



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 01:43 AM UTC

PDB ID : 7P7U / pdb_00007p7u
EMDB ID : EMD-13245
Title : E. faecalis 70S ribosome with P-tRNA, state IV
Authors : Crowe-McAuliffe, C.; Wilson, D.N.
Deposited on : 2021-07-20
Resolution : 3.10 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

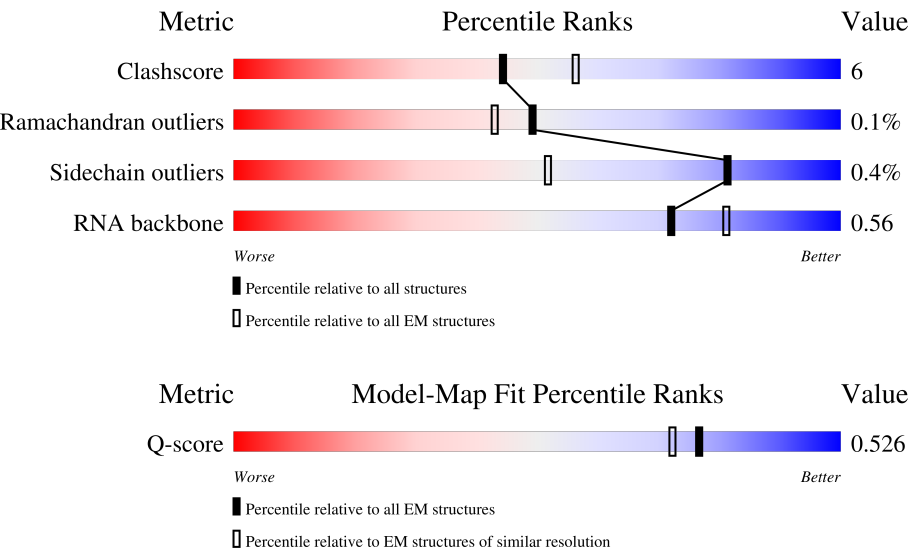
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.10 Å.

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



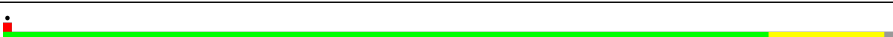
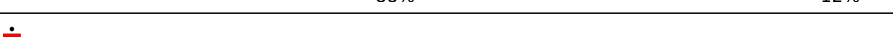
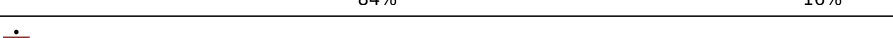
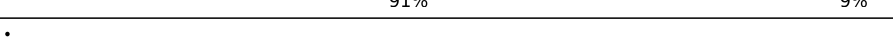
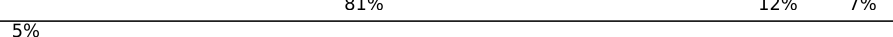
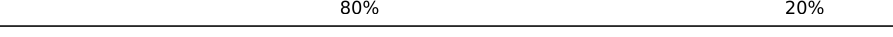
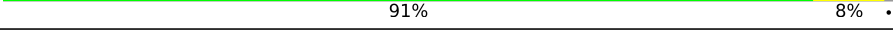
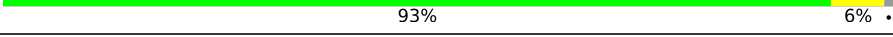
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	1	62	94% 5%
2	2	59	85% 12%
3	3	89	19% 82% 8% 10%

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Mol	Chain	Length	Quality of chain
4	4	59	
5	5	49	
6	6	44	
7	7	66	
8	8	38	
9	A	2912	
10	B	116	
11	D	77	
12	G	276	
13	H	209	
14	I	207	
15	J	179	
16	K	178	
17	M	147	
18	N	122	
19	O	146	
20	P	144	
21	Q	127	
22	R	118	
23	S	115	
24	T	119	
25	U	102	
26	V	115	
27	W	96	
28	X	103	

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Mol	Chain	Length	Quality of chain
29	Y	95	
30	Z	62	
31	a	1558	
32	b	19	
33	c	261	
34	d	218	
35	e	203	
36	f	166	
37	g	100	
38	h	156	
39	i	132	
40	j	130	
41	k	102	
42	l	129	
43	m	137	
44	n	121	
45	o	61	
46	p	89	
47	q	91	
48	r	88	
49	s	79	
50	t	92	
51	u	83	

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 139826 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 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	59	Total	C	N	O	S	0	0
			491	307	91	92	1		

- Molecule 2 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	57	Total	C	N	O	S	0	0
			428	266	80	81	1		

- Molecule 3 is a protein called 50S ribosomal protein L31 type B.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	80	Total	C	N	O	S	0	0
			647	409	110	126	2		

- Molecule 4 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	53	Total	C	N	O	S	0	0
			406	248	84	69	5		

- Molecule 5 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	48	Total	C	N	O	S	0	0
			410	247	84	75	4		

- Molecule 6 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	44	Total	C	N	O	S	0	0
			374	227	91	54	2		

- Molecule 7 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	7	64	Total	C	N	O	S	0	0
			522	320	122	78	2		

- Molecule 8 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	8	38	Total	C	N	O	S	0	0
			305	188	66	45	6		

- Molecule 9 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	A	2824	Total	C	N	O	P	0	0
			60606	27054	11141	19587	2824		

- Molecule 10 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	B	114	Total	C	N	O	P	0	0
			2439	1088	439	798	114		

- Molecule 11 is a RNA chain called tRNA-fMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	D	77	Total	C	N	O	P	0	0
			1644	733	298	536	77		

- Molecule 12 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	G	274	Total	C	N	O	S	0	0
			2106	1305	414	380	7		

- Molecule 13 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	H	206	Total	C	N	O	S	0	0
			1572	990	291	287	4		

- Molecule 14 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	I	205	Total	C	N	O	S	0	0
			1572	984	289	297	2		

- Molecule 15 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	177	Total	C	N	O	S	0	0
			1392	887	239	260	6		

- Molecule 16 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	174	Total	C	N	O	S	0	0
			1335	838	242	251	4		

- Molecule 17 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	M	147	Total	C	N	O	S	0	0
			1146	726	207	209	4		

- Molecule 18 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	N	122	Total	C	N	O	S	0	0
			923	574	176	171	2		

- Molecule 19 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	O	146	Total	C	N	O	S	0	0
			1096	677	212	206	1		

- Molecule 20 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	P	134	Total	C	N	O	S	0	0
			1070	683	209	173	5		

- Molecule 21 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Q	125	Total	C	N	O	S	0	0
			997	615	192	187	3		

- Molecule 22 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	R	118	Total	C	N	O	S	0	0
			908	561	176	169	2		

- Molecule 23 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	S	114	Total	C	N	O	S	0	0
			925	582	185	158			

- Molecule 24 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	T	118	Total	C	N	O	S	0	0
			950	602	184	160	4		

- Molecule 25 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	U	101	Total	C	N	O	S	0	0
			779	497	138	142	2		

- Molecule 26 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	V	111	Total	C	N	O	S	0	0
			841	527	154	158	2		

- Molecule 27 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	W	91	Total	C	N	O	S	0	0
			736	469	129	134	4		

- Molecule 28 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	X	101	Total	C	N	O	S	0	0
			763	486	135	140	2		

- Molecule 29 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Y	74	Total	C	N	O		0	0
			559	344	107	108			

- Molecule 30 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Z	61	Total	C	N	O	S	0	0
			480	299	97	82	2		

- Molecule 31 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	a	1521	Total	C	N	O	P	0	0
			32595	14542	5954	10578	1521		

- Molecule 32 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	b	13	Total	C	N	O	P	0	0
			285	127	57	88	13		

- Molecule 33 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	c	222	Total	C	N	O	S	0	0
			1773	1126	312	326	9		

- Molecule 34 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	d	205	Total	C	N	O	S	0	0
			1618	1018	304	293	3		

- Molecule 35 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	e	200	Total	C	N	O	S	0	0
			1611	1010	301	296	4		

- Molecule 36 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	f	163	Total	C	N	O	S	0	0
			1204	759	222	221	2		

- Molecule 37 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	g	96	Total	C	N	O	S	0	0
			786	496	135	152	3		

- Molecule 38 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	h	153	Total	C	N	O	S	0	0
			1218	759	232	221	6		

- Molecule 39 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	131	Total	C	N	O	S	0	0
			1041	662	184	193	2		

- Molecule 40 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	j	127	Total	C	N	O	S	0	0
			980	610	195	174	1		

- Molecule 41 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	k	96	Total	C	N	O	S	0	0
			773	487	142	142	2		

- Molecule 42 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	l	116	Total	C	N	O	S	0	0
			854	527	163	160	4		

- Molecule 43 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	m	134	Total	C	N	O	S	0	0
			1051	652	211	186	2		

- Molecule 44 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	n	114	Total	C	N	O	S	0	0
			902	552	183	166	1		

- Molecule 45 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	o	60	Total	C	N	O	S	0	0
			492	310	100	77	5		

- Molecule 46 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	p	85	Total	C	N	O	S	0	0
			716	440	146	129	1		

- Molecule 47 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	q	87	Total	C	N	O	S	0	0
			692	437	128	125	2		

- Molecule 48 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	r	80	Total	C	N	O	S	0	0
			660	414	124	119	3		

- Molecule 49 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	s	63	Total	C	N	O	S	0	0
			511	328	95	87	1		

- Molecule 50 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	t	82	Total	C	N	O	S	0	0
			663	426	122	113	2		

- Molecule 51 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	u	81	Total	C	N	O	S	0	0
			608	371	118	117	2		

- Molecule 52 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
52	4	1	Total	Zn	0
			1	1	
52	5	1	Total	Zn	0
			1	1	
52	8	1	Total	Zn	0
			1	1	
52	o	1	Total	Zn	0
			1	1	

- Molecule 53 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
53	7	2	Total	K	0
			2	2	
53	A	103	Total	K	0
			103	103	
53	B	3	Total	K	0
			3	3	
53	G	3	Total	K	0
			3	3	
53	P	1	Total	K	0
			1	1	
53	a	38	Total	K	0
			38	38	

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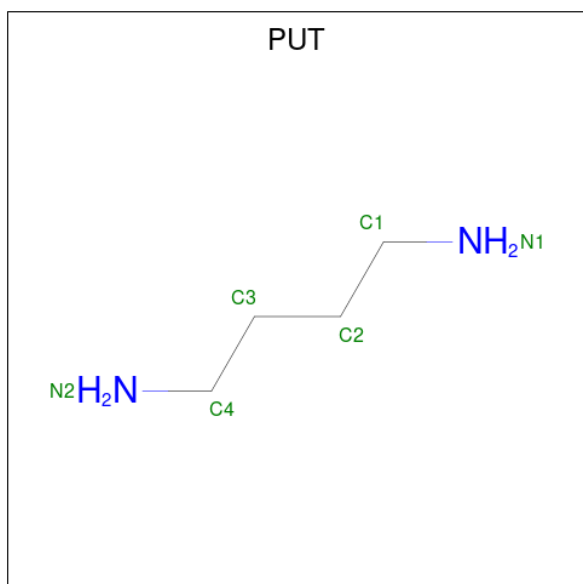
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Mol	Chain	Residues	Atoms		AltConf
53	g	1	Total	K	0
			1	1	
53	o	1	Total	K	0
			1	1	

- Molecule 54 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

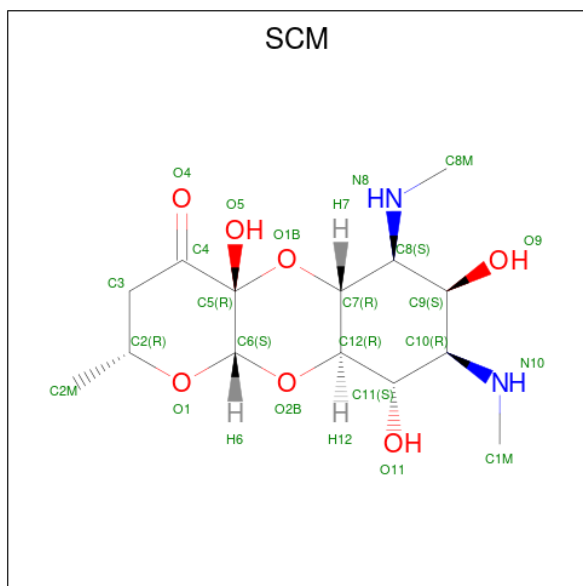
Mol	Chain	Residues	Atoms		AltConf
54	A	138	Total	Mg	0
			138	138	
54	B	1	Total	Mg	0
			1	1	
54	G	1	Total	Mg	0
			1	1	
54	Q	1	Total	Mg	0
			1	1	
54	a	44	Total	Mg	0
			44	44	
54	n	1	Total	Mg	0
			1	1	

- Molecule 55 is 1,4-DIAMINOBUTANE (CCD ID: PUT) (formula: C₄H₁₂N₂).



Mol	Chain	Residues	Atoms			AltConf
55	a	1	Total	C	N	0
			6	4	2	

- Molecule 56 is SPECTINOMYCIN (CCD ID: SCM) (formula: $C_{14}H_{24}N_2O_7$).

