



## wwPDB EM Validation Summary Report ⓘ

May 21, 2024 – 12:59 PM EDT

PDB ID : 8UPR  
EMDB ID : EMD-42454  
Title : Escherichia coli transcription-translation coupled complex class A (TTC-A) containing RfaH bound to ops signal, mRNA with a 21 nt long spacer, and fMet-tRNAs in E-site and P-site of the ribosome  
Authors : Molodtsov, V.; Wang, C.; Ebright, R.H.  
Deposited on : 2023-10-23  
Resolution : 5.30 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:

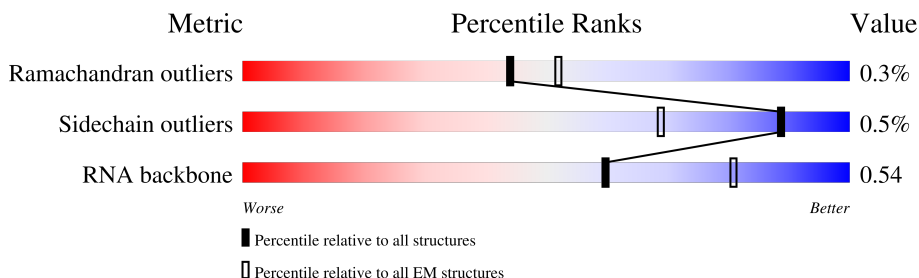
EMDB validation analysis : 0.0.1.dev92  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36.2

# 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 5.30 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.






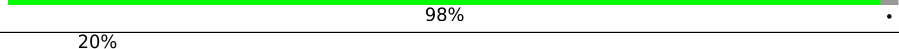
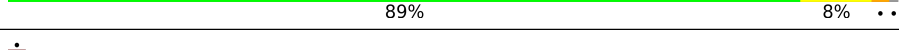
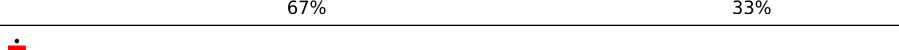
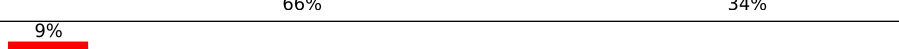
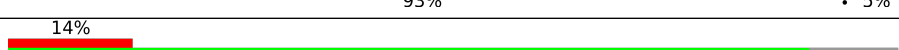
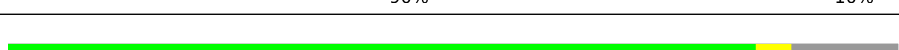


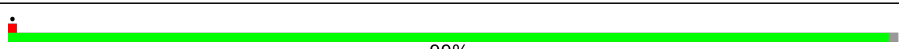



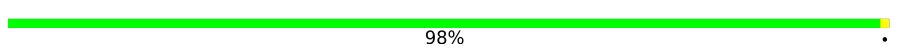



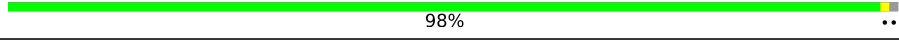
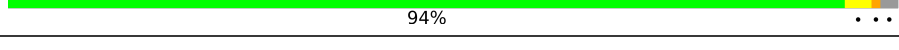
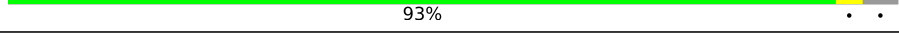
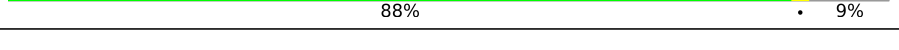
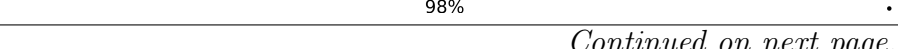

Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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

Mol	Chain	Length	Quality of chain
1	0	103	
2	1	110	
3	2	100	
4	3	104	
5	4	94	
6	5	38	
7	6	38	
8	7	38	

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Mol	Chain	Length	Quality of chain
9	9	165	 84% 10%
10	A	76	 51% 47%
10	B	76	 51% 47%
11	AA	1342	 12% 98%
12	AB	162	 20% 89% 8%
13	AC	329	 67% 33%
13	AD	329	 66% 34%
14	AE	1407	 9% 93% 5%
15	AF	91	 14% 90% 10%
16	C	75	 84% 12%
17	D	1542	 79% 20%
18	E	87	 99%
19	F	71	 99%
20	G	241	 90% 7%
21	H	557	 45% 54%
22	I	233	 87% 11%
23	J	206	 98%
24	K	167	 91% 7%
25	L	135	 74% 23%
26	M	179	 83% 16%
27	N	130	 98%
28	O	130	 94%
29	P	103	 93%
30	Q	129	 88% 9%
31	R	124	 98%


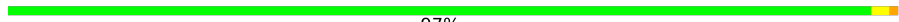







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Mol	Chain	Length	Quality of chain
32	S	101	98% ..
33	T	89	98% ..
34	U	82	98% .
35	V	84	94% . 5%
36	W	92	87% . 10%
37	X	118	95% ..
38	Y	142	7% 98% ...
39	Z	121	25% 75%
40	a	2904	80% 19% ..
41	b	85	89% 11%
42	c	78	96% ..
43	d	120	88% 12%
44	e	63	95% ..
45	f	59	97% ..
46	g	70	93% . 6%
47	h	273	98% ..
48	i	57	96% ..
49	j	209	99% .
50	k	55	95% 5%
51	l	201	99% .
52	m	46	100%
53	n	179	97% ..
54	o	65	94% 5% .
55	p	177	98% ..
56	q	38	100%

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Mol	Chain	Length	Quality of chain
57	r	149	 100%
58	s	142	 97%
59	t	123	 97%
60	u	144	 98%
61	v	136	 99%
62	w	127	 89% 5% 6%
63	x	117	 99%
64	y	115	 97%
65	z	118	 97%

## 2 Entry composition [i](#)

There are 67 unique types of molecules in this entry. The entry contains 276059 atoms, of which 98639 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 Ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
1	0	103	1655	516	839	153	145	2	0	0

- Molecule 2 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
2	1	110	1779	532	922	166	156	3	0	0

- Molecule 3 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
3	2	94	1557	470	811	140	134	2	0	0

- Molecule 4 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
4	3	103	1632	498	844	148	142	0	0

- Molecule 5 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
5	4	94	1533	479	780	137	134	3	0	0

- Molecule 6 is a DNA chain called NT DNA ops.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
6	5	35	726	342	141	208	35	0	0

- Molecule 7 is a DNA chain called T DNA ops.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
7	6	35	703	336	117	215	35	0	0

- Molecule 8 is a RNA chain called mRNA with 21 nt long spacer.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
8	7	38	792	354	112	288	38	0	0

- Molecule 9 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	9	148	1117	705	196	209	7	0	0

- Molecule 10 is a RNA chain called E-site and P-site tRNA (fMet).

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			P
10	A	76	2446	723	826	295	527	75	0	0
10	B	76	2434	723	814	295	527	75	0	0

- Molecule 11 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	AA	1316	10381	6514	1810	2014	43	0	0

- Molecule 12 is a protein called Transcription antitermination protein RfaH.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	AB	161	1286	828	222	232	4	0	0

- Molecule 13 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	AC	221	1698	1060	299	333	6	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	AD	218	1677	1048	297	326	6	0	0

- Molecule 14 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	AE	1337	10404	6535	1856	1963	50	0	0

- Molecule 15 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	AF	82	650	396	122	131	1	0	0

- Molecule 16 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
16	C	66	1103	344	559	102	97	1	0	0

- Molecule 17 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	P		
17	D	1524	49126	14585	16423	6003	10591	1524	0	0

- Molecule 18 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
18	E	86	1388	414	719	138	114	3	0	0

- Molecule 19 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
19	F	70	1218	366	629	125	97	1	0	0

- Molecule 20 is a protein called 30S ribosomal protein S2.



Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
20	G	225	3545	1113	1785	316	323	8	0	0

- Molecule 21 is a protein called 30S ribosomal protein S1.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
21	H	259	3184	1073	1454	305	349	3	0	0

- Molecule 22 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
22	I	208	3346	1036	1710	307	290	3	0	0

- Molecule 23 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
23	J	205	3350	1026	1707	315	298	4	0	0

- Molecule 24 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
24	K	156	2348	717	1196	217	212	6	0	0

- Molecule 25 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
25	L	104	1694	536	846	153	152	7	0	0

- Molecule 26 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
26	M	151	2416	735	1235	227	215	4	0	0

- Molecule 27 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
27	N	129	2010	616	1031	173	184	6	0	0

- Molecule 28 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
28	O	127	2092	634	1070	206	179	3	0	0

- Molecule 29 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
29	P	99	1621	495	831	151	143	1	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
30	Q	117	1764	540	887	174	160	3	0	0

- Molecule 31 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
31	R	121	1940	580	1001	194	161	4	0	0

- Molecule 32 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
32	S	100	1649	499	844	164	139	3	0	0

- Molecule 33 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
33	T	88	1448	439	734	144	130	1	0	0

- Molecule 34 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace	
34	U	82	Total	C	H	N	O	S	0	0
			1315	406	666	128	114	1		

- Molecule 35 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace	
35	V	80	Total	C	H	N	O	S	0	0
			1339	411	691	121	113	3		

- Molecule 36 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace	
36	W	83	Total	C	H	N	O	S	0	0
			1351	424	688	126	111	2		

- Molecule 37 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace	
37	X	116	Total	C	H	N	O	S	0	0
			1864	558	964	181	158	3		

- Molecule 38 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Y	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 39 is a protein called 50S ribosomal protein L7/L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Z	30	Total	C	N	O	S	0	0
			227	144	33	47	3		

- Molecule 40 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace	
40	a	2880	Total	C	H	N	O	P	0	0
			92918	27587	31077	11398	19976	2880		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	887	A	U	conflict	GB 937521852

- Molecule 41 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
41	b	76	1181	360	599	117	104	1	0	0

- Molecule 42 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
42	c	77	1277	388	652	129	106	2	0	0

- Molecule 43 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			P
43	d	120	3870	1144	1301	468	837	120	0	0

- Molecule 44 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
44	e	62	1032	308	531	98	94	1	0	0

- Molecule 45 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
45	f	58	936	281	488	87	78	2	0	0

- Molecule 46 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
46	g	66	1042	323	520	99	94	6	0	0

- Molecule 47 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
47	h	271	4236	1288	2154	423	364	7	0	0

- Molecule 48 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
48	i	56	903	269	459	94	80	1	0	0

- Molecule 49 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
49	j	209	3182	979	1617	288	294	4	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			
50	k	52	890	275	464	78	73		0	0

- Molecule 51 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
51	l	201	3171	974	1619	283	290	5	0	0

- Molecule 52 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
52	m	46	795	228	418	90	57	2	0	0

- Molecule 53 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
53	n	177	2853	899	1443	249	256	6	0	0

- Molecule 54 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace	
54	o	64	Total	C	H	N	O	S	0	0
			1076	323	572	105	74	2		

- Molecule 55 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace	
55	p	175	Total	C	H	N	O	S	0	0
			2671	826	1358	241	244	2		

- Molecule 56 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace	
56	q	38	Total	C	H	N	O	S	0	0
			645	185	343	65	48	4		

- Molecule 57 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace	
57	r	149	Total	C	H	N	O	S	0	0
			2259	699	1148	197	214	1		

- Molecule 58 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace	
58	s	142	Total	C	H	N	O	S	0	0
			2291	714	1162	212	199	4		

- Molecule 59 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace	
59	t	123	Total	C	H	N	O	S	0	0
			1969	593	1023	181	166	6		

- Molecule 60 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace	
60	u	144	Total	C	H	N	O	S	0	0
			2182	654	1129	207	190	2		

- Molecule 61 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace	
61	v	136	Total	C	H	N	O	S	0	0
			2231	686	1157	205	177	6		

- Molecule 62 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace	
62	w	119	Total	C	H	N	O	S	0	0
			1945	588	994	195	163	5		

- Molecule 63 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace	
63	x	116	Total	C	H	N	O		0	0
			1815	552	923	178	162			

- Molecule 64 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace	
64	y	114	Total	C	H	N	O	S	0	0
			1879	574	962	179	163	1		

- Molecule 65 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace	
65	z	117	Total	C	H	N	O		0	0
			1967	604	1020	192	151			

- Molecule 66 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
66	AE	1	Total	Mg	0
			1	1	

- Molecule 67 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
67	AE	2	Total	Zn	0
			2	2	

### 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: Ribosomal protein L21

Chain 0:  100%

There are no outlier residues recorded for this chain.

