



wwPDB EM Validation Summary Report ⓘ

Oct 27, 2024 – 11:37 AM EDT

PDB ID : 7TOO
EMDB ID : EMD-26033
Title : Yeast 80S ribosome bound with the ALS/FTD-associated dipeptide repeat protein GR20
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 : 2.70 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

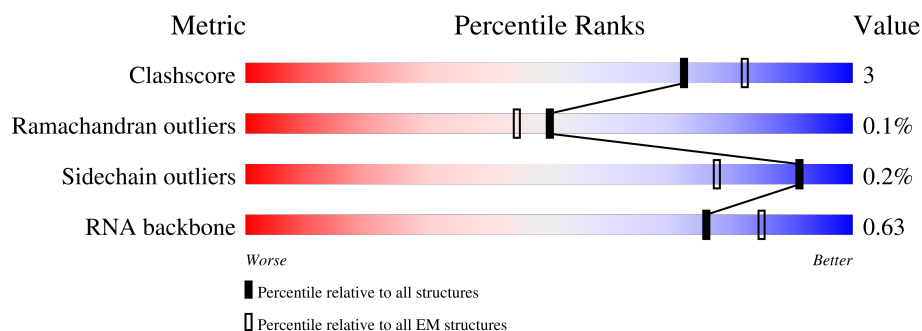
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.70 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.



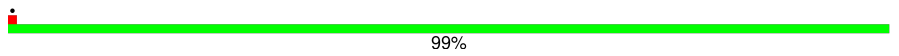

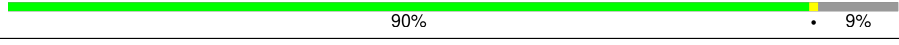

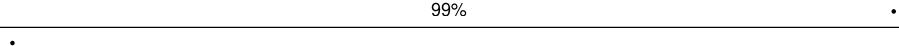
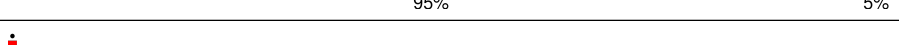
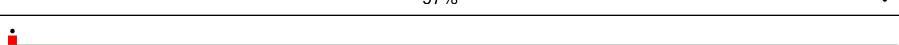
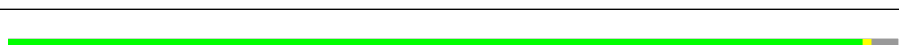



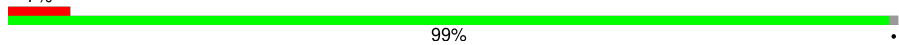
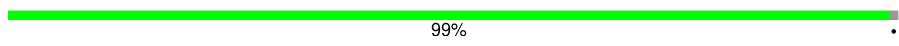
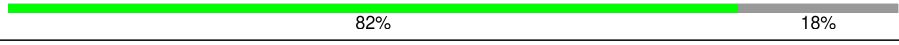
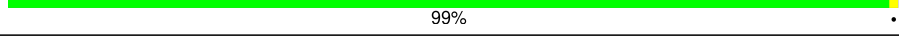
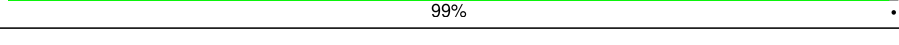
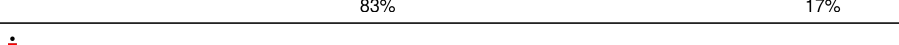
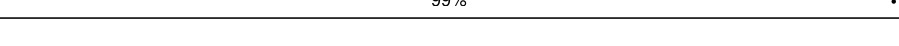



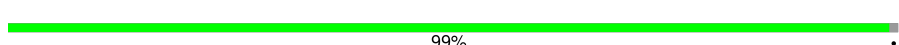
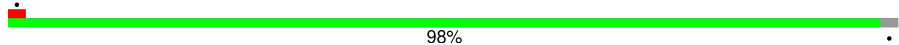


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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

Mol	Chain	Length	Quality of chain
1	A25S	3396	
2	A58S	158	
3	A5S	121	
4	AGR	40	
5	AL02	254	
6	AL03	387	
7	AL04	362	


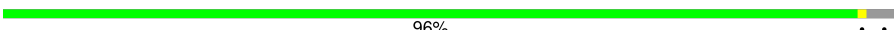

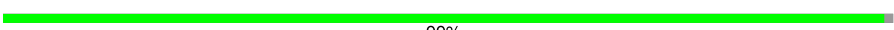








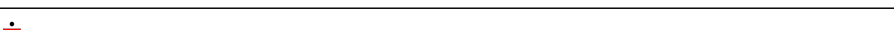
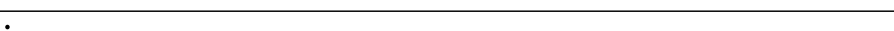
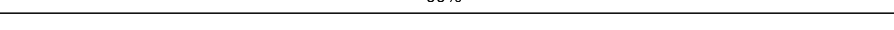
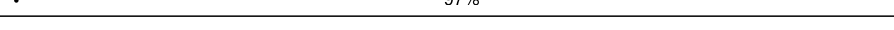
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Mol	Chain	Length	Quality of chain
8	AL05	297	
9	AL06	176	
10	AL07	244	
11	AL08	256	
12	AL09	191	
13	AL10	221	
14	AL11	174	
15	AL12	155	
16	AL13	199	
17	AL14	138	
18	AL15	204	
19	AL16	199	
20	AL17	184	
21	AL18	186	
22	AL19	189	
23	AL20	172	
24	AL21	160	
25	AL22	121	
26	AL23	137	
27	AL24	155	
28	AL25	142	
29	AL26	127	
30	AL27	136	
31	AL28	149	
32	AL29	59	

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Mol	Chain	Length	Quality of chain
33	AL30	105	 92% 8%
34	AL31	113	 96% . .
35	AL32	130	 98% .
36	AL33	107	 99% .
37	AL34	121	 93% 7%
38	AL35	120	 99% .
39	AL36	100	 98% ..
40	AL37	88	 99% .
41	AL38	78	 99% .
42	AL39	51	 98% .
43	AL40	128	 40% 68% 59%
44	AL41	25	 68% 92% 8%
45	AL42	106	 99% .
46	AL43	92	 99% .
47	ALP0	221	 97%
48	APTN	77	 88% 12%

2 Entry composition

There are 49 unique types of molecules in this entry. The entry contains 125395 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
1	A25S	3194	Total	C	N	O	P	0	0
			68318	30516	12315	22293	3194		

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

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

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

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

- Molecule 4 is a protein called ALS-FTD-associated dipeptide repeat protein, GR20.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	AGR	17	Total	C	N	O	0	0
			131	70	44	17		

- Molecule 5 is a protein called 60S ribosomal protein L2-A.

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

- Molecule 6 is a protein called RPL3 isoform 1.

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

- Molecule 7 is a protein called RPL4A isoform 1.

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

- Molecule 8 is a protein called RPL5 isoform 1.

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

- Molecule 9 is a protein called 60S ribosomal protein L6-A.

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

- Molecule 10 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 11 is a protein called 60S ribosomal protein L8-A.

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

- Molecule 12 is a protein called 60S ribosomal protein L9-A.

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

- Molecule 13 is a protein called RPL10 isoform 1.

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

- Molecule 14 is a protein called RPL11A isoform 1.

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

- Molecule 15 is a protein called Ribosomal protein L12.

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

- Molecule 16 is a protein called 60S ribosomal protein L13-A.

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

- Molecule 17 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 18 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 19 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 20 is a protein called 60S ribosomal protein L17-A.

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

- Molecule 21 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 22 is a protein called 60S ribosomal protein L19-A.

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

- Molecule 23 is a protein called 60S ribosomal protein L20-A.

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

- Molecule 24 is a protein called 60S ribosomal protein L21-A.

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

- Molecule 25 is a protein called 60S ribosomal protein L22-A.

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

- Molecule 26 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 27 is a protein called RPL24A isoform 1.

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

- Molecule 28 is a protein called 60S ribosomal protein L25.

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

- Molecule 29 is a protein called 60S ribosomal protein L26-A.

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

- Molecule 30 is a protein called 60S ribosomal protein L27-A.

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

- Molecule 31 is a protein called 60S ribosomal protein L28.

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

- Molecule 32 is a protein called RPL29 isoform 1.

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

- Molecule 33 is a protein called 60S ribosomal protein L30.

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

- Molecule 34 is a protein called 60S ribosomal protein L31-A.

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

- Molecule 35 is a protein called RPL32 isoform 1.

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

- Molecule 36 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 37 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 38 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 39 is a protein called 60S ribosomal protein L36-A.

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

- Molecule 40 is a protein called 60S ribosomal protein L37-A.

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

- Molecule 41 is a protein called RPL38 isoform 1.

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

- Molecule 42 is a protein called 60S ribosomal protein L39.

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

- Molecule 43 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 44 is a protein called 60S ribosomal protein L41-A.

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

- Molecule 45 is a protein called 60S ribosomal protein L42-A.

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

- Molecule 46 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 47 is a protein called 60S acidic ribosomal protein P0.

