



wwPDB EM Validation Summary Report ⓘ

Feb 13, 2024 – 11:29 AM EST

PDB ID : 7TOS
EMDB ID : EMD-26037
Title : E. coli 70S ribosomes bound with the ALS/FTD-associated dipeptide repeat protein PR20
Authors : Loveland, A.B.; Svidritskiy, E.; Susorov, D.; Lee, S.; Park, A.; Zvornicanin, S.; Demo, G.; Gao, F.B.; Korostelev, A.A.
Deposited on : 2022-01-24
Resolution : 2.90 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

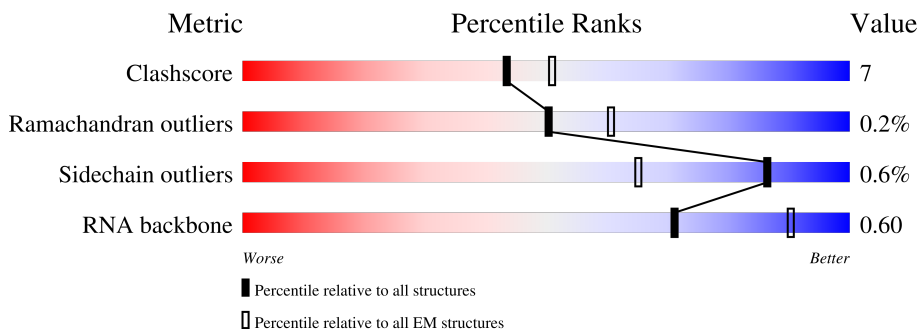
EMDB validation analysis : 0.0.1.dev70
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

1 Overall quality at a glance

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

The reported resolution of this entry is 2.90 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
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 $\leq 5\%$. 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	L02	271	
2	L03	209	
3	L04	201	
4	L05	177	
5	L06	176	
6	L09	149	
7	L10	131	

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Mol	Chain	Length	Quality of chain
8	L11	141	21% 84% 16%
9	L13	142	82% 18%
10	L14	122	83% 17%
11	L15	143	78% 22%
12	L16	136	83% 17%
13	L17	120	85% 15%
14	L18	116	85% 15%
15	L19	114	82% 18%
16	L20	117	91% 9%
17	L21	103	78% 22%
18	L22	110	84% 16%
19	L23	93	89% 11%
20	L24	102	79% 21%
21	L25	94	83% 17%
22	L27	75	92% 8%
23	L28	77	91% 9%
24	L29	63	78% 21%
25	L30	58	88% 12%
26	L31	66	5% 91% 9%
27	L32	56	89% 11%
28	L33	50	16% 78% 22%
29	L34	46	74% 26%
30	L35	64	80% 17%
31	L36	38	79% 21%
32	S02	225	79% 21%

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Mol	Chain	Length	Quality of chain
33	S03	206	80% 20%
34	S04	205	76% 24%
35	S05	157	81% 18%
36	S06	100	80% 19%
37	S07	151	81% 19%
38	S08	129	85% 15%
39	S09	127	75% 24%
40	S10	98	9% 86% 14%
41	S11	116	72% 28%
42	S12	123	79% 21%
43	S13	114	89% 11%
44	S14	100	78% 22%
45	S15	88	94% 6%
46	S16	82	73% 27%
47	S17	80	80% 20%
48	S18	65	80% 20%
49	S19	79	75% 25%
50	S20	85	86% 14%
51	S21	65	68% 29%
52	L1	223	29% 46% 14% 40%
53	16S	1539	59% 37%
54	23S	2903	60% 36%
55	5S	120	54% 42%
56	PR	40	15% 20% 62%

2 Entry composition [i](#)

There are 56 unique types of molecules in this entry. The entry contains 145427 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 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	L02	271	2083	1288	423	365	7	0	0

- Molecule 2 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	L03	209	1565	979	288	294	4	0	0

- Molecule 3 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	L04	201	1552	974	283	290	5	0	0

- Molecule 4 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	L05	177	1411	899	249	257	6	0	0

- Molecule 5 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	L06	176	1323	832	243	246	2	0	0

- Molecule 6 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	L09	149	1111	699	197	214	1	0	0

- Molecule 7 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	L10	131	989	625	175	184	5	0	0

- Molecule 8 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	L11	141	1032	651	179	196	6	0	0

- Molecule 9 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	L13	142	1129	714	212	199	4	0	0

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	L14	122	939	587	180	166	6	0	0

- Molecule 11 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	L15	143	1045	649	206	189	1	0	0

- Molecule 12 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	L16	136	1074	686	205	177	6	0	0

- Molecule 13 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	L17	120	961	593	196	167	5	0	0

- Molecule 14 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	L18	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 15 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	L19	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 16 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	L20	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 17 is a protein called Ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L21	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 18 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	L22	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 19 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	L23	93	Total	C	N	O	S	0	0
			739	466	139	132	2		

- Molecule 20 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	L24	102	Total	C	N	O	0	0
			780	492	146	142		

- Molecule 21 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	L25	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	L27	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 23 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	L28	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 24 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	L29	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 25 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	L30	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 26 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	L31	66	Total	C	N	O	S	0	0
			523	323	99	95	6		

- Molecule 27 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	L32	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
28	L33	50	Total	C	N	O	0	0
			410	263	75	72		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
29	L34	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
30	L35	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
31	L36	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 32 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	S02	225	Total	C	N	O	S	0	0
			1757	1111	315	323	8		

- Molecule 33 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	S03	206	Total	C	N	O	S	0	0
			1625	1028	305	289	3		

- Molecule 34 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	S04	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 35 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	S05	157	1157	719	218	214	6	0	0

- Molecule 36 is a protein called 30S ribosomal protein S6, non-modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	S06	100	818	515	148	149	6	0	0

- Molecule 37 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	S07	151	1182	735	227	216	4	0	0

- Molecule 38 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	S08	129	979	616	173	184	6	0	0

- Molecule 39 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	S09	127	1022	634	206	179	3	0	0

- Molecule 40 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	S10	98	787	493	150	143	1	0	0

- Molecule 41 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	S11	116	869	534	173	159	3	0	0

- Molecule 42 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	S12	123	955	590	196	165	4	0	0

- Molecule 43 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	S13	114	884	546	178	157	3	0	0

- Molecule 44 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	S14	100	805	499	164	139	3	0	0

- Molecule 45 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	S15	88	714	439	144	130	1	0	0

- Molecule 46 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	S16	82	649	406	128	114	1	0	0

- Molecule 47 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	S17	80	649	411	121	114	3	0	0

- Molecule 48 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	S18	65	536	339	100	96	1	0	0

- Molecule 49 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	S19	79	Total	C	N	O	S	0	0
			638	408	120	108	2		

- Molecule 50 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	S20	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 51 is a protein called Ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	S21	65	Total	C	N	O	S	0	0
			545	335	117	92	1		

- Molecule 52 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	L1	134	Total	C	N	O	S	0	0
			1027	645	186	194	2		

- Molecule 53 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	16S	1532	Total	C	N	O	P	0	0
			32870	14661	6031	10647	1531		

- Molecule 54 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	23S	2903	Total	C	N	O	P	0	0
			62317	27801	11468	20146	2902		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
23S	747	C	U	variant	GB 1036415628

- Molecule 55 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
55	5S	120	2568	1145	471	833	119	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
5S	120	A	-	insertion	GB 1370526515


- Molecule 56 is a protein called PR20, ALS/FTD dipeptide repeat protein.

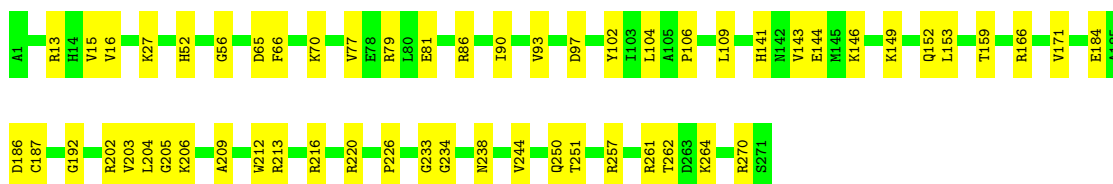
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
56	PR	15	133	82	36	15	0	0

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: 50S ribosomal protein L2

Chain L02:  79% 21%




- Molecule 2: 50S ribosomal protein L3

Chain L03:  91% 9%




- Molecule 3: 50S ribosomal protein L4

Chain L04:  79% 21%




- Molecule 4: 50S ribosomal protein L5

Chain L05:  86% 14%




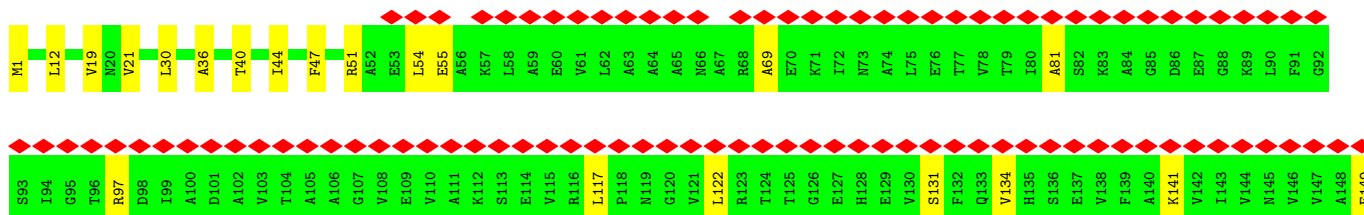
- Molecule 5: 50S ribosomal protein L6

Chain L06:  85% 15%



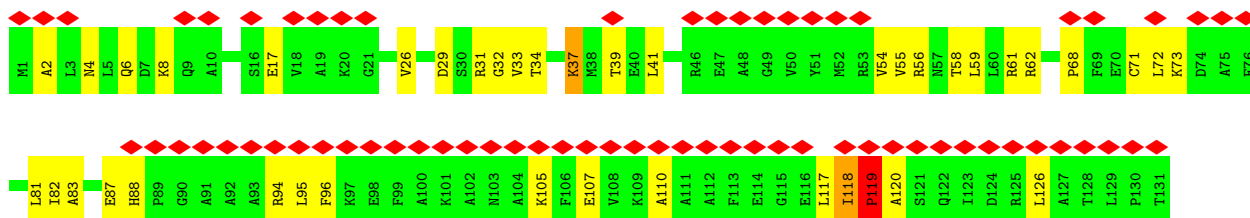
• Molecule 6: 50S ribosomal protein L9

Chain L09:  64% 86% 14%




• Molecule 7: 50S ribosomal protein L10

Chain L10:  52% 69% 29% ..