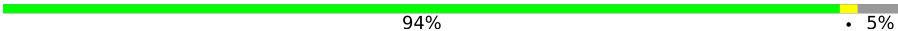


Mol	Chain	Residues	Atoms				AltConf
56	a	1	Total	C	N	O	0
			23	14	2	7	

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: 50S ribosomal protein L29

Chain 1:  94% • 5%



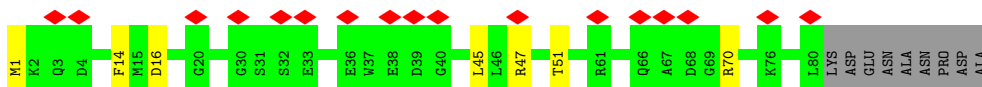
- Molecule 2: 50S ribosomal protein L30

Chain 2:  85% 12% •



- Molecule 3: 50S ribosomal protein L31 type B

Chain 3:  19% 82% 8% 10%



- Molecule 4: 50S ribosomal protein L32

Chain 4:  78% 12% 10%



- Molecule 5: 50S ribosomal protein L33

Chain 5:  84% 14% •



- Molecule 6: 50S ribosomal protein L34

Chain 6:  82% 18%



- Molecule 7: 50S ribosomal protein L35

Chain 7:  80% 17% .



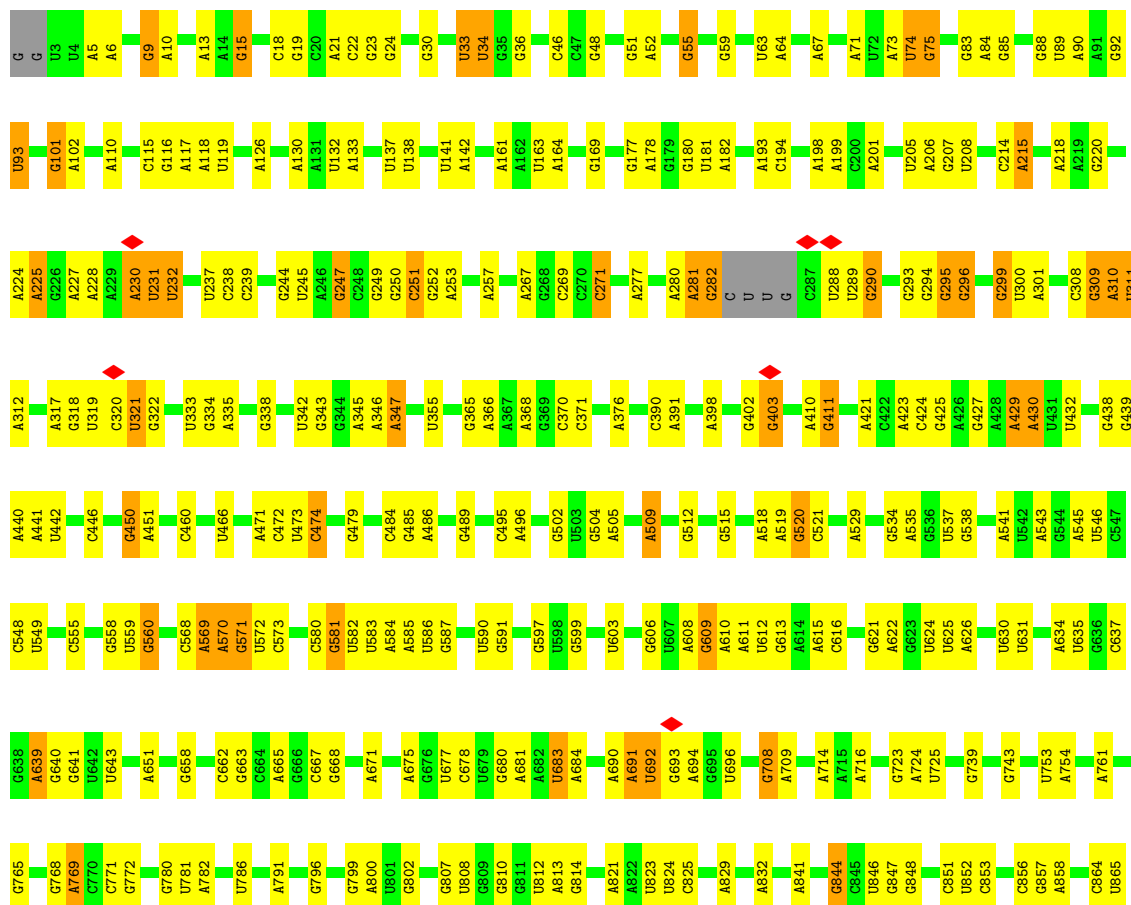
- Molecule 8: 50S ribosomal protein L36

Chain 8:  87% 13%

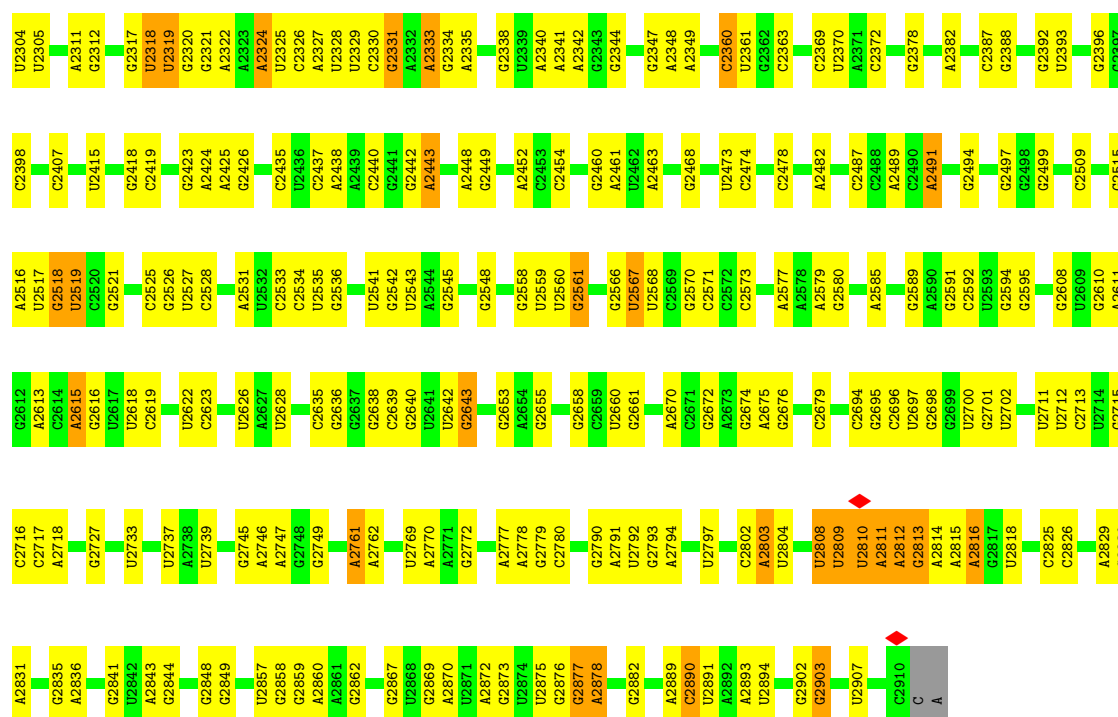


- Molecule 9: 23S rRNA

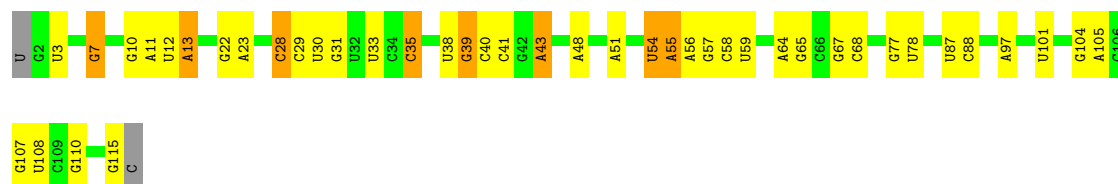
Chain A:  61% 31% 6% .







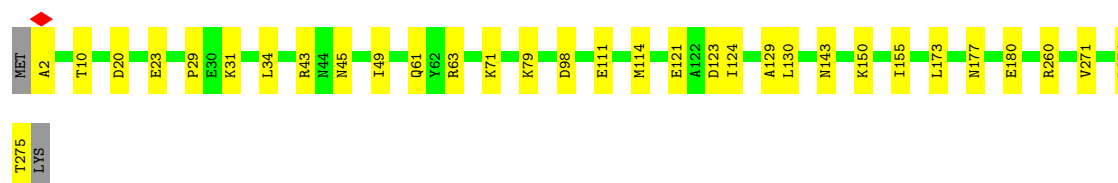
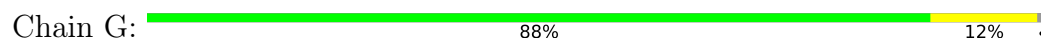
• Molecule 10: 5S rRNA



• Molecule 11: tRNA-fMet

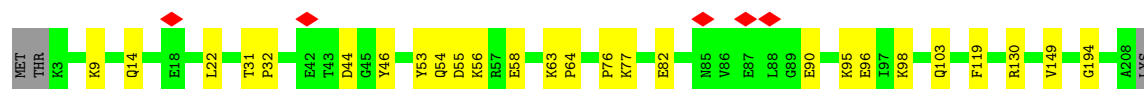


• Molecule 12: 50S ribosomal protein L2



• Molecule 13: 50S ribosomal protein L3

Chain H:  86% 12%



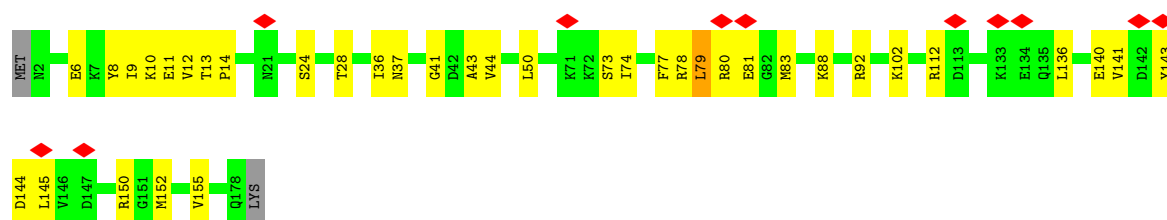
- Molecule 14: 50S ribosomal protein L4

Chain I:  86% 13%



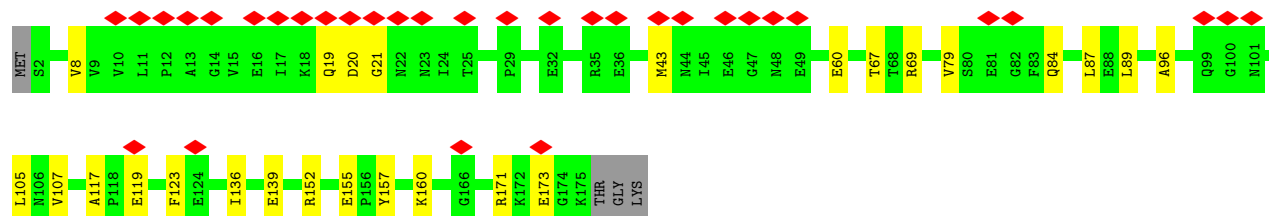
- Molecule 15: 50S ribosomal protein L5

Chain J:  6% 78% 20%



- Molecule 16: 50S ribosomal protein L6

Chain K:  19% 83% 15%



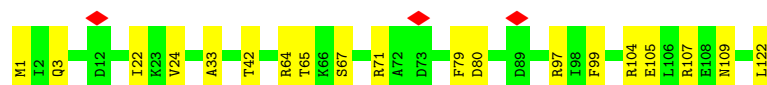
- Molecule 17: 50S ribosomal protein L13

Chain M:  88% 12%



- Molecule 18: 50S ribosomal protein L14

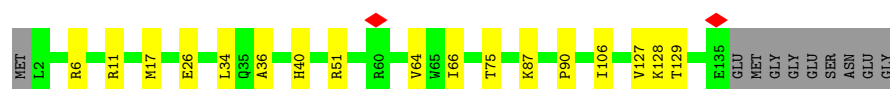
Chain N:  84% 16%



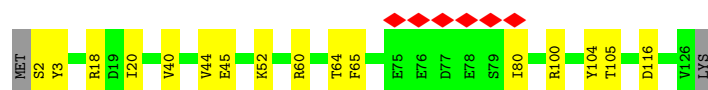
• Molecule 19: 50S ribosomal protein L15

Chain O:  91% 9%

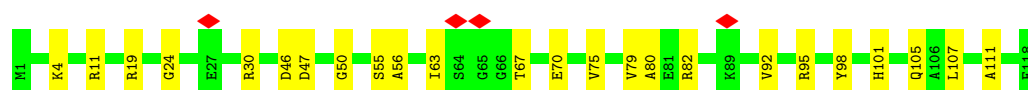
• Molecule 20: 50S ribosomal protein L16

Chain P:  81% 12% 7%

• Molecule 21: 50S ribosomal protein L17

Chain Q:  5% 86% 13%

• Molecule 22: 50S ribosomal protein L18

Chain R:  80% 20%

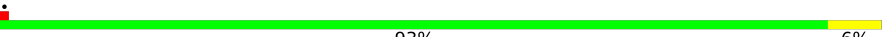
• Molecule 23: 50S ribosomal protein L19

Chain S:  91% 8%

• Molecule 24: 50S ribosomal protein L20

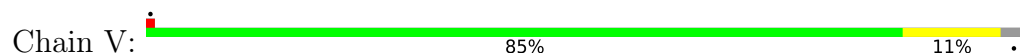
Chain T:  82% 18%

• Molecule 25: 50S ribosomal protein L21

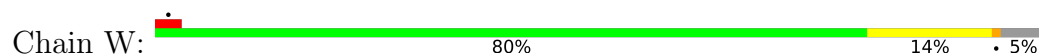
Chain U:  93% 6%



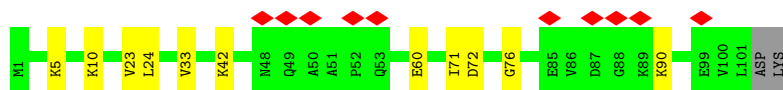
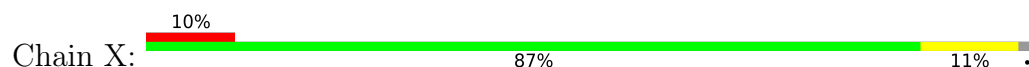
- Molecule 26: 50S ribosomal protein L22



