



## Full wwPDB EM Validation Report ⓘ

Feb 13, 2024 – 11:46 AM EST

PDB ID : 7TOP  
EMDB ID : EMD-26034  
Title : Yeast 80S ribosome 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 : 2.40 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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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

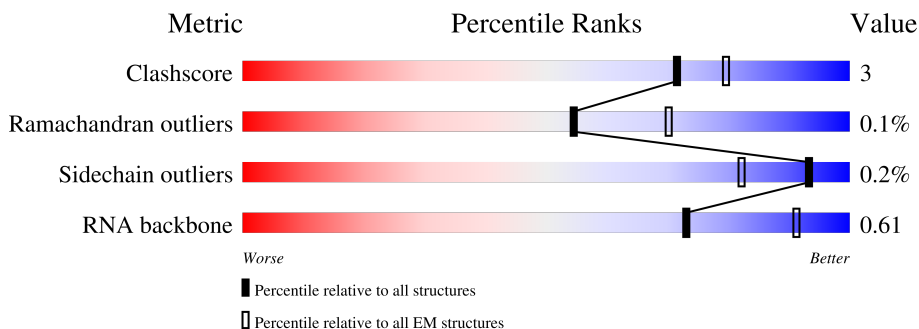
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.40 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.



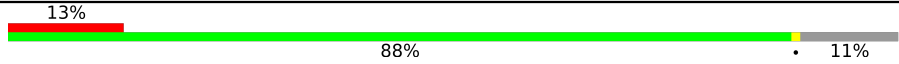
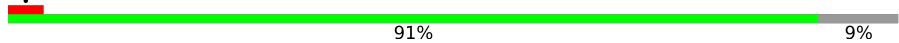

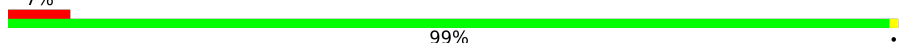
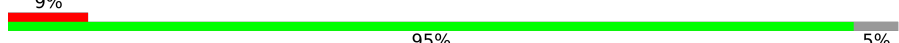
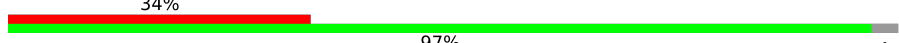


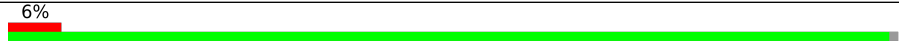

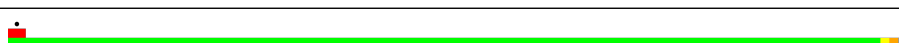

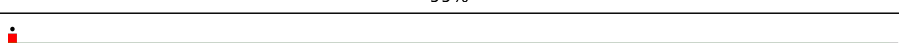
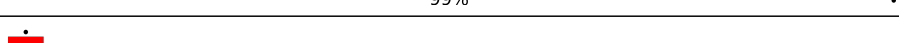
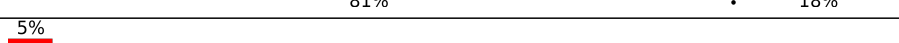
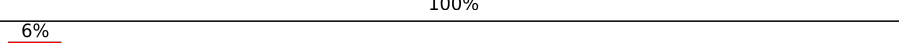
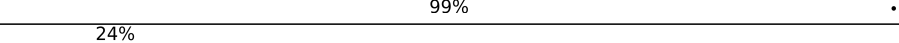
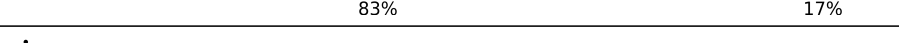
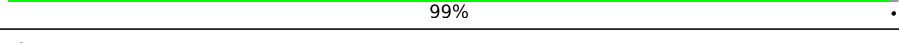


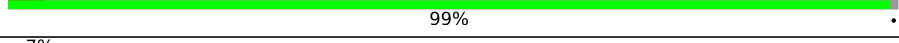
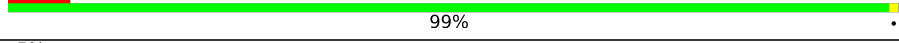
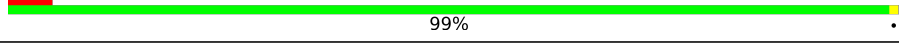
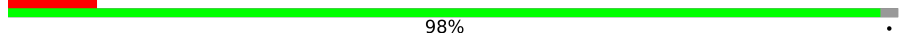
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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  $\geq 3$ , 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	A25S	3396	
2	A58S	158	
3	A5S	121	
4	AL02	254	
5	AL03	387	
6	AL04	362	
7	AL05	297	

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Mol	Chain	Length	Quality of chain
8	AL06	176	
9	AL07	244	
10	AL08	256	
11	AL09	191	
12	AL10	221	
13	AL11	174	
14	AL12	155	
15	AL13	199	
16	AL14	138	
17	AL15	204	
18	AL16	199	
19	AL17	184	
20	AL18	186	
21	AL19	189	
22	AL20	172	
23	AL21	160	
24	AL22	121	
25	AL23	137	
26	AL24	155	
27	AL25	142	
28	AL26	127	
29	AL27	136	
30	AL28	149	
31	AL29	59	
32	AL30	105	

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Mol	Chain	Length	Quality of chain
33	AL31	113	 9% 96%
34	AL32	130	 98%
35	AL33	107	 99%
36	AL34	121	 9% 92% 7%
37	AL35	120	 99%
38	AL36	100	 10% 99%
39	AL37	88	 99%
40	AL38	78	 21% 97%
41	AL39	51	 98%
42	AL40	128	 41% 41% 59%
43	AL41	25	 100% 100%
44	AL42	106	 11% 98%
45	AL43	92	 5% 99%
46	ALP0	221	 97%
47	APTN	77	 73% 88% 12%
48	PR	40	 30% 45% 52%

## 2 Entry composition

There are 49 unique types of molecules in this entry. The entry contains 125433 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A25S	3194	68318	30516	12315	22293	3194	0	0

- Molecule 2 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	A58S	158	3354	1500	586	1110	158	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	A5S	121	2580	1152	461	846	121	0	0

- Molecule 4 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	AL02	252	1914	1191	388	334	1	0	0

- Molecule 5 is a protein called RPL3 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	AL03	386	3075	1950	584	533	8	0	0

- Molecule 6 is a protein called RPL4A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	AL04	361	2748	1729	522	494	3	0	0

- Molecule 7 is a protein called RPL5 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	AL05	296	2375	1501	414	458	2	0	0

- Molecule 8 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	AL06	156	1239	800	222	216	1	0	0

- Molecule 9 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	AL07	222	1784	1151	324	308	1	0	0

- Molecule 10 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	AL08	233	1804	1151	323	327	3	0	0

- Molecule 11 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	AL09	191	1518	963	274	277	4	0	0

- Molecule 12 is a protein called RPL10 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	AL10	211	1705	1083	322	294	6	0	0

- Molecule 13 is a protein called RPL11A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	AL11	169	1353	847	253	249	4	0	0

- Molecule 14 is a protein called Ribosomal protein L12.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	AL12	12	Total	C	N	O	0	0
			60	36	12	12		

- Molecule 15 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	AL13	193	Total	C	N	O	0	0
			1543	962	315	266		

- Molecule 16 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AL14	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 17 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AL15	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 18 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AL16	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 19 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	AL17	183	Total	C	N	O	0	0
			1420	882	281	257		

- Molecule 20 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AL18	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 21 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	AL19	155	Total	C	N	O	0	0
			1249	776	264	209		

- Molecule 22 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AL20	172	Total	C	N	O	S	0	0
			1445	930	267	244	4		

- Molecule 23 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AL21	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 24 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	AL22	100	Total	C	N	O	0	0
			796	516	131	149		

- Molecule 25 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AL23	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 26 is a protein called RPL24A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AL24	63	Total	C	N	O	S	0	0
			521	336	102	82	1		

- Molecule 27 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AL25	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

- Molecule 28 is a protein called 60S ribosomal protein L26-A.



Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
28	AL26	126	993	625	192	176	0	0

- Molecule 29 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
29	AL27	135	1092	710	202	180	0	0

- Molecule 30 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	AL28	148	1173	749	231	190	3	0	0

- Molecule 31 is a protein called RPL29 isoform 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
31	AL29	58	462	289	100	73	0	0

- Molecule 32 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	AL30	97	743	479	124	139	1	0	0

- Molecule 33 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	AL31	109	876	556	167	152	1	0	0

- Molecule 34 is a protein called RPL32 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	AL32	127	1020	647	205	167	1	0	0

- Molecule 35 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	AL33	106	850	540	165	144	1	0	0

- Molecule 36 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	AL34	112	880	545	179	152	4	0	0

- Molecule 37 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	AL35	119	969	615	186	167	1	0	0

- Molecule 38 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	AL36	99	771	481	156	132	2	0	0

- Molecule 39 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	AL37	87	681	414	148	114	5	0	0

- Molecule 40 is a protein called RPL38 isoform 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
40	AL38	77	612	391	115	106	0	0

- Molecule 41 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	AL39	50	436	272	97	65	2	0	0

- Molecule 42 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	AL40	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 43 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	AL41	25	Total	C	N	O	S	0	0
			233	142	63	27	1		

- Molecule 44 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	AL42	105	Total	C	N	O	S	0	0
			847	534	170	138	5		

- Molecule 45 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	AL43	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 46 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	ALP0	7	Total	C	N	O	S	0	0
			54	32	12	9	1		

- Molecule 47 is a RNA chain called tRNAfMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	APTn	77	Total	C	N	O	P	0	0
			1644	732	297	538	77		

- Molecule 48 is a protein called PR20.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	PR	19	Total	C	N	O	0	0
			169	104	46	19		

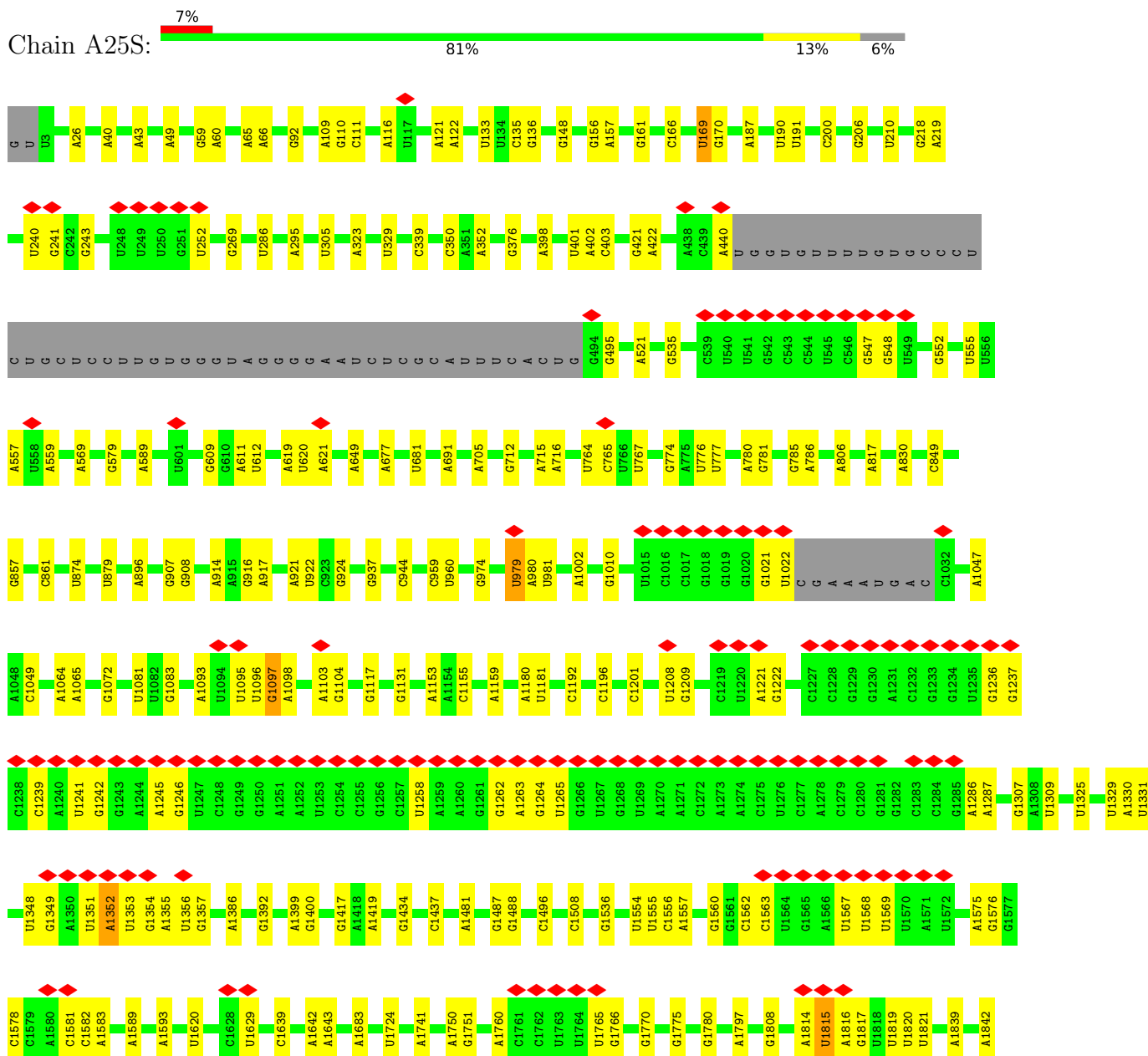
- Molecule 49 is ZINC ION (three-letter code: ZN) (formula: Zn).

