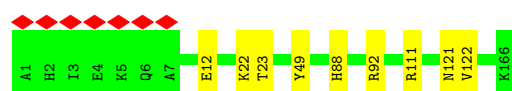
- Molecule 14: 30S ribosomal protein S3



- Molecule 15: 30S ribosomal protein S4



- Molecule 16: 30S ribosomal protein S5



- Molecule 17: 30S ribosomal protein S6



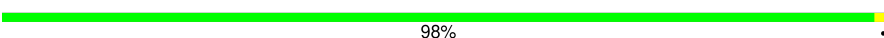
- Molecule 18: 30S ribosomal protein S7



- Molecule 19: 30S ribosomal protein S8

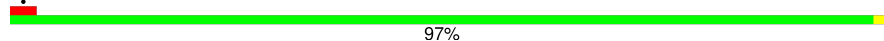


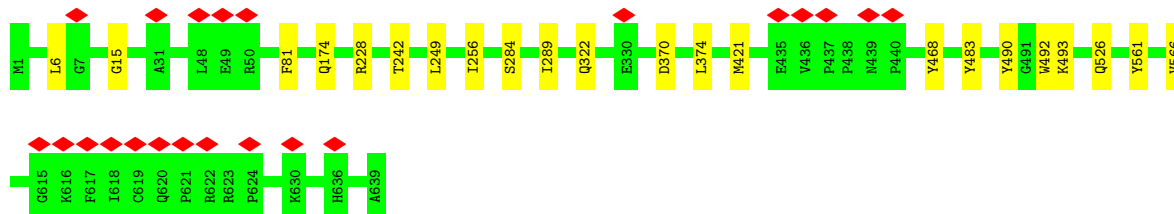
- Molecule 20: 30S ribosomal protein S9

Chain AI:  98%

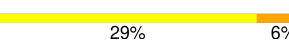


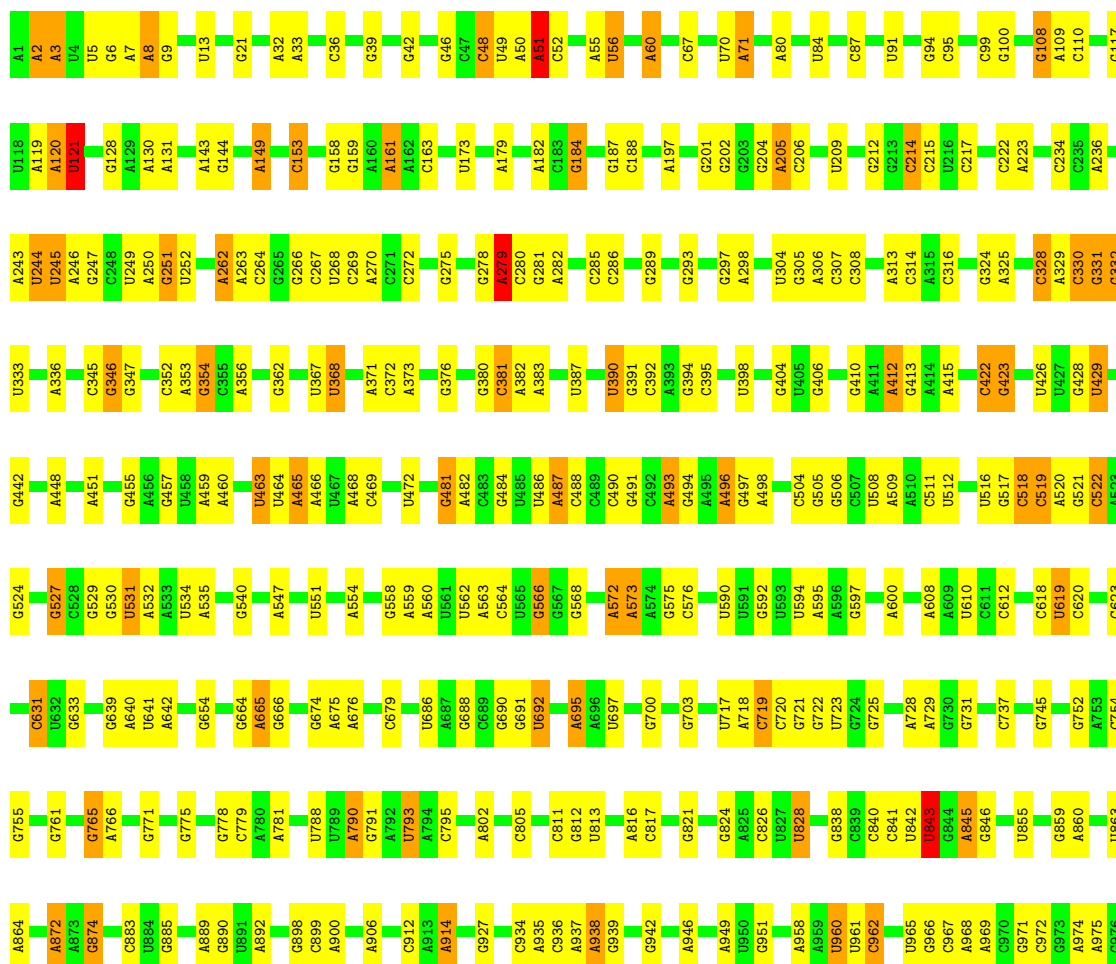
- Molecule 21: Tetracycline resistance protein TetO

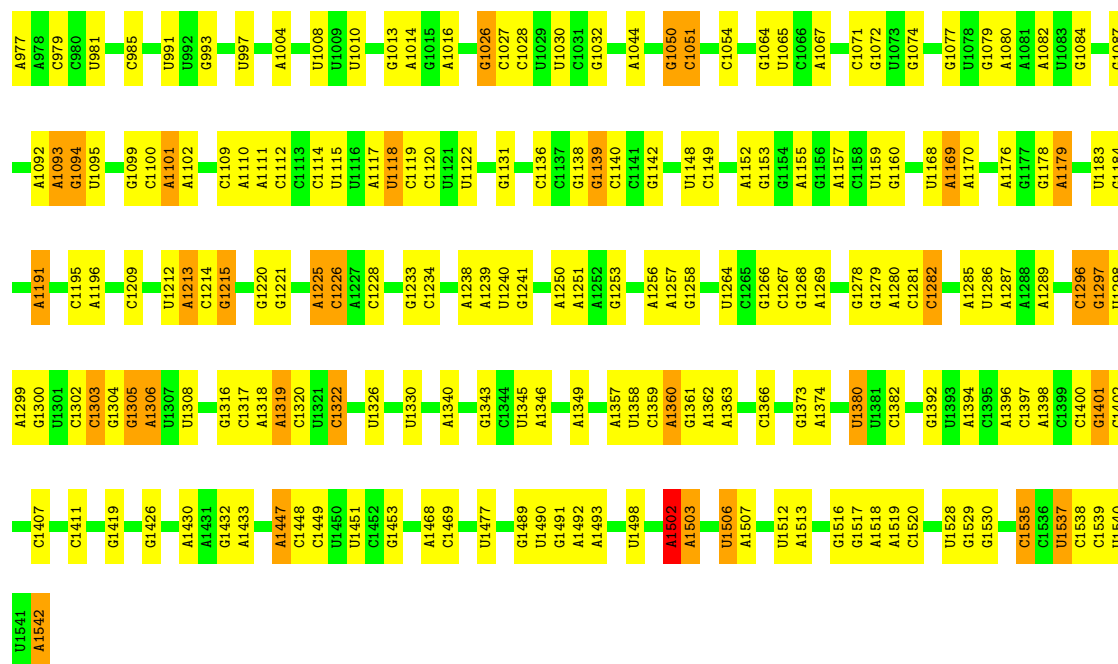
Chain A1:  97%



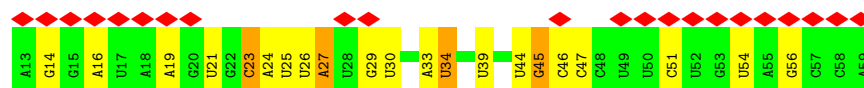
- Molecule 22: 16S ribosomal RNA

Chain AA:  65%  29%  6%





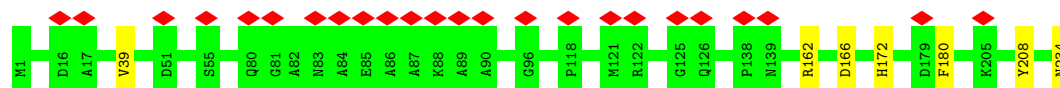
- Molecule 23: mRNA



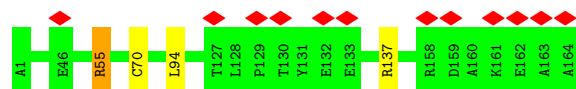
- Molecule 24: P-tRNA



- Molecule 25: 50S ribosomal protein L1

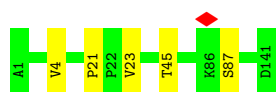


- Molecule 26: 50S ribosomal protein L10



- Molecule 27: 50S ribosomal protein L11

Chain BK:  96% .



- Molecule 28: 50S ribosomal protein L13

Chain BN:  94% 6% .



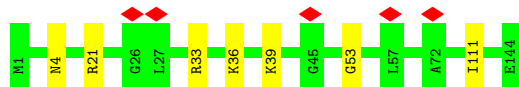
- Molecule 29: 50S ribosomal protein L14

Chain BO:  94% 5% .



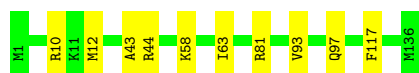
- Molecule 30: 50S ribosomal protein L15

Chain BP:  95% 5% .

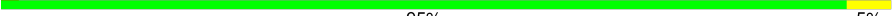


- Molecule 31: 50S ribosomal protein L16

Chain BQ:  93% 7% .



- Molecule 32: 50S ribosomal protein L17

Chain BR:  95% 5% .

