



## wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 04:45 PM UTC

PDB ID : 7TOP / pdb\_00007top  
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 wwPDB EM Validation Summary 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:

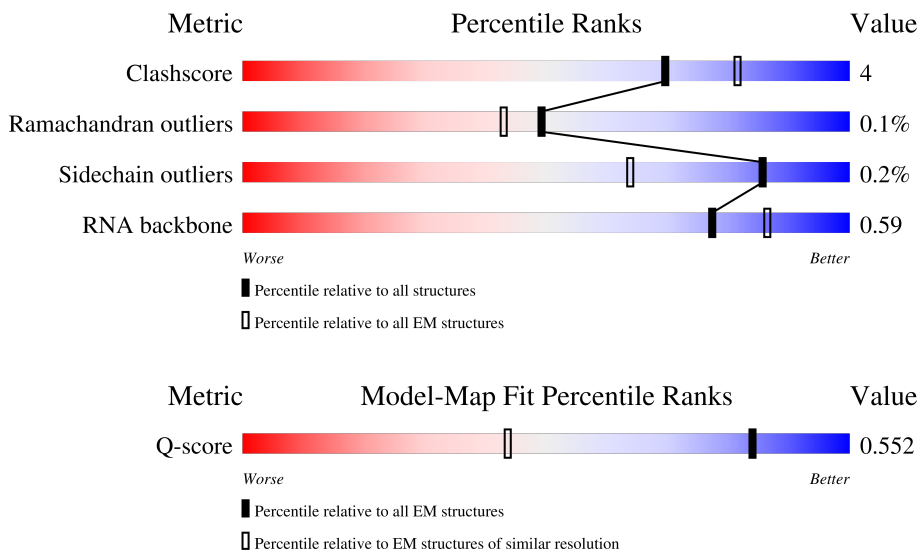
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins)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

# 1 Overall quality at a glance

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

The reported resolution of this entry is 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	5628 ( 1.90 - 2.90 )

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	 7% 81% 13% 6%
2	A58S	158	 1% 85% 15%
3	A5S	121	 92% 8%

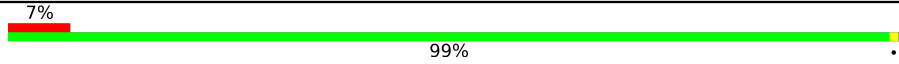
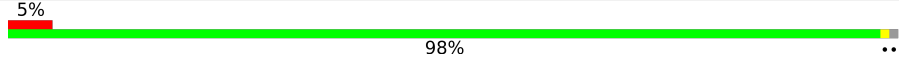
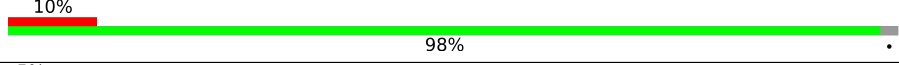
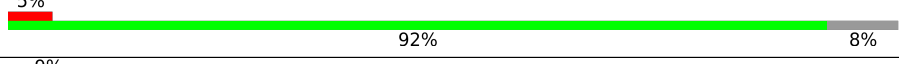
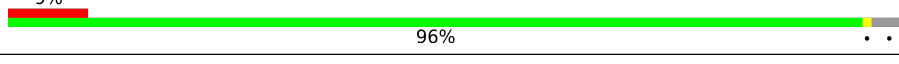
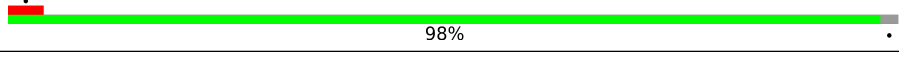
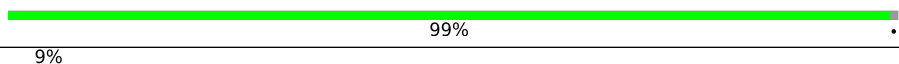
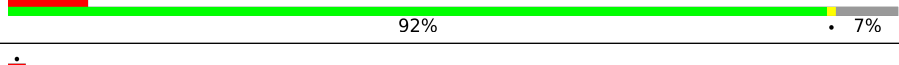
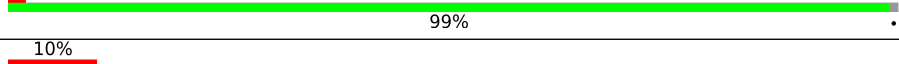
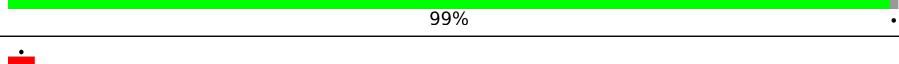
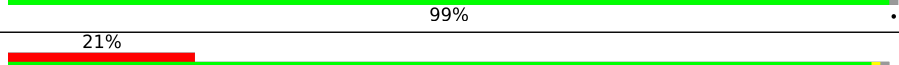
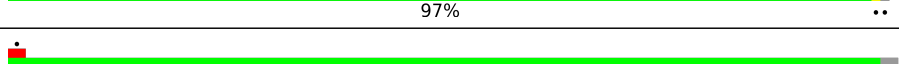
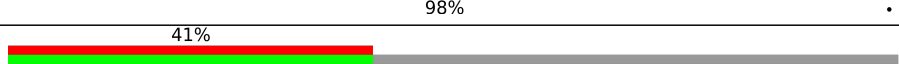
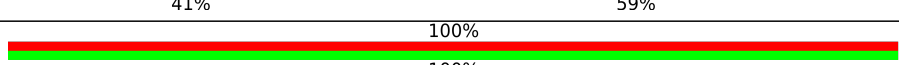
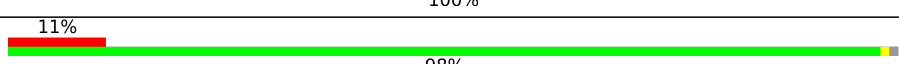
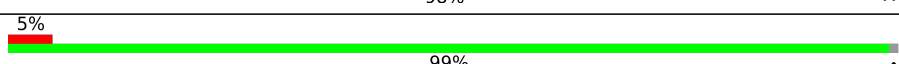
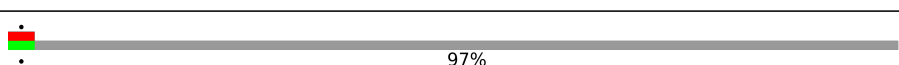
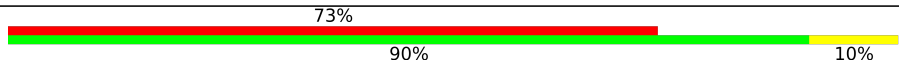
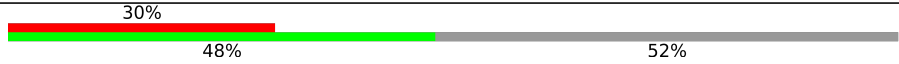

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Mol	Chain	Length	Quality of chain
4	AL02	254	99%
5	AL03	387	99%
6	AL04	362	99%
7	AL05	297	18% 100%
8	AL06	176	13% 88% 11%
9	AL07	244	9% 91% 9%
10	AL08	256	13% 91% 9%
11	AL09	191	7% 99%
12	AL10	221	9% 95% 5%
13	AL11	174	34% 97%
14	AL12	155	8% 8% 92%
15	AL13	199	12% 95%
16	AL14	138	6% 99%
17	AL15	204	100%
18	AL16	199	98%
19	AL17	184	17% 99%
20	AL18	186	99%
21	AL19	189	5% 81% 18%
22	AL20	172	5% 100%
23	AL21	160	6% 99%
24	AL22	121	24% 83% 17%
25	AL23	137	99%
26	AL24	155	41% 59%
27	AL25	142	85% 15%
28	AL26	127	99%

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Mol	Chain	Length	Quality of chain
29	AL27	136	 7% 99%
30	AL28	149	 5% 98%
31	AL29	59	 10% 98%
32	AL30	105	 5% 92% 8%
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% 90% 10%
48	PR	40	 30% 48% 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		

