



## wwPDB EM Validation Summary Report ⓘ

Feb 27, 2023 – 06:04 pm GMT

PDB ID : 8AGT  
EMDB ID : EMD-15423  
Title : Yeast RQC complex in state F  
Authors : Tesina, P.; Buschauer, R.; Beckmann, R.  
Deposited on : 2022-07-20  
Resolution : 2.60 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:

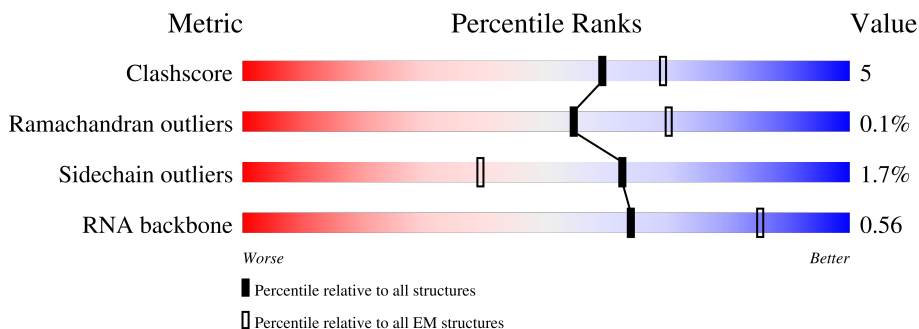
EMDB validation analysis : 0.0.1.dev43  
Mogul : 1.8.4, CSD as541be (2020)  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.32.1

# 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 2.60 Å.

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







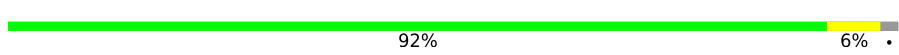
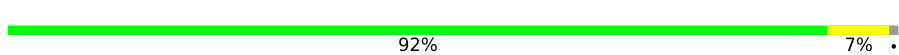
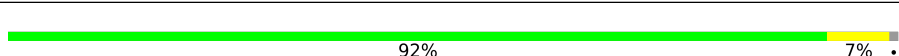
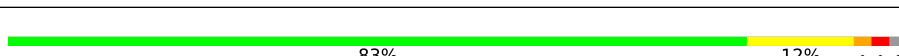
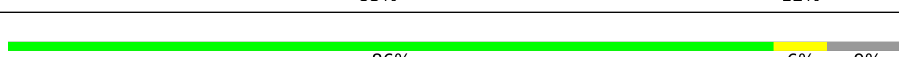

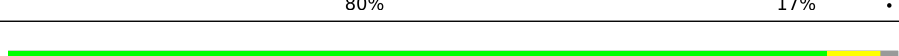
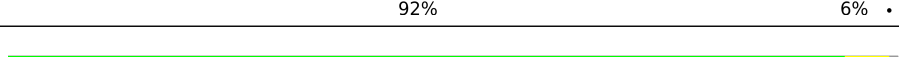
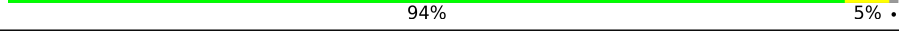

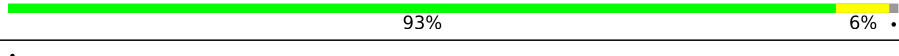
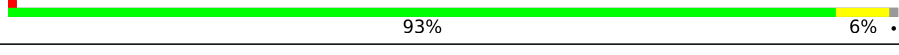
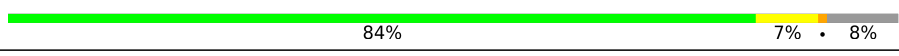

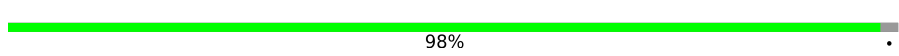

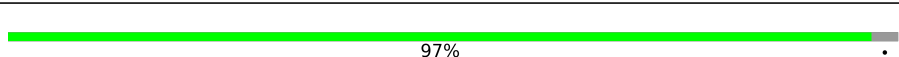
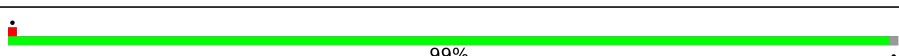
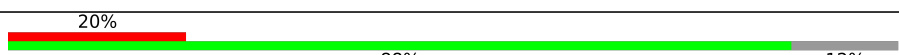
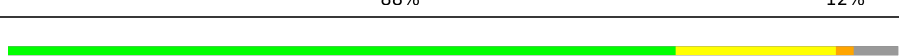

Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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

Mol	Chain	Length	Quality of chain
1	A	204	
2	B	199	
3	C	184	
4	D	186	
5	E	189	
6	F	172	
7	G	160	

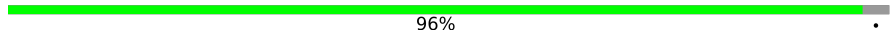
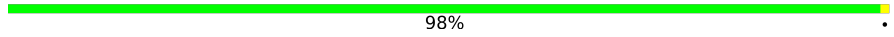
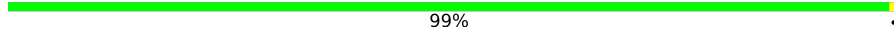
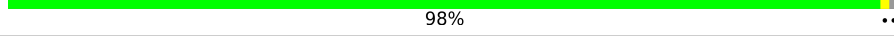
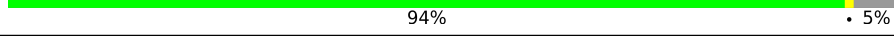
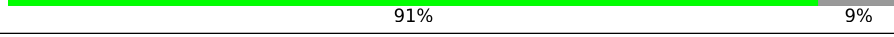

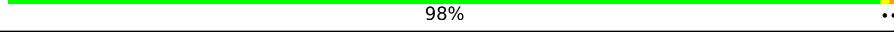
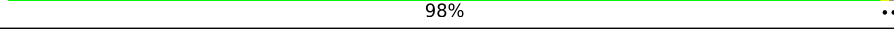
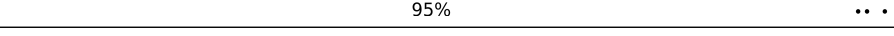
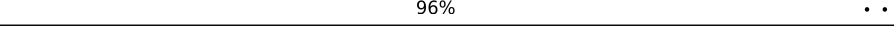
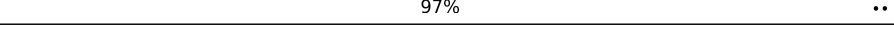

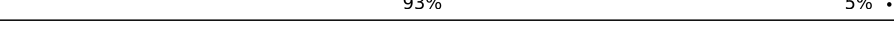
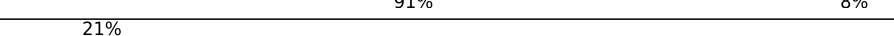
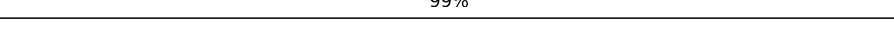
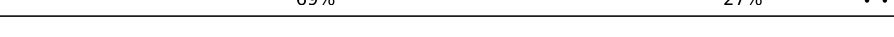

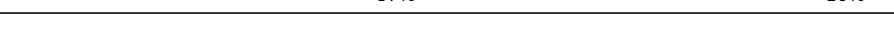



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Mol	Chain	Length	Quality of chain
8	H	121	 74% 9% 17%
9	I	137	 90% 9%
10	J	155	 37% 59%
11	K	142	 84% 15%
12	L	127	 92% 6%
13	M	136	 92% 7%
14	N	149	 92% 7%
15	O	59	 83% 12%
16	P	105	 86% 6% 9%
17	Q	113	 80% 17%
18	R	130	 92% 6%
19	S	107	 94% 5%
20	T	121	 88% 5% 7%
21	U	120	 93% 6%
22	V	100	 93% 6%
23	W	88	 84% 7% 8%
24	X	78	 88% 10%
25	Y	51	 98%
26	Z	128	 41% 59%
27	b	106	 97%
28	c	92	 99%
29	d	25	 20% 88% 12%
30	f	3395	 75% 18% 5%
31	h	121	 85% 15%
32	i	158	 78% 20%

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Mol	Chain	Length	Quality of chain
33	j	254	 96%
34	k	387	 98%
35	l	362	 99%
36	m	297	 98%
37	n	176	 94% 5%
38	o	244	 91% 9%
39	p	256	 89% 9%
40	q	191	 98%
41	r	221	 98%
42	s	174	 95%
43	t	199	 96%
44	u	138	 97%
45	a	1038	 78% 18%
46	e	1562	 62% 93% 5%
47	g	245	 91% 8%
48	w	217	 21% 99%
49	x	77	 69% 27%
50	y	76	 66% 30%
51	z	165	 87% 10%
52	0	312	 30% 7% 61%
53	1	18	 94% 6%
54	v	157	 8% 87% 10%

## 2 Entry composition [i](#)

There are 56 unique types of molecules in this entry. The entry contains 151341 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 2 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 3 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	C	183	Total	C	N	O	0	0
			1416	879	284	253		

- Molecule 4 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 5 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
5	E	156	Total	C	N	O	0	0
			1258	781	265	212		

- Molecule 6 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	171	Total	C	N	O	S	0	0
			1437	925	266	243	3		

- Molecule 7 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	G	159	1272	802	245	221	4	0	0

- Molecule 8 is a protein called 60S ribosomal protein L22-A.

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

- Molecule 9 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 10 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	J	63	518	333	102	82	1	0	0

- Molecule 11 is a protein called 60S ribosomal protein L25.

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

- Molecule 12 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
12	L	125	984	620	191	173	0	0

- Molecule 13 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
13	M	135	1080	701	199	180	0	0

- Molecule 14 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	N	148	1169	747	231	188	3	0	0

- Molecule 15 is a protein called 60S ribosomal protein L29.

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

- Molecule 16 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	P	96	737	476	123	137	1	0	0

- Molecule 17 is a protein called 60S ribosomal protein L31-A.

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

- Molecule 18 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	R	127	1013	642	205	165	1	0	0

- Molecule 19 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 20 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 21 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 22 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	99	Total	C	N	O	S	0	0
			766	478	154	132	2		

- Molecule 23 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	81	Total	C	N	O	S	0	0
			645	393	141	106	5		

- Molecule 24 is a protein called 60S ribosomal protein L38.

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

- Molecule 25 is a protein called 60S ribosomal protein L39.

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

- Molecule 26 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	52	Total	C	N	O	S	0	0
			410	254	86	65	5		

- Molecule 27 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	103	Total	C	N	O	S	0	0
			824	517	167	135	5		

- Molecule 28 is a protein called 60S ribosomal protein L43-A.