- Molecule 27: 50S ribosomal protein L23



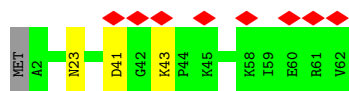
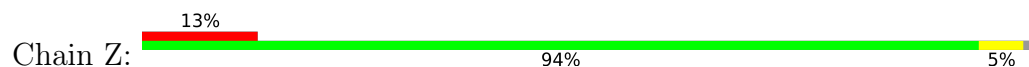
- Molecule 28: 50S ribosomal protein L24



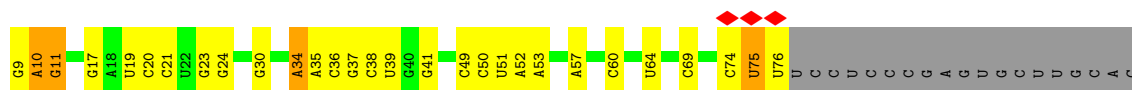
- Molecule 29: 50S ribosomal protein L27



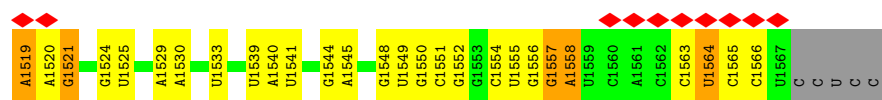
- Molecule 30: 50S ribosomal protein L28



- Molecule 31: 16S rRNA



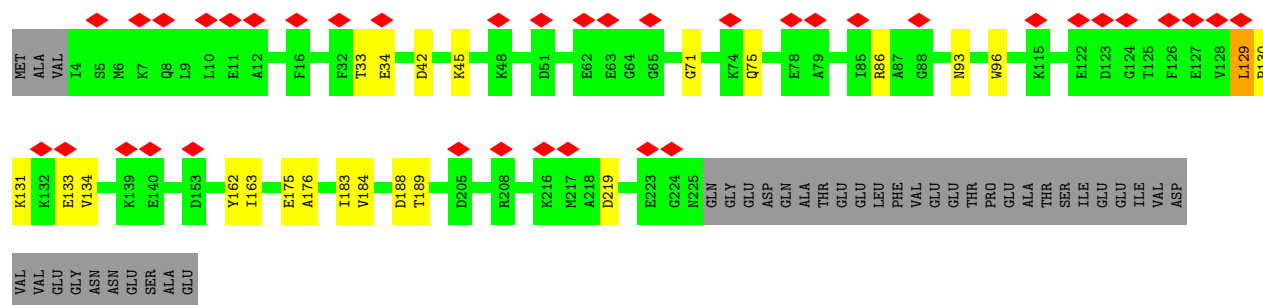
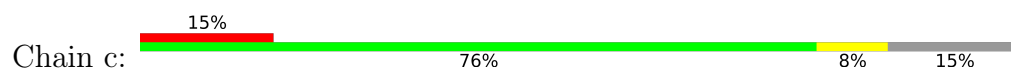
C1393	G1302	A1205	A1107	U1036	U948	C837	A713	A585	A493	A399	G302	A196	U
G1396	A1306	G1207	U1113	A1039	G949	G838	G714	U590	A495	A400	C303	U197	C
G1397	U1307	G1208	U1113	G1040	A950	A841	C715	U591	U495	U401	C304	A198	A
U1398	A1313	U1209	G1121	A1043	G952	A842	U727	G592	A498	G402	A308	C200	U
A1401	A1314	G1210	U1122	U1044	G953	C943	A728	A598	C499	C405	A314	A201	U
U1402	C1317	G1216	G1126	A1045	G954	G844	G729	A599	G500	G406	G315	G202	G
G1413	U1318	A1128	A1127	A1047	C961	U846	A730	A600	U501	A409	G315	U203	U
A1420	C1322	A1222	A1129	G1048	C963	A848	G736	C602	C502	G414	U322	U204	A
			C1130	C1049	A964	G849	G739	G603	G510	G414	G323	A213	A
			U1050	U1050	A965		G740	A604	G511	C417	G323	U214	U
			U1051	U1051	G966	A855	A741	G695	G511	G418	A326	G215	U
			U1052	U1052	G967	G956	A742	G606	A517	G418	A332	G222	C
			C1053	C1053	G968	U857	G424	A518	A518	A332	G222	G222	G
			U1145	U1145		G858	U749	G607	A523	A423	G335	G224	U
			U1146	U1146	G971	G862	G750	G627	A523	G425	G336	A132	A
			G1147	U1056	G972		A754	G630	A524	G426	C337	A227	A
			U1148	U1056	A973	G865		G630	A524	C427	C338	A228	A
			U1149	U1056	G974	G866	G757	A633	C527	G428	A339	A229	A
			A1150	U1057	U987	G866	G757	A633	C527	G428	A339	A229	A
			G1151	C1058		U867	C758	G636	A529	G430	C348	U235	G
			U1152	G1059	G993	U869	U762	G636	C533	U431	C348	U235	G
			C1154	G1060	C994	C870	G763	C638	U534	A438	A353	G	A
			C1155	G1061	A995	C871	U764	C639	A535	A439	C354	C	A
			C1156	G1062	A996	G872	U766	G644	C537	A440	A355	G240	A
			C1159	A1065	G997	C873	G767	G644	A441	G442	C356	G241	U
			A1160	U1066	G998	C874	G768	A647	C540	G442	G357	U242	U
			U1161	A1066	A1001	C874		A647	C540	G442	G357	U242	U
			U1162	U1067	A1002	G882	A775	G652	U542	U446	C358	G161	G
			U1163	G1068	A1003	G882	U783	A688	C542	U447	C359	G246	G
			A1164	U1069	A1004	G888	G784	U659	G543	U447	C360	C247	G
					A1005	A899	G784	A661	C544	C448	C361	G164	G
					C1006	A900	G786	A661	C545	G449	A362	G165	G
					C1007	G900	G786	A661	A546	G450	G363	G267	U
					U1008	G901	G787	G664	G547	A451	A364	U167	U
					U1009	G902	G787	G664	G547	U451	C365	U271	U
					A1010	C902		U664	G550	U455	A272	U271	U
					A1011	A903	G791	A668	C551	U455	A272	G273	A
					C1012	C904	A792	G675	G552	A458	C371	G272	U
					A1013	U905	A793	G675	G553	A459	G372	U173	U
					G1014	G905	A794	G675	G553	A459	G373	G277	U
						G908	G795	U679	G556	U465	G373	U278	U
					C909	C909		U679	U557	U465	C378	U278	U
					U1019	A803	A803	G690	U557	U465	C378	U278	U
					G1020	G804	A691	G690	A561	A470	A379	G281	A
					A1021	C805	A691	A691	A561	G471	G380	G281	A
					C1022	A806	G692	G692	A561	G471	G380	G281	A
					A1023	G925	G693	G693	A561	G471	G380	G281	A
						G925	G693	G693	A561	G471	G380	G281	A
					U1027	A928	U815	G699	C571	A477	G386	A288	A
					U1028	A928	A816	G700	A572	A478	G387	A288	A
					U1029	G933	G817	A701	A573	C479	C387	C290	G
					C1030	U938	A818	A702	U580	U391	U391	G291	G
					A1031	C939	U819	U703	C581	C485	C392	G292	A
					U1032	C939	A820	U703	C581	C485	C392	G292	A
					C1033	A940	C821	U710	C582	U487	U393	C297	U
					A1034	A941	C822	U711	C582	U487	C397	C297	U
					C1035	U947	C822	U711	C582	U487	C397	C297	U
						U947	C822	U711	C582	U487	C397	C297	U
												G301	U



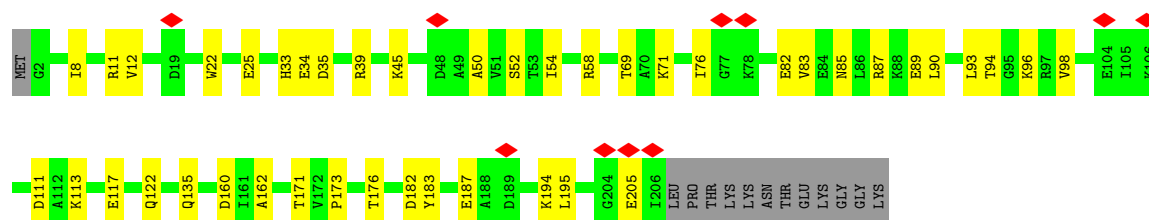
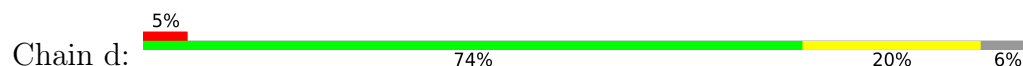
- Molecule 32: mRNA



- Molecule 33: 30S ribosomal protein S2



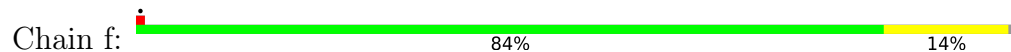
- Molecule 34: 30S ribosomal protein S3



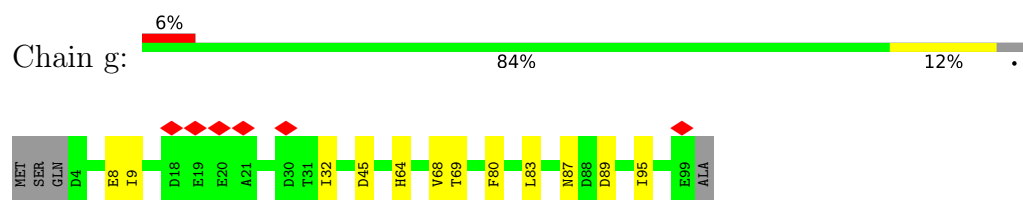
- Molecule 35: 30S ribosomal protein S4



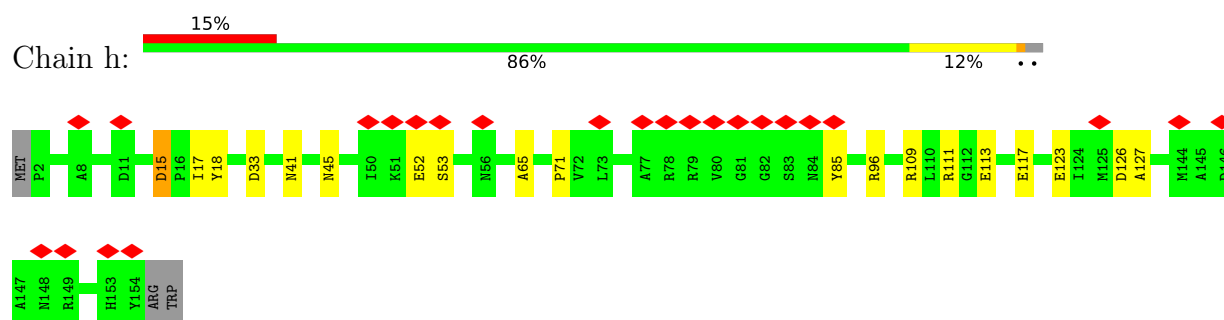
- Molecule 36: 30S ribosomal protein S5



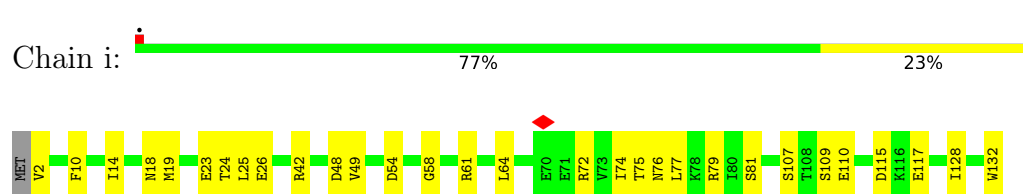
- Molecule 37: 30S ribosomal protein S6



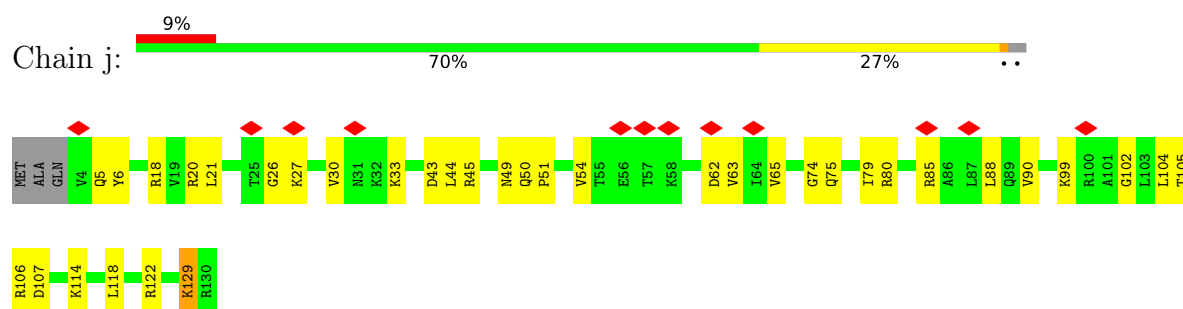
- Molecule 38: 30S ribosomal protein S7



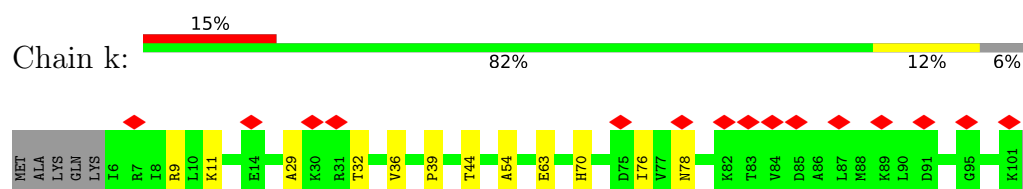
- Molecule 39: 30S ribosomal protein S8



- Molecule 40: 30S ribosomal protein S9

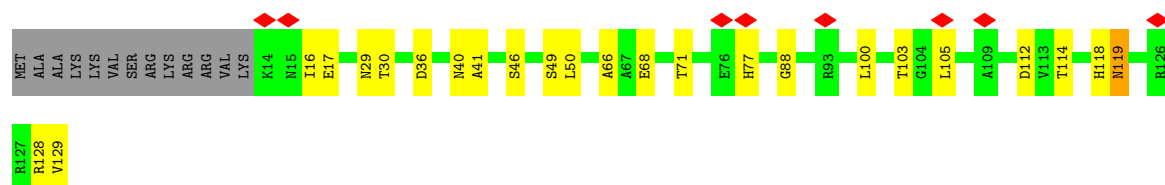


- Molecule 41: 30S ribosomal protein S10

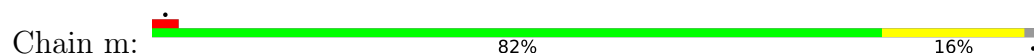


- Molecule 42: 30S ribosomal protein S11

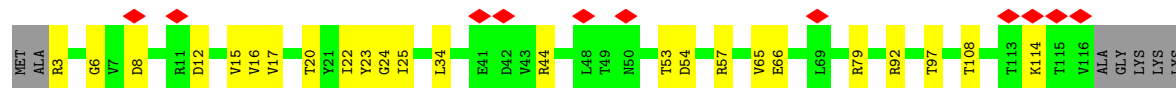
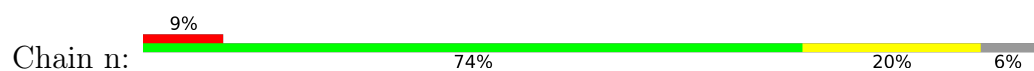