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

- Molecule 48 is a RNA chain called tRNA^{fMet}.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	APT ^N	77	Total	C	N	O	P	0	0
			1644	732	297	538	77		

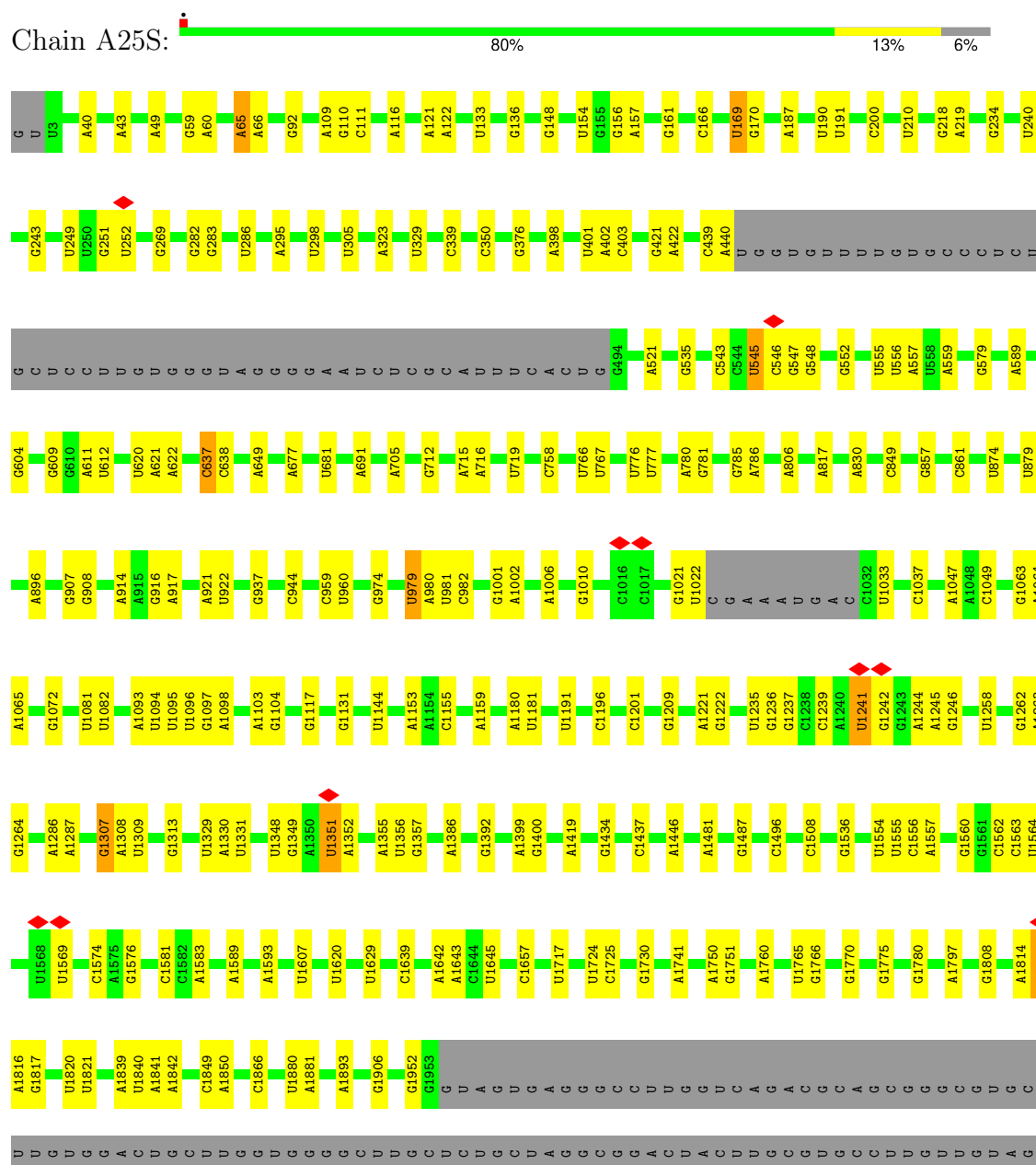
- Molecule 49 is ZINC ION (three-letter code: ZN) (formula: Zn).

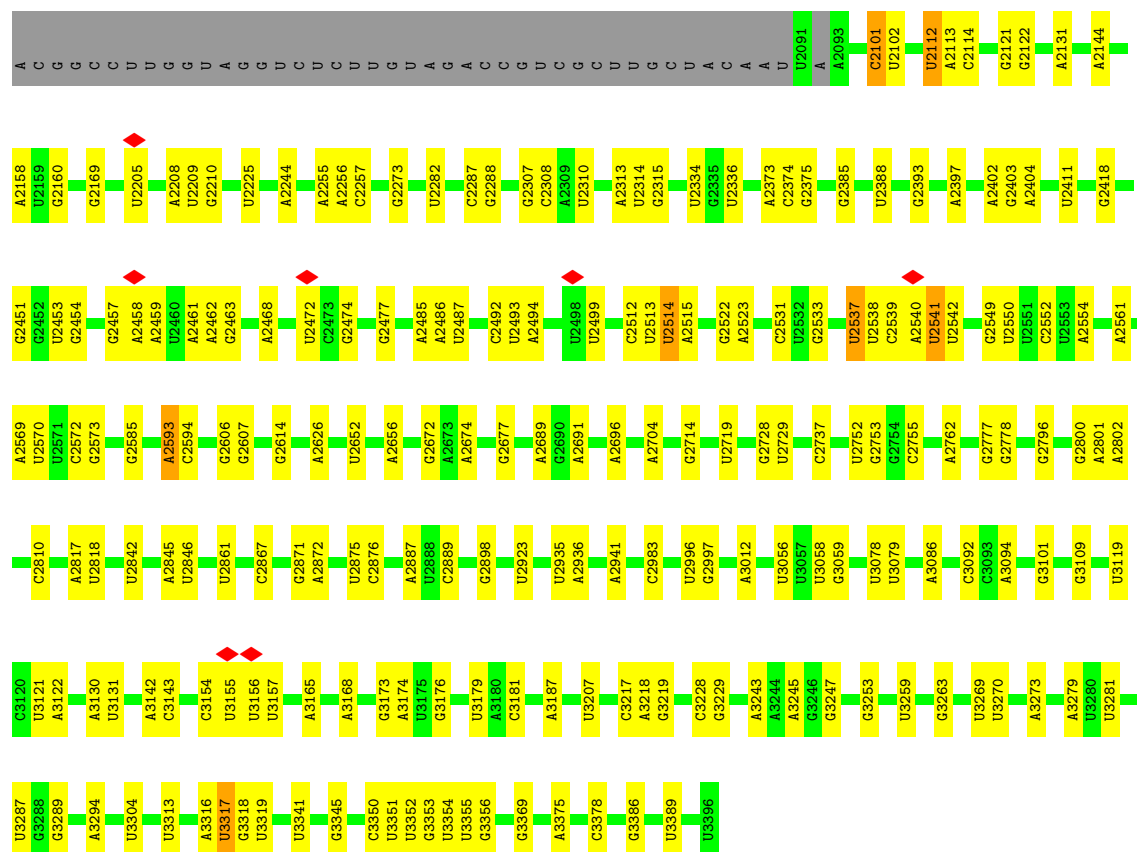
Mol	Chain	Residues	Atoms		AltConf
49	AL37	1	Total 1	Zn 1	0
49	AL40	1	Total 1	Zn 1	0
49	AL42	1	Total 1	Zn 1	0
49	AL43	1	Total 1	Zn 1	0

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





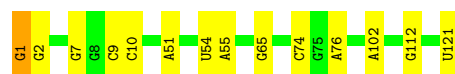
• Molecule 2: 5.8S rRNA

Chain A58S: 82% 18%



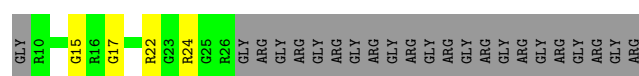
• Molecule 3: 5S rRNA

Chain A5S: 88% 11%



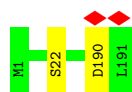
• Molecule 4: ALS-FTD-associated dipeptide repeat protein, GR20

Chain AGR: 32% 10% 58%



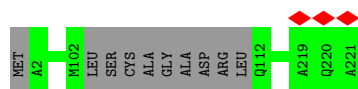
• Molecule 5: 60S ribosomal protein L2-A

Chain AL02: 99%



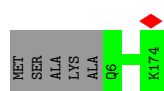
- Molecule 13: RPL10 isoform 1

Chain AL10: 95% 5%



- Molecule 14: RPL11A isoform 1

Chain AL11: 97%



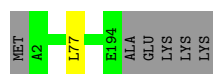
- Molecule 15: Ribosomal protein L12

Chain AL12: 8% 92%



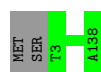
- Molecule 16: 60S ribosomal protein L13-A

Chain AL13: 96%



- Molecule 17: 60S ribosomal protein L14-A

Chain AL14: 99%



- Molecule 18: 60S ribosomal protein L15-A

Chain AL15: 100%



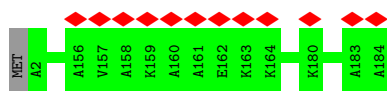
- Molecule 19: 60S ribosomal protein L16-A

Chain AL16: 97%



- Molecule 20: 60S ribosomal protein L17-A

Chain AL17: 7% 99%



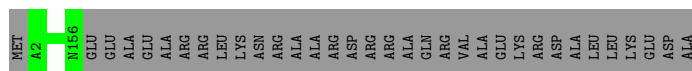
- Molecule 21: 60S ribosomal protein L18-A

Chain AL18: 99%



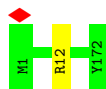
- Molecule 22: 60S ribosomal protein L19-A

Chain AL19: 82% 18%



- Molecule 23: 60S ribosomal protein L20-A

Chain AL20: 99%



- Molecule 24: 60S ribosomal protein L21-A

Chain AL21: 99%



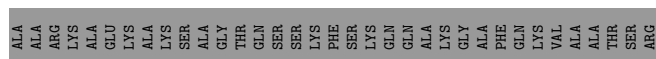
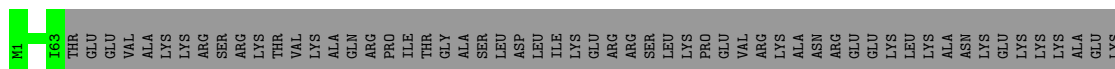
- Molecule 25: 60S ribosomal protein L22-A

Chain AL22: 83% 17%

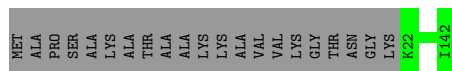
- Molecule 26: 60S ribosomal protein L23-A



