



## wwPDB EM Validation Summary Report ⓘ

Dec 30, 2024 – 08:21 AM EST

PDB ID : 8AGX  
EMDB ID : EMD-15427  
Title : Yeast RQC complex in state with the RING domain of Ltn1 in the IN position  
Authors : Tesina, P.; Buschauer, R.; Beckmann, R.  
Deposited on : 2022-07-20  
Resolution : 2.40 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.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

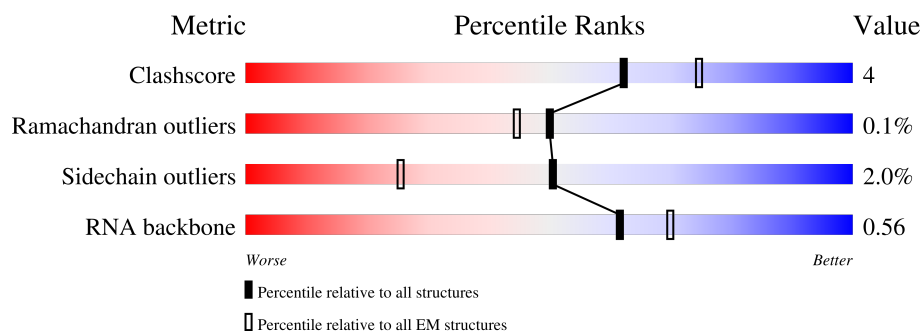
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.40 Å.

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









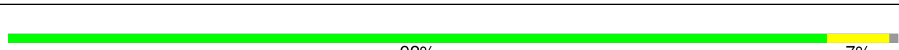

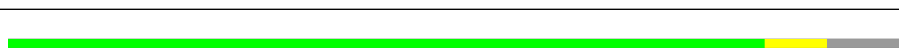

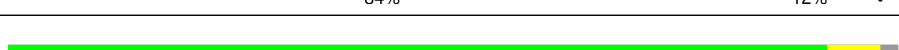
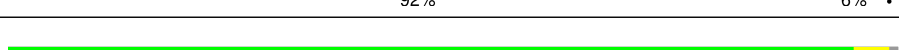
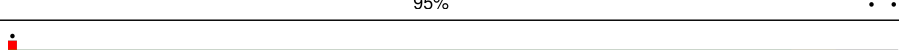
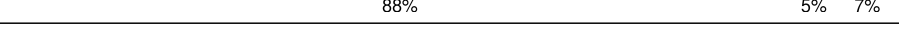
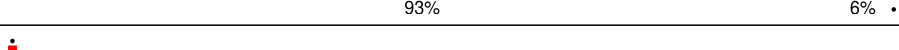
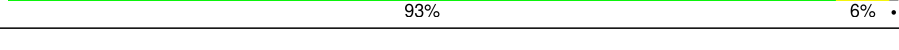


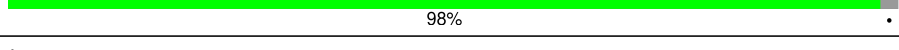

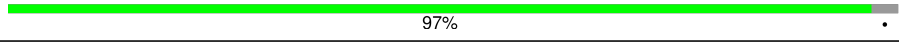
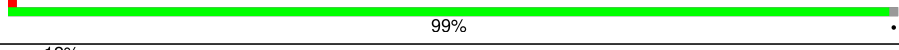
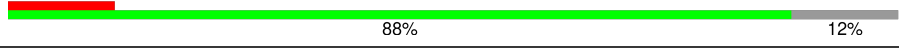


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	

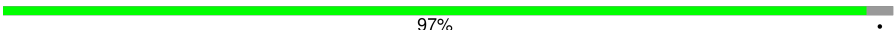
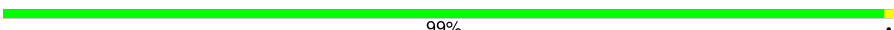
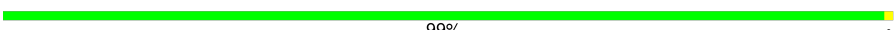
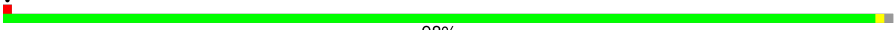






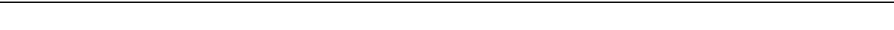

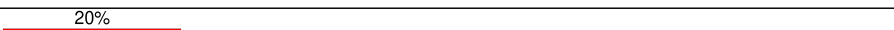
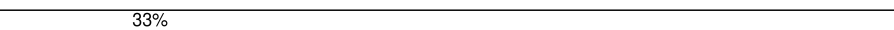
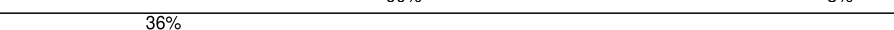

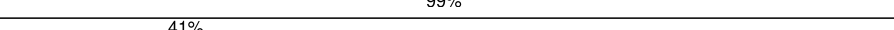




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Mol	Chain	Length	Quality of chain
8	H	121	
9	I	137	
10	J	155	
11	K	142	
12	L	127	
13	M	136	
14	N	149	
15	O	59	
16	P	105	
17	Q	113	
18	R	130	
19	S	107	
20	T	121	
21	U	120	
22	V	100	
23	W	88	
24	X	78	
25	Y	51	
26	Z	128	
27	b	106	
28	c	92	
29	d	25	
30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

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Mol	Chain	Length	Quality of chain
33	j	254	 97% .
34	k	387	 99% .
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	 94% . . .
43	t	199	 96% . .
44	u	138	 97% ..
45	a	1038	 20% 81% . 18%
46	e	1562	 33% 90% 8% .
47	v	157	 36% 89% . 10%
48	w	217	 87% 99%
49	x	76	 41% 66% 30% . .
49	y	76	 67% 25% . .
50	z	165	 89% . 10%
51	0	312	 31% 7% . 61%
52	1	18	 72% 28%

## 2 Entry composition [i](#)

There are 55 unique types of molecules in this entry. The entry contains 149706 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	102	Total	C	N	O	S	0	0
			812	526	134	152			

- 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	S	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	S	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		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	0	0
			68782	30723	12389	22454	3216		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
f	?	-	G	deletion	GB 2211412835
f	1956	U	-	insertion	GB 2211412835
f	?	-	A	deletion	GB 2211412835
f	2255	U	-	insertion	GB 2211412835
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
			6579	4194	1142	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 5A-1.

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

- 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 Ala tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	x	74	Total	C	N	O	P	0	0
			1579	702	277	526	74		
49	y	73	Total	C	N	O	P	0	0
			1556	692	272	519	73		

- Molecule 50 is a protein called 60S ribosomal protein L12-A.

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

- Molecule 51 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	0	121	Total	C	N	O	S	0	0
			961	618	167	173	3		

- Molecule 52 is a protein called CAT-tailed nascent peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	1	18	Total	C	N	O	0	0
			90	54	18	18		

- Molecule 53 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
53	A	1	Total	Mg	0
			1	1	
53	C	1	Total	Mg	0
			1	1	
53	E	1	Total	Mg	0
			1	1	
53	I	1	Total	Mg	0
			1	1	
53	R	1	Total	Mg	0
			1	1	

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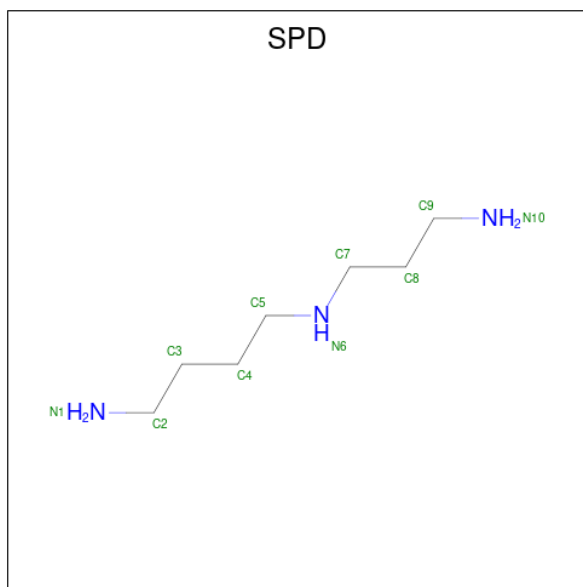
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Mol	Chain	Residues	Atoms		AltConf
53	T	1	Total 1	Mg 1	0
53	f	3	Total 3	Mg 3	0
53	h	1	Total 1	Mg 1	0
53	j	2	Total 2	Mg 2	0
53	k	1	Total 1	Mg 1	0

- Molecule 54 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 55 is SPERMIDINE (three-letter code: SPD) (formula: C<sub>7</sub>H<sub>19</sub>N<sub>3</sub>).

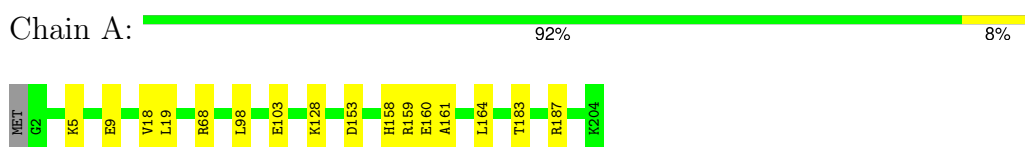


Mol	Chain	Residues	Atoms			AltConf
55	f	1	Total	C	N	0
			10	7	3	

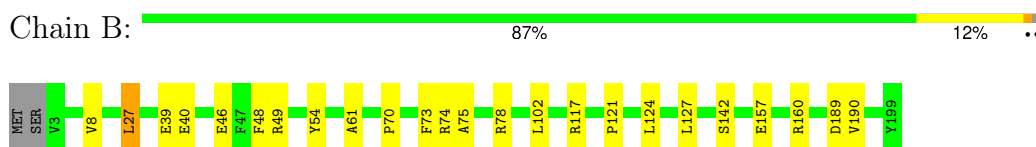
### 3 Residue-property plots

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

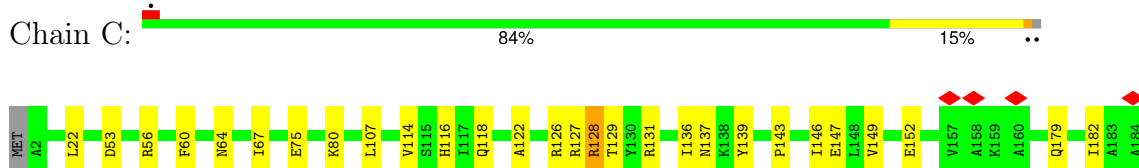
- Molecule 1: 60S ribosomal protein L15-A



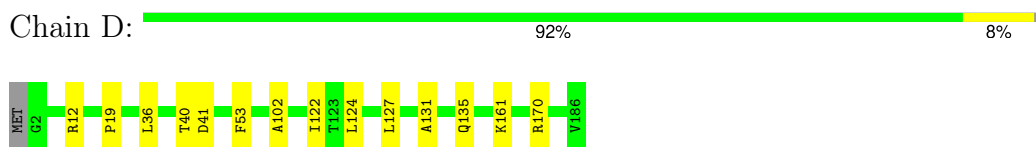
- Molecule 2: 60S ribosomal protein L16-A