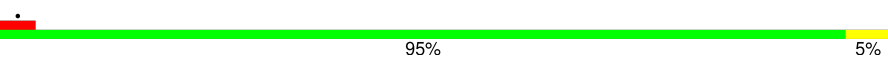


- Molecule 33: 50S ribosomal protein L18

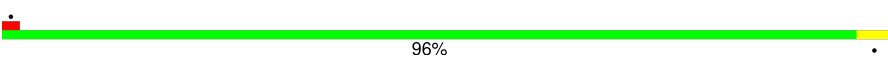
Chain BS:  99% .



• Molecule 34: 50S ribosomal protein L19

Chain BT:  95% 5%

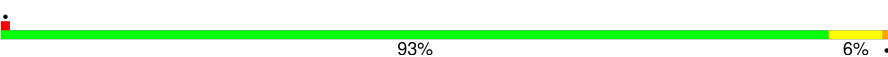
• Molecule 35: 50S ribosomal protein L2

Chain BD:  96% .

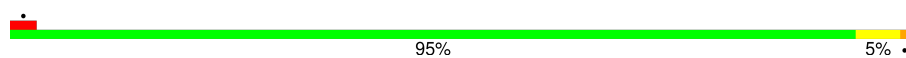
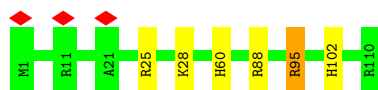
• Molecule 36: 50S ribosomal protein L20

Chain BU:  93% 6% .

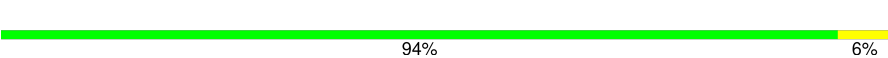
• Molecule 37: 50S ribosomal protein L21

Chain BV:  93% 6% .

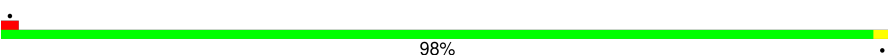
• Molecule 38: 50S ribosomal protein L22

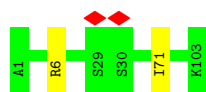
Chain BW:  95% 5% .

• Molecule 39: 50S ribosomal protein L23

Chain BX:  94% 6%

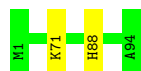
• Molecule 40: 50S ribosomal protein L24

Chain BY:  98% .



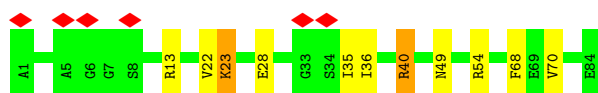
- Molecule 41: 50S ribosomal protein L25

Chain BZ: 98%



- Molecule 42: 50S ribosomal protein L27

Chain B0: 7% 87% 11%



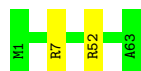
- Molecule 43: 50S ribosomal protein L28

Chain B1: 91% 9%



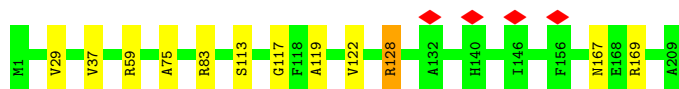
- Molecule 44: 50S ribosomal protein L29

Chain B2: 97%



- Molecule 45: 50S ribosomal protein L3

Chain BE: 94% 5%

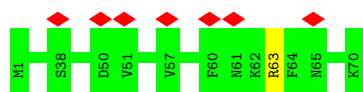


- Molecule 46: 50S ribosomal protein L30

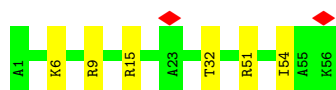
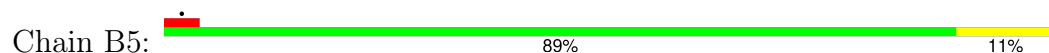
Chain B3: 91% 9%



- Molecule 47: 50S ribosomal protein L31



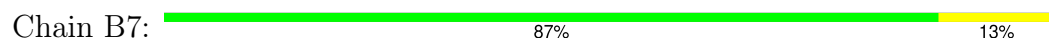
- Molecule 48: 50S ribosomal protein L32



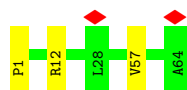
- Molecule 49: 50S ribosomal protein L33



- Molecule 50: 50S ribosomal protein L34



- Molecule 51: 50S ribosomal protein L35



- Molecule 52: 50S ribosomal protein L36



- Molecule 53: 50S ribosomal protein L4

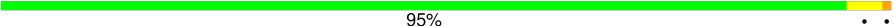


- Molecule 54: 50S ribosomal protein L5

Chain BG:  93% 7%

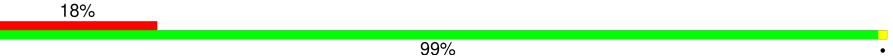


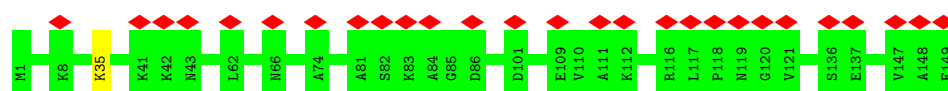
- Molecule 55: 50S ribosomal protein L6

Chain BH:  95%



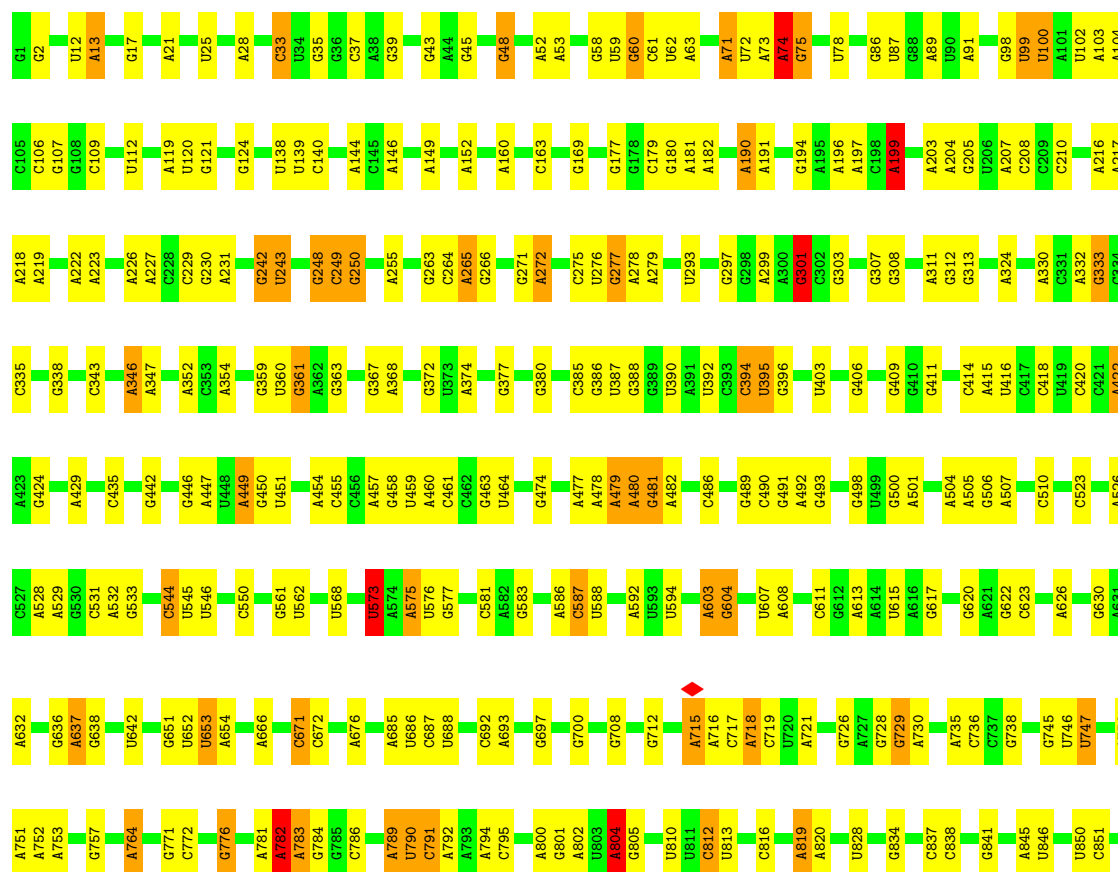
- Molecule 56: 50S ribosomal protein L9

Chain BL:  18% 99%

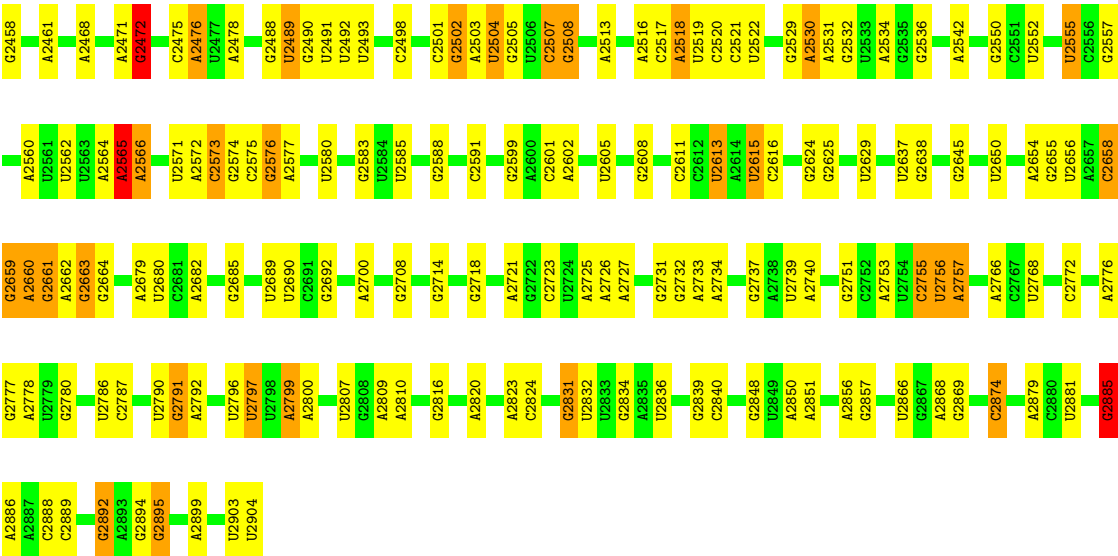


- Molecule 57: 23S ribosomal RNA

Chain BA:  63% 30% 6%







● Molecule 58: 5S ribosomal RNA

Chain Ba:

77%

19%

●●



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	98000	Depositor
Resolution determination method	FSC	Depositor
CTF correction method	group defocus	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	10	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	Not provided	
Maximum map value	253.190	Depositor
Minimum map value	-113.794	Depositor
Average map value	4.829	Depositor
Map value standard deviation	25.951	Depositor
Recommended contour level	22	Depositor
Map size ($\text{\AA}$)	365.85, 365.85, 365.85	wwPDB
Map dimensions	135, 135, 135	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	2.71, 2.71, 2.71	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 2MG, PSU, 4OC, OMU, 7MG, 2MA, OMG, H2U, 3TD, UR3, 6MZ, 4SU, 5MC, 1MG, MA6, OMC, 5MU

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	AJ	0.86	0/742	1.35	2/941 (0.2%)
2	AK	0.88	0/856	1.39	0/1069
3	AL	0.88	0/873	1.35	0/1110
4	AM	0.89	0/817	1.36	0/1022
5	AN	0.89	0/715	1.33	0/883
6	AO	0.86	0/646	1.31	0/813
7	AP	0.87	0/572	1.35	2/711 (0.3%)
8	AQ	0.83	0/636	1.31	0/822
9	AR	0.95	0/568	1.34	0/713
10	AS	0.91	0/687	1.35	1/880 (0.1%)
11	AB	0.82	0/1703	1.28	4/2161 (0.2%)
12	AT	0.85	0/574	1.33	0/694
13	AU	0.96	0/520	1.40	3/636 (0.5%)
14	AC	0.83	0/1669	1.25	1/2122 (0.0%)
15	AD	0.85	0/1497	1.30	1/1890 (0.1%)
16	AE	0.85	0/1110	1.34	3/1405 (0.2%)
17	AF	0.86	0/1001	1.31	0/1268
18	AG	0.83	0/1263	1.30	2/1590 (0.1%)
19	AH	0.79	0/896	1.28	0/1141
20	AI	0.89	0/940	1.35	2/1180 (0.2%)
21	A1	0.86	0/4864	1.38	9/6363 (0.1%)
22	AA	0.85	1/36769 (0.0%)	1.19	70/57354 (0.1%)
23	A2	0.91	0/1108	1.24	8/1724 (0.5%)
24	A3	0.88	1/1717 (0.1%)	1.17	2/2675 (0.1%)
25	BC	0.90	0/1748	1.39	2/2355 (0.1%)
26	BJ	0.89	0/1247	1.40	1/1679 (0.1%)
27	BK	0.88	0/1046	1.44	3/1410 (0.2%)
28	BN	0.96	0/1152	1.44	3/1551 (0.2%)
29	BO	0.95	0/956	1.39	1/1279 (0.1%)
30	BP	0.98	0/1062	1.48	1/1413 (0.1%)
31	BQ	0.95	1/1093 (0.1%)	1.47	4/1460 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	BR	0.96	0/1021	1.48	0/1364
33	BS	0.91	0/910	1.38	0/1219
34	BT	0.94	0/929	1.41	2/1242 (0.2%)
35	BD	0.97	0/2131	1.45	4/2863 (0.1%)
36	BU	0.90	0/960	1.49	2/1278 (0.2%)
37	BV	0.90	0/829	1.39	4/1107 (0.4%)
38	BW	0.88	0/864	1.36	3/1156 (0.3%)
39	BX	0.88	0/794	1.41	2/1060 (0.2%)
40	BY	0.88	0/797	1.36	0/1062
41	BZ	0.87	0/766	1.36	1/1025 (0.1%)
42	B0	1.00	0/642	1.53	3/848 (0.4%)
43	B1	0.97	0/635	1.48	6/848 (0.7%)
44	B2	0.87	0/510	1.48	2/677 (0.3%)
45	BE	0.91	0/1586	1.49	6/2134 (0.3%)
46	B3	0.95	0/453	1.48	7/605 (1.2%)
47	B4	1.02	0/559	1.44	0/745
48	B5	1.02	0/450	1.54	3/599 (0.5%)
49	B6	0.87	0/448	1.32	0/594
50	B7	1.04	0/380	1.60	6/498 (1.2%)
51	B8	1.02	0/513	1.49	1/676 (0.1%)
52	B9	0.93	0/303	1.37	0/397
53	BF	0.89	0/1571	1.44	10/2113 (0.5%)
54	BG	0.91	0/1444	1.40	5/1937 (0.3%)
55	BH	0.92	0/1343	1.44	1/1816 (0.1%)
56	BL	0.91	0/1122	1.39	0/1515
57	BA	0.85	1/69280 (0.0%)	1.20	135/108078 (0.1%)
58	Ba	0.85	0/2869	1.17	7/4474 (0.2%)
All	All	0.87	4/165156 (0.0%)	1.26	335/244244 (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
3	AL	0	1
6	AO	0	1
7	AP	0	1
9	AR	0	1
10	AS	0	1
15	AD	0	1
18	AG	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
21	A1	0	2
22	AA	0	350
23	A2	0	5
24	A3	0	15
26	BJ	0	1
28	BN	0	2
29	BO	0	1
32	BR	0	1
34	BT	0	1
35	BD	0	1
36	BU	0	2
38	BW	0	1
40	BY	0	1
42	B0	0	1
51	B8	0	1
55	BH	0	2
57	BA	0	660
58	Ba	0	15
All	All	0	1070

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	AA	1498	UR3	O3'-P	6.64	1.62	1.56
57	BA	2552	OMU	O3'-P	6.55	1.62	1.56
24	A3	8	4SU	O3'-P	5.43	1.61	1.56
31	BQ	81	ARG	CZ-NH2	-5.06	1.26	1.33

The worst 5 of 335 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	BA	2061	G	C2'-C3'-O3'	8.75	122.63	109.50
22	AA	1118	U	C5'-C4'-C3'	-8.37	103.45	116.00
57	BA	2658	C	C4'-C3'-C2'	-8.09	94.51	102.60
57	BA	2661	G	C1'-O4'-C4'	-8.02	101.89	109.90
48	B5	9	ARG	NE-CZ-NH2	7.62	126.06	119.20

There are no chirality outliers.

5 of 1070 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	AL	109	ARG	Sidechain
6	AO	88	ARG	Sidechain
7	AP	25	ARG	Sidechain
9	AR	2	ARG	Sidechain
10	AS	79	TYR	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AJ	794	0	803	0	0
2	AK	923	0	912	0	0
3	AL	923	0	954	0	0
4	AM	876	0	910	0	0
5	AN	771	0	777	0	0
6	AO	690	0	691	0	0
7	AP	620	0	611	0	0
8	AQ	657	0	687	0	0
9	AR	603	0	602	0	0
10	AS	708	0	732	0	0
11	AB	1805	0	1750	0	0
12	AT	636	0	652	0	0
13	AU	564	0	579	0	0
14	AC	1761	0	1793	0	0
15	AD	1587	0	1596	0	0
16	AE	1182	0	1185	0	0
17	AF	1061	0	971	0	0
18	AG	1347	0	1347	0	0
19	AH	948	0	975	0	0
20	AI	1000	0	1011	0	0
21	A1	4989	0	4915	0	0
22	AA	33089	0	16668	0	0
23	A2	993	0	501	0	0
24	A3	1640	0	845	0	0
25	BC	1733	0	1824	0	0
26	BJ	1233	0	1283	0	0
27	BK	1032	0	1088	0	0
28	BN	1129	0	1162	0	0
29	BO	947	0	1023	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	BP	1053	0	1129	0	0
31	BQ	1074	0	1157	0	0
32	BR	1008	0	1045	0	0
33	BS	900	0	935	0	0
34	BT	917	0	965	0	0
35	BD	2092	0	2170	0	0
36	BU	947	0	1022	0	0
37	BV	816	0	839	0	0
38	BW	857	0	922	0	0
39	BX	787	0	846	0	0
40	BY	789	0	847	0	0
41	BZ	753	0	780	0	0
42	B0	634	0	656	0	0
43	B1	625	0	655	0	0
44	B2	509	0	543	0	0
45	BE	1565	0	1616	0	0
46	B3	449	0	491	0	0
47	B4	549	0	552	0	0
48	B5	444	0	461	0	0
49	B6	441	0	485	0	0
50	B7	377	0	418	0	0
51	B8	504	0	574	0	0
52	B9	302	0	343	0	0
53	BF	1552	0	1619	0	0
54	BG	1420	0	1460	0	0
55	BH	1323	0	1374	0	0
56	BL	1111	0	1148	0	0
57	BA	62351	0	31378	0	0
58	Ba	2566	0	1302	0	0
All	All	154956	0	106579	0	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). Clashscore could not be calculated for this entry.

There are no clashes within the asymmetric unit.