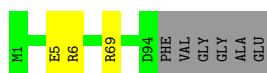
- Molecule 2: 50S ribosomal protein L22

Chain 1:  100%

There are no outlier residues recorded for this chain.

- Molecule 3: 50S ribosomal protein L23

Chain 2:  91% 6%



- Molecule 4: 50S ribosomal protein L24

Chain 3:  99%



- Molecule 5: 50S ribosomal protein L25

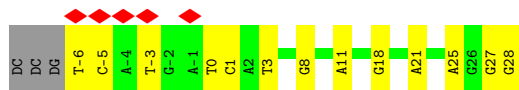
Chain 4:  98%



- Molecule 6: NT DNA ops

Chain 5:  13% 58% 34% 8%

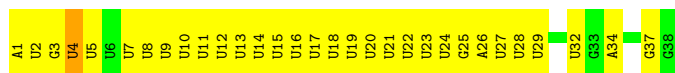




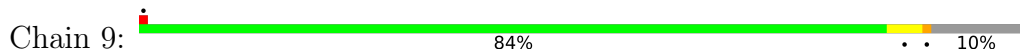
• Molecule 7: T DNA ops



• Molecule 8: mRNA with 21 nt long spacer



• Molecule 9: 50S ribosomal protein L10



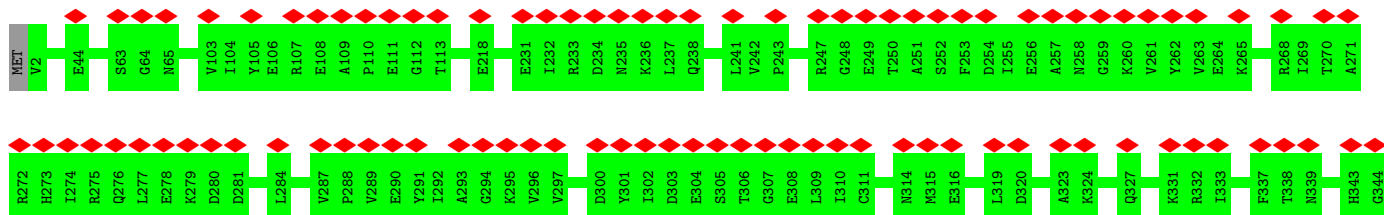
• Molecule 10: E-site and P-site tRNA (fMet)



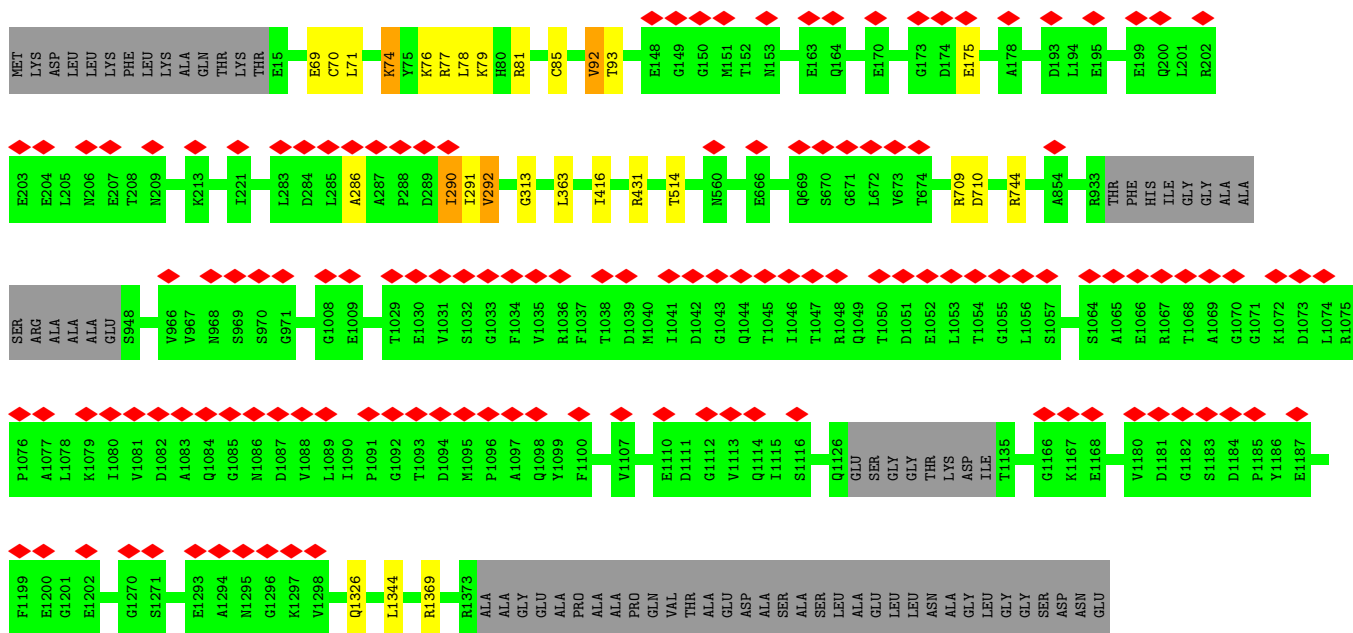
• Molecule 10: E-site and P-site tRNA (fMet)



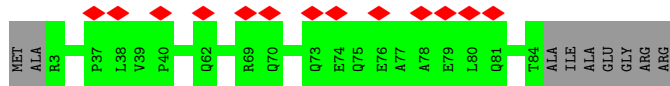
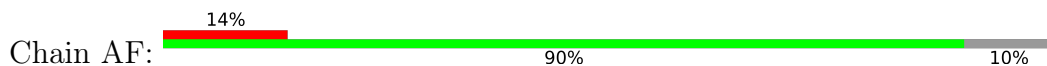
• Molecule 11: DNA-directed RNA polymerase subunit beta



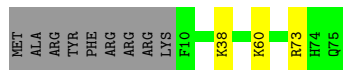
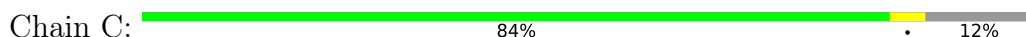




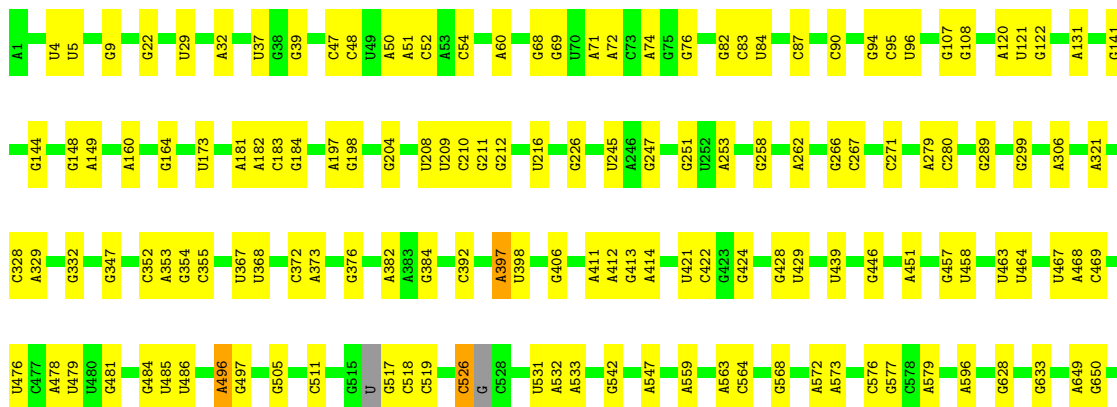
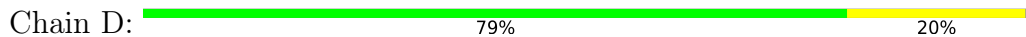
- Molecule 15: DNA-directed RNA polymerase subunit omega

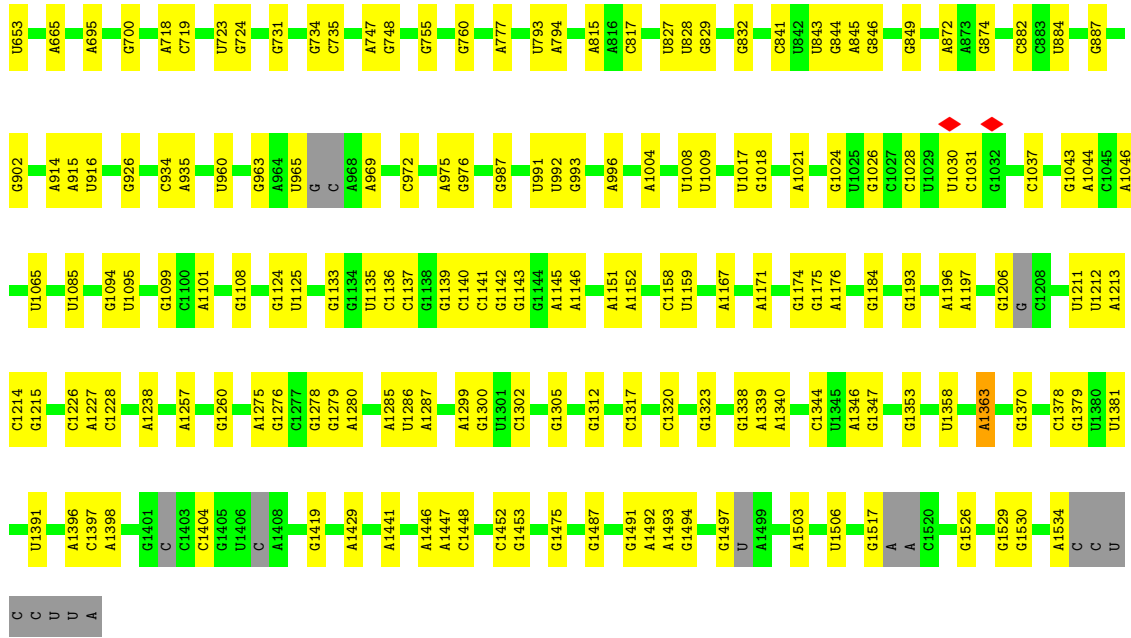


- Molecule 16: 30S ribosomal protein S18



- Molecule 17: 16S rRNA

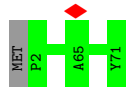




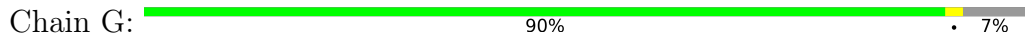
• Molecule 18: 30S ribosomal protein S20



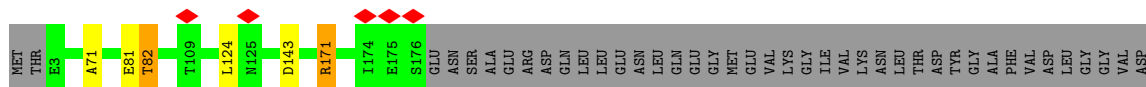
• Molecule 19: 30S ribosomal protein S21



• Molecule 20: 30S ribosomal protein S2



• Molecule 21: 30S ribosomal protein S1





- Molecule 27: 30S ribosomal protein S8

Chain N:  98% ..