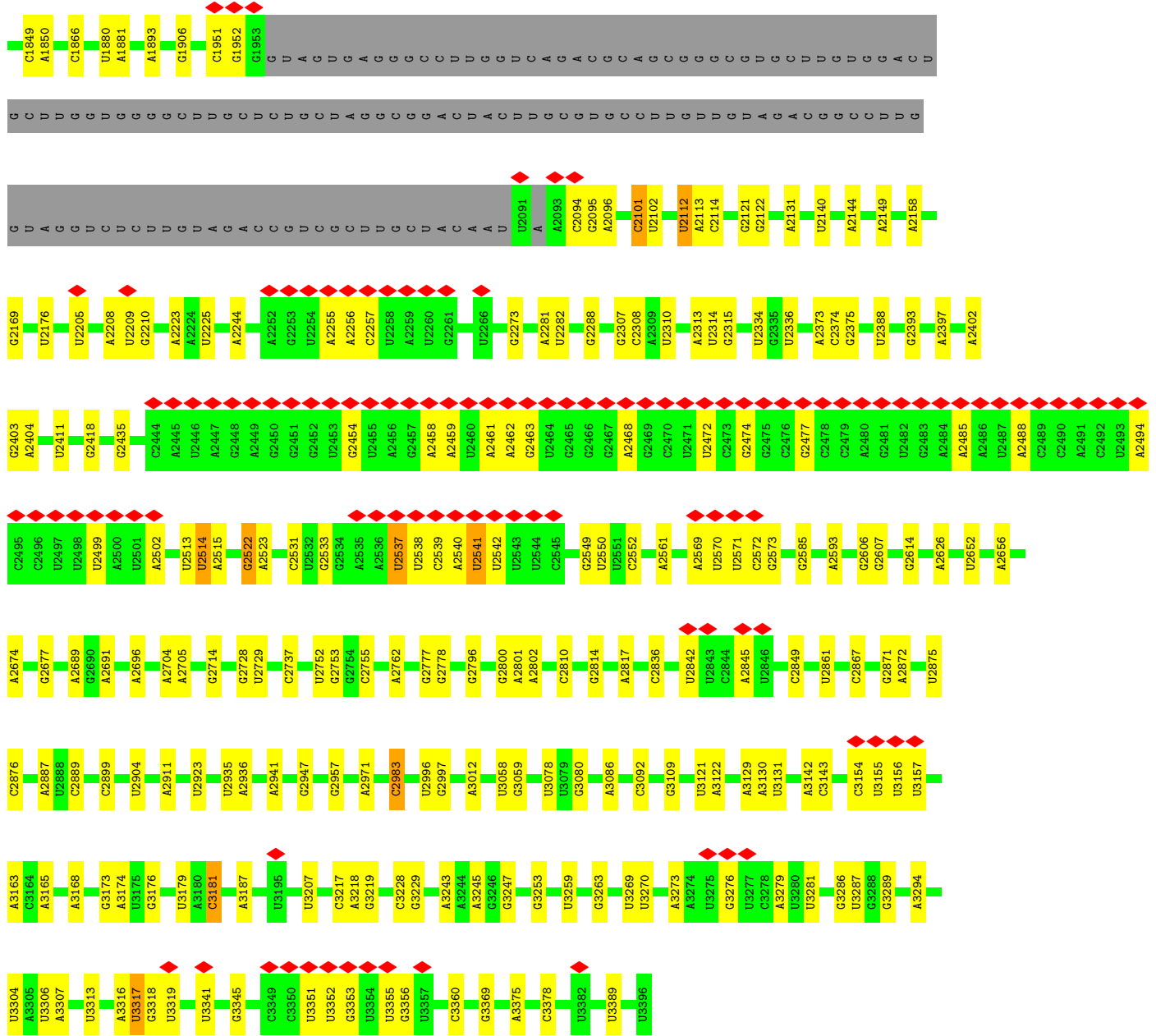
<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>AltConf</b>
49	AL37	1	Total 1	Zn 1	0
49	AL40	1	Total 1	Zn 1	0
49	AL42	1	Total 1	Zn 1	0
49	AL43	1	Total 1	Zn 1	0

### 3 Residue-property plots

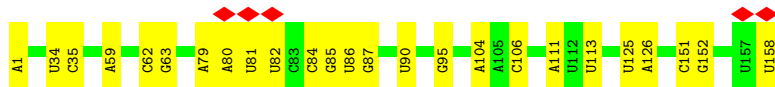
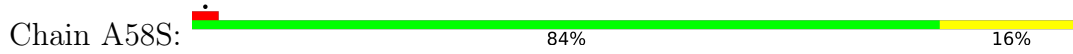
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

#### • Molecule 1: 25S rRNA





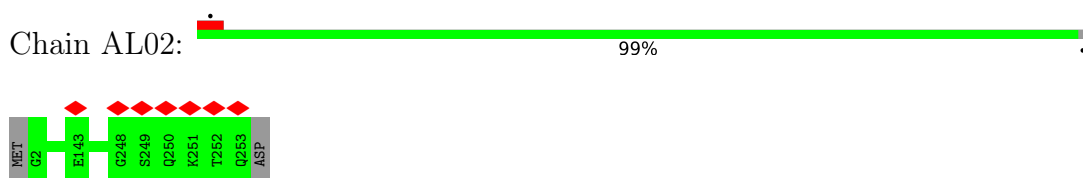
- Molecule 2: 5.8S rRNA



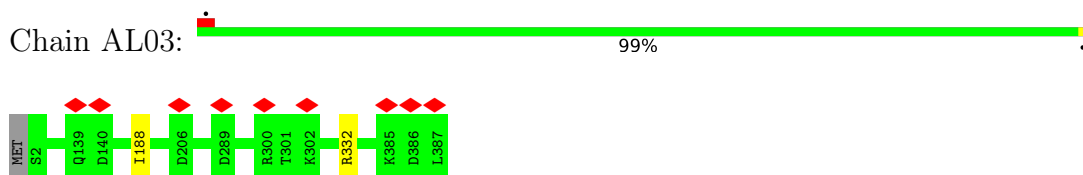
- Molecule 3: 5S rRNA



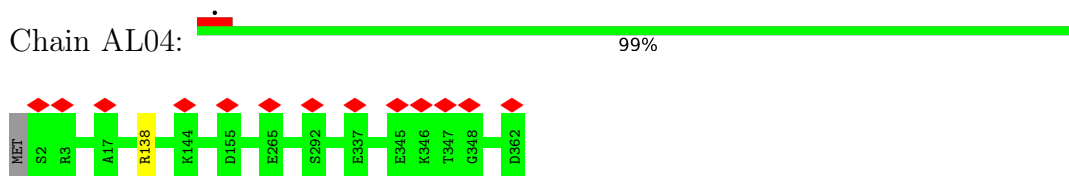
- Molecule 4: 60S ribosomal protein L2-A



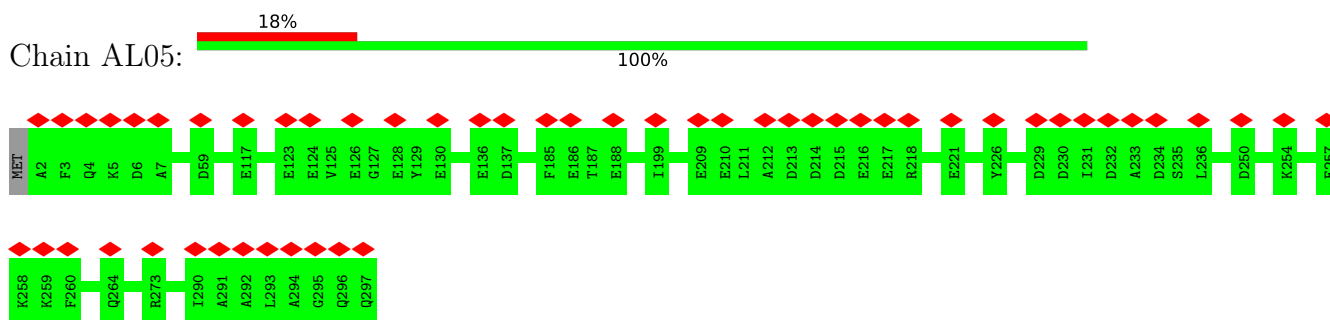
- Molecule 5: RPL3 isoform 1



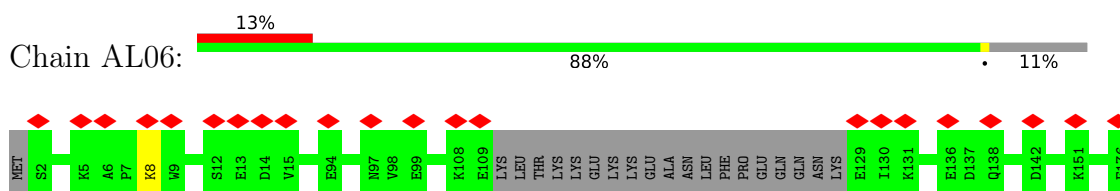
- Molecule 6: RPL4A isoform 1



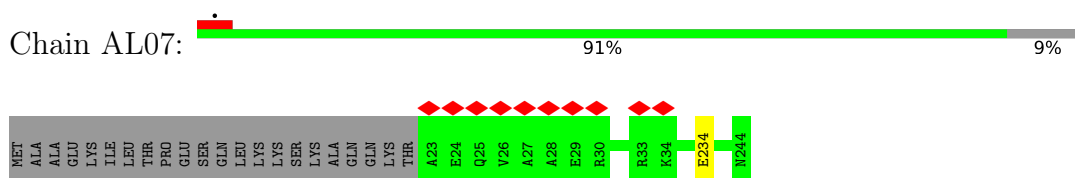
- Molecule 7: RPL5 isoform 1



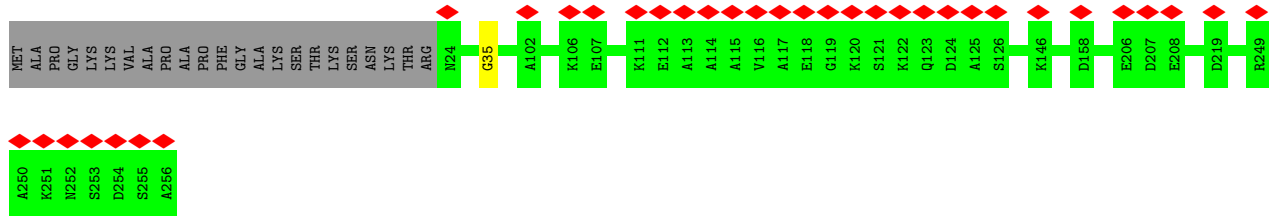
- Molecule 8: 60S ribosomal protein L6-A



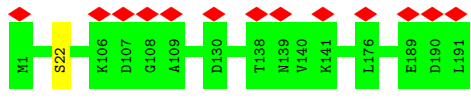
- Molecule 9: 60S ribosomal protein L7-A



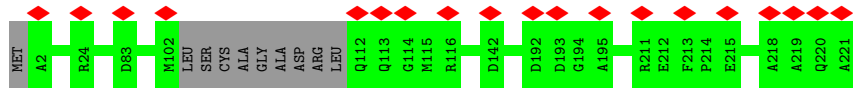
- Molecule 10: 60S ribosomal protein L8-A



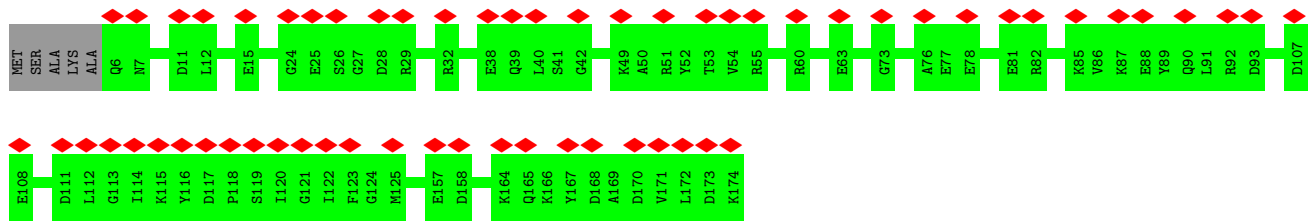
- Molecule 11: 60S ribosomal protein L9-A



- Molecule 12: RPL10 isoform 1



- Molecule 13: RPL11A isoform 1

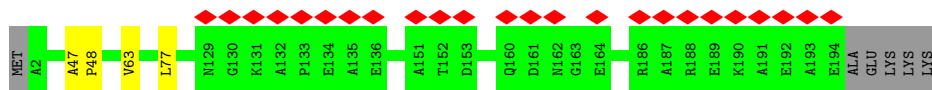


- Molecule 14: Ribosomal protein L12

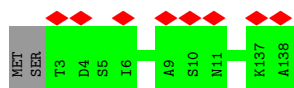


- Molecule 15: 60S ribosomal protein L13-A





• Molecule 16: 60S ribosomal protein L14-A



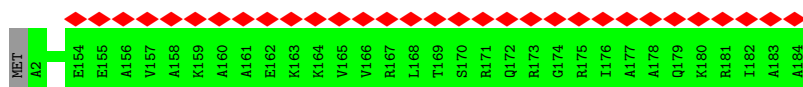
• Molecule 17: 60S ribosomal protein L15-A



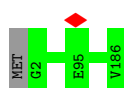
• Molecule 18: 60S ribosomal protein L16-A



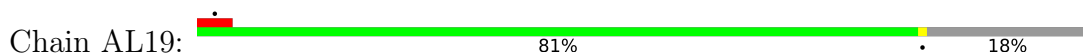
• Molecule 19: 60S ribosomal protein L17-A



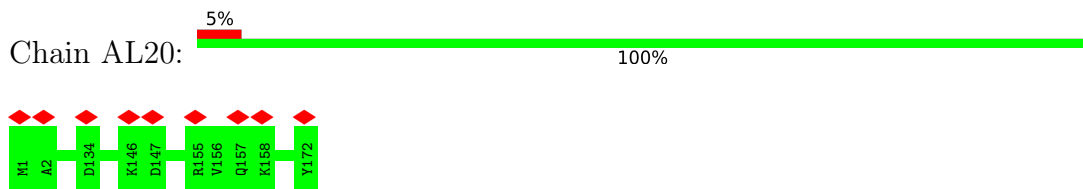
• Molecule 20: 60S ribosomal protein L18-A