- Molecule 27: RPL24A isoform 1



- Molecule 28: 60S ribosomal protein L25



- Molecule 29: 60S ribosomal protein L26-A



- Molecule 30: 60S ribosomal protein L27-A



- Molecule 31: 60S ribosomal protein L28



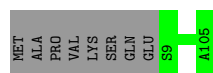
- Molecule 32: RPL29 isoform 1

Chain AL29:  98%



- Molecule 33: 60S ribosomal protein L30

Chain AL30:  92% 8%



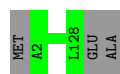
- Molecule 34: 60S ribosomal protein L31-A

Chain AL31:  96%



- Molecule 35: RPL32 isoform 1

Chain AL32:  98%



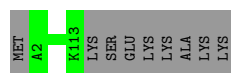
- Molecule 36: 60S ribosomal protein L33-A

Chain AL33:  99%



- Molecule 37: 60S ribosomal protein L34-A

Chain AL34:  93% 7%



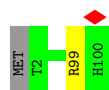
- Molecule 38: 60S ribosomal protein L35-A

Chain AL35:  99%



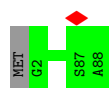
- Molecule 39: 60S ribosomal protein L36-A

Chain AL36:  98%



- Molecule 40: 60S ribosomal protein L37-A

Chain AL37:  99%



- Molecule 41: RPL38 isoform 1

Chain AL38:  99%



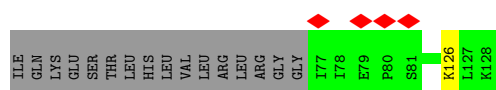
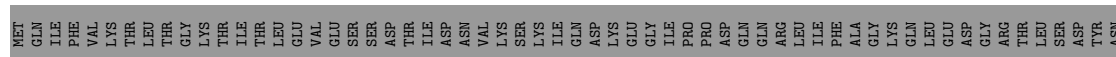
- Molecule 42: 60S ribosomal protein L39

Chain AL39:  98%

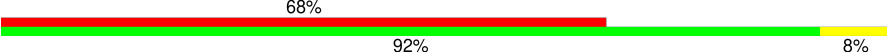


- Molecule 43: Ubiquitin-60S ribosomal protein L40

Chain AL40:  40%



- Molecule 44: 60S ribosomal protein L41-A

Chain AL41:  68%



- Molecule 45: 60S ribosomal protein L42-A

Chain AL42:  99%

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	467615	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	17.879	Depositor
Minimum map value	-4.667	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.774	Depositor
Recommended contour level	1	Depositor
Map size (\AA)	406.656, 406.656, 406.656	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.059, 1.059, 1.059	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	0.15	0/76471	0.73	35/119222 (0.0%)
2	A58S	0.22	1/3747 (0.0%)	0.70	0/5832
3	A5S	0.23	1/2884 (0.0%)	0.69	0/4491
4	AGR	0.22	0/130	0.57	0/163
5	AL02	0.24	0/1948	0.45	0/2617
6	AL03	0.23	0/3146	0.45	0/4228
7	AL04	0.24	0/2800	0.44	0/3790
8	AL05	0.24	0/2425	0.43	0/3271
9	AL06	0.25	0/1260	0.42	0/1694
10	AL07	0.24	0/1821	0.42	0/2451
11	AL08	0.24	0/1836	0.47	0/2481
12	AL09	0.26	0/1539	0.50	1/2073 (0.0%)
13	AL10	0.24	0/1741	0.42	0/2335
14	AL11	0.25	0/1374	0.50	0/1842
16	AL13	0.24	0/1568	0.47	0/2106
17	AL14	0.23	0/1068	0.42	0/1438
18	AL15	0.22	0/1757	0.41	0/2354
19	AL16	0.24	0/1585	0.40	0/2128
20	AL17	0.24	0/1443	0.43	0/1944
21	AL18	0.24	0/1465	0.41	0/1965
22	AL19	0.22	0/1266	0.40	0/1690
23	AL20	0.25	0/1481	0.44	0/1990
24	AL21	0.24	0/1300	0.46	0/1743
25	AL22	0.25	0/812	0.44	0/1099
26	AL23	0.25	0/1018	0.44	0/1369
27	AL24	0.25	0/533	0.40	0/707
28	AL25	0.23	0/979	0.42	0/1321
29	AL26	0.23	0/1004	0.44	0/1341
30	AL27	0.24	0/1118	0.42	0/1497
31	AL28	0.24	0/1204	0.45	0/1612
32	AL29	0.23	0/473	0.38	0/629
33	AL30	0.24	0/751	0.42	0/1008

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
34	AL31	0.24	0/890	0.46	0/1196
35	AL32	0.23	0/1041	0.41	0/1394
36	AL33	0.25	0/868	0.42	0/1168
37	AL34	0.23	0/890	0.45	0/1189
38	AL35	0.23	0/978	0.43	0/1301
39	AL36	0.24	0/778	0.43	0/1034
40	AL37	0.23	0/696	0.44	0/923
41	AL38	0.25	0/618	0.46	0/826
42	AL39	0.22	0/443	0.41	0/588
43	AL40	0.24	0/423	0.44	0/562
44	AL41	0.20	0/234	0.36	0/300
45	AL42	0.25	0/860	0.44	0/1136
46	AL43	0.24	0/701	0.48	0/934
47	ALP0	0.23	0/53	0.53	0/68
48	APTN	0.28	1/1836 (0.1%)	0.72	0/2859
All	All	0.19	3/135256 (0.0%)	0.65	36/199909 (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
6	AL03	0	1
10	AL07	0	1
11	AL08	0	2
12	AL09	0	1
19	AL16	0	1
23	AL20	0	1
All	All	0	7

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
48	APTN	1	C	OP3-P	-10.60	1.48	1.61
3	A5S	1	G	OP3-P	-10.60	1.48	1.61
2	A58S	1	A	OP3-P	-10.59	1.48	1.61

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A25S	1351	U	C2-N1-C1'	7.95	127.23	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A25S	1351	U	N1-C2-O2	7.54	128.08	122.80
1	A25S	922	U	C2-N1-C1'	7.15	126.28	117.70
1	A25S	1351	U	N3-C2-O2	-7.00	117.30	122.20
1	A25S	1574	C	N3-C2-O2	-6.98	117.01	121.90

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	AL03	4	ARG	Peptide
10	AL07	233	GLU	Peptide
11	AL08	156	ASP	Peptide
11	AL08	35	GLY	Peptide
12	AL09	22	SER	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A25S	68318	0	0	0	0
2	A58S	3354	0	0	0	0
3	A5S	2580	0	1304	2	0
4	AGR	131	0	140	2	0
5	AL02	1914	0	0	0	0
6	AL03	3075	0	0	0	0
7	AL04	2748	0	0	0	0
8	AL05	2375	0	0	0	0
9	AL06	1239	0	0	0	0
10	AL07	1784	0	0	0	0
11	AL08	1804	0	0	0	0
12	AL09	1518	0	0	0	0
13	AL10	1705	0	0	0	0
14	AL11	1353	0	0	0	0
15	AL12	60	0	0	0	0
16	AL13	1543	0	0	0	0
17	AL14	1053	0	0	0	0
18	AL15	1720	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	AL16	1555	0	0	0	0
20	AL17	1420	0	0	0	0
21	AL18	1441	0	0	0	0
22	AL19	1249	0	0	0	0
23	AL20	1445	0	0	0	0
24	AL21	1276	0	0	0	0
25	AL22	796	0	0	0	0
26	AL23	1003	0	0	0	0
27	AL24	521	0	0	0	0
28	AL25	964	0	0	0	0
29	AL26	993	0	0	0	0
30	AL27	1092	0	0	0	0
31	AL28	1173	0	0	0	0
32	AL29	462	0	0	0	0
33	AL30	743	0	0	0	0
34	AL31	876	0	0	0	0
35	AL32	1020	0	0	0	0
36	AL33	850	0	0	0	0
37	AL34	880	0	0	0	0
38	AL35	969	0	0	0	0
39	AL36	771	0	0	0	0
40	AL37	681	0	0	0	0
41	AL38	612	0	0	0	0
42	AL39	436	0	0	0	0
43	AL40	417	0	0	0	0
44	AL41	233	0	0	0	0
45	AL42	847	0	0	0	0
46	AL43	694	0	0	0	0
47	ALP0	54	0	0	0	0
48	APTN	1644	0	0	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	125395	0	1444	4	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 (4) 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)
4:AGR:17:GLY:HA2	4:AGR:24:ARG:HD2	1.68	0.73
3:A5S:1:G:H2'	3:A5S:2:G:H8	1.80	0.45
3:A5S:9:C:OP2	3:A5S:10:C:N4	2.50	0.45
4:AGR:15:GLY:O	4:AGR:22:ARG:NH1	2.52	0.42