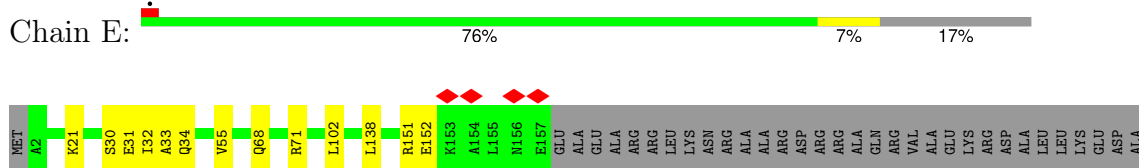
- Molecule 3: 60S ribosomal protein L17-A




- Molecule 4: 60S ribosomal protein L18-A



- Molecule 5: 60S ribosomal protein L19-A




- Molecule 6: 60S ribosomal protein L20-A

Chain F:  88% 12%



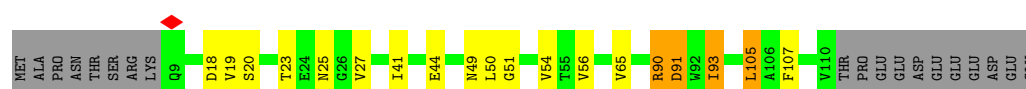
- Molecule 7: 60S ribosomal protein L21-A

Chain G:  89% 11%



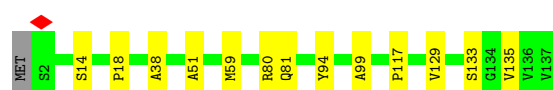
- Molecule 8: 60S ribosomal protein L22-A

Chain H:  69% 12% 16%



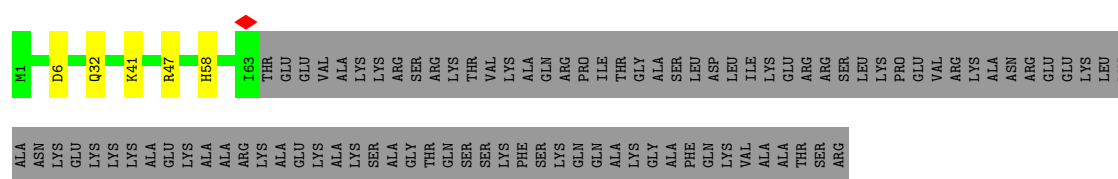
- Molecule 9: 60S ribosomal protein L23-A

Chain I:  90% 9%




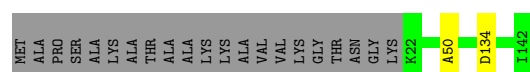
- Molecule 10: 60S ribosomal protein L24-A

Chain J:  37% 59%



- Molecule 11: 60S ribosomal protein L25

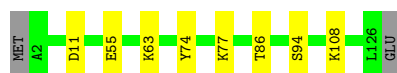
Chain K:  84% 15%



- Molecule 12: 60S ribosomal protein L26-A

Chain L:  92% 6%





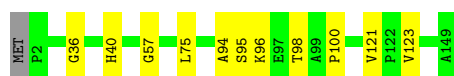
- Molecule 13: 60S ribosomal protein L27-A

Chain M: 92% 7%



- Molecule 14: 60S ribosomal protein L28

Chain N: 92% 7%



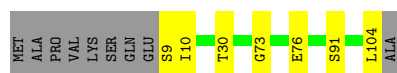
- Molecule 15: 60S ribosomal protein L29

Chain O: 83% 12%



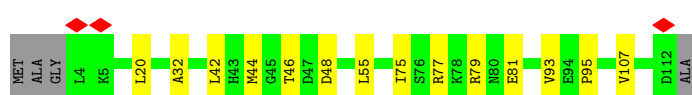
- Molecule 16: 60S ribosomal protein L30

Chain P: 85% 7% 9%



- Molecule 17: 60S ribosomal protein L31-A

Chain Q: 84% 12%



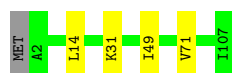
- Molecule 18: 60S ribosomal protein L32

Chain R: 92% 6%

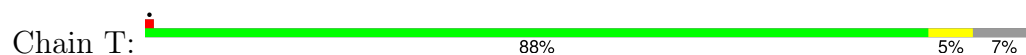


- Molecule 19: 60S ribosomal protein L33-A

Chain S: 95%



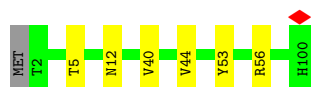
- Molecule 20: 60S ribosomal protein L34-A



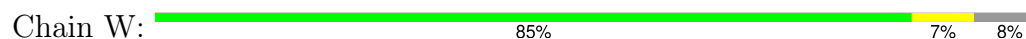
- Molecule 21: 60S ribosomal protein L35-A



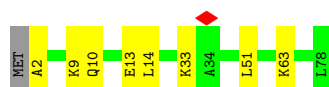
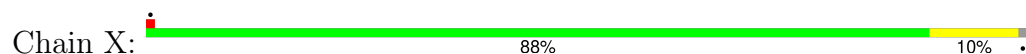
- Molecule 22: 60S ribosomal protein L36-A



- Molecule 23: 60S ribosomal protein L37-A



- Molecule 24: 60S ribosomal protein L38

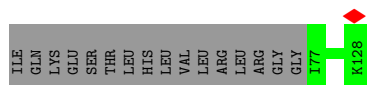


- Molecule 25: 60S ribosomal protein L39



- Molecule 26: Ubiquitin-60S ribosomal protein L40

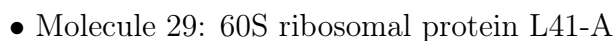


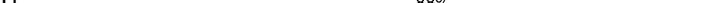


- Chain b:  97%



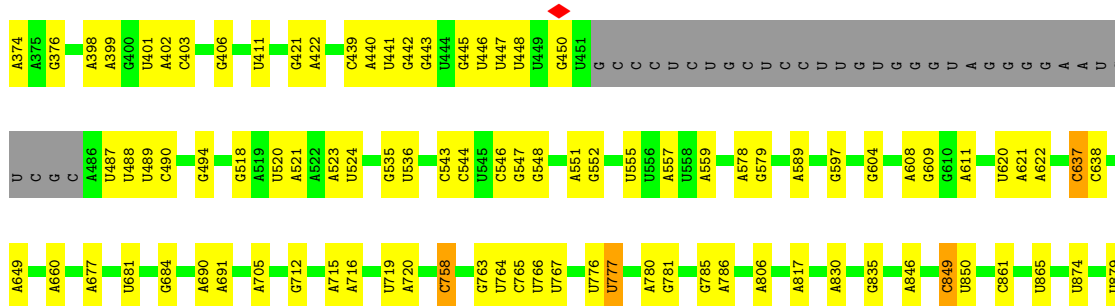
- Chain c:  99%



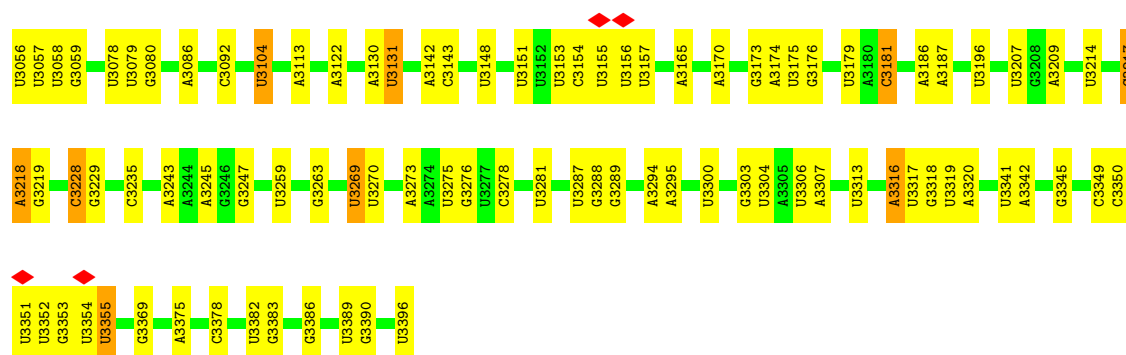
- Chain d:  88% 12%



- Chain f:  75% 18% • 5%



G2834	A2515	A2404	A2223	U	A1760	A1566	G1349	A1217	U1028	U885
U2835	G2522	C2405	A2224	G	C1761	U1567	A1350	A1219	A1036	U1218
C2836	G2526	U2411	U2225	A	C1762	U1568	U1351	C1219	A1041	C890
U2842	C2526	U2419	A2228	G	U1765	U1569	U1352	G1222	U1041	A896
U2843	C2531	G2437	C2235	C	G1766	U1572	A1354	A1047	A1047	G907
C2844	U2537	C2444	G2249	C	G1770	C1573	A1355	A1225	A1048	G908
A2845	U2538	A2445	U2254	U	G1775	C1574	U1356	G1226	C1049	
U2846	C2539	U2446	U	A	A1575	G1576	G1357	C1227		
C2849	A2540	A2447	A	U	G1780	G1577	A1386	U1235	G1063	A914
U2860	U2542	G2450	A	A	A1797	A1580	G1392	G1236	A1064	A915
C2867	U2543	G2451	U	U	C1797	C1581	A1399	G1237	A1065	G916
A2871	U2544	G2452	C	U	A1814	C1582	G1400	C1238	A1065	A917
U2872	A2547	U2453	A	A	U1815	A1583	A1419	C1239	G1072	A920
U2873	C2548	G2454	U	C	A1816	A1589	U1425	U1241	U1081	A921
G2874	U2549	A2455	A2262	C	U1819	G1590	U1425	G1242	G1087	C923
U2875	U2550	U2456	G2272	G	U1820	C1597	G1434	A1243	A1093	G924
G2876	U2551	G2457	G2273	A	U1821	G1604	U1437	A1244	A1094	A925
U2877	C2552	A2458	U2274	C	A1835	A1605	A1446	A1245	U1095	G937
A2887	U2553	U2459	U2274	U	U1839	U1607	U1448	A1252	U1096	
G2888	A2554	U2460	A2281	G	A1840	C1608	A1449	A1253	G1097	C944
C2889	G2555	A2461	U2282	U	U1842	U1609	G1450	C1254	A1098	
A2911	U2561	A2462	G2288	C	C1846	U1629	A1481	U1258	A1103	U954
G2914	C2568	U2463	G2307	G	U1849	C1639	A1482	A1259	G1104	C959
U2914	U2570	G2464	A2308	U	A1850	U1642	G1483	U1263	G1115	C969
U2923	G2571	U2465	U2310	C	C1866	A1643	G1488	G1264	G1116	
C2936	C2572	A2466	U2313	G	A1867	U1645	C1496	U1265	G1117	U981
A2941	G2573	U2467	U2314	C	U1872	C1657	C1502	U1269	G1131	C982
C2942	U2581	G2474	G2315	C	G1878	U1688	G1508	G1272	U1144	U985
G2947	C2585	A2475	U2334	U	U1879	C1725	G1525	C1277	A1153	U986
U2971	A2593	U2479	G2335	G	U1880	U1716	G1536	A1278	A1159	G991
C2983	C2594	A2480	U2336	U	A1881	U1717	A1539	C1279	C1160	G994
G2990	G2607	A2484	C2366	A	A1893	C1907	U1554	G1282	G1177	U1015
A2991	G2614	A2485	A2373	G	U1906	G1943	U1555	G1285	U1191	C1016
U2992	U2617	U2486	C2374	U	C1907	C1951	A1556	A1286	A1180	C1017
U2996	C2622	A2488	G2375	C	U1907	G1952	C1557	A1287	U1181	G1018
G2997	C2638	U2489	U2378	C	G1954	G1953	G1560	G1313	A1197	G1021
A3006	G2648	U2499	G2385	A	U1955	A1741	G1561	A1308	C1192	G1024
A3012	G2651	A2500	U2388	C	U1955	A1750	C1562	U1309	A1193	A1025
C3034	U2652	U2501	G2393	C	U1955	G1751	C1563	G1307	G1196	A1026
A3048	A2656	G2503	A2397	U	U1955			A1287	A1197	A1027
		U2504	A2402	G	U1955			G1282	C1201	
		U2505	G2403	G	U1955			A1287	A1202	
				U	U1955			G1282	U1208	