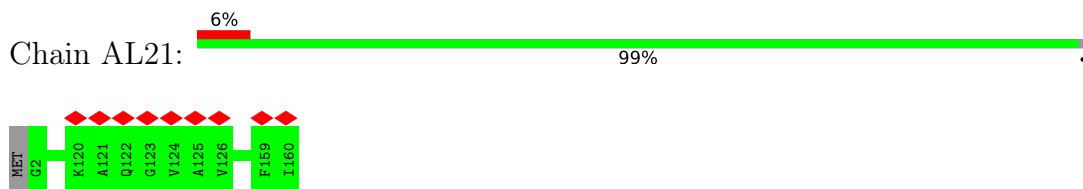
• Molecule 21: 60S ribosomal protein L19-A



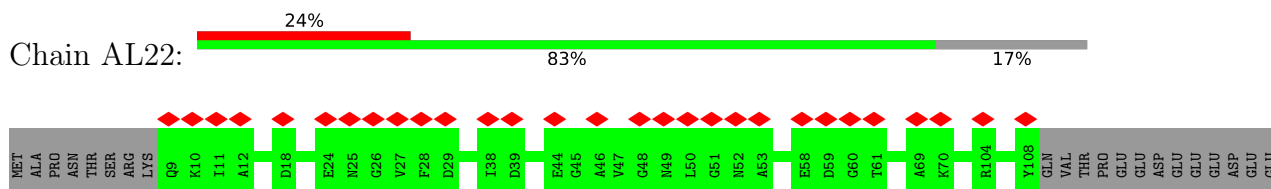
- Molecule 22: 60S ribosomal protein L20-A



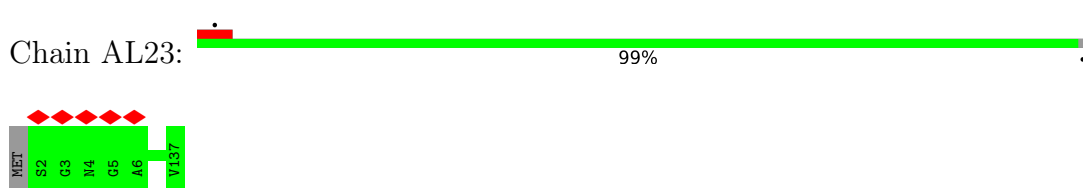
- Molecule 23: 60S ribosomal protein L21-A



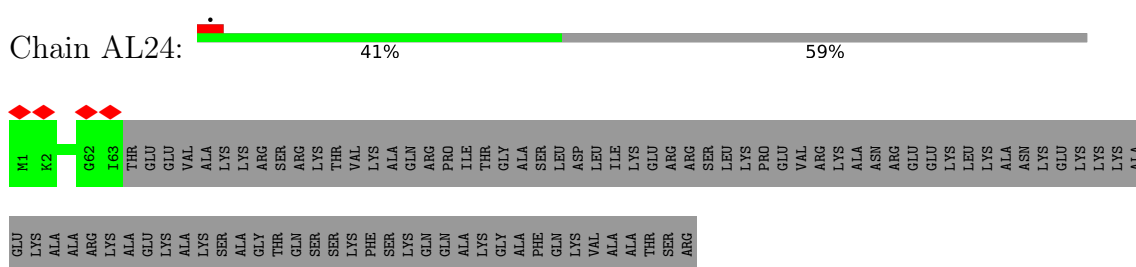
- Molecule 24: 60S ribosomal protein L22-A



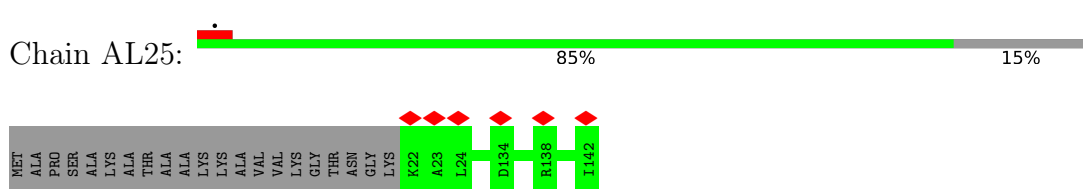
- Molecule 25: 60S ribosomal protein L23-A



- Molecule 26: RPL24A isoform 1

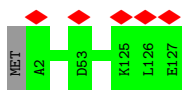


- Molecule 27: 60S ribosomal protein L25



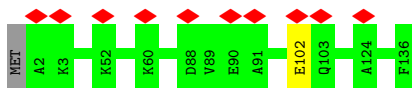
- Molecule 28: 60S ribosomal protein L26-A

Chain AL26:  99%



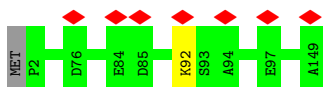
- Molecule 29: 60S ribosomal protein L27-A

Chain AL27:  99%



- Molecule 30: 60S ribosomal protein L28

Chain AL28:  99%



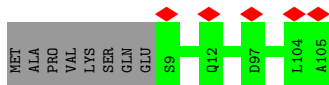
- Molecule 31: RPL29 isoform 1

Chain AL29:  98%



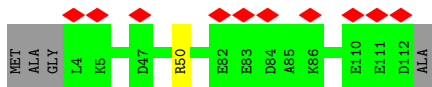
- Molecule 32: 60S ribosomal protein L30

Chain AL30:  92% 8%



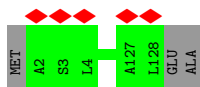
- Molecule 33: 60S ribosomal protein L31-A

Chain AL31:  96%



- Molecule 34: RPL32 isoform 1

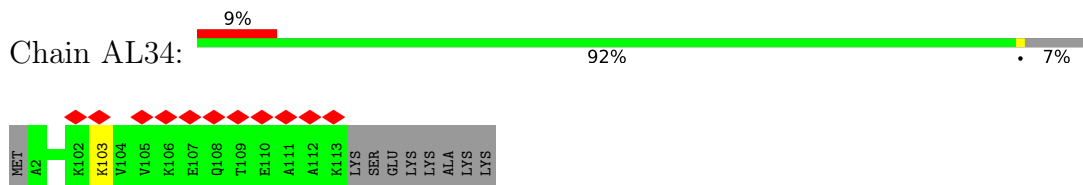
Chain AL32:  98%



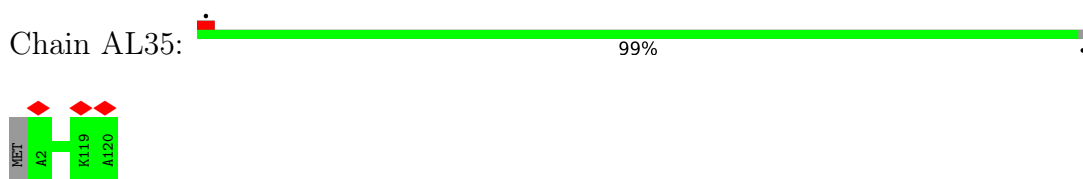
- Molecule 35: 60S ribosomal protein L33-A



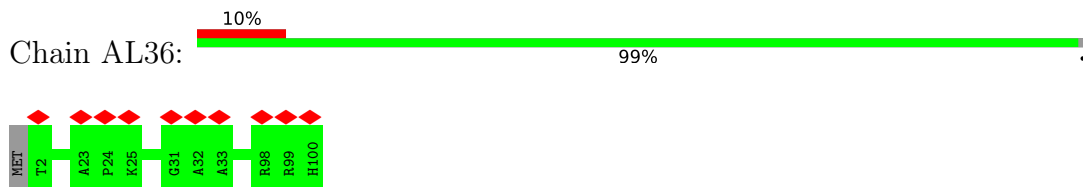
- Molecule 36: 60S ribosomal protein L34-A



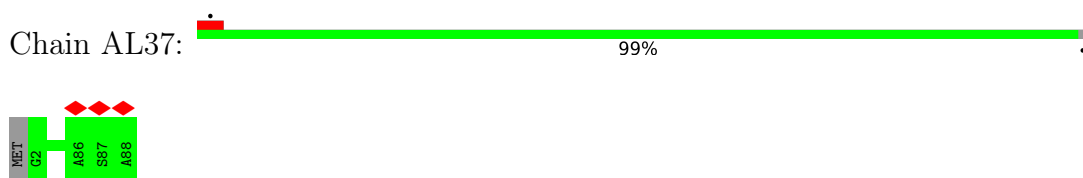
- Molecule 37: 60S ribosomal protein L35-A



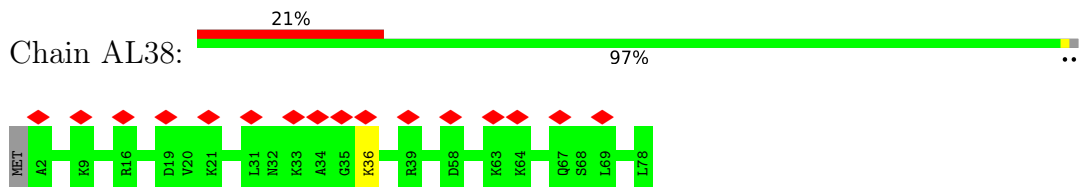
- Molecule 38: 60S ribosomal protein L36-A



- Molecule 39: 60S ribosomal protein L37-A



- Molecule 40: RPL38 isoform 1



- Molecule 41: 60S ribosomal protein L39







## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	203089	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	30	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	29.872	Depositor
Minimum map value	-7.203	Depositor
Average map value	0.010	Depositor
Map value standard deviation	1.068	Depositor
Recommended contour level	4.0	Depositor
Map size ( $\text{\AA}$ )	403.19998, 403.19998, 403.19998	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.05, 1.05, 1.05	Depositor

## 5 Model quality i

### 5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section:  
ZN

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	A25S	0.16	0/76471	0.75	29/119222 (0.0%)
2	A58S	0.22	1/3747 (0.0%)	0.71	0/5832
3	A5S	0.24	1/2884 (0.0%)	0.71	0/4491
4	AL02	0.24	0/1948	0.46	0/2617
5	AL03	0.24	0/3146	0.45	0/4228
6	AL04	0.24	0/2800	0.45	0/3790
7	AL05	0.24	0/2425	0.45	0/3271
8	AL06	0.25	0/1260	0.45	0/1694
9	AL07	0.24	0/1821	0.42	0/2451
10	AL08	0.25	0/1836	0.46	0/2481
11	AL09	0.26	0/1539	0.49	0/2073
12	AL10	0.25	0/1741	0.44	0/2335
13	AL11	0.26	0/1374	0.53	0/1842
15	AL13	0.24	0/1568	0.47	0/2106
16	AL14	0.24	0/1068	0.42	0/1438
17	AL15	0.23	0/1757	0.43	0/2354
18	AL16	0.24	0/1585	0.40	0/2128
19	AL17	0.23	0/1443	0.44	0/1944
20	AL18	0.24	0/1465	0.43	0/1965
21	AL19	0.22	0/1266	0.40	0/1690
22	AL20	0.25	0/1481	0.46	0/1990
23	AL21	0.24	0/1300	0.46	0/1743
24	AL22	0.26	0/812	0.47	0/1099
25	AL23	0.24	0/1018	0.44	0/1369
26	AL24	0.26	0/533	0.43	0/707
27	AL25	0.24	0/979	0.44	0/1321
28	AL26	0.24	0/1004	0.45	0/1341
29	AL27	0.26	0/1118	0.47	0/1497
30	AL28	0.24	0/1204	0.47	0/1612
31	AL29	0.25	0/473	0.44	0/629
32	AL30	0.24	0/751	0.41	0/1008
33	AL31	0.24	0/890	0.43	0/1196



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
34	AL32	0.22	0/1041	0.42	0/1394
35	AL33	0.25	0/868	0.42	0/1168
36	AL34	0.23	0/890	0.44	0/1189
37	AL35	0.23	0/978	0.43	0/1301
38	AL36	0.24	0/778	0.45	0/1034
39	AL37	0.24	0/696	0.45	0/923
40	AL38	0.25	0/618	0.49	0/826
41	AL39	0.23	0/443	0.45	0/588
42	AL40	0.24	0/423	0.44	0/562
43	AL41	0.20	0/234	0.37	0/300
44	AL42	0.25	0/860	0.47	0/1136
45	AL43	0.24	0/701	0.48	0/934
46	ALP0	0.20	0/53	0.34	0/68
47	APTN	0.28	1/1836 (0.1%)	0.71	0/2859
48	PR	0.28	0/178	0.51	0/242
All	All	0.20	3/135304 (0.0%)	0.66	29/199988 (0.0%)

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
10	AL08	0	1
11	AL09	0	1
15	AL13	0	1
18	AL16	0	1
21	AL19	0	1
29	AL27	0	1
All	All	0	6

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A5S	1	G	OP3-P	-10.62	1.48	1.61
2	A58S	1	A	OP3-P	-10.60	1.48	1.61
47	APTN	1	C	OP3-P	-10.60	1.48	1.61