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AJ	44/103 (43%)	40 (91%)	1 (2%)	3 (7%)	1	11
2	AK	57/128 (44%)	52 (91%)	5 (9%)	0	100	100
3	AL	64/123 (52%)	54 (84%)	8 (12%)	2 (3%)	3	22
4	AM	56/117 (48%)	51 (91%)	4 (7%)	1 (2%)	6	34
5	AN	41/100 (41%)	37 (90%)	3 (7%)	1 (2%)	4	27
6	AO	44/88 (50%)	43 (98%)	1 (2%)	0	100	100
7	AP	34/82 (42%)	31 (91%)	3 (9%)	0	100	100
8	AQ	52/83 (63%)	48 (92%)	4 (8%)	0	100	100
9	AR	36/74 (49%)	34 (94%)	2 (6%)	0	100	100
10	AS	54/91 (59%)	53 (98%)	1 (2%)	0	100	100
11	AB	123/240 (51%)	114 (93%)	7 (6%)	2 (2%)	7	38
12	AT	32/86 (37%)	30 (94%)	2 (6%)	0	100	100
13	AU	24/70 (34%)	18 (75%)	3 (12%)	3 (12%)	0	4
14	AC	126/232 (54%)	122 (97%)	4 (3%)	0	100	100
15	AD	107/205 (52%)	102 (95%)	5 (5%)	0	100	100
16	AE	89/166 (54%)	84 (94%)	4 (4%)	1 (1%)	11	46
17	AF	65/135 (48%)	61 (94%)	4 (6%)	0	100	100
18	AG	84/178 (47%)	79 (94%)	5 (6%)	0	100	100
19	AH	77/129 (60%)	70 (91%)	7 (9%)	0	100	100
20	AI	69/129 (54%)	63 (91%)	6 (9%)	0	100	100
21	A1	434/639 (68%)	390 (90%)	38 (9%)	6 (1%)	9	40
25	BC	232/234 (99%)	213 (92%)	18 (8%)	1 (0%)	30	67
26	BJ	162/164 (99%)	158 (98%)	3 (2%)	1 (1%)	21	59
27	BK	139/141 (99%)	133 (96%)	6 (4%)	0	100	100
28	BN	140/142 (99%)	131 (94%)	9 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	BO	121/123 (98%)	107 (88%)	11 (9%)	3 (2%)	4	26
30	BP	142/144 (99%)	127 (89%)	13 (9%)	2 (1%)	9	40
31	BQ	134/136 (98%)	126 (94%)	6 (4%)	2 (2%)	8	40
32	BR	125/127 (98%)	112 (90%)	11 (9%)	2 (2%)	7	38
33	BS	115/117 (98%)	115 (100%)	0	0	100	100
34	BT	112/114 (98%)	107 (96%)	3 (3%)	2 (2%)	6	34
35	BD	270/272 (99%)	252 (93%)	15 (6%)	3 (1%)	11	46
36	BU	115/117 (98%)	108 (94%)	5 (4%)	2 (2%)	7	36
37	BV	101/103 (98%)	94 (93%)	4 (4%)	3 (3%)	3	23
38	BW	108/110 (98%)	103 (95%)	4 (4%)	1 (1%)	14	51
39	BX	98/100 (98%)	83 (85%)	12 (12%)	3 (3%)	3	22
40	BY	101/103 (98%)	97 (96%)	4 (4%)	0	100	100
41	BZ	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
42	B0	82/84 (98%)	72 (88%)	6 (7%)	4 (5%)	1	16
43	B1	75/77 (97%)	69 (92%)	5 (7%)	1 (1%)	9	42
44	B2	61/63 (97%)	54 (88%)	7 (12%)	0	100	100
45	BE	207/209 (99%)	181 (87%)	20 (10%)	6 (3%)	3	23
46	B3	56/58 (97%)	53 (95%)	3 (5%)	0	100	100
47	B4	68/70 (97%)	62 (91%)	6 (9%)	0	100	100
48	B5	54/56 (96%)	50 (93%)	3 (6%)	1 (2%)	6	32
49	B6	52/54 (96%)	51 (98%)	1 (2%)	0	100	100
50	B7	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
51	B8	62/64 (97%)	61 (98%)	1 (2%)	0	100	100
52	B9	36/38 (95%)	31 (86%)	3 (8%)	2 (6%)	1	14
53	BF	199/201 (99%)	186 (94%)	7 (4%)	6 (3%)	3	23
54	BG	176/178 (99%)	155 (88%)	15 (8%)	6 (3%)	3	21
55	BH	174/176 (99%)	157 (90%)	14 (8%)	3 (2%)	7	36
56	BL	147/149 (99%)	133 (90%)	13 (9%)	1 (1%)	18	56
All	All	5512/7062 (78%)	5089 (92%)	349 (6%)	74 (1%)	12	42

5 of 74 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
21	A1	242	THR
21	A1	493	LYS
32	BR	13	ASN
35	BD	140	VAL
42	B0	40	ARG

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AJ	90/90 (100%)	88 (98%)	2 (2%)	45	64
2	AK	98/98 (100%)	96 (98%)	2 (2%)	48	66
3	AL	103/103 (100%)	102 (99%)	1 (1%)	68	78
4	AM	95/95 (100%)	95 (100%)	0	100	100
5	AN	83/83 (100%)	82 (99%)	1 (1%)	63	75
6	AO	76/76 (100%)	75 (99%)	1 (1%)	61	74
7	AP	65/65 (100%)	64 (98%)	1 (2%)	57	72
8	AQ	77/77 (100%)	77 (100%)	0	100	100
9	AR	64/64 (100%)	62 (97%)	2 (3%)	35	56
10	AS	78/78 (100%)	75 (96%)	3 (4%)	29	50
11	AB	198/198 (100%)	197 (100%)	1 (0%)	81	83
12	AT	65/65 (100%)	65 (100%)	0	100	100
13	AU	60/60 (100%)	58 (97%)	2 (3%)	33	55
14	AC	189/189 (100%)	184 (97%)	5 (3%)	40	62
15	AD	172/172 (100%)	170 (99%)	2 (1%)	63	75
16	AE	125/125 (100%)	119 (95%)	6 (5%)	23	44
17	AF	116/116 (100%)	112 (97%)	4 (3%)	32	54
18	AG	146/146 (100%)	144 (99%)	2 (1%)	59	72
19	AH	104/104 (100%)	104 (100%)	0	100	100
20	AI	106/106 (100%)	105 (99%)	1 (1%)	70	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	A1	568/568 (100%)	559 (98%)	9 (2%)	55	70
25	BC	181/181 (100%)	177 (98%)	4 (2%)	45	64
26	BJ	122/122 (100%)	120 (98%)	2 (2%)	55	70
27	BK	109/109 (100%)	106 (97%)	3 (3%)	38	60
28	BN	116/116 (100%)	111 (96%)	5 (4%)	26	47
29	BO	104/104 (100%)	101 (97%)	3 (3%)	37	58
30	BP	103/103 (100%)	99 (96%)	4 (4%)	28	49
31	BQ	109/109 (100%)	105 (96%)	4 (4%)	30	51
32	BR	103/103 (100%)	100 (97%)	3 (3%)	37	58
33	BS	87/87 (100%)	86 (99%)	1 (1%)	65	76
34	BT	99/99 (100%)	98 (99%)	1 (1%)	68	78
35	BD	217/217 (100%)	214 (99%)	3 (1%)	59	72
36	BU	89/89 (100%)	86 (97%)	3 (3%)	32	54
37	BV	84/84 (100%)	83 (99%)	1 (1%)	63	75
38	BW	93/93 (100%)	91 (98%)	2 (2%)	45	64
39	BX	84/84 (100%)	83 (99%)	1 (1%)	63	75
40	BY	84/84 (100%)	83 (99%)	1 (1%)	63	75
41	BZ	78/78 (100%)	77 (99%)	1 (1%)	61	74
42	B0	62/62 (100%)	56 (90%)	6 (10%)	8	24
43	B1	67/67 (100%)	67 (100%)	0	100	100
44	B2	55/55 (100%)	55 (100%)	0	100	100
45	BE	164/164 (100%)	162 (99%)	2 (1%)	63	75
46	B3	48/48 (100%)	48 (100%)	0	100	100
47	B4	62/62 (100%)	61 (98%)	1 (2%)	55	70
48	B5	47/47 (100%)	45 (96%)	2 (4%)	26	47
49	B6	48/48 (100%)	48 (100%)	0	100	100
50	B7	38/38 (100%)	38 (100%)	0	100	100
51	B8	51/51 (100%)	50 (98%)	1 (2%)	48	66
52	B9	34/34 (100%)	34 (100%)	0	100	100
53	BF	165/165 (100%)	163 (99%)	2 (1%)	63	75
54	BG	149/149 (100%)	145 (97%)	4 (3%)	39	61

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
55	BH	137/137 (100%)	134 (98%)	3 (2%)	45	64
56	BL	114/114 (100%)	114 (100%)	0	100	100
All	All	5781/5781 (100%)	5673 (98%)	108 (2%)	49	67

5 of 108 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
28	BN	61	LYS
32	BR	16	HIS
53	BF	67	ARG
29	BO	47	ILE
30	BP	111	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
22	AA	1541/1542 (99%)	204 (13%)	57 (3%)
23	A2	46/47 (97%)	13 (28%)	1 (2%)
24	A3	75/77 (97%)	12 (16%)	2 (2%)
57	BA	2903/2904 (99%)	434 (14%)	115 (3%)
58	Ba	119/120 (99%)	14 (11%)	0
All	All	4684/4690 (99%)	677 (14%)	175 (3%)

5 of 677 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
22	AA	2	A
22	AA	3	A
22	AA	5	U
22	AA	6	G
22	AA	7	A

5 of 175 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
57	BA	1325	U
57	BA	2062	A

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Mol	Chain	Res	Type
57	BA	1393	A
57	BA	1653	G
57	BA	2248	C