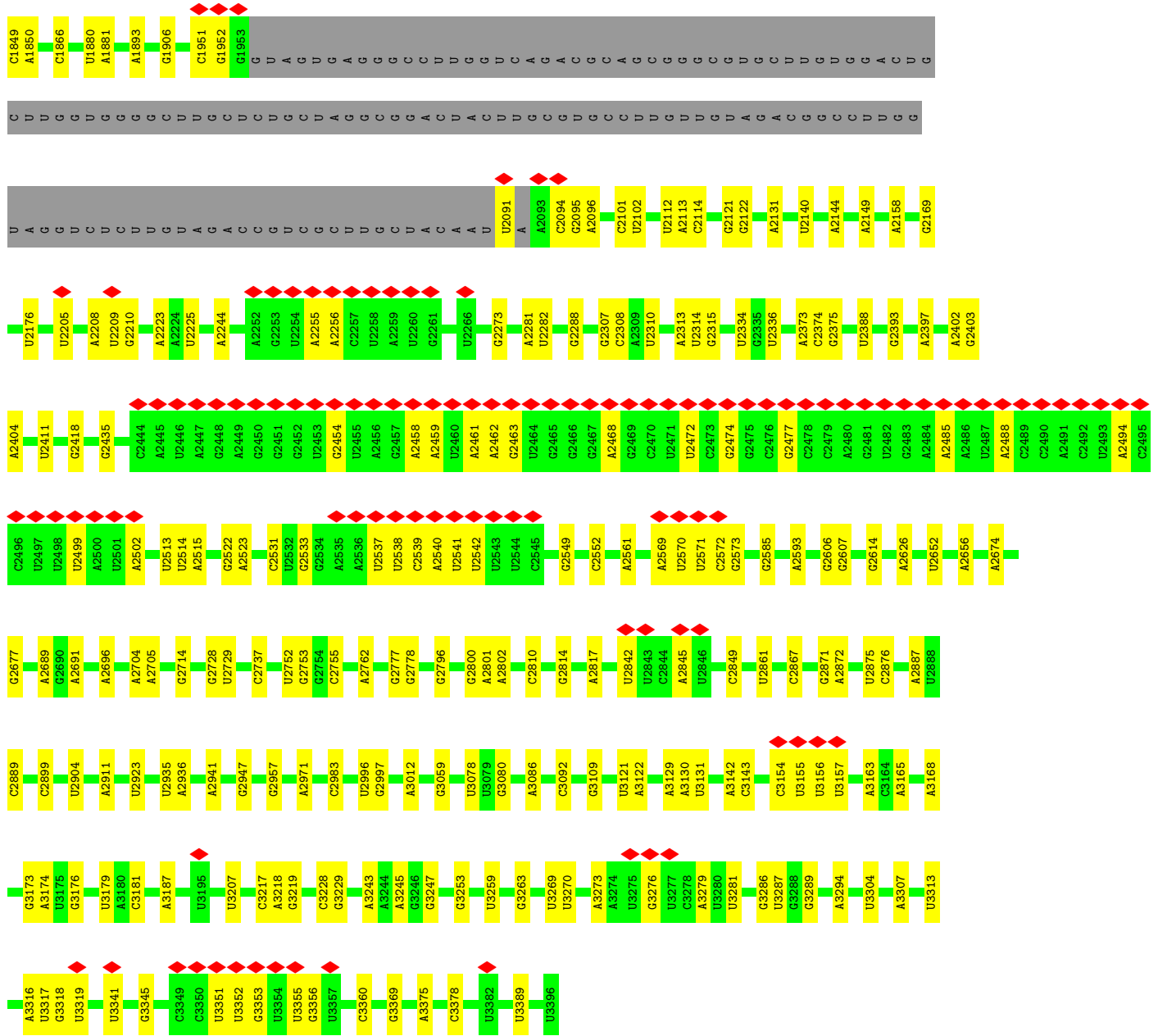
- Molecule 48 is a protein called PR20.

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

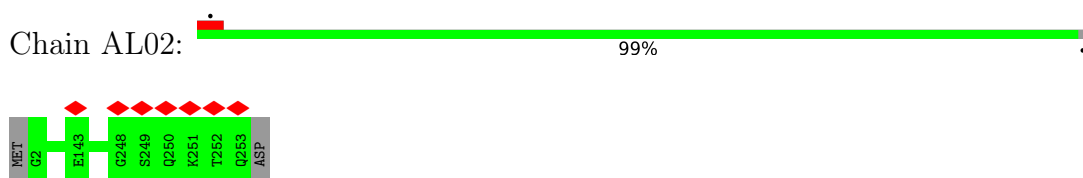
- Molecule 49 is ZINC ION (CCD ID: ZN) (formula: Zn).

<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

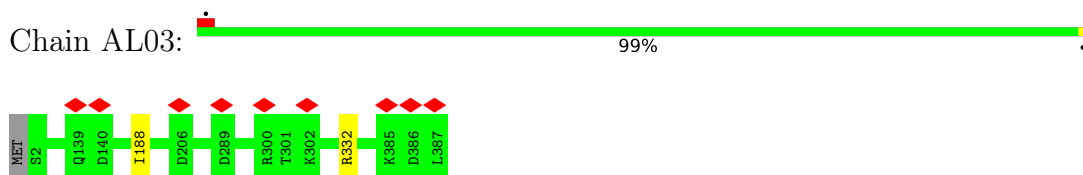




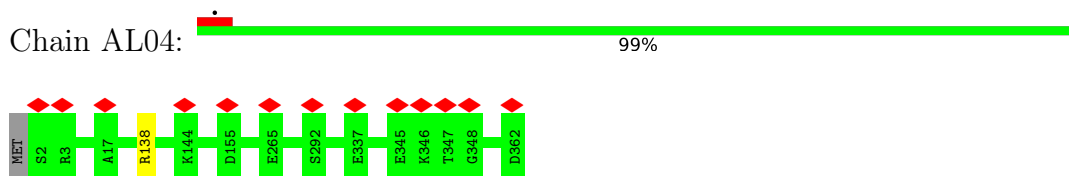
- Molecule 4: 60S ribosomal protein L2-A



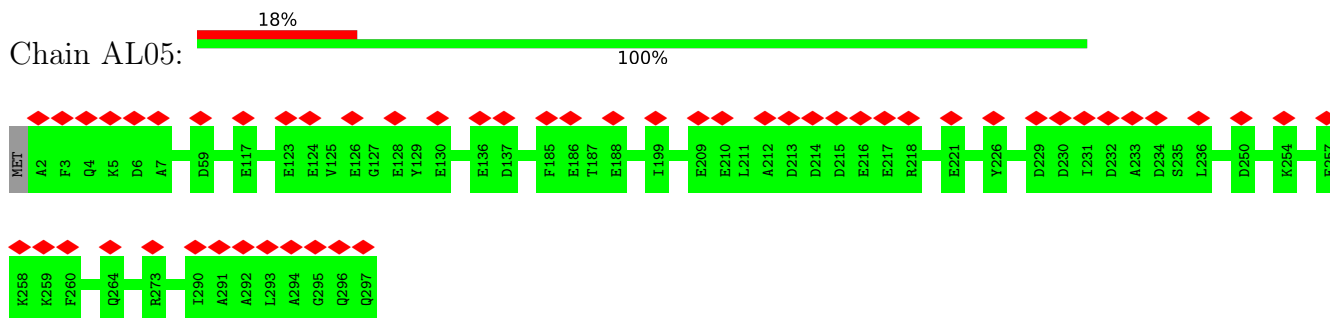
- Molecule 5: RPL3 isoform 1



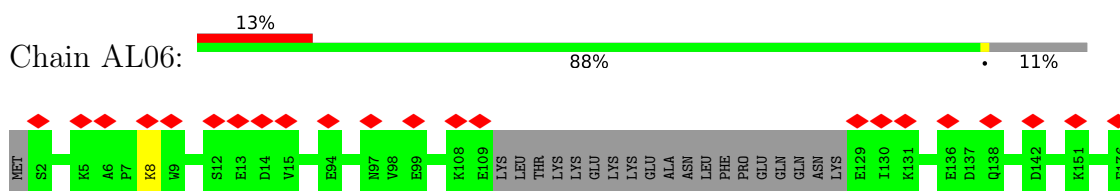
- Molecule 6: RPL4A isoform 1



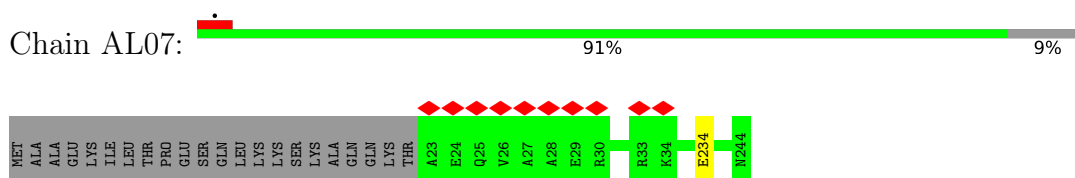
- Molecule 7: RPL5 isoform 1



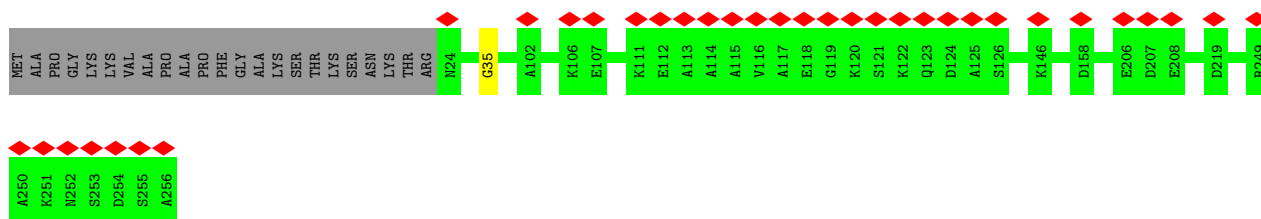
- Molecule 8: 60S ribosomal protein L6-A



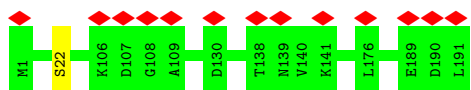
- Molecule 9: 60S ribosomal protein L7-A



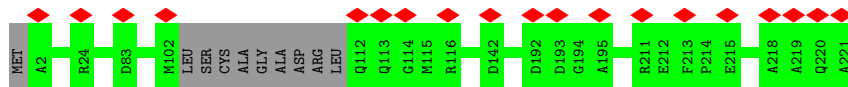
- Molecule 10: 60S ribosomal protein L8-A



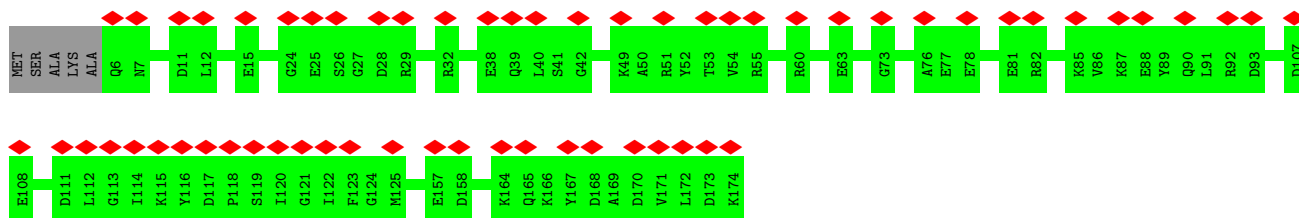
- Molecule 11: 60S ribosomal protein L9-A