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A25S	922	U	C2-N1-C1'	7.81	127.07	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A25S	922	U	N1-C2-O2	7.27	127.89	122.80
1	A25S	922	U	N3-C2-O2	-6.59	117.59	122.20
1	A25S	2983	C	C2-N1-C1'	6.39	125.83	118.80
1	A25S	2541	U	P-O3'-C3'	5.88	126.75	119.70
1	A25S	979	U	P-O3'-C3'	5.80	126.66	119.70
1	A25S	3317	U	P-O3'-C3'	5.79	126.65	119.70
1	A25S	1815	U	P-O3'-C3'	5.74	126.58	119.70
1	A25S	2112	U	P-O3'-C3'	5.72	126.57	119.70
1	A25S	2522	G	C4-N9-C1'	5.65	133.84	126.50
1	A25S	2514	U	P-O3'-C3'	5.64	126.47	119.70
1	A25S	2514	U	OP1-P-O3'	5.62	117.56	105.20
1	A25S	2101	C	P-O3'-C3'	5.57	126.38	119.70
1	A25S	1352	A	OP1-P-O3'	5.56	117.43	105.20
1	A25S	3306	U	C2-N1-C1'	5.56	124.37	117.70
1	A25S	2550	U	C2-N1-C1'	5.47	124.27	117.70
1	A25S	1352	A	P-O3'-C3'	5.44	126.23	119.70
1	A25S	2257	C	C2-N1-C1'	5.33	124.67	118.80
1	A25S	3058	U	C2-N1-C1'	5.23	123.98	117.70
1	A25S	2101	C	OP1-P-O3'	5.22	116.69	105.20
1	A25S	169	U	P-O3'-C3'	5.21	125.95	119.70
1	A25S	1097	G	P-O3'-C3'	5.20	125.94	119.70
1	A25S	2522	G	N3-C4-C5	-5.19	126.01	128.60
1	A25S	2537	U	P-O3'-C3'	5.13	125.85	119.70
1	A25S	922	U	C6-N1-C1'	-5.10	114.05	121.20
1	A25S	3181	C	C2-N1-C1'	5.08	124.39	118.80
1	A25S	2983	C	N1-C2-O2	5.08	121.95	118.90
1	A25S	2836	C	C2-N1-C1'	5.05	124.35	118.80
1	A25S	2522	G	N3-C4-N9	5.04	129.03	126.00

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	AL08	35	GLY	Peptide
11	AL09	22	SER	Peptide
15	AL13	47	ALA	Peptide
18	AL16	110	PRO	Peptide
21	AL19	129	GLY	Peptide
29	AL27	102	GLU	Peptide

## 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A25S	68318	0	0	0	0
2	A58S	3354	0	0	0	0
3	A5S	2580	0	1304	1	0
4	AL02	1914	0	0	0	0
5	AL03	3075	0	0	0	0
6	AL04	2748	0	0	0	0
7	AL05	2375	0	0	0	0
8	AL06	1239	0	0	0	0
9	AL07	1784	0	0	0	0
10	AL08	1804	0	0	0	0
11	AL09	1518	0	0	0	0
12	AL10	1705	0	0	0	0
13	AL11	1353	0	0	0	0
14	AL12	60	0	0	0	0
15	AL13	1543	0	0	0	0
16	AL14	1053	0	0	0	0
17	AL15	1720	0	0	0	0
18	AL16	1555	0	0	0	0
19	AL17	1420	0	0	0	0
20	AL18	1441	0	0	0	0
21	AL19	1249	0	0	0	0
22	AL20	1445	0	0	0	0
23	AL21	1276	0	0	0	0
24	AL22	796	0	0	0	0
25	AL23	1003	0	0	0	0
26	AL24	521	0	0	0	0
27	AL25	964	0	0	0	0
28	AL26	993	0	0	0	0
29	AL27	1092	0	0	0	0
30	AL28	1173	0	0	0	0
31	AL29	462	0	0	0	0
32	AL30	743	0	0	0	0
33	AL31	876	0	0	0	0
34	AL32	1020	0	0	0	0
35	AL33	850	0	0	0	0
36	AL34	880	0	0	0	0
37	AL35	969	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	AL36	771	0	0	0	0
39	AL37	681	0	0	0	0
40	AL38	612	0	0	0	0
41	AL39	436	0	0	0	0
42	AL40	417	0	0	0	0
43	AL41	233	0	0	0	0
44	AL42	847	0	0	0	0
45	AL43	694	0	0	0	0
46	ALP0	54	0	0	0	0
47	APTN	1644	0	0	0	0
48	PR	169	0	187	0	0
49	AL37	1	0	0	0	0
49	AL40	1	0	0	0	0
49	AL42	1	0	0	0	0
49	AL43	1	0	0	0	0
All	All	125433	0	1491	1	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 3.

All (1) 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)
3:A5S:9:C:OP2	3:A5S:10:C:N4	2.54	0.40

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
4	AL02	250/254 (98%)	240 (96%)	10 (4%)	0	<b>100</b> <b>100</b>

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	AL03	384/387 (99%)	371 (97%)	12 (3%)	1 (0%)	41	55
6	AL04	359/362 (99%)	323 (90%)	36 (10%)	0	100	100
7	AL05	294/297 (99%)	278 (95%)	16 (5%)	0	100	100
8	AL06	152/176 (86%)	144 (95%)	8 (5%)	0	100	100
9	AL07	220/244 (90%)	209 (95%)	10 (4%)	1 (0%)	29	41
10	AL08	231/256 (90%)	216 (94%)	15 (6%)	0	100	100
11	AL09	189/191 (99%)	173 (92%)	16 (8%)	0	100	100
12	AL10	207/221 (94%)	201 (97%)	6 (3%)	0	100	100
13	AL11	167/174 (96%)	149 (89%)	18 (11%)	0	100	100
15	AL13	191/199 (96%)	173 (91%)	15 (8%)	3 (2%)	9	13
16	AL14	134/138 (97%)	128 (96%)	6 (4%)	0	100	100
17	AL15	201/204 (98%)	187 (93%)	14 (7%)	0	100	100
18	AL16	195/199 (98%)	191 (98%)	2 (1%)	2 (1%)	15	23
19	AL17	181/184 (98%)	172 (95%)	9 (5%)	0	100	100
20	AL18	183/186 (98%)	180 (98%)	3 (2%)	0	100	100
21	AL19	153/189 (81%)	147 (96%)	6 (4%)	0	100	100
22	AL20	170/172 (99%)	160 (94%)	10 (6%)	0	100	100
23	AL21	157/160 (98%)	148 (94%)	9 (6%)	0	100	100
24	AL22	98/121 (81%)	95 (97%)	3 (3%)	0	100	100
25	AL23	134/137 (98%)	133 (99%)	1 (1%)	0	100	100
26	AL24	61/155 (39%)	58 (95%)	3 (5%)	0	100	100
27	AL25	119/142 (84%)	114 (96%)	5 (4%)	0	100	100
28	AL26	124/127 (98%)	122 (98%)	2 (2%)	0	100	100
29	AL27	133/136 (98%)	124 (93%)	9 (7%)	0	100	100
30	AL28	146/149 (98%)	131 (90%)	15 (10%)	0	100	100
31	AL29	56/59 (95%)	51 (91%)	5 (9%)	0	100	100
32	AL30	95/105 (90%)	95 (100%)	0	0	100	100
33	AL31	107/113 (95%)	101 (94%)	6 (6%)	0	100	100
34	AL32	125/130 (96%)	123 (98%)	2 (2%)	0	100	100
35	AL33	104/107 (97%)	99 (95%)	5 (5%)	0	100	100
36	AL34	110/121 (91%)	107 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	AL35	117/120 (98%)	111 (95%)	6 (5%)	0	100	100
38	AL36	97/100 (97%)	91 (94%)	6 (6%)	0	100	100
39	AL37	85/88 (97%)	81 (95%)	4 (5%)	0	100	100
40	AL38	75/78 (96%)	75 (100%)	0	0	100	100
41	AL39	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
42	AL40	50/128 (39%)	48 (96%)	2 (4%)	0	100	100
43	AL41	23/25 (92%)	23 (100%)	0	0	100	100
44	AL42	103/106 (97%)	93 (90%)	10 (10%)	0	100	100
45	AL43	89/92 (97%)	84 (94%)	5 (6%)	0	100	100
46	ALP0	5/221 (2%)	5 (100%)	0	0	100	100
48	PR	17/40 (42%)	13 (76%)	4 (24%)	0	100	100
All	All	6139/6844 (90%)	5813 (95%)	319 (5%)	7 (0%)	54	68

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
18	AL16	111	PRO
9	AL07	234	GLU
15	AL13	77	LEU
15	AL13	63	VAL
15	AL13	48	PRO
18	AL16	110	PRO
5	AL03	188	ILE

### 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	
4	AL02	193/196 (98%)	193 (100%)	0	100	100
5	AL03	320/323 (99%)	319 (100%)	1 (0%)	92	97
6	AL04	288/289 (100%)	287 (100%)	1 (0%)	92	97

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	AL05	244/245 (100%)	244 (100%)	0	100	100
8	AL06	134/153 (88%)	133 (99%)	1 (1%)	84	92
9	AL07	186/205 (91%)	186 (100%)	0	100	100
10	AL08	187/208 (90%)	187 (100%)	0	100	100
11	AL09	171/171 (100%)	171 (100%)	0	100	100
12	AL10	177/187 (95%)	177 (100%)	0	100	100
13	AL11	147/150 (98%)	147 (100%)	0	100	100
15	AL13	154/159 (97%)	154 (100%)	0	100	100
16	AL14	107/109 (98%)	107 (100%)	0	100	100
17	AL15	175/176 (99%)	175 (100%)	0	100	100
18	AL16	160/162 (99%)	160 (100%)	0	100	100
19	AL17	140/146 (96%)	140 (100%)	0	100	100
20	AL18	150/151 (99%)	150 (100%)	0	100	100
21	AL19	128/154 (83%)	128 (100%)	0	100	100
22	AL20	156/156 (100%)	156 (100%)	0	100	100
23	AL21	136/137 (99%)	136 (100%)	0	100	100
24	AL22	87/107 (81%)	87 (100%)	0	100	100
25	AL23	104/105 (99%)	104 (100%)	0	100	100
26	AL24	55/129 (43%)	55 (100%)	0	100	100
27	AL25	104/118 (88%)	104 (100%)	0	100	100
28	AL26	109/110 (99%)	109 (100%)	0	100	100
29	AL27	115/116 (99%)	115 (100%)	0	100	100
30	AL28	118/119 (99%)	117 (99%)	1 (1%)	81	91
31	AL29	46/47 (98%)	46 (100%)	0	100	100
32	AL30	81/88 (92%)	81 (100%)	0	100	100
33	AL31	92/97 (95%)	91 (99%)	1 (1%)	73	87
34	AL32	109/111 (98%)	109 (100%)	0	100	100
35	AL33	90/91 (99%)	90 (100%)	0	100	100
36	AL34	95/103 (92%)	94 (99%)	1 (1%)	73	87
37	AL35	104/105 (99%)	104 (100%)	0	100	100
38	AL36	81/82 (99%)	81 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	AL37	70/71 (99%)	70 (100%)	0	100	100
40	AL38	68/69 (99%)	67 (98%)	1 (2%)	65	80
41	AL39	45/46 (98%)	45 (100%)	0	100	100
42	AL40	47/116 (40%)	47 (100%)	0	100	100
43	AL41	23/23 (100%)	23 (100%)	0	100	100
44	AL42	90/91 (99%)	89 (99%)	1 (1%)	73	87
45	AL43	71/72 (99%)	71 (100%)	0	100	100
46	ALP0	6/166 (4%)	6 (100%)	0	100	100
48	PR	19/40 (48%)	18 (95%)	1 (5%)	22	37
All	All	5182/5699 (91%)	5173 (100%)	9 (0%)	93	97

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	AL03	332	ARG
6	AL04	138	ARG
8	AL06	8	LYS
30	AL28	92	LYS
33	AL31	50	ARG
36	AL34	103	LYS
40	AL38	36	LYS
44	AL42	15	LYS
48	PR	20	ARG

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
1	A25S	3189/3396 (93%)	441 (13%)	29 (0%)
2	A58S	157/158 (99%)	24 (15%)	1 (0%)
3	A5S	120/121 (99%)	8 (6%)	0
47	APTN	76/77 (98%)	8 (10%)	0
All	All	3542/3752 (94%)	481 (13%)	30 (0%)

All (481) RNA backbone outliers are listed below:



Mol	Chain	Res	Type
1	A25S	26	A
1	A25S	40	A
1	A25S	43	A
1	A25S	49	A
1	A25S	59	G
1	A25S	60	A
1	A25S	65	A
1	A25S	66	A
1	A25S	92	G
1	A25S	109	A
1	A25S	110	G
1	A25S	111	C
1	A25S	116	A
1	A25S	121	A
1	A25S	122	A
1	A25S	133	U
1	A25S	135	C
1	A25S	136	G
1	A25S	148	G
1	A25S	156	G
1	A25S	157	A
1	A25S	161	G
1	A25S	166	C
1	A25S	170	G
1	A25S	187	A
1	A25S	190	U
1	A25S	191	U
1	A25S	200	C
1	A25S	206	G
1	A25S	210	U
1	A25S	218	G
1	A25S	219	A
1	A25S	240	U
1	A25S	241	G
1	A25S	243	G
1	A25S	252	U
1	A25S	269	G
1	A25S	286	U
1	A25S	295	A
1	A25S	305	U
1	A25S	323	A
1	A25S	329	U
1	A25S	339	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A25S	350	C
1	A25S	352	A
1	A25S	376	G
1	A25S	398	A
1	A25S	401	U
1	A25S	402	A
1	A25S	403	C
1	A25S	421	G
1	A25S	422	A
1	A25S	440	A
1	A25S	495	G
1	A25S	521	A
1	A25S	535	G
1	A25S	547	G
1	A25S	548	G
1	A25S	552	G
1	A25S	555	U
1	A25S	557	A
1	A25S	559	A
1	A25S	569	A
1	A25S	579	G
1	A25S	589	A
1	A25S	609	G
1	A25S	611	A
1	A25S	612	U
1	A25S	620	U
1	A25S	621	A
1	A25S	649	A
1	A25S	677	A
1	A25S	681	U
1	A25S	691	A
1	A25S	705	A
1	A25S	712	G
1	A25S	715	A
1	A25S	716	A
1	A25S	765	C
1	A25S	767	U
1	A25S	774	G
1	A25S	776	U
1	A25S	777	U
1	A25S	780	A
1	A25S	781	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A25S	785	G
1	A25S	786	A
1	A25S	806	A
1	A25S	817	A
1	A25S	830	A
1	A25S	849	C
1	A25S	857	G
1	A25S	861	C
1	A25S	874	U
1	A25S	879	U
1	A25S	896	A
1	A25S	907	G
1	A25S	908	G
1	A25S	914	A
1	A25S	916	G
1	A25S	917	A
1	A25S	921	A
1	A25S	924	G
1	A25S	937	G
1	A25S	944	C
1	A25S	959	C
1	A25S	960	U
1	A25S	974	G
1	A25S	979	U
1	A25S	980	A
1	A25S	981	U
1	A25S	1002	A
1	A25S	1010	G
1	A25S	1021	G
1	A25S	1022	U
1	A25S	1047	A
1	A25S	1049	C
1	A25S	1064	A
1	A25S	1065	A
1	A25S	1072	G
1	A25S	1081	U
1	A25S	1083	G
1	A25S	1093	A
1	A25S	1095	U
1	A25S	1096	U
1	A25S	1097	G
1	A25S	1098	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A25S	1103	A
1	A25S	1104	G
1	A25S	1117	G
1	A25S	1131	G
1	A25S	1153	A
1	A25S	1155	C
1	A25S	1159	A
1	A25S	1180	A
1	A25S	1181	U
1	A25S	1192	C
1	A25S	1196	C
1	A25S	1201	C
1	A25S	1208	U
1	A25S	1209	G
1	A25S	1221	A
1	A25S	1222	G
1	A25S	1236	G
1	A25S	1237	G
1	A25S	1239	C
1	A25S	1242	G
1	A25S	1245	A
1	A25S	1246	G
1	A25S	1258	U
1	A25S	1262	G
1	A25S	1263	A
1	A25S	1264	G
1	A25S	1265	U
1	A25S	1286	A
1	A25S	1287	A
1	A25S	1307	G
1	A25S	1309	U
1	A25S	1325	U
1	A25S	1330	A
1	A25S	1331	U
1	A25S	1348	U
1	A25S	1349	G
1	A25S	1351	U
1	A25S	1352	A
1	A25S	1353	U
1	A25S	1354	G
1	A25S	1355	A
1	A25S	1356	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A25S	1357	G
1	A25S	1386	A
1	A25S	1392	G
1	A25S	1399	A
1	A25S	1400	G
1	A25S	1417	G
1	A25S	1419	A
1	A25S	1434	G
1	A25S	1437	C
1	A25S	1481	A
1	A25S	1487	G
1	A25S	1488	G
1	A25S	1496	C
1	A25S	1508	C
1	A25S	1536	G
1	A25S	1555	U
1	A25S	1556	C
1	A25S	1557	A
1	A25S	1560	G
1	A25S	1562	C
1	A25S	1563	C
1	A25S	1567	U
1	A25S	1568	U
1	A25S	1569	U
1	A25S	1575	A
1	A25S	1576	G
1	A25S	1578	C
1	A25S	1581	C
1	A25S	1582	C
1	A25S	1583	A
1	A25S	1589	A
1	A25S	1593	A
1	A25S	1620	U
1	A25S	1629	U
1	A25S	1639	C
1	A25S	1642	A
1	A25S	1643	A
1	A25S	1683	A
1	A25S	1724	U
1	A25S	1741	A
1	A25S	1750	A
1	A25S	1751	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A25S	1760	A
1	A25S	1765	U
1	A25S	1766	G
1	A25S	1770	G
1	A25S	1775	G
1	A25S	1780	G
1	A25S	1797	A
1	A25S	1808	G
1	A25S	1814	A
1	A25S	1816	A
1	A25S	1817	G
1	A25S	1819	U
1	A25S	1820	U
1	A25S	1821	U
1	A25S	1839	A
1	A25S	1842	A
1	A25S	1849	C
1	A25S	1850	A
1	A25S	1866	C
1	A25S	1880	U
1	A25S	1881	A
1	A25S	1893	A
1	A25S	1906	G
1	A25S	1951	C
1	A25S	1952	G
1	A25S	2094	C
1	A25S	2095	G
1	A25S	2096	A
1	A25S	2101	C
1	A25S	2102	U
1	A25S	2113	A
1	A25S	2114	C
1	A25S	2121	G
1	A25S	2122	G
1	A25S	2131	A
1	A25S	2140	U
1	A25S	2144	A
1	A25S	2149	A
1	A25S	2158	A
1	A25S	2169	G
1	A25S	2176	U
1	A25S	2205	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A25S	2208	A
1	A25S	2209	U
1	A25S	2210	G
1	A25S	2223	A
1	A25S	2225	U
1	A25S	2244	A
1	A25S	2255	A
1	A25S	2256	A
1	A25S	2273	G
1	A25S	2281	A
1	A25S	2282	U
1	A25S	2288	G
1	A25S	2307	G
1	A25S	2308	C
1	A25S	2310	U
1	A25S	2313	A
1	A25S	2314	U
1	A25S	2315	G
1	A25S	2334	U
1	A25S	2336	U
1	A25S	2373	A
1	A25S	2374	C
1	A25S	2375	G
1	A25S	2388	U
1	A25S	2393	G
1	A25S	2397	A
1	A25S	2402	A
1	A25S	2403	G
1	A25S	2404	A
1	A25S	2411	U
1	A25S	2418	G
1	A25S	2435	G
1	A25S	2454	G
1	A25S	2458	A
1	A25S	2459	A
1	A25S	2461	A
1	A25S	2462	A
1	A25S	2463	G
1	A25S	2468	A
1	A25S	2472	U
1	A25S	2474	G
1	A25S	2477	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A25S	2485	A
1	A25S	2488	A
1	A25S	2494	A
1	A25S	2499	U
1	A25S	2502	A
1	A25S	2513	U
1	A25S	2514	U
1	A25S	2515	A
1	A25S	2522	G
1	A25S	2523	A
1	A25S	2531	C
1	A25S	2533	G
1	A25S	2537	U
1	A25S	2538	U
1	A25S	2539	C
1	A25S	2540	A
1	A25S	2541	U
1	A25S	2542	U
1	A25S	2549	G
1	A25S	2552	C
1	A25S	2561	A
1	A25S	2569	A
1	A25S	2570	U
1	A25S	2571	U
1	A25S	2572	C
1	A25S	2573	G
1	A25S	2585	G
1	A25S	2593	A
1	A25S	2606	G
1	A25S	2607	G
1	A25S	2614	G
1	A25S	2626	A
1	A25S	2652	U
1	A25S	2656	A
1	A25S	2674	A
1	A25S	2677	G
1	A25S	2689	A
1	A25S	2691	A
1	A25S	2696	A
1	A25S	2704	A
1	A25S	2705	A
1	A25S	2714	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A25S	2728	G
1	A25S	2729	U
1	A25S	2737	C
1	A25S	2752	U
1	A25S	2753	G
1	A25S	2755	C
1	A25S	2762	A
1	A25S	2777	G
1	A25S	2778	G
1	A25S	2796	G
1	A25S	2800	G
1	A25S	2801	A
1	A25S	2802	A
1	A25S	2810	C
1	A25S	2814	G
1	A25S	2817	A
1	A25S	2842	U
1	A25S	2845	A
1	A25S	2849	C
1	A25S	2861	U
1	A25S	2867	C
1	A25S	2871	G
1	A25S	2872	A
1	A25S	2875	U
1	A25S	2876	C
1	A25S	2887	A
1	A25S	2889	C
1	A25S	2899	C
1	A25S	2904	U
1	A25S	2911	A
1	A25S	2923	U
1	A25S	2935	U
1	A25S	2936	A
1	A25S	2941	A
1	A25S	2947	G
1	A25S	2957	G
1	A25S	2971	A
1	A25S	2983	C
1	A25S	2996	U
1	A25S	2997	G
1	A25S	3012	A
1	A25S	3059	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A25S	3078	U
1	A25S	3080	G
1	A25S	3086	A
1	A25S	3092	C
1	A25S	3109	G
1	A25S	3122	A
1	A25S	3129	A
1	A25S	3130	A
1	A25S	3131	U
1	A25S	3142	A
1	A25S	3143	C
1	A25S	3154	C
1	A25S	3155	U
1	A25S	3156	U
1	A25S	3157	U
1	A25S	3163	A
1	A25S	3165	A
1	A25S	3168	A
1	A25S	3173	G
1	A25S	3174	A
1	A25S	3176	G
1	A25S	3179	U
1	A25S	3181	C
1	A25S	3187	A
1	A25S	3207	U
1	A25S	3217	C
1	A25S	3218	A
1	A25S	3219	G
1	A25S	3229	G
1	A25S	3243	A
1	A25S	3245	A
1	A25S	3247	G
1	A25S	3253	G
1	A25S	3259	U
1	A25S	3263	G
1	A25S	3269	U
1	A25S	3270	U
1	A25S	3273	A
1	A25S	3276	G
1	A25S	3279	A
1	A25S	3281	U
1	A25S	3286	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A25S	3287	U
1	A25S	3289	G
1	A25S	3294	A
1	A25S	3304	U
1	A25S	3307	A
1	A25S	3313	U
1	A25S	3316	A
1	A25S	3318	G
1	A25S	3319	U
1	A25S	3341	U
1	A25S	3345	G
1	A25S	3352	U
1	A25S	3353	G
1	A25S	3355	U
1	A25S	3356	G
1	A25S	3360	C
1	A25S	3369	G
1	A25S	3375	A
1	A25S	3378	C
1	A25S	3389	U
2	A58S	34	U
2	A58S	35	C
2	A58S	59	A
2	A58S	62	C
2	A58S	63	G
2	A58S	79	A
2	A58S	80	A
2	A58S	81	U
2	A58S	82	U
2	A58S	84	C
2	A58S	85	G
2	A58S	86	U
2	A58S	87	G
2	A58S	90	U
2	A58S	95	G
2	A58S	104	A
2	A58S	106	C
2	A58S	111	A
2	A58S	113	U
2	A58S	125	U
2	A58S	126	A
2	A58S	151	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
2	A58S	152	G
2	A58S	158	U
3	A5S	7	G
3	A5S	11	A
3	A5S	51	A
3	A5S	54	U
3	A5S	65	G
3	A5S	102	A
3	A5S	112	G
3	A5S	121	U
47	APTN	9	G
47	APTN	18	G
47	APTN	19	G
47	APTN	20	U
47	APTN	47	U
47	APTN	48	C
47	APTN	75	C
47	APTN	76	A

All (30) RNA pucker outliers are listed below:

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A25S	169	U
1	A25S	547	G
1	A25S	619	A
1	A25S	764	U
1	A25S	916	G
1	A25S	979	U
1	A25S	1064	A
1	A25S	1097	G
1	A25S	1103	A
1	A25S	1241	U
1	A25S	1329	U
1	A25S	1352	A
1	A25S	1355	A
1	A25S	1554	U
1	A25S	1562	C
1	A25S	1815	U
1	A25S	1816	A
1	A25S	2101	C
1	A25S	2112	U
1	A25S	2209	U

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Mol	Chain	Res	Type
1	A25S	2514	U
1	A25S	2537	U
1	A25S	2541	U
1	A25S	3121	U
1	A25S	3218	A
1	A25S	3228	C
1	A25S	3269	U
1	A25S	3317	U
1	A25S	3351	U
2	A58S	85	G

#### 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](#)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

#### 5.7 Other polymers [i](#)

There are no such residues in this entry.

#### 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

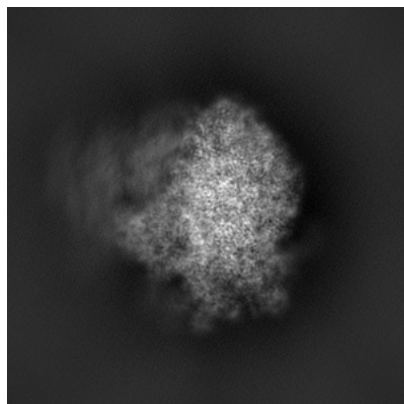
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26034. These allow visual inspection of the internal detail of the map and identification of artifacts.