• Molecule 8: 50S ribosomal protein L11

Chain L11:  21% 84% 16%




• Molecule 9: 50S ribosomal protein L13

Chain L13:  82% 18%

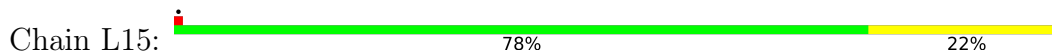


• Molecule 10: 50S ribosomal protein L14

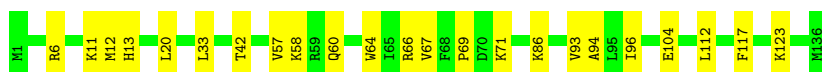
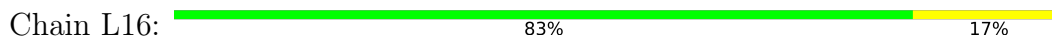
Chain L14:  83% 17%



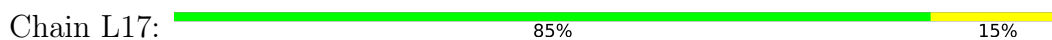
- Molecule 11: 50S ribosomal protein L15



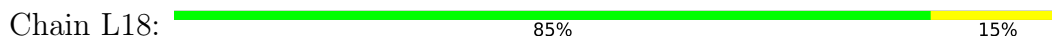
- Molecule 12: 50S ribosomal protein L16



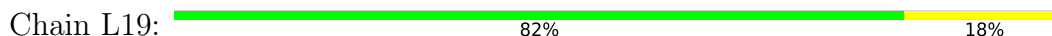
- Molecule 13: 50S ribosomal protein L17



- Molecule 14: 50S ribosomal protein L18



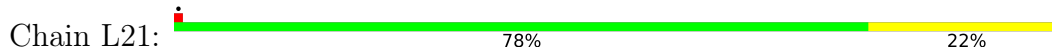
- Molecule 15: 50S ribosomal protein L19



- Molecule 16: 50S ribosomal protein L20

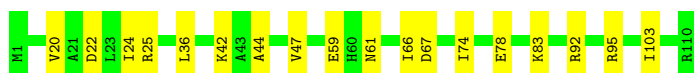
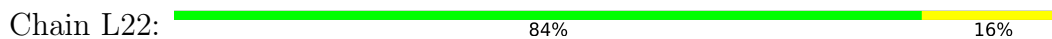


- Molecule 17: Ribosomal protein L21





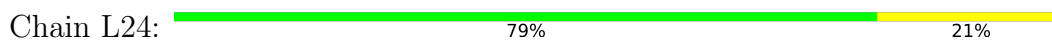
- Molecule 18: 50S ribosomal protein L22



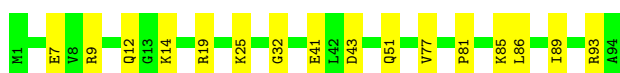
- Molecule 19: 50S ribosomal protein L23



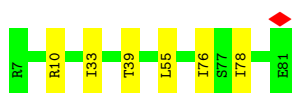
- Molecule 20: Ribosomal protein L24



- Molecule 21: 50S ribosomal protein L25



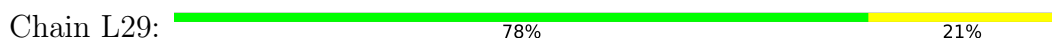
- Molecule 22: 50S ribosomal protein L27



- Molecule 23: 50S ribosomal protein L28

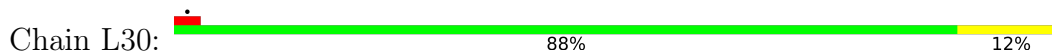


- Molecule 24: 50S ribosomal protein L29

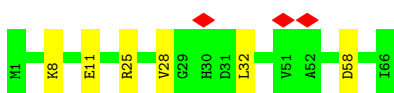




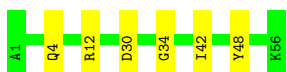
- Molecule 25: 50S ribosomal protein L30



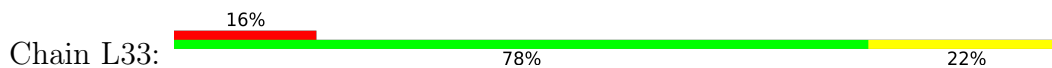
- Molecule 26: 50S ribosomal protein L31



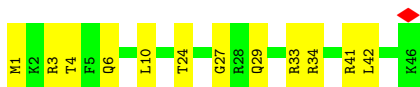
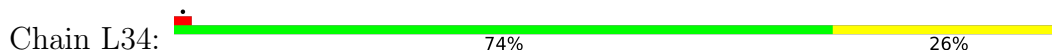
- Molecule 27: 50S ribosomal protein L32



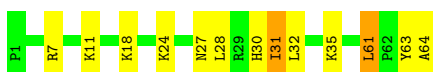
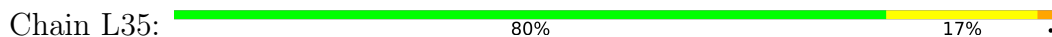
- Molecule 28: 50S ribosomal protein L33




- Molecule 29: 50S ribosomal protein L34



- Molecule 30: 50S ribosomal protein L35




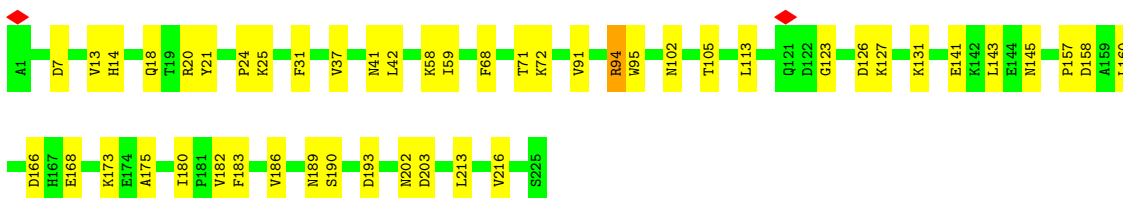
- Molecule 31: 50S ribosomal protein L36

Chain L36:  79% 21%




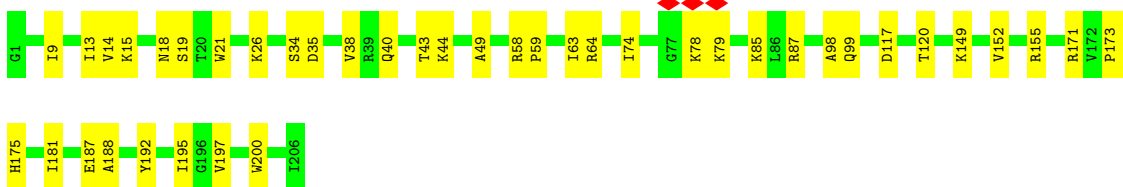
- Molecule 32: 30S ribosomal protein S2

Chain S02:  79% 21%




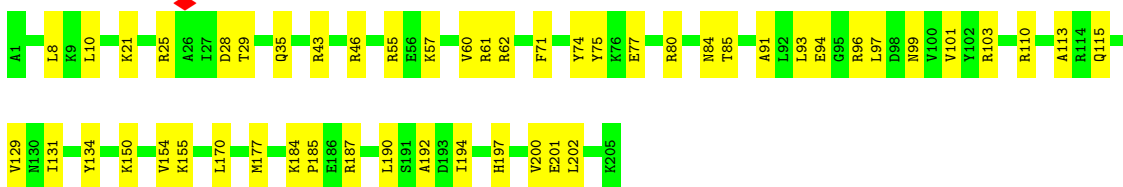
- Molecule 33: 30S ribosomal protein S3

Chain S03:  80% 20%




- Molecule 34: 30S ribosomal protein S4

Chain S04:  76% 24%




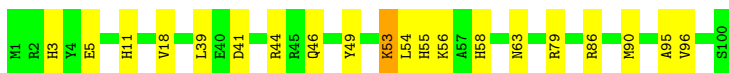
- Molecule 35: 30S ribosomal protein S5

Chain S05:  81% 18%

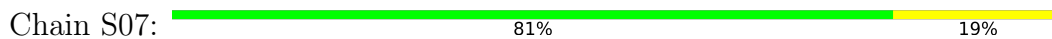


- Molecule 36: 30S ribosomal protein S6, non-modified isoform

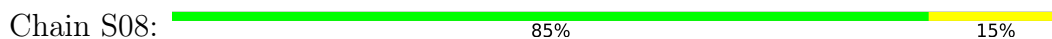
Chain S06:  80% 19%



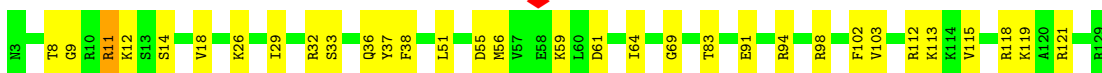
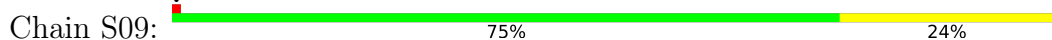
- Molecule 37: 30S ribosomal protein S7



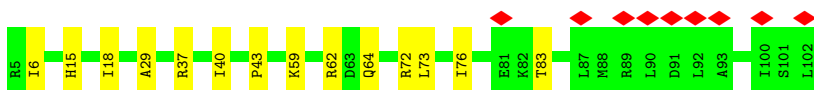
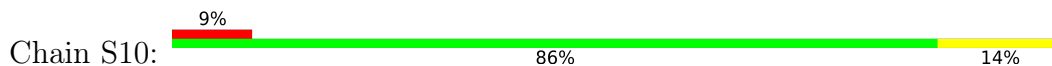
- Molecule 38: 30S ribosomal protein S8



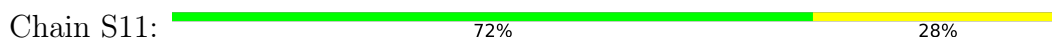
- Molecule 39: 30S ribosomal protein S9



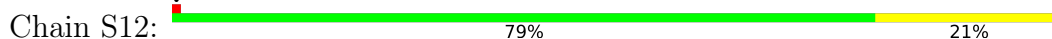
- Molecule 40: 30S ribosomal protein S10



- Molecule 41: 30S ribosomal protein S11



- Molecule 42: 30S ribosomal protein S12

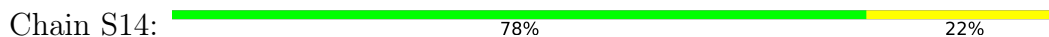


- Molecule 43: 30S ribosomal protein S13

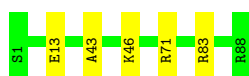




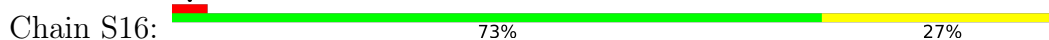
- Molecule 44: 30S ribosomal protein S14



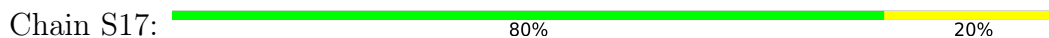
- Molecule 45: 30S ribosomal protein S15



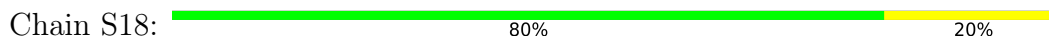
- Molecule 46: 30S ribosomal protein S16



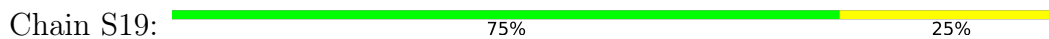
- Molecule 47: 30S ribosomal protein S17



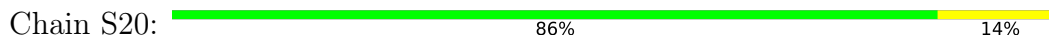
- Molecule 48: 30S ribosomal protein S18



- Molecule 49: 30S ribosomal protein S19



- Molecule 50: 30S ribosomal protein S20

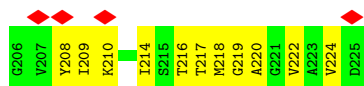
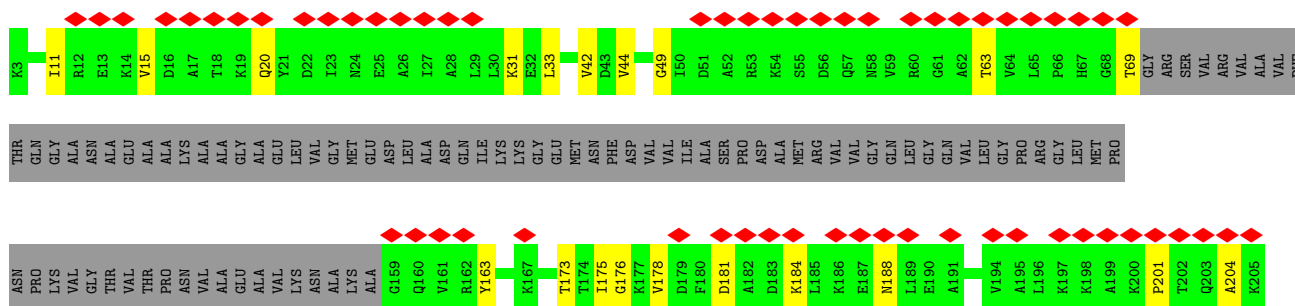