- Molecule 12: RPL10 isoform 1



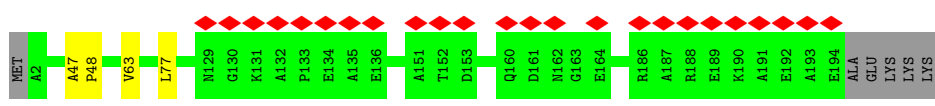
- Molecule 13: RPL11A isoform 1



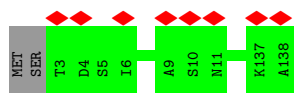
- Molecule 14: Ribosomal protein L12



- Molecule 15: 60S ribosomal protein L13-A



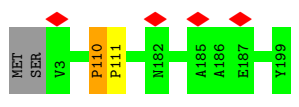
• Molecule 16: 60S ribosomal protein L14-A



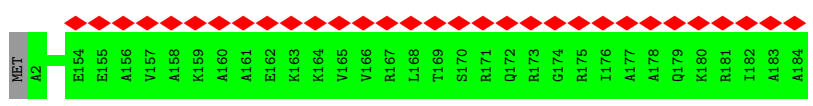
• Molecule 17: 60S ribosomal protein L15-A



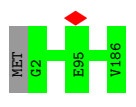
• Molecule 18: 60S ribosomal protein L16-A



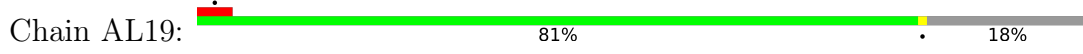
• Molecule 19: 60S ribosomal protein L17-A



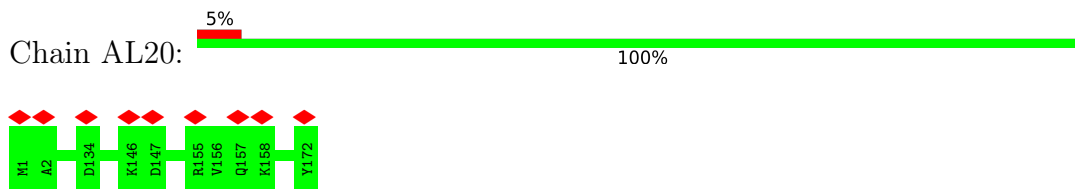
• Molecule 20: 60S ribosomal protein L18-A



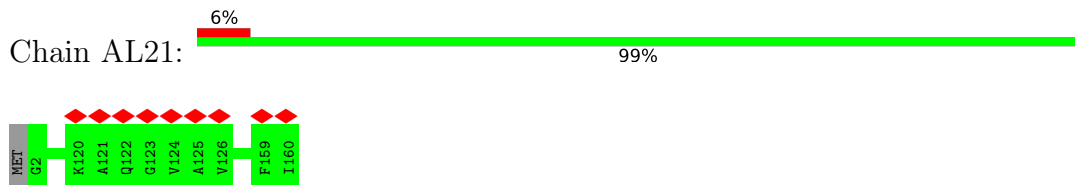
• Molecule 21: 60S ribosomal protein L19-A



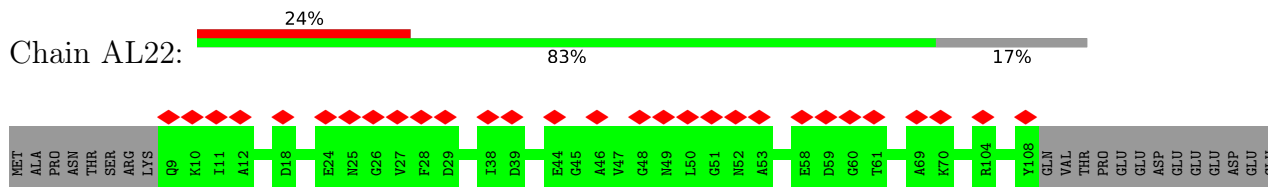
- Molecule 22: 60S ribosomal protein L20-A



- Molecule 23: 60S ribosomal protein L21-A



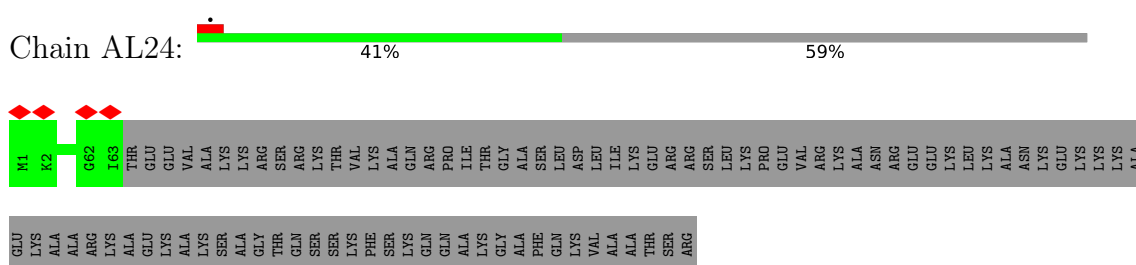
- Molecule 24: 60S ribosomal protein L22-A



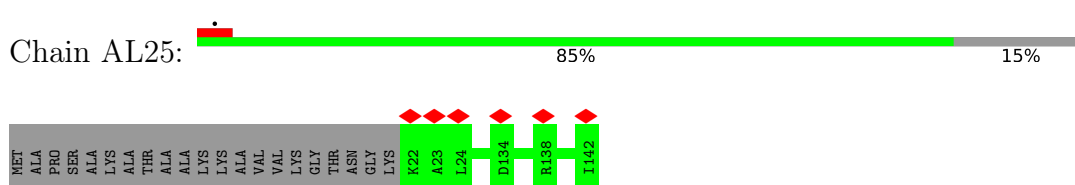
- Molecule 25: 60S ribosomal protein L23-A



- Molecule 26: RPL24A isoform 1

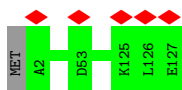


- Molecule 27: 60S ribosomal protein L25



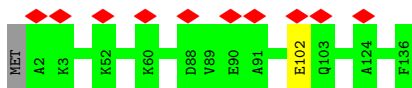
- Molecule 28: 60S ribosomal protein L26-A

Chain AL26:  99%



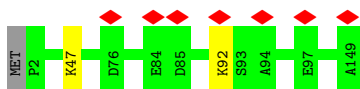
- Molecule 29: 60S ribosomal protein L27-A

Chain AL27:  99%



- Molecule 30: 60S ribosomal protein L28

Chain AL28:  98%



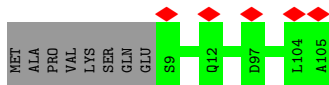
- Molecule 31: RPL29 isoform 1

Chain AL29:  98%



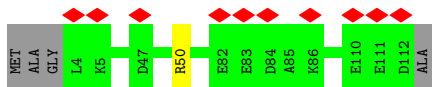
- Molecule 32: 60S ribosomal protein L30

Chain AL30:  92% 8%



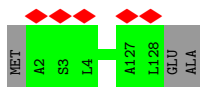
- Molecule 33: 60S ribosomal protein L31-A

Chain AL31:  96%



- Molecule 34: RPL32 isoform 1

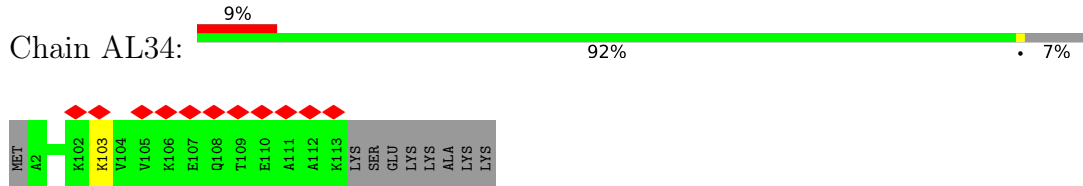
Chain AL32:  98%



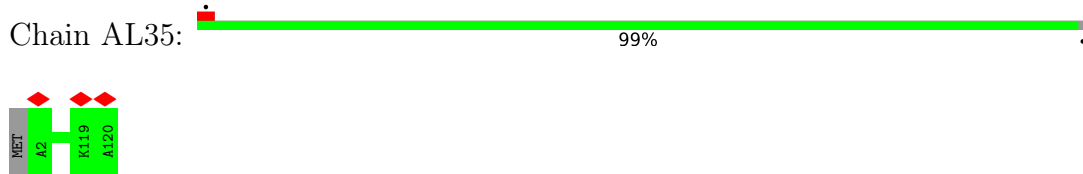
- Molecule 35: 60S ribosomal protein L33-A



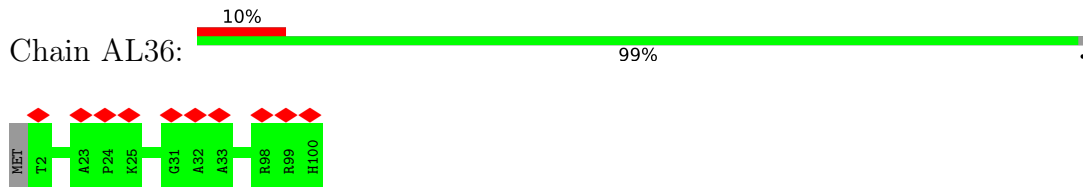
- Molecule 36: 60S ribosomal protein L34-A



