



## wwPDB EM Validation Summary Report ⓘ

Dec 30, 2024 – 02:34 AM EST

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)

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<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.dev113
Mogul	:	2022.3.0, CSD as543be (2022)
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)	:	2.40

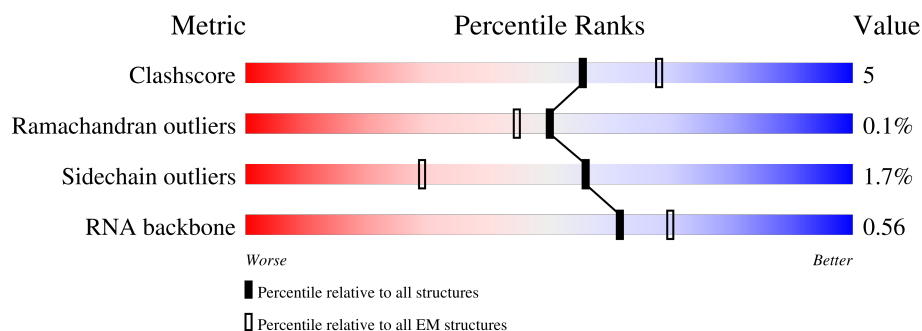
# 1 Overall quality at a glance

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.




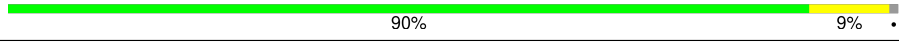
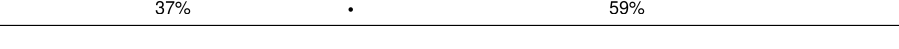
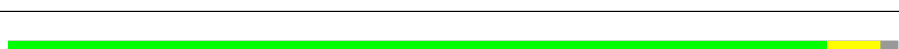

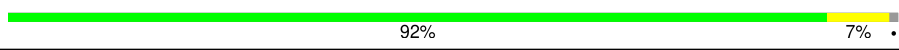

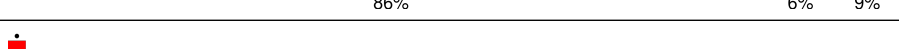
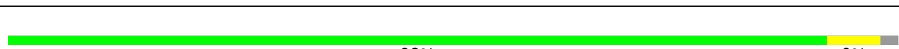
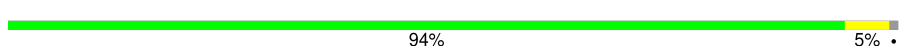

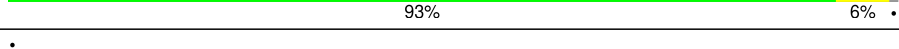
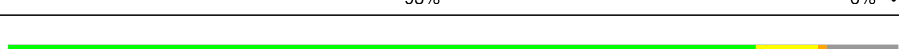
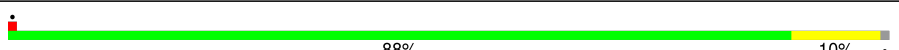
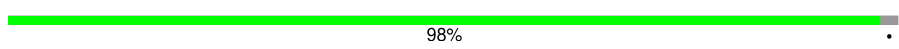

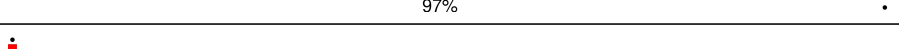







Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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  $\geq 3$ , 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	

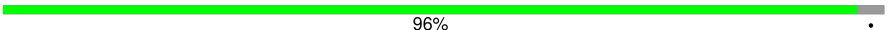
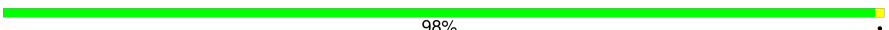
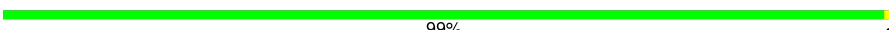
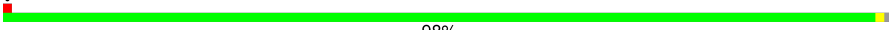






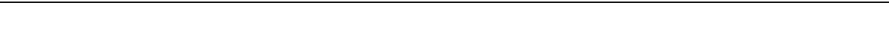

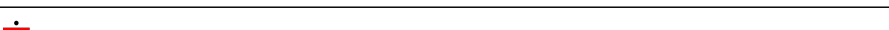
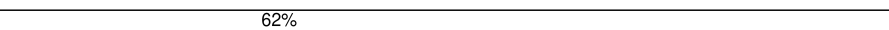
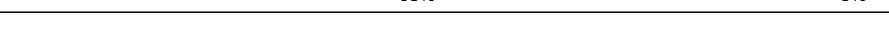

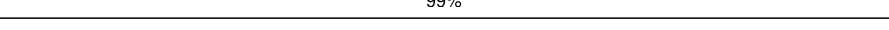




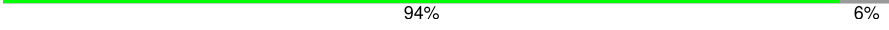
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Mol	Chain	Length	Quality of chain
8	H	121	
9	I	137	
10	J	155	
11	K	142	
12	L	127	
13	M	136	
14	N	149	
15	O	59	
16	P	105	
17	Q	113	
18	R	130	
19	S	107	
20	T	121	
21	U	120	
22	V	100	
23	W	88	
24	X	78	
25	Y	51	
26	Z	128	
27	b	106	
28	c	92	
29	d	25	
30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

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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
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
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
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
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
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
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
7	G	159	Total	C	N	O	S	0	0
			1272	802	245	221	4		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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
28	c	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

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

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

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

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

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
31	h	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

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

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

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

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

- 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
54	v	142	Total	C	N	O	S	0	0
			1085	676	183	217	9		

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

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

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

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

### 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

Chain A: 




#### • Molecule 2: 60S ribosomal protein L16-A

Chain B: 



#### • Molecule 3: 60S ribosomal protein L17-A

Chain C: 




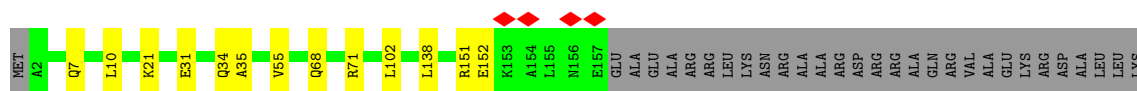
#### • Molecule 4: 60S ribosomal protein L18-A

Chain D: 



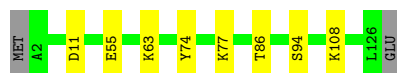
#### • Molecule 5: 60S ribosomal protein L19-A

Chain E: 





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% .




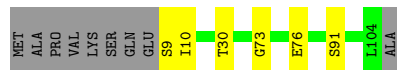
- Molecule 15: 60S ribosomal protein L29

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

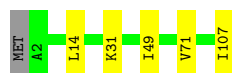
Chain R:  92% 6% .




- 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%



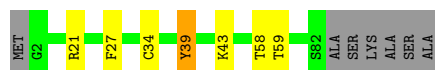
- Molecule 22: 60S ribosomal protein L36-A

Chain V:  93% 6%




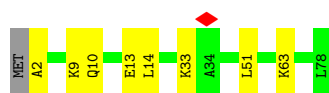
- Molecule 23: 60S ribosomal protein L37-A