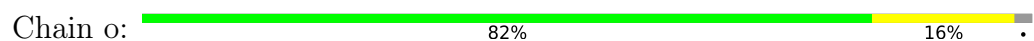
- Molecule 43: 30S ribosomal protein S12



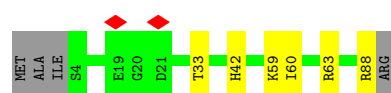
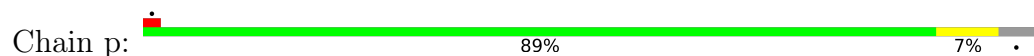
- Molecule 44: 30S ribosomal protein S13



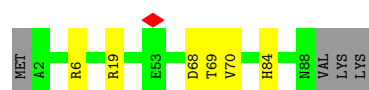
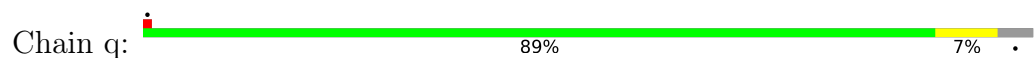
- Molecule 45: 30S ribosomal protein S14 type Z



- Molecule 46: 30S ribosomal protein S15



- Molecule 47: 30S ribosomal protein S16

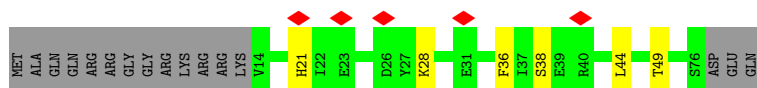


- Molecule 48: 30S ribosomal protein S17

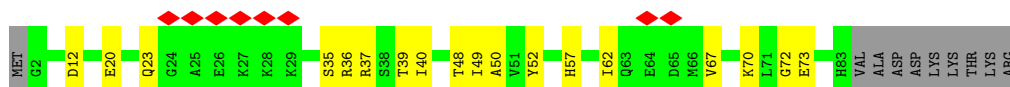




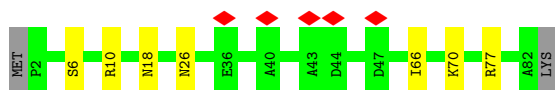
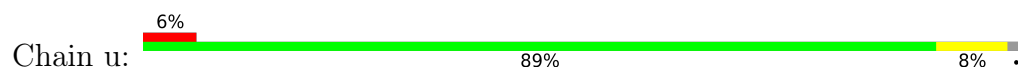
- Molecule 49: 30S ribosomal protein S18



- Molecule 50: 30S ribosomal protein S19



- Molecule 51: 30S ribosomal protein S20



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	18512	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 ($e^-/\text{\AA}^2$)	30.255	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	165000	Depositor
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.052	Depositor
Minimum map value	-0.010	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.015	Depositor
Map size (Å)	344.4, 344.4, 344.4	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82, 0.82, 0.82	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, SCM, K, MG, PUT

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	1	0.15	0/492	0.24	0/654
2	2	0.17	0/430	0.29	0/579
3	3	0.18	0/664	0.34	0/896
4	4	0.18	0/413	0.30	0/549
5	5	0.20	0/414	0.29	0/552
6	6	0.20	0/377	0.27	0/491
7	7	0.19	0/528	0.29	0/689
8	8	0.20	0/310	0.32	0/409
9	A	0.21	0/67888	0.28	0/105890
10	B	0.17	0/2728	0.24	0/4252
11	D	0.16	0/1837	0.28	0/2862
12	G	0.20	0/2141	0.31	0/2881
13	H	0.19	0/1594	0.31	0/2140
14	I	0.19	0/1595	0.28	0/2157
15	J	0.18	0/1411	0.37	0/1897
16	K	0.15	0/1355	0.30	0/1825
17	M	0.20	0/1167	0.28	0/1576
18	N	0.20	0/930	0.30	0/1247
19	O	0.19	0/1106	0.27	0/1474
20	P	0.20	0/1093	0.28	0/1457
21	Q	0.19	0/1006	0.33	0/1349
22	R	0.19	0/917	0.34	0/1226
23	S	0.18	0/939	0.31	0/1262
24	T	0.20	0/963	0.28	0/1280
25	U	0.24	0/791	0.30	0/1061
26	V	0.20	0/850	0.32	0/1145
27	W	0.19	0/743	0.30	0/993
28	X	0.18	0/772	0.32	0/1035
29	Y	0.20	0/565	0.30	0/755
30	Z	0.16	0/486	0.28	0/648
31	a	0.19	0/36487	0.27	1/56905 (0.0%)
32	b	0.12	0/319	0.33	0/494

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	c	0.32	0/1803	0.48	0/2430
34	d	0.18	0/1643	0.31	0/2208
35	e	0.17	0/1641	0.32	0/2206
36	f	0.18	0/1217	0.30	0/1641
37	g	0.18	0/798	0.31	0/1075
38	h	0.15	0/1238	0.30	0/1668
39	i	0.18	0/1054	0.33	0/1417
40	j	0.16	0/993	0.30	0/1331
41	k	0.18	0/785	0.29	0/1059
42	l	0.16	0/869	0.29	0/1174
43	m	0.18	0/1068	0.35	0/1435
44	n	0.15	0/908	0.31	0/1219
45	o	0.17	0/504	0.26	0/669
46	p	0.17	0/726	0.27	0/969
47	q	0.17	0/704	0.34	0/945
48	r	0.17	0/668	0.30	0/891
49	s	0.16	0/518	0.29	0/694
50	t	0.16	0/680	0.28	0/911
51	u	0.17	0/611	0.33	0/818
All	All	0.20	0/151739	0.29	1/227390 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
31	a	1390	C	N1-C1'-C2'	5.16	119.74	112.00

There are no chirality outliers.

There are no planarity outliers.

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	1	491	0	527	0	0
2	2	428	0	463	4	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	3	647	0	616	5	0
4	4	406	0	417	7	0
5	5	410	0	422	5	0
6	6	374	0	424	16	0
7	7	522	0	575	9	0
8	8	305	0	337	5	0
9	A	60606	0	30437	620	0
10	B	2439	0	1228	21	0
11	D	1644	0	835	29	0
12	G	2106	0	2189	21	0
13	H	1572	0	1654	18	0
14	I	1572	0	1614	17	0
15	J	1392	0	1454	43	0
16	K	1335	0	1369	18	0
17	M	1146	0	1191	14	0
18	N	923	0	985	16	0
19	O	1096	0	1149	10	0
20	P	1070	0	1136	13	0
21	Q	997	0	1033	13	0
22	R	908	0	944	16	0
23	S	925	0	979	8	0
24	T	950	0	1009	16	0
25	U	779	0	821	4	0
26	V	841	0	898	11	0
27	W	736	0	795	10	0
28	X	763	0	823	8	0
29	Y	559	0	568	9	0
30	Z	480	0	522	2	0
31	a	32595	0	16412	378	0
32	b	285	0	143	3	0
33	c	1773	0	1810	16	0
34	d	1618	0	1664	29	0
35	e	1611	0	1628	20	0
36	f	1204	0	1280	21	0
37	g	786	0	781	10	0
38	h	1218	0	1246	12	0
39	i	1041	0	1092	21	0
40	j	980	0	1027	24	0
41	k	773	0	814	16	0
42	l	854	0	869	19	0
43	m	1051	0	1115	18	0
44	n	902	0	956	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
45	o	492	0	508	9	0
46	p	716	0	727	5	0
47	q	692	0	724	7	0
48	r	660	0	699	15	0
49	s	511	0	549	6	0
50	t	663	0	675	12	0
51	u	608	0	635	7	0
52	4	1	0	0	0	0
52	5	1	0	0	0	0
52	8	1	0	0	0	0
52	o	1	0	0	0	0
53	7	2	0	0	0	0
53	A	103	0	0	0	0
53	B	3	0	0	0	0
53	G	3	0	0	0	0
53	P	1	0	0	0	0
53	a	38	0	0	0	0
53	g	1	0	0	0	0
53	o	1	0	0	0	0
54	A	138	0	0	0	0
54	B	1	0	0	0	0
54	G	1	0	0	0	0
54	Q	1	0	0	0	0
54	a	44	0	0	0	0
54	n	1	0	0	0	0
55	a	6	0	12	0	0
56	a	23	0	24	2	0
All	All	139826	0	92804	1441	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 6.

The worst 5 of 1441 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)
6:6:1:MET:HE2	6:6:3:ARG:NH2	1.46	1.28
6:6:1:MET:CE	6:6:3:ARG:NH2	2.10	1.13
41:k:36:VAL:HG12	41:k:76:ILE:CD1	1.85	1.07
36:f:86:ILE:HG12	36:f:95:LEU:HD13	1.36	1.06
9:A:295:G:O2'	9:A:296:G:O5'	1.72	1.05

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	1	57/62 (92%)	56 (98%)	1 (2%)	0	100	100
2	2	55/59 (93%)	54 (98%)	1 (2%)	0	100	100
3	3	78/89 (88%)	73 (94%)	5 (6%)	0	100	100
4	4	51/59 (86%)	49 (96%)	2 (4%)	0	100	100
5	5	46/49 (94%)	45 (98%)	1 (2%)	0	100	100
6	6	42/44 (96%)	42 (100%)	0	0	100	100
7	7	62/66 (94%)	62 (100%)	0	0	100	100
8	8	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
12	G	272/276 (99%)	265 (97%)	6 (2%)	1 (0%)	30	61
13	H	204/209 (98%)	195 (96%)	9 (4%)	0	100	100
14	I	203/207 (98%)	201 (99%)	2 (1%)	0	100	100
15	J	175/179 (98%)	167 (95%)	8 (5%)	0	100	100
16	K	172/178 (97%)	165 (96%)	7 (4%)	0	100	100
17	M	145/147 (99%)	144 (99%)	1 (1%)	0	100	100
18	N	120/122 (98%)	116 (97%)	4 (3%)	0	100	100
19	O	144/146 (99%)	140 (97%)	3 (2%)	1 (1%)	18	49
20	P	132/144 (92%)	131 (99%)	1 (1%)	0	100	100
21	Q	123/127 (97%)	120 (98%)	3 (2%)	0	100	100
22	R	116/118 (98%)	113 (97%)	3 (3%)	0	100	100
23	S	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
24	T	116/119 (98%)	114 (98%)	2 (2%)	0	100	100
25	U	99/102 (97%)	97 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	V	109/115 (95%)	107 (98%)	2 (2%)	0	100	100
27	W	89/96 (93%)	88 (99%)	1 (1%)	0	100	100
28	X	99/103 (96%)	96 (97%)	3 (3%)	0	100	100
29	Y	72/95 (76%)	68 (94%)	4 (6%)	0	100	100
30	Z	59/62 (95%)	59 (100%)	0	0	100	100
33	c	220/261 (84%)	209 (95%)	10 (4%)	1 (0%)	24	57
34	d	203/218 (93%)	197 (97%)	6 (3%)	0	100	100
35	e	198/203 (98%)	193 (98%)	5 (2%)	0	100	100
36	f	161/166 (97%)	159 (99%)	2 (1%)	0	100	100
37	g	94/100 (94%)	92 (98%)	2 (2%)	0	100	100
38	h	151/156 (97%)	148 (98%)	3 (2%)	0	100	100
39	i	129/132 (98%)	126 (98%)	3 (2%)	0	100	100
40	j	125/130 (96%)	119 (95%)	6 (5%)	0	100	100
41	k	94/102 (92%)	93 (99%)	1 (1%)	0	100	100
42	l	114/129 (88%)	110 (96%)	3 (3%)	1 (1%)	14	44
43	m	132/137 (96%)	125 (95%)	7 (5%)	0	100	100
44	n	112/121 (93%)	110 (98%)	2 (2%)	0	100	100
45	o	58/61 (95%)	58 (100%)	0	0	100	100
46	p	83/89 (93%)	82 (99%)	1 (1%)	0	100	100
47	q	85/91 (93%)	83 (98%)	2 (2%)	0	100	100
48	r	78/88 (89%)	75 (96%)	3 (4%)	0	100	100
49	s	61/79 (77%)	59 (97%)	2 (3%)	0	100	100
50	t	80/92 (87%)	80 (100%)	0	0	100	100
51	u	79/83 (95%)	77 (98%)	2 (2%)	0	100	100
All	All	5245/5564 (94%)	5107 (97%)	134 (3%)	4 (0%)	49	78