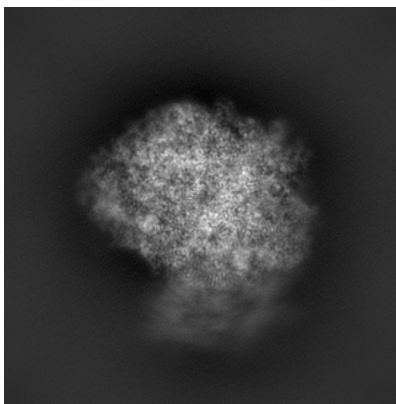
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

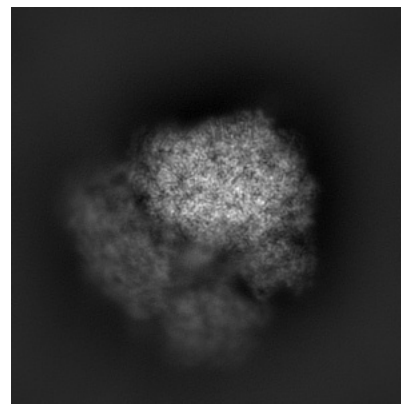
#### 6.1.1 Primary map



X

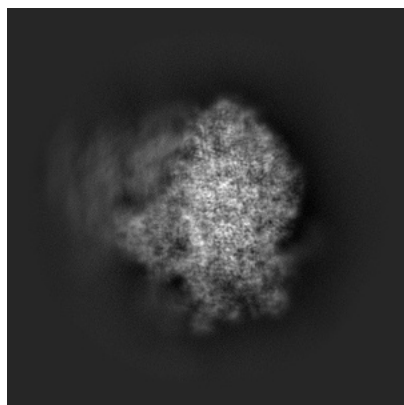


Y

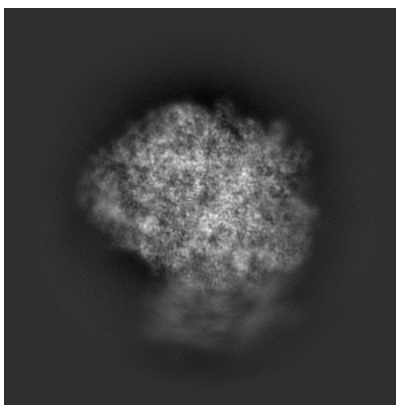


Z

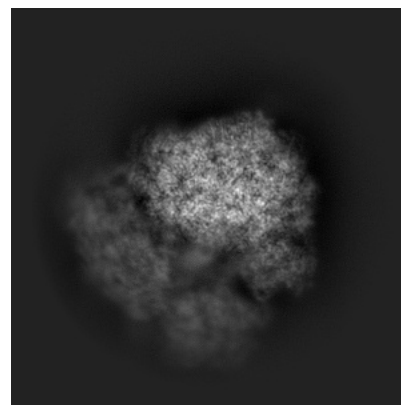
#### 6.1.2 Raw map



X



Y

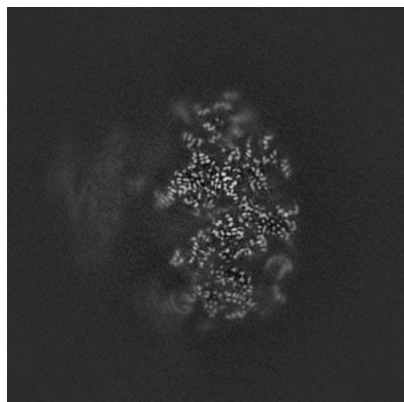


Z

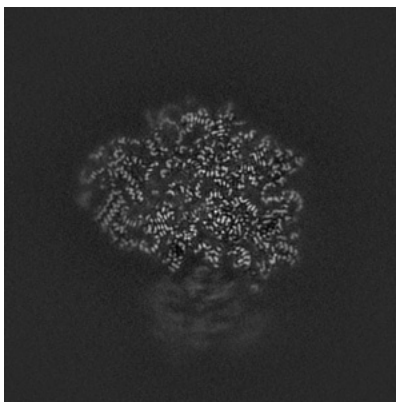
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

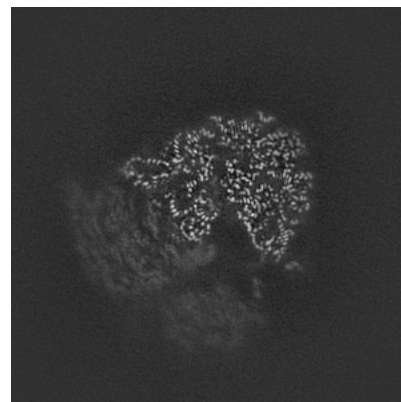
### 6.2.1 Primary map



X Index: 192

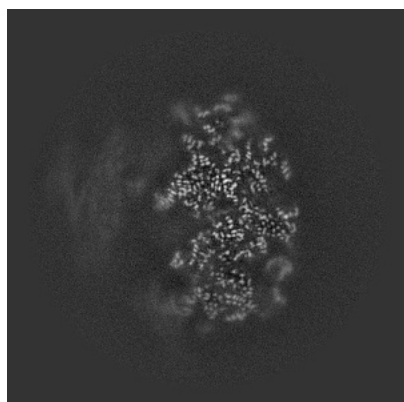


Y Index: 192

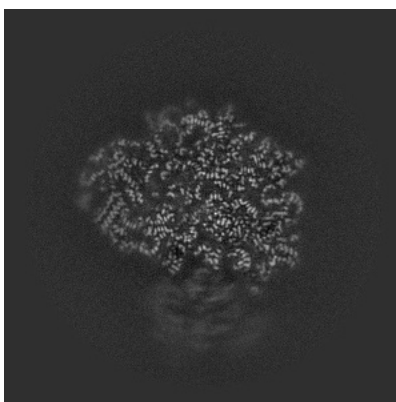


Z Index: 192

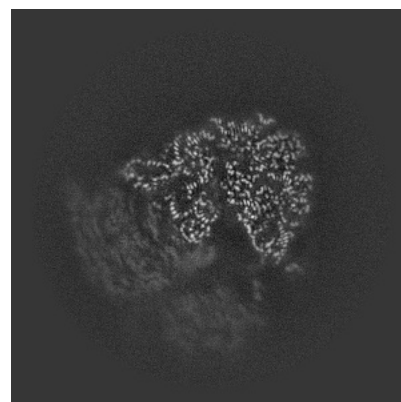
### 6.2.2 Raw map



X Index: 192



Y Index: 192

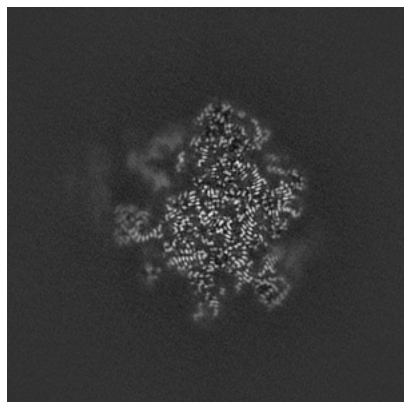


Z Index: 192

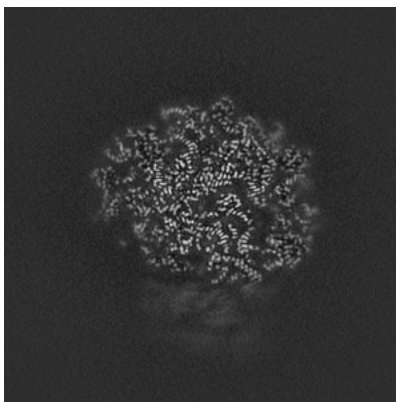
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

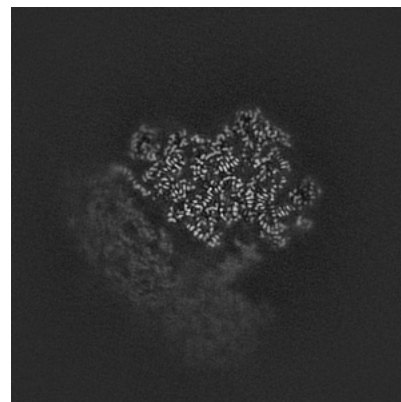
### 6.3.1 Primary map



X Index: 235

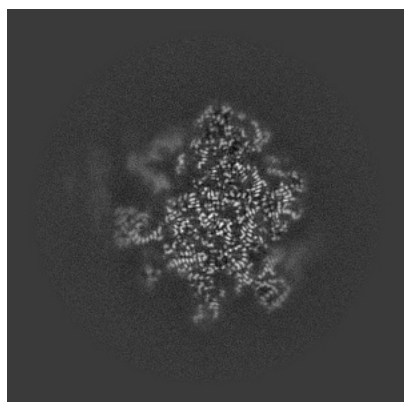


Y Index: 206

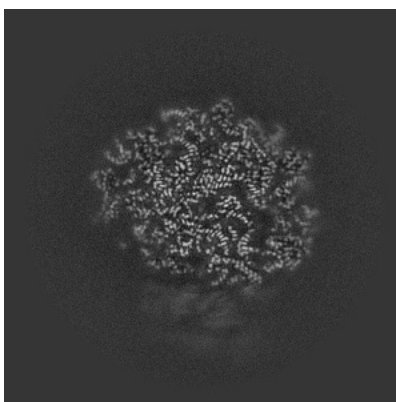


Z Index: 210

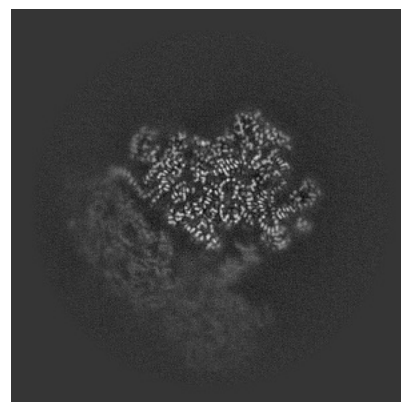
### 6.3.2 Raw map



X Index: 235



Y Index: 206



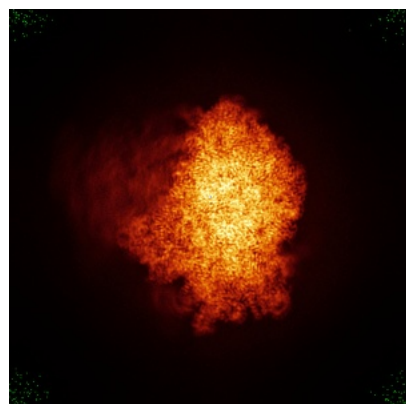
Z Index: 209

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

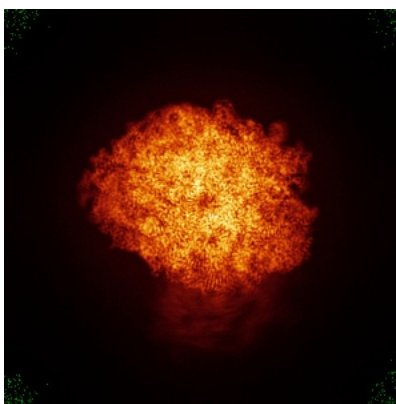


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

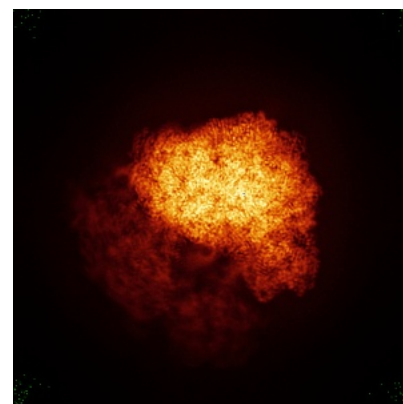
### 6.4.1 Primary map



X

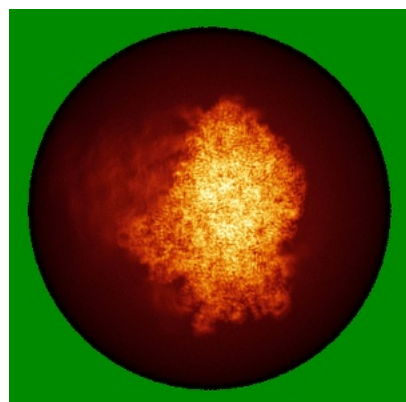


Y

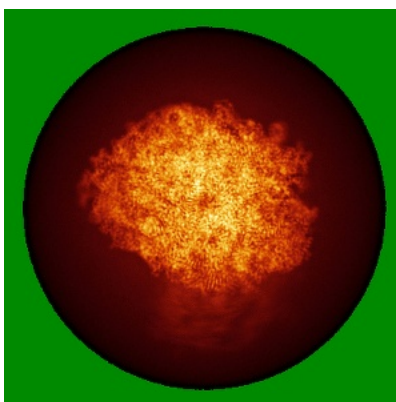


Z

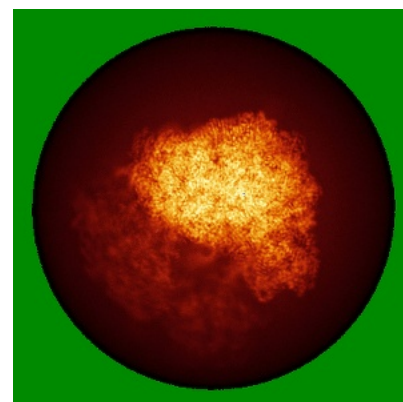
### 6.4.2 Raw map



X



Y

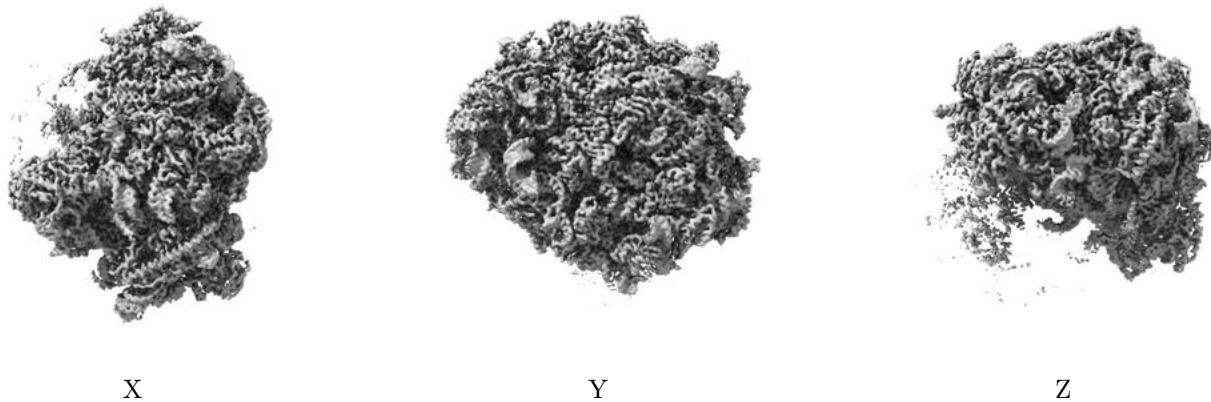


Z

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.