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

- Molecule 29 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	d	22	207	127	56	23	1	0	0

- Molecule 30 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
30	f	3216	68802	30732	12391	22462	3217	1	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
f	?	-	G	deletion	GB 2211412835

- Molecule 31 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
31	h	121	2579	1152	461	845	121	0	0

- Molecule 32 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
32	i	158	3353	1500	586	1109	158	0	0

- Molecule 33 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	j	246	1874	1168	380	325	1	0	0

- Molecule 34 is a protein called 60S ribosomal protein L3.

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

- Molecule 35 is a protein called 60S ribosomal protein L4-A.

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

- Molecule 36 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	m	294	Total	C	N	O	S	0	0
			2351	1484	410	455	2		

- Molecule 37 is a protein called 60S ribosomal protein L6-B.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	n	167	Total	C	N	O	0	0
			1307	843	234	230		

- Molecule 38 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 39 is a protein called 60S ribosomal protein L8-A.

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

- Molecule 40 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	q	191	Total	C	N	O	S	0	0
			1508	957	274	273	4		

- Molecule 41 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	r	218	Total	C	N	O	S	0	0
			1764	1117	334	306	7		

- Molecule 42 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	s	169	Total	C	N	O	S	0	0
			1346	843	252	247	4		

- Molecule 43 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	t	193	Total	C	N	O	S	0	0
			1543	962	315	266			

- Molecule 44 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 45 is a protein called Ribosome quality control complex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	a	848	Total	C	N	O	S	0	0
			6569	4188	1138	1226	17		

- Molecule 46 is a protein called E3 ubiquitin-protein ligase listerin.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	e	1527	Total	C	N	O	S	0	0
			11508	7354	1936	2180	38		

- Molecule 47 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	g	225	Total	C	N	O	S	0	0
			1651	1030	282	332	7		

- Molecule 48 is a protein called 60S ribosomal protein L1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	w	216	Total	C	N	O	S	0	0
			1709	1092	298	310	9		

- Molecule 49 is a RNA chain called A-site Ala aminoacyl-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	x	75	Total	C	N	O	P	0	0
			1584	705	279	526	74		

- Molecule 50 is a RNA chain called P-site petidyl-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	y	73	Total	C	N	O	P	0	0
			1556	692	273	518	73		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
y	72	C	-	insertion	GB 1554469083
y	73	G	-	insertion	GB 1554469083
y	75	C	A	conflict	GB 1554469083

- Molecule 51 is a protein called 60S ribosomal protein L12-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	z	148	Total	C	N	O	0	0
			728	432	148	148		

- Molecule 52 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	0	121	Total	C	N	O	S	0	0
			961	618	167	173	3		

- Molecule 53 is a protein called CAT tailed nascent peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	1	17	Total	C	N	O	0	0
			85	51	17	17		

- Molecule 54 is a protein called Eukaryotic translation initiation factor 5A-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	v	142	1085	676	183	217	9	0	0

- Molecule 55 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
55	A	1	Total 1	Mg 1	0
55	C	1	Total 1	Mg 1	0
55	E	1	Total 1	Mg 1	0
55	I	1	Total 1	Mg 1	0
55	R	1	Total 1	Mg 1	0
55	T	1	Total 1	Mg 1	0
55	f	3	Total 3	Mg 3	0
55	h	1	Total 1	Mg 1	0
55	j	2	Total 2	Mg 2	0
55	k	1	Total 1	Mg 1	0

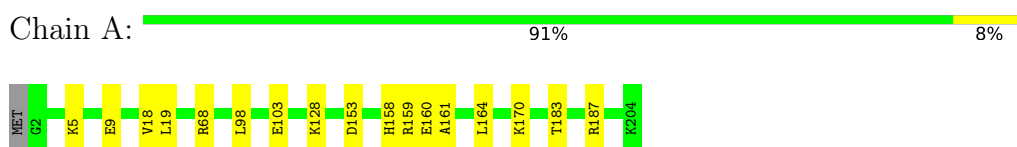
- Molecule 56 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
56	T	1	Total 1	Zn 1	0
56	W	1	Total 1	Zn 1	0
56	Z	1	Total 1	Zn 1	0
56	b	1	Total 1	Zn 1	0
56	c	1	Total 1	Zn 1	0
56	e	2	Total 2	Zn 2	0

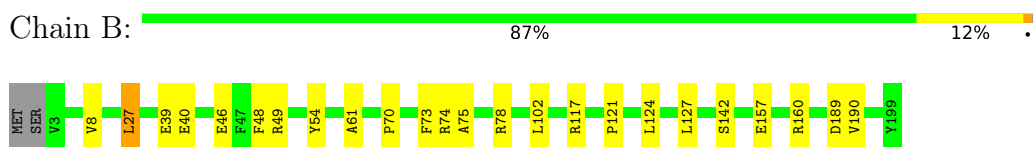
### 3 Residue-property plots [i](#)

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

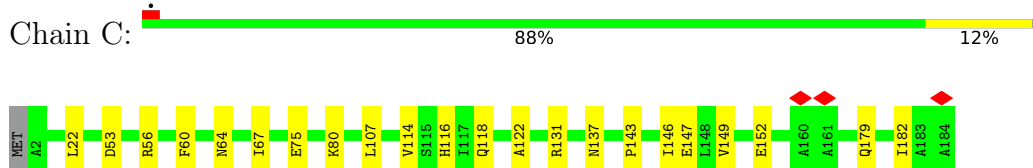
- Molecule 1: 60S ribosomal protein L15-A



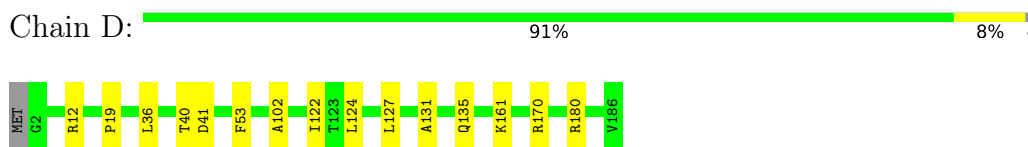
- Molecule 2: 60S ribosomal protein L16-A



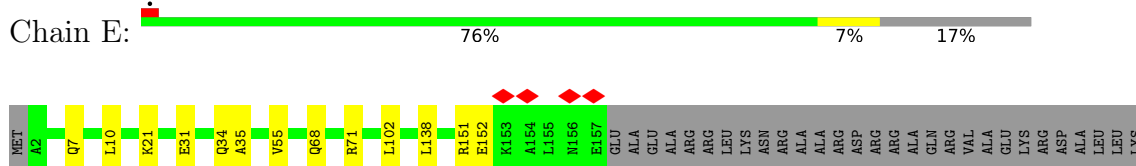
- Molecule 3: 60S ribosomal protein L17-A



- Molecule 4: 60S ribosomal protein L18-A

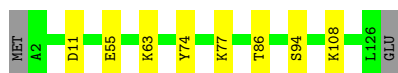


- Molecule 5: 60S ribosomal protein L19-A





Chain L:  92% 6%



- Molecule 13: 60S ribosomal protein L27-A

Chain M:  92% 7%




- Molecule 14: 60S ribosomal protein L28

Chain N:  92% 7%




- Molecule 15: 60S ribosomal protein L29

Chain O:  83% 12%




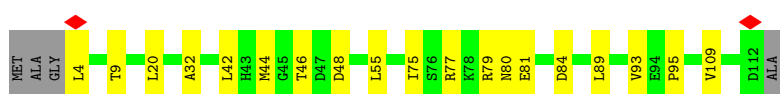
- Molecule 16: 60S ribosomal protein L30

Chain P:  86% 6% 9%



- Molecule 17: 60S ribosomal protein L31-A

Chain Q:  80% 17%



- Molecule 18: 60S ribosomal protein L32

Chain R:  92% 6%




- Molecule 19: 60S ribosomal protein L33-A



Chain S:  94% 5%



- Molecule 20: 60S ribosomal protein L34-A

Chain T:  88% 5% 7%



- Molecule 21: 60S ribosomal protein L35-A

Chain U:  93% 6%




- Molecule 22: 60S ribosomal protein L36-A

Chain V:  93% 6%




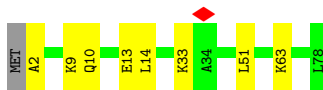
- Molecule 23: 60S ribosomal protein L37-A

Chain W:  84% 7% 8%



- Molecule 24: 60S ribosomal protein L38

Chain X:  88% 10%



- Molecule 25: 60S ribosomal protein L39

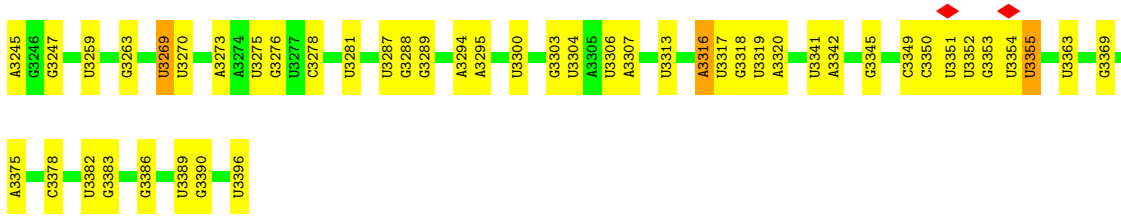
Chain Y:  98%



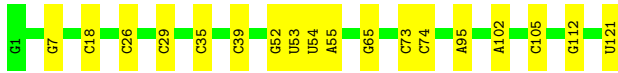
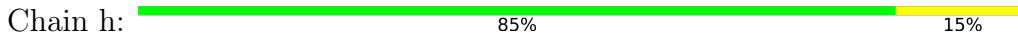
- Molecule 26: Ubiquitin-60S ribosomal protein L40



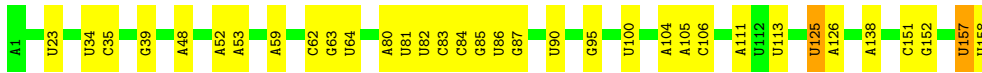
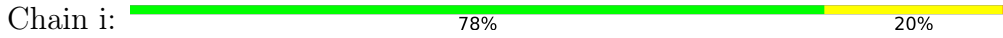




• Molecule 31: 5S rRNA



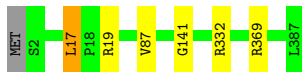
• Molecule 32: 5.8S rRNA



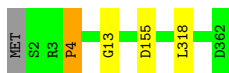
• Molecule 33: 60S ribosomal protein L2-A



• Molecule 34: 60S ribosomal protein L3



• Molecule 35: 60S ribosomal protein L4-A

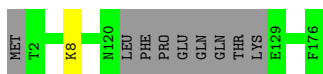


• Molecule 36: 60S ribosomal protein L5



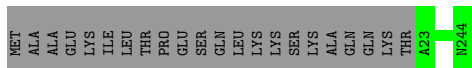
- Molecule 37: 60S ribosomal protein L6-B

Chain n:  94% 5%




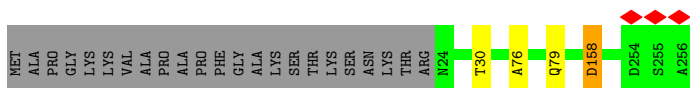
- Molecule 38: 60S ribosomal protein L7-A

Chain o:  91% 9%



- Molecule 39: 60S ribosomal protein L8-A

Chain p:  89% 9%



- Molecule 40: 60S ribosomal protein L9-A

Chain q:  98% ..