- Molecule 28: 30S ribosomal protein S9

Chain O:  94% ...




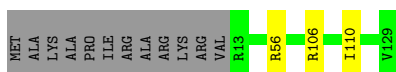
- Molecule 29: 30S ribosomal protein S10

Chain P:  93% ..



- Molecule 30: 30S ribosomal protein S11

Chain Q:  88% . 9%



- Molecule 31: 30S ribosomal protein S12

Chain R:  98% .



- Molecule 32: 30S ribosomal protein S14

Chain S:  98% ..



- Molecule 33: 30S ribosomal protein S15

Chain T:  98% ..

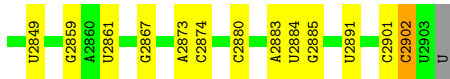


- Molecule 34: 30S ribosomal protein S16



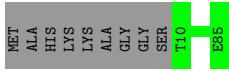
A181	G411	A609	A819	C995	G1107	C1345	U1554	U1758	U1923	C2055	G2162	A2322	G2458	U2609
A196	A412	A613	U827	A996	A1111	U1352	U1559	C1764	C1924	G2056	A2163	G2325	G2470	C2610
G215	C420	A614	A845	U999	G1112	A1365	A1566	C1773	C1925	A2060	C2164	C2326	U2474	C2611
A216	G424	U615	U846	C1005	U1119	G1388	A1569	U1775	U1926	G2061	C2165	A2327	G2475	C2612
A221	U451	A626	G858	U1012	G1122	A1378	A1579	A1791	G1929	A2068	A2169	U2329	A2476	U2613
A222	A457	A627	G859	C1013	G1128	A1379	U1578	C1800	A1936	U2068	A2171	C2332	A2477	U2629
C235	A457	A637	G869	U1019	U1132	G1380	A1580	U1808	U1937	G	U2172	U2333	G2484	G2638
G248	A477	C645	A878	A1020	U1133	A1383	G1581	A1808	U1940	A2070	C2178	A2335	U2491	G2663
C249	G451	U646	G881	G1022	A1134	A1392	C1582	G1811	U1955	C2073	U2182	C2338	A2497	G2669
C253	G491	G647	G882	U1023	C1135	A1395	U1584	G1816	U1961	U	A2183	C2339	C	A2670
G251	A501	A654	G883	G1026	U1141	A1406	C1585	G1817	C	U2075	A2184	G2345	C2499	G2671
C264	A503	A668	U884	U1033	A1142	U1407	C1588	U1818	U1963	A2097	U2185	G2346	G	U2689
A265	A504	U686	C885	G1041	A1169	G1408	U1589	G1829	G1964	U2098	U2188	C2347	U2502	U2690
G266	A505	G704	C888	G1045	C1170	G1409	A1590	A1833	U1965	U2099	G2190	C2350	A	G2714
C267	G509	U710	G891	G1046	U1173	U1409	A1608	C1833	A1966	A2108	U2194	G2351	U	C2715
G271	G520	U717	G892	A1046	U1174	A1414	A1609	G	U1967	G2109	A2198	G2361	C2512	C2716
A272	G521	C717	G893	G1047	A1175	U4415	A1610	C1836	A1971	G2110	G2198	U2372	A2513	A2726
C275	A522	U729	U894	U1053	U1176	G1416	G1613	A1847	G1972	U2111	G2204	A2376	A2518	G2744
G276	A522	G730	G895	U1060	C1177	C1417	U1617	A1848	A1987	G2112	A2211	G2383	U2519	G2744
U277	A522	A730	A896	U1061	G1179	G1418	A	U1848	U1991	G2114	A2212	U2384	C2520	A2748
A278	G529	G738	C898	U1083	U1180	A1420	G1519	G1857	U1992	G2116	A2212	C2385	G2525	G2756
G285	C551	U742	A899	C1084	G1186	C1428	U1647	U1859	U1993	U2118	A2225	U2402	G2529	A2757
G291	A532	A743	G907	U1065	G1225	G1452	U1648	G1862	C1997	G2121	C2226	C2403	G2529	A2758
A311	G537	U744	A910	G1068	G1238	A1453	U1649	U1864	G2002	U2122	U2229	A2406	G2535	A2765
G329	C542	G	G914	A1069	G1248	U1460	A1655	G1869	G2012	G2124	G2238	A2406	G2551	G2777
A330	G543	U	C915	U1070	U1253	G1482	A1665	C1870	G2013	G2125	G2239	U2423	U	A2778
C353	C544	G748	U931	C1072	A1253	G1482	U1665	A1872	A2013	A2126	G2250	C2424	G2553	G2791
G361	U546	G757	A941	G1074	G1256	A1490	U1674	G1873	A2020	G2127	G	A2425	U2554	C2791
A362	A547	G757	G942	U1074	C1257	U1497	G1674	G1873	G2021	G2128	G2252	A2426	A2566	C2793
A371	G549	A764	U945	C1079	G1266	U1497	A1677	G1906	U2021	U2131	A2268	G2429	A2567	U2796
G372	C551	C765	A945	U1081	U1271	A1503	G1703	G1907	G2027	U2132	A2268	A2430	G2573	U2797
U373	G551	G775	C946	U1082	A1272	G1497	U1714	U	U2028	U2133	A2278	U2431	G2574	U2797
A374	A563	G776	C946	A1084	U1273	A1508	G1715	A1912	G2029	G2133	C2283	A2434	A2435	U2799
G375	U569	A782	U	A1085	A1276	G1510	U1715	A1912	A	U2139	G2283	A2435	C2435	A2800
C383	G784	A785	G956	U1086	G1300	A1515	U1729	A1913	A2031	G2140	A2287	U2441	U2441	G2801
C385	G785	G784	U	G1087	A1301	G1529	C1730	C1914	G2032	G2141	A2288	A2444	G	U2818
G386	A960	G785	A960	A1088	G1300	G1529	G1731	U	A2033	C2146	A2297	G2444	G2446	G2819
G396	C961	A800	C961	A1090	A1321	G1530	C1732	U	A2043	A2154	A2297	G2446	G2446	A2820
U405	G805	G805	G974	A1095	A1321	U1534	G1738	A1918	C2043	A2154	U2305	G2446	A2448	A2823
	C812	C812	A953	U1101	G1331	A1536	G1750	A1919	G2049	G2157	G2308	G2446	A2448	C2824
					G1334	C1536	G1750	C1920	C2050	A2158	A2309	G2446	A2448	G2825
						G1537	G1750	G1921	A2052	A2158	A2309	C2456	A2448	U2825
								G1922	A2052	A2158	A2309	U		A2835





- Molecule 41: 50S ribosomal protein L27

Chain b: 89% 11%



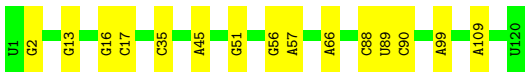
- Molecule 42: 50S ribosomal protein L28

Chain c: 96% ..



- Molecule 43: 5S rRNA

Chain d: 88% 12%



- Molecule 44: 50S ribosomal protein L29

Chain e: 95% ..



- Molecule 45: 50S ribosomal protein L30

Chain f: 97% ..



- Molecule 46: 50S ribosomal protein L31

Chain g: 93% • 6%



- Molecule 47: 50S ribosomal protein L2

Chain h: 98% ..



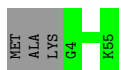
- Molecule 48: 50S ribosomal protein L32



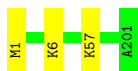
- Molecule 49: 50S ribosomal protein L3



- Molecule 50: 50S ribosomal protein L33



- Molecule 51: 50S ribosomal protein L4



- Molecule 52: 50S ribosomal protein L34



There are no outlier residues recorded for this chain.

- Molecule 53: 50S ribosomal protein L5



- Molecule 54: 50S ribosomal protein L35



- Molecule 55: 50S ribosomal protein L6

Chain p:  98%



- Molecule 56: 50S ribosomal protein L36

Chain q:  100%

There are no outlier residues recorded for this chain.

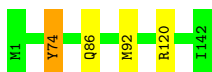
- Molecule 57: 50S ribosomal protein L9

Chain r:  100%

There are no outlier residues recorded for this chain.

- Molecule 58: 50S ribosomal protein L13

Chain s:  97%



- Molecule 59: 50S ribosomal protein L14

Chain t:  97%



- Molecule 60: 50S ribosomal protein L15

Chain u:  98%




- Molecule 61: 50S ribosomal protein L16

Chain v:  99%



- Molecule 62: 50S ribosomal protein L17

Chain w:  89% 5% 6%



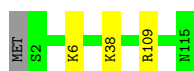
- Molecule 63: 50S ribosomal protein L18