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
33	c	131	LYS
42	l	119	ASN
19	O	29	LYS
12	G	155	ILE

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	1	54/56 (96%)	53 (98%)	1 (2%)	50	73
2	2	48/50 (96%)	48 (100%)	0	100	100
3	3	72/79 (91%)	71 (99%)	1 (1%)	59	76
4	4	43/48 (90%)	43 (100%)	0	100	100
5	5	48/49 (98%)	48 (100%)	0	100	100
6	6	39/39 (100%)	39 (100%)	0	100	100
7	7	51/53 (96%)	51 (100%)	0	100	100
8	8	35/35 (100%)	35 (100%)	0	100	100
12	G	224/226 (99%)	224 (100%)	0	100	100
13	H	169/172 (98%)	169 (100%)	0	100	100
14	I	172/173 (99%)	171 (99%)	1 (1%)	78	83
15	J	154/156 (99%)	151 (98%)	3 (2%)	50	73
16	K	145/148 (98%)	144 (99%)	1 (1%)	76	82
17	M	124/124 (100%)	124 (100%)	0	100	100
18	N	98/98 (100%)	98 (100%)	0	100	100
19	O	112/112 (100%)	111 (99%)	1 (1%)	70	80
20	P	107/114 (94%)	107 (100%)	0	100	100
21	Q	107/109 (98%)	107 (100%)	0	100	100
22	R	92/92 (100%)	91 (99%)	1 (1%)	65	78
23	S	97/98 (99%)	97 (100%)	0	100	100
24	T	94/95 (99%)	93 (99%)	1 (1%)	65	78
25	U	83/83 (100%)	83 (100%)	0	100	100
26	V	94/98 (96%)	94 (100%)	0	100	100
27	W	82/85 (96%)	81 (99%)	1 (1%)	63	78
28	X	85/87 (98%)	85 (100%)	0	100	100
29	Y	59/75 (79%)	59 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	Z	54/55 (98%)	54 (100%)	0	100	100
33	c	187/220 (85%)	186 (100%)	1 (0%)	81	85
34	d	163/174 (94%)	163 (100%)	0	100	100
35	e	174/177 (98%)	173 (99%)	1 (1%)	78	83
36	f	126/128 (98%)	126 (100%)	0	100	100
37	g	85/88 (97%)	85 (100%)	0	100	100
38	h	130/133 (98%)	128 (98%)	2 (2%)	57	75
39	i	112/113 (99%)	112 (100%)	0	100	100
40	j	100/102 (98%)	98 (98%)	2 (2%)	48	72
41	k	87/92 (95%)	87 (100%)	0	100	100
42	l	90/101 (89%)	89 (99%)	1 (1%)	65	78
43	m	117/119 (98%)	117 (100%)	0	100	100
44	n	98/102 (96%)	97 (99%)	1 (1%)	68	79
45	o	51/52 (98%)	51 (100%)	0	100	100
46	p	76/79 (96%)	76 (100%)	0	100	100
47	q	77/81 (95%)	77 (100%)	0	100	100
48	r	74/81 (91%)	74 (100%)	0	100	100
49	s	54/67 (81%)	54 (100%)	0	100	100
50	t	70/79 (89%)	70 (100%)	0	100	100
51	u	62/64 (97%)	62 (100%)	0	100	100
All	All	4475/4661 (96%)	4456 (100%)	19 (0%)	81	86

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
38	h	85	TYR
42	l	77	HIS
44	n	79	ARG
40	j	129	LYS
22	R	4	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
34	d	122	GLN
35	e	86	ASN
46	p	76	GLN
35	e	59	HIS
35	e	93	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	B	113/116 (97%)	23 (20%)	0
11	D	76/77 (98%)	20 (26%)	0
31	a	1518/1558 (97%)	219 (14%)	0
32	b	11/19 (57%)	2 (18%)	0
9	A	2820/2912 (96%)	405 (14%)	30 (1%)
All	All	4538/4682 (96%)	669 (14%)	30 (0%)

5 of 669 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	A	10	A
9	A	15	G
9	A	34	U
9	A	46	C
9	A	51	G

5 of 30 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
9	A	1451	G
9	A	2808	U
9	A	1583	G
9	A	2877	G
9	A	2216	G

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 344 ligands modelled in this entry, 342 are monoatomic - leaving 2 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
56	SCM	a	1660	-	23,25,25	1.34	3 (13%)	27,39,39	1.57	4 (14%)
55	PUT	a	1610	-	5,5,5	0.11	0	4,4,4	0.15	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
56	SCM	a	1660	-	-	0/4/57/57	0/3/3/3
55	PUT	a	1610	-	-	0/3/3/3	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	a	1660	SCM	C10-N10	-2.35	1.43	1.47
56	a	1660	SCM	C3-C4	-2.17	1.47	1.50
56	a	1660	SCM	C8-N8	-2.10	1.44	1.47

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	a	1660	SCM	C8M-N8-C8	-4.24	108.75	114.23
56	a	1660	SCM	C1M-N10-C10	-4.17	108.84	114.23
56	a	1660	SCM	C2M-C2-C3	-2.75	108.33	113.27
56	a	1660	SCM	O1-C2-C3	2.52	112.14	108.62

There are no chirality outliers.

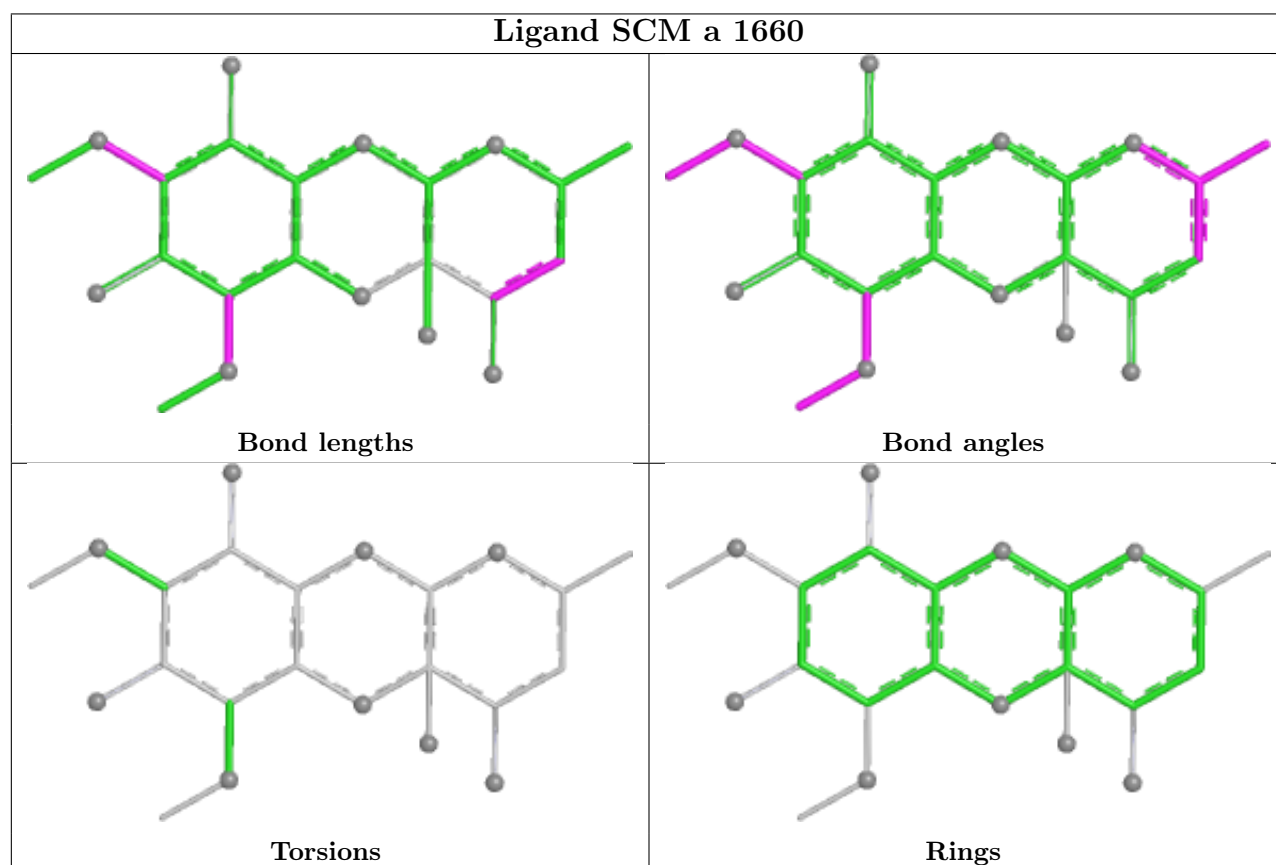
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
56	a	1660	SCM	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

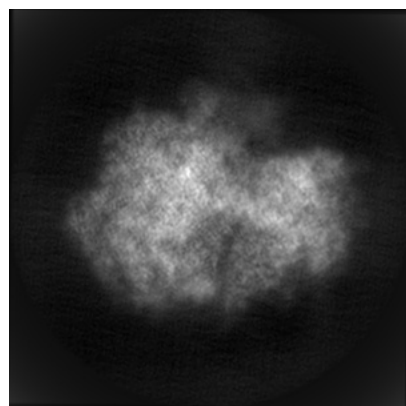
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13245. These allow visual inspection of the internal detail of the map and identification of artifacts.

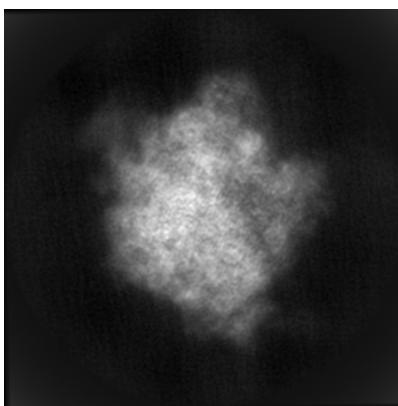
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

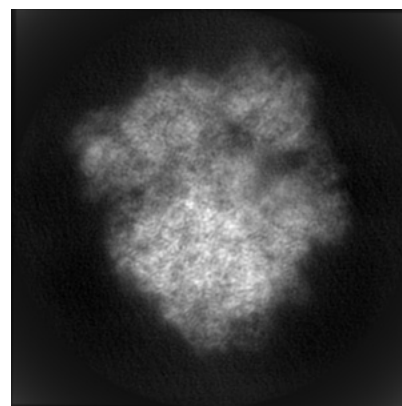
6.1.1 Primary map



X

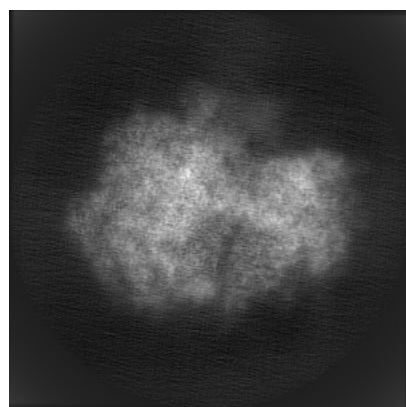


Y

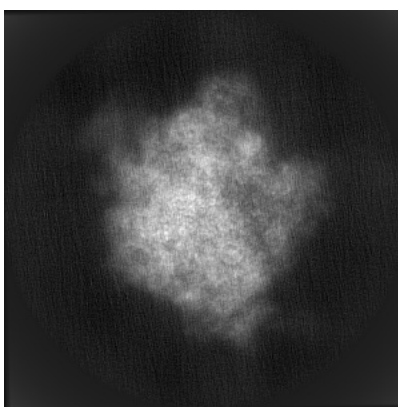


Z

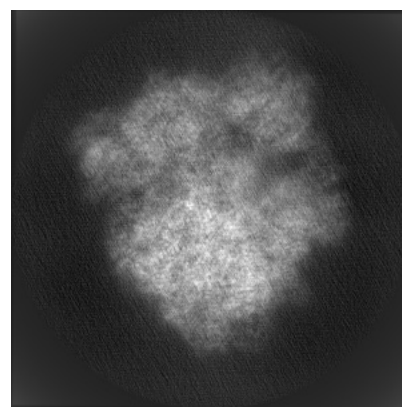
6.1.2 Raw map



X



Y

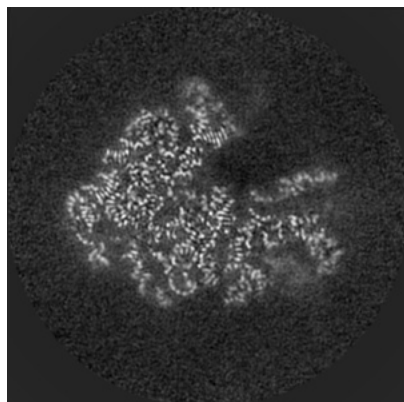


Z

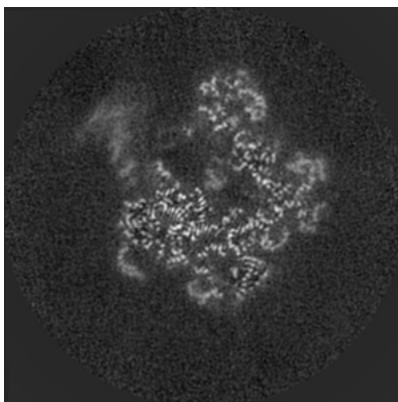
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