Chain W:  84% 7% 8%



- Molecule 24: 60S ribosomal protein L38

Chain X:  88% 10%

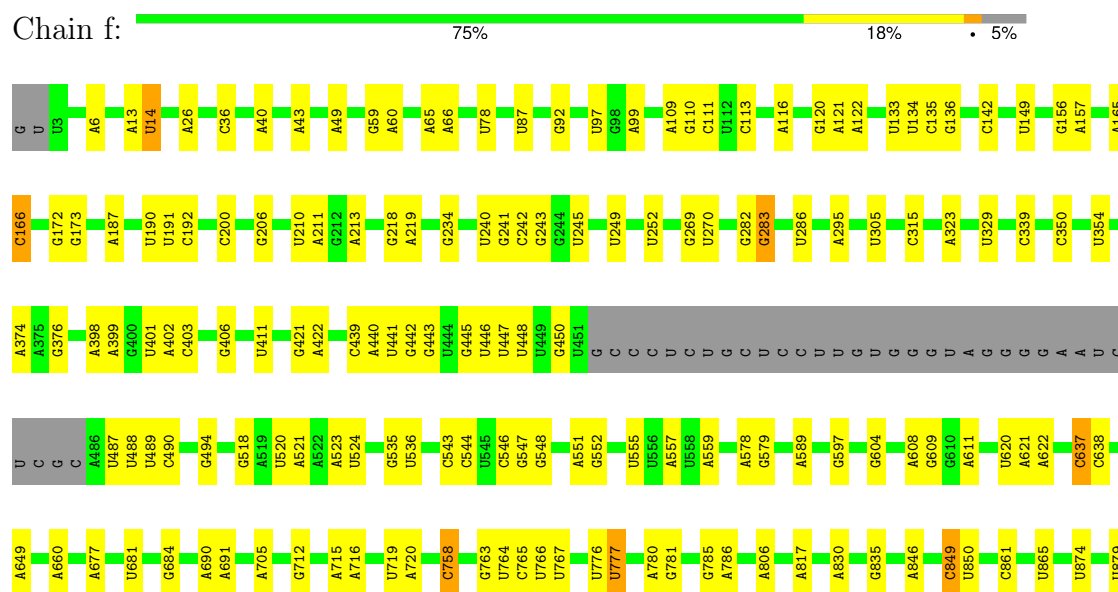


- Molecule 25: 60S ribosomal protein L39

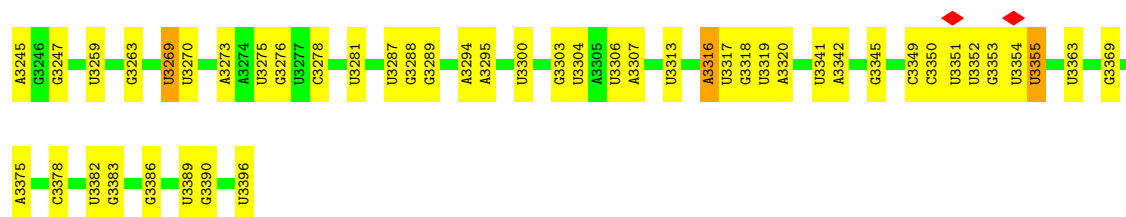
Chain Y:  98%



- Molecule 26: Ubiquitin-60S ribosomal protein L40



C3092	A2691	U2537	A2404	A2223	G	U	G	A1760	A1566	G1349	A1217	U1028	U885
U2860	A2694	U2538	C2405	A2224	C	A	A	C1761	U1567	A1350	A1218	A1036	C890
C2867	A2695	A2539	U2411	U2225	U	G	G	U1764	U1568	U1351	C1219	U1041	A896
G2871	A2696	A2540	U2419	A2226	G	C	C	U1765	U1569	G1352	G1222	A1047	G907
A2872	U2541	U2542	G2437	C2235	C	U	A	G1766	U1572	U1353	G1225	C1049	G908
A2887	U2543	U2544	G2444	G2249	U	G	C	G1770	G1573	A1355	A1226	G1063	A914
G2898	U2545	A2547	A2445	U2254	A	U	A	G1775	A1574	U1356	G1227	A1064	A915
C2899	U2550	U2551	U2446	A	A	C	U	G1780	G1576	G1357	G1235	A1065	G916
A2911	U2552	C2553	A2447	C	U	U	C	A1797	G1577	A1386	G1236	A1066	A917
G2914	U2554	U2555	G2450	U	U	U	C	A1814	A1580	G1392	G1237	G1072	A920
U2923	U2556	A2561	A2461	A	A	U	C	A1816	C1581	A1399	C1238	U1081	A921
U2935	U2557	C2568	G2463	G2262	C2093	G	C	U1819	C1582	G1400	C1239	G1087	U922
A2936	U2558	U2569	U2464	A	C2094	C	A	U1820	A1583	A1419	A1240	A1093	G924
A2941	U2559	U2570	G2465	U	U	U	C	A1821	C1584	U1425	G1242	U1094	A925
C2942	U2560	U2571	U2466	G	C2101	C	C	A1835	U1606	U1434	A1243	U1095	G937
G2947	U2561	U2572	U2467	A2262	U2102	C	C	U1839	U1607	C1437	A1251	U1096	C944
U2954	A2562	G2752	U2468	G2272	G2111	C	A	U1840	C1608	A1446	U1252	G1097	U954
A2971	C2569	G2753	A2469	U2273	U2112	C	C	A1841	U1609	A1447	C1254	A1103	C959
C2972	U2570	C2754	C2470	U2274	A2113	U	U	A1842	U1610	G1448	U1258	G1104	U960
A2983	U2571	C2755	U2471	A2281	C2114	G	G	C1846	U1611	A1481	A1263	G1115	C969
C2990	U2572	U2756	U2472	U2282	G2121	U	C	U1849	U1612	A1482	G1264	G1116	U981
A3179	U2573	C2772	C2473	G2288	G2122	G	G	A1866	C1644	G1487	U1265	G1117	C982
A3180	C2773	C2773	U2474	A2289	A2131	C	C	A1867	U1645	U1488	U1269	G1131	U985
C3181	U2774	U2774	U2475	G2290	U2132	U	U	C1872	C1657	C1496	C1272	U1144	U986
A3186	G2775	G2775	A2484	G2291	U2133	C	C	U1878	C1658	C1502	C1277	A1153	G991
A3187	C2776	C2776	A2485	U2292	G2134	A	U	A1879	U1716	C1508	A1278	A1159	G994
U3196	U2777	U2777	A2486	G2293	U2135	G	G	U1880	U1717	G1509	C1279	C1180	U995
U3207	C2778	C2778	U2487	A2334	G2136	U	U	A1881	U1688	G1525	G1282	G1177	G1001
G3208	U2779	U2779	U2488	G2335	U2137	C	C	A1893	U1718	G1536	G1285	A1180	A1002
A3209	A2800	U2800	A2489	U2336	U2138	U	U	G1906	U1719	U1554	A1286	U1181	G1010
U3214	A2801	C2801	C2490	U2337	G2139	C	C	U1907	C1725	U1555	A1287	A1190	U1015
C3217	A2802	U2802	U2491	G2338	U2140	U	U	A1908	U1724	U1556	G1307	U1191	C1016
A3218	A2803	C2803	U2492	U2339	U2141	C	C	A1909	U1725	C1556	A1308	A1192	C1017
G3228	U2804	U2804	U2493	G2340	U2142	G	G	U1910	U1726	U1557	U1309	C1196	G1018
G3229	A2805	U2805	A2494	U2341	U2143	U	U	G1911	U1727	G1560	G1313	A1197	G1021
C3235	A2806	C2806	U2495	G2342	U2144	C	C	C1912	U1728	U1561	C1201	C1201	G1024
A3243	U2807	U2807	U2496	U2343	U2145	U	U	U1913	U1729	C1562	A1202	A1025	A1026
A3244	A2808	U2808	U2497	G2344	U2146	C	C	U1914	U1730	U1563	U1348	U1208	A1027



• Molecule 31: 5S rRNA

Chain h: 85% 15%



• Molecule 32: 5.8S rRNA

Chain i: 78% 20%



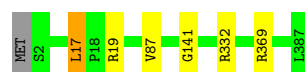
• Molecule 33: 60S ribosomal protein L2-A

Chain j: 96%



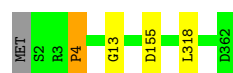
• Molecule 34: 60S ribosomal protein L3

Chain k: 98%



• Molecule 35: 60S ribosomal protein L4-A

Chain l: 99%



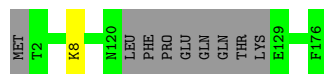
• Molecule 36: 60S ribosomal protein L5

Chain m: 98%



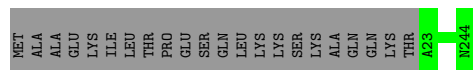
- Molecule 37: 60S ribosomal protein L6-B

Chain n:  94% • 5%




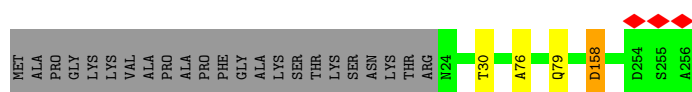
- Molecule 38: 60S ribosomal protein L7-A

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% ..



- MET  
SER  
T3  
W12  
D47  
A138

- 

[illegible][illegible][illegible][illegible]

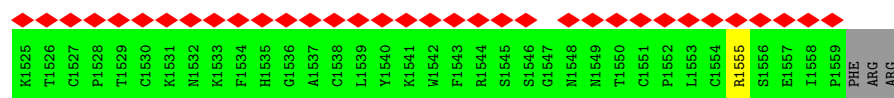
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- | Category | Gene Count |
|----------|------------|
| MET      | 1          |
| S2       | 1          |
| T8       | 1          |
| V23      | 1          |
| F30      | 1          |
| I125     | 1          |
| L143     | 1          |
| T156     | 1          |
| L178     | 1          |
| S194     | 1          |
| E205     | 1          |
| S230     | 1          |
| I240     | 1          |
| W247     | 1          |
| L249     | 1          |
| K253     | 1          |
| N254     | 1          |
| G255     | 1          |
| Q256     | 1          |
| Y276     | 1          |
| H297     | 1          |
| L298     | 1          |
| T299     | 1          |
| S300     | 1          |
| K301     | 1          |
| K305     | 1          |
| V309     | 1          |
| Y323     | 1          |
| E324     | 1          |
| D325     | 1          |
| G326     | 1          |
| S330     | 1          |
| Y331     | 1          |
| D332     | 1          |
| K333     | 1          |
| S334     | 1          |
| K338     | 1          |
| F342     | 1          |