- Molecule 41: 60S ribosomal protein L10

Chain r:  98% ..



- Molecule 42: 60S ribosomal protein L11-A

Chain s:  95% ..



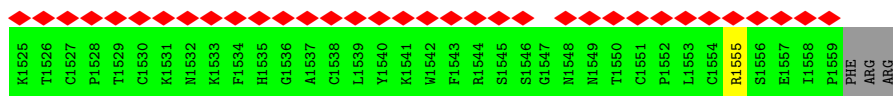
- Molecule 43: 60S ribosomal protein L13-A

Chain t:  96% ..

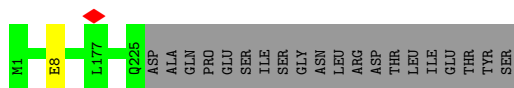




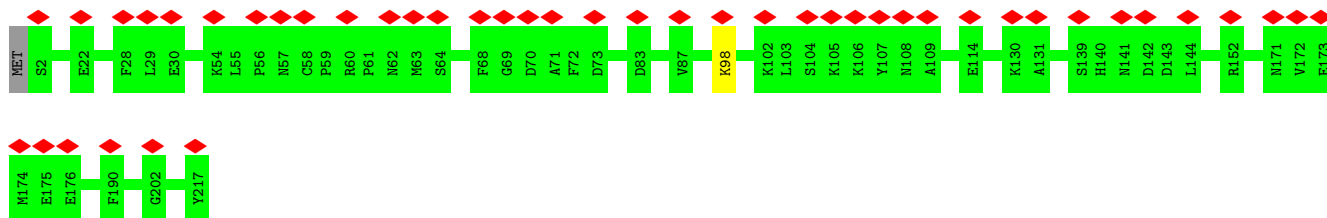
D1436	K1349	I1283	I1212	F1151	D1091	I1031	R911	L851	S791	L731	F671
D1437	K1350	Y1284	E1212	Y1152	T1092	L1032	V912	S852	T792	Q732	C672
K1438	L1351	L1287	Y1213	Q1153	L1093	K1033	L913	E853	T793	H733	A673
E1440	L1352	R1287	E1214	K1154	Y1094	W1034	Y914	E854	T794	A734	V674
I1441	H1353	L1215	L1215	L1155	L1095	L1035	K915	P855	H795	Q735	L675
S1442	T1355	R1216	R1216	Y1156	L1096	D1036	K916	P856	L796	V736	S676
F1443	L1356	I1217	I1217	K1157	E1097	S1037	L917	D857	L797	Y737	K677
Y1449	L1357	GLN	GLN	W1158	L1098	D1038	L918	L858	L798	F738	L678
I1454	Q1358	LYS	LYS	I1159	R1099	L1039	L919	Y859	T799	S739	D679
S1460	L1359	GLN	GLN	K1295	S1100	A1040	S920	Y860	D800	P740	E680
R1461	F1360	THR	THR	S1160	L980	Y1041	I921	D861	D801	G741	T681
V1462	M1361	GLY	GLY	S1161	A981	E1042	I922	F862	K802	A742	F682
G1463	M1362	ASP	ASP	E1163	C1102	L1043	T923	G863	P803	K743	F683
I1464	V1363	ASP	ASP	L1164	N1104	S1044	Y924	H864	I804	E744	S684
T1387	G1364	GLY	GLY	K1165	L1105	F1045	S925	T865	N805	K745	T685
L1379	T1387	SER	SER	K1166	Y1106	S1046	S926	F866	L806	Y746	L686
K1385	R1302	ALA	ALA	L1167	E1107	T1047	T927	F867	K807	V747	L687
F1386	M1303	ASP	ASP	L1168	R888	V1048	T928	K868	N808	T748	L688
E1389	F1304	ASN	ASN	S1169	E989	R1049	L929	H869	M809	H749	N689
F1400	D1305	ASP	ASP	Q1170	V990	L1050	N930	G870	Q810	A750	T690
D1401	D1309	VAL	VAL	Y1171	E991	L1051	G931	K871	K811	V751	D691
F1402	D1312	GLY	GLY	K1172	L992	L1052	G932	K872	L812	E752	F692
I1403	L1313	SER	SER	R1173	V993	L1053	L933	N873	I813	L753	L693
I1404	L1314	LYS	LYS	I1174	D994	D1054	A934	L874	R814	I754	S694
M1405	D1315	ASN	ASN	F1175	Q995	F1055	S935	N875	Y815	N755	C695
S1406	T1316	GLY	GLY	E1176	E996	F1056	V936	F876	A816	G756	A696
K1406	E1317	GLU	GLU	V1177	F997	T1057	E937	S877	L817	C757	L697
M1407	K1242	ILE	ILE	Y1178	K998	K1058	S938	D878	F818	N758	Y698
D1408	K1243	SER	SER	L1179	S999	M1059	F939	I879	L819	D759	E699
H1409	L1244	E1122	E1122	M1180	L1000	M1060	V940	V880	D820	T760	V700
L1410	L1245	Y1123	Y1123	D1181	A1001	R1061	T941	G881	A821	S761	S701
T1411	K1246	G1124	G1124	K1182	L1002	F1062	K942	N882	L822	Q762	E702
SER	K1247	D1125	D1125	D1183	L1003	E1063	T943	V883	L823	I763	D703
ASN	V1248	E1126	E1126	I1184	M1004	G1064	V944	I884	D824	F764	T704
ASP	T1249	I1127	I1127	G1185	M1005	V1065	R945	Q885	A825	F765	N705
A1416	E1250	Q1128	Q1128	S1186	L1006	R1066	D946	P886	P827	P766	E706
L1417	V1251	I1129	I1129	I1187	L1007	D1067	Q947	A887	E828	A767	K707
L1420	V1252	M1130	M1130	I1188	D1008	M1068	K948	N888	R829	N768	L708
K1421	K1254	L1131	L1131	M1189	I1009	G1069	S949	G889	V830	A769	F709
M1422	E1255	E1133	E1133	Q1190	P1010	T1070	T950	G890	N831	I770	K710
N1423	Y1256	L1134	L1134	S1191	Q1011	A1072	D951	D891	N832	E771	L711
I1424	E1260	F1136	F1136	R1192	D1012	E1073	K952	A892	N833	V772	S712
N1426	E1261	L1137	L1137	L1193	D1013	F1073	D953	M893	H833	F773	L713
N1427	N1261	L1137	L1137	L1194	K1014	E1074	Y954	L894	I834	A774	Q714
V1428	N1263	L1137	L1137	L1195	Q1015	L1075	L955	T895	V835	R775	L715
K1429	S1264	M1138	M1138	T1196	V1016	S1076	L956	F896	A836	V776	A716
A1430	L1269	F1139	F1139	L1197	E1077	E1077	C957	D897	F837	M777	K717
S1431	E1269	M1140	M1140	L1197	P1018	R1078	A958	I898	G718	P778	G718
L1432	W1272	E1142	E1142	L1079	I1019	L1079	I959	A899	N719	A779	N719
L1433	F1279	R1143	R1143	L1080	A1020	L1080	L960	E900	V840	I780	S720
L1434		V1202	V1202	A1081	P1021	A1081	L961	S901	S842	D781	E721
L1435		V1203	V1203	D1082	Q1022	D1082	L962	N902	S843	Y782	I722
F1436		K1204	K1204	S1083	R1023	S1083	M963	S903	E843	R783	A723
E1437		T1205	T1205	S1085	L1024	L1024	F964	V904	L844	S784	N724
E1438		Q1206	Q1206	S1086	M1025	M1025	N965	Y905	V845	S785	K725
E1439		Q1207	Q1207	M1086	M1026	M1026	R966	F906	T846	L786	L726
E1440		D1208	D1208	C1087	I1027	I1027	S967	F907	D847	V787	A727
S1524		L1150	L1150	Q1088	F1028	F1028	N968	Y908	N849	S788	Q728
		I1089	I1089	I1089	R1029	R1029	S969	Y909	N850	S789	V729
		I1210	I1210	I1090	S1030	S1030	K970	S910	C850	L790	I730



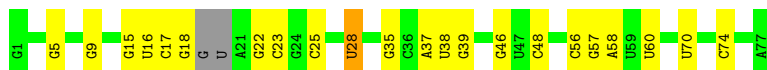
- Molecule 47: Eukaryotic translation initiation factor 6



- Molecule 48: 60S ribosomal protein L1-A



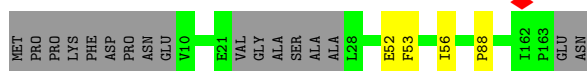
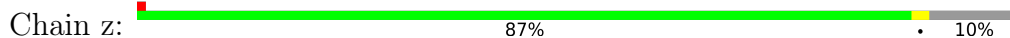
- Molecule 49: A-site Ala aminoacyl-tRNA



- Molecule 50: P-site peptidyl-tRNA



- Molecule 51: 60S ribosomal protein L12-A



- Molecule 52: 60S acidic ribosomal protein P0







## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	74128	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	46	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	3.681	Depositor
Minimum map value	-0.788	Depositor
Average map value	0.020	Depositor
Map value standard deviation	0.128	Depositor
Recommended contour level	0.35	Depositor
Map size ( $\text{\AA}$ )	476.55002, 476.55002, 476.55002	wwPDB
Map dimensions	450, 450, 450	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.059, 1.059, 1.059	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, MG, 5CT