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

39 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	$\# Z > 2$
57	3TD	BA	1915	57	19,22,23	0.81	0	23,32,35	1.44	3 (13%)
57	OMC	BA	2498	57	19,22,23	0.75	0	25,31,34	1.29	1 (4%)
22	MA6	AA	1518	22	23,26,27	0.64	0	33,38,41	0.98	1 (3%)
57	PSU	BA	746	57	18,21,22	0.79	0	21,30,33	1.28	4 (19%)
57	PSU	BA	2504	57	18,21,22	0.78	0	21,30,33	1.21	2 (9%)
57	2MG	BA	2445	57	23,26,27	0.55	0	33,38,41	0.84	0
57	PSU	BA	1917	57	18,21,22	0.77	0	21,30,33	1.18	2 (9%)
22	MA6	AA	1519	22	23,26,27	0.66	0	33,38,41	1.07	1 (3%)
22	5MC	AA	967	22	19,22,23	0.67	0	26,32,35	1.49	5 (19%)
22	2MG	AA	1516	22	23,26,27	0.56	0	33,38,41	0.93	1 (3%)
22	4OC	AA	1402	22	20,23,24	0.63	0	25,32,35	1.23	3 (12%)
57	2MG	BA	1835	57	23,26,27	0.59	0	33,38,41	0.73	0
57	6MZ	BA	2030	57	22,25,26	0.66	0	29,36,39	1.09	2 (6%)
57	OMU	BA	2552	57	19,22,23	0.57	0	25,31,34	0.93	1 (4%)
57	7MG	BA	2069	57	23,26,27	3.90	2 (8%)	27,39,42	1.47	1 (3%)
57	PSU	BA	2457	57	18,21,22	0.78	0	21,30,33	1.20	2 (9%)
24	H2U	A3	21	24	18,21,22	1.05	2 (11%)	19,30,33	0.71	0
57	6MZ	BA	1618	57	22,25,26	0.72	1 (4%)	29,36,39	1.20	3 (10%)
57	OMG	BA	2251	57	23,26,27	0.62	0	32,38,41	1.03	2 (6%)
22	PSU	AA	516	22	18,21,22	0.81	0	21,30,33	1.30	2 (9%)
57	PSU	BA	955	57	18,21,22	0.79	0	21,30,33	1.15	2 (9%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
24	5MU	A3	55	24	19,22,23	0.66	0	27,32,35	1.34	4 (14%)
57	1MG	BA	745	57	23,26,27	0.64	0	33,39,42	1.18	3 (9%)
22	7MG	AA	527	22	23,26,27	3.84	3 (13%)	27,39,42	1.55	2 (7%)
24	PSU	A3	56	24	18,21,22	0.84	0	21,30,33	1.18	2 (9%)
57	PSU	BA	2605	57	18,21,22	0.87	0	21,30,33	1.35	3 (14%)
22	2MG	AA	966	22	23,26,27	0.58	0	33,38,41	0.81	0
57	PSU	BA	1911	57	18,21,22	0.83	0	21,30,33	1.06	2 (9%)
57	2MA	BA	2503	57	22,25,26	0.83	1 (4%)	32,37,40	1.30	4 (12%)
22	5MC	AA	1407	22	19,22,23	0.69	0	26,32,35	1.45	5 (19%)
57	5MC	BA	1962	57	19,22,23	0.72	1 (5%)	26,32,35	1.59	6 (23%)
57	H2U	BA	2449	57	18,21,22	1.16	2 (11%)	19,30,33	1.01	0
24	OMC	A3	33	24	19,22,23	0.69	0	25,31,34	1.13	1 (4%)
57	PSU	BA	2580	57	18,21,22	0.82	0	21,30,33	1.55	4 (19%)
57	5MU	BA	747	57	19,22,23	0.71	0	27,32,35	1.34	3 (11%)
22	UR3	AA	1498	22	19,22,23	0.69	0	26,32,35	1.06	3 (11%)
22	2MG	AA	1207	22	23,26,27	0.60	0	33,38,41	0.72	0
57	5MU	BA	1939	57	19,22,23	0.69	0	27,32,35	1.31	3 (11%)
24	4SU	A3	8	24	18,21,22	1.47	2 (11%)	25,30,33	1.16	2 (8%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
57	3TD	BA	1915	57	-	2/7/25/26	0/2/2/2
57	OMC	BA	2498	57	-	0/9/27/28	0/2/2/2
22	MA6	AA	1518	22	-	0/11/29/30	0/3/3/3
57	PSU	BA	746	57	-	0/7/25/26	0/2/2/2
57	PSU	BA	2504	57	-	2/7/25/26	0/2/2/2
57	2MG	BA	2445	57	-	0/9/27/28	0/3/3/3
57	PSU	BA	1917	57	-	0/7/25/26	0/2/2/2
22	MA6	AA	1519	22	-	0/11/29/30	0/3/3/3
22	5MC	AA	967	22	-	0/7/25/26	0/2/2/2
22	2MG	AA	1516	22	-	0/9/27/28	0/3/3/3
22	4OC	AA	1402	22	-	0/9/29/30	0/2/2/2
57	2MG	BA	1835	57	-	0/9/27/28	0/3/3/3
57	6MZ	BA	2030	57	-	0/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
57	OMU	BA	2552	57	-	0/9/27/28	0/2/2/2
57	7MG	BA	2069	57	-	0/7/37/38	0/3/3/3
57	PSU	BA	2457	57	-	0/7/25/26	0/2/2/2
24	H2U	A3	21	24	-	0/7/38/39	0/2/2/2
57	6MZ	BA	1618	57	-	0/9/27/28	0/3/3/3
57	OMG	BA	2251	57	-	0/9/27/28	0/3/3/3
22	PSU	AA	516	22	-	0/7/25/26	0/2/2/2
57	PSU	BA	955	57	-	0/7/25/26	0/2/2/2
24	5MU	A3	55	24	-	0/7/25/26	0/2/2/2
57	1MG	BA	745	57	-	0/7/25/26	0/3/3/3
22	7MG	AA	527	22	-	0/7/37/38	0/3/3/3
24	PSU	A3	56	24	-	2/7/25/26	0/2/2/2
57	PSU	BA	2605	57	-	0/7/25/26	0/2/2/2
22	2MG	AA	966	22	-	0/9/27/28	0/3/3/3
57	PSU	BA	1911	57	-	0/7/25/26	0/2/2/2
57	2MA	BA	2503	57	-	2/7/25/26	0/3/3/3
22	5MC	AA	1407	22	-	0/7/25/26	0/2/2/2
57	5MC	BA	1962	57	-	0/7/25/26	0/2/2/2
57	H2U	BA	2449	57	-	0/7/38/39	0/2/2/2
24	OMC	A3	33	24	-	0/9/27/28	0/2/2/2
57	PSU	BA	2580	57	-	0/7/25/26	0/2/2/2
57	5MU	BA	747	57	-	0/7/25/26	0/2/2/2
22	UR3	AA	1498	22	-	0/7/25/26	0/2/2/2
22	2MG	AA	1207	22	-	0/9/27/28	0/3/3/3
57	5MU	BA	1939	57	-	0/7/25/26	0/2/2/2
24	4SU	A3	8	24	-	0/7/25/26	0/2/2/2

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	BA	2069	7MG	C8-N9	-18.24	1.34	1.45
22	AA	527	7MG	C8-N9	-17.94	1.34	1.45
24	A3	8	4SU	C5-C4	-5.29	1.36	1.42
57	BA	2449	H2U	C4-N3	-3.12	1.32	1.37
57	BA	2449	H2U	C2-N3	-3.00	1.32	1.38

The worst 5 of 85 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	BA	2069	7MG	N9-C8-N7	6.12	112.04	103.37
22	AA	527	7MG	N9-C8-N7	5.87	111.68	103.37
57	BA	1915	3TD	C6-C5-C4	4.02	120.89	118.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	BA	745	1MG	N2-C2-N1	4.02	122.02	118.79
57	BA	2580	PSU	C6-C5-C4	3.96	120.85	118.17

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
24	A3	56	PSU	O4'-C1'-C5-C4
57	BA	2504	PSU	O4'-C1'-C5-C4
57	BA	2503	2MA	O4'-C1'-N9-C8
57	BA	2503	2MA	O4'-C1'-N9-C4
24	A3	56	PSU	O4'-C1'-C5-C6

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

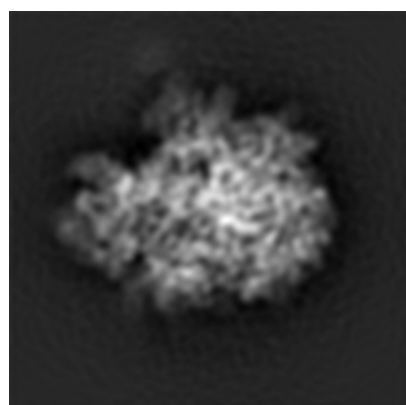
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5562. These allow visual inspection of the internal detail of the map and identification of artifacts.

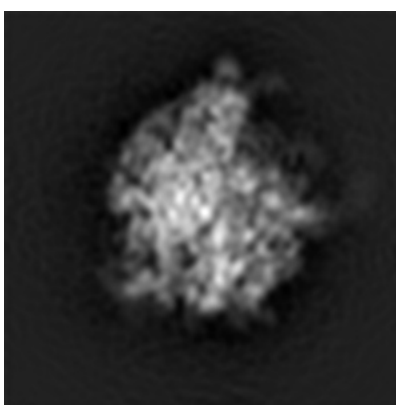
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

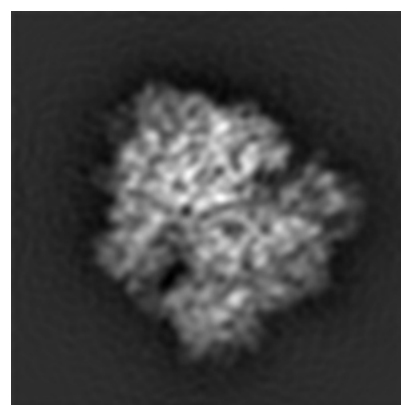
6.1.1 Primary map



X



Y

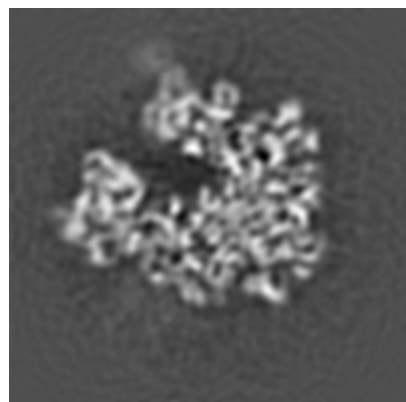


Z

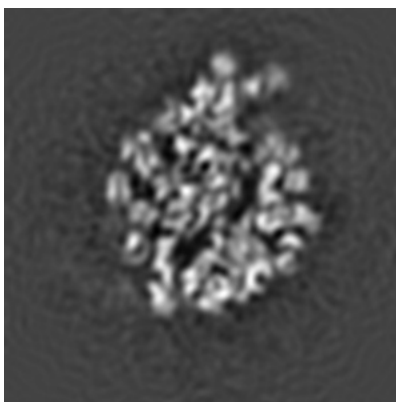
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