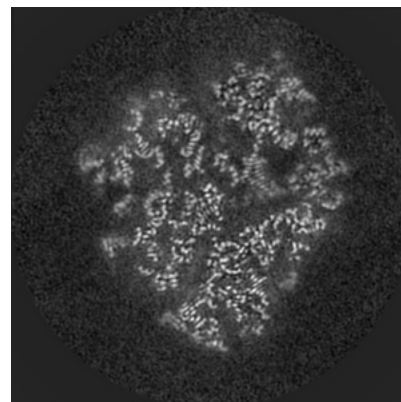
6.2.1 Primary map



X Index: 210

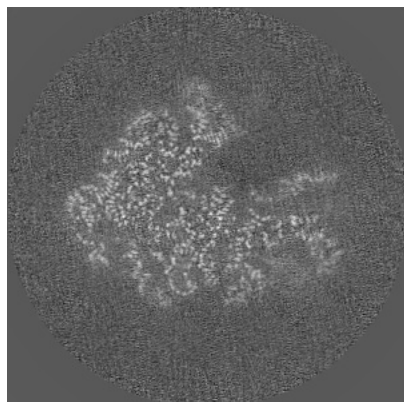


Y Index: 210

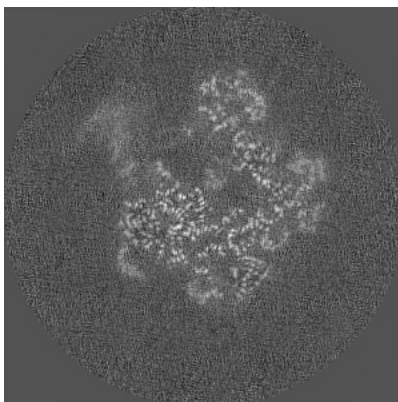


Z Index: 210

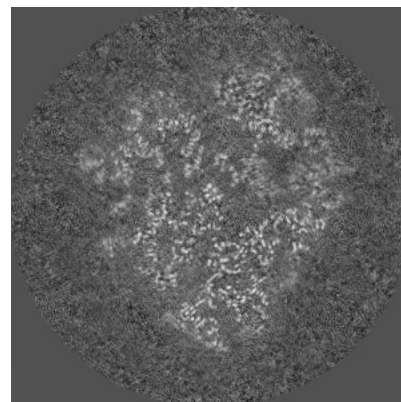
6.2.2 Raw map



X Index: 210



Y Index: 210

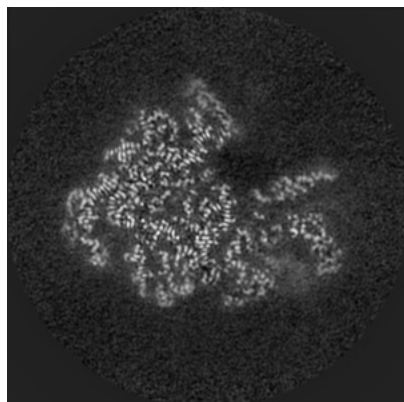


Z Index: 210

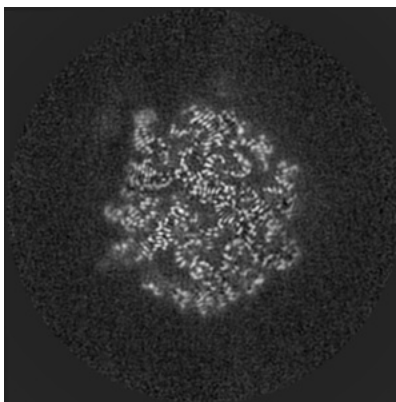
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

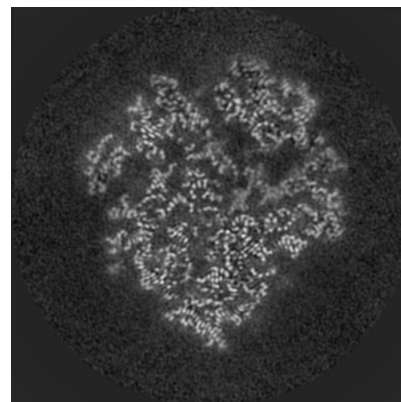
6.3.1 Primary map



X Index: 207

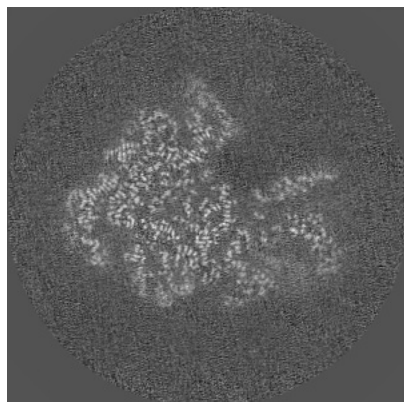


Y Index: 170

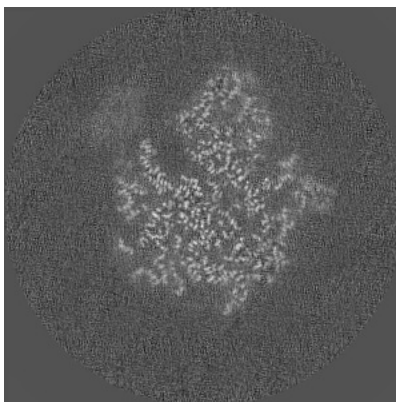


Z Index: 218

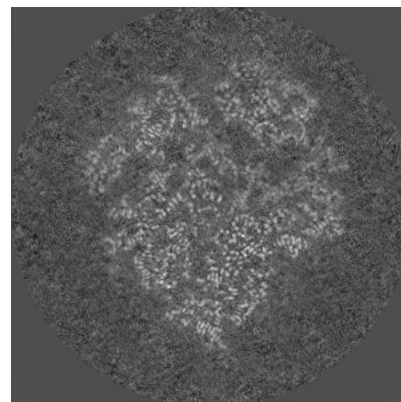
6.3.2 Raw map



X Index: 207



Y Index: 191

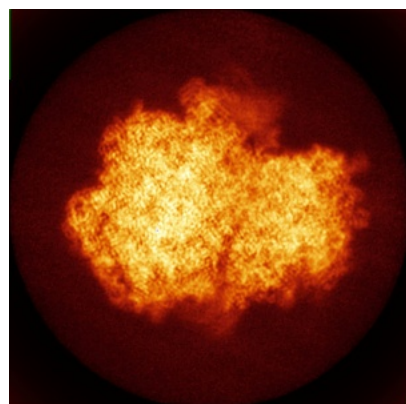


Z Index: 217

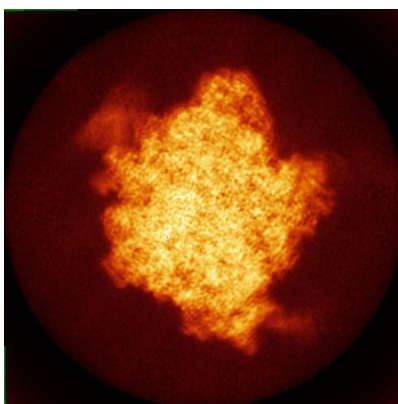
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) ⓘ

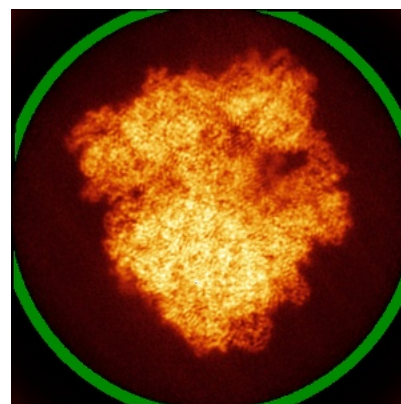
6.4.1 Primary map



X

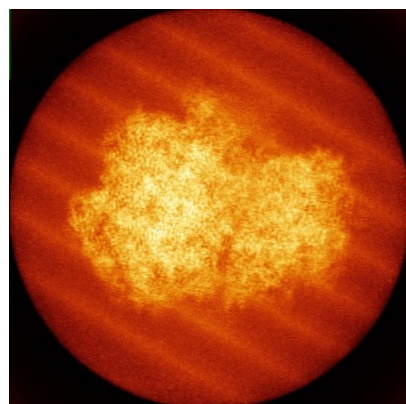


Y

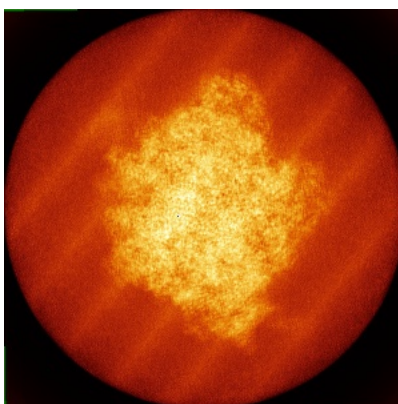


Z

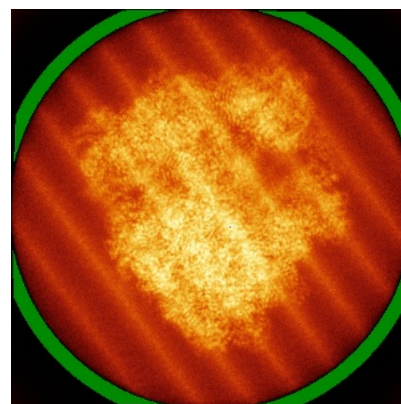
6.4.2 Raw map



X



Y

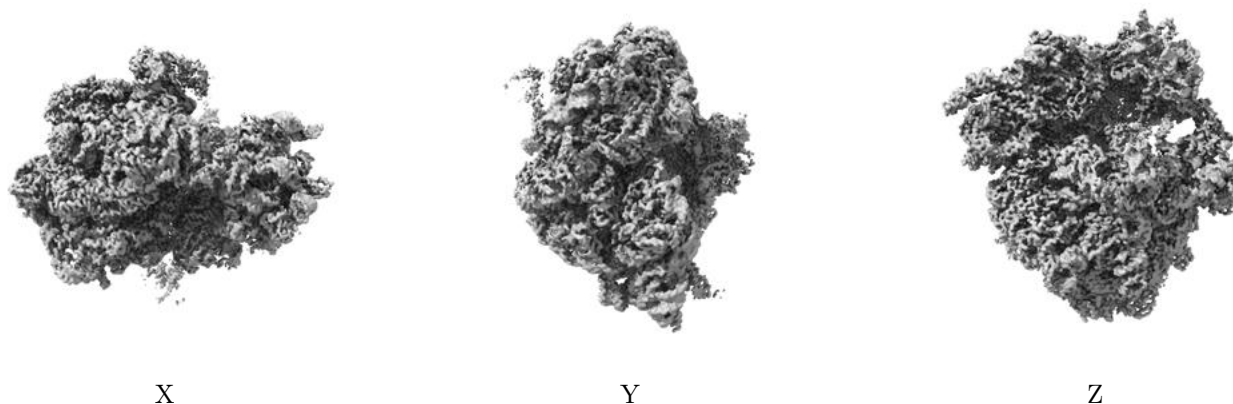


Z

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.

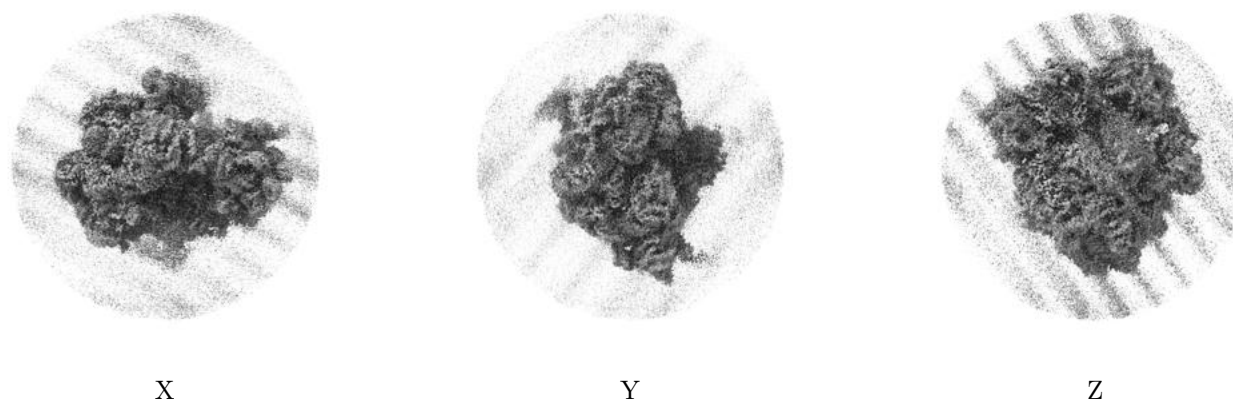
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.015. 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.