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	A	0.39	0/1757	0.70	1/2354 (0.0%)
2	B	0.39	0/1585	0.64	1/2128 (0.0%)
3	C	0.38	0/1439	0.71	2/1938 (0.1%)
4	D	0.34	0/1465	0.67	1/1965 (0.1%)
5	E	0.37	0/1275	0.67	1/1702 (0.1%)
6	F	0.38	0/1473	0.65	0/1980
7	G	0.36	0/1296	0.62	0/1739
8	H	0.37	0/812	0.73	3/1099 (0.3%)
9	I	0.35	0/1018	0.64	0/1369
10	J	0.36	0/530	0.63	0/703
11	K	0.41	0/979	0.69	1/1321 (0.1%)
12	L	0.35	0/995	0.67	1/1329 (0.1%)
13	M	0.36	0/1106	0.61	0/1485
14	N	0.40	0/1200	0.62	0/1607
15	O	0.32	0/473	0.72	2/629 (0.3%)
16	P	0.35	0/745	0.68	0/1001
17	Q	0.39	0/890	0.77	2/1196 (0.2%)
18	R	0.32	0/1034	0.59	0/1385
19	S	0.50	0/868	0.64	0/1168
20	T	0.35	0/890	0.67	0/1189
21	U	0.34	0/978	0.65	1/1301 (0.1%)
22	V	0.34	0/772	0.66	0/1026
23	W	0.39	0/660	0.67	0/875
24	X	0.33	0/618	0.78	1/826 (0.1%)
25	Y	0.33	0/443	0.65	0/588
26	Z	0.34	0/416	0.70	0/553
27	b	0.36	0/836	0.66	0/1104
28	c	0.36	0/701	0.66	0/934
29	d	0.26	0/208	0.84	0/267
30	f	0.61	0/77011	1.03	296/120065 (0.2%)
31	h	0.53	0/2883	0.98	9/4491 (0.2%)
32	i	0.61	0/3746	0.96	7/5832 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	j	0.38	0/1908	0.67	0/2564
34	k	0.36	0/3146	0.63	1/4228 (0.0%)
35	l	0.36	0/2800	0.64	2/3790 (0.1%)
36	m	0.34	0/2400	0.67	4/3239 (0.1%)
37	n	0.36	0/1329	0.67	0/1794
38	o	0.37	0/1821	0.61	0/2451
39	p	0.34	0/1836	0.62	2/2481 (0.1%)
40	q	0.37	0/1529	0.68	2/2060 (0.1%)
41	r	0.33	0/1801	0.63	0/2416
42	s	0.33	0/1367	0.70	3/1834 (0.2%)
43	t	0.36	0/1568	0.69	1/2106 (0.0%)
44	u	0.34	0/1068	0.66	1/1438 (0.1%)
45	a	0.29	0/6679	0.49	0/9012
46	e	0.28	0/11707	0.49	0/15897
47	g	0.32	0/1672	0.63	0/2281
48	w	0.33	0/1736	0.65	0/2332
49	x	0.33	0/1765	1.00	8/2746 (0.3%)
50	y	0.22	0/1735	0.65	0/2701
51	z	0.37	0/726	0.60	0/1006
52	0	0.33	0/976	0.55	0/1313
54	v	0.33	0/1084	0.63	1/1456 (0.1%)
All	All	0.50	0/161755	0.87	354/236294 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
15	O	0	1
21	U	0	1
23	W	0	1
34	k	0	2
35	l	0	2
39	p	0	3
40	q	0	1
44	u	0	1
46	e	0	2
47	g	0	1
All	All	0	15

There are no bond length outliers.

The worst 5 of 354 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	f	3217	C	N1-C2-O2	12.17	126.20	118.90
30	f	3217	C	C2-N1-C1'	11.30	131.23	118.80
30	f	3217	C	N3-C2-O2	-9.78	115.05	121.90
11	K	134	ASP	CB-CG-OD1	9.65	126.99	118.30
30	f	922	U	C2-N1-C1'	9.29	128.84	117.70

There are no chirality outliers.

5 of 15 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
15	O	20	GLY	Peptide
21	U	83	LYS	Peptide
23	W	39	TYR	Peptide
34	k	141	GLY	Peptide
34	k	17	LEU	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	A	1720	0	1779	10	0
2	B	1555	0	1659	13	0
3	C	1416	0	1433	11	0
4	D	1441	0	1543	8	0
5	E	1258	0	1342	6	0
6	F	1437	0	1475	15	0
7	G	1272	0	1312	9	0
8	H	796	0	812	4	0
9	I	1003	0	1048	7	0
10	J	518	0	542	3	0
11	K	964	0	1025	1	0
12	L	984	0	1075	4	0
13	M	1080	0	1122	5	0
14	N	1169	0	1211	7	0
15	O	462	0	491	6	0
16	P	737	0	792	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	Q	876	0	912	9	0
18	R	1013	0	1077	5	0
19	S	850	0	880	2	0
20	T	880	0	942	3	0
21	U	969	0	1078	3	0
22	V	766	0	844	4	0
23	W	645	0	645	5	0
24	X	612	0	682	3	0
25	Y	436	0	475	0	0
26	Z	410	0	442	0	0
27	b	824	0	888	0	0
28	c	694	0	734	0	0
29	d	207	0	250	0	0
30	f	68802	0	34573	0	0
31	h	2579	0	1304	0	0
32	i	3353	0	1695	0	0
33	j	1874	0	1943	0	0
34	k	3075	0	3142	0	0
35	l	2748	0	2859	0	0
36	m	2351	0	2294	0	0
37	n	1307	0	1377	0	0
38	o	1784	0	1862	0	0
39	p	1804	0	1877	0	0
40	q	1508	0	1572	0	0
41	r	1764	0	1804	0	0
42	s	1346	0	1370	0	0
43	t	1543	0	1608	0	0
44	u	1053	0	1149	0	0
45	a	6569	0	6460	0	0
46	e	11508	0	10762	0	0
47	g	1651	0	1613	0	0
48	w	1709	0	1799	0	0
49	x	1584	0	803	0	0
50	y	1556	0	788	0	0
51	z	728	0	337	0	0
52	0	961	0	979	12	0
53	1	85	0	20	0	0
54	v	1085	0	1086	0	0
55	A	1	0	0	0	0
55	C	1	0	0	0	0
55	E	1	0	0	0	0
55	I	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
55	R	1	0	0	0	0
55	T	1	0	0	0	0
55	f	3	0	0	0	0
55	h	1	0	0	0	0
55	j	2	0	0	0	0
55	k	1	0	0	0	0
56	T	1	0	0	0	0
56	W	1	0	0	0	0
56	Z	1	0	0	0	0
56	b	1	0	0	0	0
56	c	1	0	0	0	0
56	e	2	0	0	0	0
All	All	151341	0	113586	149	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 5.

The worst 5 of 149 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)
15:O:16:ALA:O	15:O:20:GLY:HA3	1.68	0.90
15:O:16:ALA:O	15:O:20:GLY:CA	2.36	0.73
52:O:26:PHE:HB2	52:O:87:VAL:HB	1.73	0.68
2:B:46[A]:GLU:HB3	2:B:49[A]:ARG:HG3	1.75	0.68
7:G:84:TYR:HB2	15:O:24:PRO:HD3	1.78	0.64

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	201/204 (98%)	190 (94%)	11 (6%)	0	100	100
2	B	195/199 (98%)	192 (98%)	3 (2%)	0	100	100
3	C	181/184 (98%)	172 (95%)	9 (5%)	0	100	100
4	D	183/186 (98%)	176 (96%)	7 (4%)	0	100	100
5	E	154/189 (82%)	151 (98%)	3 (2%)	0	100	100
6	F	169/172 (98%)	163 (96%)	6 (4%)	0	100	100
7	G	157/160 (98%)	149 (95%)	8 (5%)	0	100	100
8	H	98/121 (81%)	93 (95%)	5 (5%)	0	100	100
9	I	134/137 (98%)	132 (98%)	2 (2%)	0	100	100
10	J	61/155 (39%)	61 (100%)	0	0	100	100
11	K	119/142 (84%)	118 (99%)	1 (1%)	0	100	100
12	L	123/127 (97%)	119 (97%)	4 (3%)	0	100	100
13	M	133/136 (98%)	126 (95%)	7 (5%)	0	100	100
14	N	146/149 (98%)	136 (93%)	10 (7%)	0	100	100
15	O	56/59 (95%)	52 (93%)	3 (5%)	1 (2%)	8	16
16	P	94/105 (90%)	93 (99%)	1 (1%)	0	100	100
17	Q	107/113 (95%)	98 (92%)	9 (8%)	0	100	100
18	R	125/130 (96%)	123 (98%)	2 (2%)	0	100	100
19	S	104/107 (97%)	100 (96%)	4 (4%)	0	100	100
20	T	110/121 (91%)	108 (98%)	2 (2%)	0	100	100
21	U	117/120 (98%)	112 (96%)	5 (4%)	0	100	100
22	V	97/100 (97%)	93 (96%)	4 (4%)	0	100	100
23	W	79/88 (90%)	74 (94%)	5 (6%)	0	100	100
24	X	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
25	Y	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
26	Z	50/128 (39%)	47 (94%)	3 (6%)	0	100	100
27	b	101/106 (95%)	95 (94%)	6 (6%)	0	100	100
28	c	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
29	d	20/25 (80%)	19 (95%)	1 (5%)	0	100	100
33	j	244/254 (96%)	226 (93%)	18 (7%)	0	100	100
34	k	384/387 (99%)	364 (95%)	20 (5%)	0	100	100
35	l	359/362 (99%)	329 (92%)	29 (8%)	1 (0%)	41	64

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	m	292/297 (98%)	278 (95%)	14 (5%)	0	100	100
37	n	163/176 (93%)	153 (94%)	10 (6%)	0	100	100
38	o	220/244 (90%)	207 (94%)	13 (6%)	0	100	100
39	p	231/256 (90%)	220 (95%)	11 (5%)	0	100	100
40	q	189/191 (99%)	174 (92%)	14 (7%)	1 (0%)	29	52
41	r	216/221 (98%)	206 (95%)	10 (5%)	0	100	100
42	s	167/174 (96%)	161 (96%)	5 (3%)	1 (1%)	25	47
43	t	191/199 (96%)	174 (91%)	16 (8%)	1 (0%)	29	52
44	u	134/138 (97%)	125 (93%)	9 (7%)	0	100	100
45	a	842/1038 (81%)	832 (99%)	10 (1%)	0	100	100
46	e	1519/1562 (97%)	1503 (99%)	14 (1%)	2 (0%)	51	75
47	g	223/245 (91%)	215 (96%)	8 (4%)	0	100	100
48	w	214/217 (99%)	211 (99%)	3 (1%)	0	100	100
51	z	144/165 (87%)	135 (94%)	5 (4%)	4 (3%)	5	7
52	0	117/312 (38%)	116 (99%)	0	1 (1%)	17	35
54	v	139/157 (88%)	139 (100%)	0	0	100	100
All	All	9314/10279 (91%)	8965 (96%)	337 (4%)	12 (0%)	54	75

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
46	e	437	LYS
51	z	88	PRO
51	z	52	GLU
51	z	53	PHE
35	l	4	PRO