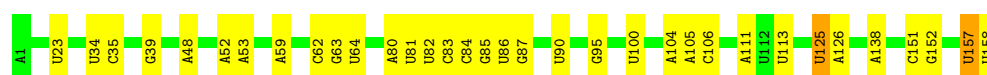
• Molecule 31: 5S rRNA

Chain h: 86% 14%



• Molecule 32: 5.8S rRNA

Chain i: 78% 20%



• Molecule 33: 60S ribosomal protein L2-A

Chain j: 97%



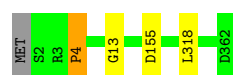
• Molecule 34: 60S ribosomal protein L3

Chain k: 99%



• Molecule 35: 60S ribosomal protein L4-A

Chain l: 99%



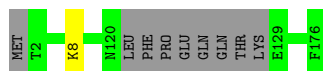
• Molecule 36: 60S ribosomal protein L5

Chain m: 98%



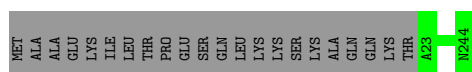
- Molecule 37: 60S ribosomal protein L6-B

Chain n: 94% 5%



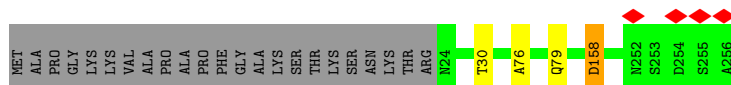
- Molecule 38: 60S ribosomal protein L7-A

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% 2%



- Molecule 41: 60S ribosomal protein L10

Chain r: 98% 2%



- Molecule 42: 60S ribosomal protein L11-A

Chain s: 94% 6%



- Molecule 43: 60S ribosomal protein L13-A

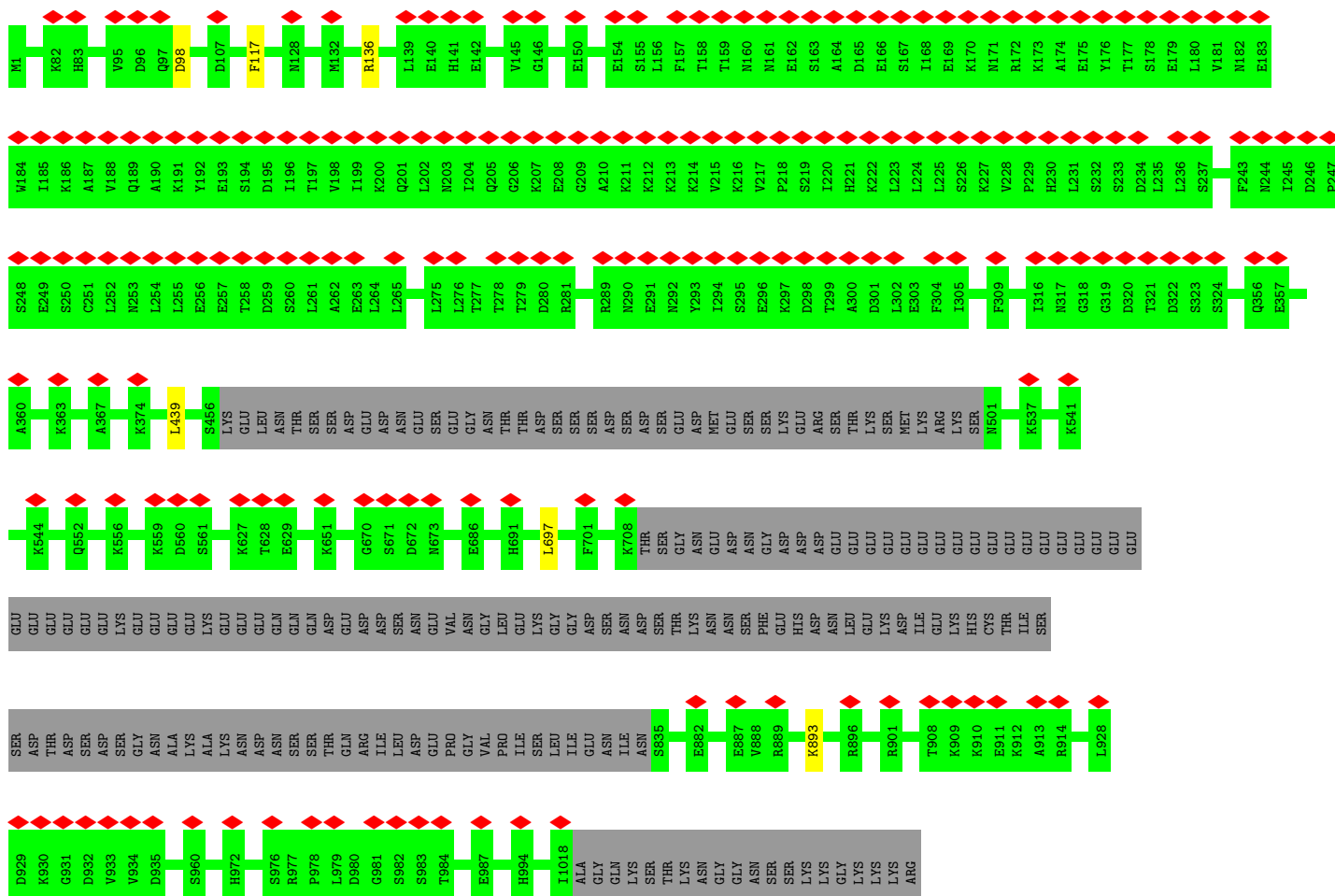
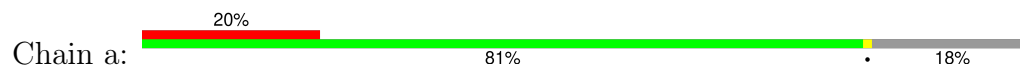
Chain t: 96% 4%



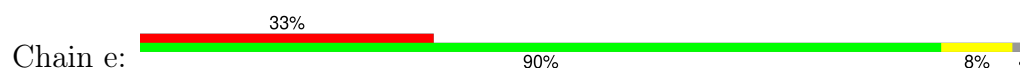
- Molecule 44: 60S ribosomal protein L14-A