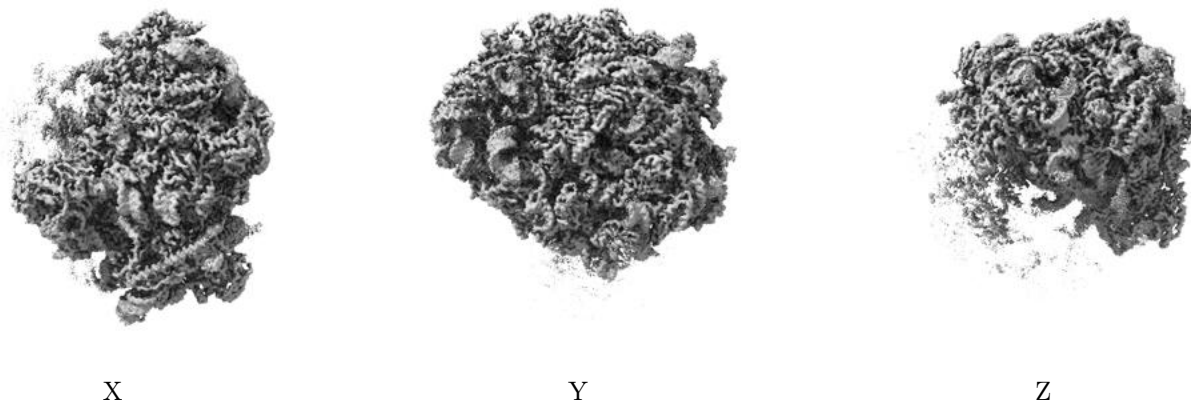
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 4.0. 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.

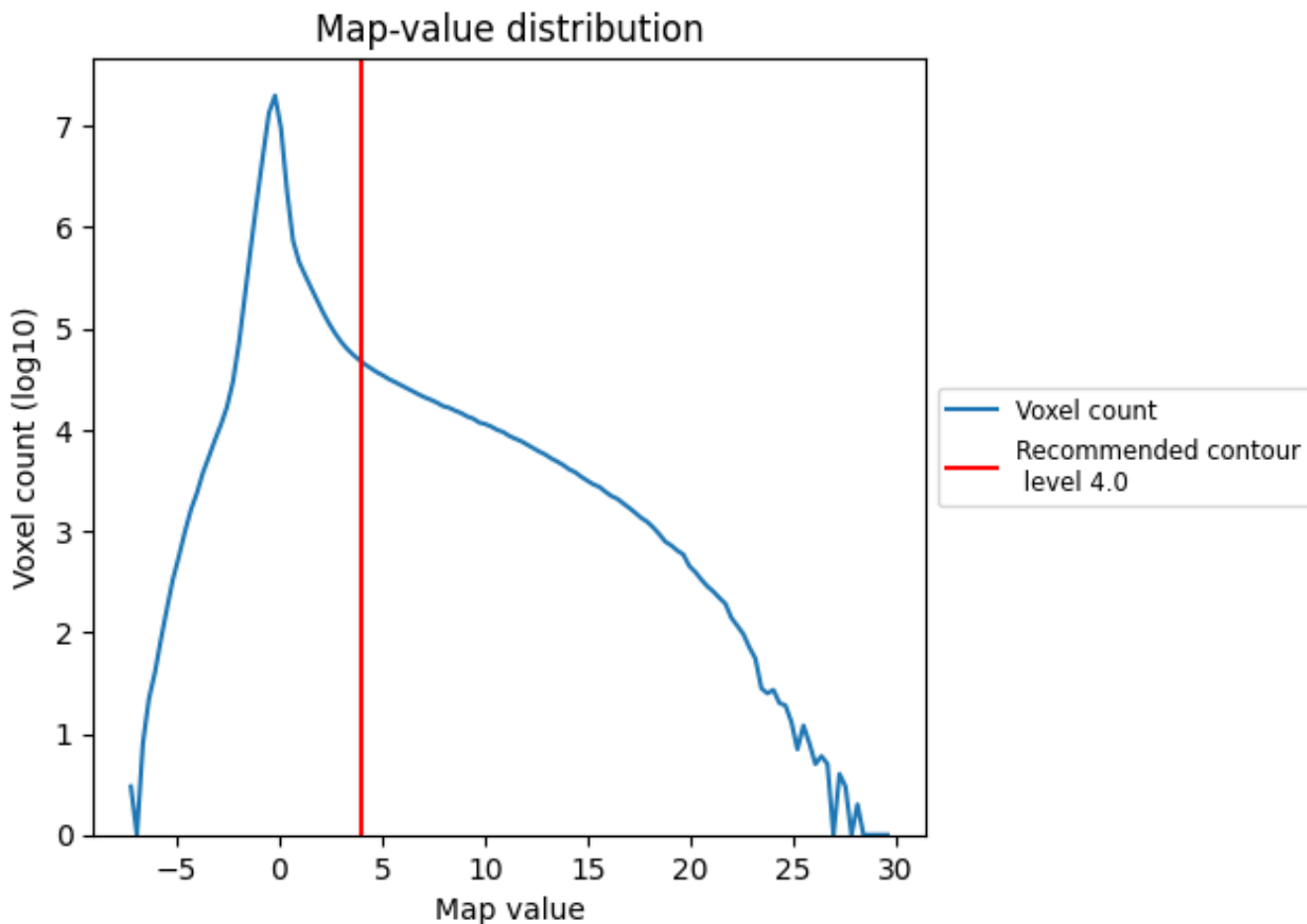
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

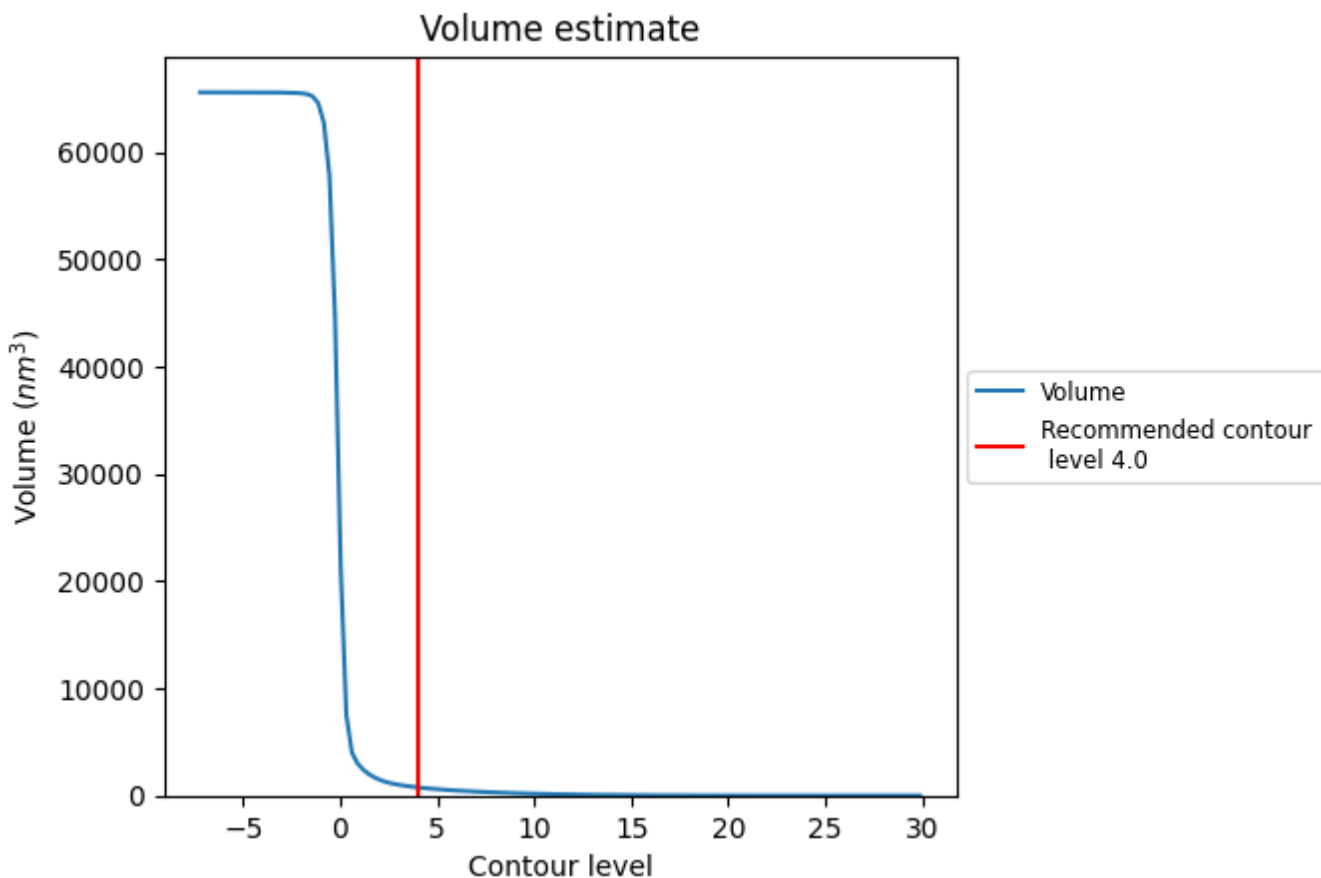
This section contains the results of statistical analysis of the map.

### 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.

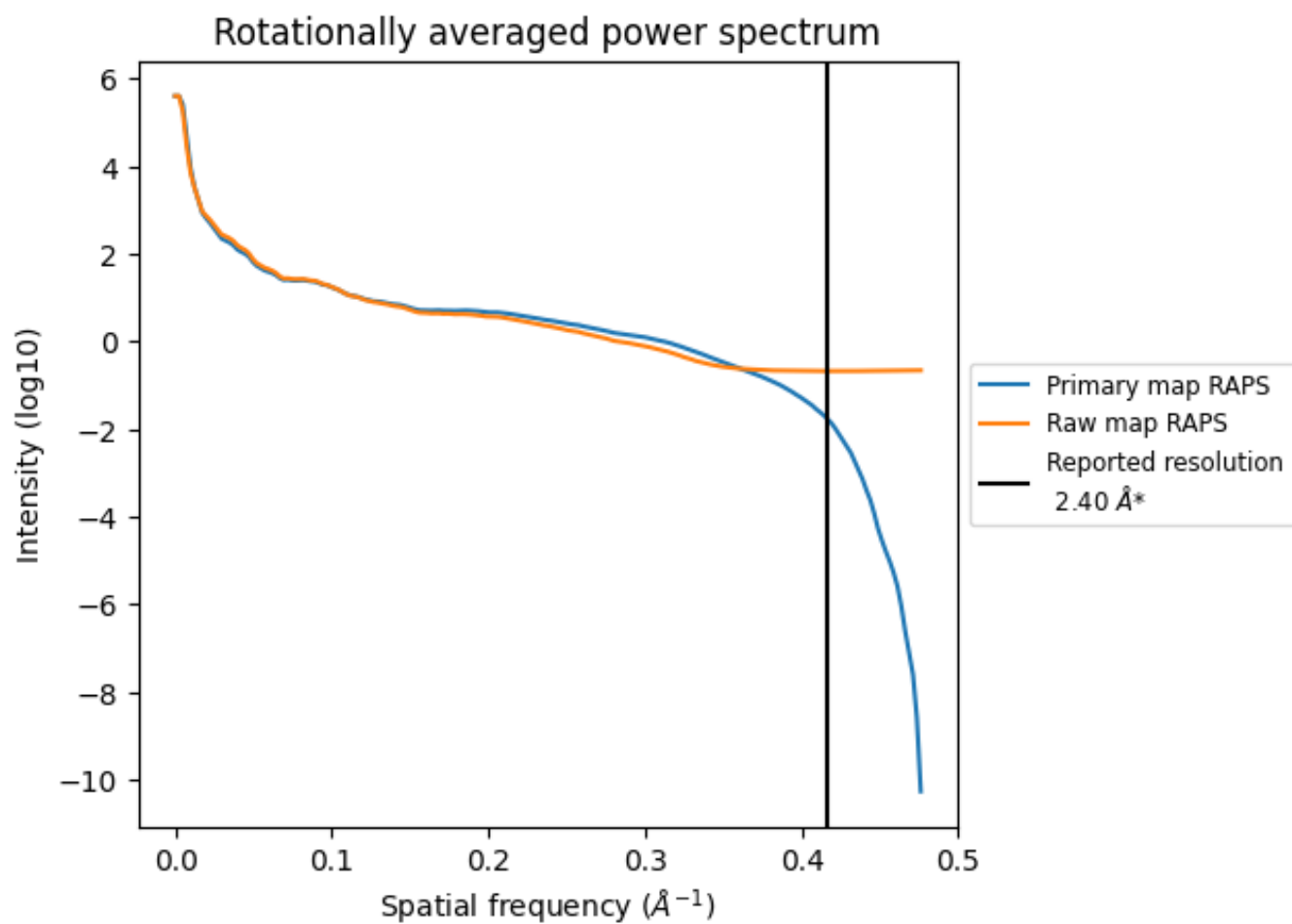
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 761  $\text{nm}^3$ ; this corresponds to an approximate mass of 688 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](#)