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	175/176 (99%)	175 (100%)	0	100	100
2	B	160/162 (99%)	160 (100%)	0	100	100
3	C	138/146 (94%)	138 (100%)	0	100	100
4	D	150/151 (99%)	149 (99%)	1 (1%)	84	94
5	E	129/154 (84%)	129 (100%)	0	100	100
6	F	155/156 (99%)	155 (100%)	0	100	100
7	G	135/137 (98%)	134 (99%)	1 (1%)	84	94
8	H	87/107 (81%)	87 (100%)	0	100	100
9	I	104/105 (99%)	104 (100%)	0	100	100
10	J	54/129 (42%)	54 (100%)	0	100	100
11	K	104/118 (88%)	104 (100%)	0	100	100
12	L	108/110 (98%)	108 (100%)	0	100	100
13	M	112/116 (97%)	112 (100%)	0	100	100
14	N	117/119 (98%)	117 (100%)	0	100	100
15	O	46/47 (98%)	45 (98%)	1 (2%)	52	76
16	P	81/88 (92%)	81 (100%)	0	100	100
17	Q	92/97 (95%)	92 (100%)	0	100	100
18	R	107/111 (96%)	107 (100%)	0	100	100
19	S	90/91 (99%)	89 (99%)	1 (1%)	73	88
20	T	95/103 (92%)	94 (99%)	1 (1%)	73	88
21	U	104/105 (99%)	104 (100%)	0	100	100
22	V	80/82 (98%)	80 (100%)	0	100	100
23	W	67/71 (94%)	67 (100%)	0	100	100
24	X	68/69 (99%)	66 (97%)	2 (3%)	42	68
25	Y	45/46 (98%)	45 (100%)	0	100	100
26	Z	45/116 (39%)	45 (100%)	0	100	100
27	b	87/91 (96%)	87 (100%)	0	100	100
28	c	71/72 (99%)	71 (100%)	0	100	100
29	d	20/23 (87%)	20 (100%)	0	100	100
33	j	189/196 (96%)	188 (100%)	1 (0%)	88	96
34	k	320/323 (99%)	316 (99%)	4 (1%)	69	86
35	l	288/289 (100%)	288 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	m	241/245 (98%)	241 (100%)	0	100	100
37	n	139/155 (90%)	138 (99%)	1 (1%)	84	94
38	o	186/205 (91%)	186 (100%)	0	100	100
39	p	187/208 (90%)	187 (100%)	0	100	100
40	q	168/171 (98%)	168 (100%)	0	100	100
41	r	185/187 (99%)	183 (99%)	2 (1%)	73	88
42	s	145/150 (97%)	145 (100%)	0	100	100
43	t	154/159 (97%)	154 (100%)	0	100	100
44	u	107/109 (98%)	107 (100%)	0	100	100
45	a	676/949 (71%)	642 (95%)	34 (5%)	24	47
46	e	1150/1451 (79%)	1080 (94%)	70 (6%)	18	38
47	g	180/211 (85%)	180 (100%)	0	100	100
48	w	197/198 (100%)	196 (100%)	1 (0%)	88	96
52	0	104/254 (41%)	95 (91%)	9 (9%)	10	20
54	v	119/132 (90%)	116 (98%)	3 (2%)	47	73
All	All	7561/8690 (87%)	7429 (98%)	132 (2%)	62	81

5 of 132 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
46	e	1480	ILE
48	w	98	LYS
54	v	71	GLU
45	a	1014	LEU
45	a	1003	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
46	e	805	ASN
46	e	1288	GLN
46	e	1111	GLN
46	e	1499	HIS
45	a	696	GLN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
30	f	3211/3395 (94%)	590 (18%)	0
31	h	120/121 (99%)	12 (10%)	0
32	i	157/158 (99%)	32 (20%)	0
49	x	72/77 (93%)	19 (26%)	0
50	y	71/76 (93%)	23 (32%)	0
All	All	3631/3827 (94%)	676 (18%)	0

5 of 676 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
30	f	6	A
30	f	13	A
30	f	14	U
30	f	26	A
30	f	40	A

There are no RNA pucker outliers to report.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
54	5CT	v	51	54	13,14,15	0.77	0	9,15,17	1.29	1 (11%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
54	5CT	v	51	54	-	9/13/14/16	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	v	51	5CT	C4-C3-C2	-2.19	108.86	113.47

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
54	v	51	5CT	NZ-C1-C2-C3
54	v	51	5CT	O1-C2-C3-C4
54	v	51	5CT	C2-C3-C4-N1
54	v	51	5CT	C-CA-CB-CG
54	v	51	5CT	N-CA-CB-CG

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 20 ligands modelled in this entry, 20 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

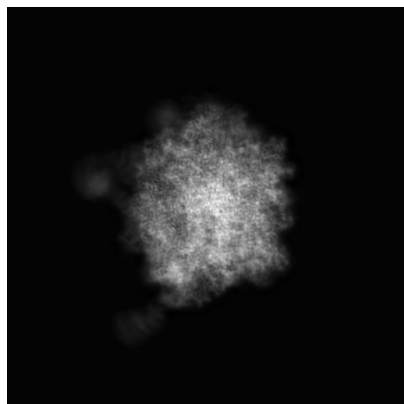
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-15423. These allow visual inspection of the internal detail of the map and identification of artifacts.

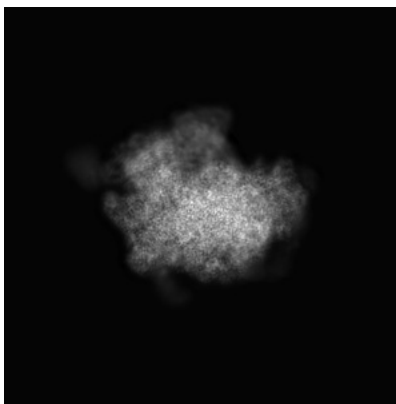
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

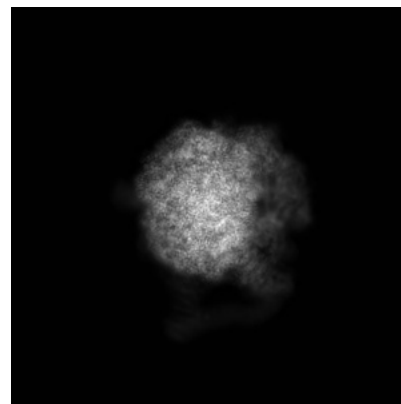
#### 6.1.1 Primary map



X

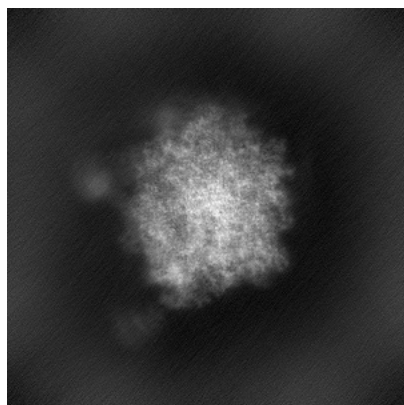


Y

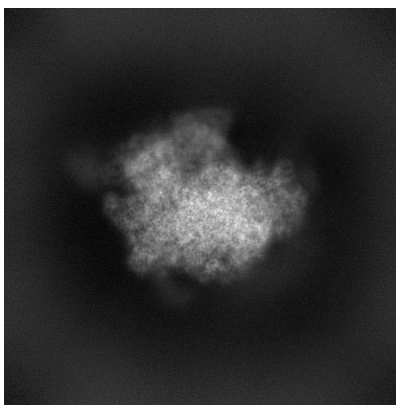


Z

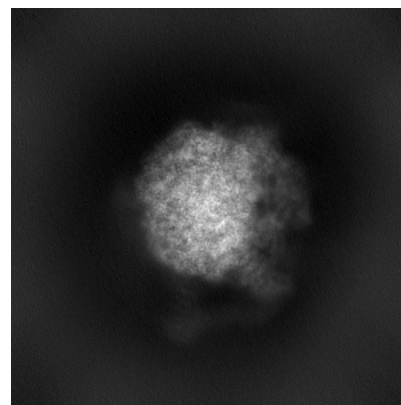
#### 6.1.2 Raw map



X



Y

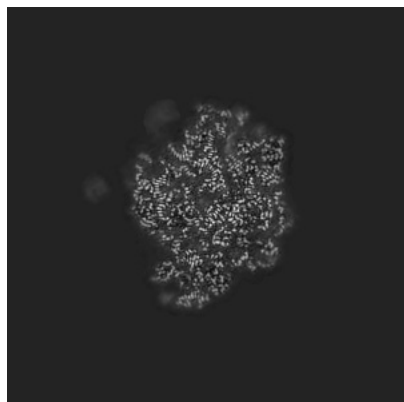


Z

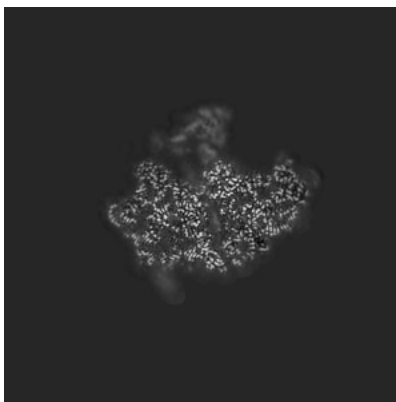
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