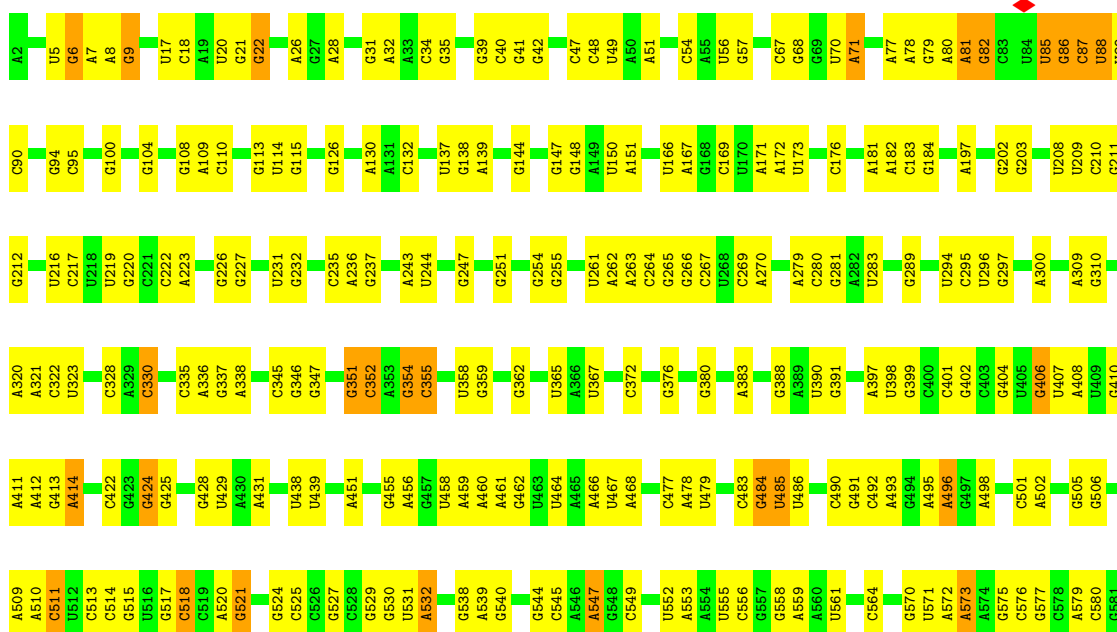
• Molecule 51: Ribosomal protein S21

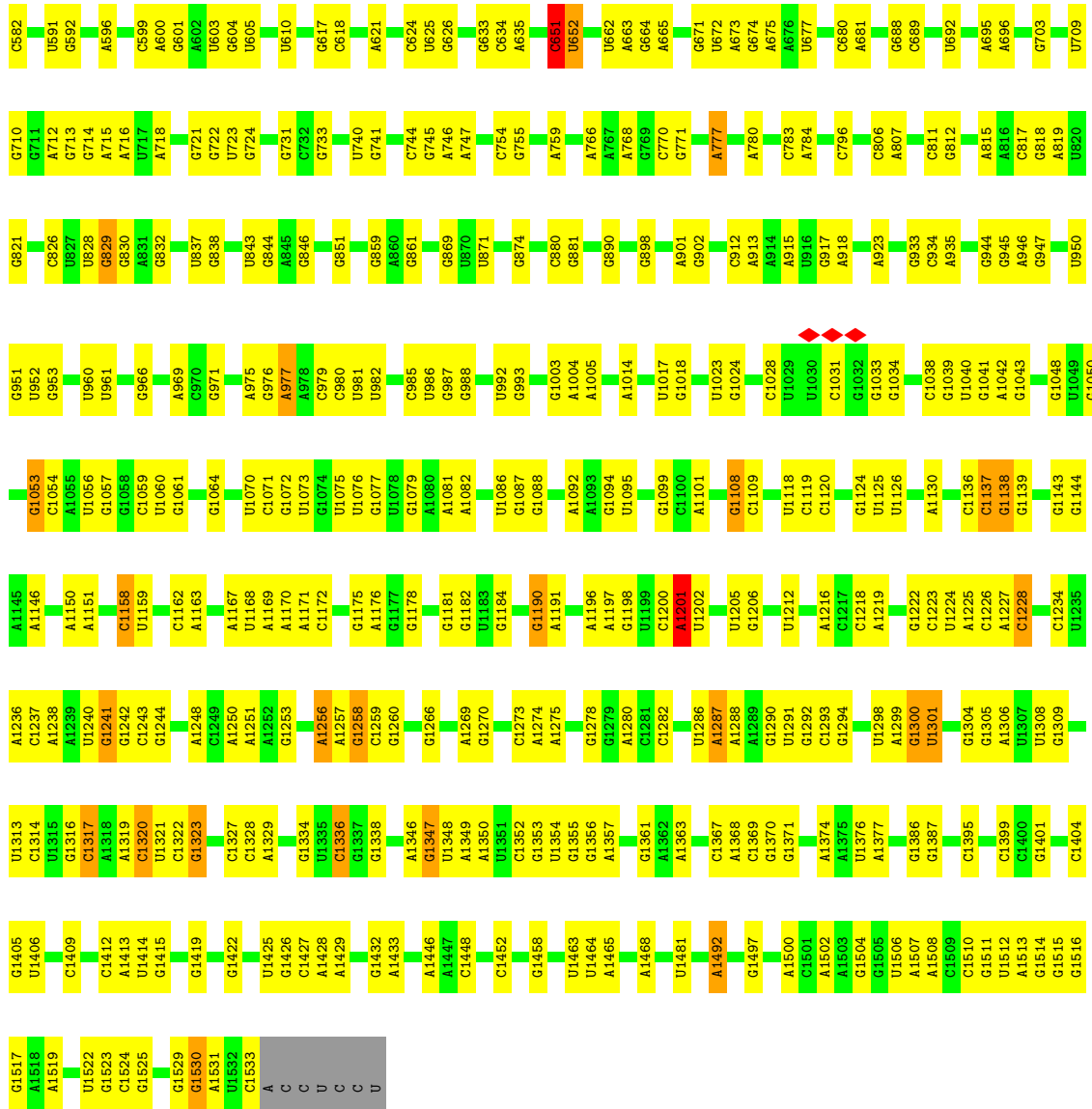


• Molecule 52: 50S ribosomal protein L1

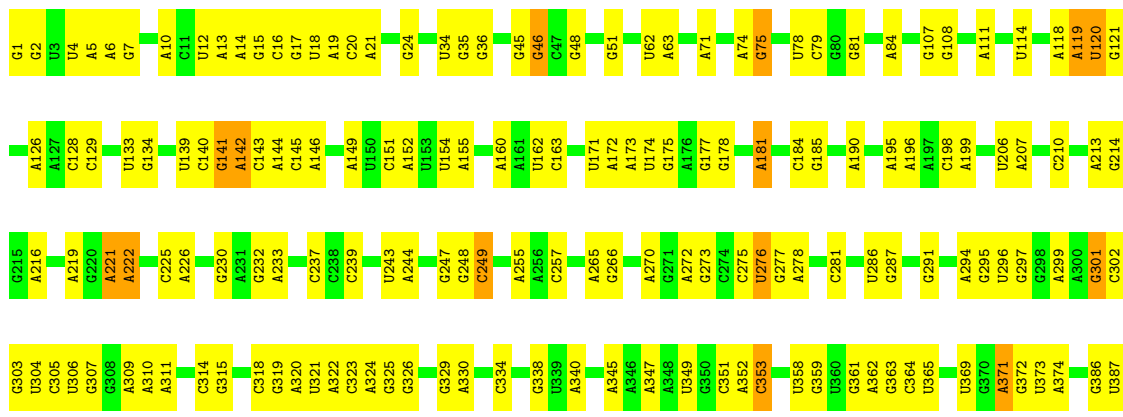


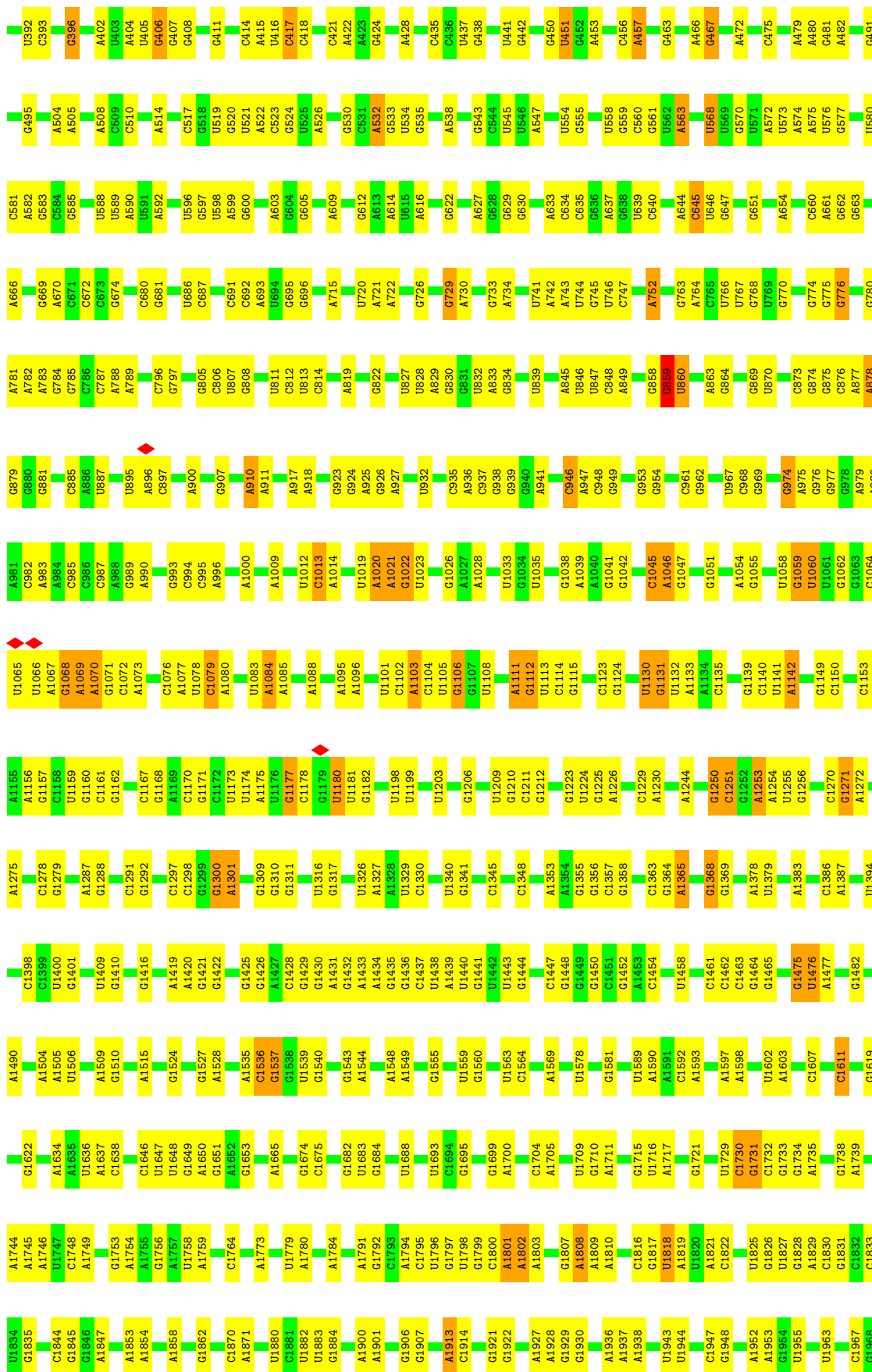
• Molecule 53: 16S ribosomal RNA

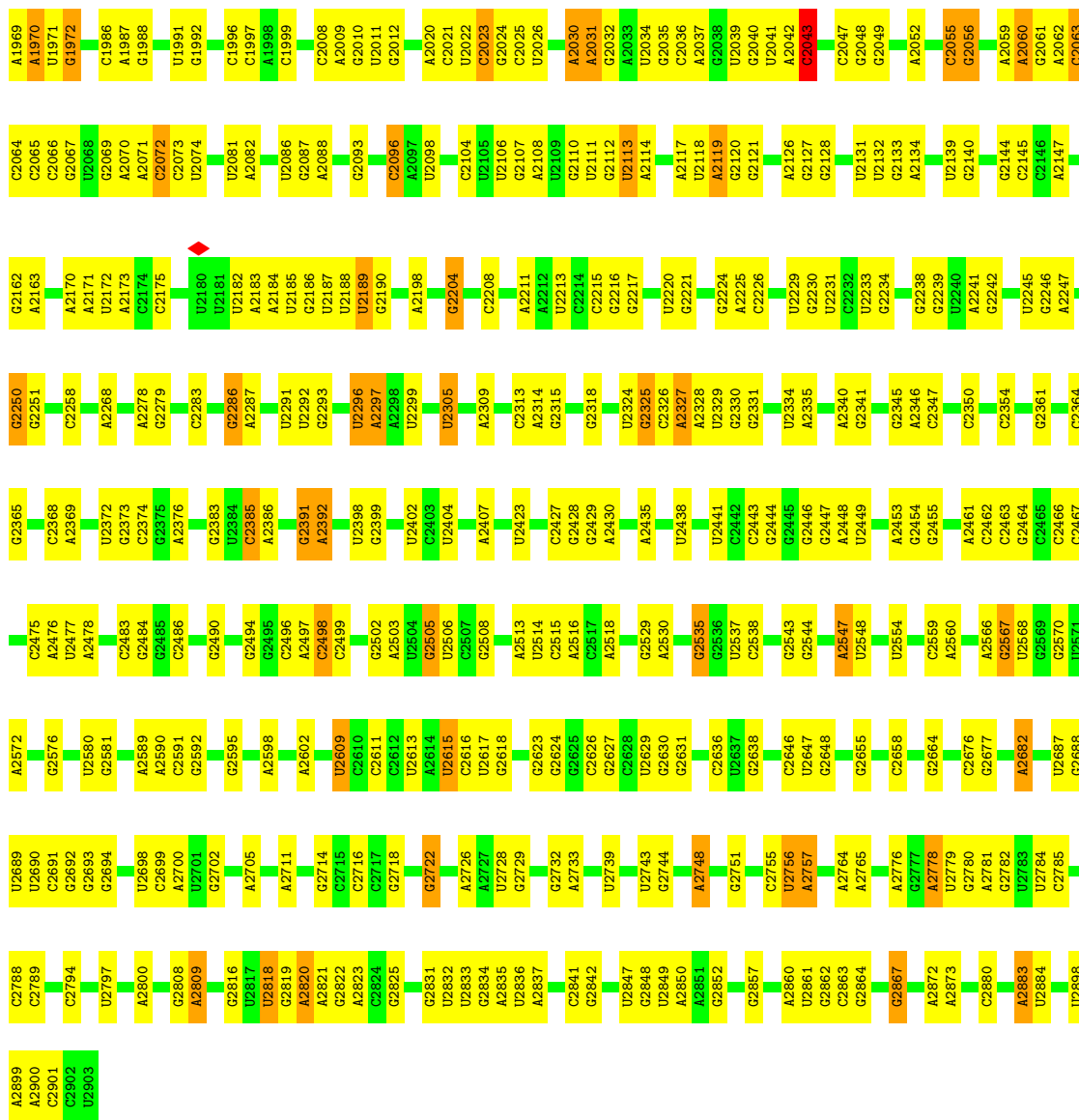




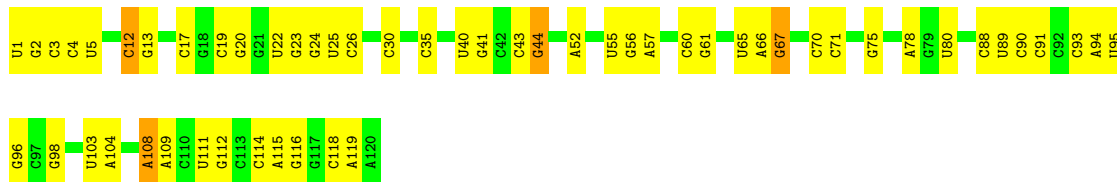
• Molecule 54: 23S ribosomal RNA



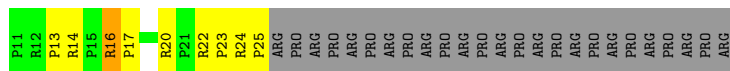




• Molecule 55: 5S ribosomal RNA



• Molecule 56: PR20, ALS/FTD dipeptide repeat protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	49219	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	26.145	Depositor
Minimum map value	-6.229	Depositor
Average map value	0.018	Depositor
Map value standard deviation	2.086	Depositor
Recommended contour level	3.0	Depositor
Map size (\AA)	375.84, 375.84, 375.84	wwPDB
Map dimensions	432, 432, 432	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.87, 0.87, 0.87	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	L02	0.25	0/2122	0.47	0/2852
2	L03	0.25	0/1586	0.47	0/2134
3	L04	0.25	0/1571	0.47	0/2113
4	L05	0.26	0/1435	0.48	0/1926
5	L06	0.24	0/1343	0.44	0/1816
6	L09	0.27	0/1122	0.54	1/1515 (0.1%)
7	L10	0.29	0/1002	0.64	0/1350
8	L11	0.27	0/1046	0.50	0/1410
9	L13	0.24	0/1152	0.42	0/1551
10	L14	0.25	0/948	0.50	0/1268
11	L15	0.26	0/1054	0.52	0/1403
12	L16	0.25	0/1093	0.50	0/1460
13	L17	0.24	0/974	0.46	0/1301
14	L18	0.23	0/902	0.43	0/1209
15	L19	0.24	0/929	0.48	1/1242 (0.1%)
16	L20	0.23	0/960	0.33	0/1278
17	L21	0.25	0/829	0.52	0/1107
18	L22	0.23	0/864	0.45	0/1156
19	L23	0.24	0/745	0.45	0/994
20	L24	0.25	0/788	0.49	1/1051 (0.1%)
21	L25	0.24	0/766	0.44	0/1025
22	L27	0.26	0/582	0.45	0/769
23	L28	0.23	0/635	0.42	0/848
24	L29	0.26	0/510	0.46	0/677
25	L30	0.22	0/453	0.44	0/605
26	L31	0.24	0/532	0.44	0/709
27	L32	0.22	0/450	0.45	0/599
28	L33	0.24	0/417	0.44	0/554
29	L34	0.23	0/380	0.45	0/498
30	L35	0.24	0/513	0.52	1/676 (0.1%)
31	L36	0.24	0/303	0.51	0/397
32	S02	0.26	0/1788	0.50	0/2408
33	S03	0.26	0/1652	0.50	0/2225
34	S04	0.25	0/1665	0.50	0/2227

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	S05	0.28	0/1170	0.56	0/1573
36	S06	0.25	0/836	0.54	0/1128
37	S07	0.25	0/1196	0.50	0/1602
38	S08	0.26	0/989	0.49	0/1326
39	S09	0.24	0/1034	0.50	0/1375
40	S10	0.24	0/797	0.54	0/1077
41	S11	0.24	0/883	0.48	0/1189
42	S12	0.25	0/969	0.52	0/1300
43	S13	0.23	0/893	0.49	0/1193
44	S14	0.24	0/817	0.45	0/1088
45	S15	0.23	0/722	0.43	0/964