[illegible]

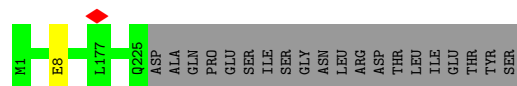
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------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

I611	I612	Q613	Q614	L615	M616	K617	S618	D619	S620	E621	E622	L623	E624	L625	Y626	I627	E628	D629	F630	M631	K632	N633	Y634	F636	D637	D638	S639	G640	E641	I642	F643	K644	G645	N646	N647	K648	F649	L650	N651	Q652	R653	T654	L655	T656	T657	L658	Y659	R660	S661	A662	V663	A664	N665	G666	Q667	V668	E669	E670
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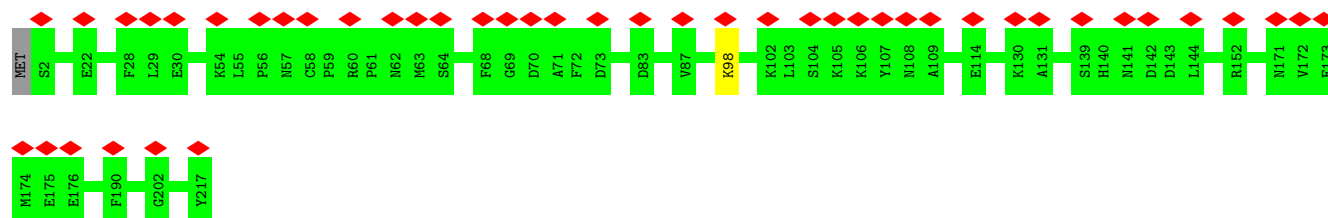
D1436	K1349	F1151	D1091	R911	L851	S791	L731	F671
D1437	K1350	Y1152	T1092	V912	S852	T792	Q732	C672
K1438	L1351	Q1153	L1093	L913	E853	T793	H733	A673
L1439	L1352	K1154	Y1094	Y914	E854	T794	A734	V674
E1440	G1353	L1155	L1095	K915	P855	H795	Q735	L675
I1441	H1354	Y1156	L1096	V916	N856	H796	V736	S676
S1442	T1355	K1157	E1097	L917	D857	L797	Y737	K677
F1443	E1292	V1158	L1098	L918	L958	L798	F738	L678
Y1449	Q1293	LYS	L1099	N919	Y859	T799	S739	D679
I1454	L1294	L1159	R1099	N920	Y860	D800	P740	E680
I1455	Q1358	K1295	S1100	S920	D861	D801	G741	T681
I1456	L1359	L1160	S1101	I921	F862	K802	A742	F682
F1460	F1360	S1161	C1102	T923	G863	I804	K743	F683
N1362	ASP	E1163	L1103	V924	H864	N805	E744	S684
V1363	ASP	L1164	L1104	S925	T865	N806	K745	T685
G1364	GLY	K1165	L1105	S926	F866	L806	Y746	L686
I1367	ALA	K1166	Y1106	T927	F867	K807	V747	L687
T1379	ASP	L1167	E1107	T928	K868	N808	T748	L688
K1385	ASP	E1168	T1108	T929	H869	M809	H749	N689
F1386	ASP	S1169	L1109	L929	G870	Q810	A750	T690
I1387	ASP	Q1170	S1110	N930	K871	K811	V751	D691
F1388	VAL	Y1171	Q1111	G931	V872	L812	E752	F692
E1399	N1235	K1172	GLY	L933	N873	I813	L753	L693
F1400	K1237	R1173	VAL	A934	L874	R814	I754	S694
D1401	F1238	I1174	LYS	S935	N875	Y815	N755	C695
D1402	K1239	F1175	ASN	V936	F876	A816	G756	A696
I1403	L1240	E1176	GLY	E937	S877	L817	C757	L697
N1404	F1241	V1177	GLU	S938	D878	F818	N758	Y698
S1405	K1242	V1178	ILE	S939	I879	L819	D759	E699
K1406	K1243	L1179	SER	V940	V880	D820	T760	V700
M1407	L1244	M1180	E1122	T941	G881	A821	S761	S701
D1408	L1245	D1181	Y1123	K942	N882	L823	Q762	E702
H1409	K1246	K1182	G1124	T943	V883	D824	I763	D703
L1410	Q1247	D1183	E1125	V944	I884	A825	F764	T704
L1411	V1248	I1184	E1126	R945	Q885	L826	F765	N705
SER	T1249	G1185	I1127	D946	P886	P827	P766	E706
ASN	E1250	S1186	Q1128	K947	A887	E828	A767	K707
ASP	E1251	L1187	E1129	Q948	N888	R829	A768	F709
ASP	V1252	I1188	M1130	S949	G889	V830	I770	K710
A1416	P1253	N1189	L1131	T950	G890	N831	E771	L711
L1417	K1254	Q1190	I1132	D951	D891	N832	V772	S712
L1420	E1255	S1191	E1133	K952	A892	H833	F773	L713
L1421	Y1256	R1192	L1134	D953	M893	I834	A774	Q714
N1422	L1257	L1193	M1135	Y954	L894	V835	R775	L715
I1510	E1258	L1194	F1136	L955	T895	A836	Y776	A716
C1511	Y1259	T1195	L1137	L956	F896	F837	M777	K717
Y1512	E1260	L1196	M1138	C957	D897	I838	P778	G718
S1513	N1261	L1197	F1139	A958	I898	T839	A779	N719
L1514	K1262	L1198	M1140	S959	A899	V840	I780	S720
L1515	N1263	Q1199	E1142	L960	E900	V841	D781	E721
H1516	S1264	G1199	Q1141	L961	S901	S842	Y782	T722
A1517	L1269	L1201	R1143	L962	N902	E843	F783	A723
V1518	E1342	V1202	M1144	M963	S903	L844	S784	N724
D1519	D1343	V1203	N1145	N965	Y905	V845	S785	K725
L1520	I1344	K1204	Q1146	R966	F906	D847	L786	L726
K1521	F1345	T1205	V1147	S967	F907	Y848	V787	A727
S1524	E1346	Q1206	S1148	N968	F908	N849	S788	G728
	E1347	D1208	T1149	S969	Y909	C850	S789	V729
	C1348	I1209	L1150	K970	S910		L790	I730



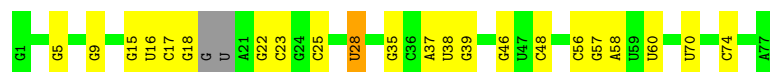
- Molecule 47: Eukaryotic translation initiation factor 6



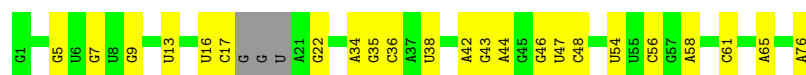
- Molecule 48: 60S ribosomal protein L1-A



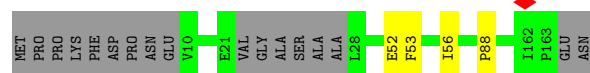
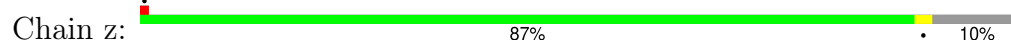
- Molecule 49: A-site Ala aminoacyl-tRNA



- Molecule 50: P-site petidyl-tRNA



- Molecule 51: 60S ribosomal protein L12-A



- Molecule 52: 60S acidic ribosomal protein P0



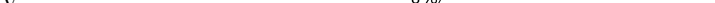


- Molecule 53: CAT tailed nascent peptide

Chain 1:  94% 6%



- Molecule 54: Eukaryotic translation initiation factor 5A-1

Chain v:  8% 87% 10%



## 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 (Å)	476.55002, 476.55002, 476.55002	wwPDB
Map dimensions	450, 450, 450	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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, 5CT, MG

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%)	7	14
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%)	37	59

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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%)	25	47
41	r	216/221 (98%)	206 (95%)	10 (5%)	0	100	100
42	s	167/174 (96%)	161 (96%)	5 (3%)	1 (1%)	22	43
43	t	191/199 (96%)	174 (91%)	16 (8%)	1 (0%)	25	47
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%)	48	71
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%)	4	7
52	0	117/312 (38%)	116 (99%)	0	1 (1%)	14	31
54	v	139/157 (88%)	139 (100%)	0	0	100	100
All	All	9314/10279 (91%)	8965 (96%)	337 (4%)	12 (0%)	50	71

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 ⓘ

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%)	81	93
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%)	81	93
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%)	47	72
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%)	70	86
20	T	95/103 (92%)	94 (99%)	1 (1%)	70	86
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%)	37	64
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%)	86	95
34	k	320/323 (99%)	316 (99%)	4 (1%)	65	84
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%)	81	93
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%)	70	86
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%)	20	43
46	e	1150/1451 (79%)	1080 (94%)	70 (6%)	15	34
47	g	180/211 (85%)	180 (100%)	0	100	100
48	w	197/198 (100%)	196 (100%)	1 (0%)	86	95
52	0	104/254 (41%)	95 (91%)	9 (9%)	8	17
54	v	119/132 (90%)	116 (98%)	3 (2%)	42	68
All	All	7561/8690 (87%)	7429 (98%)	132 (2%)	56	78