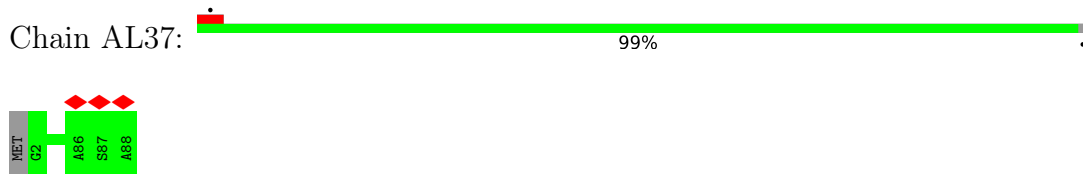
- Molecule 37: 60S ribosomal protein L35-A



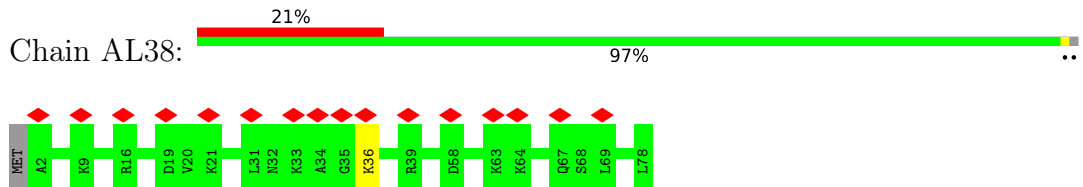
- Molecule 38: 60S ribosomal protein L36-A



- 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	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	0.08	0/76471	0.20	0/119222
2	A58S	0.07	0/3747	0.16	0/5832
3	A5S	0.06	0/2884	0.13	0/4491
4	AL02	0.13	0/1948	0.39	0/2617
5	AL03	0.13	0/3146	0.38	0/4228
6	AL04	0.15	0/2800	0.44	0/3790
7	AL05	0.14	0/2425	0.44	0/3271
8	AL06	0.14	0/1260	0.39	0/1694
9	AL07	0.14	0/1821	0.41	0/2451
10	AL08	0.16	0/1836	0.47	0/2481
11	AL09	0.16	0/1539	0.44	0/2073
12	AL10	0.13	0/1741	0.39	0/2335
13	AL11	0.18	0/1374	0.54	0/1842
15	AL13	0.15	0/1568	0.50	0/2106
16	AL14	0.12	0/1068	0.33	0/1438
17	AL15	0.14	0/1757	0.39	0/2354
18	AL16	0.12	0/1585	0.34	0/2128
19	AL17	0.12	0/1443	0.38	0/1944
20	AL18	0.13	0/1465	0.39	0/1965
21	AL19	0.11	0/1266	0.38	0/1690
22	AL20	0.14	0/1481	0.40	0/1990
23	AL21	0.14	0/1300	0.41	0/1743
24	AL22	0.15	0/812	0.41	0/1099
25	AL23	0.11	0/1018	0.33	0/1369
26	AL24	0.15	0/533	0.41	0/707
27	AL25	0.11	0/979	0.37	0/1321
28	AL26	0.14	0/1004	0.36	0/1341
29	AL27	0.17	0/1118	0.44	0/1497
30	AL28	0.16	0/1204	0.49	2/1612 (0.1%)
31	AL29	0.17	0/473	0.44	0/629
32	AL30	0.11	0/751	0.30	0/1008
33	AL31	0.13	0/890	0.38	0/1196

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
34	AL32	0.11	0/1041	0.37	0/1394
35	AL33	0.12	0/868	0.33	0/1168
36	AL34	0.13	0/890	0.37	0/1189
37	AL35	0.12	0/978	0.41	0/1301
38	AL36	0.15	0/778	0.41	0/1034
39	AL37	0.14	0/696	0.43	0/923
40	AL38	0.12	0/618	0.36	0/826
41	AL39	0.13	0/443	0.44	0/588
42	AL40	0.15	0/423	0.43	0/562
43	AL41	0.14	0/234	0.43	0/300
44	AL42	0.15	0/860	0.45	0/1136
45	AL43	0.15	0/701	0.47	0/934
46	ALP0	0.10	0/53	0.31	0/68
47	APTN	0.06	0/1836	0.14	0/2859
48	PR	0.29	0/178	0.62	0/242
All	All	0.11	0/135304	0.29	2/199988 (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

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	AL28	47	LYS	CA-C-N	5.20	131.47	121.54
30	AL28	47	LYS	C-N-CA	5.20	131.47	121.54

There are no chirality outliers.

5 of 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

## 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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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
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	APT0	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 4.

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

### 5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	AL02	250/254 (98%)	240 (96%)	10 (4%)	0	100	100
5	AL03	384/387 (99%)	371 (97%)	12 (3%)	1 (0%)	36	50
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%)	24	37
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%)	7	11
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%)	12	20
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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
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%)	49	64

5 of 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

### 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%)	86	93
6	AL04	288/289 (100%)	287 (100%)	1 (0%)	86	93
7	AL05	244/245 (100%)	244 (100%)	0	100	100
8	AL06	134/153 (88%)	133 (99%)	1 (1%)	76	88
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%)	73	86
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%)	65	82
34	AL32	109/111 (98%)	109 (100%)	0	100	100
35	AL33	90/91 (99%)	90 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	AL34	95/103 (92%)	94 (99%)	1 (1%)	65	82
37	AL35	104/105 (99%)	104 (100%)	0	100	100
38	AL36	81/82 (99%)	81 (100%)	0	100	100
39	AL37	70/71 (99%)	70 (100%)	0	100	100
40	AL38	68/69 (99%)	67 (98%)	1 (2%)	57	77
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%)	65	82
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%)	19 (100%)	0	100	100
All	All	5182/5699 (91%)	5174 (100%)	8 (0%)	85	94

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
44	AL42	15	LYS
40	AL38	36	LYS
33	AL31	50	ARG
30	AL28	92	LYS
36	AL34	103	LYS

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	3191/3396 (93%)	443 (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	3544/3752 (94%)	483 (13%)	30 (0%)

5 of 483 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

5 of 30 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A25S	1562	C
1	A25S	3317	U
1	A25S	2101	C
2	A58S	85	G
1	A25S	3218	A

#### 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 oligosaccharides 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

There are no chain breaks in this entry.

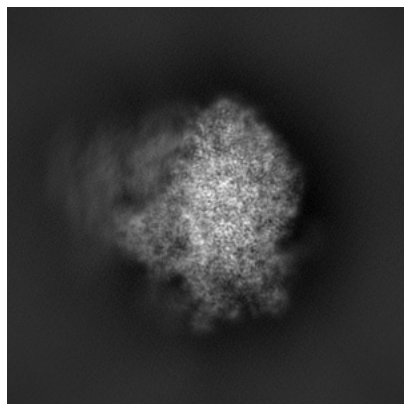
## 6 Map visualisation [i](#)

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.

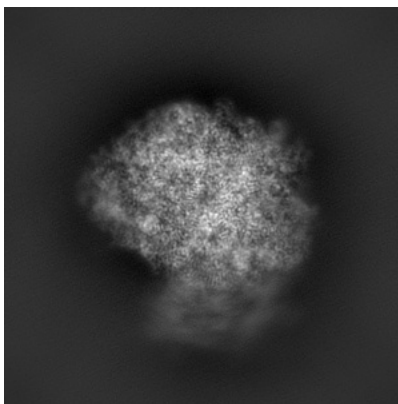
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

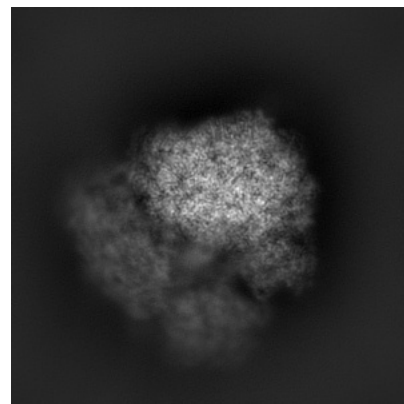
#### 6.1.1 Primary map



X

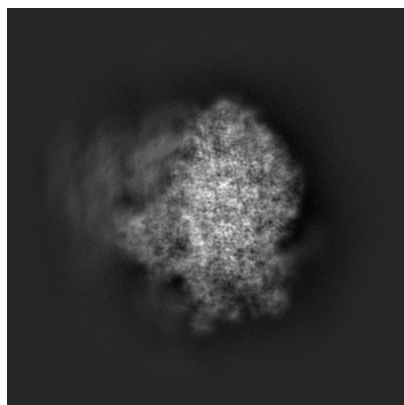


Y

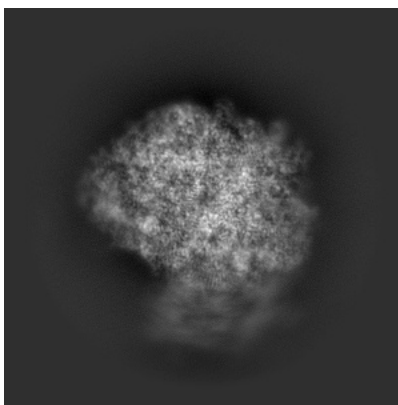


Z

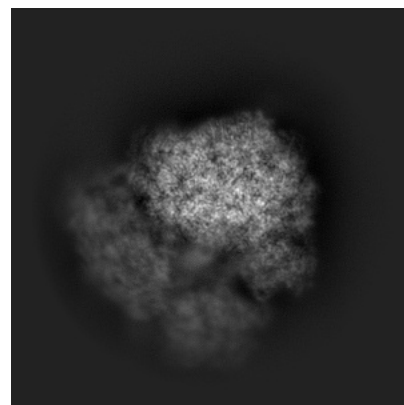
#### 6.1.2 Raw map



X



Y

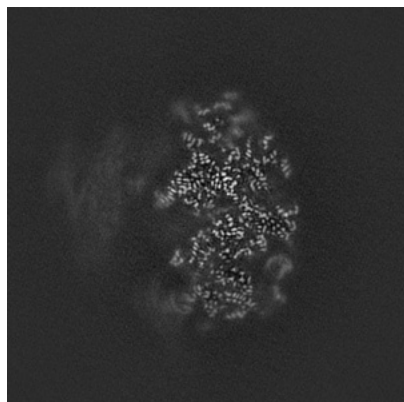


Z

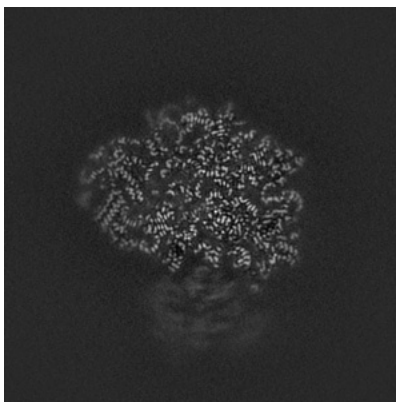
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