Chain x:  99%

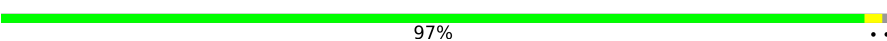


- Molecule 64: 50S ribosomal protein L19

Chain y:  97%



- Molecule 65: 50S ribosomal protein L20

Chain z:  97%



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	10509	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	28	Depositor
Minimum defocus (nm)	1250	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.032	Depositor
Minimum map value	-0.007	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0025	Depositor
Map size ( $\text{\AA}$ )	531.968, 531.968, 531.968	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.039, 1.039, 1.039	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0	0.47	0/829	0.60	0/1107
2	1	0.58	0/864	0.69	0/1156
3	2	0.67	1/752 (0.1%)	0.72	1/1005 (0.1%)
4	3	0.41	0/796	0.55	0/1062
5	4	0.65	2/766 (0.3%)	0.69	0/1025
6	5	1.14	11/816 (1.3%)	1.12	2/1259 (0.2%)
7	6	1.12	8/783 (1.0%)	1.10	0/1203
8	7	0.53	2/879 (0.2%)	0.87	3/1364 (0.2%)
9	9	0.36	0/1131	0.66	2/1524 (0.1%)
10	A	0.55	1/1810 (0.1%)	1.26	12/2821 (0.4%)
10	B	0.55	1/1810 (0.1%)	1.26	11/2821 (0.4%)
11	AA	0.43	0/10547	0.61	1/14232 (0.0%)
12	AB	0.42	0/1317	0.85	5/1786 (0.3%)
13	AC	0.41	0/1718	0.62	0/2328
13	AD	0.36	0/1696	0.62	0/2298
14	AE	0.42	0/10561	0.63	3/14258 (0.0%)
15	AF	0.33	0/652	0.57	0/879
16	C	0.70	0/553	0.92	4/743 (0.5%)
17	D	0.59	13/36610 (0.0%)	1.03	67/57091 (0.1%)
18	E	0.57	0/675	0.71	0/895
19	F	0.62	0/597	0.59	0/792
20	G	0.66	2/1791 (0.1%)	0.83	7/2413 (0.3%)
21	H	0.43	0/1746	0.70	0/2382
22	I	0.62	2/1663 (0.1%)	0.71	4/2241 (0.2%)
23	J	0.54	2/1665 (0.1%)	0.59	0/2227
24	K	0.69	1/1165 (0.1%)	0.86	4/1568 (0.3%)
25	L	0.79	3/867 (0.3%)	0.82	3/1171 (0.3%)
26	M	0.54	0/1195	0.69	2/1602 (0.1%)
27	N	0.52	0/989	0.63	1/1326 (0.1%)
28	O	0.67	4/1034 (0.4%)	0.82	4/1375 (0.3%)
29	P	0.52	0/800	0.70	2/1082 (0.2%)
30	Q	0.71	1/893 (0.1%)	0.81	4/1205 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
31	R	0.56	0/952	0.65	0/1274
32	S	0.64	1/817 (0.1%)	0.64	0/1088
33	T	0.56	0/722	0.72	1/964 (0.1%)
34	U	0.45	0/659	0.65	1/884 (0.1%)
35	V	0.57	0/657	0.70	0/881
36	W	0.56	1/680 (0.1%)	0.69	3/915 (0.3%)
37	X	0.48	0/909	0.72	1/1215 (0.1%)
38	Y	0.42	1/1046 (0.1%)	0.57	2/1410 (0.1%)
39	Z	0.23	0/227	0.38	0/304
40	a	0.61	14/69247 (0.0%)	1.03	129/107985 (0.1%)
41	b	0.47	0/589	0.57	0/779
42	c	0.56	1/635 (0.2%)	0.66	1/848 (0.1%)
43	d	0.50	0/2872	0.95	0/4478
44	e	0.81	2/502 (0.4%)	0.66	0/667
45	f	0.53	0/452	0.72	2/605 (0.3%)
46	g	0.50	1/531 (0.2%)	0.67	1/709 (0.1%)
47	h	0.53	2/2121 (0.1%)	0.67	6/2852 (0.2%)
48	i	0.42	0/450	0.65	1/599 (0.2%)
49	j	0.53	0/1586	0.64	2/2134 (0.1%)
50	k	0.51	0/433	0.67	0/576
51	l	0.54	1/1571 (0.1%)	0.64	1/2113 (0.0%)
52	m	0.43	0/380	0.61	0/498
53	n	0.51	0/1434	0.68	2/1926 (0.1%)
54	o	0.51	0/513	0.86	1/676 (0.1%)
55	p	0.50	0/1333	0.68	3/1805 (0.2%)
56	q	0.46	0/303	0.61	0/397
57	r	0.34	0/1122	0.52	0/1515
58	s	0.83	5/1152 (0.4%)	0.81	5/1551 (0.3%)
59	t	0.55	1/955 (0.1%)	0.89	5/1279 (0.4%)
60	u	0.47	1/1062 (0.1%)	0.63	0/1413
61	v	0.61	1/1093 (0.1%)	0.75	1/1460 (0.1%)
62	w	0.90	5/964 (0.5%)	0.95	9/1289 (0.7%)
63	x	0.42	0/902	0.57	0/1209
64	y	0.46	0/929	0.58	1/1242 (0.1%)
65	z	0.63	1/960 (0.1%)	0.59	0/1278
All	All	0.58	92/190730 (0.0%)	0.92	320/281059 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
9	9	0	3
12	AB	0	10
13	AC	0	1
13	AD	0	1
14	AE	0	4
20	G	0	1
21	H	0	5
22	I	0	1
24	K	0	2
28	O	0	1
37	X	0	1
38	Y	0	1
53	n	0	1
54	o	0	1
58	s	0	1
60	u	0	2
All	All	0	36

The worst 5 of 92 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
62	w	35	LYS	CE-NZ	-15.21	1.11	1.49
25	L	42	TRP	CB-CG	-12.38	1.27	1.50
3	2	5	GLU	CG-CD	-11.53	1.34	1.51
44	e	46	VAL	CB-CG1	-11.32	1.29	1.52
62	w	42	LYS	CD-CE	-10.77	1.24	1.51

The worst 5 of 320 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
40	a	1019	U	C5-C4-O4	30.71	144.33	125.90
40	a	1141	U	C5-C4-O4	29.52	143.61	125.90
17	D	37	U	C5-C4-O4	29.43	143.56	125.90
17	D	1358	U	C5-C4-O4	29.20	143.42	125.90
17	D	827	U	C5-C4-O4	28.66	143.10	125.90

There are no chirality outliers.

5 of 36 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	9	107	GLU	Peptide
9	9	79	PRO	Peptide

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Mol	Chain	Res	Type	Group
9	9	92	ALA	Peptide
12	AB	106	ASP	Peptide
12	AB	116	VAL	Peptide

## 5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

## 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	0	101/103 (98%)	97 (96%)	4 (4%)	0	100	100
2	1	108/110 (98%)	107 (99%)	1 (1%)	0	100	100
3	2	92/100 (92%)	87 (95%)	5 (5%)	0	100	100
4	3	101/104 (97%)	98 (97%)	3 (3%)	0	100	100
5	4	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
9	9	146/165 (88%)	101 (69%)	42 (29%)	3 (2%)	7	38
11	AA	1312/1342 (98%)	1199 (91%)	112 (8%)	1 (0%)	51	85
12	AB	159/162 (98%)	109 (69%)	45 (28%)	5 (3%)	4	30
13	AC	217/329 (66%)	203 (94%)	12 (6%)	2 (1%)	17	56
13	AD	214/329 (65%)	198 (92%)	16 (8%)	0	100	100
14	AE	1331/1407 (95%)	1210 (91%)	115 (9%)	6 (0%)	29	69
15	AF	80/91 (88%)	77 (96%)	3 (4%)	0	100	100
16	C	64/75 (85%)	63 (98%)	1 (2%)	0	100	100
18	E	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
19	F	68/71 (96%)	68 (100%)	0	0	100	100
20	G	223/241 (92%)	212 (95%)	10 (4%)	1 (0%)	34	72

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	H	255/557 (46%)	182 (71%)	66 (26%)	7 (3%)	5	33
22	I	206/233 (88%)	193 (94%)	13 (6%)	0	100	100
23	J	203/206 (98%)	201 (99%)	2 (1%)	0	100	100
24	K	154/167 (92%)	145 (94%)	8 (5%)	1 (1%)	25	65
25	L	102/135 (76%)	97 (95%)	4 (4%)	1 (1%)	15	54
26	M	149/179 (83%)	140 (94%)	8 (5%)	1 (1%)	22	62
27	N	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
28	O	125/130 (96%)	116 (93%)	8 (6%)	1 (1%)	19	60
29	P	97/103 (94%)	89 (92%)	8 (8%)	0	100	100
30	Q	115/129 (89%)	107 (93%)	8 (7%)	0	100	100
31	R	117/124 (94%)	112 (96%)	5 (4%)	0	100	100
32	S	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
33	T	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
34	U	80/82 (98%)	76 (95%)	4 (5%)	0	100	100
35	V	78/84 (93%)	74 (95%)	4 (5%)	0	100	100
36	W	81/92 (88%)	80 (99%)	1 (1%)	0	100	100
37	X	114/118 (97%)	103 (90%)	9 (8%)	2 (2%)	8	41
38	Y	139/142 (98%)	101 (73%)	38 (27%)	0	100	100
39	Z	28/121 (23%)	22 (79%)	6 (21%)	0	100	100
41	b	74/85 (87%)	73 (99%)	1 (1%)	0	100	100
42	c	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
44	e	60/63 (95%)	57 (95%)	3 (5%)	0	100	100
45	f	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
46	g	64/70 (91%)	62 (97%)	2 (3%)	0	100	100
47	h	269/273 (98%)	255 (95%)	14 (5%)	0	100	100
48	i	54/57 (95%)	49 (91%)	5 (9%)	0	100	100
49	j	207/209 (99%)	198 (96%)	9 (4%)	0	100	100
50	k	50/55 (91%)	50 (100%)	0	0	100	100
51	l	199/201 (99%)	188 (94%)	11 (6%)	0	100	100
52	m	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
53	n	175/179 (98%)	161 (92%)	13 (7%)	1 (1%)	25	65

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	o	62/65 (95%)	57 (92%)	4 (6%)	1 (2%)	9	44
55	p	173/177 (98%)	162 (94%)	11 (6%)	0	100	100
56	q	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
57	r	147/149 (99%)	139 (95%)	8 (5%)	0	100	100
58	s	140/142 (99%)	133 (95%)	7 (5%)	0	100	100
59	t	121/123 (98%)	114 (94%)	7 (6%)	0	100	100
60	u	142/144 (99%)	134 (94%)	8 (6%)	0	100	100
61	v	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
62	w	117/127 (92%)	112 (96%)	5 (4%)	0	100	100
63	x	114/117 (97%)	107 (94%)	7 (6%)	0	100	100
64	y	112/115 (97%)	105 (94%)	7 (6%)	0	100	100
65	z	115/118 (98%)	111 (96%)	4 (4%)	0	100	100
All	All	9486/10558 (90%)	8740 (92%)	713 (8%)	33 (0%)	44	76

5 of 33 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	AB	141	LEU
12	AB	152	HIS
20	G	127	ASP
21	H	304	VAL
26	M	56	LYS

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

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	84/84 (100%)	84 (100%)	0	100	100
2	1	93/93 (100%)	93 (100%)	0	100	100
3	2	81/84 (96%)	80 (99%)	1 (1%)	71	84
4	3	84/85 (99%)	84 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	4	78/78 (100%)	78 (100%)	0	100	100
9	9	112/123 (91%)	109 (97%)	3 (3%)	44	65
11	AA	1135/1157 (98%)	1134 (100%)	1 (0%)	93	97
12	AB	141/142 (99%)	140 (99%)	1 (1%)	84	90
13	AC	186/286 (65%)	186 (100%)	0	100	100
13	AD	185/286 (65%)	185 (100%)	0	100	100
14	AE	1122/1168 (96%)	1103 (98%)	19 (2%)	60	78
15	AF	70/75 (93%)	70 (100%)	0	100	100
16	C	57/65 (88%)	57 (100%)	0	100	100
18	E	65/66 (98%)	65 (100%)	0	100	100
19	F	60/61 (98%)	60 (100%)	0	100	100
20	G	187/199 (94%)	186 (100%)	1 (0%)	88	93
21	H	137/461 (30%)	137 (100%)	0	100	100
22	I	171/190 (90%)	170 (99%)	1 (1%)	86	91
23	J	172/173 (99%)	171 (99%)	1 (1%)	86	91
24	K	119/126 (94%)	119 (100%)	0	100	100
25	L	91/116 (78%)	91 (100%)	0	100	100
26	M	124/147 (84%)	124 (100%)	0	100	100
27	N	104/105 (99%)	104 (100%)	0	100	100
28	O	105/107 (98%)	104 (99%)	1 (1%)	76	86
29	P	86/90 (96%)	85 (99%)	1 (1%)	71	84
30	Q	90/99 (91%)	90 (100%)	0	100	100
31	R	101/104 (97%)	101 (100%)	0	100	100
32	S	83/84 (99%)	83 (100%)	0	100	100
33	T	76/77 (99%)	76 (100%)	0	100	100
34	U	65/65 (100%)	64 (98%)	1 (2%)	65	80
35	V	74/78 (95%)	73 (99%)	1 (1%)	67	81
36	W	72/79 (91%)	72 (100%)	0	100	100
37	X	94/96 (98%)	94 (100%)	0	100	100
38	Y	109/110 (99%)	108 (99%)	1 (1%)	78	88
39	Z	26/85 (31%)	26 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	b	58/63 (92%)	58 (100%)	0	100	100
42	c	67/68 (98%)	67 (100%)	0	100	100
44	e	54/55 (98%)	54 (100%)	0	100	100
45	f	48/49 (98%)	48 (100%)	0	100	100
46	g	59/62 (95%)	59 (100%)	0	100	100
47	h	216/218 (99%)	216 (100%)	0	100	100
48	i	47/48 (98%)	47 (100%)	0	100	100
49	j	164/164 (100%)	164 (100%)	0	100	100
50	k	47/49 (96%)	47 (100%)	0	100	100
51	l	165/165 (100%)	164 (99%)	1 (1%)	86	91
52	m	38/38 (100%)	38 (100%)	0	100	100
53	n	148/150 (99%)	148 (100%)	0	100	100
54	o	51/52 (98%)	51 (100%)	0	100	100
55	p	136/138 (99%)	136 (100%)	0	100	100
56	q	34/34 (100%)	34 (100%)	0	100	100
57	r	114/114 (100%)	114 (100%)	0	100	100
58	s	116/116 (100%)	115 (99%)	1 (1%)	78	88
59	t	104/104 (100%)	103 (99%)	1 (1%)	76	86
60	u	103/103 (100%)	103 (100%)	0	100	100
61	v	109/109 (100%)	109 (100%)	0	100	100
62	w	99/103 (96%)	98 (99%)	1 (1%)	76	86
63	x	86/87 (99%)	86 (100%)	0	100	100
64	y	99/100 (99%)	97 (98%)	2 (2%)	55	73
65	z	89/90 (99%)	88 (99%)	1 (1%)	73	84
All	All	7890/8723 (90%)	7850 (100%)	40 (0%)	89	93