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	AGR	15/40 (38%)	10 (67%)	5 (33%)	0	100	100
5	AL02	250/254 (98%)	245 (98%)	5 (2%)	0	100	100
6	AL03	384/387 (99%)	367 (96%)	16 (4%)	1 (0%)	37	61
7	AL04	359/362 (99%)	335 (93%)	23 (6%)	1 (0%)	37	61
8	AL05	294/297 (99%)	279 (95%)	15 (5%)	0	100	100
9	AL06	152/176 (86%)	148 (97%)	4 (3%)	0	100	100
10	AL07	220/244 (90%)	206 (94%)	13 (6%)	1 (0%)	25	49
11	AL08	231/256 (90%)	213 (92%)	17 (7%)	1 (0%)	30	55
12	AL09	189/191 (99%)	170 (90%)	19 (10%)	0	100	100
13	AL10	207/221 (94%)	200 (97%)	7 (3%)	0	100	100
14	AL11	167/174 (96%)	154 (92%)	13 (8%)	0	100	100
16	AL13	191/199 (96%)	176 (92%)	14 (7%)	1 (0%)	25	49
17	AL14	134/138 (97%)	127 (95%)	7 (5%)	0	100	100
18	AL15	201/204 (98%)	190 (94%)	11 (6%)	0	100	100
19	AL16	195/199 (98%)	189 (97%)	4 (2%)	2 (1%)	13	33
20	AL17	181/184 (98%)	173 (96%)	8 (4%)	0	100	100
21	AL18	183/186 (98%)	178 (97%)	5 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	AL19	153/189 (81%)	147 (96%)	6 (4%)	0	100	100
23	AL20	170/172 (99%)	162 (95%)	8 (5%)	0	100	100
24	AL21	157/160 (98%)	151 (96%)	6 (4%)	0	100	100
25	AL22	98/121 (81%)	96 (98%)	2 (2%)	0	100	100
26	AL23	134/137 (98%)	132 (98%)	2 (2%)	0	100	100
27	AL24	61/155 (39%)	59 (97%)	2 (3%)	0	100	100
28	AL25	119/142 (84%)	117 (98%)	2 (2%)	0	100	100
29	AL26	124/127 (98%)	123 (99%)	1 (1%)	0	100	100
30	AL27	133/136 (98%)	126 (95%)	7 (5%)	0	100	100
31	AL28	146/149 (98%)	137 (94%)	9 (6%)	0	100	100
32	AL29	56/59 (95%)	51 (91%)	5 (9%)	0	100	100
33	AL30	95/105 (90%)	94 (99%)	1 (1%)	0	100	100
34	AL31	107/113 (95%)	99 (92%)	8 (8%)	0	100	100
35	AL32	125/130 (96%)	122 (98%)	3 (2%)	0	100	100
36	AL33	104/107 (97%)	99 (95%)	5 (5%)	0	100	100
37	AL34	110/121 (91%)	108 (98%)	2 (2%)	0	100	100
38	AL35	117/120 (98%)	112 (96%)	5 (4%)	0	100	100
39	AL36	97/100 (97%)	88 (91%)	9 (9%)	0	100	100
40	AL37	85/88 (97%)	83 (98%)	2 (2%)	0	100	100
41	AL38	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
42	AL39	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
43	AL40	50/128 (39%)	49 (98%)	1 (2%)	0	100	100
44	AL41	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
45	AL42	103/106 (97%)	94 (91%)	9 (9%)	0	100	100
46	AL43	89/92 (97%)	84 (94%)	5 (6%)	0	100	100
47	ALP0	5/221 (2%)	5 (100%)	0	0	100	100
All	All	6137/6844 (90%)	5839 (95%)	291 (5%)	7 (0%)	50	73

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	AL04	339	LEU
10	AL07	234	GLU

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Mol	Chain	Res	Type
19	AL16	111	PRO
6	AL03	4	ARG
16	AL13	77	LEU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	AGR	9/20 (45%)	9 (100%)	0	100	100
5	AL02	193/196 (98%)	193 (100%)	0	100	100
6	AL03	320/323 (99%)	318 (99%)	2 (1%)	84	94
7	AL04	288/289 (100%)	287 (100%)	1 (0%)	91	97
8	AL05	244/245 (100%)	243 (100%)	1 (0%)	89	96
9	AL06	134/153 (88%)	134 (100%)	0	100	100
10	AL07	186/205 (91%)	186 (100%)	0	100	100
11	AL08	187/208 (90%)	187 (100%)	0	100	100
12	AL09	171/171 (100%)	171 (100%)	0	100	100
13	AL10	177/187 (95%)	177 (100%)	0	100	100
14	AL11	147/150 (98%)	147 (100%)	0	100	100
16	AL13	154/159 (97%)	154 (100%)	0	100	100
17	AL14	107/109 (98%)	107 (100%)	0	100	100
18	AL15	175/176 (99%)	175 (100%)	0	100	100
19	AL16	160/162 (99%)	159 (99%)	1 (1%)	84	94
20	AL17	140/146 (96%)	140 (100%)	0	100	100
21	AL18	150/151 (99%)	150 (100%)	0	100	100
22	AL19	128/154 (83%)	128 (100%)	0	100	100
23	AL20	156/156 (100%)	156 (100%)	0	100	100
24	AL21	136/137 (99%)	136 (100%)	0	100	100
25	AL22	87/107 (81%)	87 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
26	AL23	104/105 (99%)	104 (100%)	0	100	100
27	AL24	55/129 (43%)	55 (100%)	0	100	100
28	AL25	104/118 (88%)	104 (100%)	0	100	100
29	AL26	109/110 (99%)	109 (100%)	0	100	100
30	AL27	115/116 (99%)	115 (100%)	0	100	100
31	AL28	118/119 (99%)	118 (100%)	0	100	100
32	AL29	46/47 (98%)	46 (100%)	0	100	100
33	AL30	81/88 (92%)	81 (100%)	0	100	100
34	AL31	92/97 (95%)	91 (99%)	1 (1%)	70	87
35	AL32	109/111 (98%)	109 (100%)	0	100	100
36	AL33	90/91 (99%)	90 (100%)	0	100	100
37	AL34	95/103 (92%)	95 (100%)	0	100	100
38	AL35	104/105 (99%)	104 (100%)	0	100	100
39	AL36	81/82 (99%)	80 (99%)	1 (1%)	67	86
40	AL37	70/71 (99%)	70 (100%)	0	100	100
41	AL38	68/69 (99%)	68 (100%)	0	100	100
42	AL39	45/46 (98%)	45 (100%)	0	100	100
43	AL40	47/116 (40%)	46 (98%)	1 (2%)	48	76
44	AL41	23/23 (100%)	21 (91%)	2 (9%)	8	20
45	AL42	90/91 (99%)	90 (100%)	0	100	100
46	AL43	71/72 (99%)	71 (100%)	0	100	100
47	ALP0	6/166 (4%)	6 (100%)	0	100	100
All	All	5172/5679 (91%)	5162 (100%)	10 (0%)	91	98

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

Mol	Chain	Res	Type
43	AL40	126	LYS
44	AL41	9	ARG
44	AL41	12	ARG
8	AL05	196	ARG
19	AL16	117	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%)	453 (14%)	31 (0%)
2	A58S	157/158 (99%)	28 (17%)	1 (0%)
3	A5S	120/121 (99%)	10 (8%)	0
48	APTN	76/77 (98%)	8 (10%)	0
All	All	3542/3752 (94%)	499 (14%)	32 (0%)

5 of 499 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A25S	40	A
1	A25S	43	A
1	A25S	49	A
1	A25S	59	G
1	A25S	60	A

5 of 32 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A25S	3269	U
1	A25S	3317	U
1	A25S	1329	U
1	A25S	1307	G
1	A25S	3351	U

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

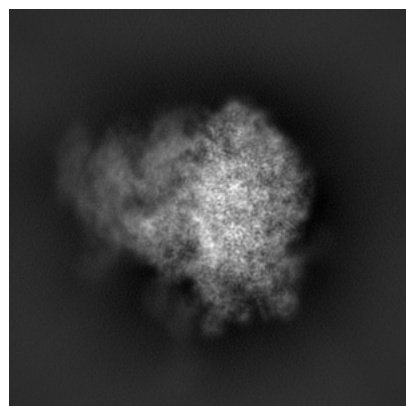
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26033. These allow visual inspection of the internal detail of the map and identification of artifacts.

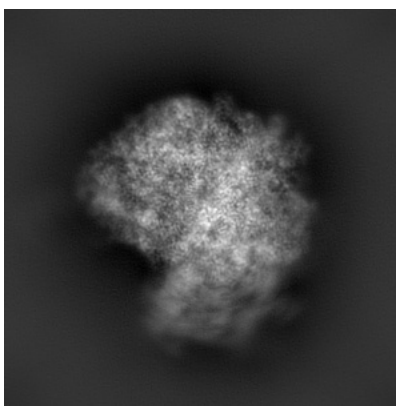
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

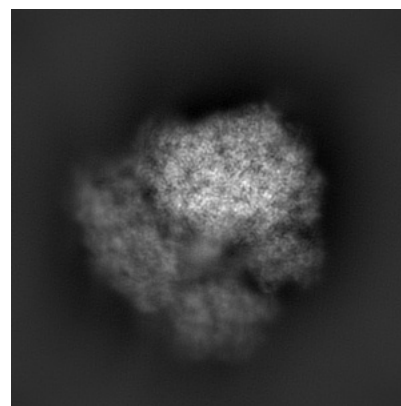
6.1.1 Primary map



X

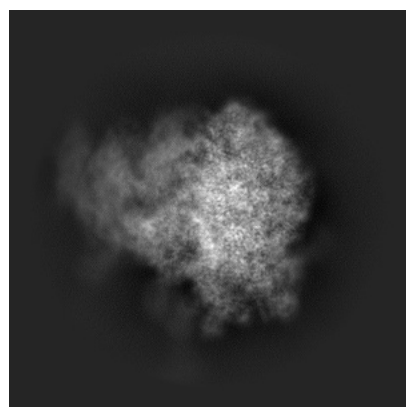


Y

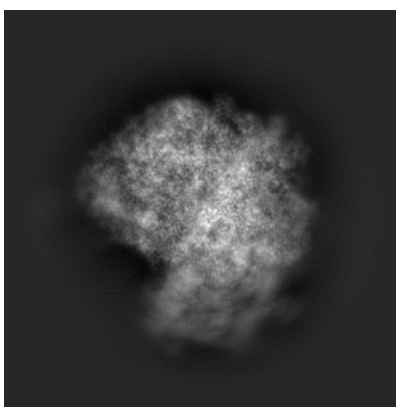


Z

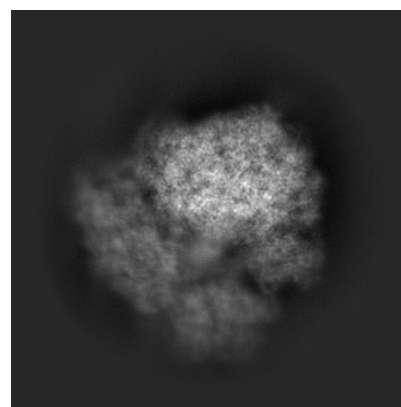
6.1.2 Raw map



X



Y

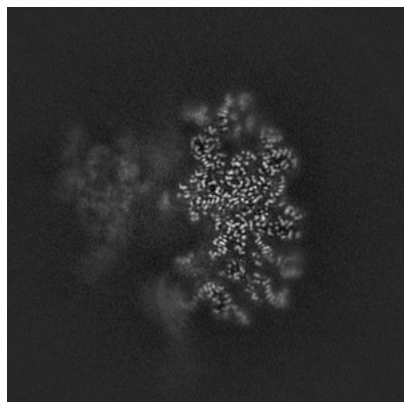


Z

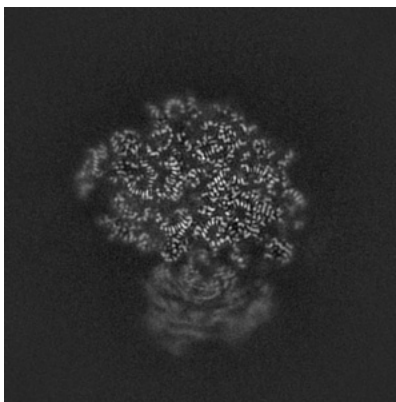
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