46	S16	0.24	0/659	0.45	0/884
47	S17	0.27	0/658	0.56	0/881
48	S18	0.24	0/545	0.45	0/731
49	S19	0.26	0/653	0.49	0/877
50	S20	0.24	0/671	0.38	0/888
51	S21	0.38	0/551	0.72	0/728
52	L1	0.24	0/1034	0.46	0/1387
53	16S	0.21	0/36806	0.82	6/57419 (0.0%)
54	23S	0.21	0/69796	0.83	19/108888 (0.0%)
55	5S	0.23	0/2872	0.91	6/4479 (0.1%)
56	PR	0.52	0/140	0.68	0/190
All	All	0.23	0/157802	0.75	35/235520 (0.0%)

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	23S	2043	C	C2-N1-C1'	5.90	125.29	118.80
54	23S	1020	A	P-O3'-C3'	5.90	126.78	119.70
54	23S	2063	C	N1-C2-O2	5.81	122.38	118.90
53	16S	1201	A	P-O3'-C3'	5.80	126.66	119.70
54	23S	1818	U	C2-N1-C1'	5.73	124.57	117.70

There are no chirality outliers.

There are no planarity outliers.

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	L02	2083	0	2157	43	0
2	L03	1565	0	1616	17	0
3	L04	1552	0	1619	31	0
4	L05	1411	0	1447	18	0
5	L06	1323	0	1374	16	0
6	L09	1111	0	1148	11	0
7	L10	989	0	1025	32	0
8	L11	1032	0	1088	14	0
9	L13	1129	0	1162	18	0
10	L14	939	0	1012	14	0
11	L15	1045	0	1117	25	0
12	L16	1074	0	1157	17	0
13	L17	961	0	1000	11	0
14	L18	892	0	923	10	0
15	L19	917	0	965	13	0
16	L20	947	0	1022	11	0
17	L21	816	0	839	16	0
18	L22	857	0	922	13	0
19	L23	739	0	807	9	0
20	L24	780	0	834	12	0
21	L25	753	0	780	14	0
22	L27	575	0	592	4	0
23	L28	625	0	655	5	0
24	L29	509	0	543	11	0
25	L30	449	0	491	3	0
26	L31	523	0	524	3	0
27	L32	444	0	461	4	0
28	L33	410	0	440	5	0
29	L34	377	0	418	9	0
30	L35	504	0	574	10	0
31	L36	302	0	343	6	0
32	S02	1757	0	1787	29	0
33	S03	1625	0	1699	24	0
34	S04	1643	0	1710	36	0
35	S05	1157	0	1199	35	0
36	S06	818	0	808	14	0
37	S07	1182	0	1240	18	0
38	S08	979	0	1034	13	0
39	S09	1022	0	1070	20	0
40	S10	787	0	828	11	0
41	S11	869	0	876	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	S12	955	0	1019	19	0
43	S13	884	0	944	9	0
44	S14	805	0	847	15	0
45	S15	714	0	737	5	0
46	S16	649	0	666	16	0
47	S17	649	0	691	11	0
48	S18	536	0	552	7	0
49	S19	638	0	665	14	0
50	S20	665	0	714	11	0
51	S21	545	0	579	17	0
52	L1	1027	0	1092	18	0
53	16S	32870	0	16543	390	0
54	23S	62317	0	31346	687	0
55	5S	2568	0	1303	33	0
56	PR	133	0	147	15	0
All	All	145427	0	99151	1670	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 1670 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:L10:118:ILE:HG22	7:L10:119:PRO:HD3	1.37	1.05
56:PR:24:ARG:HG2	56:PR:25:PRO:HD2	1.44	0.99
3:L04:61:ARG:HH22	56:PR:16:ARG:CZ	1.90	0.84
35:S05:98:ALA:HB3	35:S05:122:VAL:HA	1.60	0.81
41:S11:74:LYS:CA	41:S11:75:GLU:N	2.45	0.80