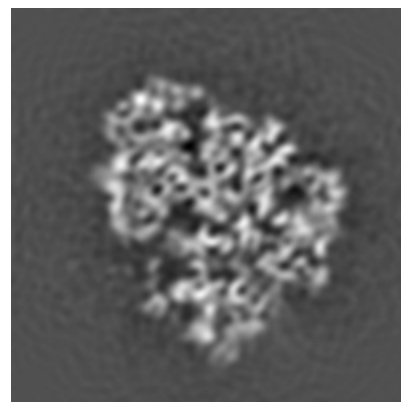
6.2.1 Primary map



X Index: 67



Y Index: 67

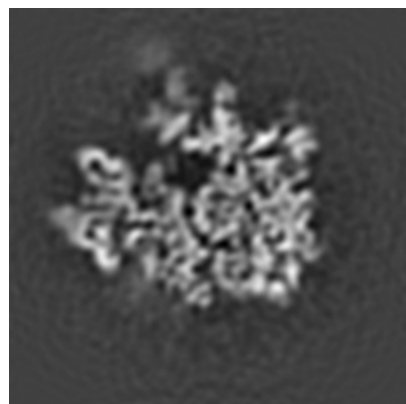


Z Index: 67

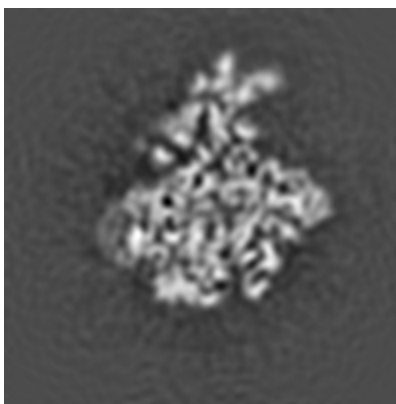
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

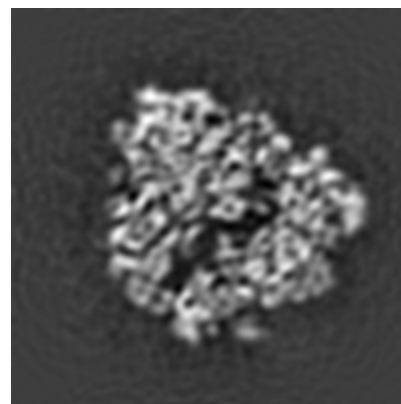
6.3.1 Primary map



X Index: 70



Y Index: 71

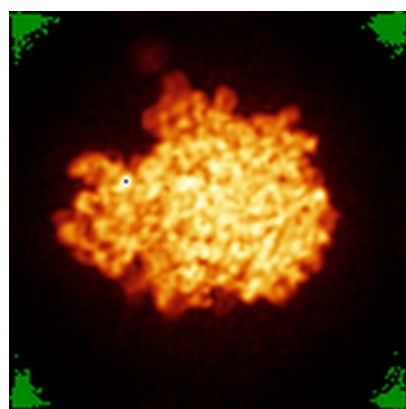


Z Index: 73

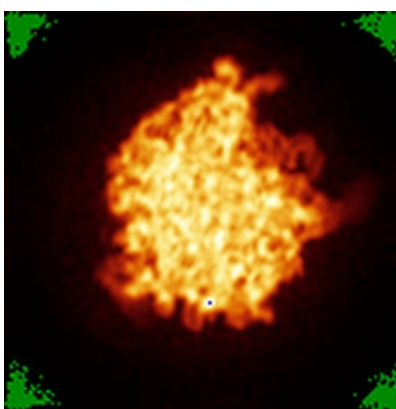
The images above show the largest variance slices of the map in three orthogonal directions.

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

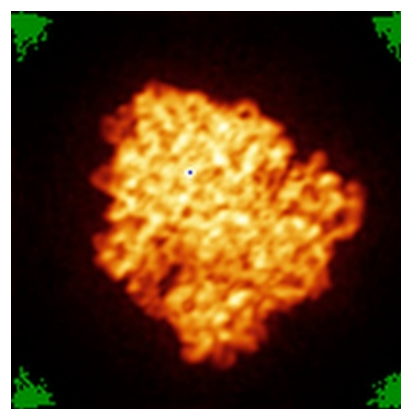
6.4.1 Primary map



X



Y

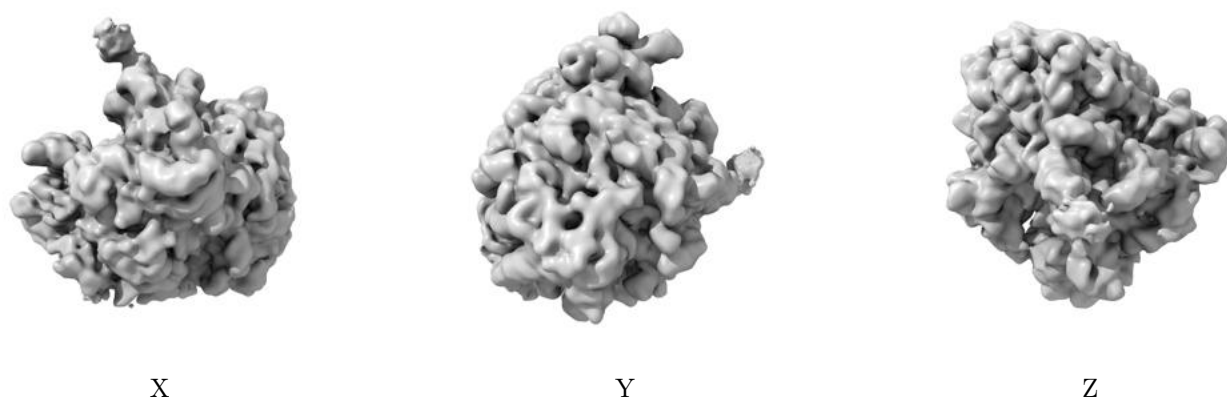


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 22.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

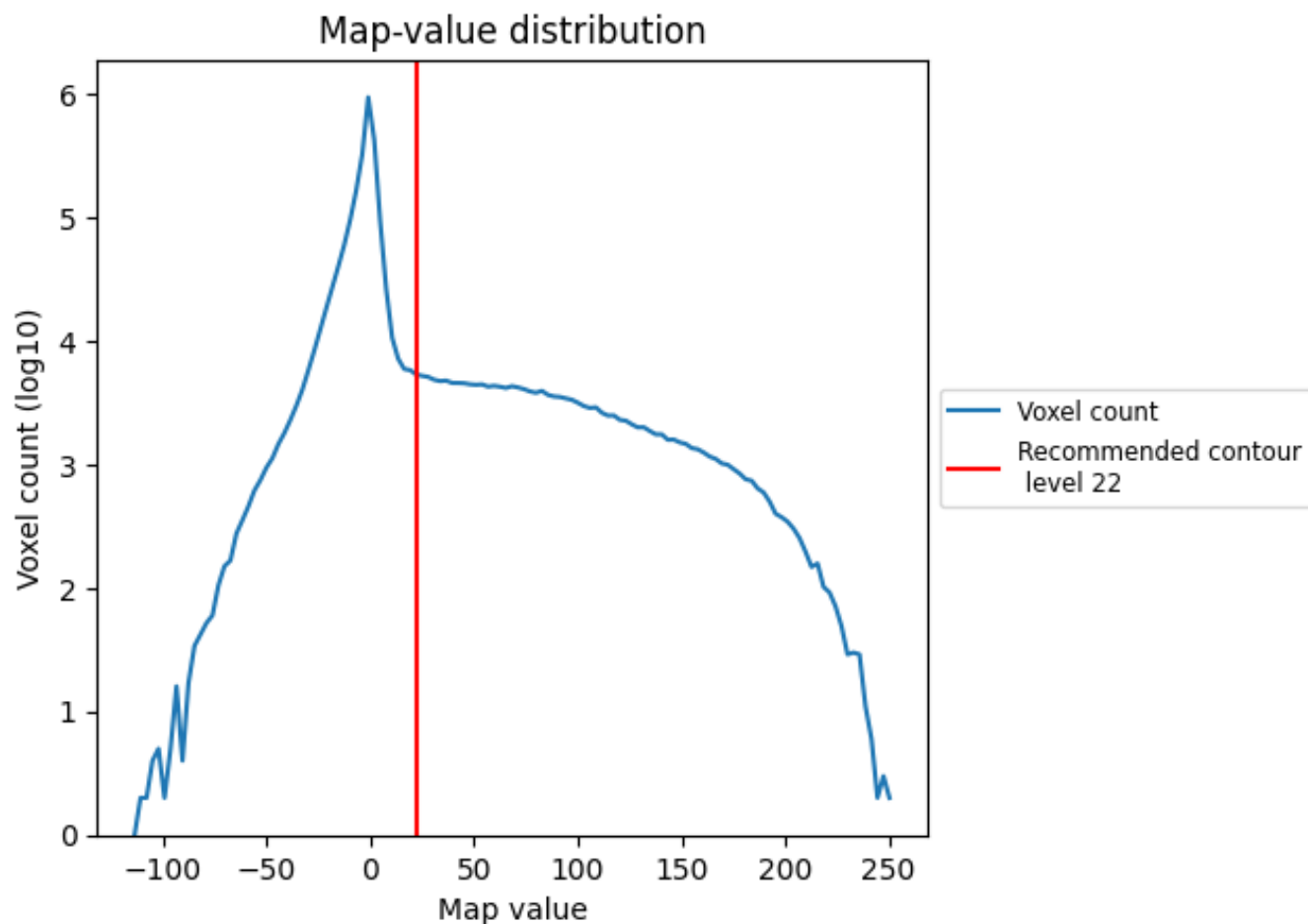
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