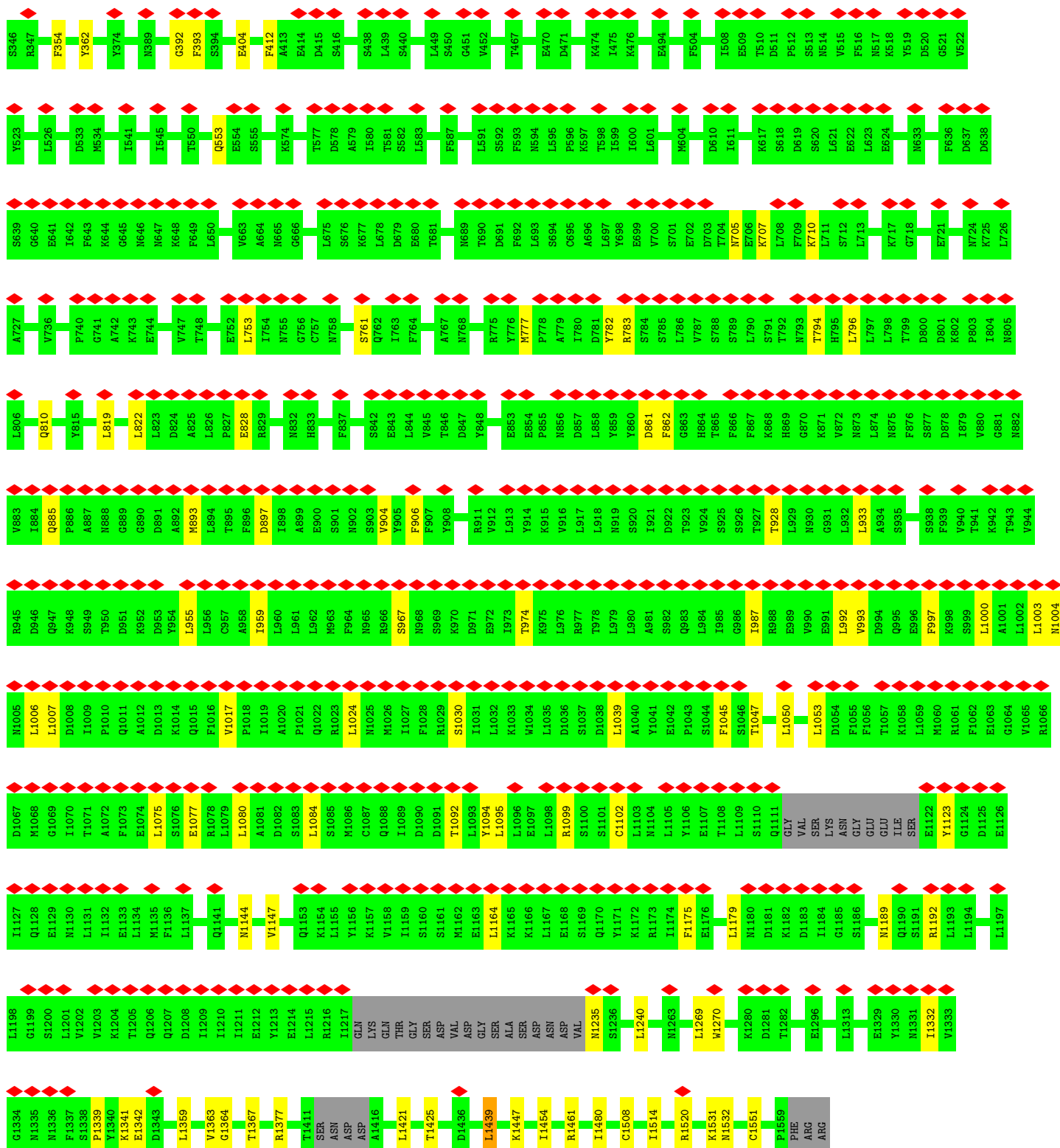


- Molecule 45: Ribosome quality control complex subunit 2

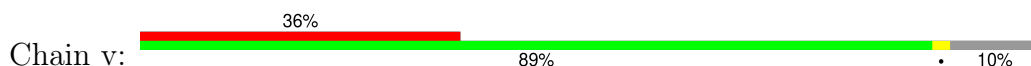


- Molecule 46: E3 ubiquitin-protein ligase listerin

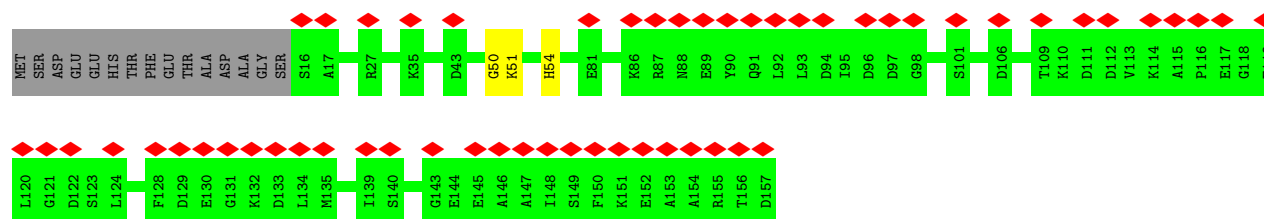




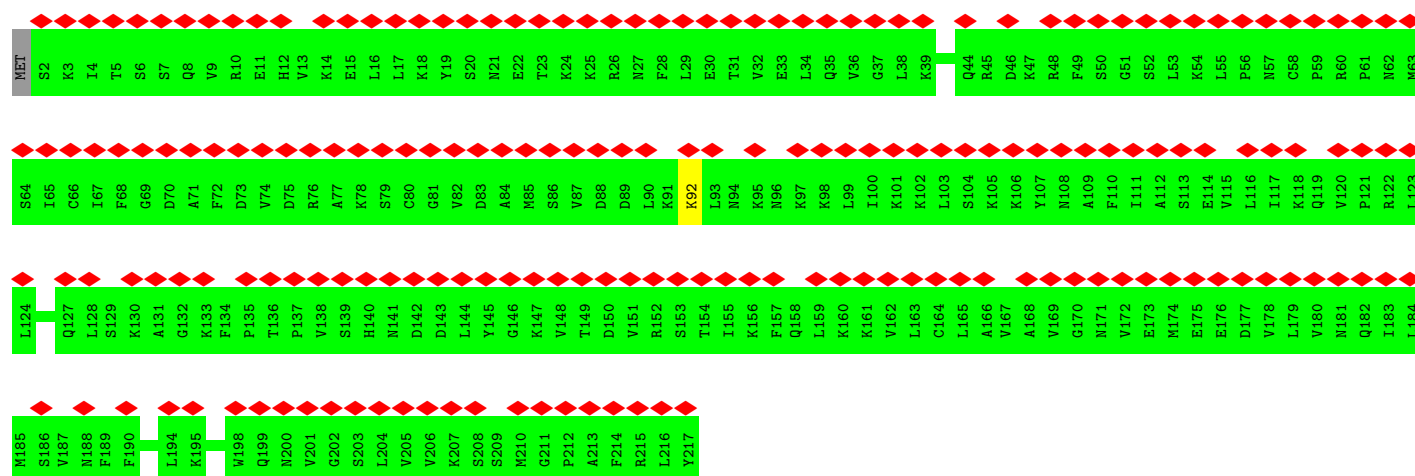
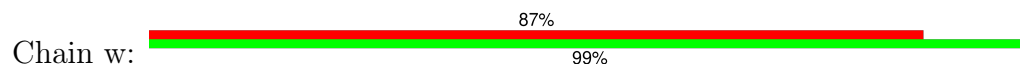
- Molecule 47: Eukaryotic translation initiation factor 5A-1



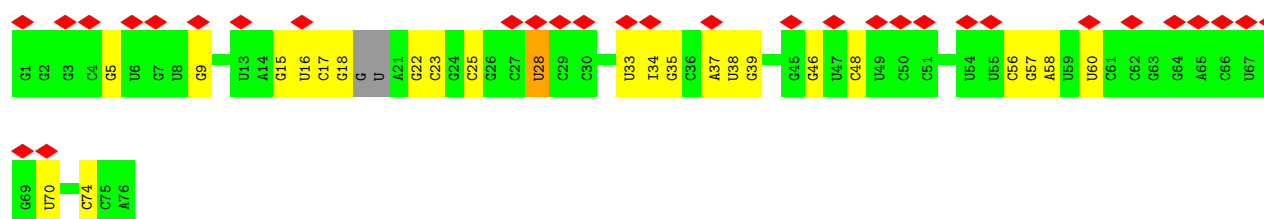
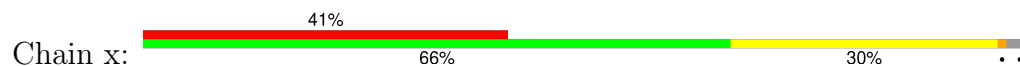




• Molecule 48: 60S ribosomal protein L1-A



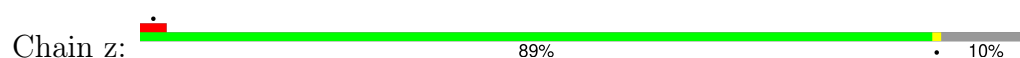
• Molecule 49: Ala tRNA



• Molecule 49: Ala tRNA



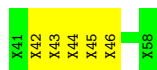
• Molecule 50: 60S ribosomal protein L12-A



- Molecule 51: 60S acidic ribosomal protein P0



- Molecule 52: CAT-tailed nascent peptide



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	124605	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	3.973	Depositor
Minimum map value	-0.648	Depositor
Average map value	0.020	Depositor
Map value standard deviation	0.132	Depositor
Recommended contour level	0.4	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: 5CT, SPD, MG, ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z  > 5$	RMSZ	# $ Z  > 5$
1	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	0.40	0/1439	0.74	2/1938 (0.1%)
4	D	0.34	0/1465	0.67	1/1965 (0.1%)
5	E	0.38	0/1275	0.69	0/1702
6	F	0.38	0/1473	0.65	0/1980
7	G	0.36	0/1296	0.62	0/1739
8	H	0.43	0/828	0.76	3/1121 (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	0.71	2/629 (0.3%)
16	P	0.35	0/745	0.67	1/1001 (0.1%)
17	Q	0.39	0/890	0.66	1/1196 (0.1%)
18	R	0.32	0/1034	0.59	0/1385
19	S	0.38	0/868	0.61	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	0.69	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	0.67	0/934
29	d	0.26	0/208	0.84	0/267
30	f	0.61	0/76989	1.03	294/120031 (0.2%)
31	h	0.53	0/2883	0.98	8/4491 (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	0.37	0/1908	0.67	0/2564
34	k	0.37	0/3146	0.64	1/4228 (0.0%)
35	l	0.36	0/2800	0.65	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	0.64	0/2416
42	s	0.36	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	0.31	0/6689	0.57	3/9023 (0.0%)
46	e	0.43	0/11707	0.63	7/15897 (0.0%)
47	v	0.31	0/1084	0.62	1/1456 (0.1%)
48	w	0.34	0/1736	0.65	0/2332
49	x	0.37	0/1760	1.02	8/2738 (0.3%)
49	y	0.40	0/1734	1.10	7/2697 (0.3%)
50	z	0.38	0/726	0.61	0/1006
51	0	0.33	0/976	0.55	0/1313
All	All	0.51	0/160081	0.89	367/234000 (0.2%)

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
3	C	0	1
5	E	0	1
8	H	0	1
15	O	0	1
21	U	0	1
34	k	0	1
35	l	0	2
39	p	0	3
40	q	0	1
44	u	0	1
46	e	0	1
All	All	0	14

There are no bond length outliers.

The worst 5 of 367 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	f	3217	C	N1-C2-O2	12.24	126.24	118.90
30	f	3217	C	C2-N1-C1'	11.26	131.19	118.80
49	y	75	C	C6-N1-C2	-10.41	116.14	120.30
30	f	3217	C	N3-C2-O2	-9.71	115.10	121.90
11	K	134	ASP	CB-CG-OD1	9.68	127.02	118.30

There are no chirality outliers.

5 of 14 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	126	ARG	Mainchain
5	E	32	ILE	Mainchain
8	H	90	ARG	Mainchain
15	O	20	GLY	Peptide
21	U	83	LYS	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	9	0
2	B	1555	0	1659	13	0
3	C	1416	0	1433	15	0
4	D	1441	0	1543	7	0
5	E	1258	0	1342	9	0
6	F	1437	0	1475	14	0
7	G	1272	0	1312	10	0
8	H	812	0	829	10	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	5	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	5	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	3	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	68782	0	34563	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	6579	0	6482	0	0
46	e	11508	0	10764	0	0
47	v	1085	0	1086	0	0
48	w	1709	0	1799	0	0
49	x	1579	0	798	0	0
49	y	1556	0	788	0	0
50	z	728	0	337	0	0
51	0	961	0	979	11	0
52	1	90	0	22	4	0
53	A	1	0	0	0	0
53	C	1	0	0	0	0
53	E	1	0	0	0	0
53	I	1	0	0	0	0
53	R	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
53	T	1	0	0	0	0
53	f	3	0	0	0	0
53	h	1	0	0	0	0
53	j	2	0	0	0	0
53	k	1	0	0	0	0
54	T	1	0	0	0	0
54	W	1	0	0	0	0
54	Z	1	0	0	0	0
54	b	1	0	0	0	0
54	c	1	0	0	0	0
54	e	2	0	0	0	0
55	f	10	0	19	0	0
All	All	149706	0	112020	156	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 156 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	1.69	0.90
15:O:16:ALA:O	15:O:20:GLY:CA	2.36	0.73
5:E:31:GLU:HA	5:E:34:GLN:HB2	1.71	0.71
23:W:21:ARG:HE	23:W:39:TYR:HB2	1.58	0.69
51:O:26:PHE:HB2	51:O:87:VAL:HB	1.73	0.69

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	100/121 (83%)	95 (95%)	4 (4%)	1 (1%)	13	20
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	9
16	P	94/105 (90%)	93 (99%)	1 (1%)	0	100	100
17	Q	107/113 (95%)	103 (96%)	4 (4%)	0	100	100
18	R	125/130 (96%)	123 (98%)	2 (2%)	0	100	100
19	S	104/107 (97%)	101 (97%)	3 (3%)	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%)	75 (95%)	4 (5%)	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%)	363 (94%)	21 (6%)	0	100	100
35	l	359/362 (99%)	329 (92%)	29 (8%)	1 (0%)	37	51

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	m	292/297 (98%)	277 (95%)	15 (5%)	0	100	100
37	n	163/176 (93%)	154 (94%)	9 (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	38
41	r	216/221 (98%)	206 (95%)	10 (5%)	0	100	100
42	s	167/174 (96%)	161 (96%)	5 (3%)	1 (1%)	22	33
43	t	191/199 (96%)	174 (91%)	16 (8%)	1 (0%)	25	38
44	u	134/138 (97%)	125 (93%)	9 (7%)	0	100	100
45	a	842/1038 (81%)	826 (98%)	16 (2%)	0	100	100
46	e	1519/1562 (97%)	1497 (99%)	20 (1%)	2 (0%)	48	65
47	v	139/157 (88%)	139 (100%)	0	0	100	100
48	w	214/217 (99%)	211 (99%)	3 (1%)	0	100	100
50	z	144/165 (87%)	136 (94%)	7 (5%)	1 (1%)	19	29
51	0	117/312 (38%)	116 (99%)	0	1 (1%)	14	22
All	All	9093/10034 (91%)	8747 (96%)	336 (4%)	10 (0%)	50	65

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
46	e	393	PHE
50	z	88	PRO
46	e	1339	PRO
8	H	91	ASP
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	160/162 (99%)	160 (100%)	0	100	100
3	C	138/146 (94%)	137 (99%)	1 (1%)	81	91
4	D	150/151 (99%)	149 (99%)	1 (1%)	81	91
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	91
8	H	89/107 (83%)	87 (98%)	2 (2%)	47	67
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	67
16	P	81/88 (92%)	81 (100%)	0	100	100
17	Q	92/97 (95%)	89 (97%)	3 (3%)	33	53
18	R	107/111 (96%)	107 (100%)	0	100	100
19	S	90/91 (99%)	90 (100%)	0	100	100
20	T	95/103 (92%)	94 (99%)	1 (1%)	70	84
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	58
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%)	189 (100%)	0	100	100
34	k	320/323 (99%)	318 (99%)	2 (1%)	84	92
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	91
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	84
42	s	145/150 (97%)	142 (98%)	3 (2%)	48	69
43	t	154/159 (97%)	154 (100%)	0	100	100
44	u	107/109 (98%)	107 (100%)	0	100	100
45	a	678/949 (71%)	675 (100%)	3 (0%)	89	95
46	e	1150/1451 (79%)	1038 (90%)	112 (10%)	6	10
47	v	119/132 (90%)	118 (99%)	1 (1%)	79	90
48	w	197/198 (100%)	196 (100%)	1 (0%)	86	94
51	0	104/254 (41%)	95 (91%)	9 (9%)	8	13
All	All	7385/8479 (87%)	7239 (98%)	146 (2%)	50	70