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 ⓘ

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 ⓘ

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	0.79	0	8,15,17	1.29	1 (12%)

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. '–' 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 oligosaccharides 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

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

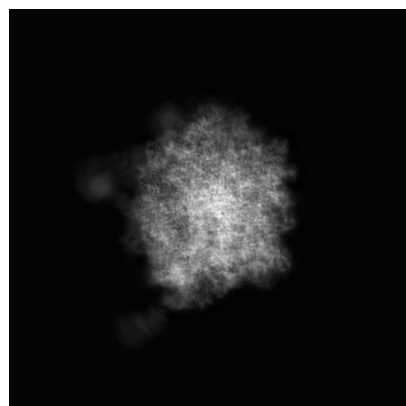
## 6 Map visualisation [i](#)

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

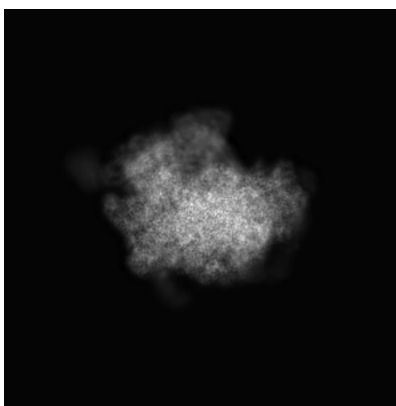
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

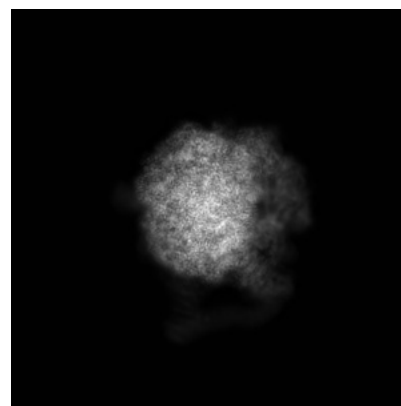
#### 6.1.1 Primary map



X

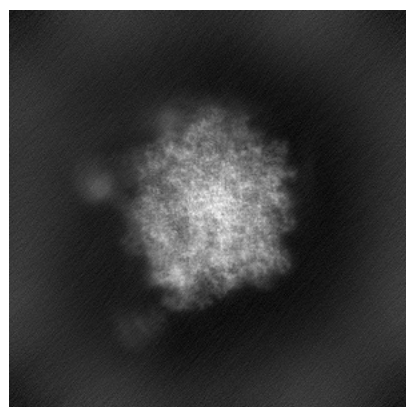


Y

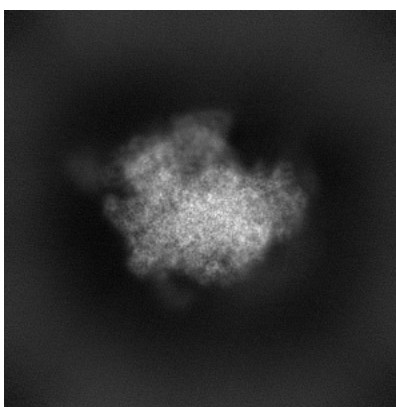


Z

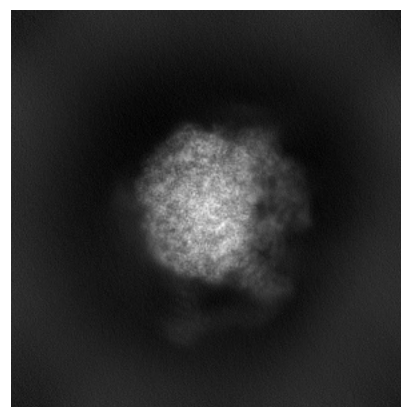
#### 6.1.2 Raw map



X



Y

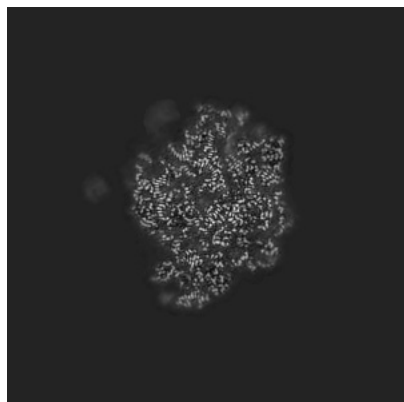


Z

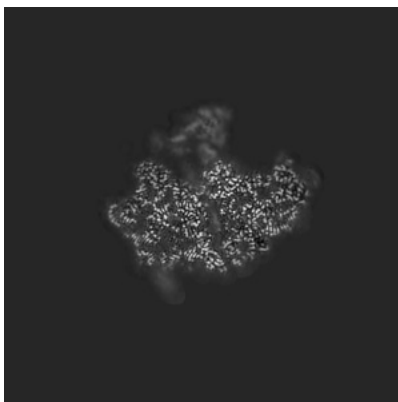
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