5 of 40 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
28	O	12	ARG
59	t	108	ARG
29	P	5	ARG
38	Y	44	LYS
64	y	6	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 72 such sidechains are listed below:

Mol	Chain	Res	Type
51	l	92	HIS
65	z	72	ASN
53	n	5	HIS
62	w	18	GLN
14	AE	777	HIS

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	A	75/76 (98%)	29 (38%)	8 (10%)
10	B	75/76 (98%)	29 (38%)	8 (10%)
17	D	1514/1542 (98%)	290 (19%)	20 (1%)
40	a	2859/2904 (98%)	508 (17%)	0
43	d	119/120 (99%)	15 (12%)	0
8	7	37/38 (97%)	28 (75%)	5 (13%)
All	All	4679/4756 (98%)	899 (19%)	41 (0%)

5 of 899 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	7	3	G
8	7	4	U
8	7	5	U
8	7	7	U
8	7	8	U

5 of 41 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
17	D	517	G
17	D	1213	A
17	D	991	U
17	D	1196	A
17	D	1447	A

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

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

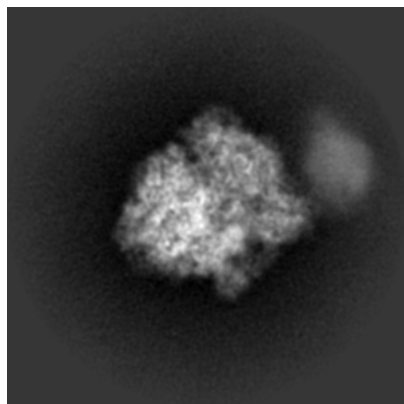
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42454. These allow visual inspection of the internal detail of the map and identification of artifacts.

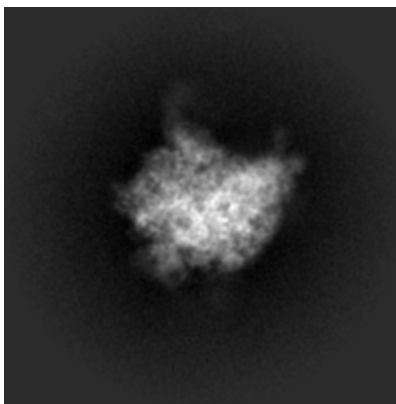
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

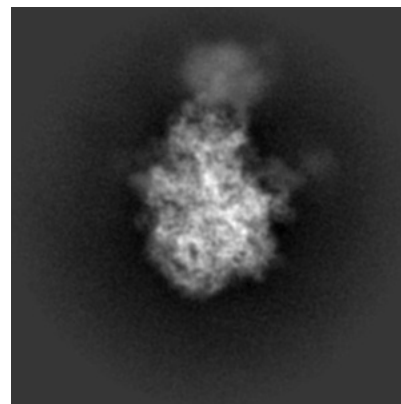
#### 6.1.1 Primary map



X

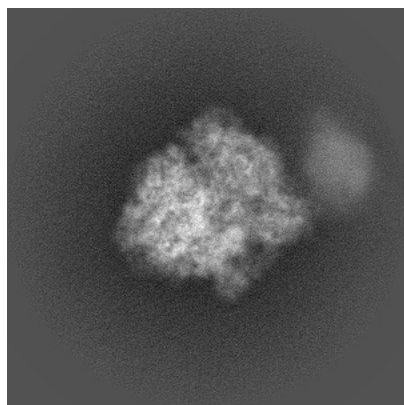


Y

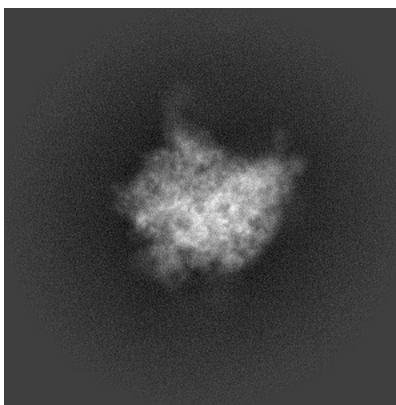


Z

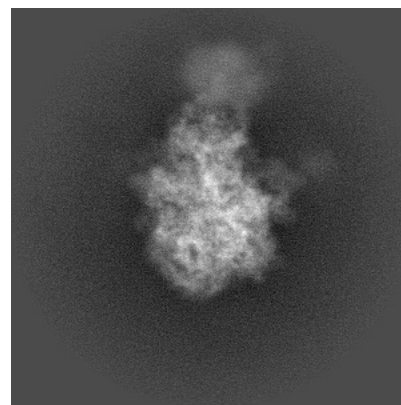
#### 6.1.2 Raw map



X



Y



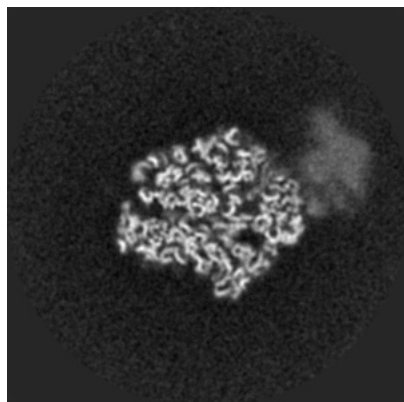
Z

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

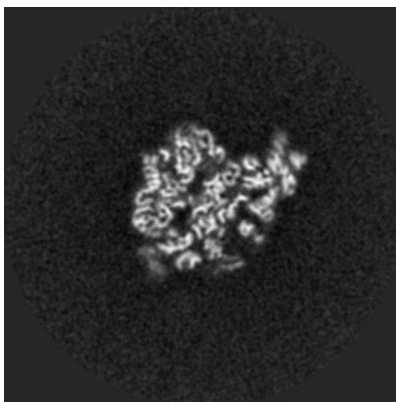


## 6.2 Central slices [i](#)

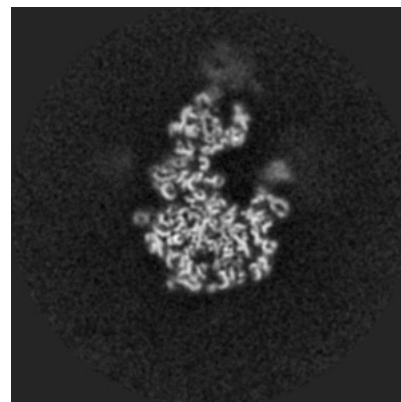
### 6.2.1 Primary map



X Index: 256

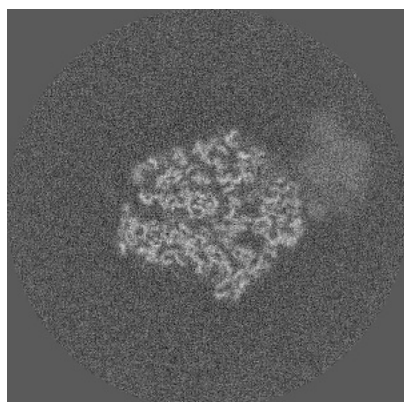


Y Index: 256

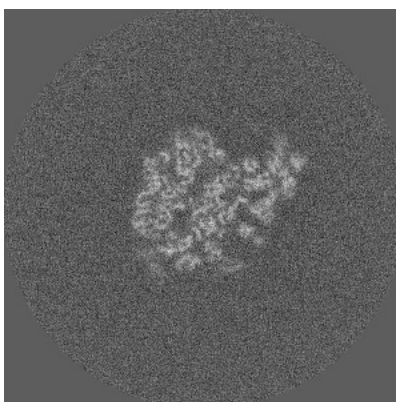


Z Index: 256

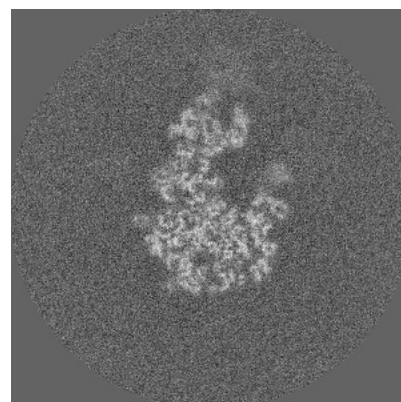
### 6.2.2 Raw map



X Index: 256



Y Index: 256

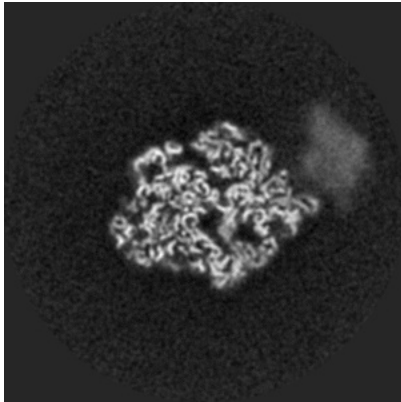


Z Index: 256

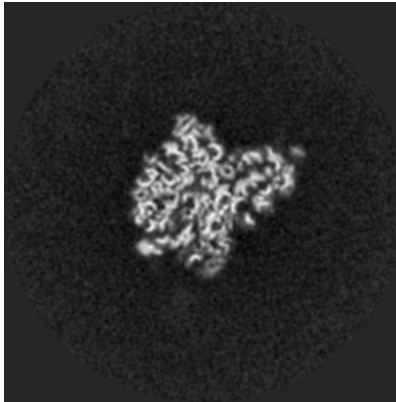
The images above show central slices of the map in three orthogonal directions.