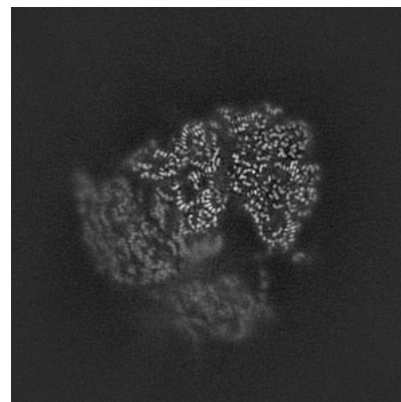
6.2.1 Primary map



X Index: 192

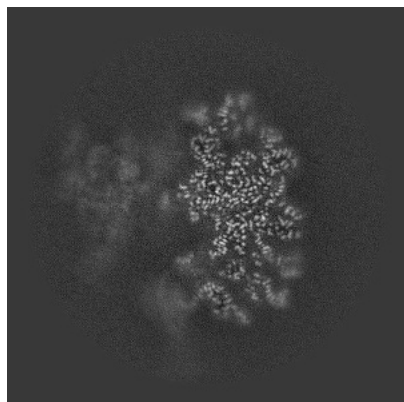


Y Index: 192

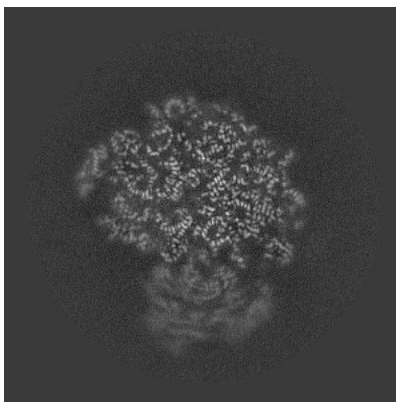


Z Index: 192

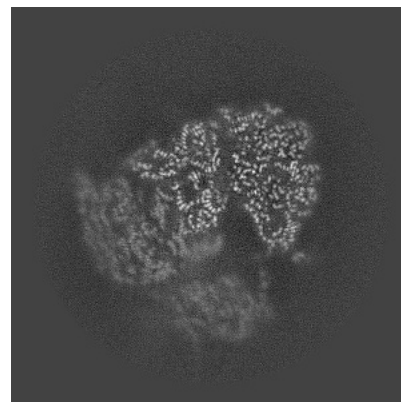
6.2.2 Raw map



X Index: 192



Y Index: 192

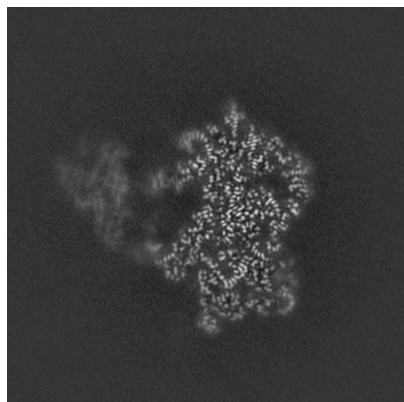


Z Index: 192

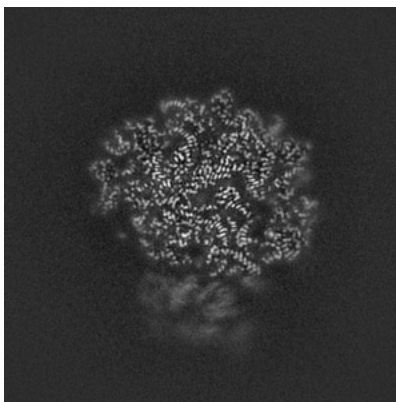
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

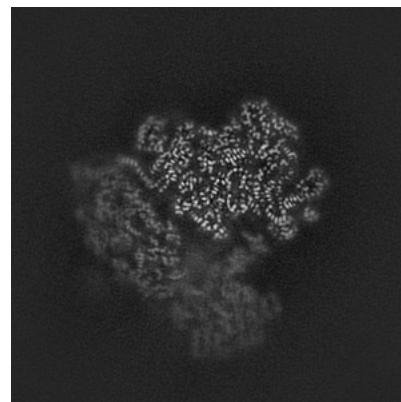
6.3.1 Primary map



X Index: 225

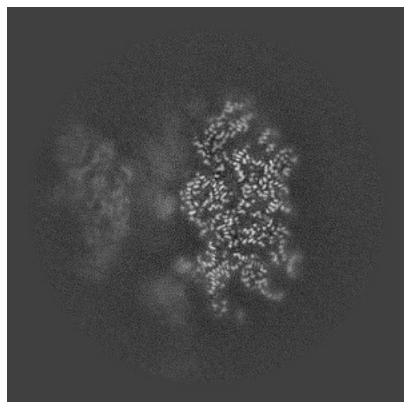


Y Index: 214

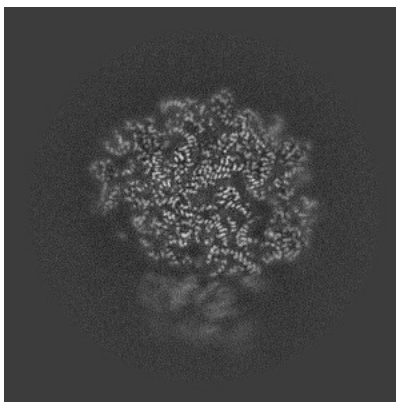


Z Index: 208

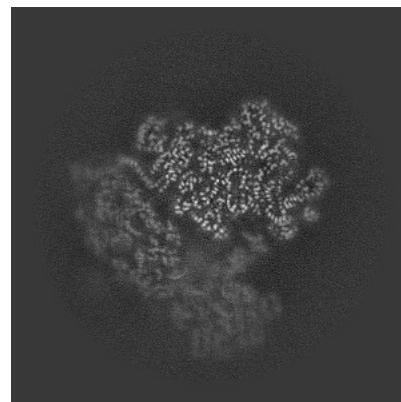
6.3.2 Raw map



X Index: 184



Y Index: 214

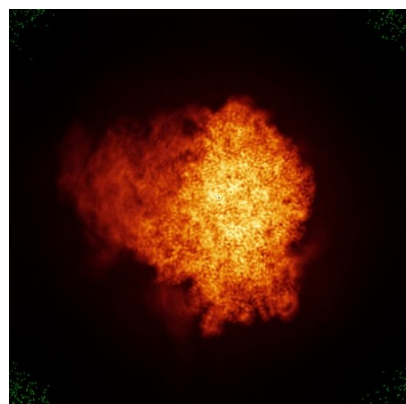


Z Index: 208

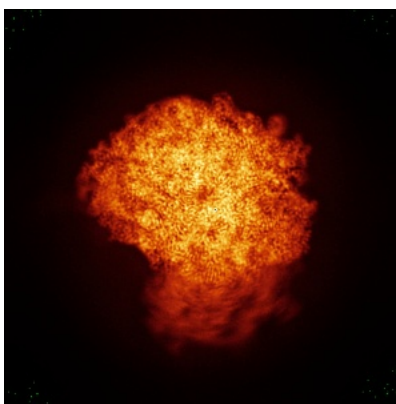
The images above show the largest variance slices of the map in three orthogonal directions.

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

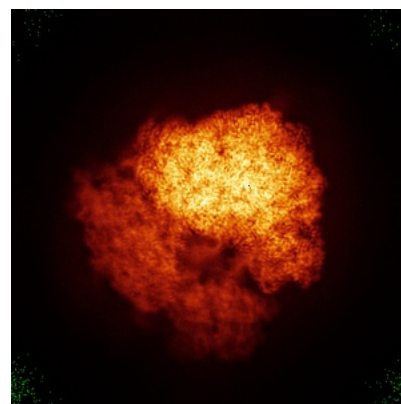
6.4.1 Primary map



X

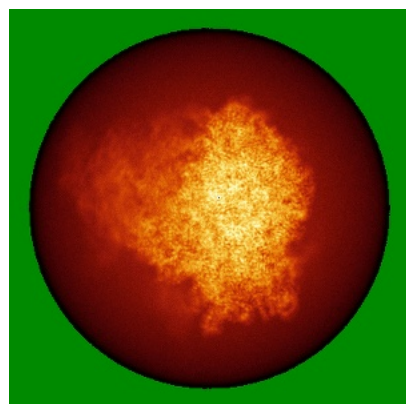


Y

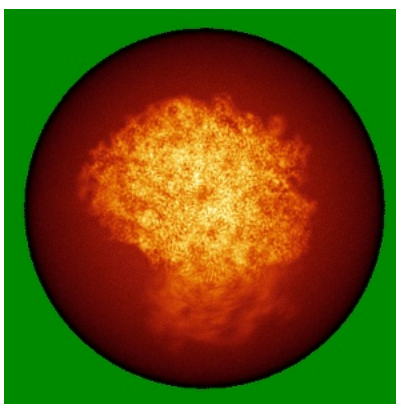


Z

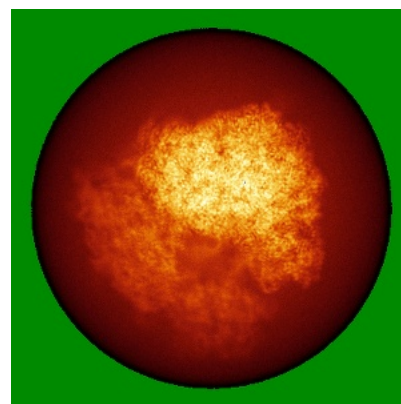
6.4.2 Raw map



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



X



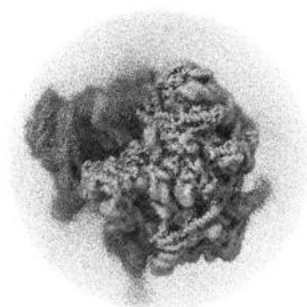
Y



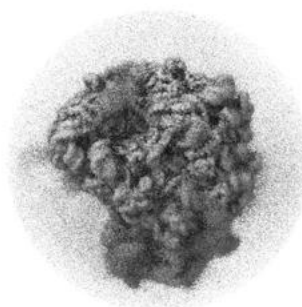
Z

The images above show the 3D surface view of the map at the recommended contour level 1.0. 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



X



Y



Z

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.