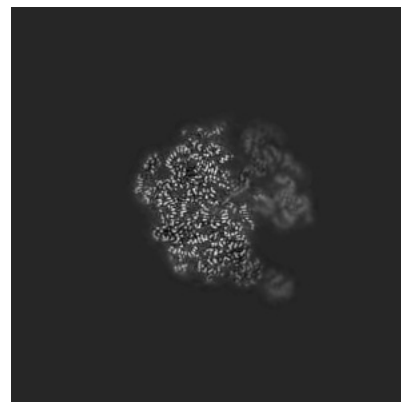
### 6.2.1 Primary map



X Index: 225

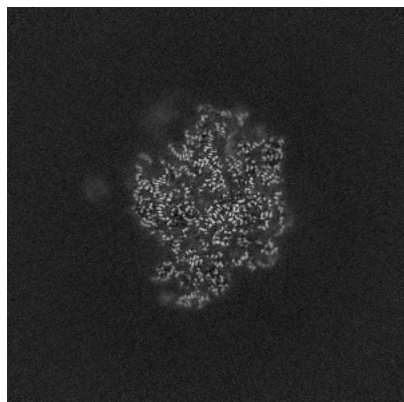


Y Index: 225

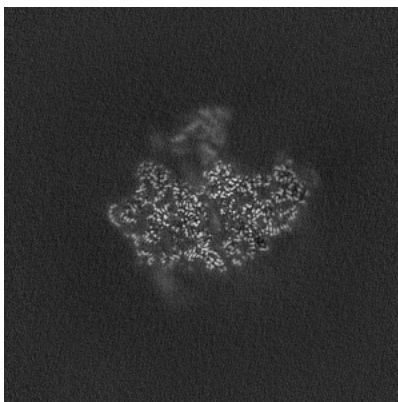


Z Index: 225

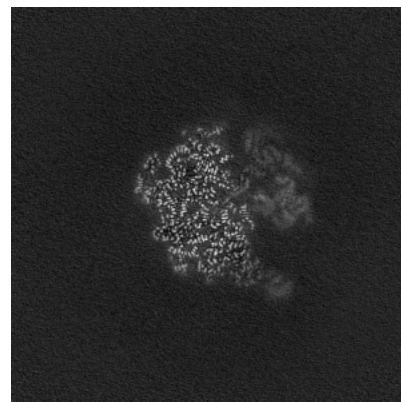
### 6.2.2 Raw map



X Index: 225



Y Index: 225



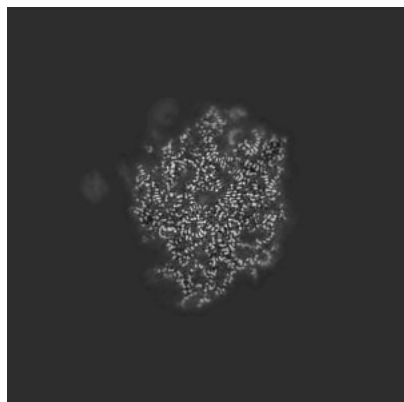
Z Index: 225

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

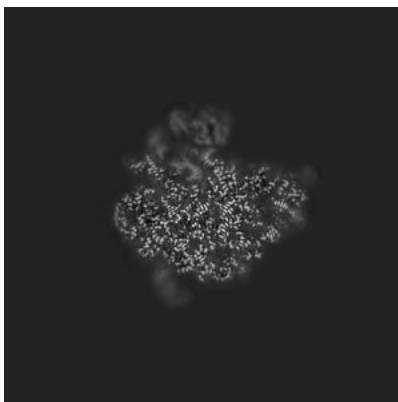


## 6.3 Largest variance slices [i](#)

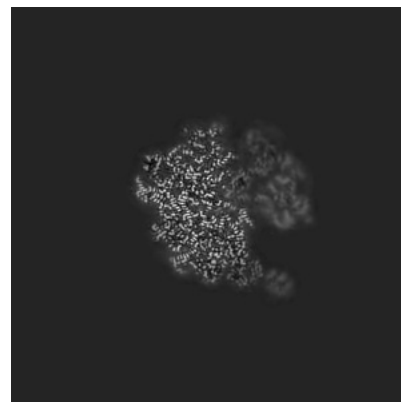
### 6.3.1 Primary map



X Index: 219

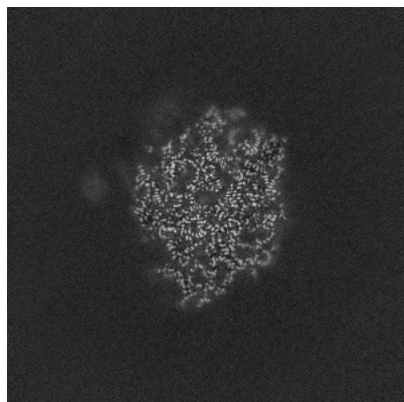


Y Index: 237

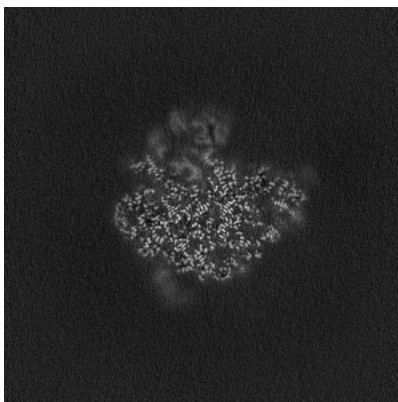


Z Index: 222

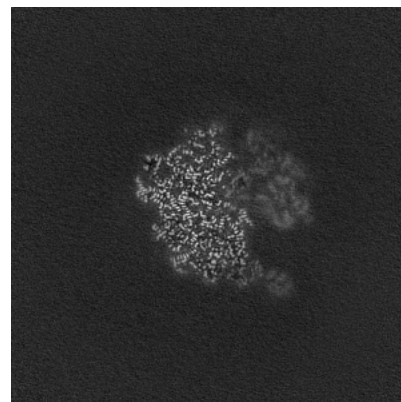
### 6.3.2 Raw map



X Index: 219



Y Index: 237

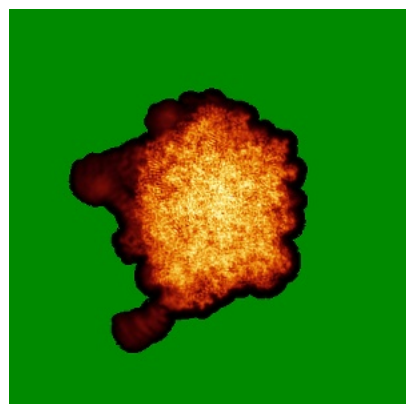


Z Index: 222

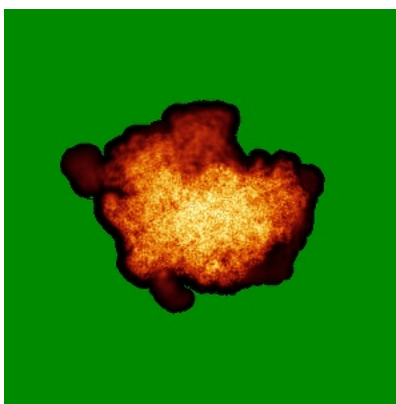
The images above show the largest variance slices of the map in three orthogonal directions.

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

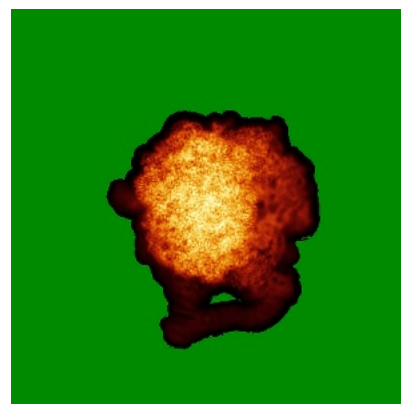
### 6.4.1 Primary map



X

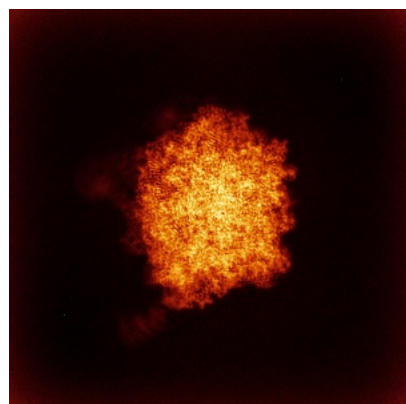


Y

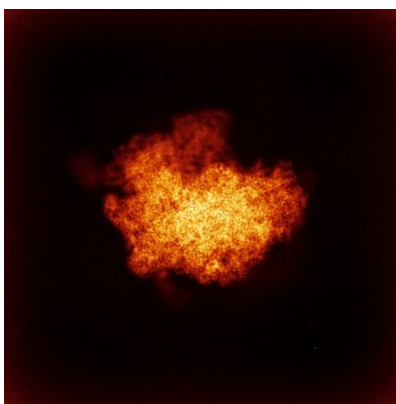


Z

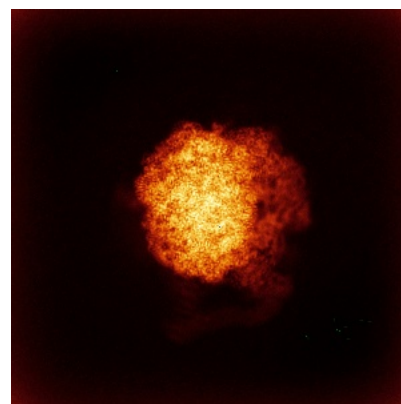
### 6.4.2 Raw map



X



Y

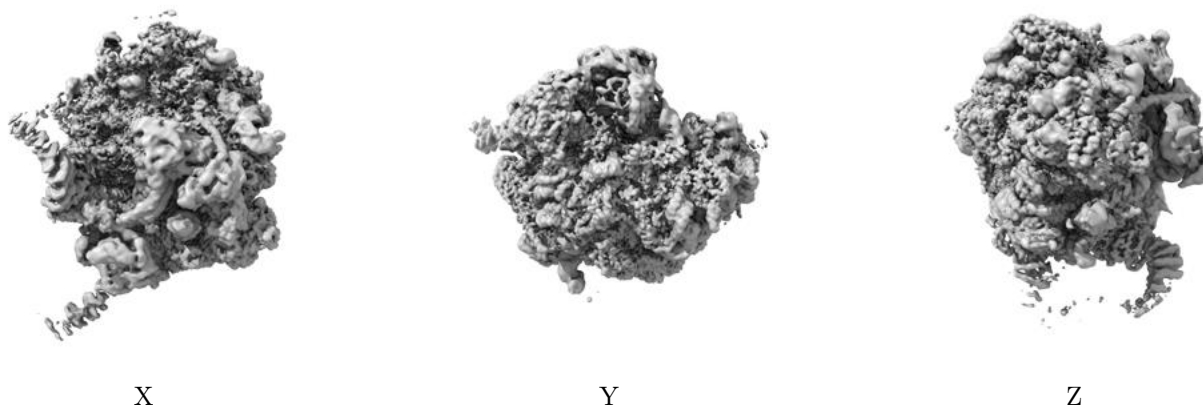


Z

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

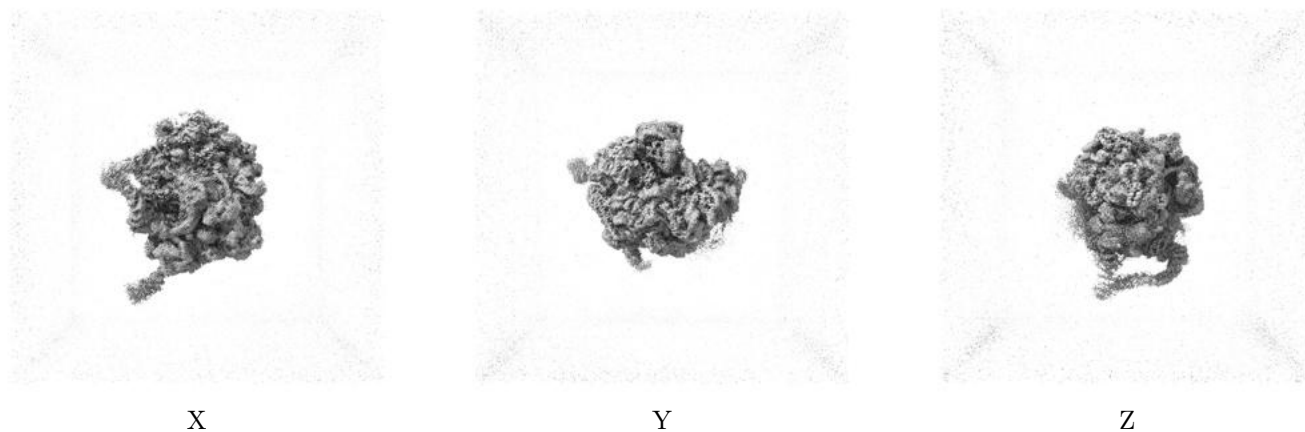
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