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

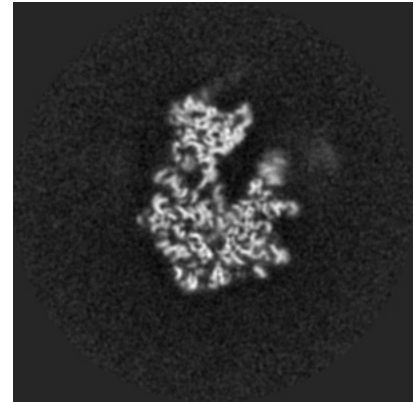
### 6.3.1 Primary map



X Index: 248

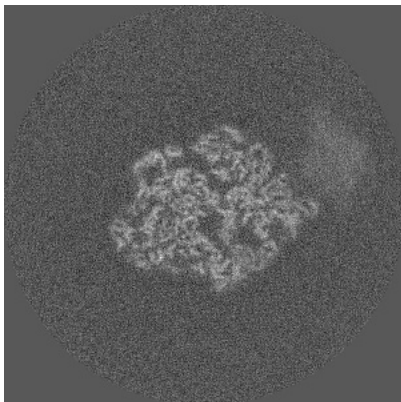


Y Index: 249

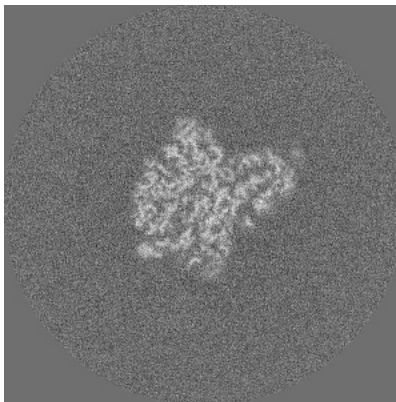


Z Index: 241

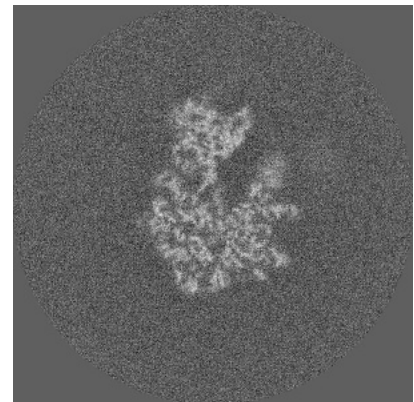
### 6.3.2 Raw map



X Index: 248



Y Index: 249

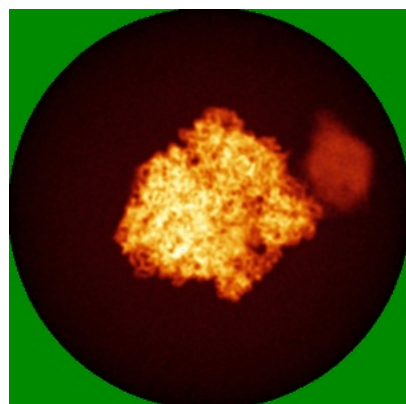


Z Index: 241

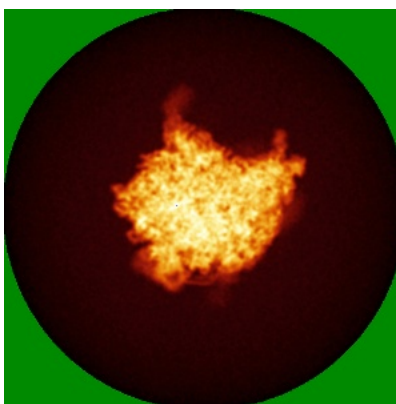
The images above show the largest variance slices of the map in three orthogonal directions.

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

### 6.4.1 Primary map



X

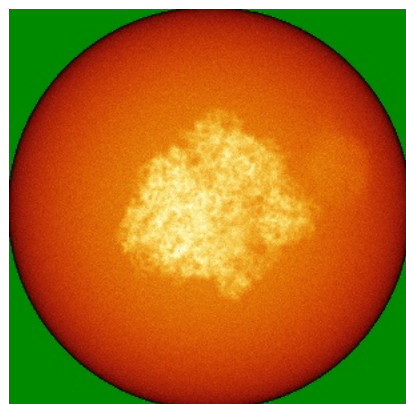


Y

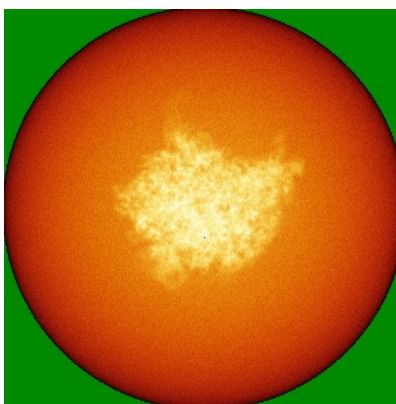


Z

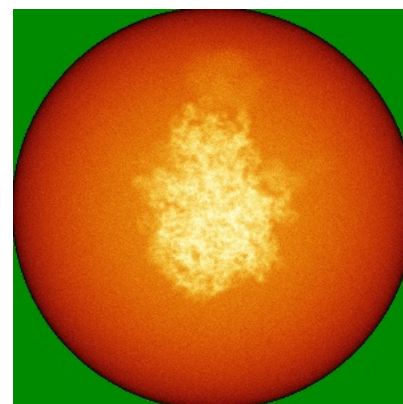
### 6.4.2 Raw map



X



Y

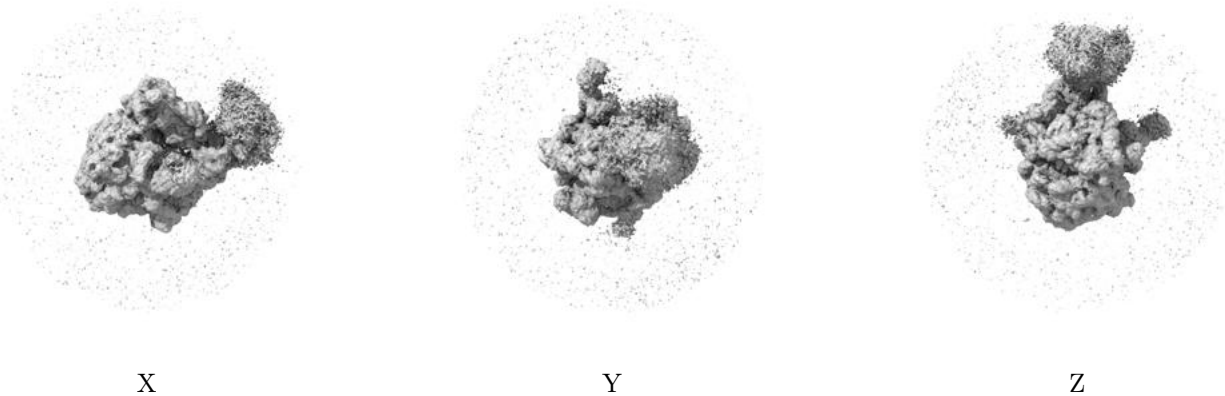


Z

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.

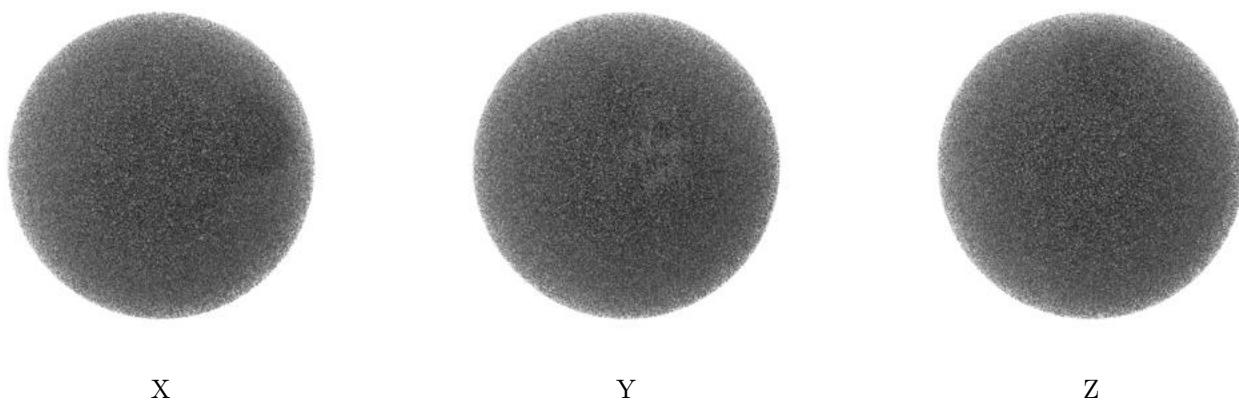
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0025. 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.

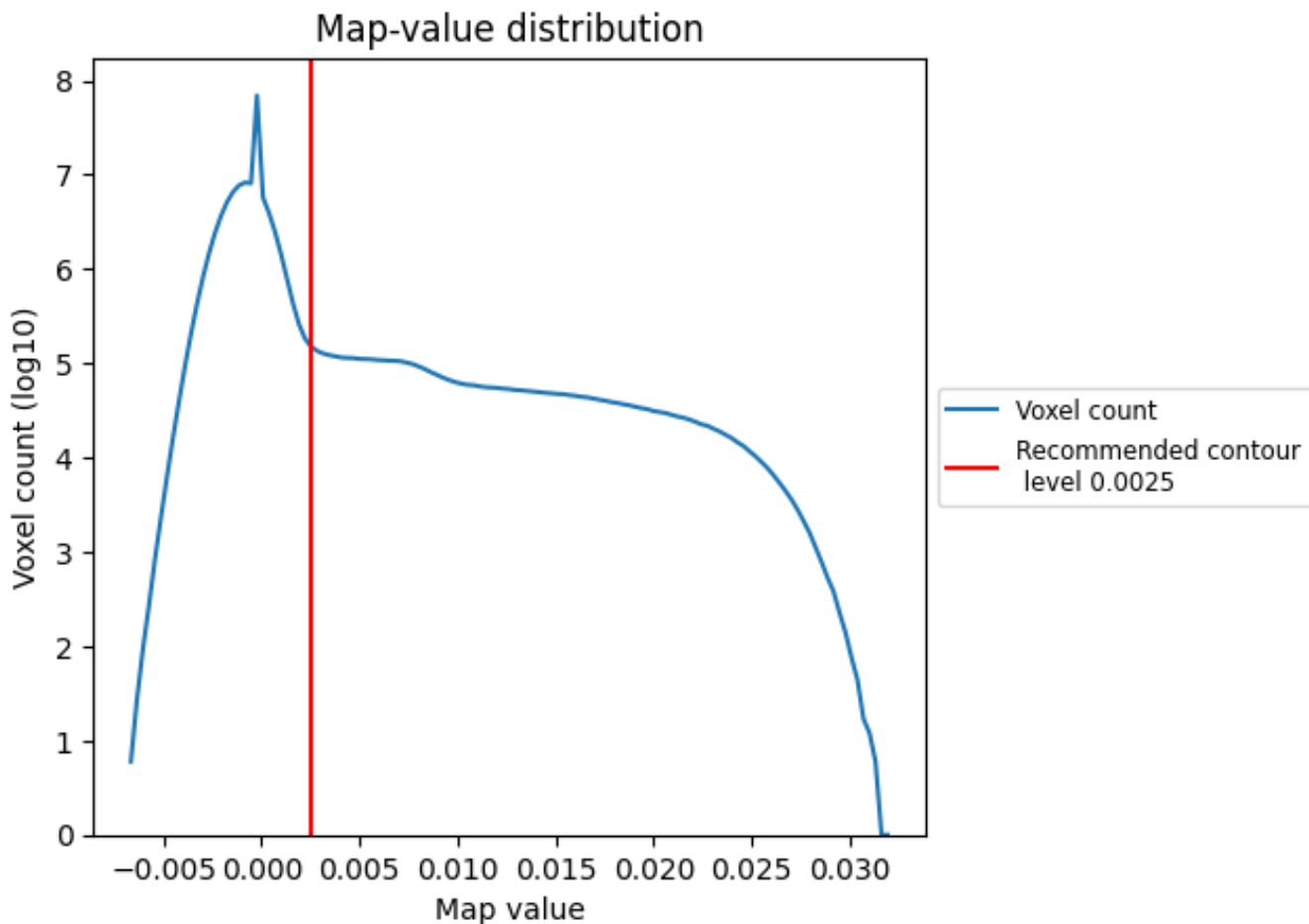
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