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	L02	269/271 (99%)	258 (96%)	11 (4%)	0	100	100
2	L03	207/209 (99%)	197 (95%)	10 (5%)	0	100	100
3	L04	199/201 (99%)	190 (96%)	8 (4%)	1 (0%)	29	61
4	L05	175/177 (99%)	169 (97%)	6 (3%)	0	100	100
5	L06	174/176 (99%)	166 (95%)	8 (5%)	0	100	100
6	L09	147/149 (99%)	135 (92%)	12 (8%)	0	100	100
7	L10	129/131 (98%)	103 (80%)	24 (19%)	2 (2%)	9	32
8	L11	139/141 (99%)	120 (86%)	19 (14%)	0	100	100
9	L13	140/142 (99%)	138 (99%)	2 (1%)	0	100	100
10	L14	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
11	L15	141/143 (99%)	129 (92%)	12 (8%)	0	100	100
12	L16	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
13	L17	118/120 (98%)	109 (92%)	9 (8%)	0	100	100
14	L18	114/116 (98%)	111 (97%)	3 (3%)	0	100	100
15	L19	112/114 (98%)	106 (95%)	6 (5%)	0	100	100
16	L20	115/117 (98%)	115 (100%)	0	0	100	100
17	L21	101/103 (98%)	96 (95%)	5 (5%)	0	100	100
18	L22	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
19	L23	91/93 (98%)	86 (94%)	5 (6%)	0	100	100
20	L24	100/102 (98%)	90 (90%)	10 (10%)	0	100	100
21	L25	92/94 (98%)	92 (100%)	0	0	100	100
22	L27	73/75 (97%)	70 (96%)	3 (4%)	0	100	100
23	L28	75/77 (97%)	73 (97%)	2 (3%)	0	100	100
24	L29	61/63 (97%)	59 (97%)	1 (2%)	1 (2%)	9	32
25	L30	56/58 (97%)	55 (98%)	1 (2%)	0	100	100
26	L31	64/66 (97%)	61 (95%)	3 (5%)	0	100	100
27	L32	54/56 (96%)	52 (96%)	2 (4%)	0	100	100
28	L33	48/50 (96%)	44 (92%)	4 (8%)	0	100	100
29	L34	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
30	L35	62/64 (97%)	58 (94%)	3 (5%)	1 (2%)	9	32
31	L36	36/38 (95%)	34 (94%)	2 (6%)	0	100	100
32	S02	223/225 (99%)	212 (95%)	11 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	S03	204/206 (99%)	197 (97%)	7 (3%)	0	100	100
34	S04	203/205 (99%)	182 (90%)	21 (10%)	0	100	100
35	S05	155/157 (99%)	138 (89%)	16 (10%)	1 (1%)	25	58
36	S06	98/100 (98%)	81 (83%)	17 (17%)	0	100	100
37	S07	149/151 (99%)	140 (94%)	9 (6%)	0	100	100
38	S08	127/129 (98%)	125 (98%)	2 (2%)	0	100	100
39	S09	125/127 (98%)	107 (86%)	18 (14%)	0	100	100
40	S10	96/98 (98%)	79 (82%)	17 (18%)	0	100	100
41	S11	112/116 (97%)	100 (89%)	12 (11%)	0	100	100
42	S12	121/123 (98%)	107 (88%)	14 (12%)	0	100	100
43	S13	112/114 (98%)	102 (91%)	10 (9%)	0	100	100
44	S14	98/100 (98%)	87 (89%)	11 (11%)	0	100	100
45	S15	86/88 (98%)	80 (93%)	6 (7%)	0	100	100
46	S16	80/82 (98%)	73 (91%)	7 (9%)	0	100	100
47	S17	78/80 (98%)	71 (91%)	7 (9%)	0	100	100
48	S18	63/65 (97%)	59 (94%)	4 (6%)	0	100	100
49	S19	77/79 (98%)	70 (91%)	7 (9%)	0	100	100
50	S20	83/85 (98%)	81 (98%)	2 (2%)	0	100	100
51	S21	63/65 (97%)	46 (73%)	15 (24%)	2 (3%)	4	16
52	L1	130/223 (58%)	122 (94%)	8 (6%)	0	100	100
56	PR	13/40 (32%)	10 (77%)	1 (8%)	2 (15%)	0	0
All	All	5994/6218 (96%)	5578 (93%)	406 (7%)	10 (0%)	50	78

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	L10	118	ILE
35	S05	122	VAL
24	L29	24	GLU
56	PR	13	PRO
7	L10	119	PRO

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	
1	L02	216/216 (100%)	216 (100%)	0	100	100
2	L03	164/164 (100%)	164 (100%)	0	100	100
3	L04	165/165 (100%)	163 (99%)	2 (1%)	71	91
4	L05	148/148 (100%)	148 (100%)	0	100	100
5	L06	137/137 (100%)	136 (99%)	1 (1%)	84	95
6	L09	114/114 (100%)	113 (99%)	1 (1%)	78	93
7	L10	100/100 (100%)	97 (97%)	3 (3%)	41	75
8	L11	109/109 (100%)	107 (98%)	2 (2%)	59	85
9	L13	116/116 (100%)	116 (100%)	0	100	100
10	L14	103/103 (100%)	103 (100%)	0	100	100
11	L15	102/102 (100%)	102 (100%)	0	100	100
12	L16	109/109 (100%)	109 (100%)	0	100	100
13	L17	100/100 (100%)	99 (99%)	1 (1%)	76	92
14	L18	86/86 (100%)	86 (100%)	0	100	100
15	L19	99/99 (100%)	99 (100%)	0	100	100
16	L20	89/89 (100%)	89 (100%)	0	100	100
17	L21	84/84 (100%)	84 (100%)	0	100	100
18	L22	93/93 (100%)	93 (100%)	0	100	100
19	L23	80/80 (100%)	80 (100%)	0	100	100
20	L24	83/83 (100%)	83 (100%)	0	100	100
21	L25	78/78 (100%)	78 (100%)	0	100	100
22	L27	57/57 (100%)	57 (100%)	0	100	100
23	L28	67/67 (100%)	67 (100%)	0	100	100
24	L29	55/55 (100%)	54 (98%)	1 (2%)	59	85
25	L30	48/48 (100%)	47 (98%)	1 (2%)	53	81
26	L31	59/59 (100%)	58 (98%)	1 (2%)	60	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	L32	47/47 (100%)	47 (100%)	0	100	100
28	L33	45/45 (100%)	44 (98%)	1 (2%)	52	81
29	L34	38/38 (100%)	38 (100%)	0	100	100
30	L35	51/51 (100%)	51 (100%)	0	100	100
31	L36	34/34 (100%)	34 (100%)	0	100	100
32	S02	186/186 (100%)	184 (99%)	2 (1%)	73	92
33	S03	170/170 (100%)	166 (98%)	4 (2%)	49	79
34	S04	172/172 (100%)	170 (99%)	2 (1%)	71	91
35	S05	119/119 (100%)	119 (100%)	0	100	100
36	S06	87/87 (100%)	86 (99%)	1 (1%)	73	92
37	S07	124/124 (100%)	124 (100%)	0	100	100
38	S08	104/104 (100%)	104 (100%)	0	100	100
39	S09	105/105 (100%)	104 (99%)	1 (1%)	76	92
40	S10	86/86 (100%)	85 (99%)	1 (1%)	71	91
41	S11	89/89 (100%)	88 (99%)	1 (1%)	73	92
42	S12	103/103 (100%)	103 (100%)	0	100	100
43	S13	92/92 (100%)	92 (100%)	0	100	100
44	S14	83/83 (100%)	83 (100%)	0	100	100
45	S15	76/76 (100%)	76 (100%)	0	100	100
46	S16	65/65 (100%)	65 (100%)	0	100	100
47	S17	74/74 (100%)	74 (100%)	0	100	100
48	S18	56/56 (100%)	55 (98%)	1 (2%)	59	85
49	S19	70/70 (100%)	70 (100%)	0	100	100
50	S20	65/65 (100%)	65 (100%)	0	100	100
51	S21	55/55 (100%)	53 (96%)	2 (4%)	35	69
52	L1	110/174 (63%)	110 (100%)	0	100	100
56	PR	15/40 (38%)	15 (100%)	0	100	100
All	All	4982/5071 (98%)	4953 (99%)	29 (1%)	86	96

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	S02	58	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
51	S21	24	LYS
33	S03	78	LYS
40	S10	37	ARG
33	S03	44	LYS

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

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
53	16S	1531/1539 (99%)	192 (12%)	6 (0%)
54	23S	2902/2903 (99%)	394 (13%)	11 (0%)
55	5S	119/120 (99%)	14 (11%)	1 (0%)
All	All	4552/4562 (99%)	600 (13%)	18 (0%)

5 of 600 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
53	16S	6	G
53	16S	7	A
53	16S	9	G
53	16S	22	G
53	16S	31	G

5 of 18 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
54	23S	2326	C
55	5S	88	C
54	23S	2756	U
54	23S	1020	A
54	23S	2296	U

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no monosaccharides 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.

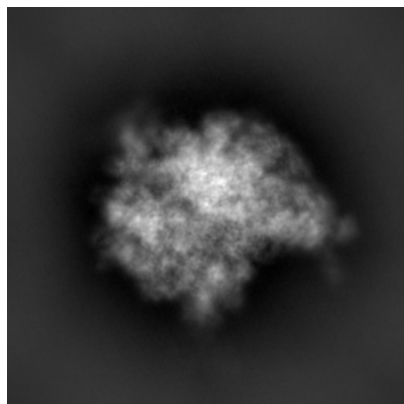
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26037. These allow visual inspection of the internal detail of the map and identification of artifacts.

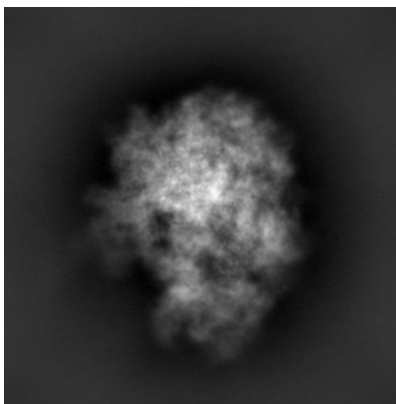
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

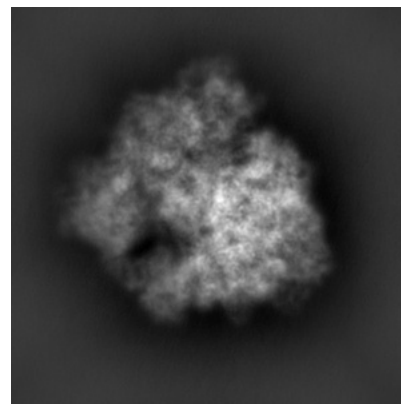
6.1.1 Primary map



X

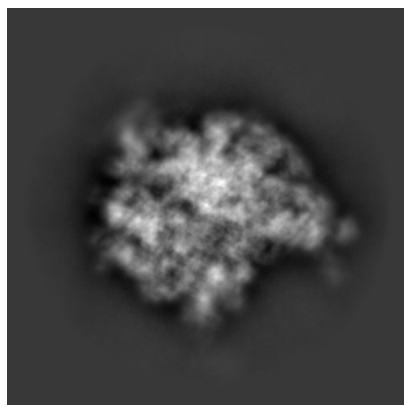


Y

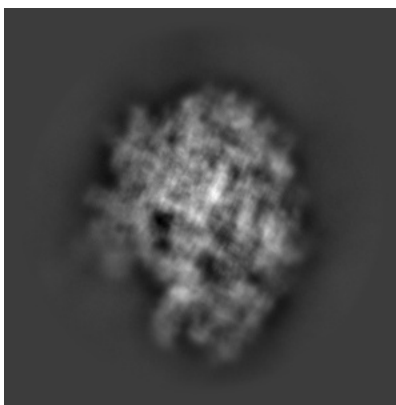


Z

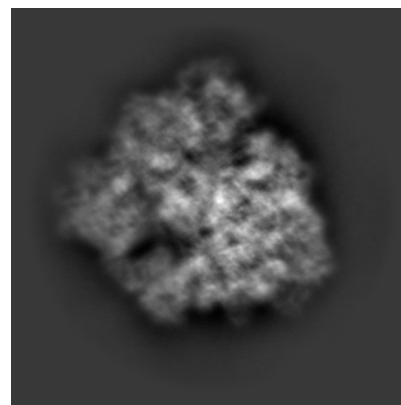
6.1.2 Raw map



X



Y

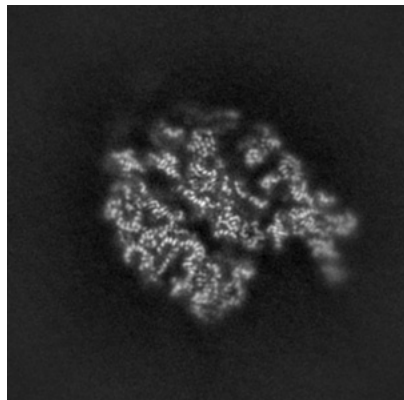


Z

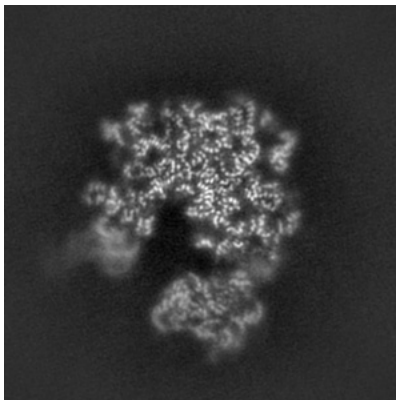
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