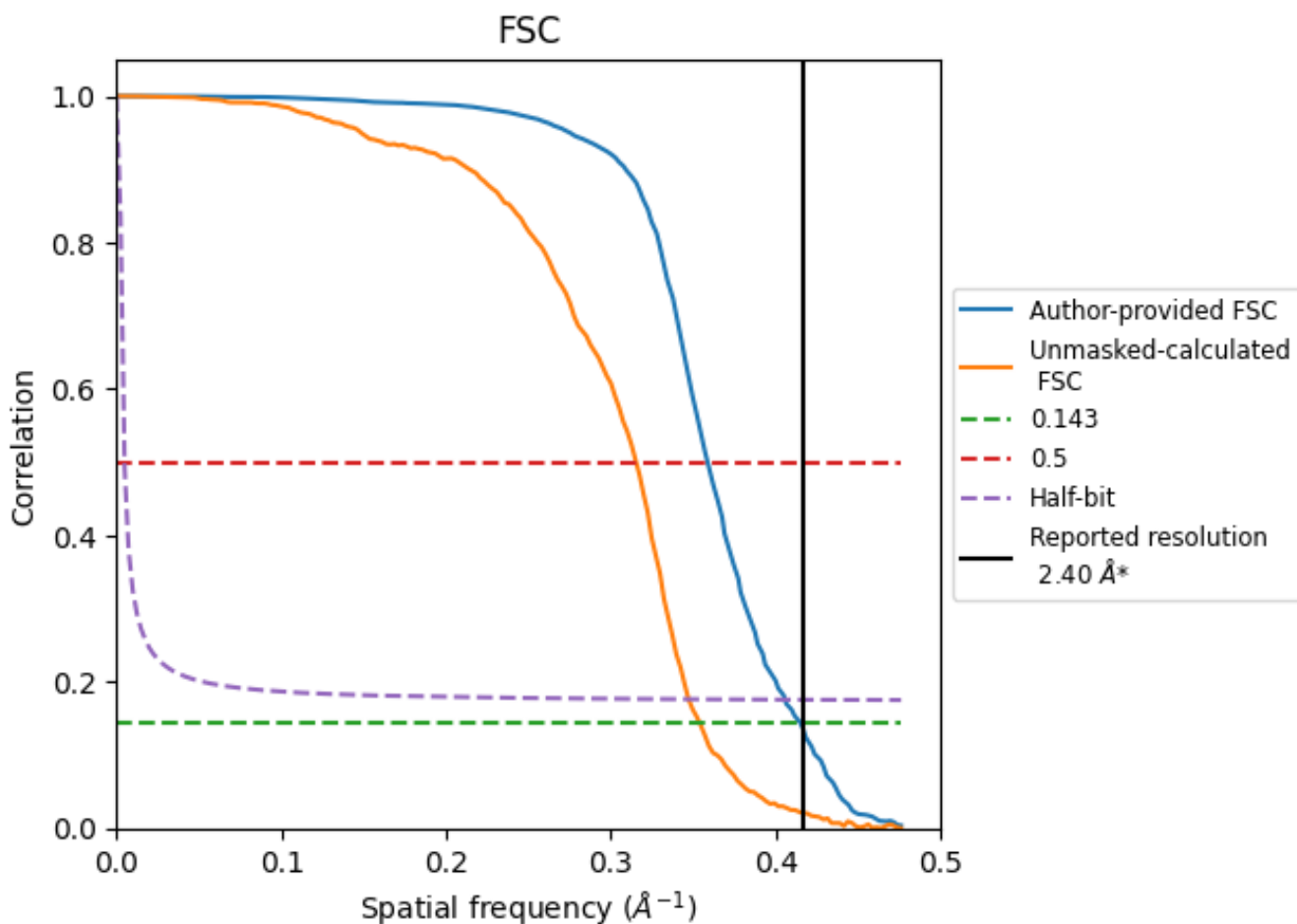


\*Reported resolution corresponds to spatial frequency of 0.417 Å<sup>-1</sup>

## 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 0.417  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

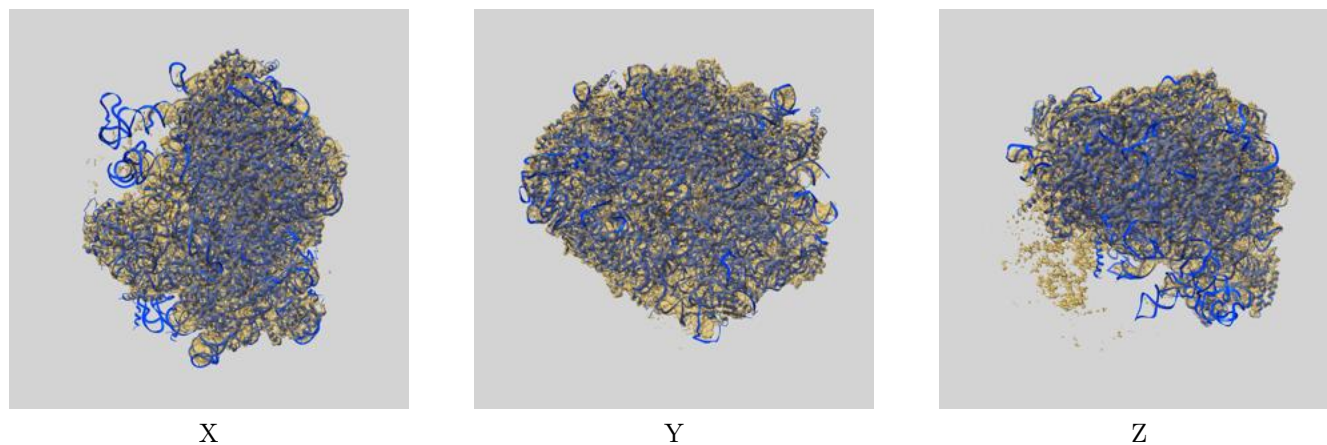
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.40	-	-
Author-provided FSC curve	2.41	2.79	2.46
Unmasked-calculated*	2.82	3.17	2.88

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 2.82 differs from the reported value 2.4 by more than 10 %

## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-26034 and PDB model 7TOP. Per-residue inclusion information can be found in section 3 on page 13.

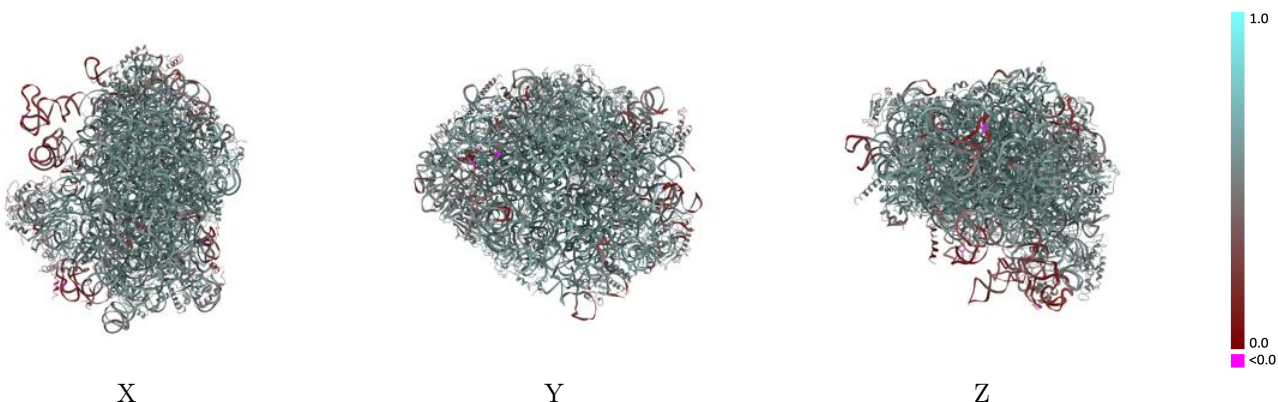
### 9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 4.0 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.

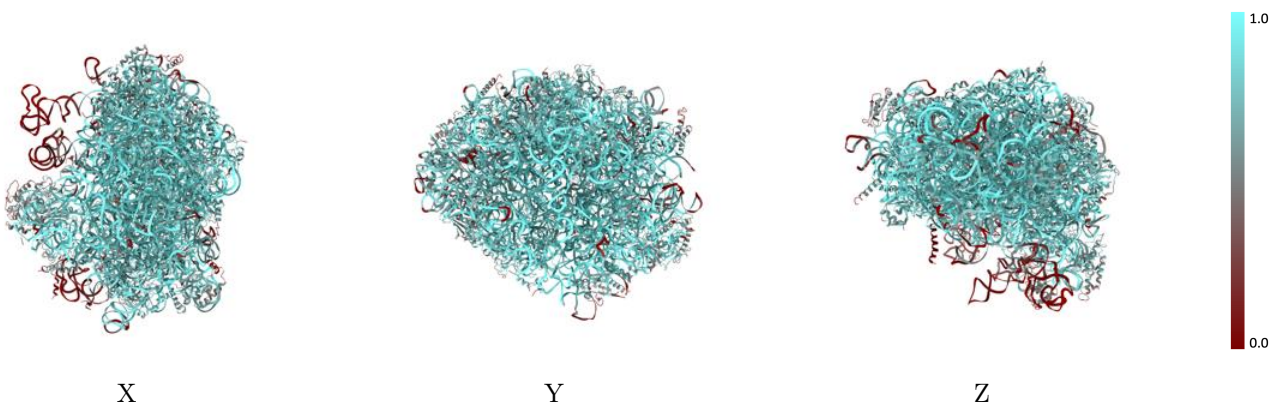


## 9.2 Q-score mapped to coordinate model [i](#)



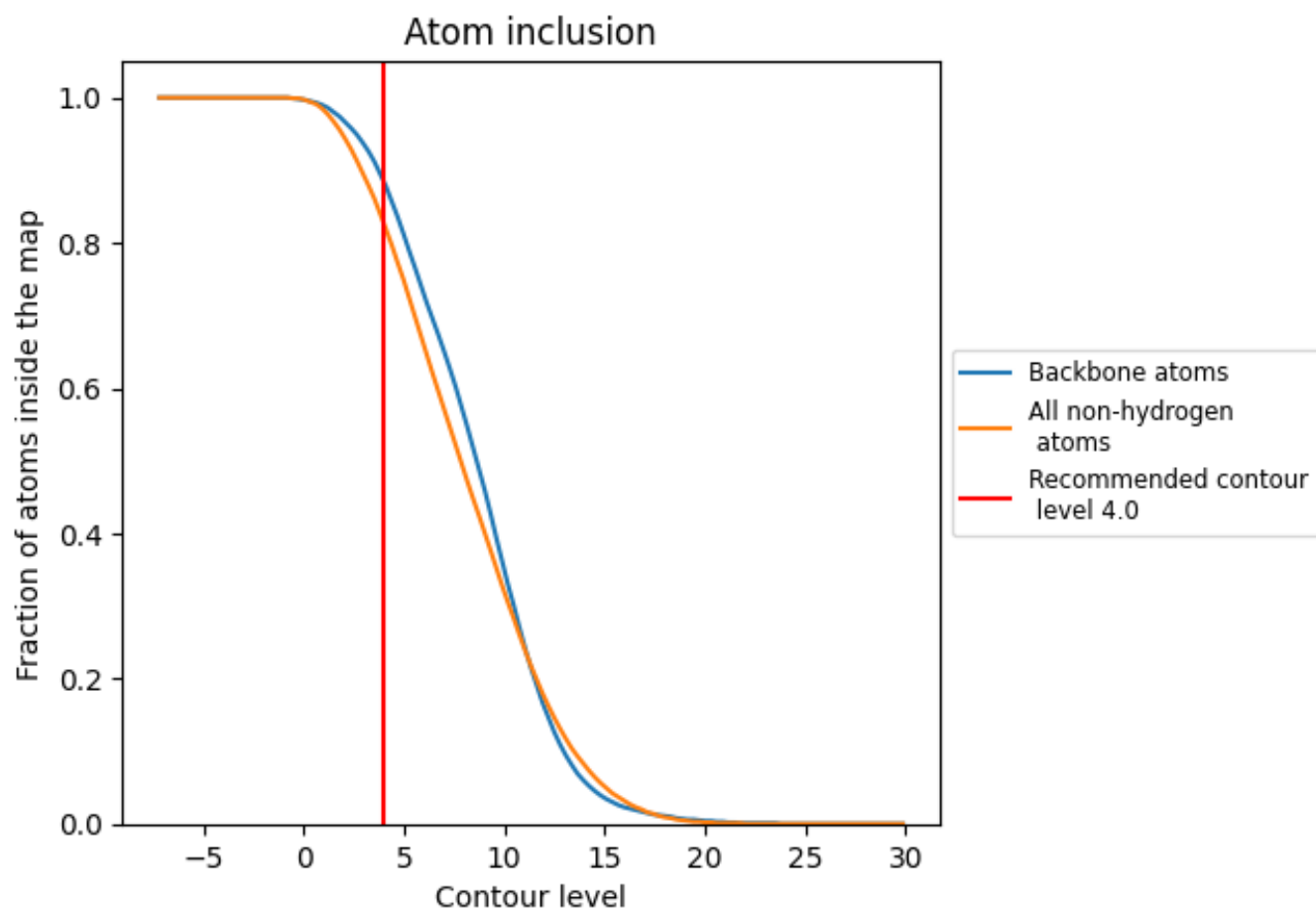
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (4.0).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 83% 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 (4.0) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8260	 0.5520
A25S	 0.8870	 0.5560
A58S	 0.9480	 0.5900
A5S	 0.9430	 0.5710
AL02	 0.8730	 0.5930
AL03	 0.8380	 0.5810
AL04	 0.7880	 0.5620
AL05	 0.6140	 0.5000
AL06	 0.6130	 0.5260
AL07	 0.7890	 0.5680
AL08	 0.6760	 0.5210
AL09	 0.6650	 0.5210
AL10	 0.7430	 0.5410
AL11	 0.4880	 0.4430
AL12	 0.0000	 0.0980
AL13	 0.7340	 0.5530
AL14	 0.6980	 0.5510
AL15	 0.8970	 0.6030
AL16	 0.8380	 0.5850
AL17	 0.7520	 0.5300
AL18	 0.8210	 0.5790
AL19	 0.8120	 0.5740
AL20	 0.7630	 0.5580
AL21	 0.7960	 0.5670
AL22	 0.5010	 0.4920
AL23	 0.7940	 0.5830
AL24	 0.7880	 0.5670
AL25	 0.7900	 0.5730
AL26	 0.7660	 0.5670
AL27	 0.7110	 0.5310
AL28	 0.8320	 0.5760
AL29	 0.7540	 0.5480
AL30	 0.7280	 0.5340
AL31	 0.7740	 0.5620
AL32	 0.8090	 0.5890



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Chain	Atom inclusion	Q-score
AL33	 0.8470	 0.5960
AL34	 0.7780	 0.5650
AL35	 0.7630	 0.5490
AL36	 0.6700	 0.5200
AL37	 0.9020	 0.5970
AL38	 0.5960	 0.5180
AL39	 0.8700	 0.5810
AL40	 0.0620	 0.4820
AL41	 0.0140	 0.2160
AL42	 0.7440	 0.5440
AL43	 0.8070	 0.5680
ALP0	 0.0000	 0.2570
APTN	 0.2810	 0.3190
PR	 0.4110	 0.5170