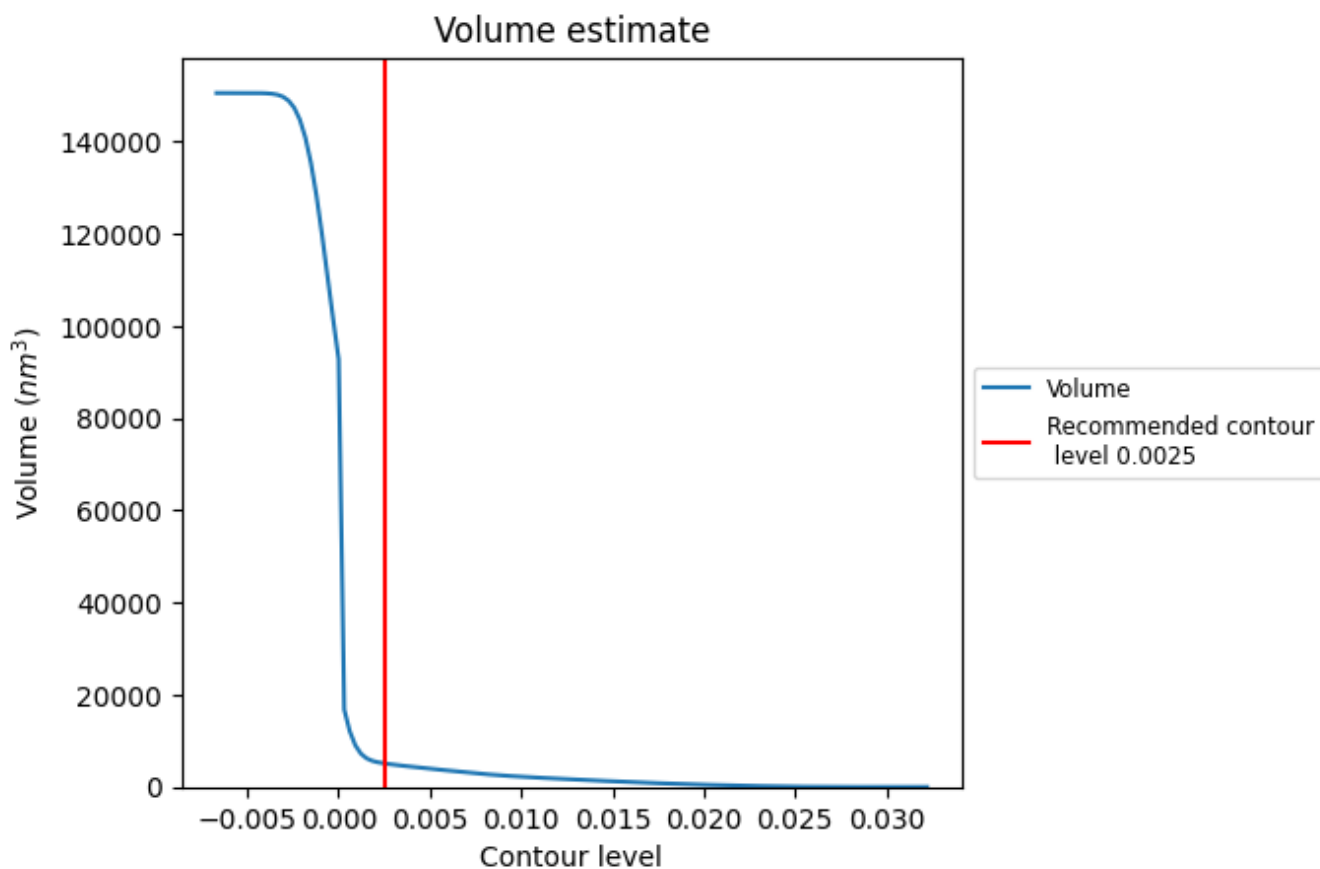
This section contains the results of statistical analysis of the map.

### 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.

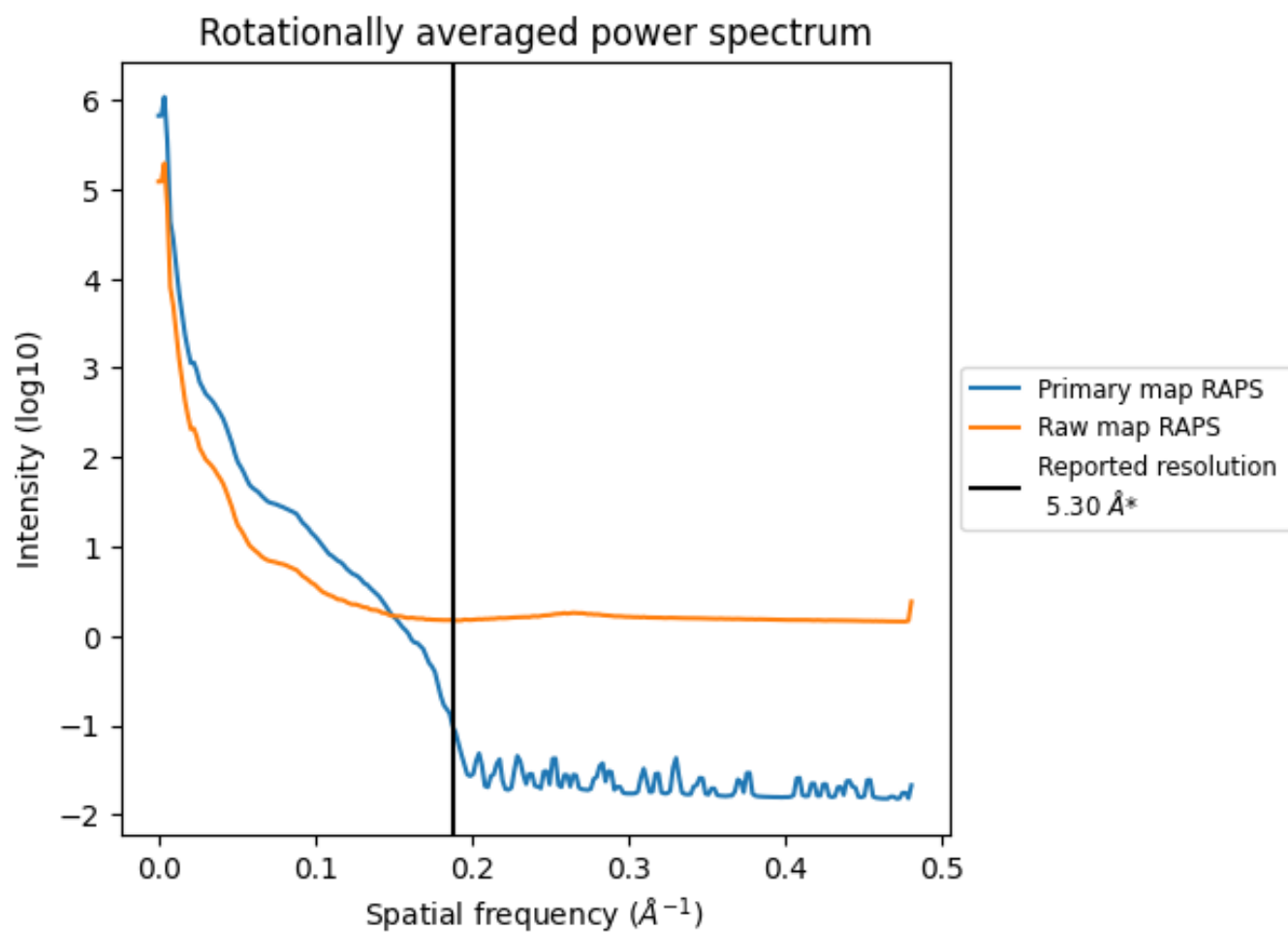
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 51200 nm<sup>3</sup>; this corresponds to an approximate mass of 4625 kDa.

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

### 7.3 Rotationally averaged power spectrum i

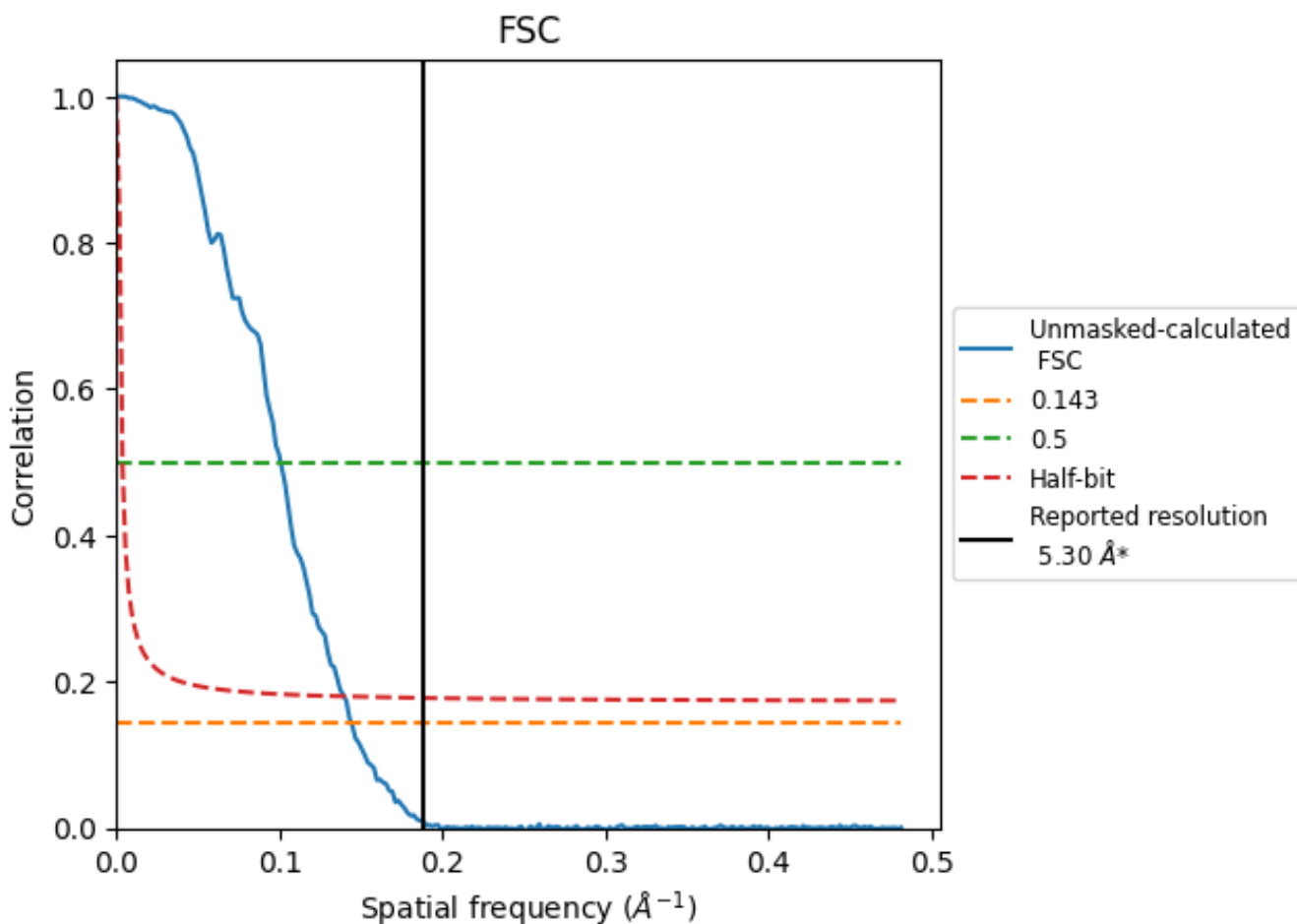


\*Reported resolution corresponds to spatial frequency of 0.189 Å<sup>-1</sup>

## 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 0.189 Å<sup>-1</sup>



## 8.2 Resolution estimates [i](#)

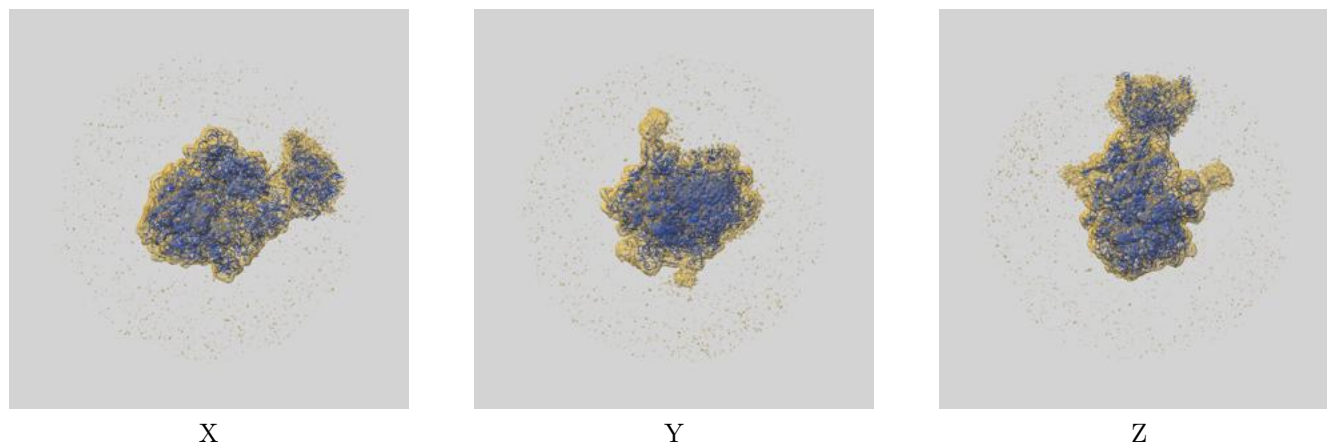
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.94	9.93	7.16