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

### 6.5.2 Raw map



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

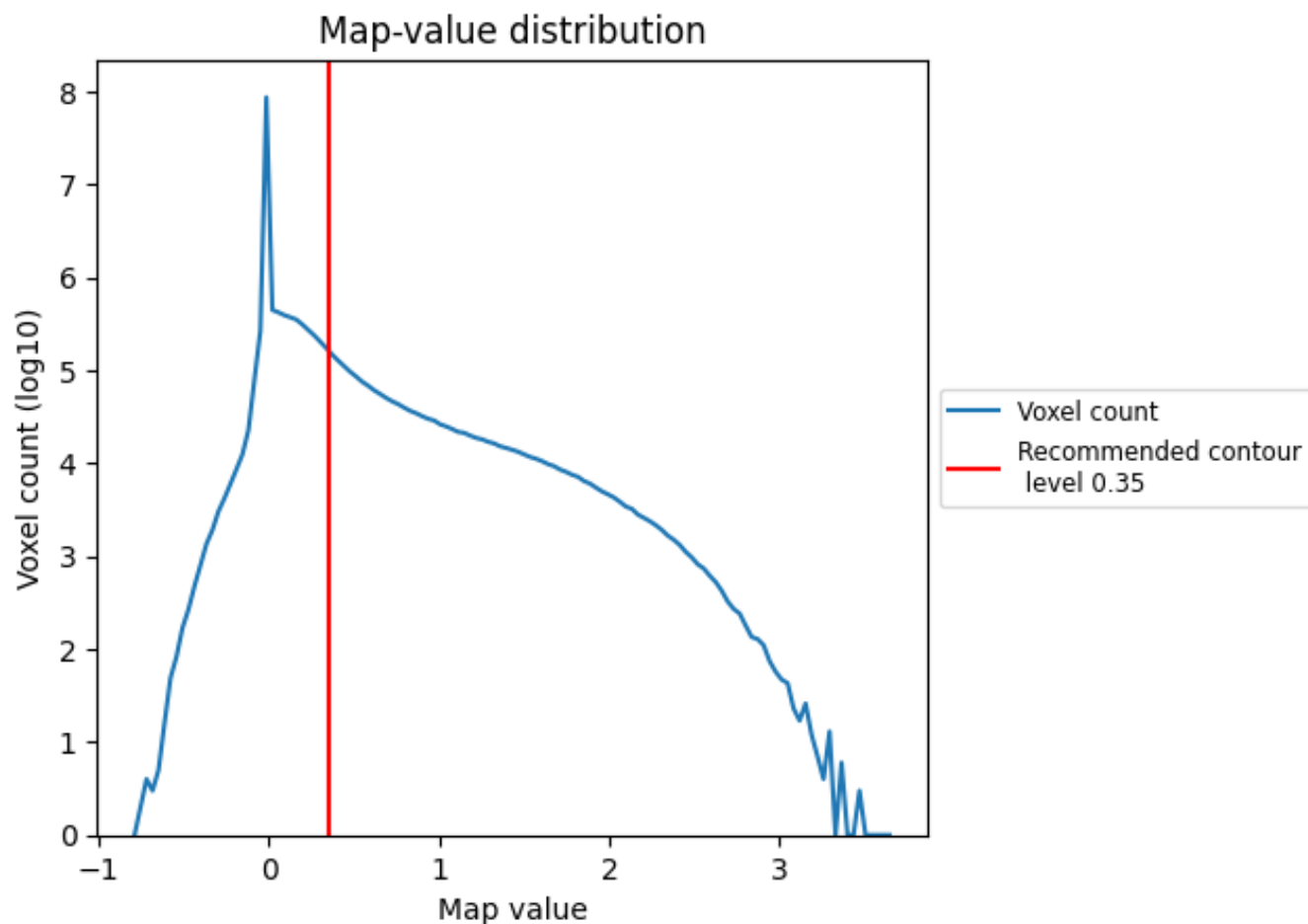
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

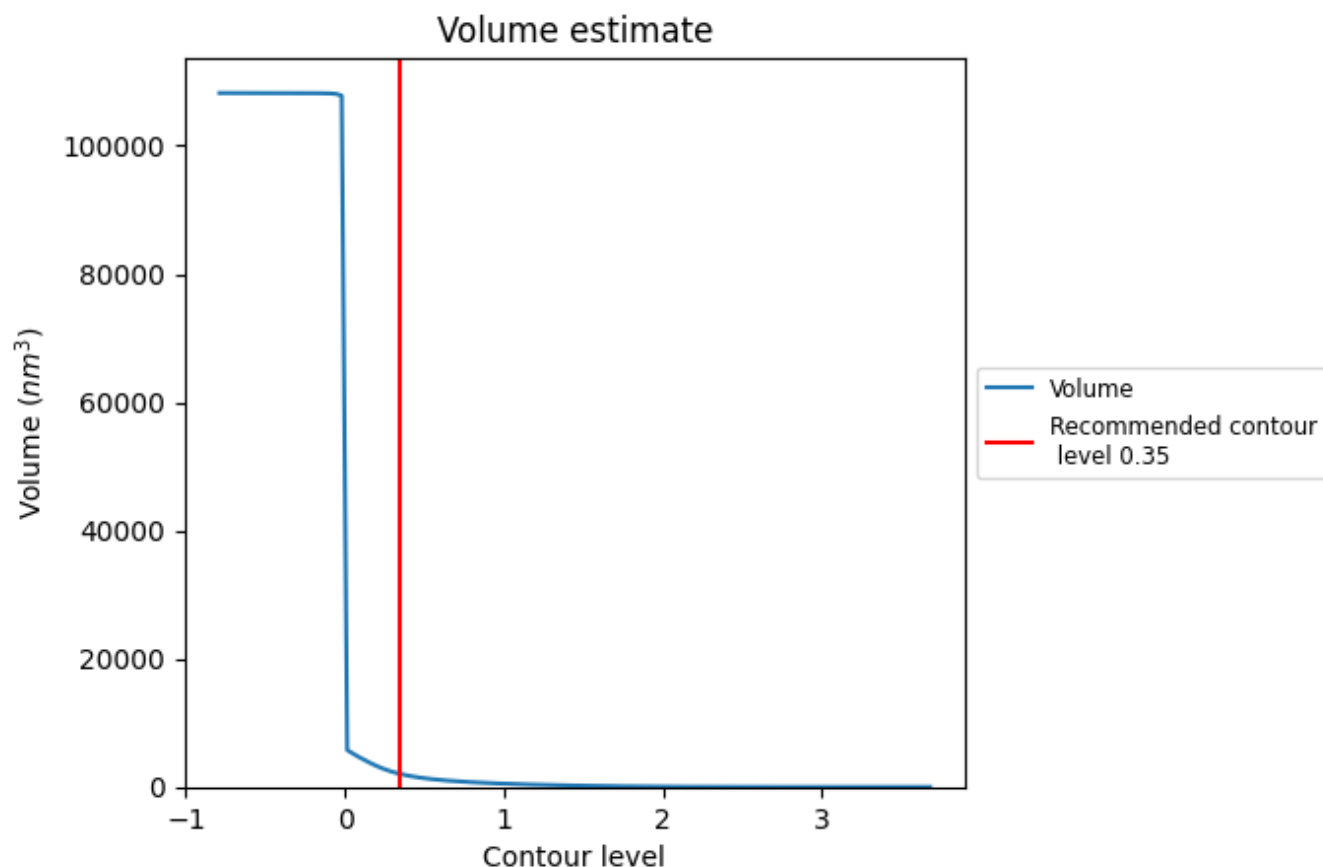
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