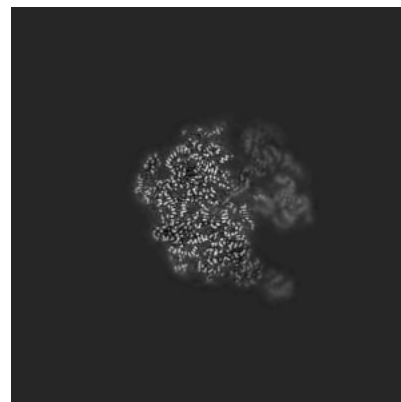
### 6.2.1 Primary map



X Index: 225

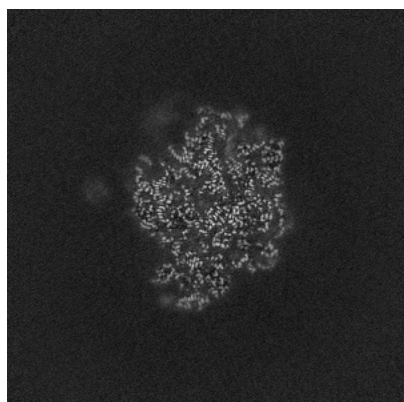


Y Index: 225

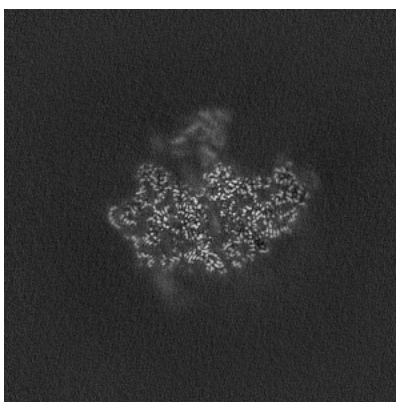


Z Index: 225

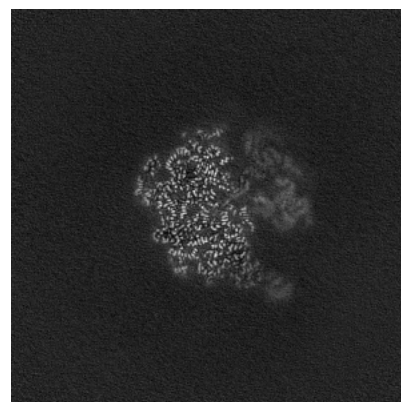
### 6.2.2 Raw map



X Index: 225



Y Index: 225



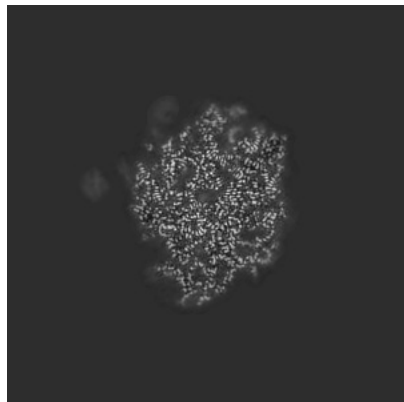
Z Index: 225

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

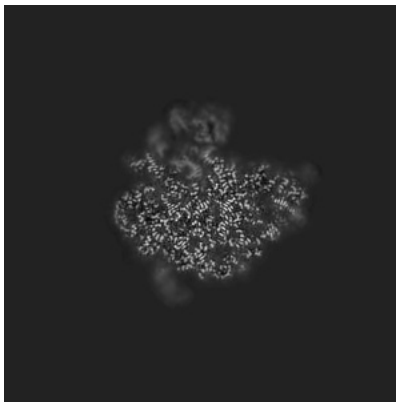


## 6.3 Largest variance slices [i](#)

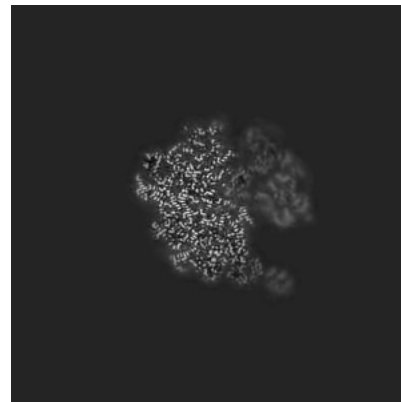
### 6.3.1 Primary map



X Index: 219

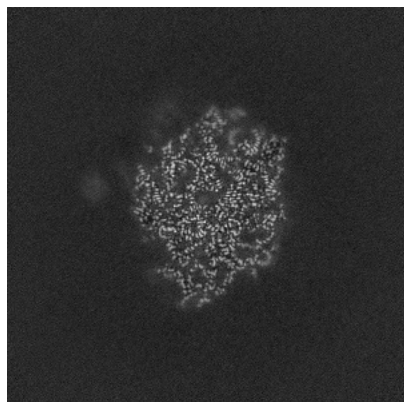


Y Index: 237

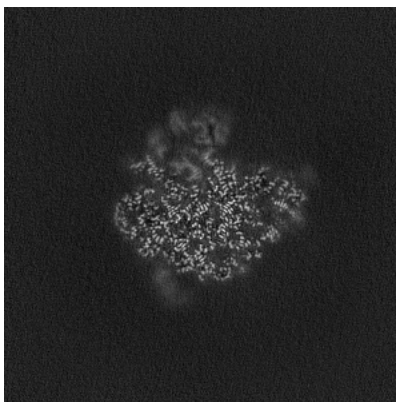


Z Index: 222

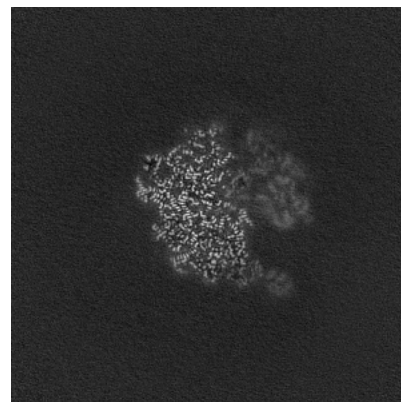
### 6.3.2 Raw map



X Index: 219



Y Index: 237



Z Index: 222

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

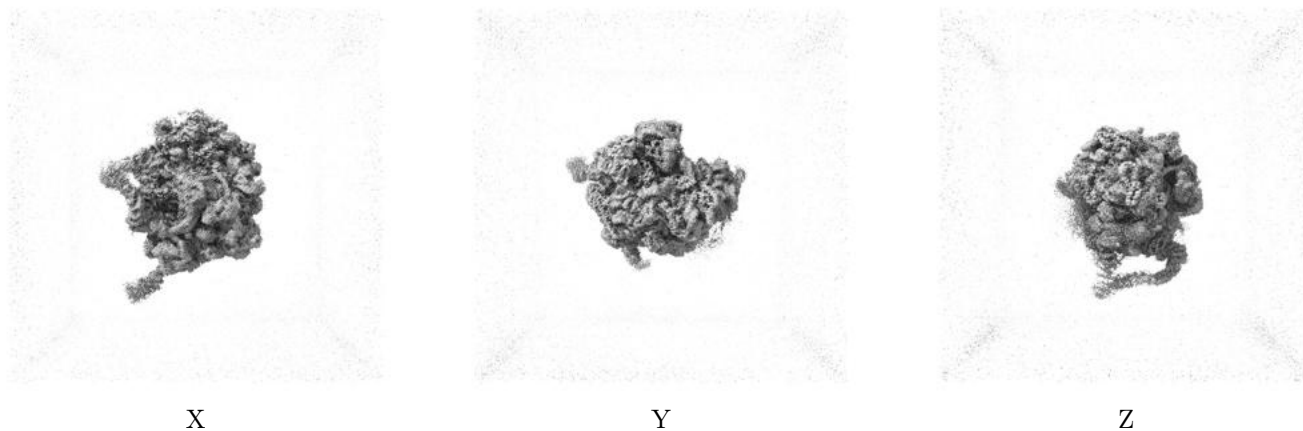
## 6.4 Orthogonal surface views [i](#)

### 6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.35. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.4.2 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.

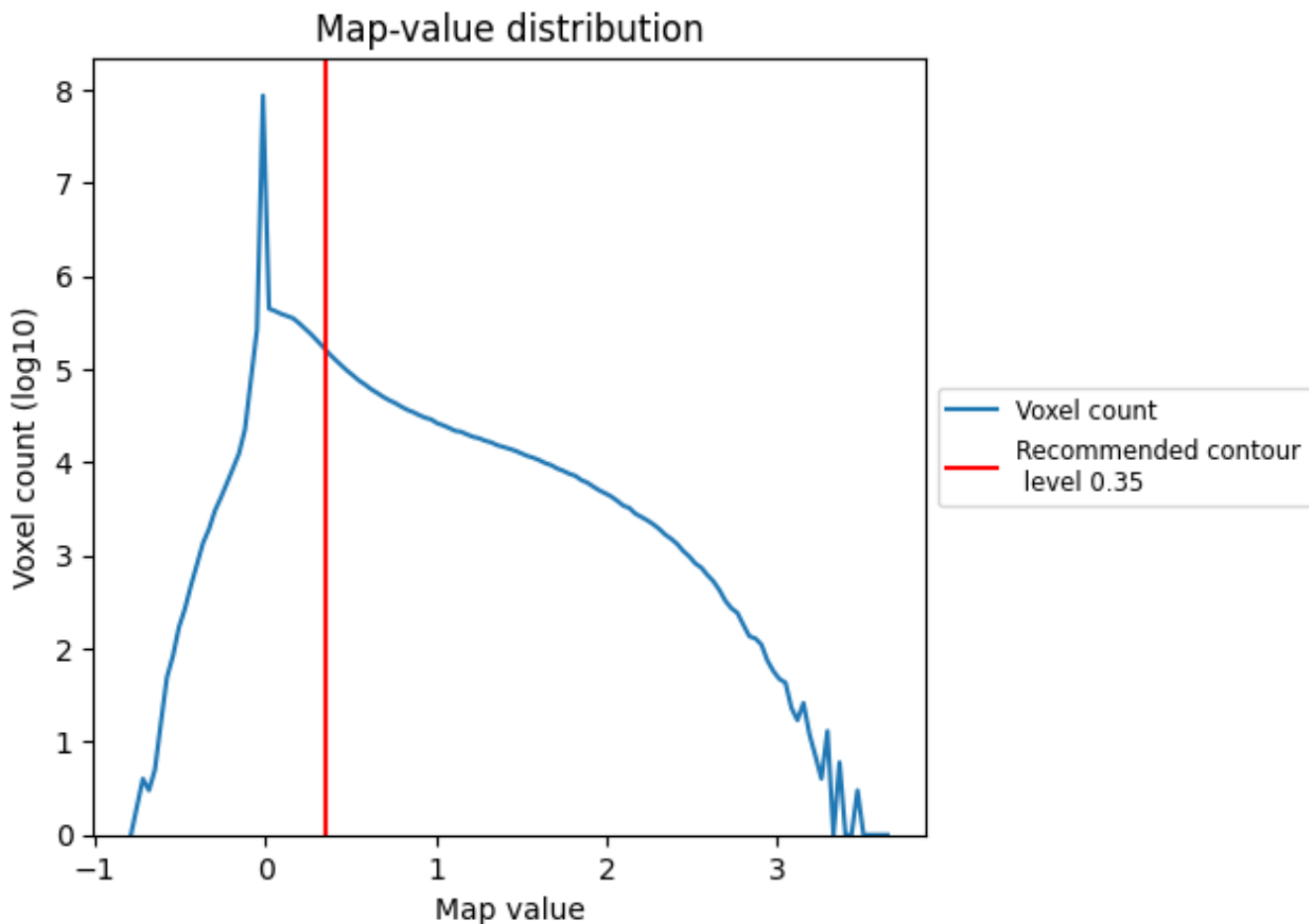
## 6.5 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