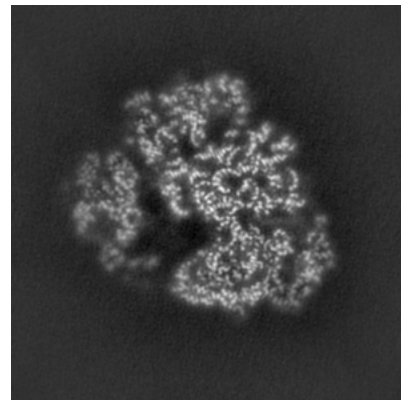
6.2.1 Primary map



X Index: 216

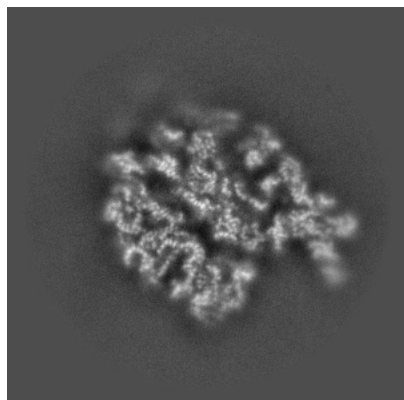


Y Index: 216

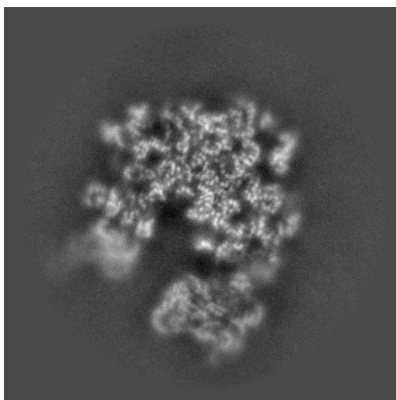


Z Index: 216

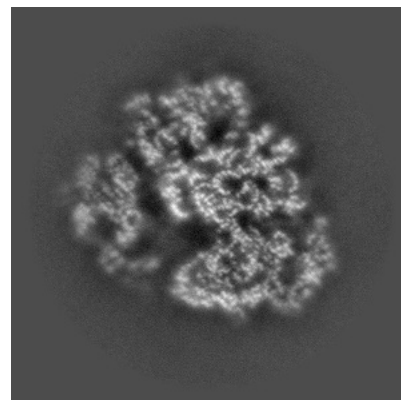
6.2.2 Raw map



X Index: 216



Y Index: 216

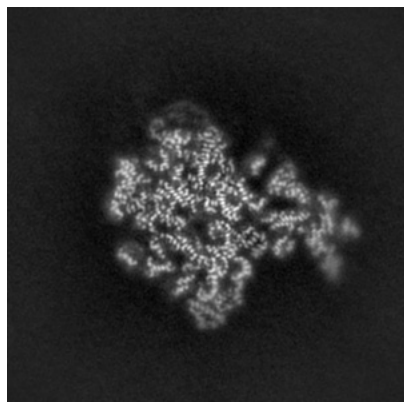


Z Index: 216

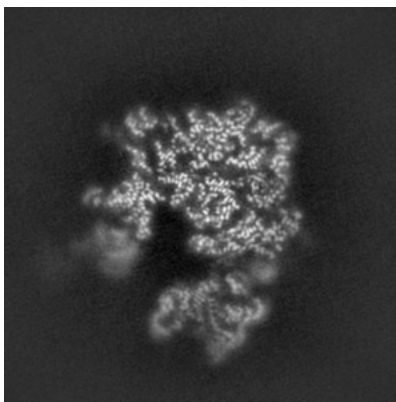
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

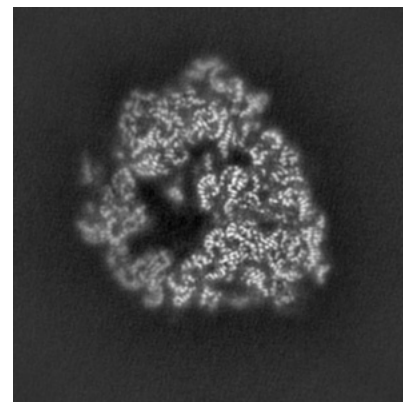
6.3.1 Primary map



X Index: 225

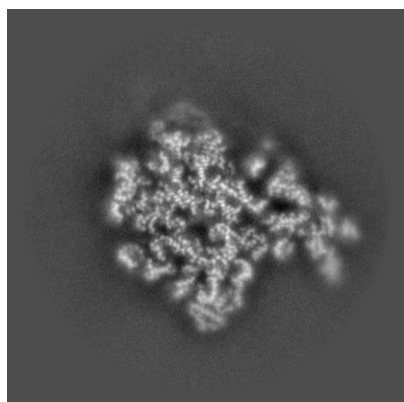


Y Index: 223

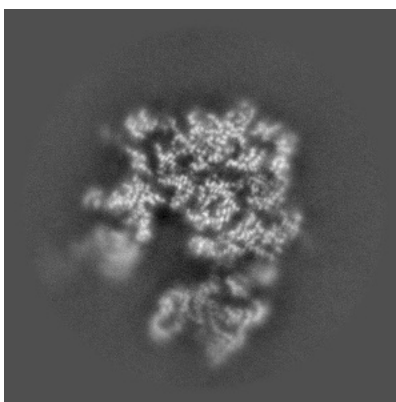


Z Index: 202

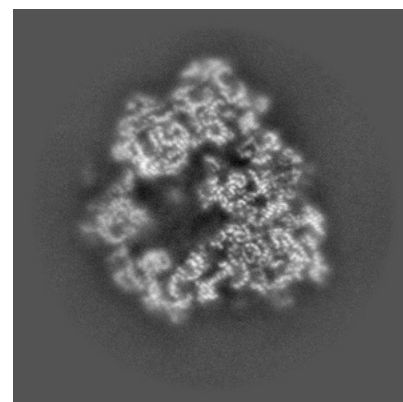
6.3.2 Raw map



X Index: 224



Y Index: 223

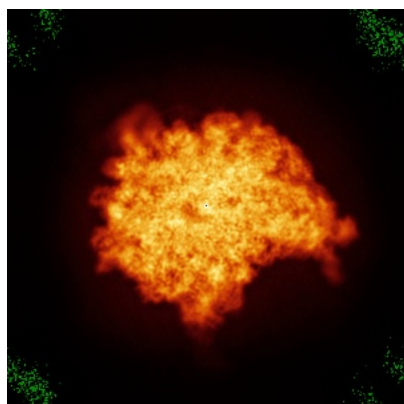


Z Index: 196

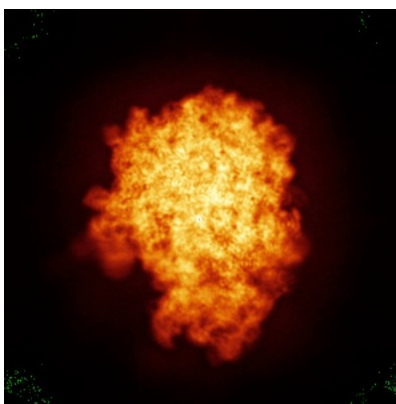
The images above show the largest variance slices of the map in three orthogonal directions.

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

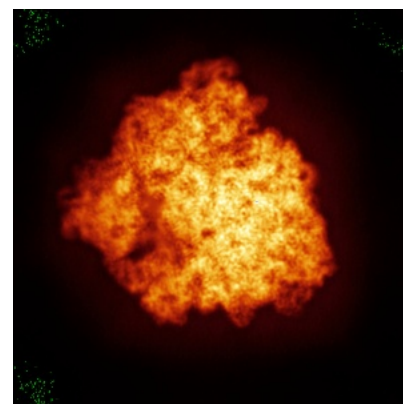
6.4.1 Primary map



X

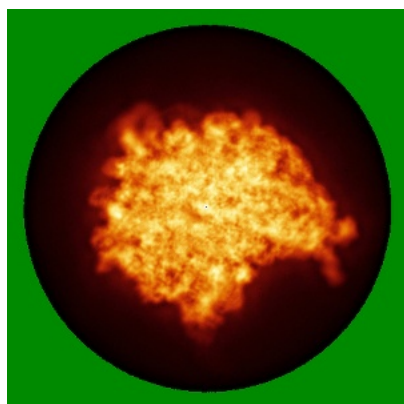


Y

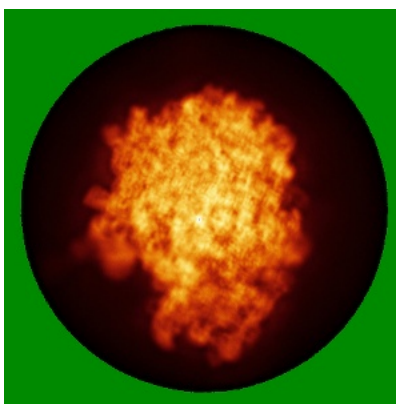


Z

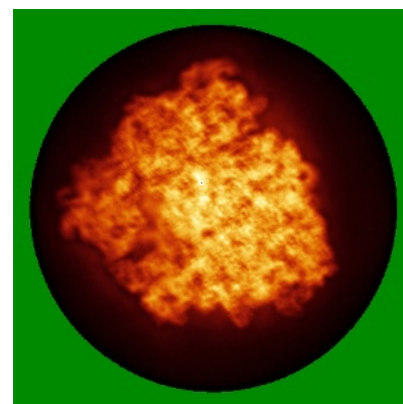
6.4.2 Raw map



X



Y

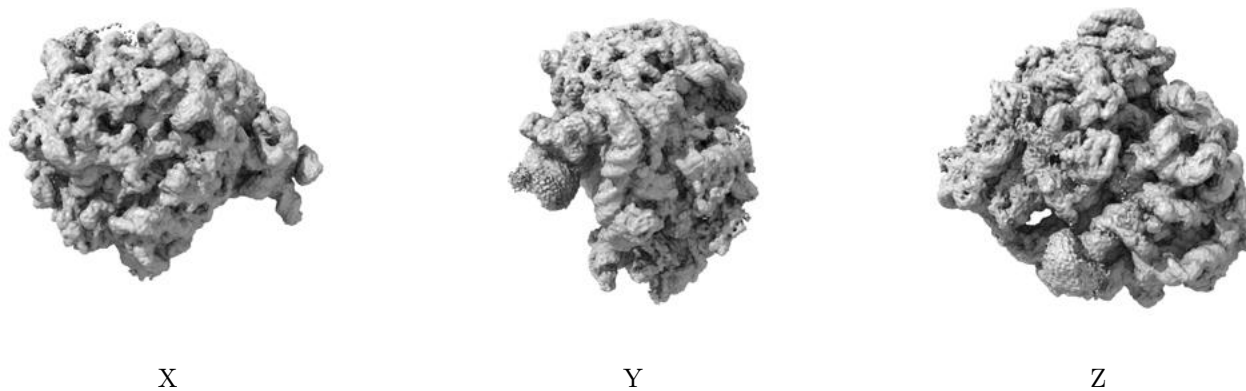


Z

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

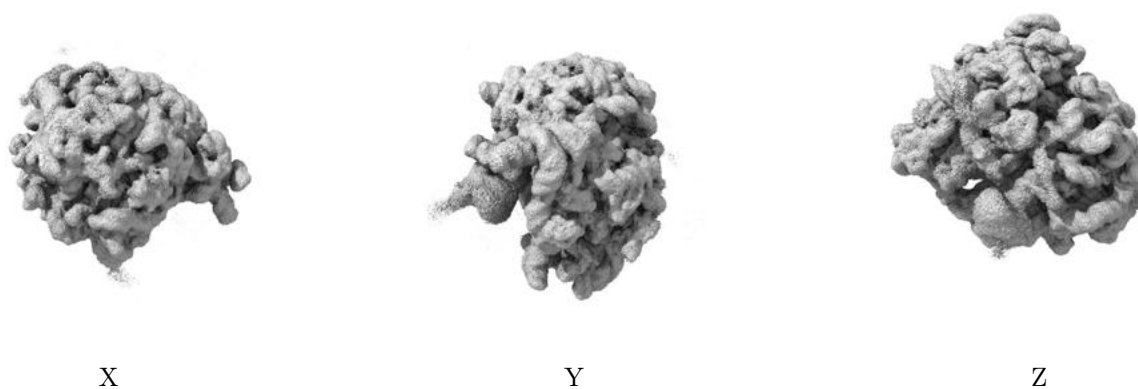
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