5 of 146 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
46	e	1270	TRP
51	0	93	LEU
46	e	1359	LEU
46	e	1508	CYS
46	e	342	PHE

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	1138	ASN
46	e	1190	GLN
46	e	1189	ASN
46	e	1288	GLN
46	e	233	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
30	f	3212/3395 (94%)	589 (18%)	0
31	h	120/121 (99%)	12 (10%)	0
32	i	157/158 (99%)	32 (20%)	0
49	x	72/76 (94%)	21 (29%)	0
49	y	71/76 (93%)	20 (28%)	0
All	All	3632/3826 (94%)	674 (18%)	0

5 of 674 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	$\# Z  > 2$
47	5CT	v	51	47	13,14,15	0.79	0	8,15,17	1.30	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
47	5CT	v	51	47	-	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(°)
47	v	51	5CT	C4-C3-C2	-2.21	108.81	113.47

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
47	v	51	5CT	NZ-C1-C2-C3
47	v	51	5CT	O1-C2-C3-C4
47	v	51	5CT	C2-C3-C4-N1
47	v	51	5CT	C-CA-CB-CG
47	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 21 ligands modelled in this entry, 20 are monoatomic - leaving 1 for Mogul analysis.

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	$\# Z  > 2$
55	SPD	f	3401	-	9,9,9	0.32	0	8,8,8	0.85	0

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
55	SPD	f	3401	-	-	5/7/7/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
55	f	3401	SPD	C3-C4-C5-N6
55	f	3401	SPD	N6-C7-C8-C9
55	f	3401	SPD	C2-C3-C4-C5
55	f	3401	SPD	C4-C5-N6-C7
55	f	3401	SPD	C8-C7-N6-C5

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.

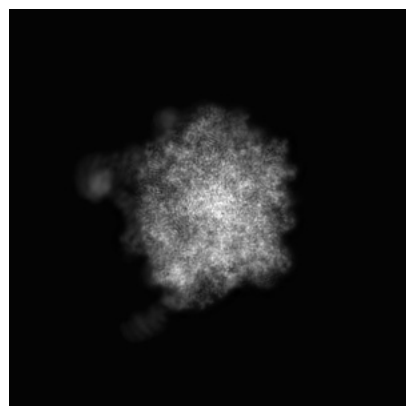
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-15427. These allow visual inspection of the internal detail of the map and identification of artifacts.

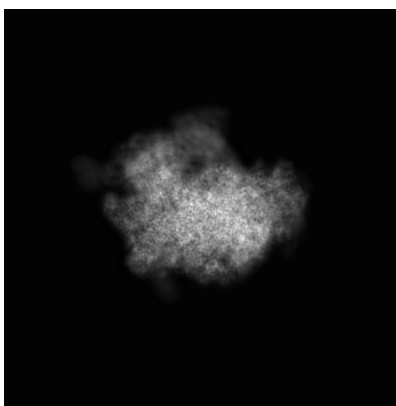
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

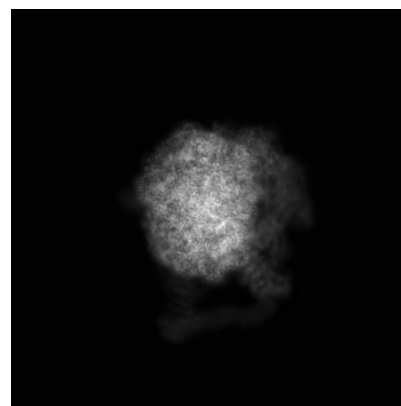
#### 6.1.1 Primary map



X

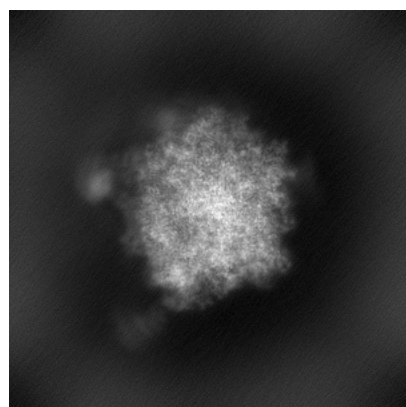


Y

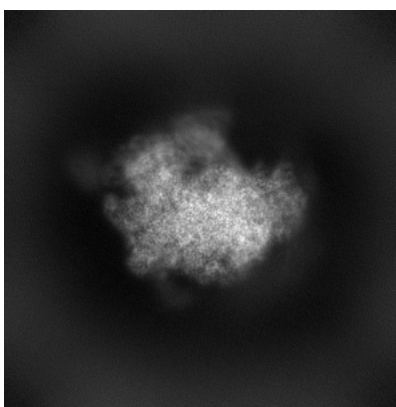


Z

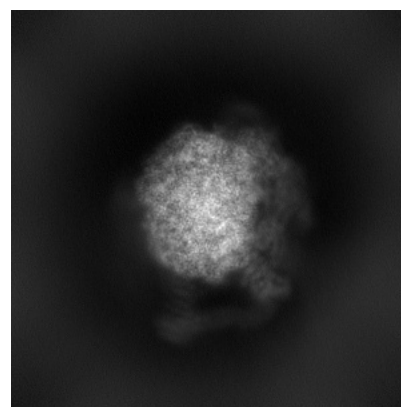
#### 6.1.2 Raw map



X



Y



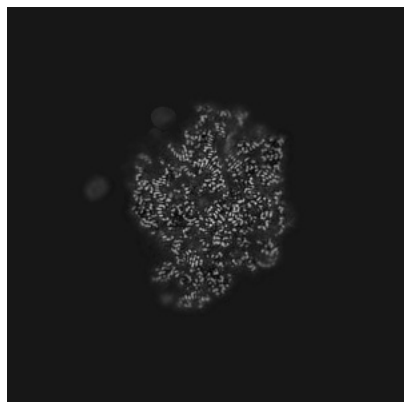
Z

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

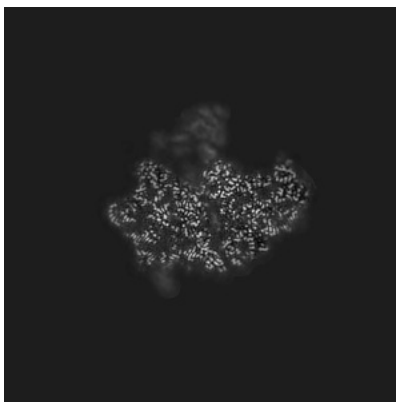


## 6.2 Central slices [i](#)

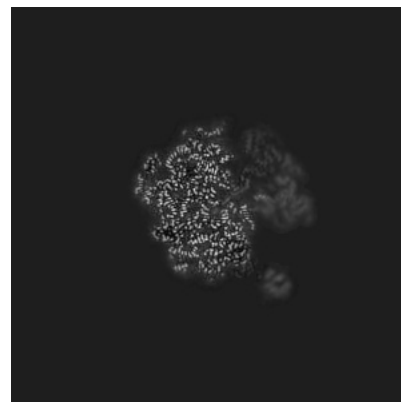
### 6.2.1 Primary map



X Index: 225

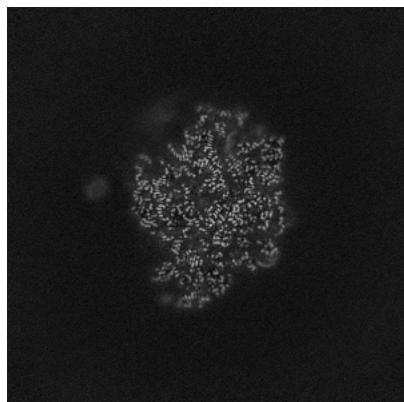


Y Index: 225

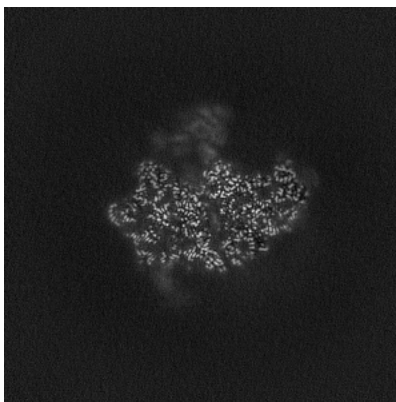


Z Index: 225

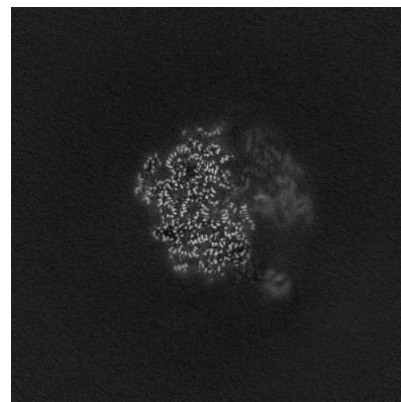
### 6.2.2 Raw map



X Index: 225



Y Index: 225

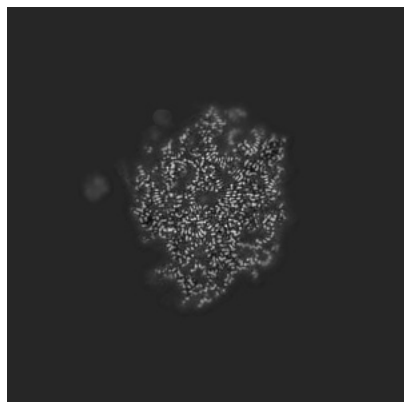


Z Index: 225

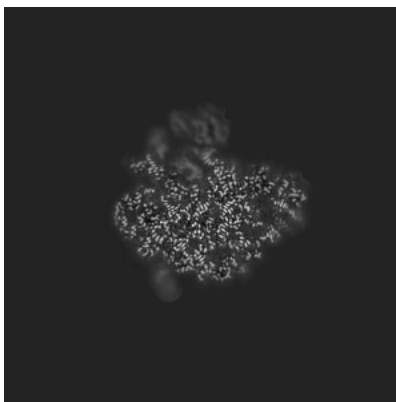
The images above show central slices of the map in three orthogonal directions.