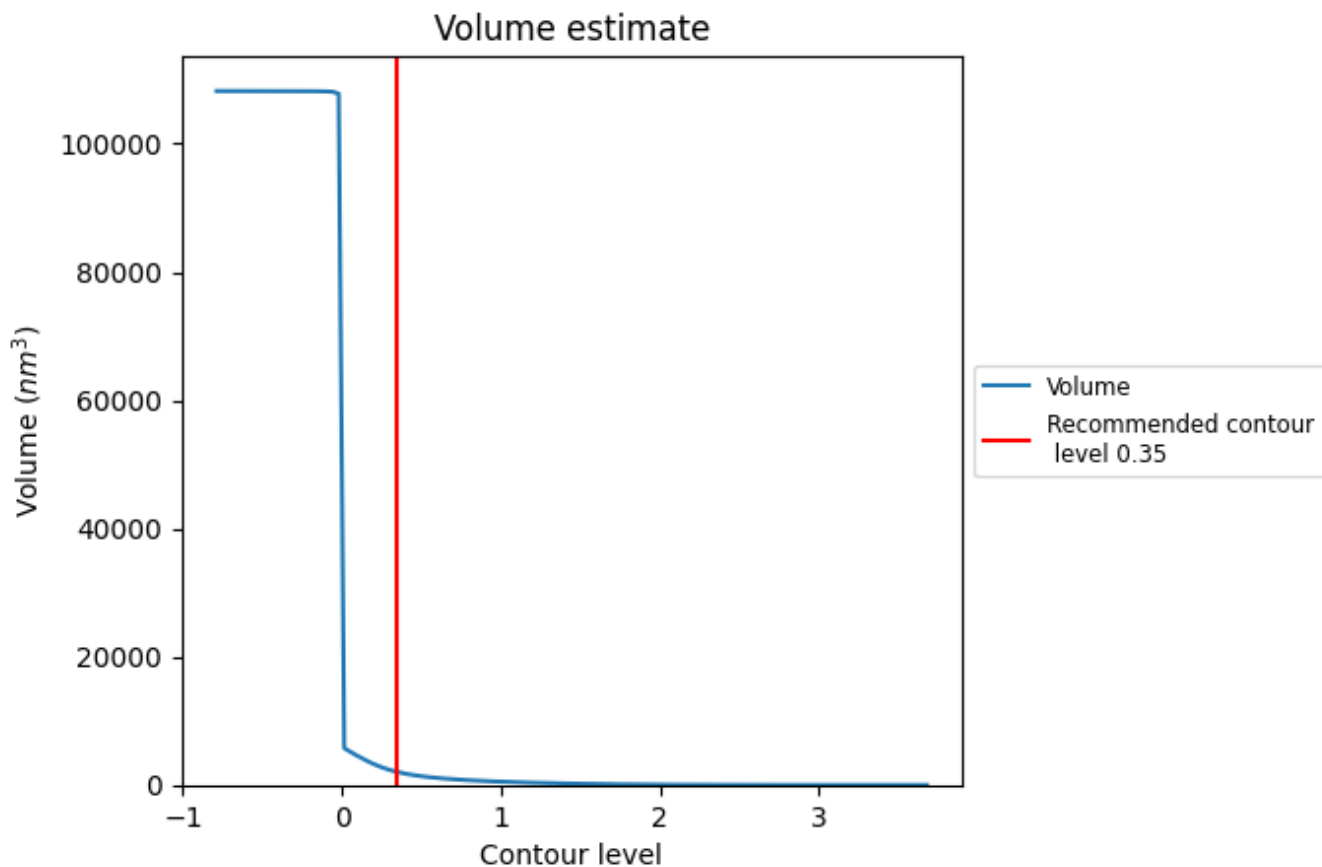
This section contains the results of statistical analysis of the map.

### 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.

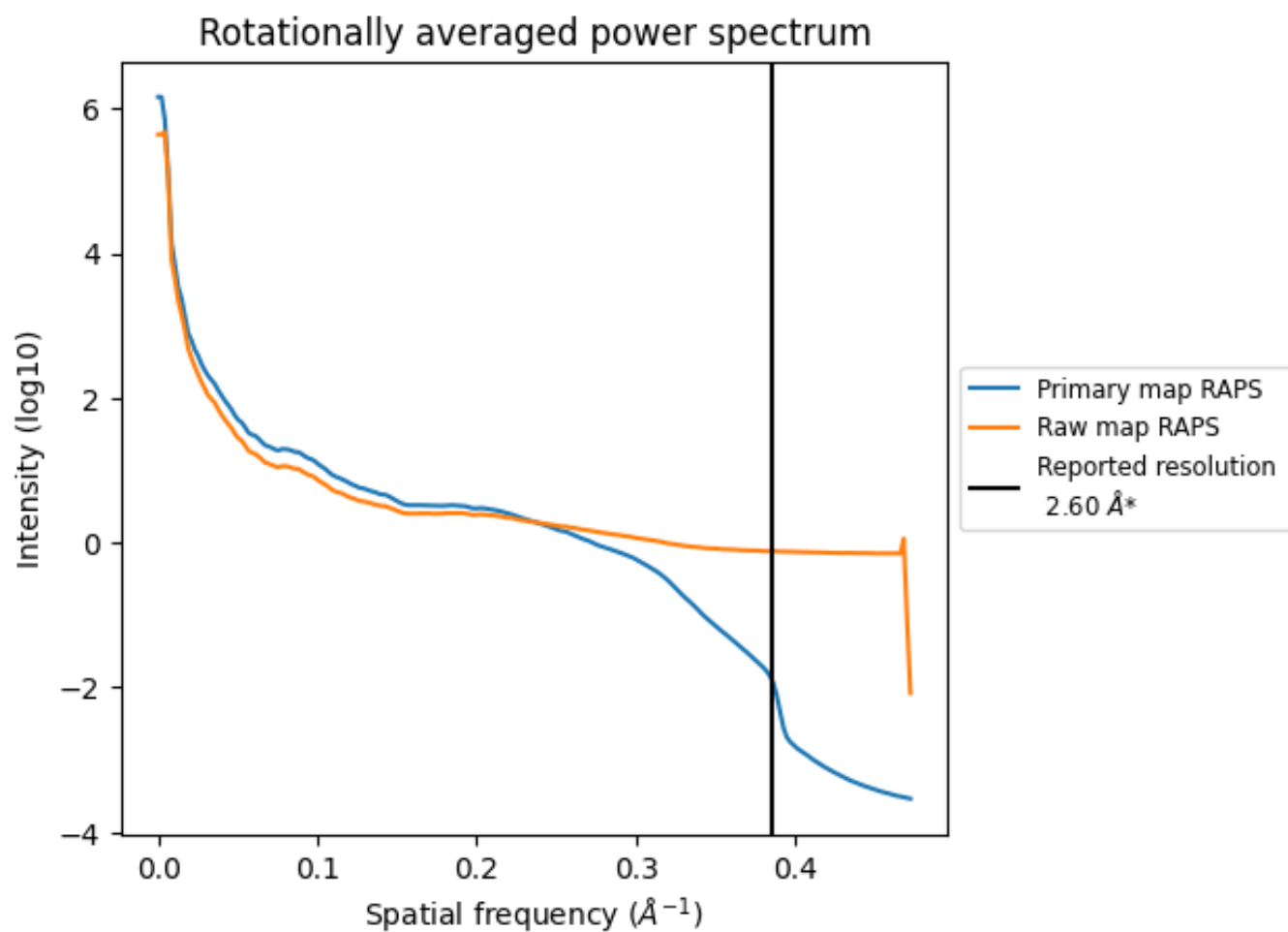
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 2020  $\text{nm}^3$ ; this corresponds to an approximate mass of 1824 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

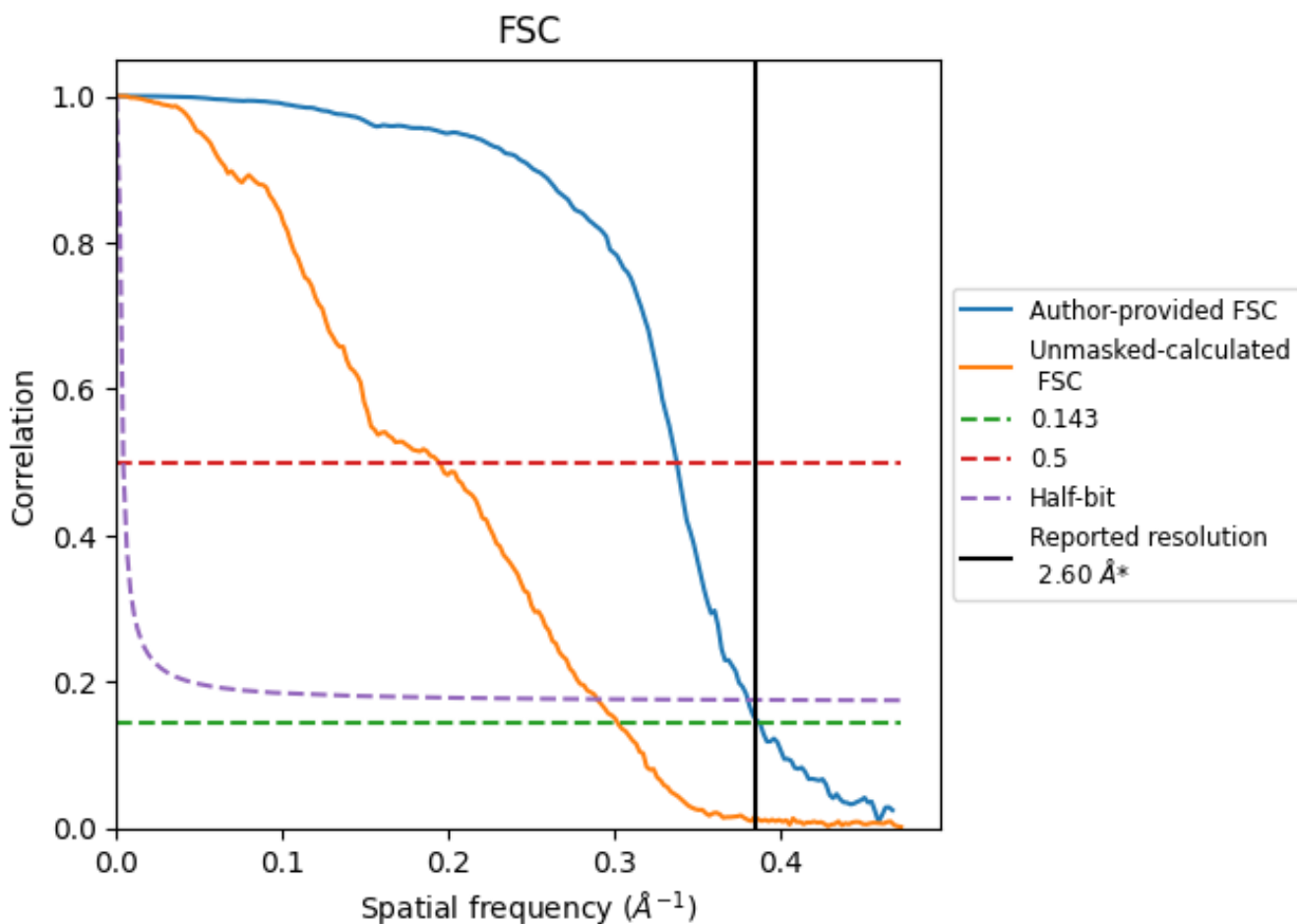


\*Reported resolution corresponds to spatial frequency of  $0.385 \text{ \AA}^{-1}$

## 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 0.385 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

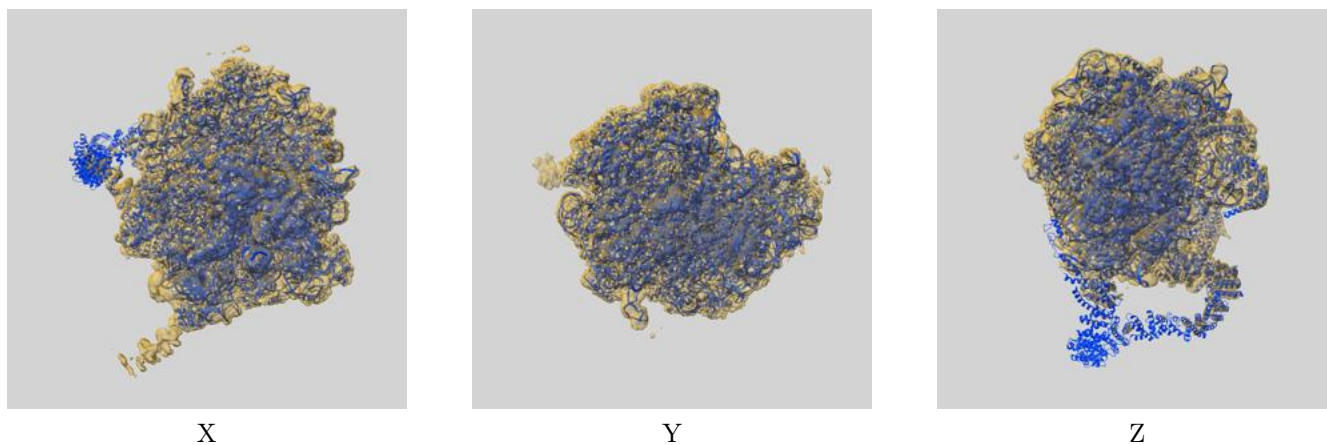
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.60	-	-
Author-provided FSC curve	2.58	2.97	2.63
Unmasked-calculated*	3.32	5.16	3.46

\*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 3.32 differs from the reported value 2.6 by more than 10 %

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

This section contains information regarding the fit between EMDB map EMD-15423 and PDB model 8AGT. Per-residue inclusion information can be found in section [3](#) on page [14](#).