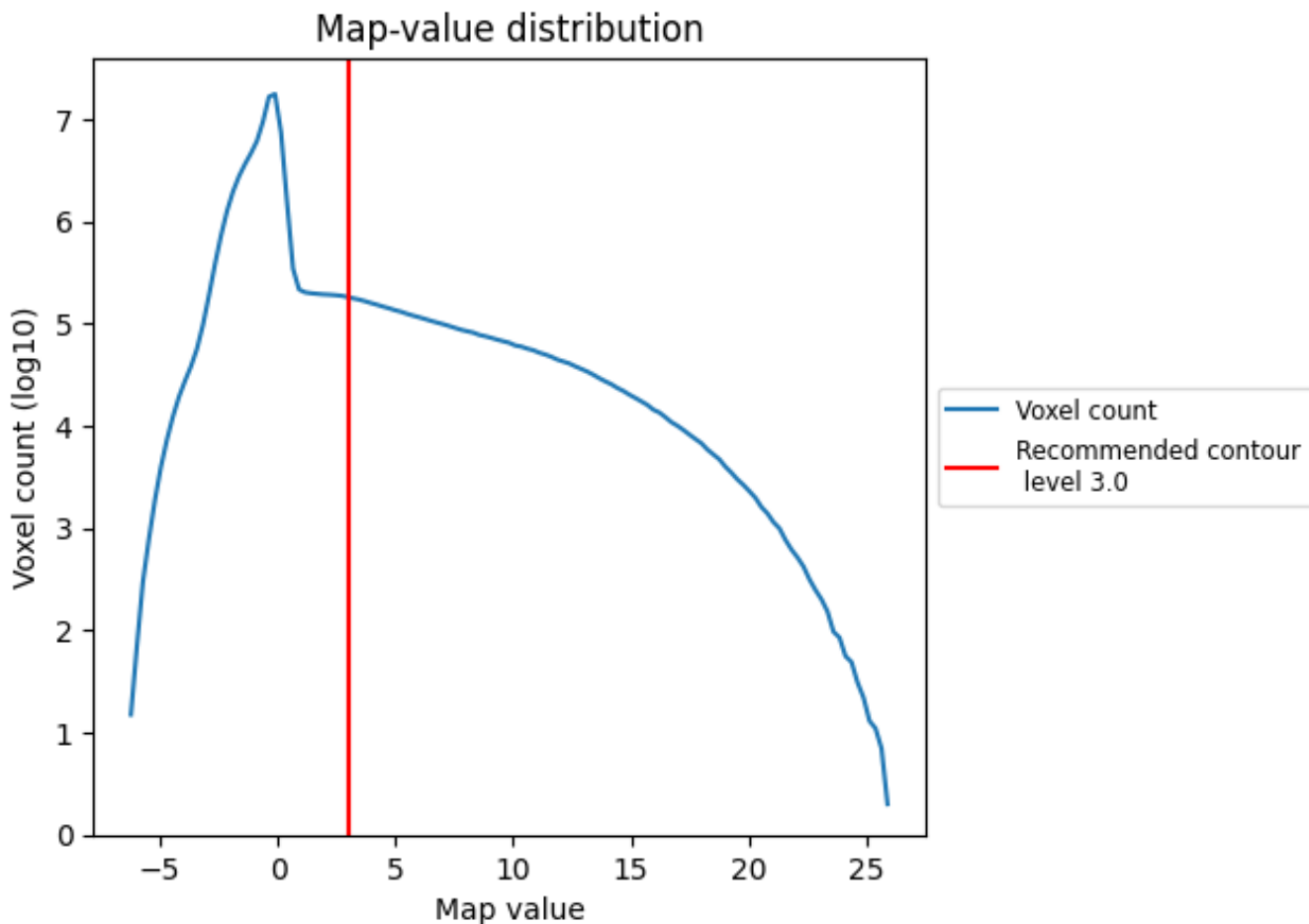
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

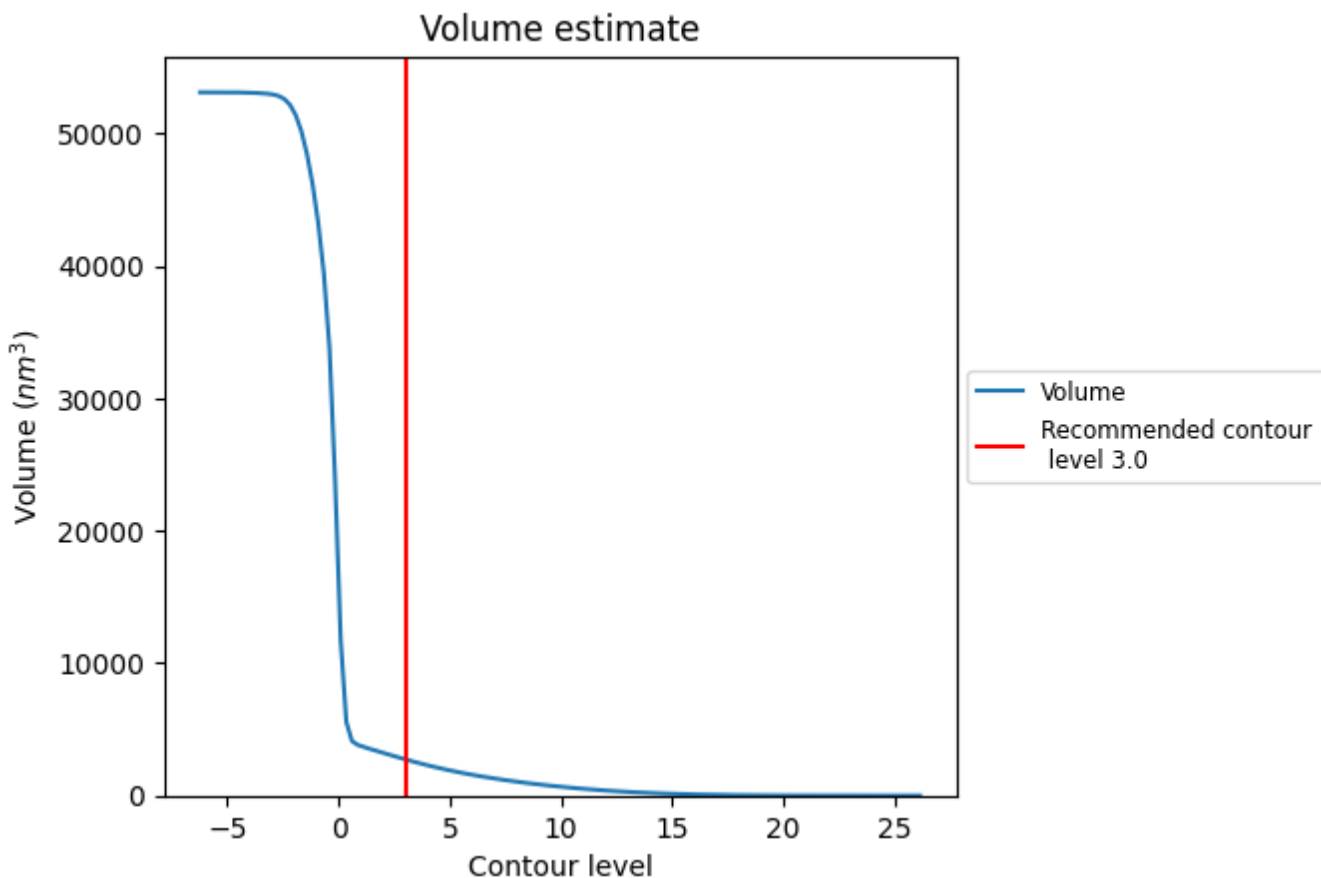
This section contains the results of statistical analysis of the map.

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.

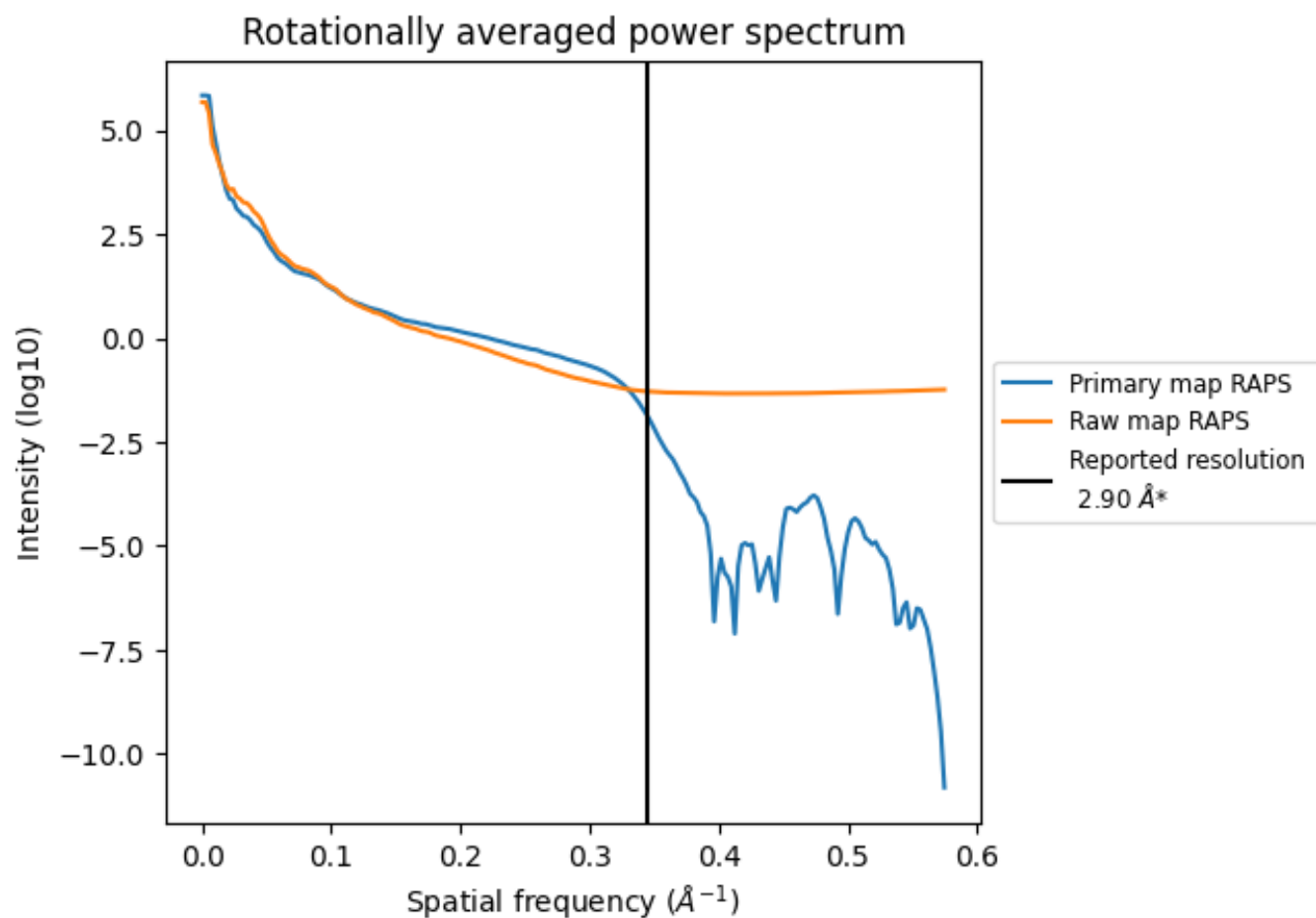
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 2732 nm^3 ; this corresponds to an approximate mass of 2468 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](#)