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

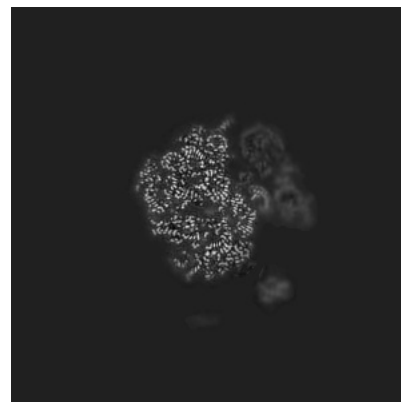
### 6.3.1 Primary map



X Index: 219

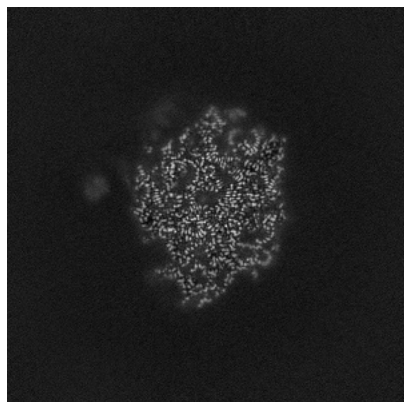


Y Index: 237

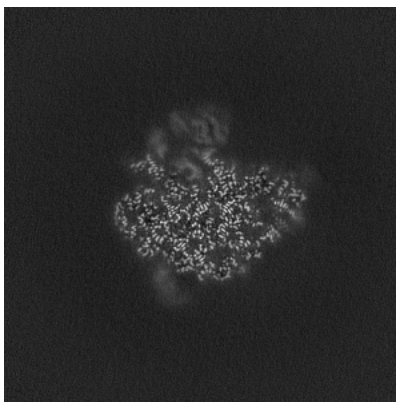


Z Index: 231

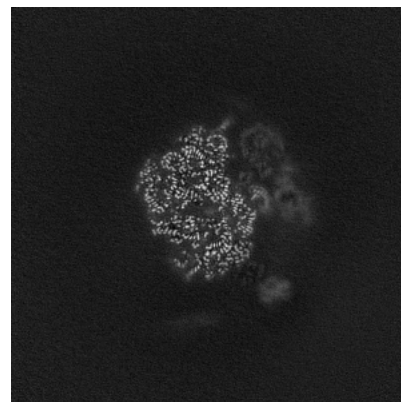
### 6.3.2 Raw map



X Index: 219



Y Index: 237

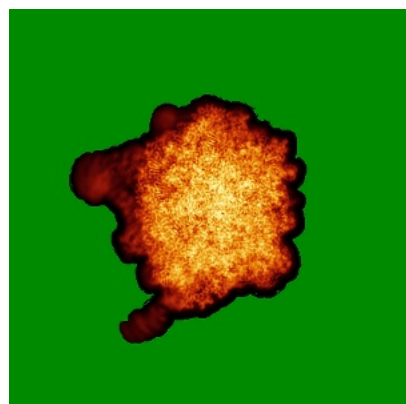


Z Index: 231

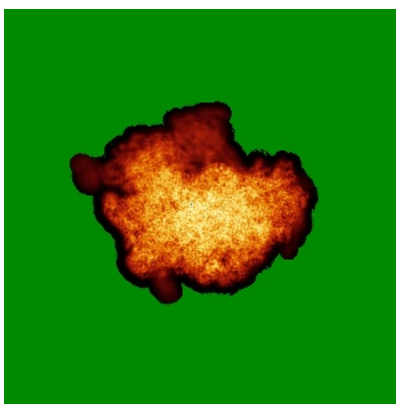
The images above show the largest variance slices of the map in three orthogonal directions.

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

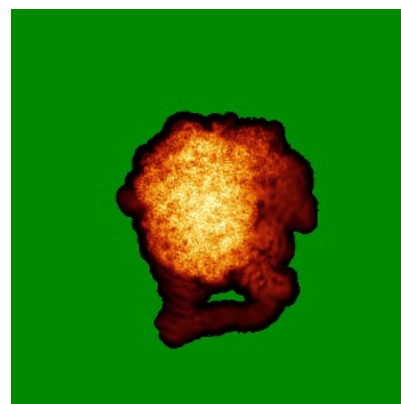
### 6.4.1 Primary map



X

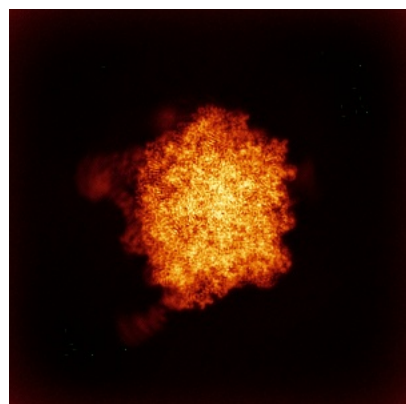


Y

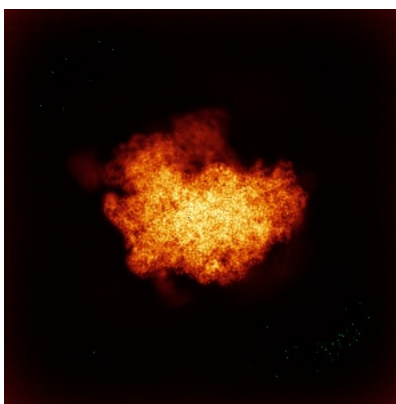


Z

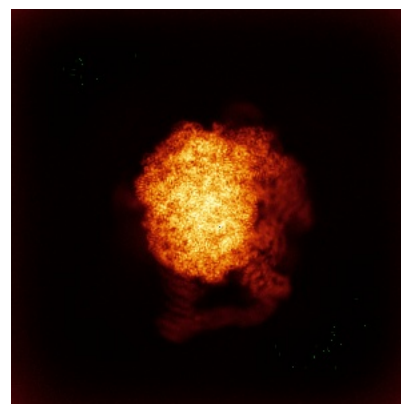
### 6.4.2 Raw map



X



Y

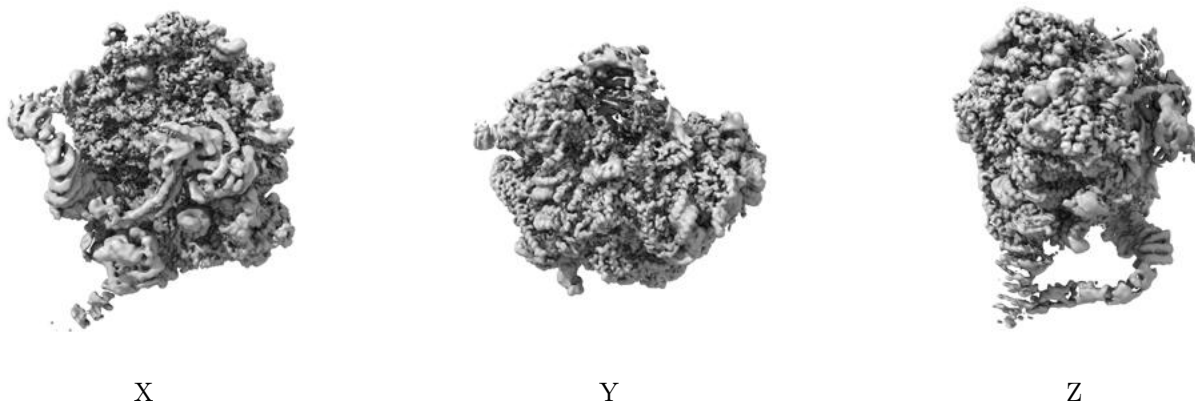


Z

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.

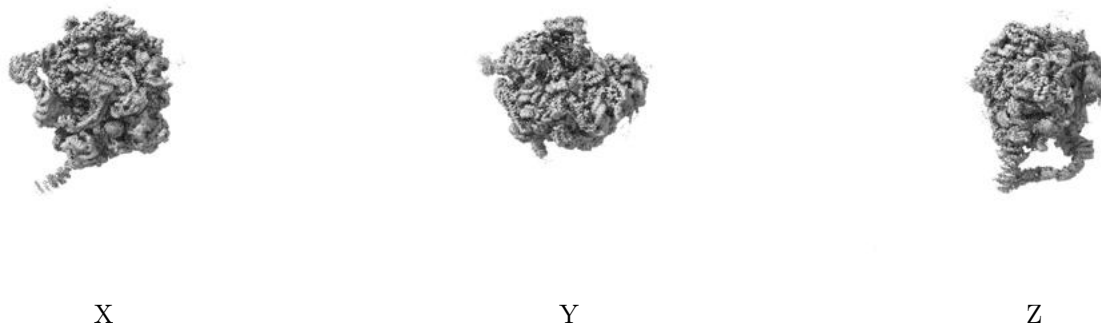
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.4. 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.

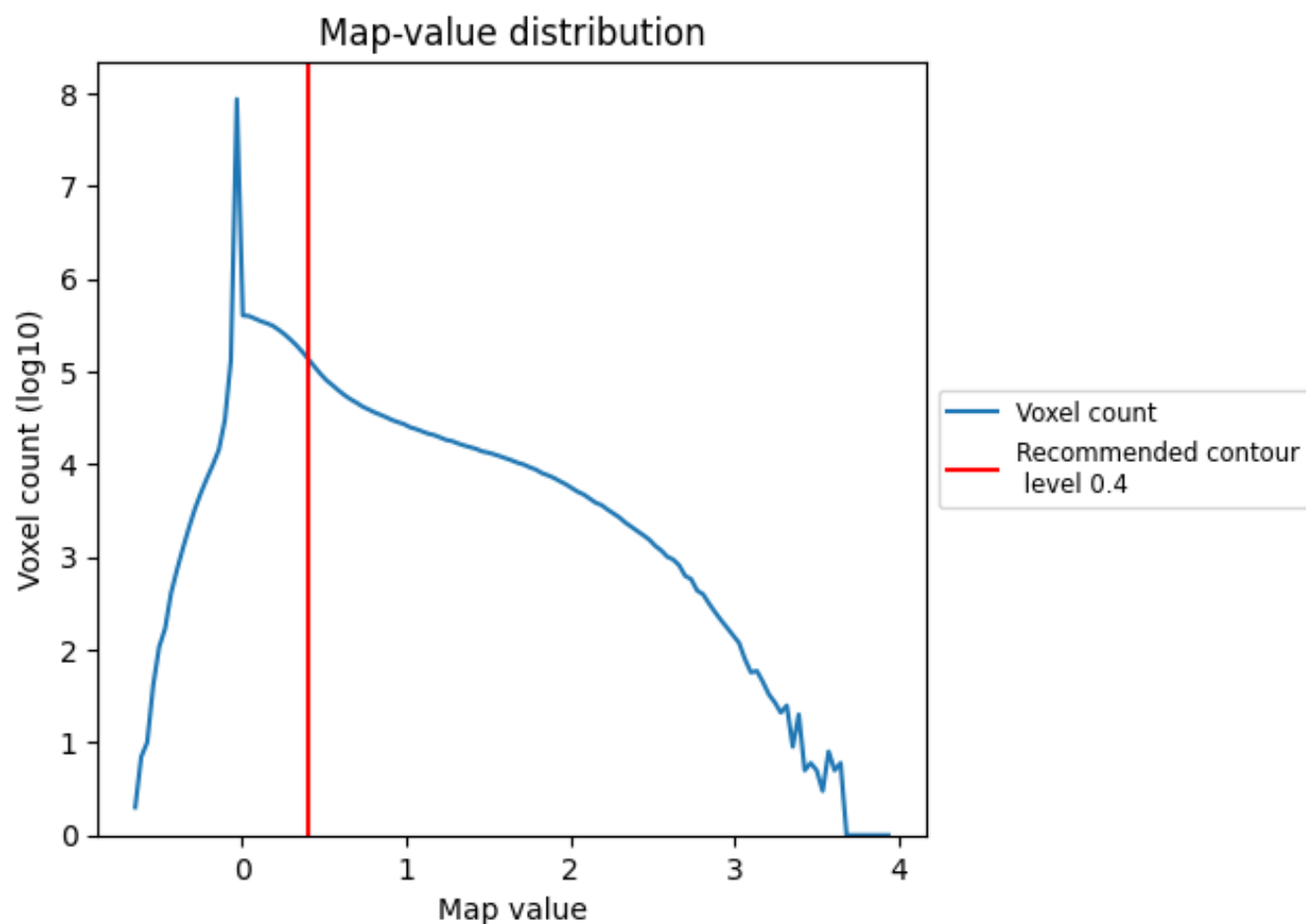
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