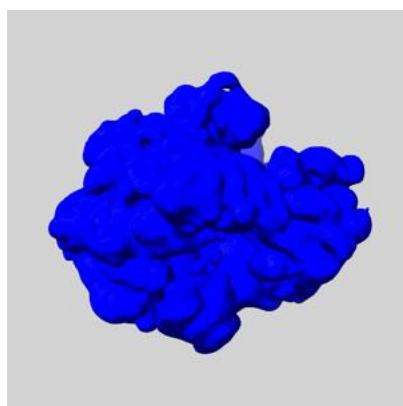
6.6 Mask visualisation [i](#)

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

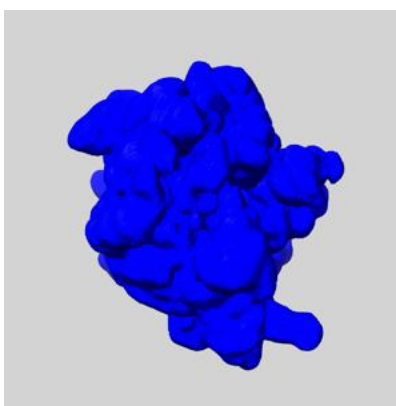
A mask typically either:

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

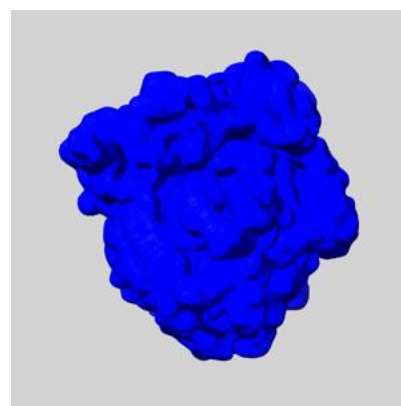
6.6.1 emd_13245_msk_1.map [i](#)



X



Y

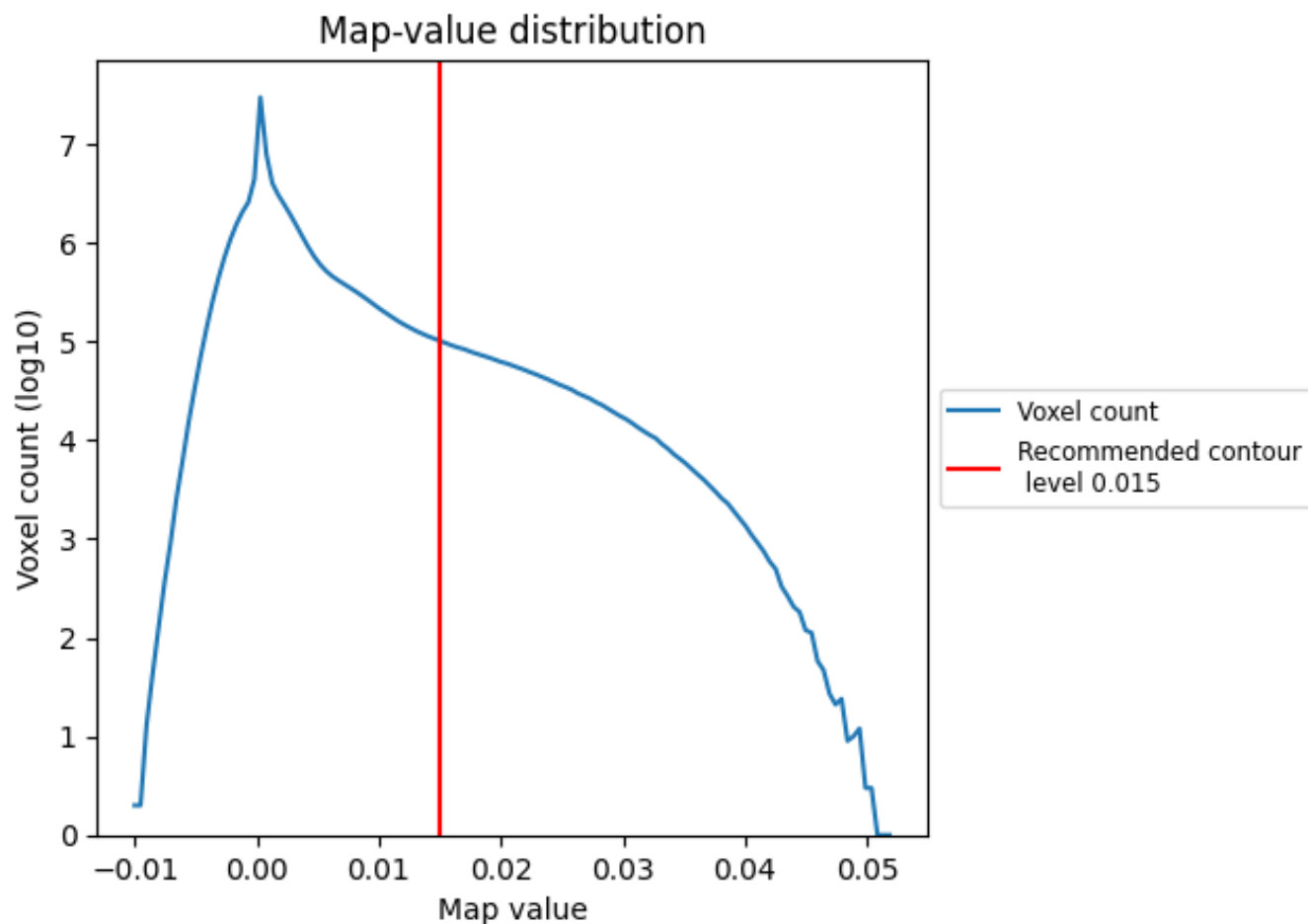


Z

7 Map analysis [i](#)

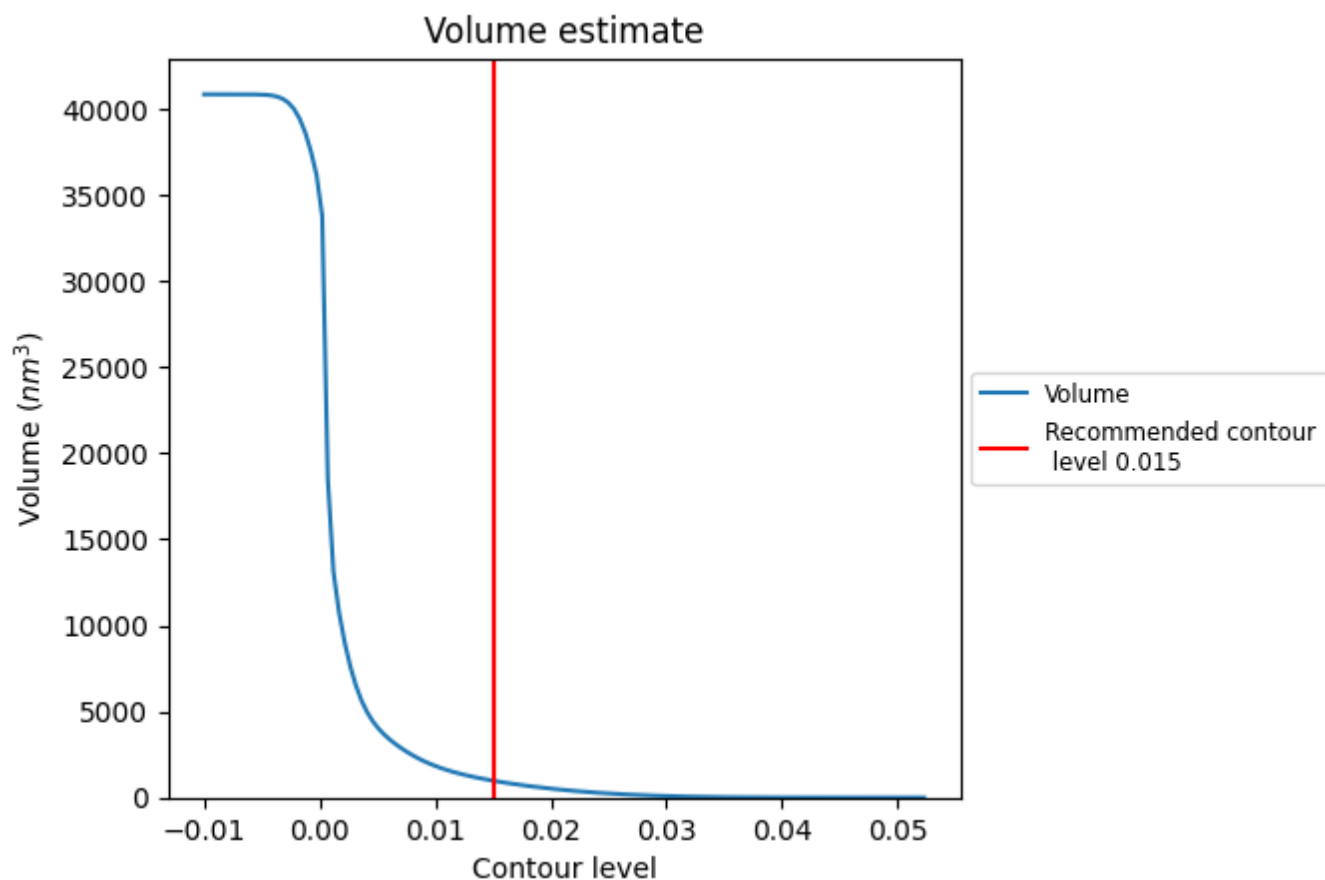
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

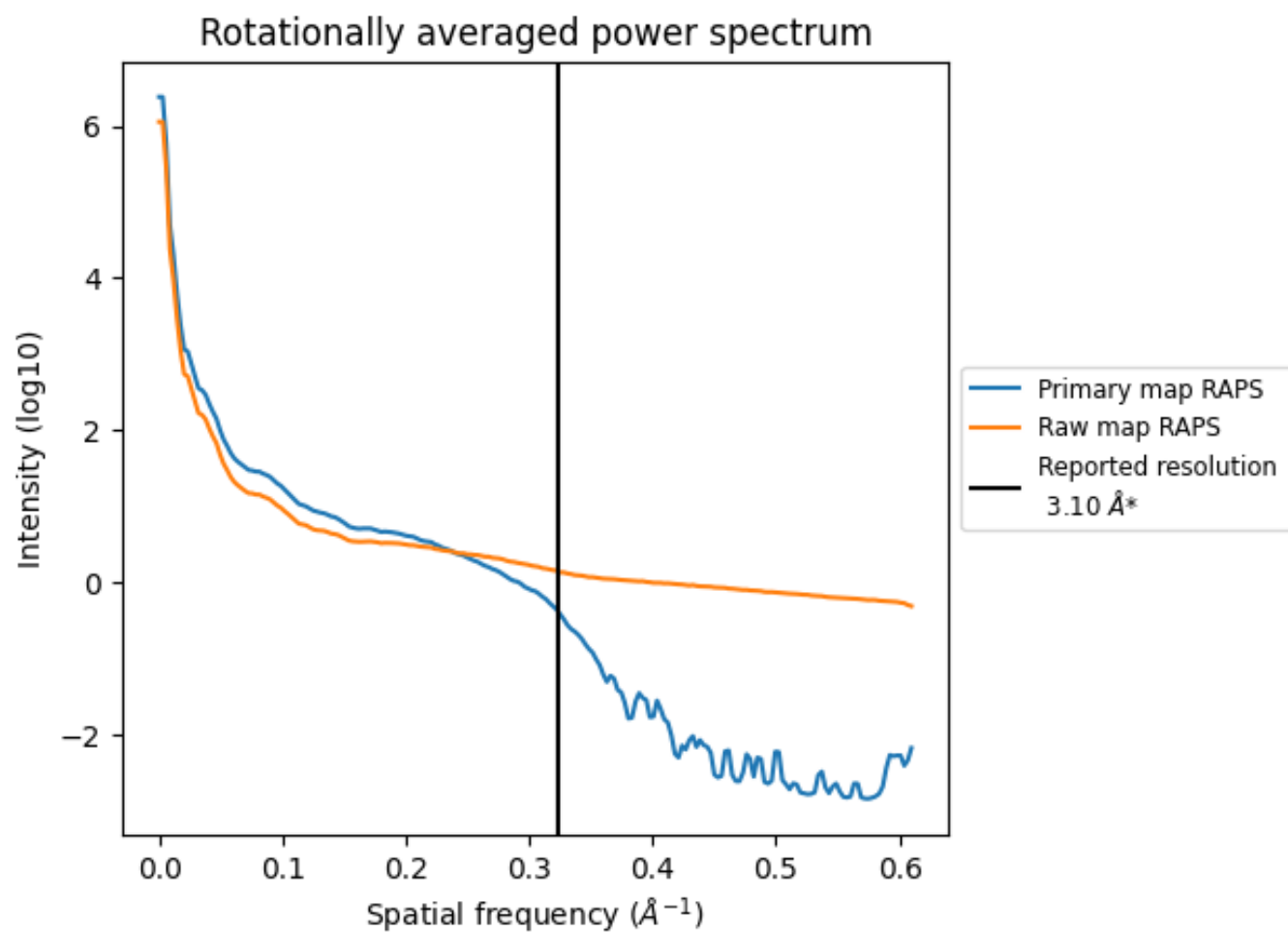
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 980 nm^3 ; this corresponds to an approximate mass of 885 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 ⓘ