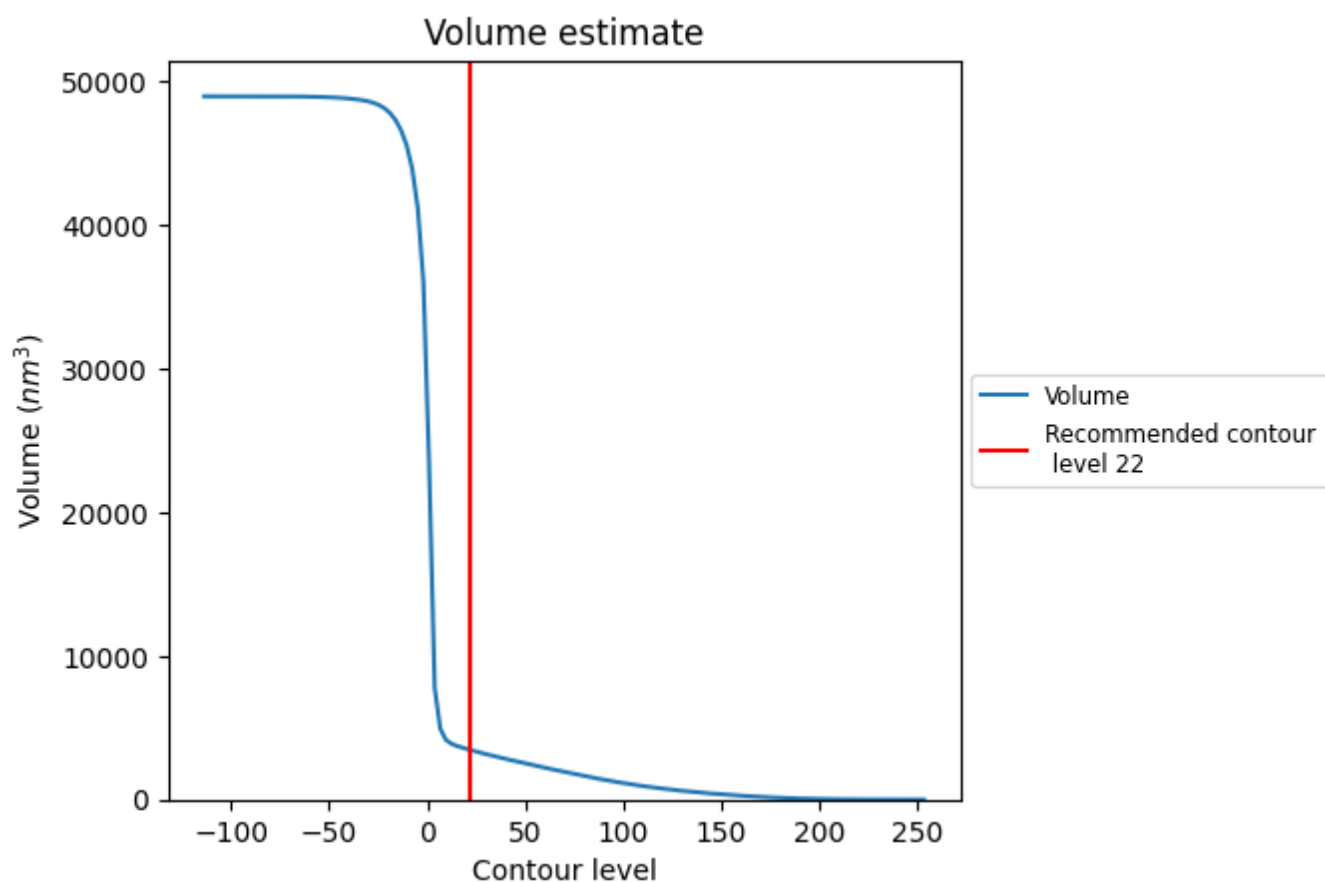
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

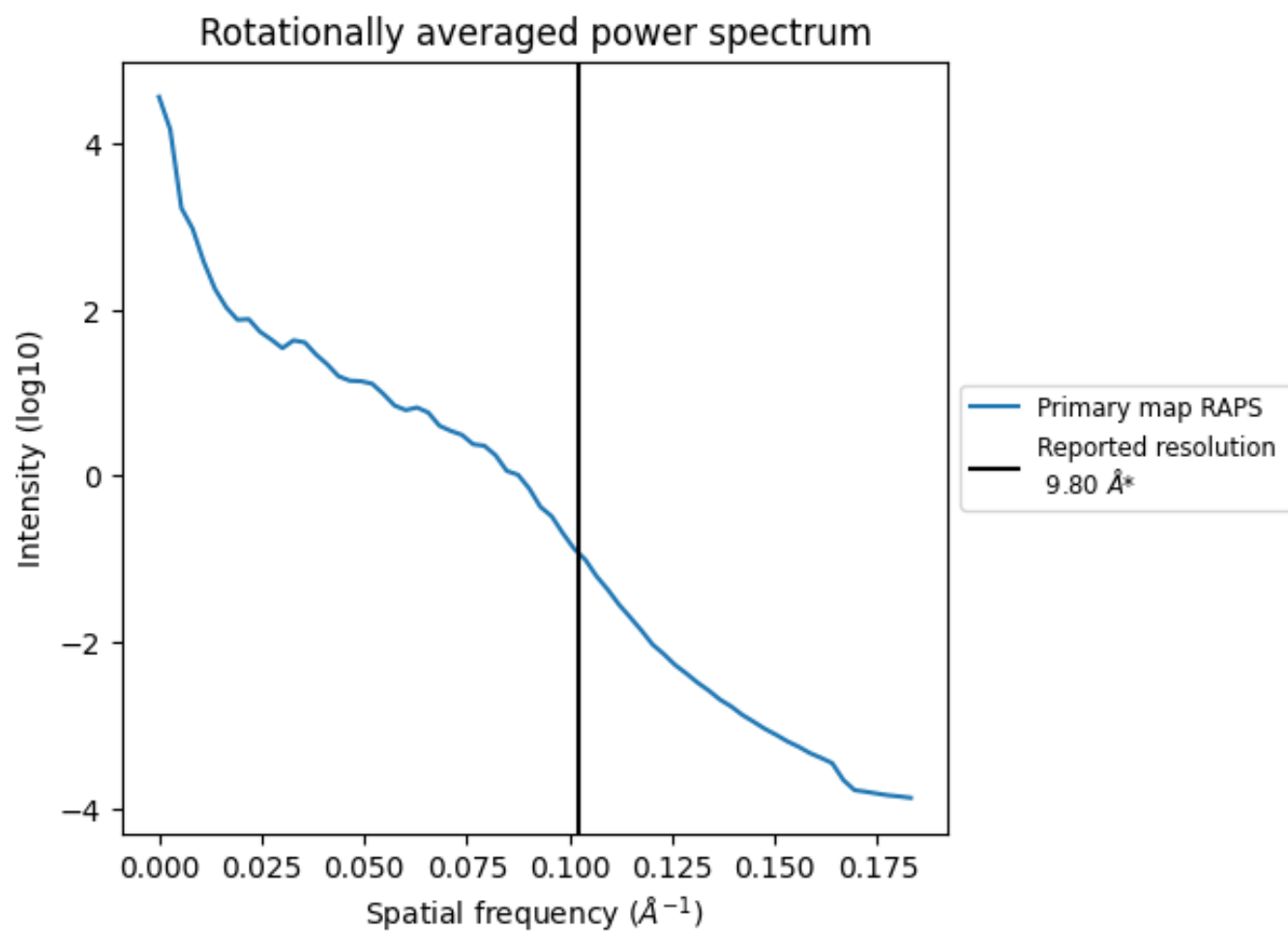
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3450 nm³; this corresponds to an approximate mass of 3116 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.102 Å⁻¹

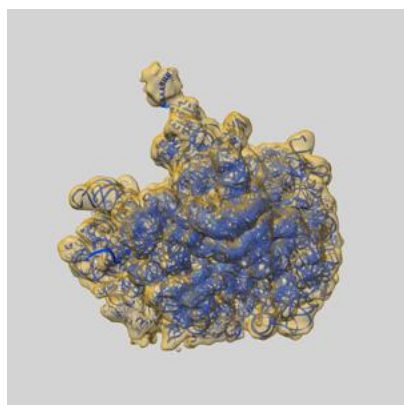
8 Fourier-Shell correlation

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

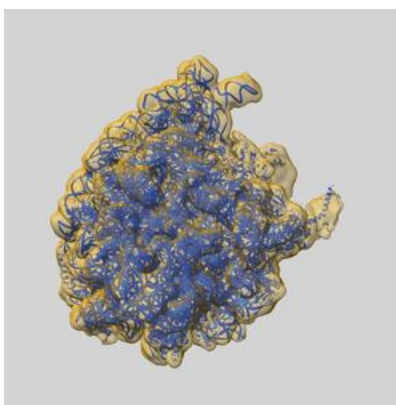
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-5562 and PDB model 4V6V. Per-residue inclusion information can be found in section [3](#) on page [15](#).