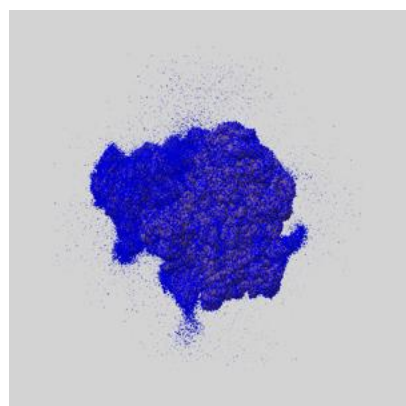
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

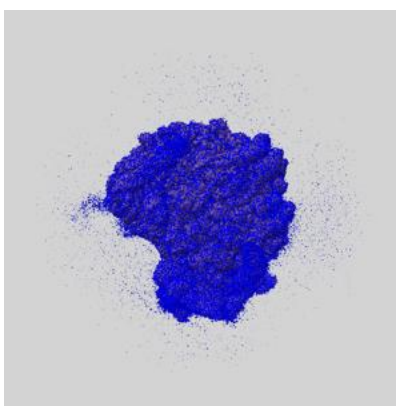
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

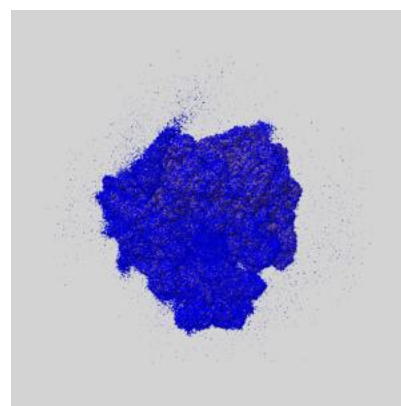
6.6.1 emd_26033_msk_1.map [i](#)



X



Y

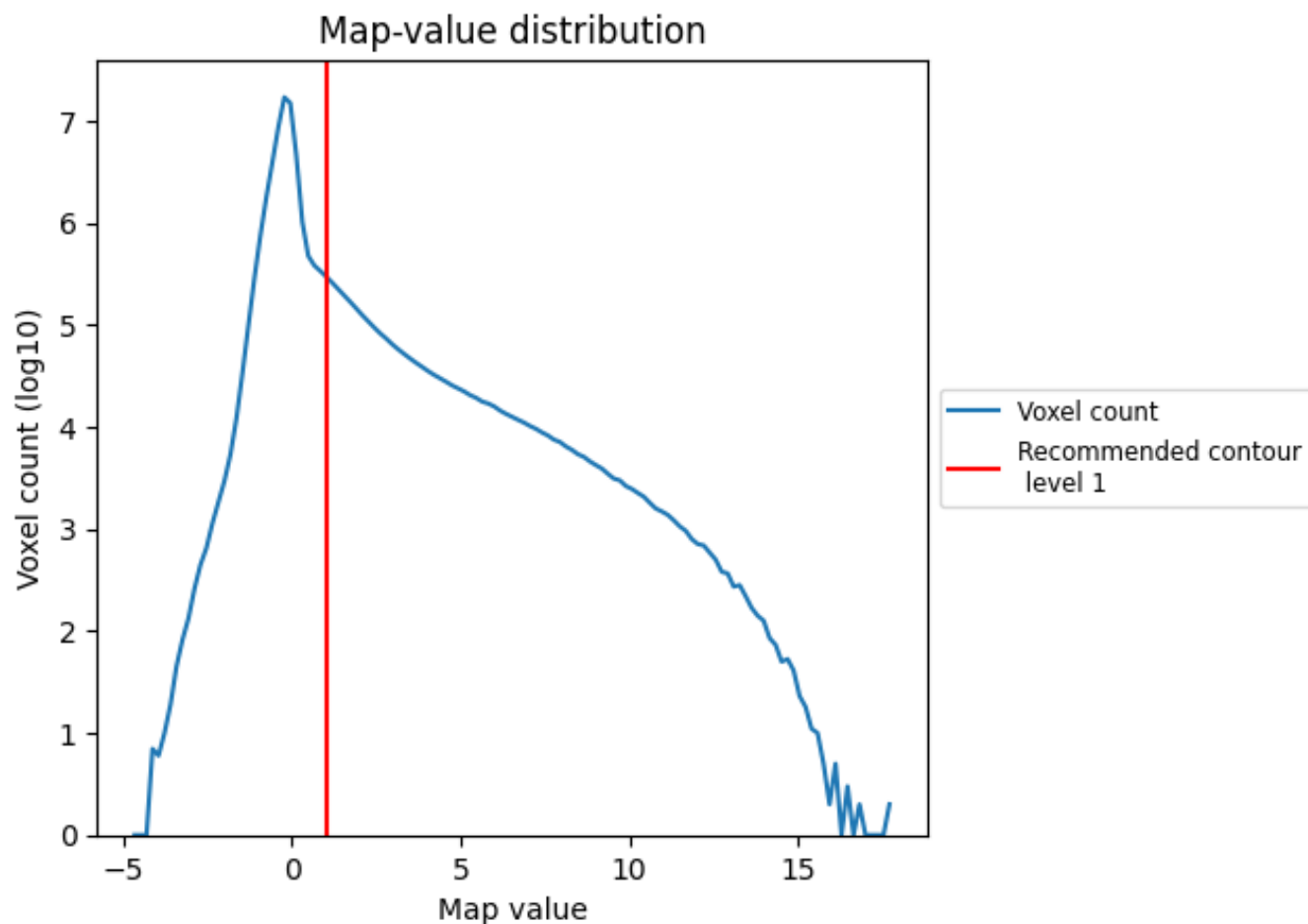


Z

7 Map analysis [i](#)

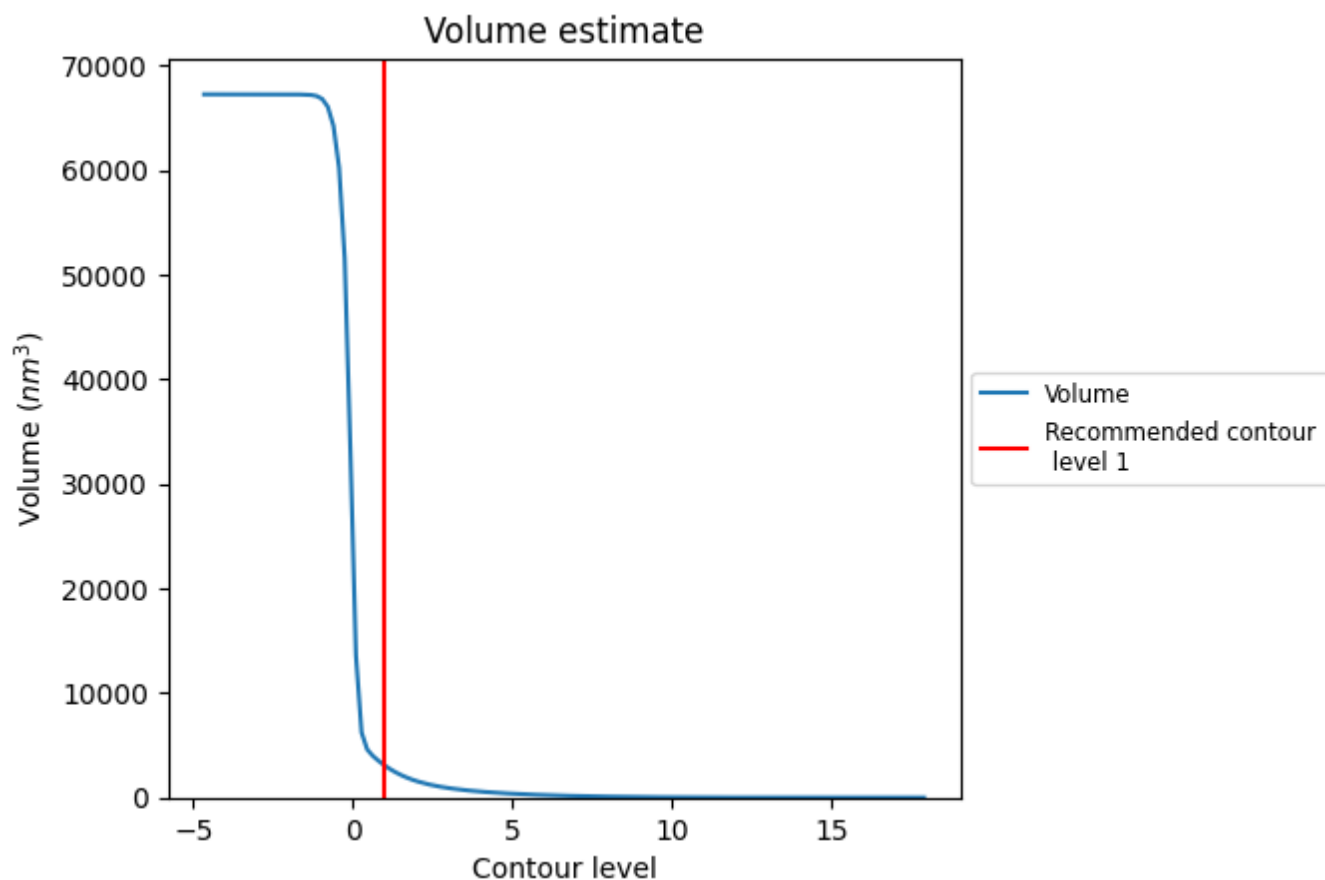
This section contains the results of statistical analysis of the map.