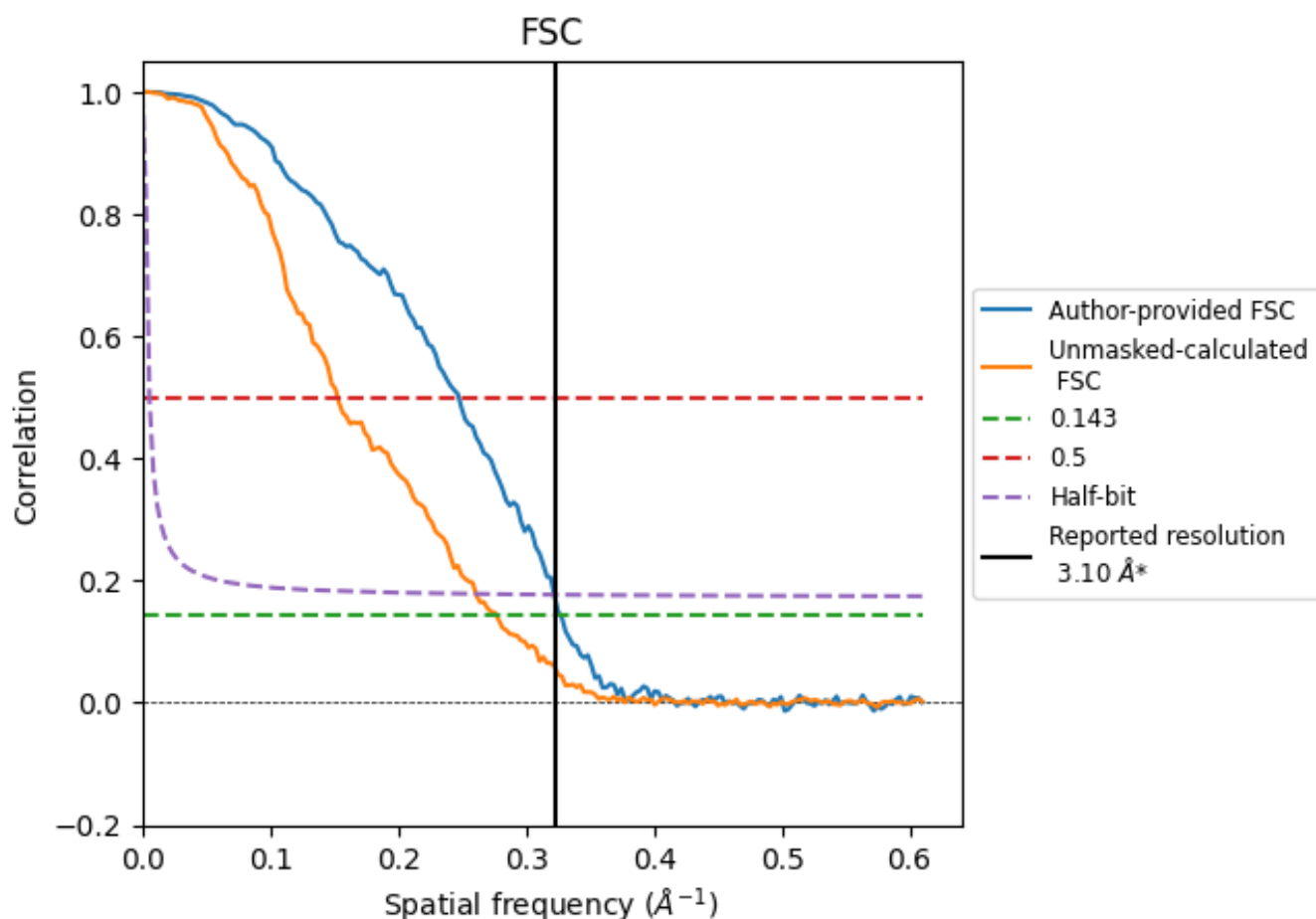


*Reported resolution corresponds to spatial frequency of 0.323 $\text{\AA}^{-1}$

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 0.323 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

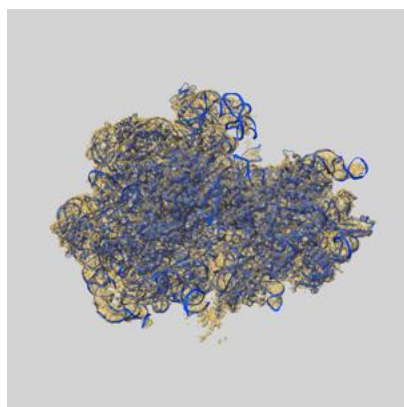
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.06	4.04	3.10
Unmasked-calculated*	3.61	6.54	3.83

*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 3.61 differs from the reported value 3.1 by more than 10 %

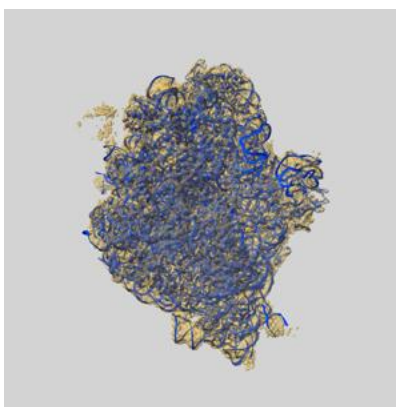
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13245 and PDB model 7P7U. Per-residue inclusion information can be found in section [3](#) on page [15](#).

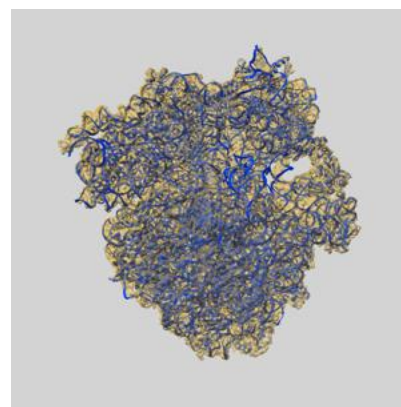
9.1 Map-model overlay [i](#)



X



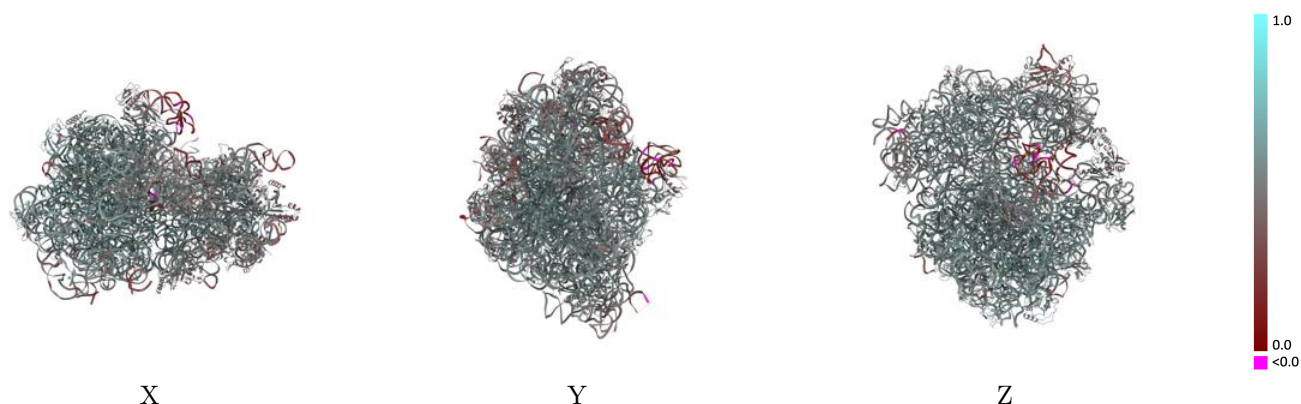
Y



Z

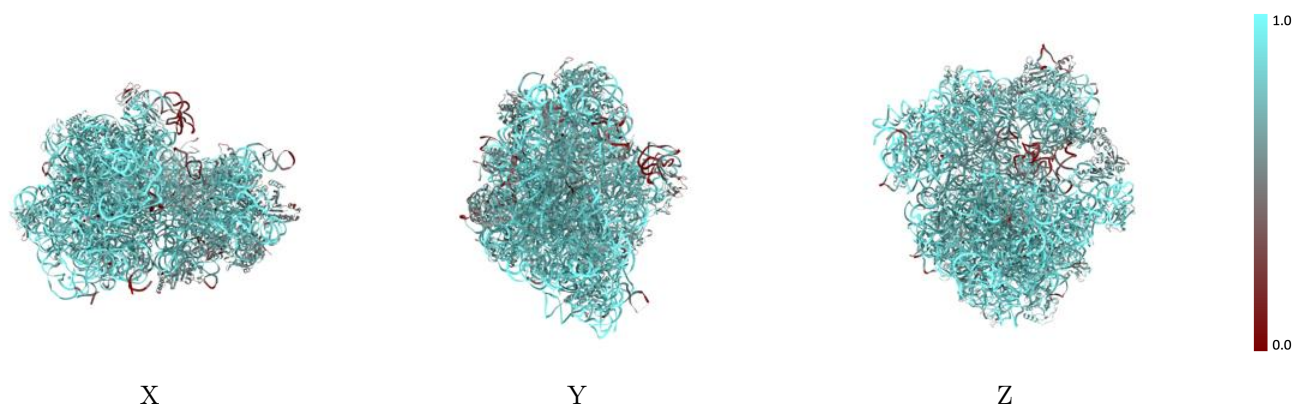
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



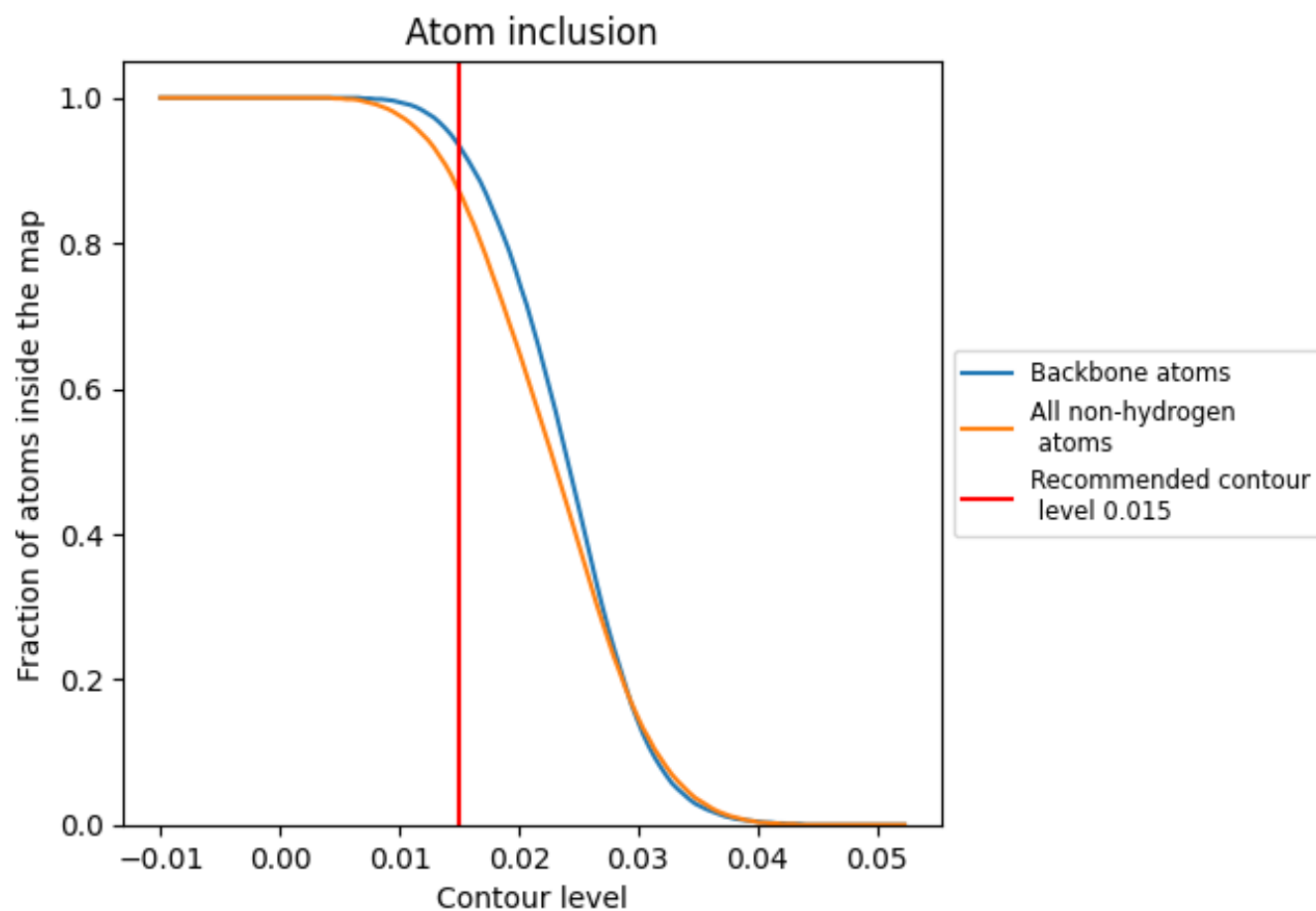
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.015).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 87% 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 (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8710	 0.5260
1	 0.7450	 0.4960
2	 0.7820	 0.5350
3	 0.5840	 0.4450
4	 0.8490	 0.5610
5	 0.8430	 0.5540
6	 0.9120	 0.5940
7	 0.9240	 0.5910
8	 0.8550	 0.5530
A	 0.9340	 0.5400
B	 0.9320	 0.4990
D	 0.6920	 0.4210
G	 0.8470	 0.5780
H	 0.7800	 0.5550
I	 0.8260	 0.5580
J	 0.6620	 0.4610
K	 0.6070	 0.4530
M	 0.8470	 0.5520
N	 0.7470	 0.5540
O	 0.8090	 0.5580
P	 0.7890	 0.5520
Q	 0.8010	 0.5290
R	 0.7350	 0.4940
S	 0.7540	 0.5350
T	 0.8580	 0.5580
U	 0.8090	 0.5700
V	 0.8190	 0.5500
W	 0.8020	 0.5230
X	 0.6740	 0.4990
Y	 0.8730	 0.5730
Z	 0.6650	 0.5470
a	 0.9210	 0.5180
b	 0.2840	 0.3380
c	 0.6020	 0.4510
d	 0.6970	 0.4970



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Chain	Atom inclusion	Q-score
e	 0.7420	 0.4990
f	 0.7850	 0.5310
g	 0.6510	 0.5050
h	 0.5890	 0.4600
i	 0.8190	 0.5320
j	 0.6870	 0.4700
k	 0.6450	 0.4590
l	 0.6660	 0.4800
m	 0.7080	 0.5400
n	 0.6540	 0.4690
o	 0.8550	 0.5330
p	 0.7450	 0.5150
q	 0.8010	 0.5110
r	 0.7870	 0.5350
s	 0.6800	 0.4910
t	 0.6630	 0.4770
u	 0.7070	 0.4800