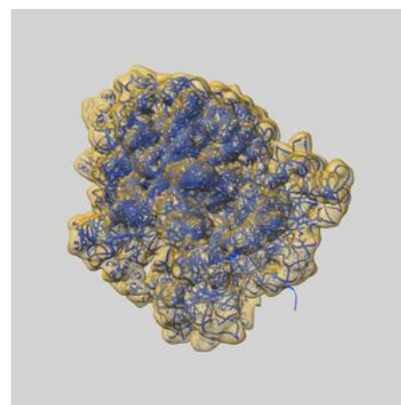
9.1 Map-model overlay [i](#)



X



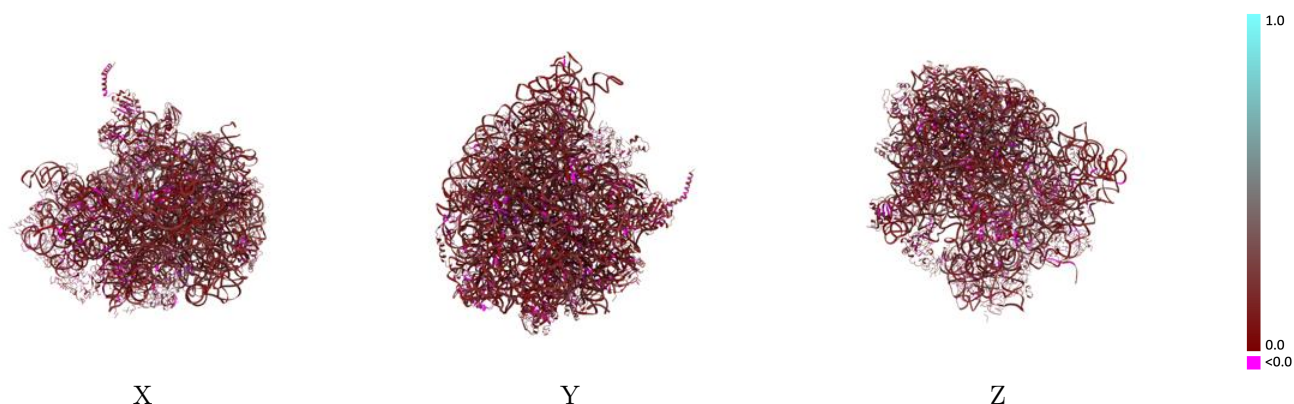
Y



Z

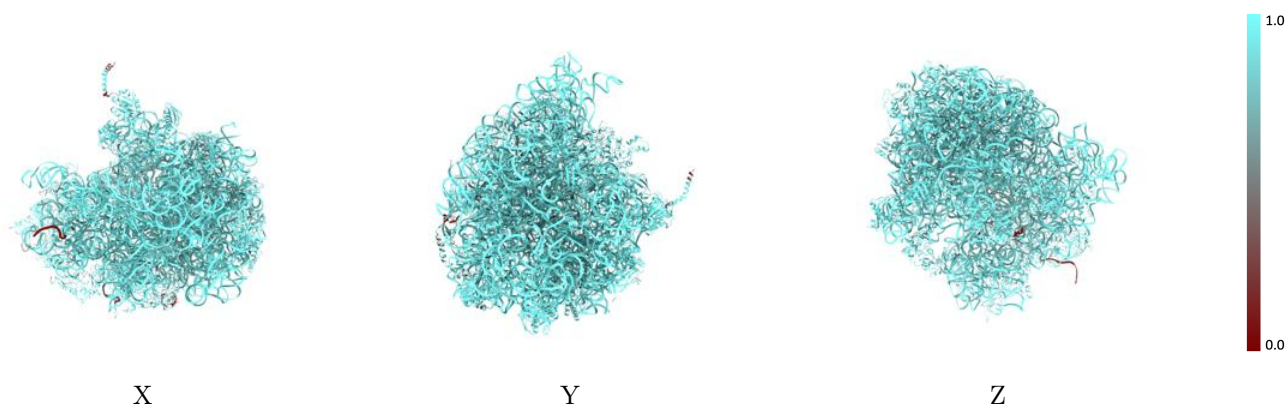
The images above show the 3D surface view of the map at the recommended contour level 22.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



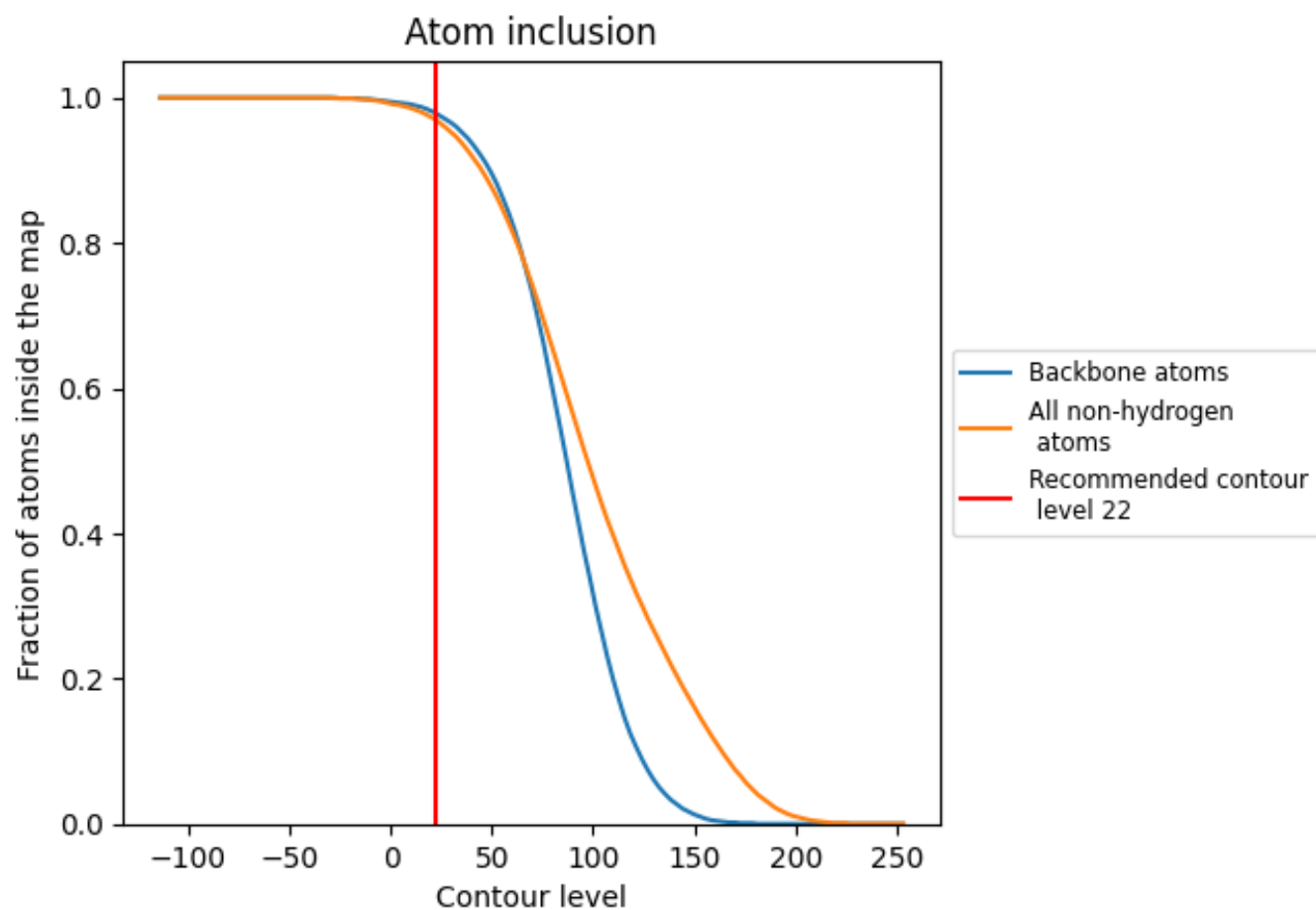
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (22).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 97% 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 (22) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9700	 0.1260
A1	 0.9130	 0.1120
A2	 0.4660	 0.0110
A3	 0.9840	 0.1530
AA	 0.9950	 0.1430
AB	 0.9200	 0.1050
AC	 0.9110	 0.0970
AD	 0.9760	 0.0960
AE	 0.8840	 0.0850
AF	 0.8220	 0.0930
AG	 0.9590	 0.1070
AH	 0.9560	 0.1020
AI	 0.9750	 0.0840
AJ	 0.9580	 0.0780
AK	 0.8950	 0.0910
AL	 0.9260	 0.0940
AM	 0.9720	 0.1100
AN	 0.9470	 0.0640
AO	 0.9800	 0.1040
AP	 0.9730	 0.0620
AQ	 0.9630	 0.1070
AR	 0.9090	 0.0770
AS	 0.9540	 0.0810
AT	 0.9610	 0.1110
AU	 0.8750	 0.0990
B0	 0.9000	 0.0370
B1	 0.9550	 0.0880
B2	 0.9660	 0.1380
B3	 0.9660	 0.1170
B4	 0.8850	 0.0850
B5	 0.9300	 0.0630
B6	 0.9540	 0.0900
B7	 0.9270	 0.0670
B8	 0.9430	 0.0620
B9	 0.9520	 0.0520



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Chain	Atom inclusion	Q-score
BA	 0.9930	 0.1450
BC	 0.8760	 0.0490
BD	 0.9380	 0.0750
BE	 0.9420	 0.0870
BF	 0.9720	 0.0950
BG	 0.9730	 0.0890
BH	 0.9810	 0.1240
BJ	 0.8870	 0.0810
BK	 0.9790	 0.0960
BL	 0.7430	 0.1000
BN	 0.9590	 0.0980
BO	 0.9100	 0.0960
BP	 0.9510	 0.0750
BQ	 0.9500	 0.0920
BR	 0.9520	 0.0900
BS	 0.9760	 0.0940
BT	 0.9350	 0.1020
BU	 0.9660	 0.0980
BV	 0.9400	 0.0990
BW	 0.9250	 0.0900
BX	 0.9600	 0.0890
BY	 0.9600	 0.1060
BZ	 0.9730	 0.1180
Ba	 0.9960	 0.1520