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.

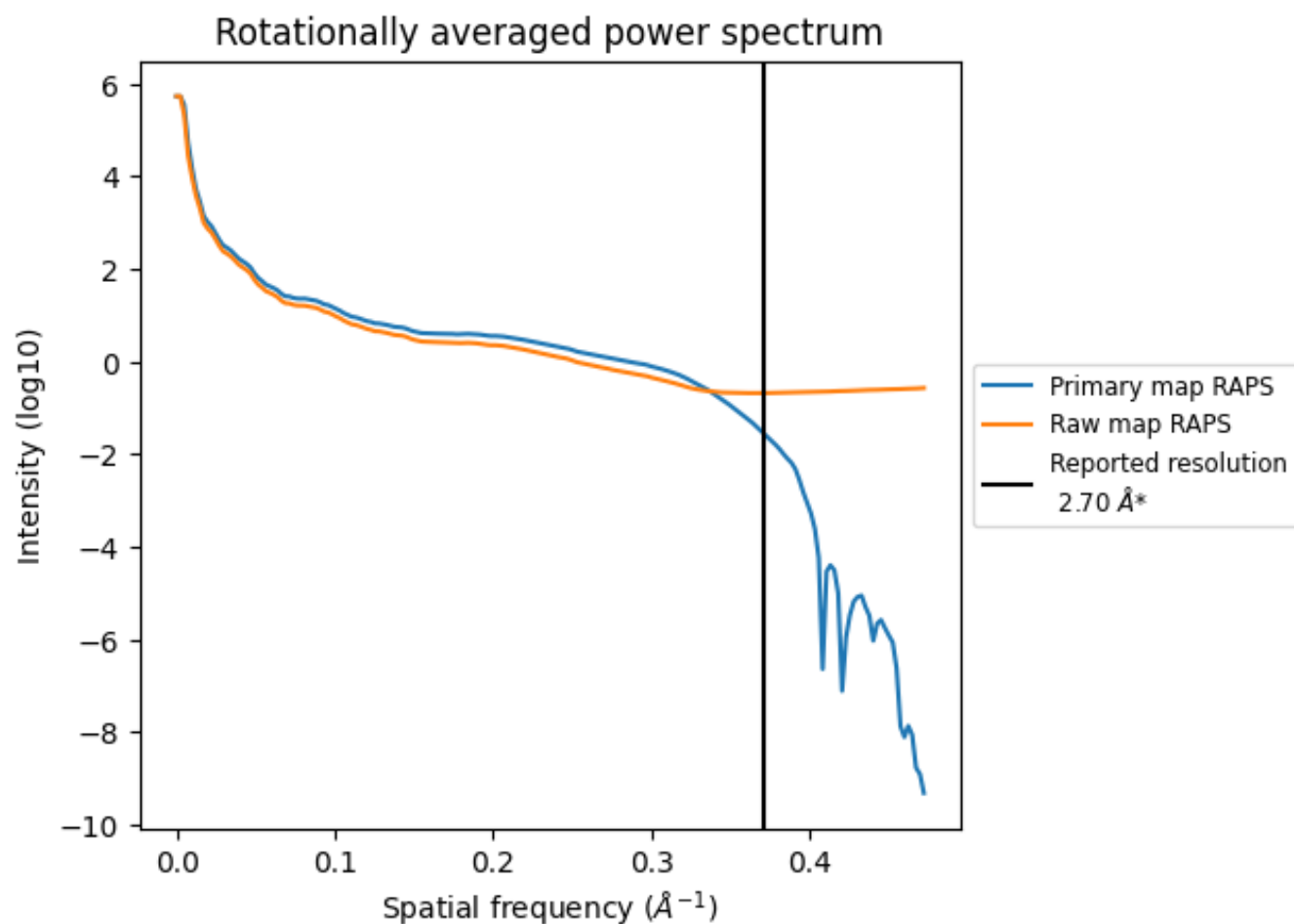
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3047 nm³; this corresponds to an approximate mass of 2752 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

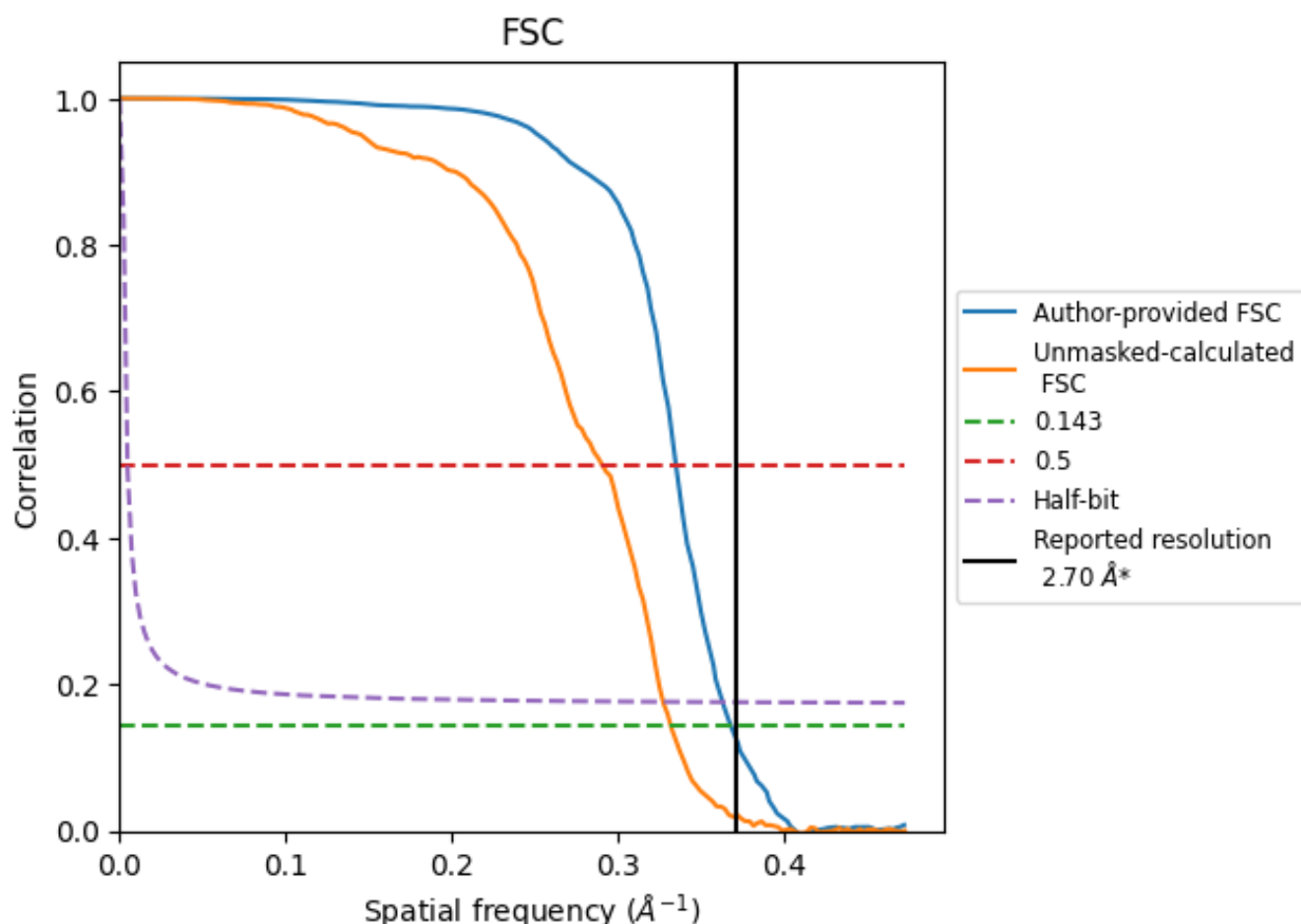


*Reported resolution corresponds to spatial frequency of 0.370 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.370 Å⁻¹

8.2 Resolution estimates [i](#)

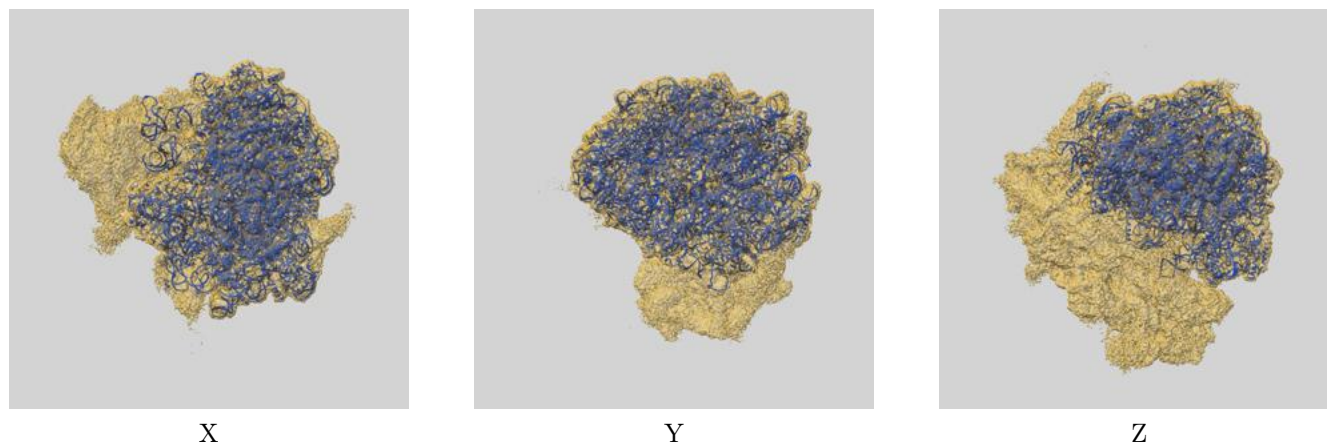
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.70	-	-
Author-provided FSC curve	2.72	2.99	2.76
Unmasked-calculated*	3.02	3.45	3.06