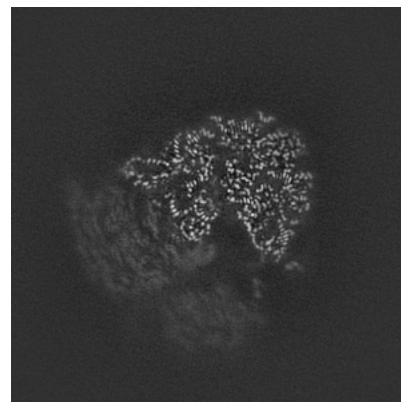
### 6.2.1 Primary map



X Index: 192

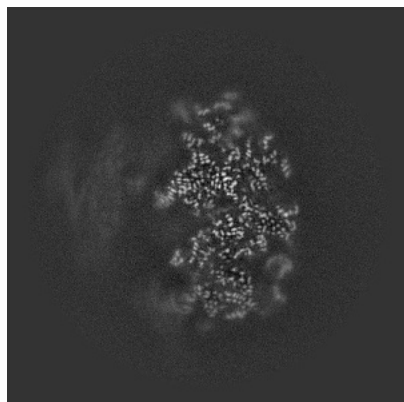


Y Index: 192

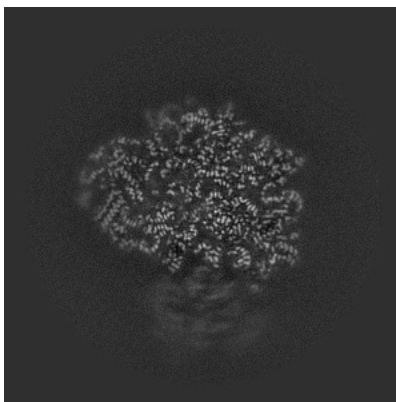


Z Index: 192

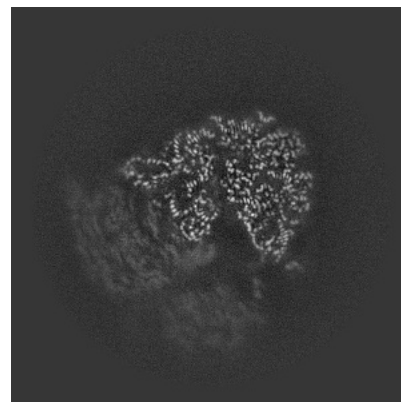
### 6.2.2 Raw map



X Index: 192



Y Index: 192

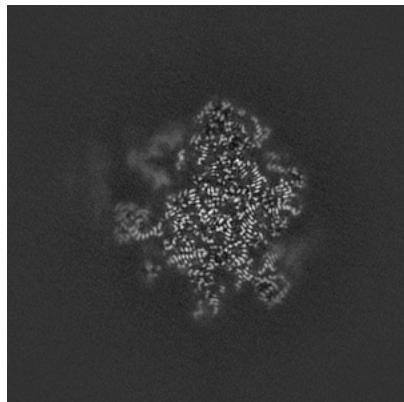


Z Index: 192

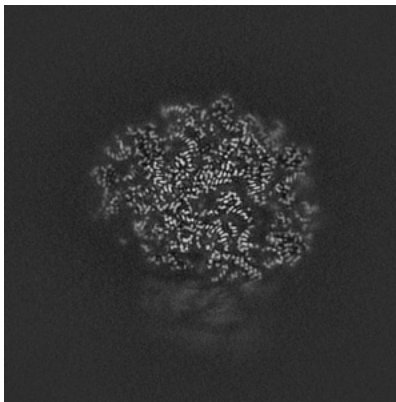
The images above show central slices of the map in three orthogonal directions.

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

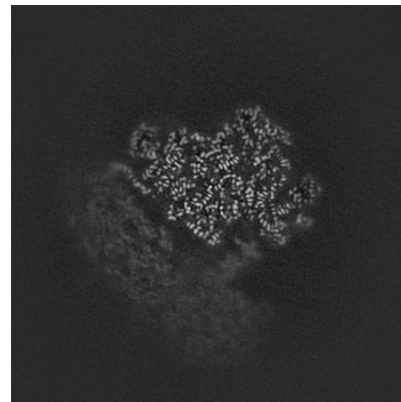
### 6.3.1 Primary map



X Index: 235

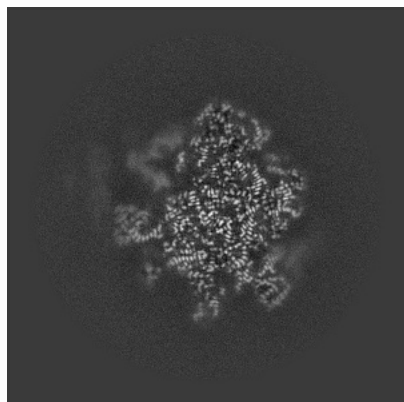


Y Index: 206

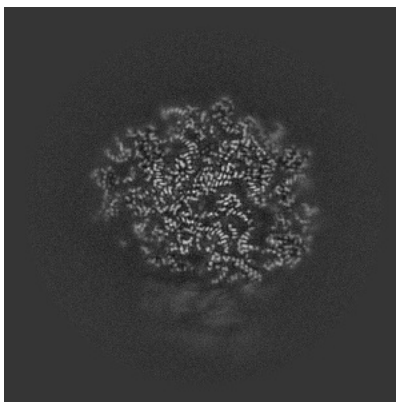


Z Index: 210

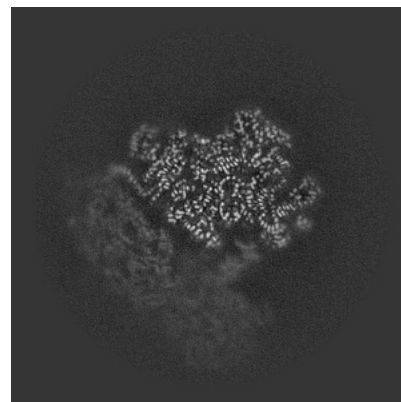
### 6.3.2 Raw map



X Index: 235



Y Index: 206

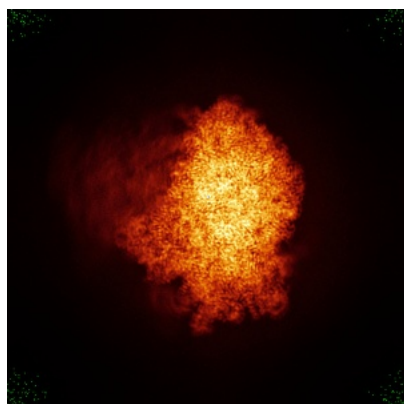


Z Index: 209

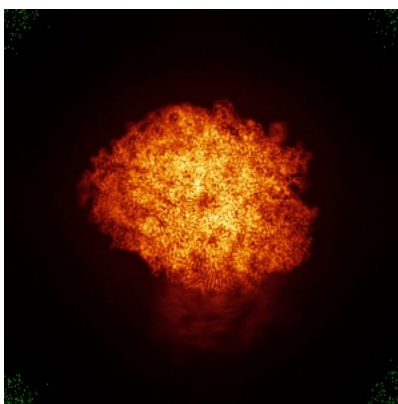
The images above show the largest variance slices of the map in three orthogonal directions.