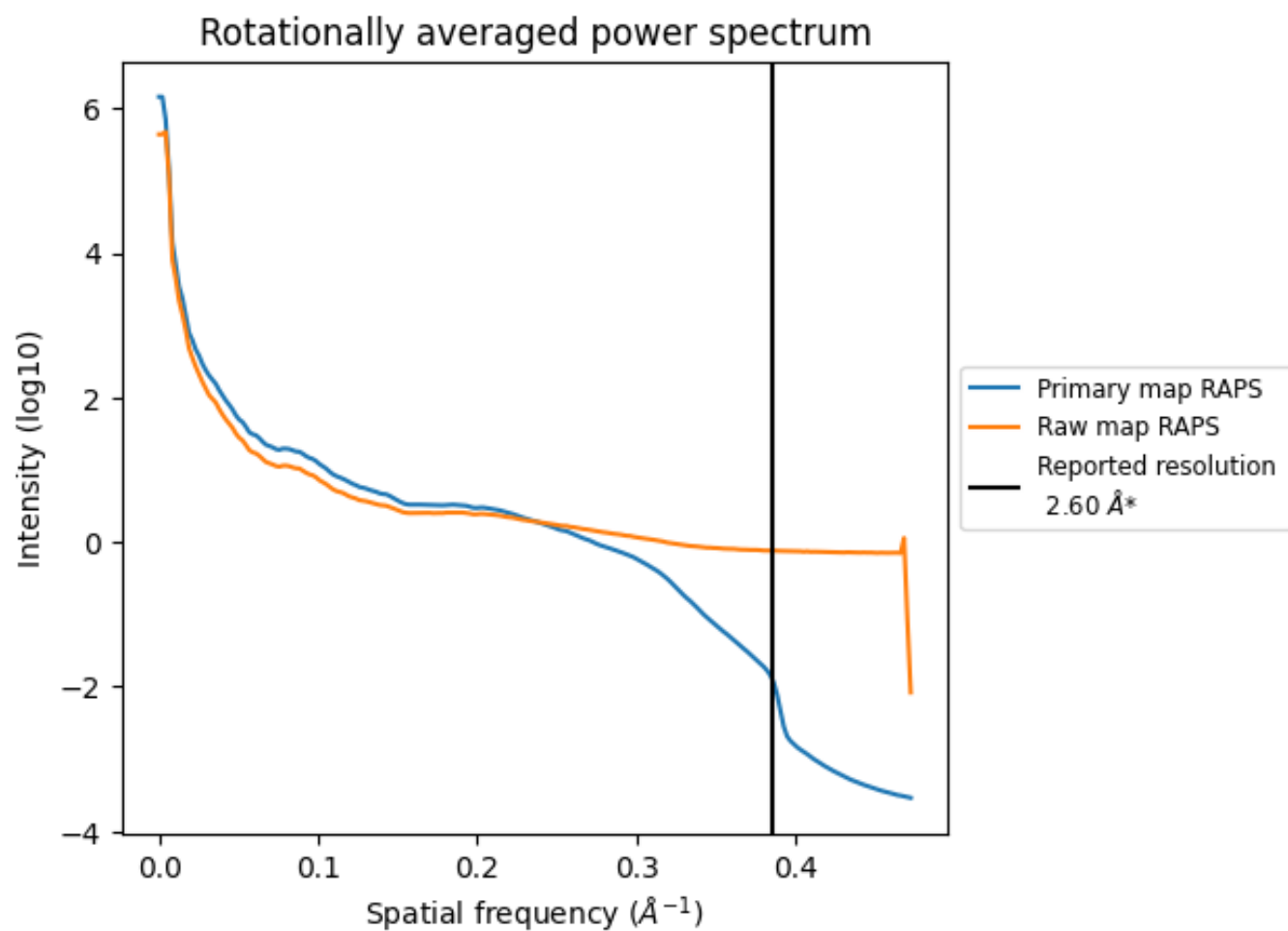
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2020 nm<sup>3</sup>; 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 ⓘ

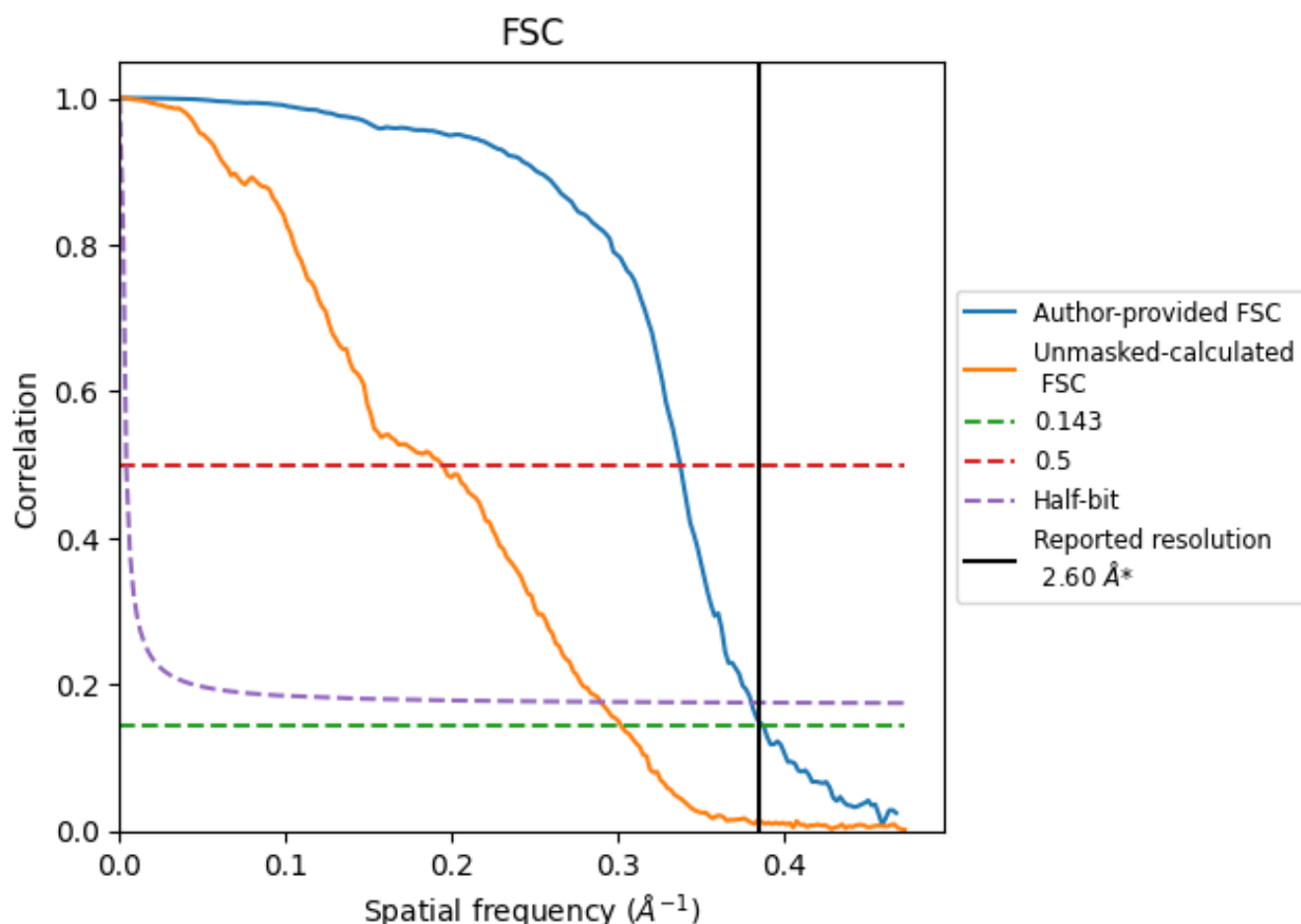


\*Reported resolution corresponds to spatial frequency of  $0.385 \text{ \AA}^{-1}$

## 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

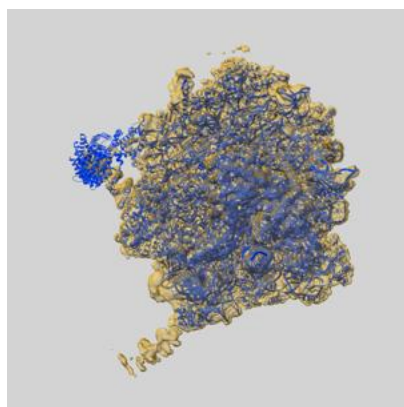
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.32 differs from the reported value 2.6 by more than 10 %



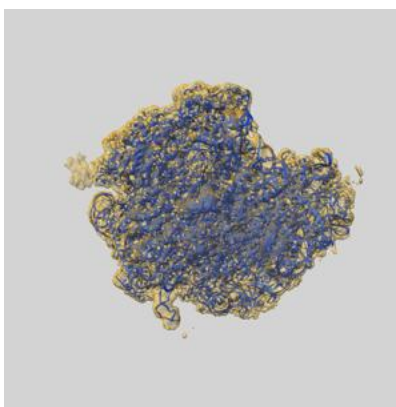
## 9 Map-model fit [i](#)

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](#).