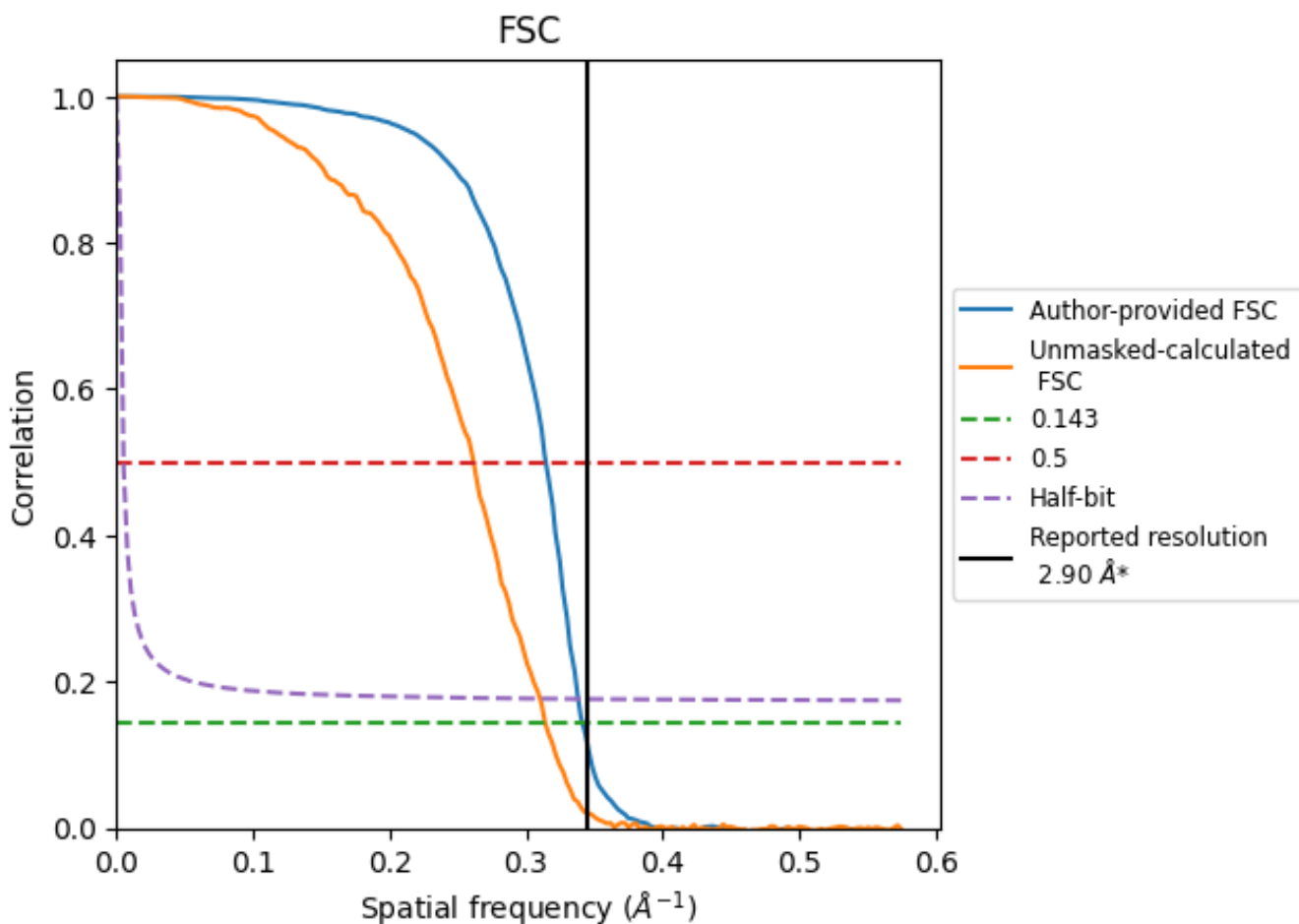


*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

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 0.345 Å⁻¹

8.2 Resolution estimates [i](#)

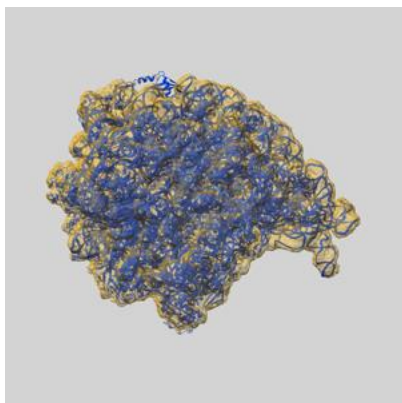
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	2.93	3.18	2.96
Unmasked-calculated*	3.18	3.82	3.22

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

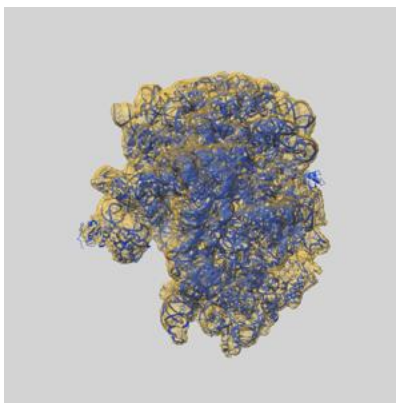
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-26037 and PDB model 7TOS. Per-residue inclusion information can be found in section 3 on page 14.

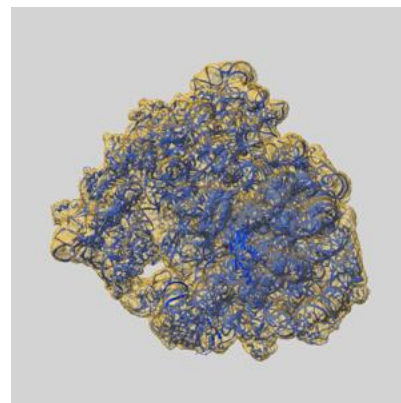
9.1 Map-model overlay [i](#)



X



Y



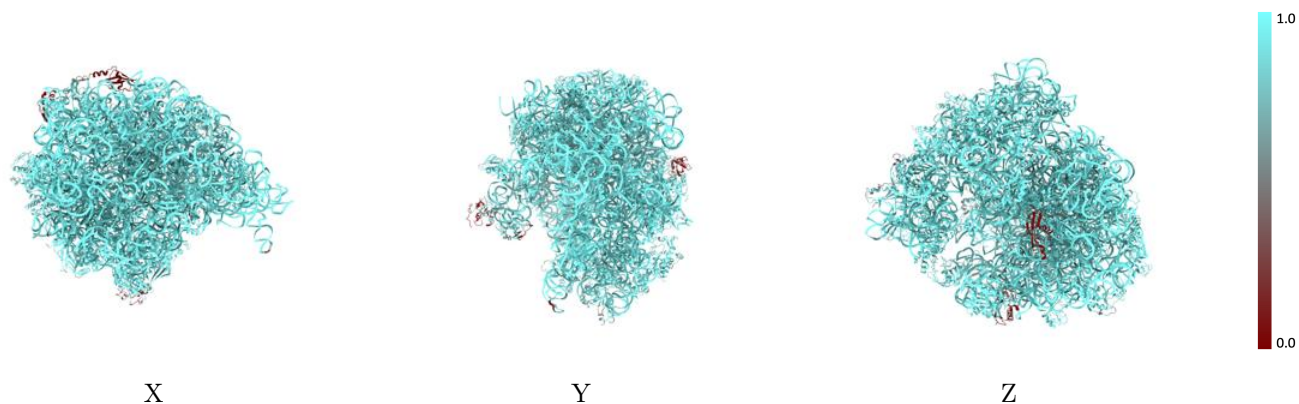
Z

The images above show the 3D surface view of the map at the recommended contour level 3.0 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](#)

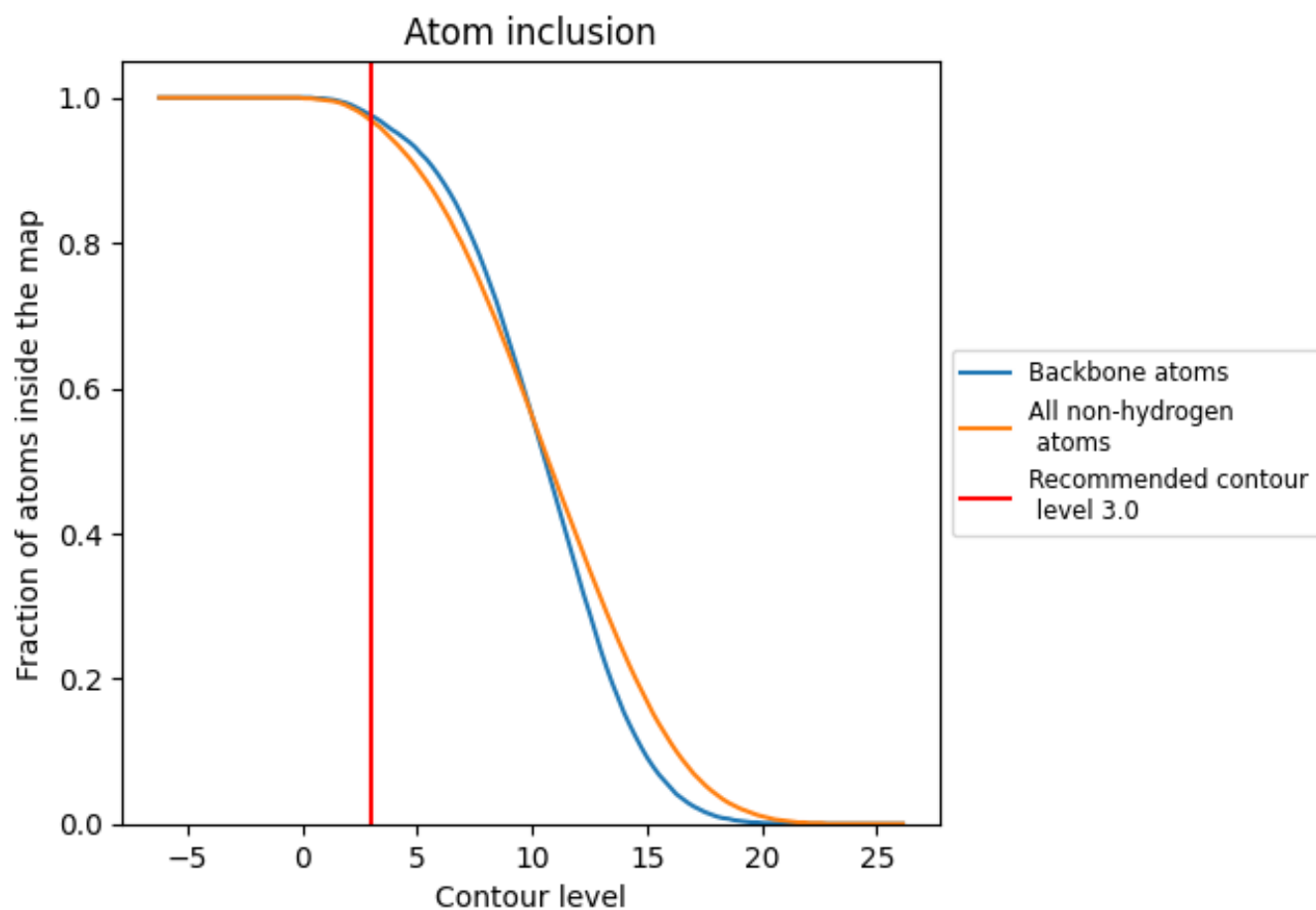
This section was not generated.

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 (3.0).




































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 (3.0) and Q-score for the entire model and for each chain.

Chain	Atom inclusion
All	 0.9680
16S	 0.9930
23S	 0.9940
5S	 0.9970
L02	 0.9900
L03	 0.9820
L04	 0.9340
L05	 0.9710
L06	 0.9700
L09	 0.3800
L1	 0.4910
L10	 0.4360
L11	 0.7170
L13	 0.9740
L14	 0.9660
L15	 0.9620
L16	 0.9650
L17	 0.9940
L18	 0.9750
L19	 0.9730
L20	 0.9860
L21	 0.9420
L22	 0.9550
L23	 0.9710
L24	 0.9490
L25	 0.9470
L27	 0.9700
L28	 0.9880
L29	 0.9620
L30	 0.9570
L31	 0.9080
L32	 0.9670
L33	 0.7260
L34	 0.9780
L35	 0.9940



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Chain	Atom inclusion
L36	 1.0000
PR	 0.9500
S02	 0.9080
S03	 0.8900
S04	 0.9420
S05	 0.9570
S06	 0.9500
S07	 0.9590
S08	 0.9670
S09	 0.9530
S10	 0.8150
S11	 0.9910
S12	 0.9510
S13	 0.9590
S14	 0.9430
S15	 0.9830
S16	 0.9510
S17	 0.9720
S18	 0.9940
S19	 0.9520
S20	 0.9750
S21	 0.9050