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

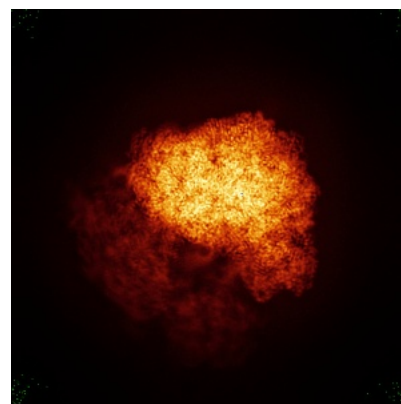
### 6.4.1 Primary map



X

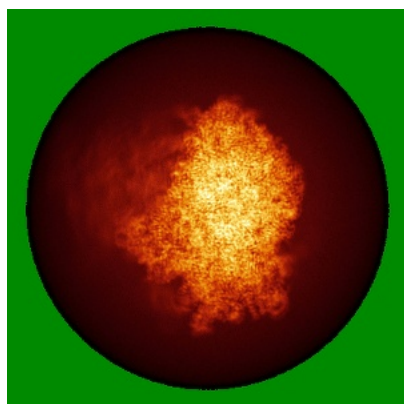


Y

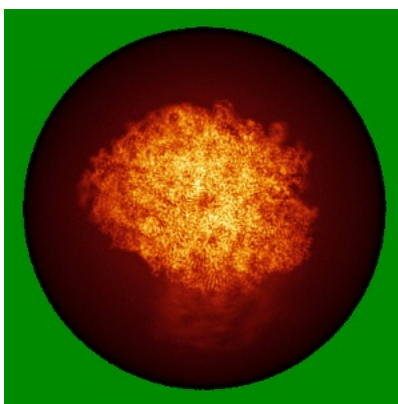


Z

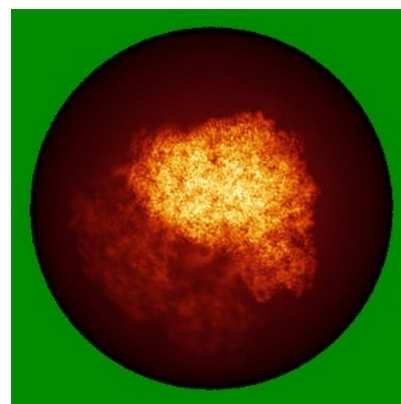
### 6.4.2 Raw map



X



Y

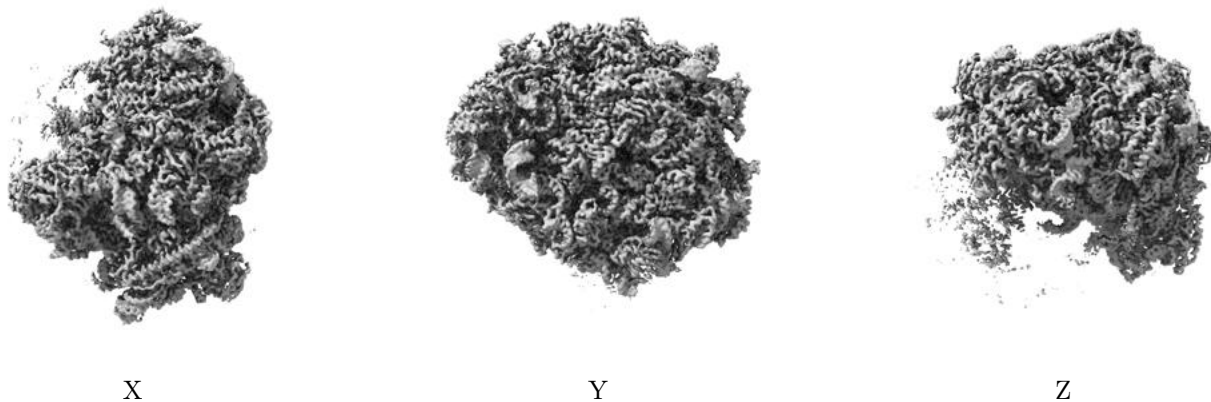


Z

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.

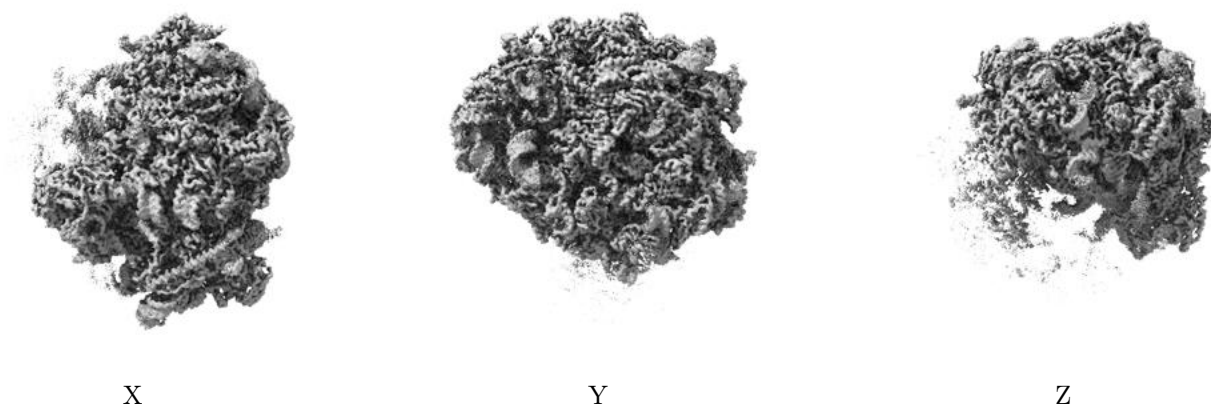
## 6.5 Orthogonal surface views [i](#)

### 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.

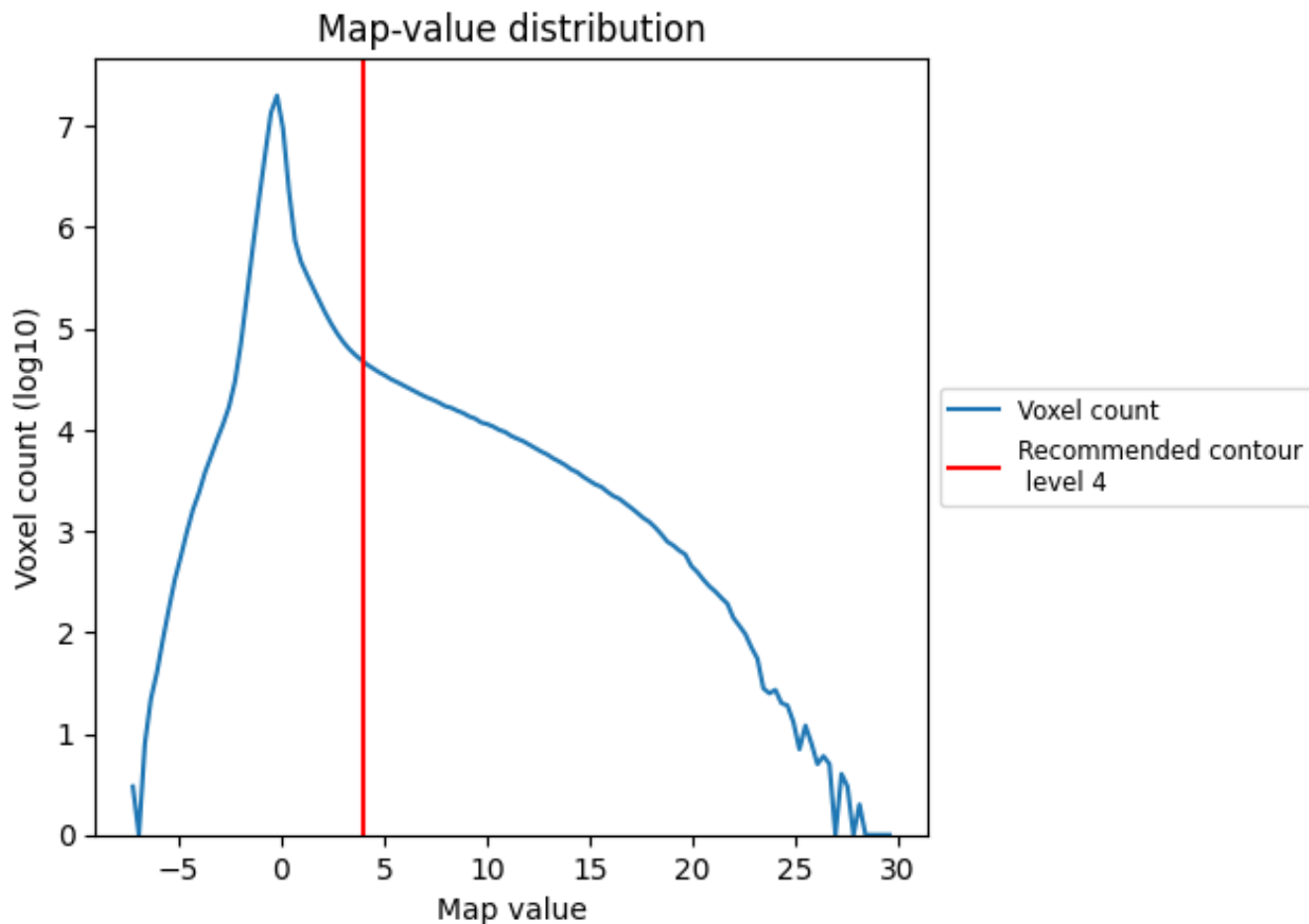
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