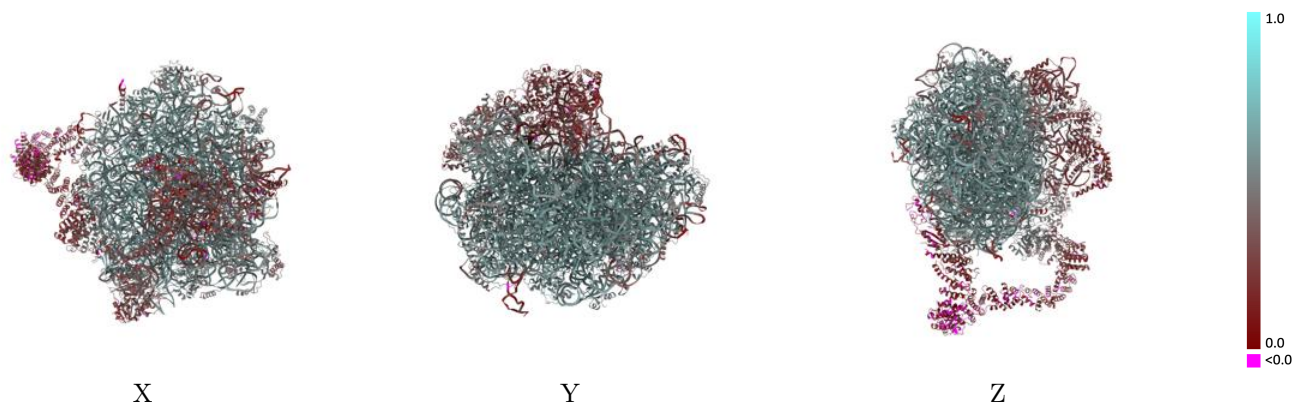
### 9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.35 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.

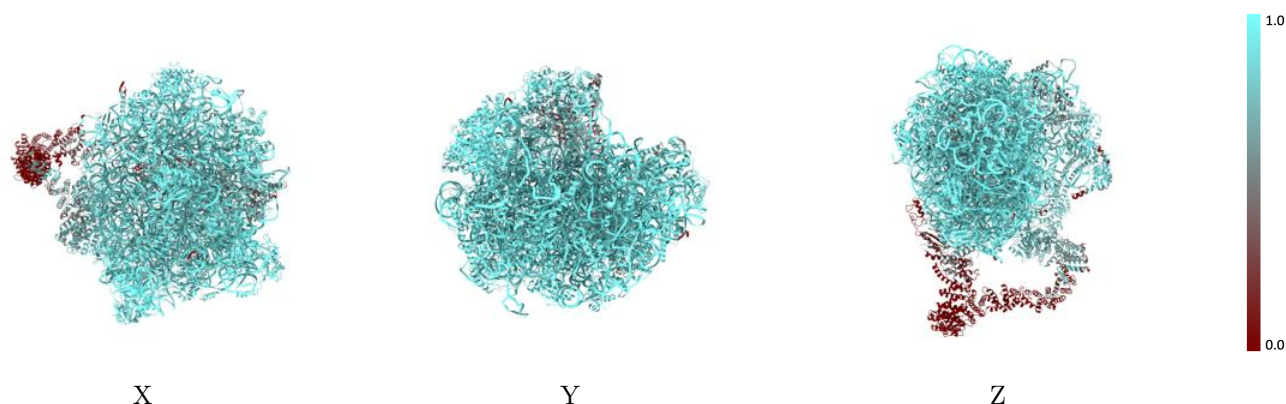


## 9.2 Q-score mapped to coordinate model [i](#)



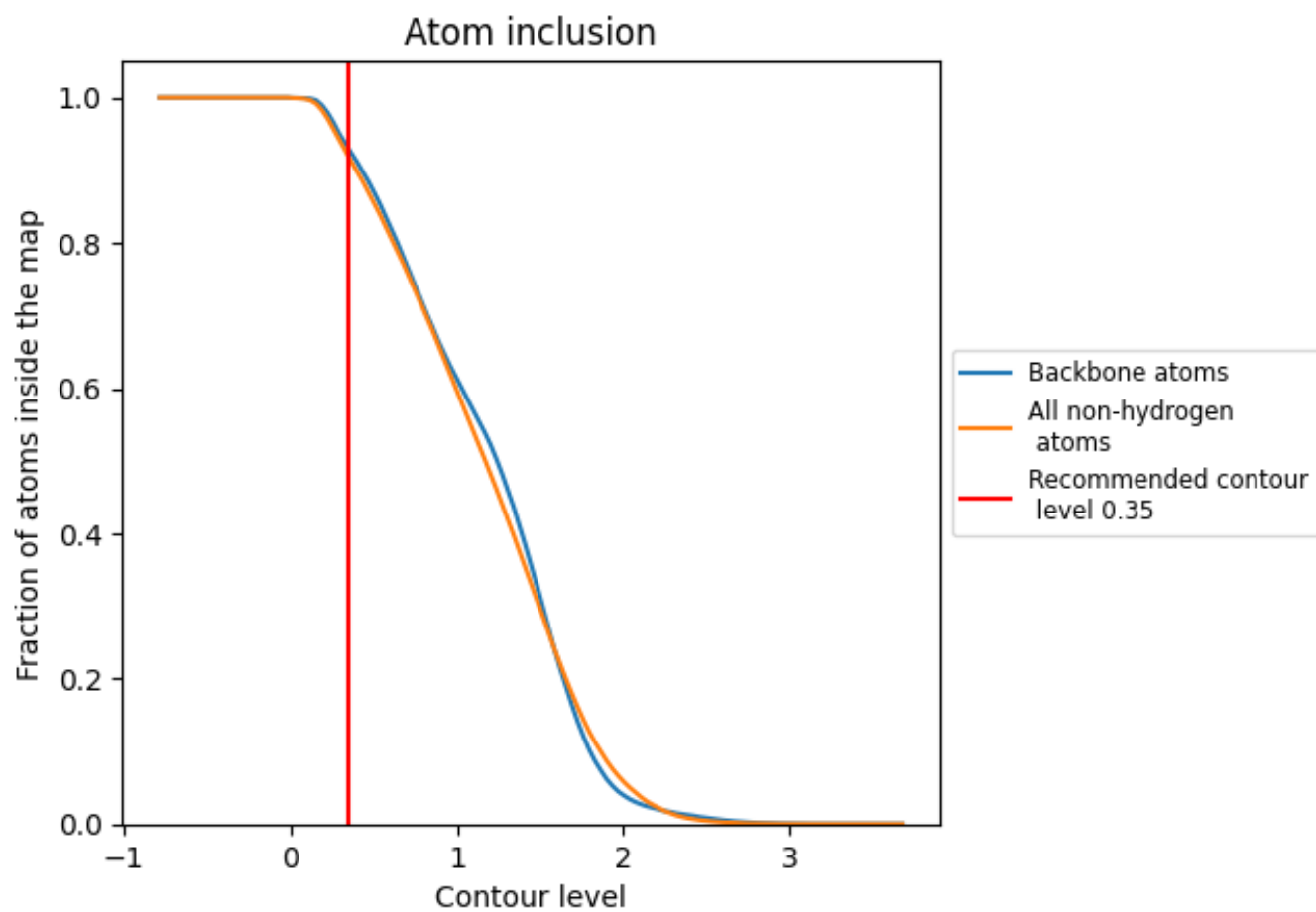
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.35).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 92% 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 (0.35) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9179	 0.5070
0	 0.8757	 0.3000
1	 0.9882	 0.4320
A	 0.9945	 0.6100
B	 0.9808	 0.5840
C	 0.9788	 0.5850
D	 0.9849	 0.5840
E	 0.9456	 0.5440
F	 0.9842	 0.5760
G	 0.9725	 0.5550
H	 0.9412	 0.4710
I	 0.9745	 0.5750
J	 0.9761	 0.5720
K	 0.9756	 0.5630
L	 0.9854	 0.5620
M	 0.9622	 0.5170
N	 0.9815	 0.5900
O	 0.9735	 0.5390
P	 0.9421	 0.5160
Q	 0.9435	 0.5440
R	 0.9899	 0.6000
S	 0.9939	 0.6160
T	 0.9801	 0.5730
U	 0.9724	 0.5520
V	 0.9689	 0.5230
W	 1.0000	 0.6240
X	 0.9416	 0.4940
Y	 1.0000	 0.5980
Z	 0.9647	 0.5730
a	 0.8545	 0.2670
b	 0.9628	 0.5730
c	 0.9776	 0.5680
d	 0.7872	 0.4160
e	 0.2942	 0.1860
f	 0.9916	 0.5680



*Continued on next page...*

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Chain	Atom inclusion	Q-score
g	 0.8200	 0.4650
h	 0.9992	 0.5650
i	 0.9970	 0.5950
j	 0.9912	 0.6000
k	 0.9853	 0.5850
l	 0.9818	 0.5720
m	 0.9524	 0.4800
n	 0.9602	 0.5210
o	 0.9759	 0.5650
p	 0.9588	 0.5220
q	 0.9655	 0.5450
r	 0.9725	 0.5430
s	 0.9457	 0.4360
t	 0.9785	 0.5600
u	 0.9786	 0.5430
v	 0.7619	 0.3880
w	 0.5792	 0.2430
x	 0.9848	 0.2700
y	 0.9923	 0.2810
z	 0.9794	 0.3160