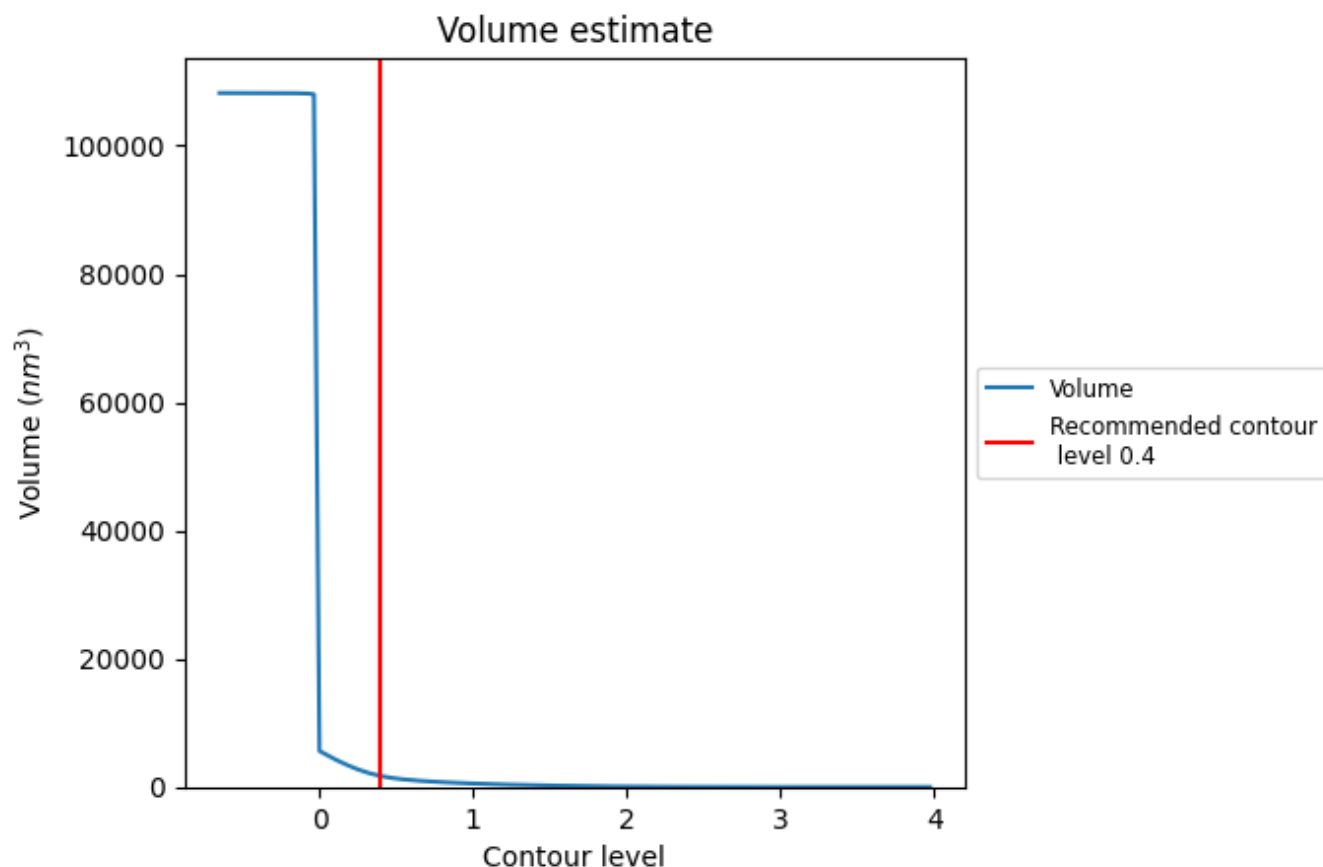
This section contains the results of statistical analysis of the map.

### 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.

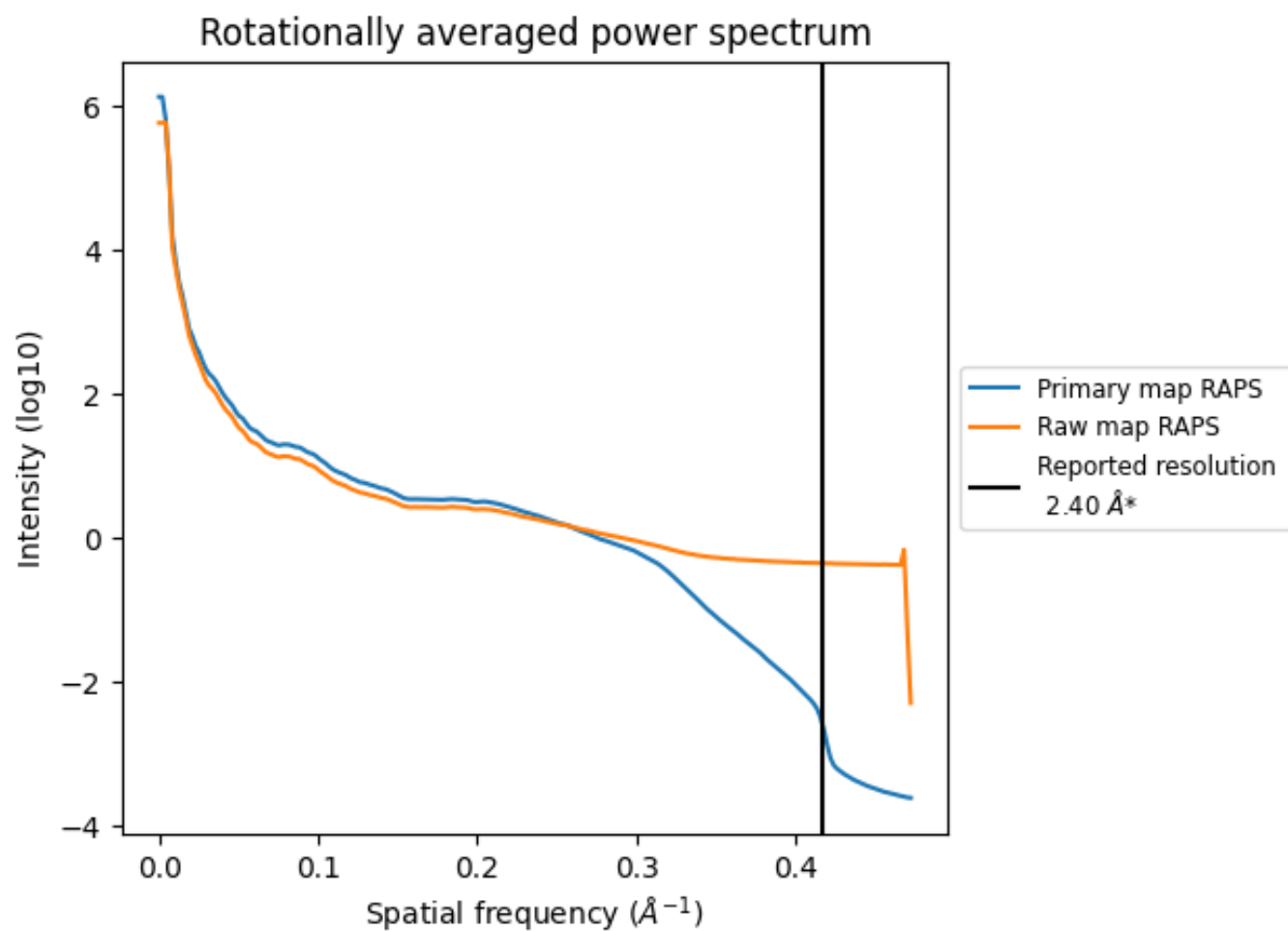
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1709  $\text{nm}^3$ ; this corresponds to an approximate mass of 1544 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 ⓘ

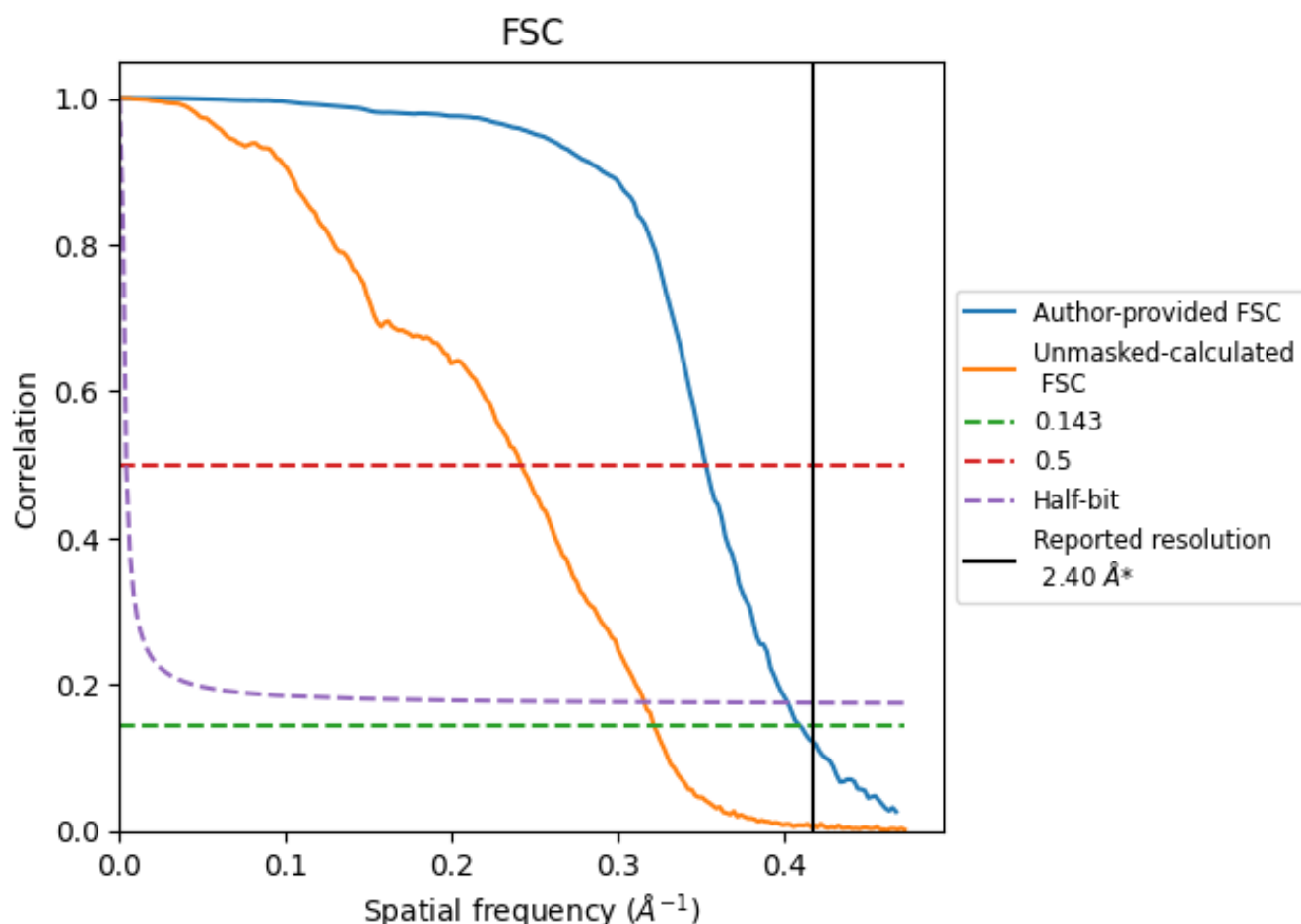


\*Reported resolution corresponds to spatial frequency of 0.417 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



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



## 8.2 Resolution estimates [i](#)

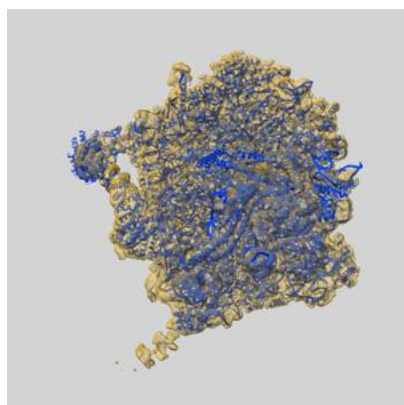
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.40	-	-
Author-provided FSC curve	2.44	2.84	2.49
Unmasked-calculated*	3.11	4.14	3.17

\*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 3.11 differs from the reported value 2.4 by more than 10 %

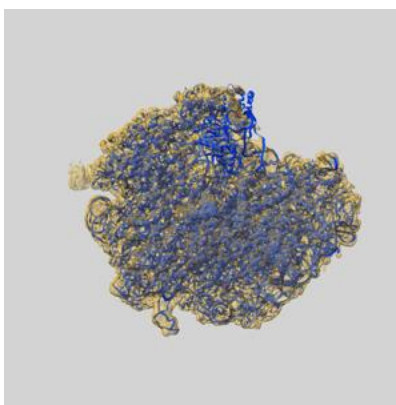
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-15427 and PDB model 8AGX. Per-residue inclusion information can be found in section [3](#) on page [15](#).