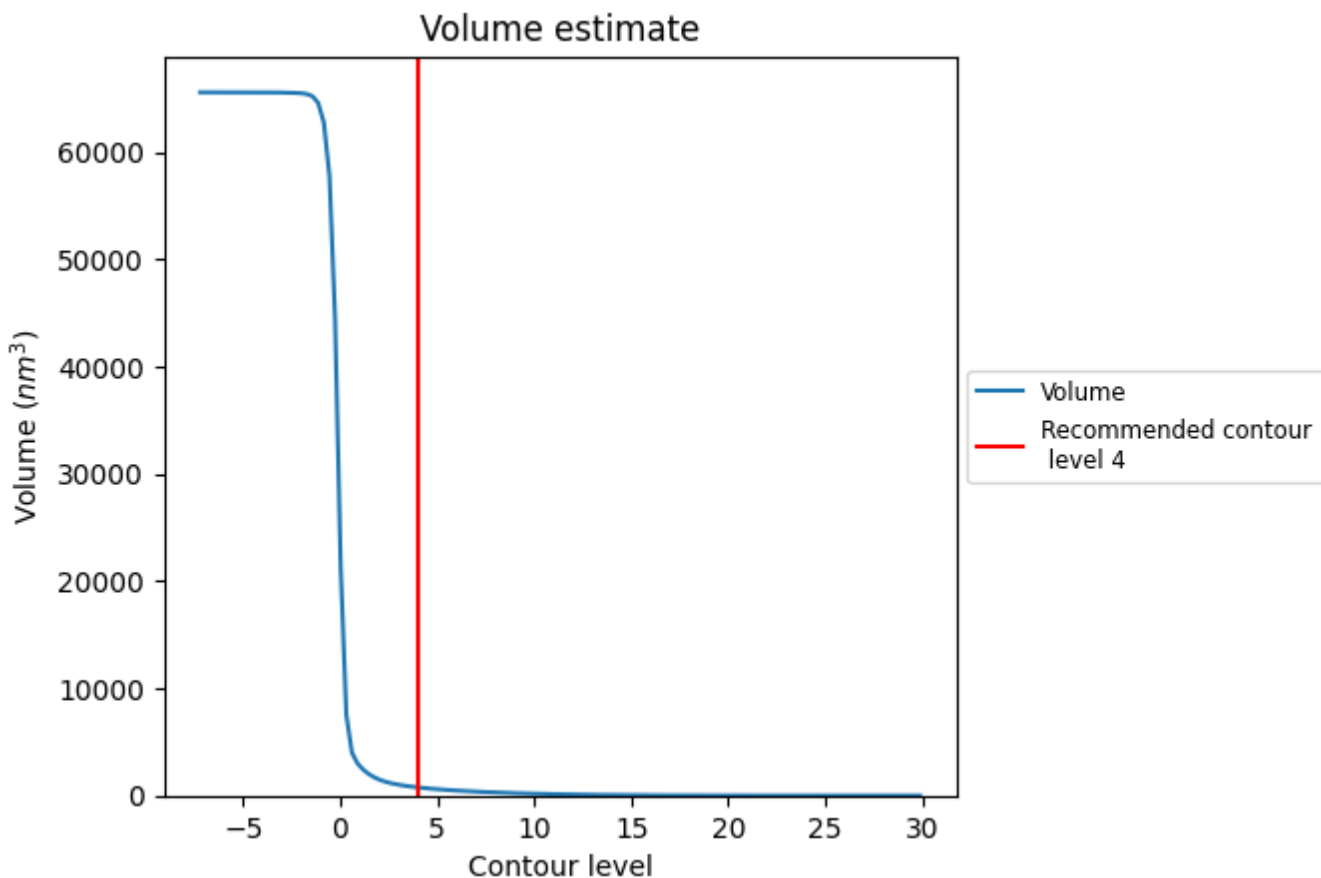
This section contains the results of statistical analysis of the map.

### 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.

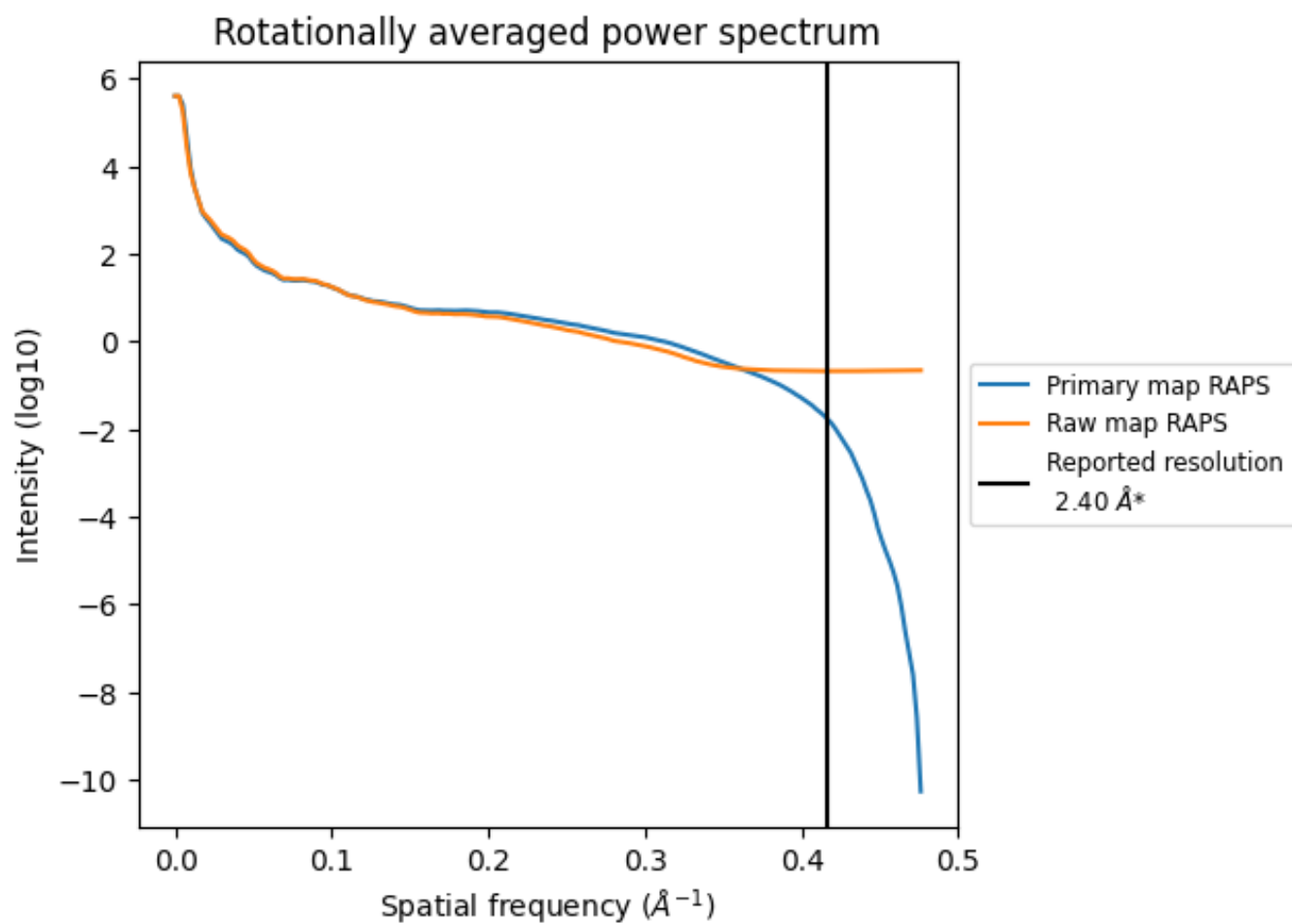
## 7.2 Volume estimate [i](#)



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](#)