\*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 6.94 differs from the reported value 5.3 by more than 10 %

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

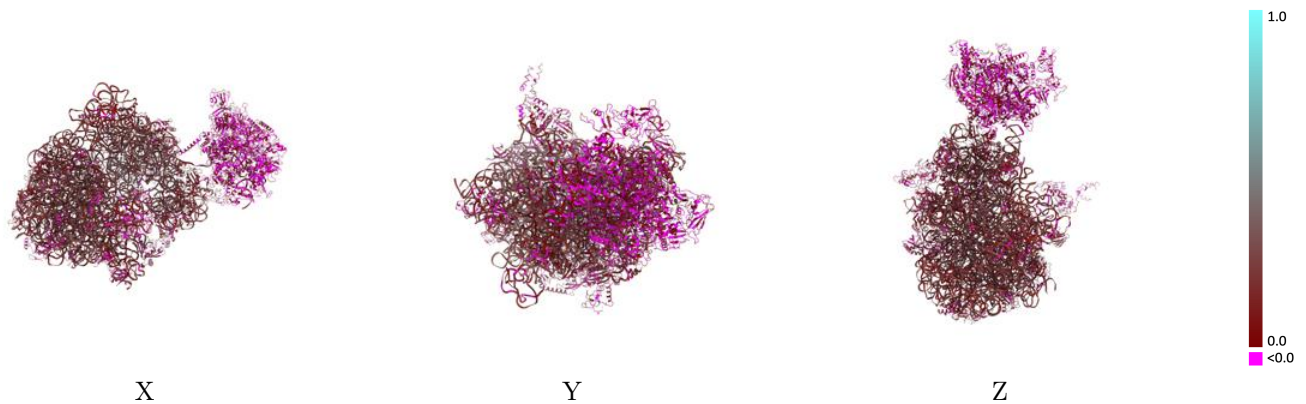
This section contains information regarding the fit between EMDB map EMD-42454 and PDB model 8UPR. Per-residue inclusion information can be found in section 3 on page 16.

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



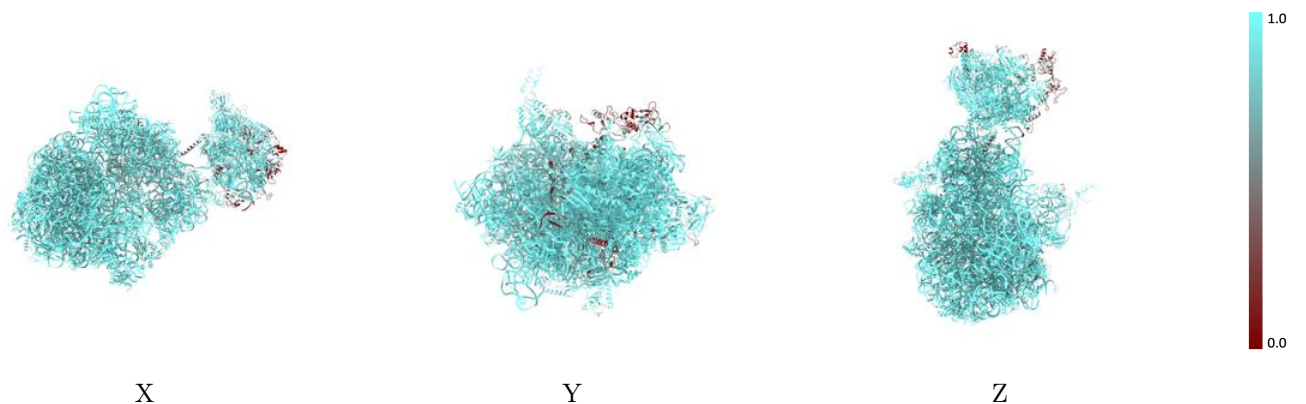
The images above show the 3D surface view of the map at the recommended contour level 0.0025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



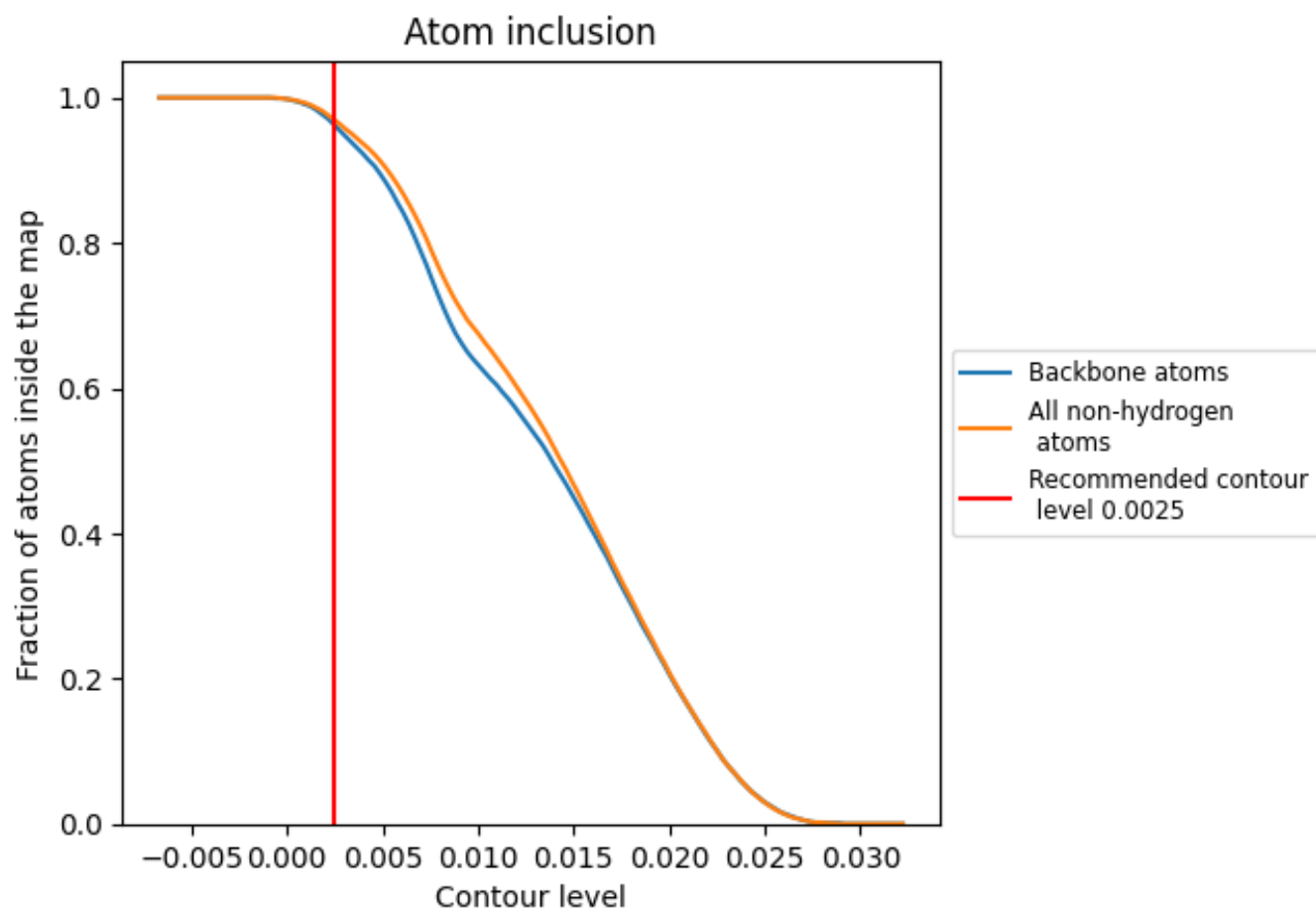
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0025).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 97% 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 (0.0025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9690	 0.1640
0	 0.9940	 0.1470
1	 0.9960	 0.1770
2	 0.9840	 0.1390
3	 0.9960	 0.1320
4	 0.9950	 0.1550
5	 0.8440	 0.0630
6	 0.8950	 0.0530
7	 0.9820	 0.0800
9	 0.9740	 0.0970
A	 1.0000	 0.1790
AA	 0.8530	 0.0180
AB	 0.7320	 0.0520
AC	 0.9780	 0.0280
AD	 0.9450	 0.0160
AE	 0.8920	 0.0320
AF	 0.7900	 0.0190
B	 0.9800	 0.1100
C	 0.9980	 0.1530
D	 0.9980	 0.2210
E	 0.9990	 0.1540
F	 0.9820	 0.1740
G	 0.9850	 0.1580
H	 0.9140	 0.0630
I	 0.9920	 0.1870
J	 0.9980	 0.1730
K	 0.9970	 0.2020
L	 1.0000	 0.1540
M	 0.9930	 0.1490
N	 0.9870	 0.1750
O	 0.9910	 0.1280
P	 1.0000	 0.1580
Q	 0.9970	 0.1510
R	 0.9980	 0.2050
S	 0.9970	 0.1650



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Chain	Atom inclusion	Q-score
T	 1.0000	 0.1490
U	 0.9980	 0.1610
V	 0.9910	 0.1670
W	 0.9750	 0.1230
X	 0.9930	 0.1390
Y	 0.9010	 0.0550
Z	 0.9690	 0.0340
a	 0.9990	 0.2090
b	 0.9970	 0.1270
c	 0.9920	 0.1580
d	 1.0000	 0.1810
e	 0.9920	 0.1320
f	 0.9930	 0.1740
g	 0.9940	 0.1140
h	 0.9930	 0.1500
i	 0.9910	 0.1870
j	 0.9960	 0.1550
k	 1.0000	 0.1360
l	 0.9890	 0.1340
m	 0.9940	 0.1680
n	 0.9880	 0.1240
o	 1.0000	 0.1240
p	 0.9980	 0.1480
q	 0.9970	 0.1410
r	 0.9660	 0.1120
s	 0.9960	 0.1710
t	 0.9900	 0.1740
u	 0.9940	 0.1280
v	 0.9920	 0.1800
w	 0.9950	 0.1510
x	 0.9820	 0.0900
y	 0.9940	 0.1690
z	 0.9970	 0.1390