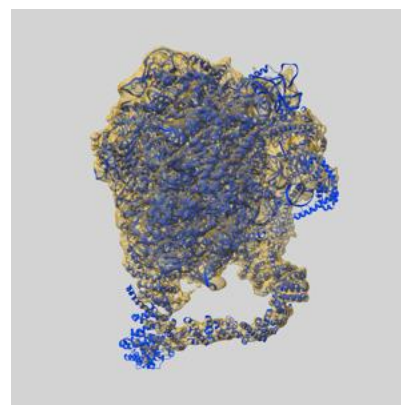
### 9.1 Map-model overlay [i](#)



X



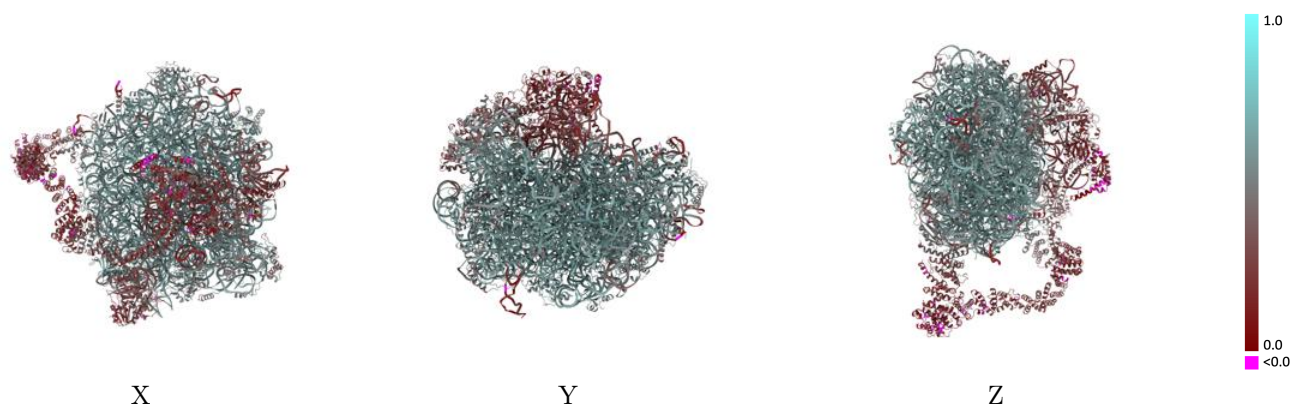
Y



Z

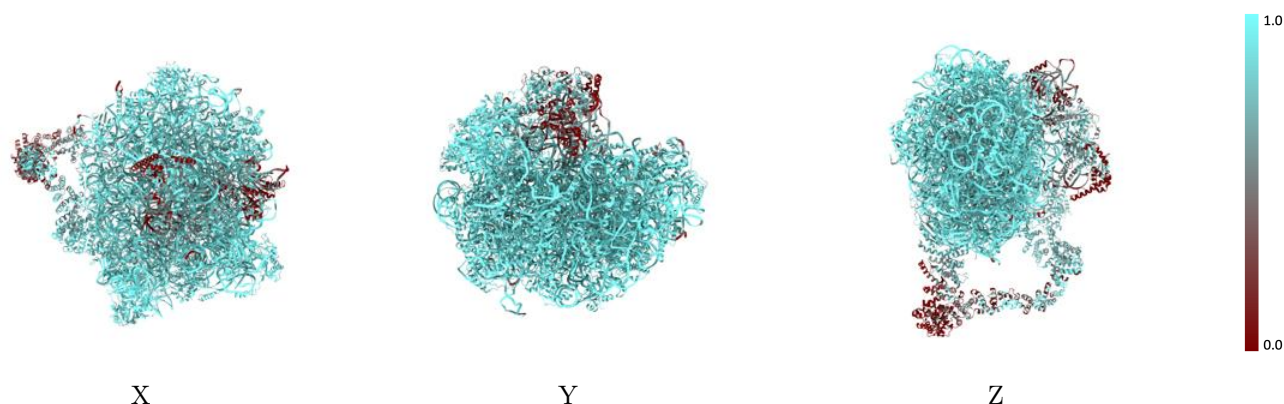
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



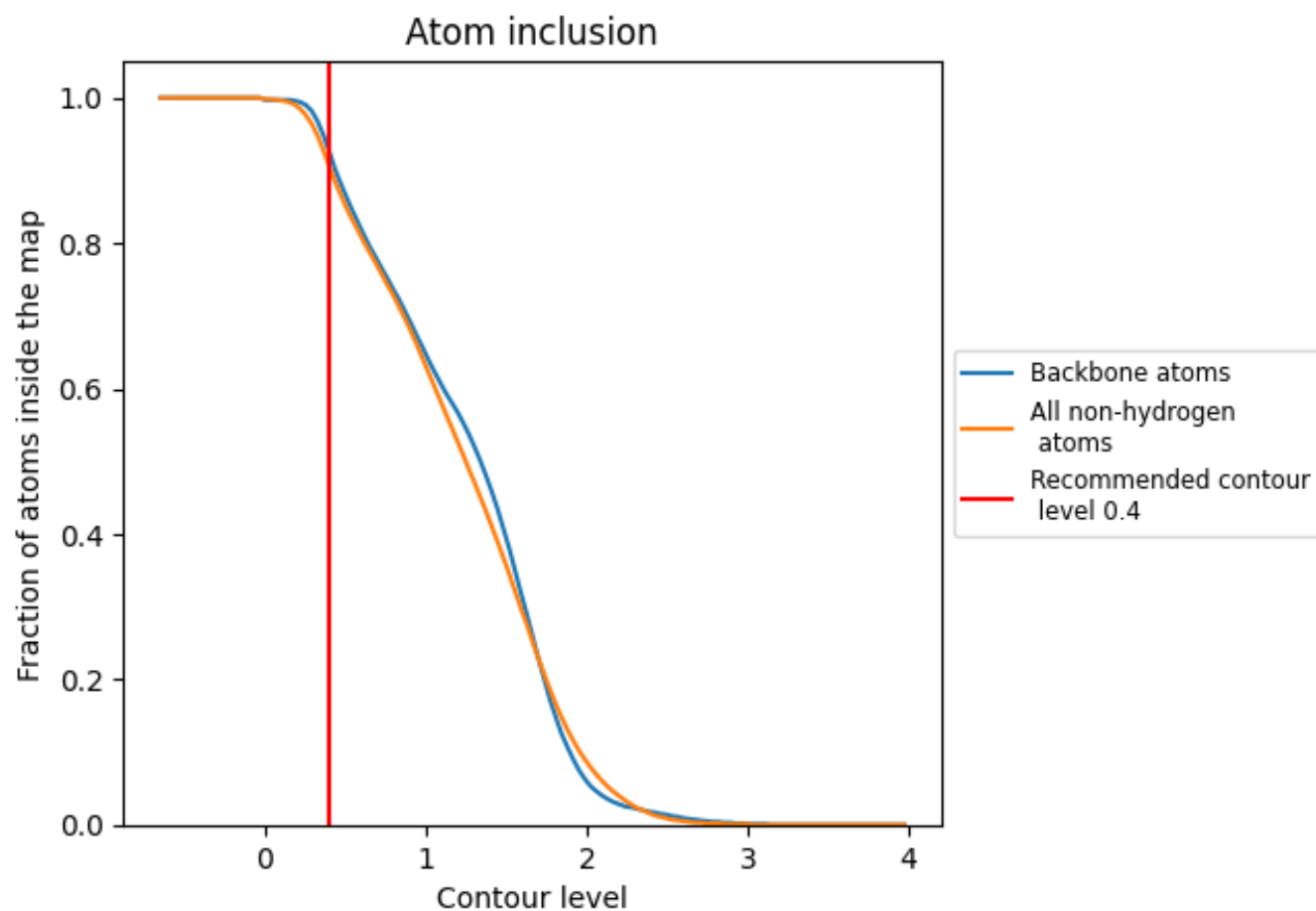
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.4).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 91% 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 (0.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9060	 0.5200
0	 0.8400	 0.2790
1	 0.9890	 0.4180
A	 0.9910	 0.6220
B	 0.9800	 0.5990
C	 0.9710	 0.5960
D	 0.9800	 0.5970
E	 0.9380	 0.5600
F	 0.9790	 0.5880
G	 0.9690	 0.5770
H	 0.9180	 0.4740
I	 0.9670	 0.5830
J	 0.9600	 0.5800
K	 0.9710	 0.5860
L	 0.9760	 0.5810
M	 0.9520	 0.5350
N	 0.9820	 0.6050
O	 0.9560	 0.5510
P	 0.9390	 0.5370
Q	 0.9390	 0.5670
R	 0.9840	 0.6140
S	 0.9920	 0.6230
T	 0.9680	 0.5850
U	 0.9680	 0.5700
V	 0.9570	 0.5380
W	 1.0000	 0.6370
X	 0.9200	 0.5010
Y	 0.9980	 0.6160
Z	 0.9650	 0.5800
a	 0.6040	 0.2130
b	 0.9600	 0.5860
c	 0.9720	 0.5850
d	 0.7710	 0.4410
e	 0.5430	 0.2500
f	 0.9830	 0.5790



*Continued on next page...*

*Continued from previous page...*

Chain	Atom inclusion	Q-score
h	 0.9990	 0.5830
i	 0.9950	 0.6070
j	 0.9880	 0.6160
k	 0.9790	 0.5960
l	 0.9750	 0.5890
m	 0.9410	 0.5020
n	 0.9530	 0.5390
o	 0.9740	 0.5840
p	 0.9520	 0.5350
q	 0.9600	 0.5600
r	 0.9580	 0.5560
s	 0.9360	 0.4690
t	 0.9720	 0.5750
u	 0.9720	 0.5610
v	 0.4730	 0.3880
w	 0.1540	 0.2370
x	 0.4690	 0.2580
y	 0.8790	 0.2370
z	 0.9150	 0.2820