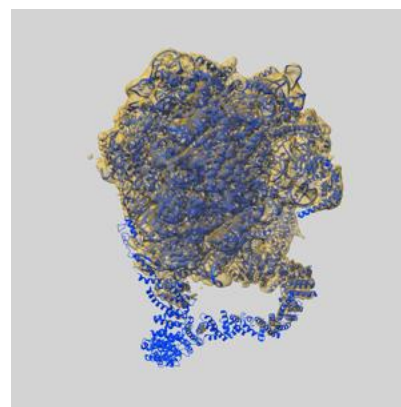
### 9.1 Map-model overlay [i](#)



X



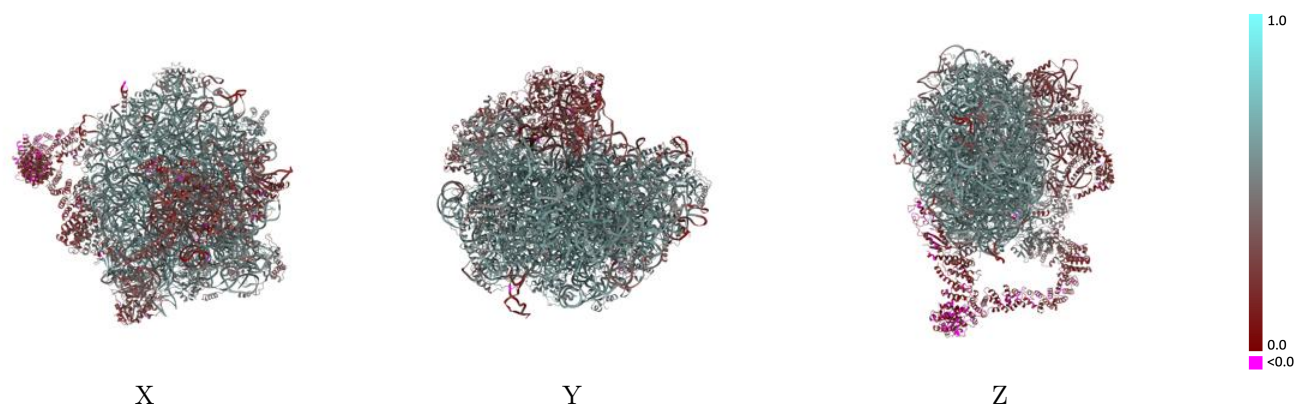
Y



Z

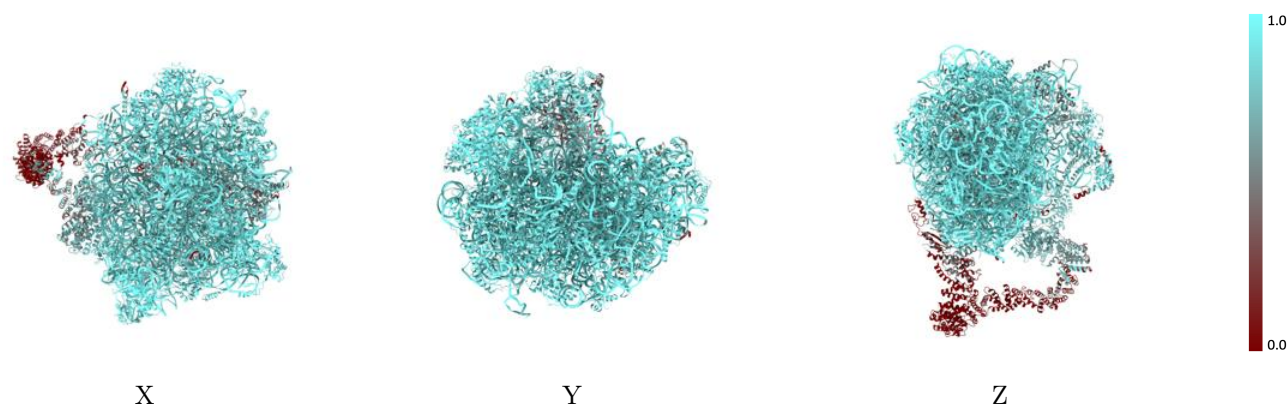
The images above show the 3D surface view of the map at the recommended contour level 0.35 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



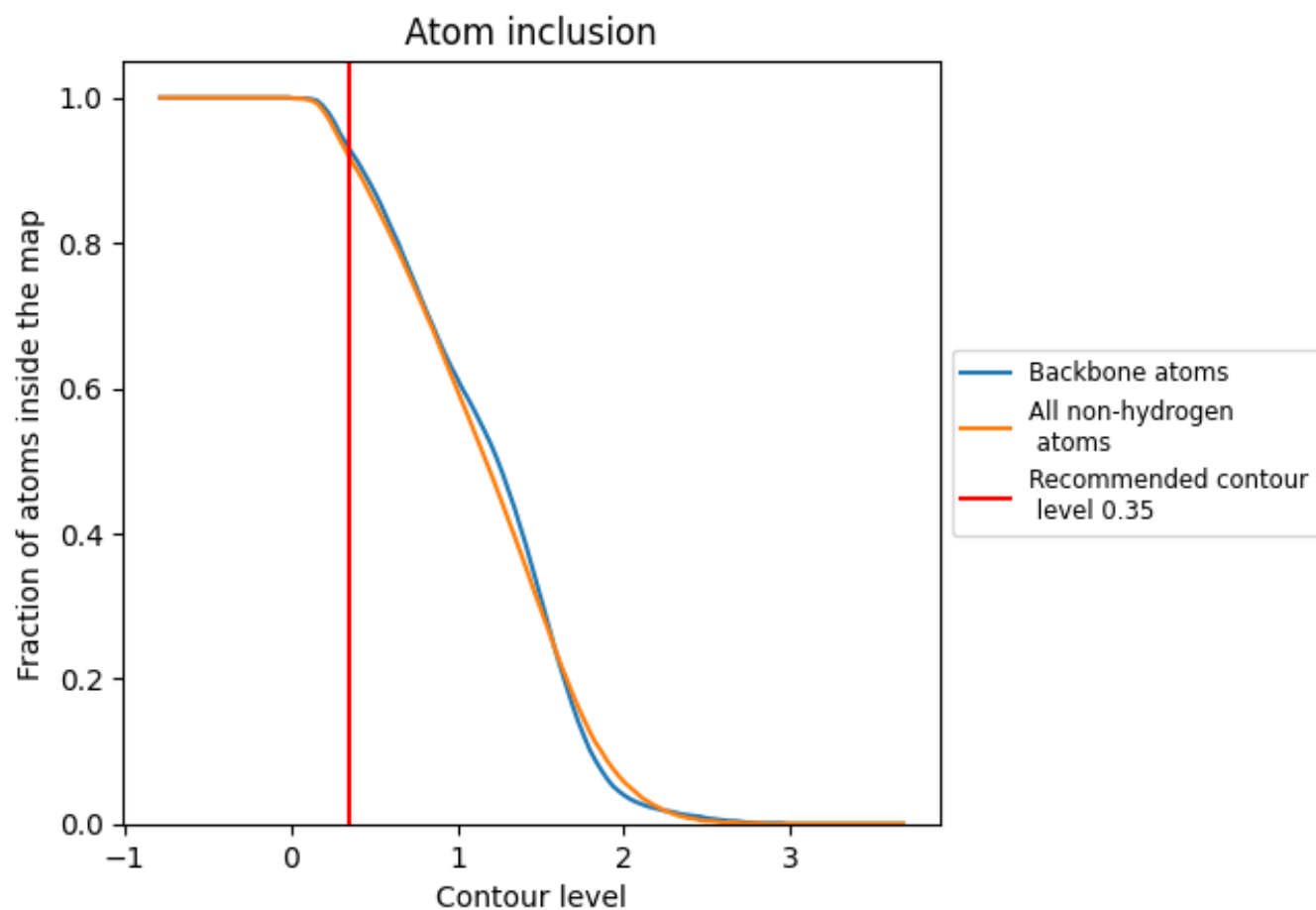
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	 0.9180	 0.5070
0	 0.8760	 0.3000
1	 0.9880	 0.4320
A	 0.9950	 0.6100
B	 0.9810	 0.5840
C	 0.9790	 0.5850
D	 0.9850	 0.5840
E	 0.9460	 0.5440
F	 0.9840	 0.5760
G	 0.9730	 0.5550
H	 0.9410	 0.4710
I	 0.9750	 0.5750
J	 0.9760	 0.5720
K	 0.9760	 0.5630
L	 0.9850	 0.5620
M	 0.9620	 0.5170
N	 0.9820	 0.5900
O	 0.9740	 0.5390
P	 0.9420	 0.5160
Q	 0.9440	 0.5440
R	 0.9900	 0.6000
S	 0.9940	 0.6160
T	 0.9800	 0.5730
U	 0.9720	 0.5520
V	 0.9690	 0.5230
W	 1.0000	 0.6240
X	 0.9420	 0.4940
Y	 1.0000	 0.5980
Z	 0.9650	 0.5730
a	 0.8550	 0.2670
b	 0.9630	 0.5730
c	 0.9780	 0.5680
d	 0.7870	 0.4160
e	 0.2940	 0.1860
f	 0.9920	 0.5680



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Chain	Atom inclusion	Q-score
g	 0.8200	 0.4650
h	 0.9990	 0.5650
i	 0.9970	 0.5950
j	 0.9910	 0.6000
k	 0.9850	 0.5850
l	 0.9820	 0.5720
m	 0.9520	 0.4800
n	 0.9600	 0.5210
o	 0.9760	 0.5650
p	 0.9590	 0.5220
q	 0.9660	 0.5450
r	 0.9730	 0.5430
s	 0.9460	 0.4360
t	 0.9790	 0.5600
u	 0.9790	 0.5430
v	 0.7620	 0.3880
w	 0.5790	 0.2430
x	 0.9850	 0.2700
y	 0.9920	 0.2810
z	 0.9790	 0.3160