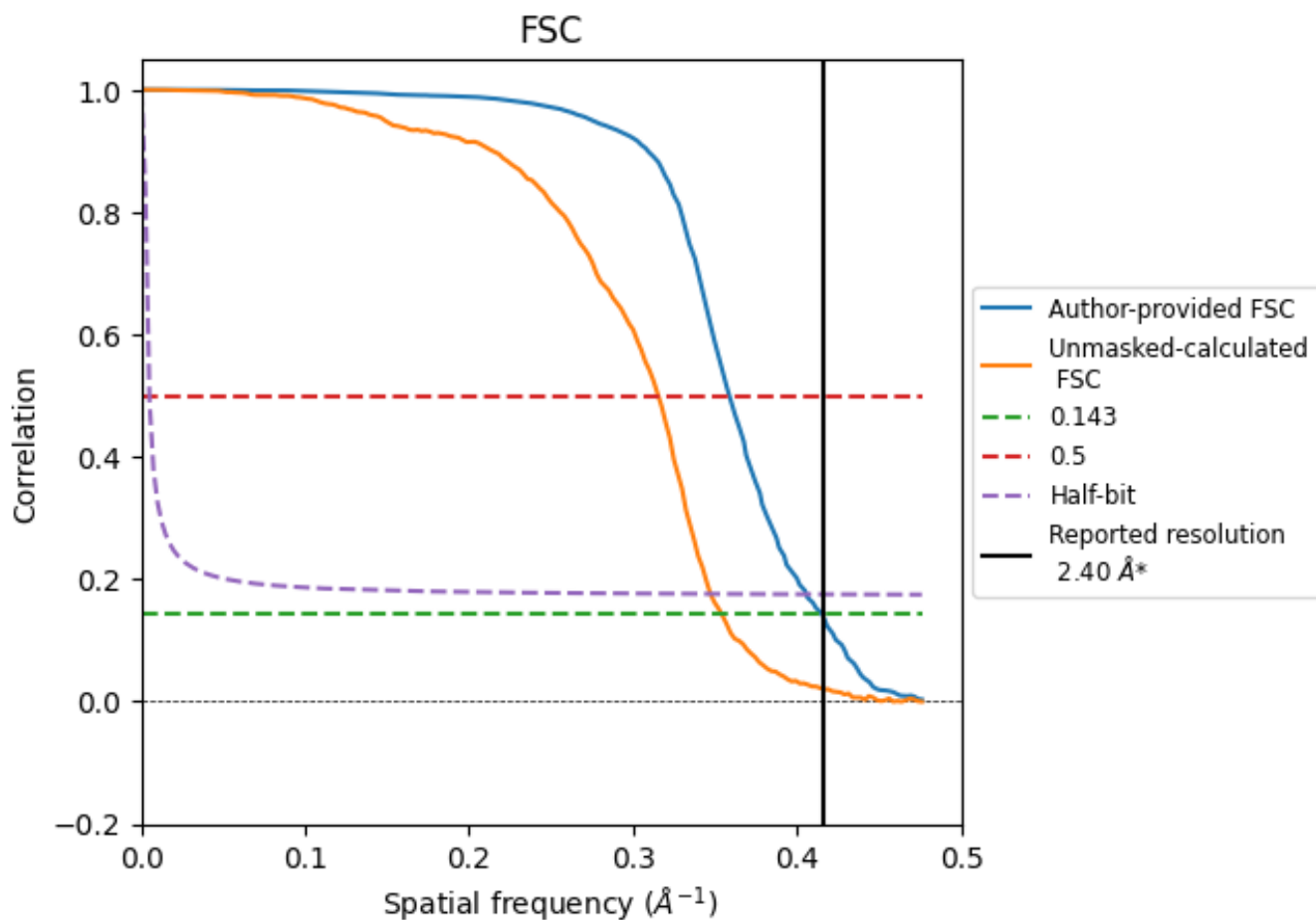


\*Reported resolution corresponds to spatial frequency of 0.417 Å<sup>-1</sup>

## 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 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

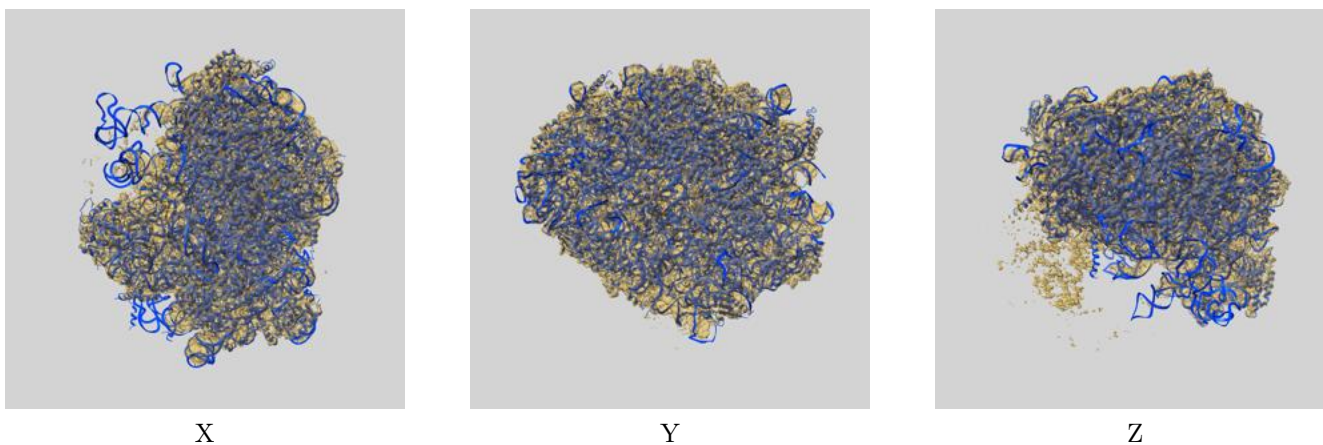
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.40	-	-
Author-provided FSC curve	2.41	2.79	2.46
Unmasked-calculated*	2.82	3.17	2.88

\*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](#)

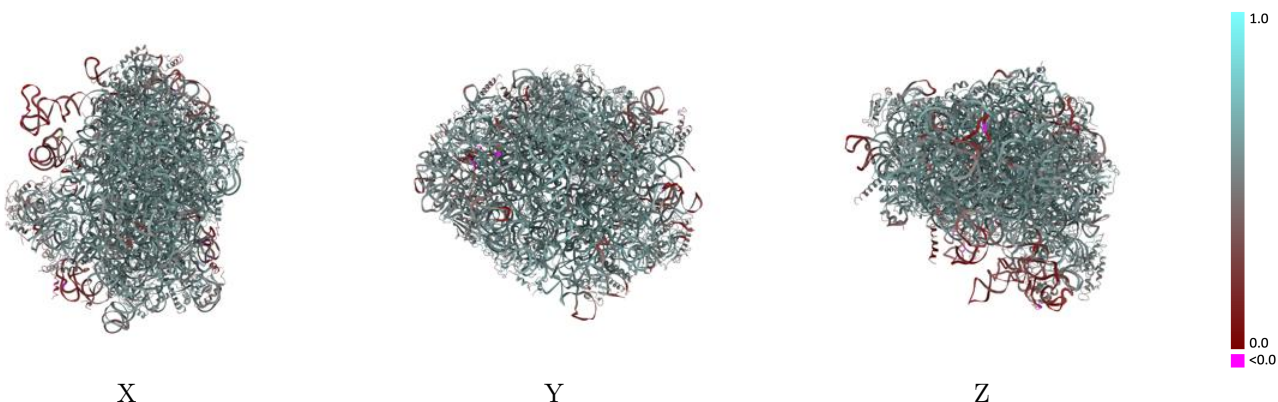
This section contains information regarding the fit between EMDB map EMD-26034 and PDB model 7TOP. Per-residue inclusion information can be found in section 3 on page 13.

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



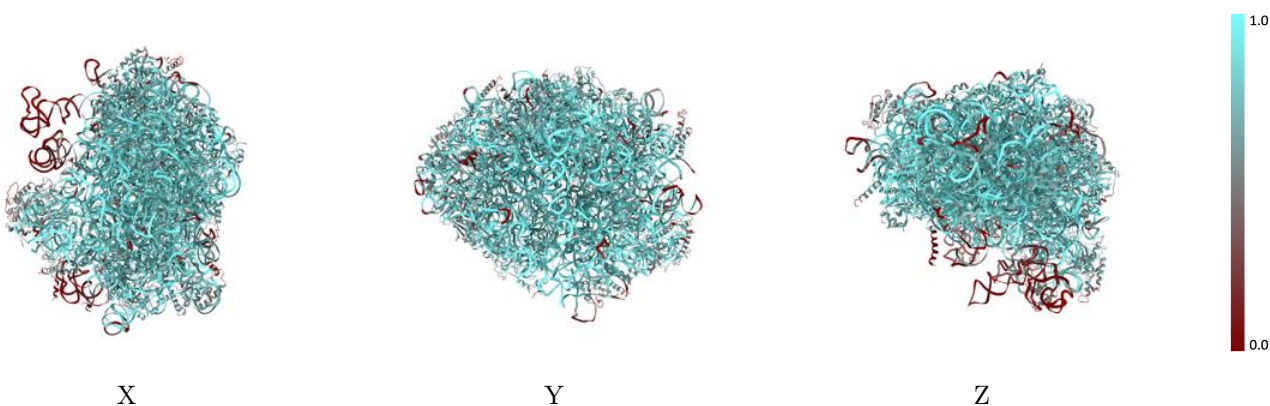
The images above show the 3D surface view of the map at the recommended contour level 4.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



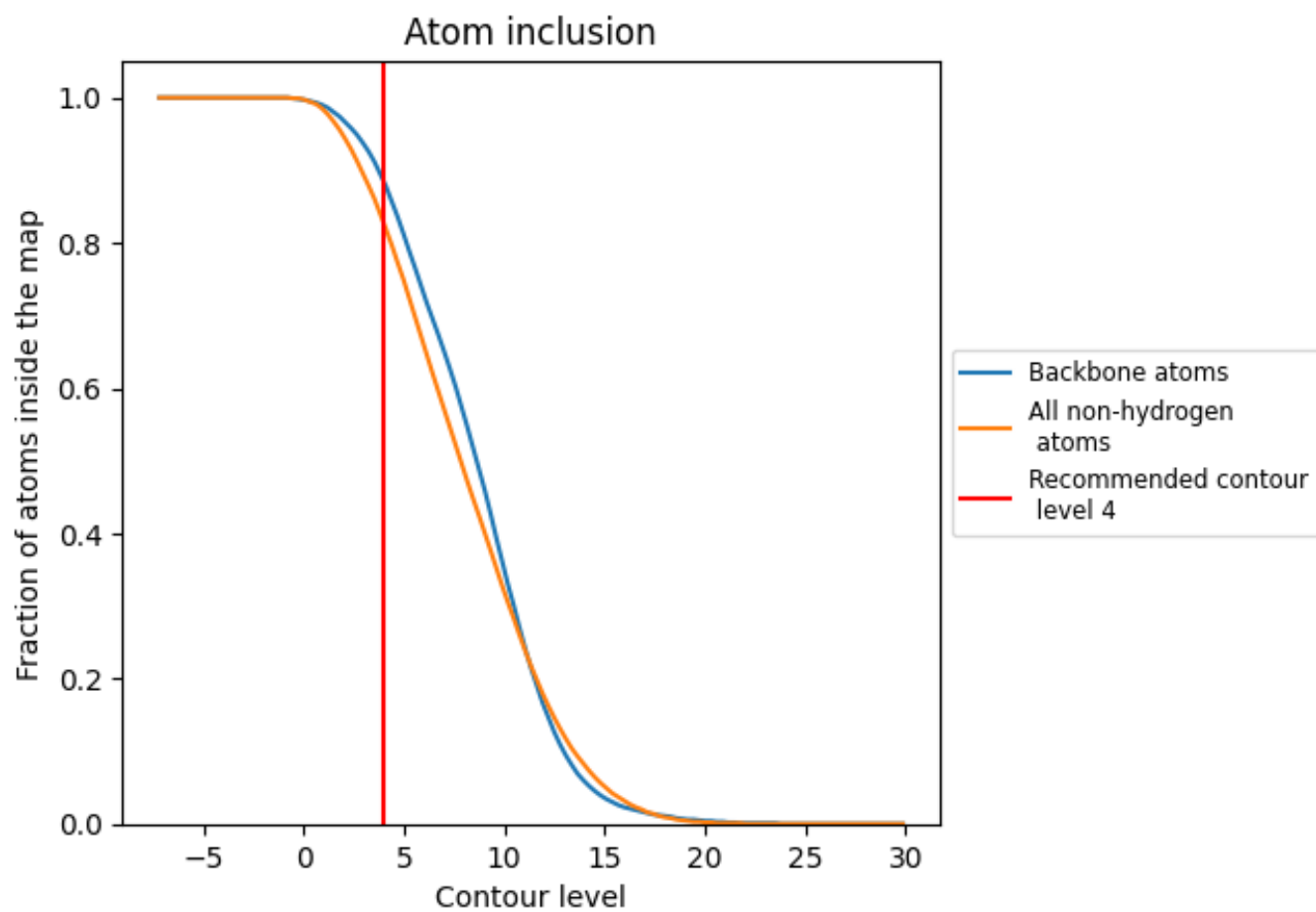
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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







































































## 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) 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	 0.5540
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



*Continued on next page...*

*Continued from previous page...*

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