*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 3.02 differs from the reported value 2.7 by more than 10 %

9 Map-model fit [i](#)

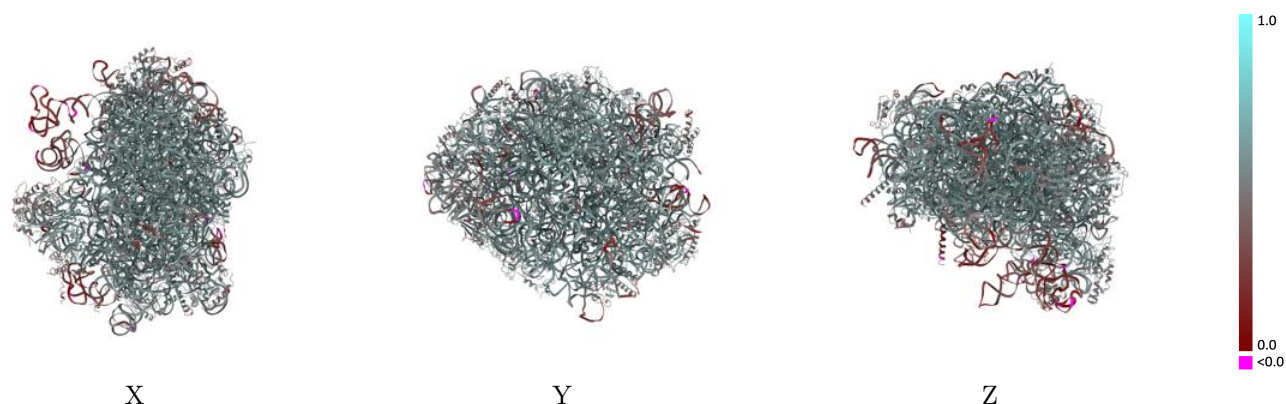
This section contains information regarding the fit between EMDB map EMD-26033 and PDB model 7TOO. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

9.1 Map-model overlay [i](#)



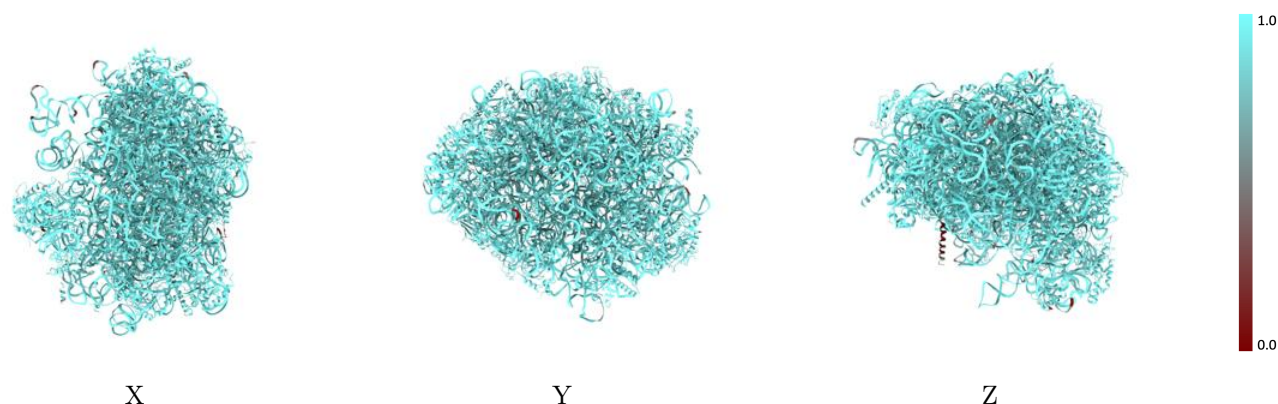
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



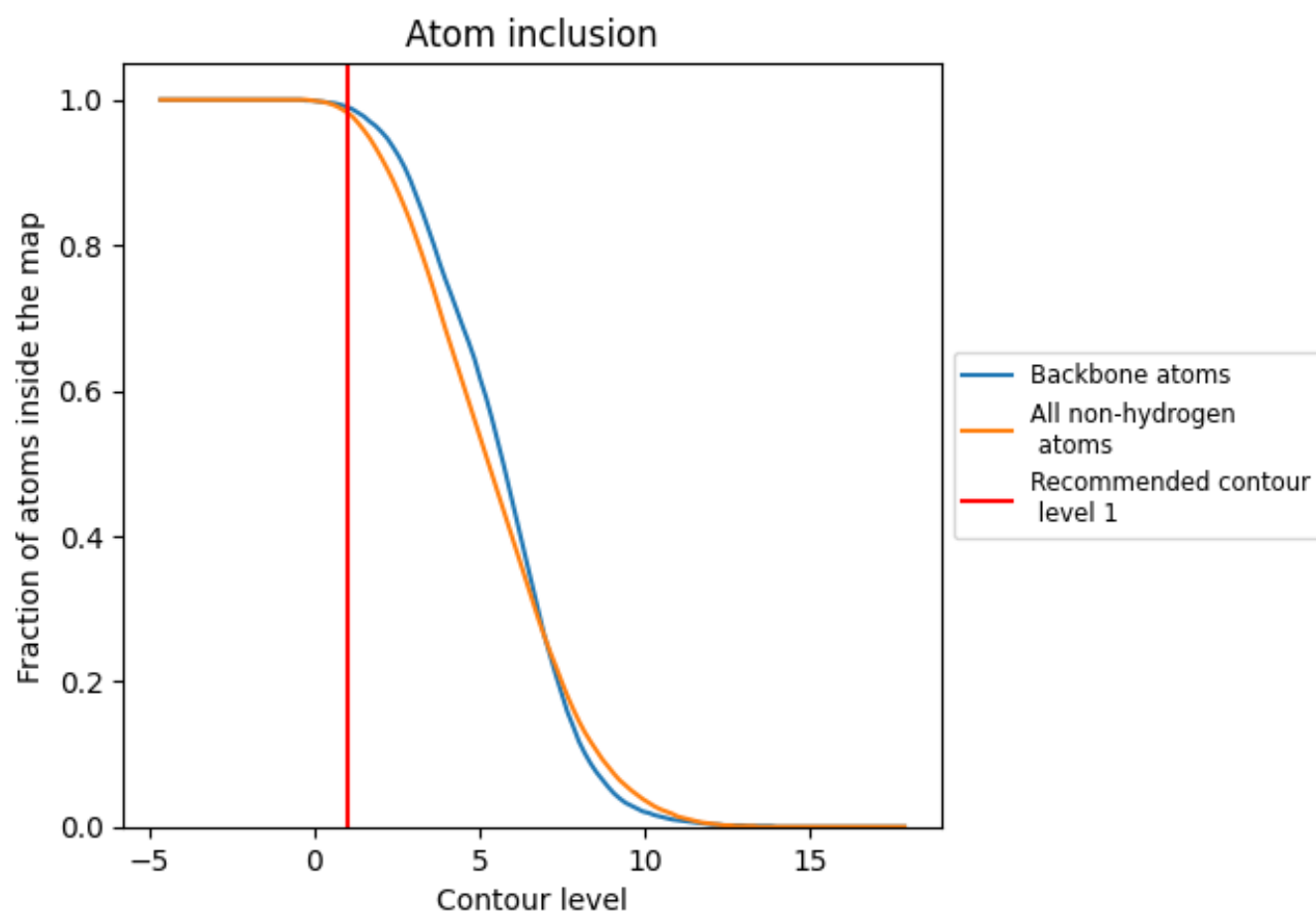
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 98% 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 (1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9820	 0.5310
A25S	 0.9900	 0.5350
A58S	 0.9970	 0.5680
A5S	 1.0000	 0.5550
AGR	 0.8940	 0.3110
AL02	 0.9700	 0.5620
AL03	 0.9860	 0.5510
AL04	 0.9770	 0.5390
AL05	 0.9720	 0.4900
AL06	 0.9790	 0.5100
AL07	 0.9820	 0.5390
AL08	 0.9710	 0.4980
AL09	 0.9700	 0.4970
AL10	 0.9770	 0.5310
AL11	 0.9550	 0.4470
AL12	 0.7830	 0.2040
AL13	 0.9700	 0.5270
AL14	 0.9750	 0.5180
AL15	 0.9900	 0.5790
AL16	 0.9860	 0.5560
AL17	 0.9370	 0.5250
AL18	 0.9790	 0.5590
AL19	 0.9820	 0.5420
AL20	 0.9700	 0.5390
AL21	 0.9810	 0.5460
AL22	 0.9760	 0.4790
AL23	 0.9830	 0.5590
AL24	 0.9660	 0.5420
AL25	 0.9860	 0.5470
AL26	 0.9750	 0.5360
AL27	 0.9840	 0.5150
AL28	 0.9820	 0.5590
AL29	 0.9670	 0.5380
AL30	 0.9660	 0.5000
AL31	 0.9670	 0.5390



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Chain	Atom inclusion	Q-score
AL32	 0.9830	 0.5700
AL33	 0.9950	 0.5730
AL34	 0.9850	 0.5320
AL35	 0.9710	 0.5280
AL36	 0.9660	 0.5030
AL37	 0.9880	 0.5740
AL38	 0.9600	 0.4920
AL39	 0.9810	 0.5670
AL40	 0.8660	 0.4010
AL41	 0.2590	 0.1620
AL42	 0.9340	 0.5270
AL43	 0.9610	 0.5310
ALP0	 1.0000	 0.2560
APTn	 0.9740	 0.3380