



## wwPDB EM Validation Summary Report ⓘ

Aug 6, 2024 – 02:48 PM EDT

PDB ID : 8UPO  
EMDB ID : EMD-42453  
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 : 5.50 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) : 2.37.1

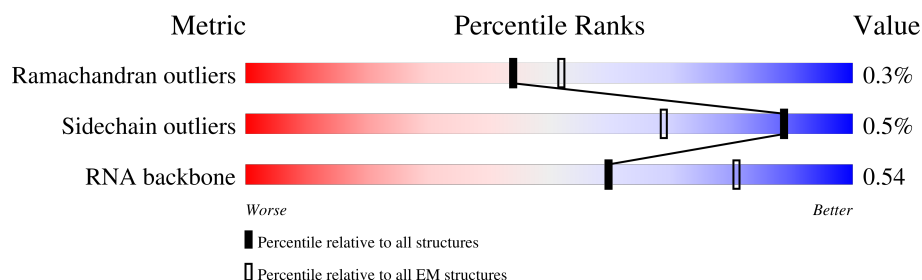
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 5.50 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.













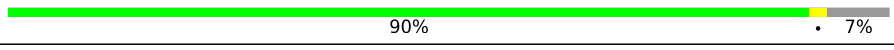
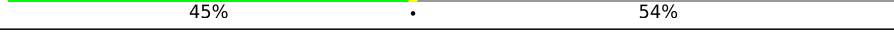



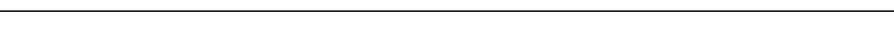
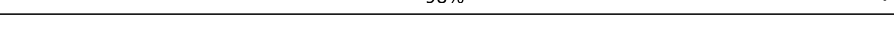
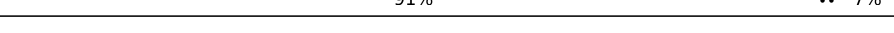


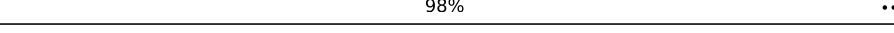
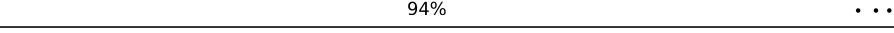
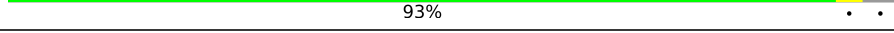

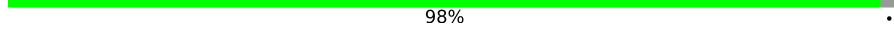
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	

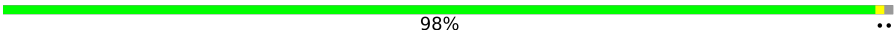
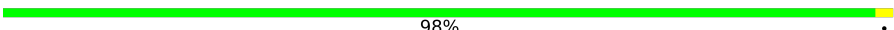


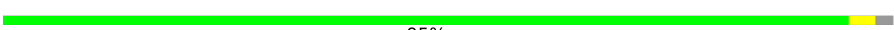





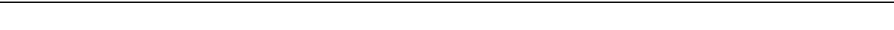

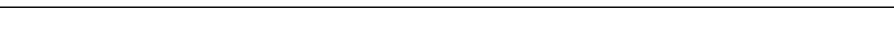
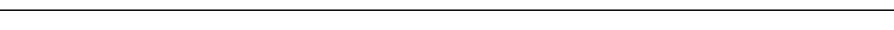
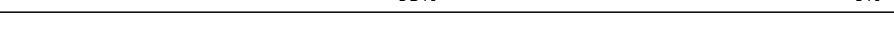
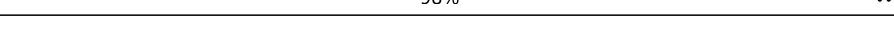
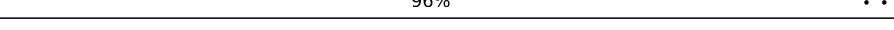
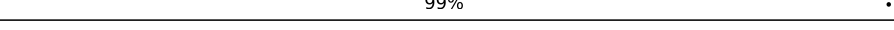
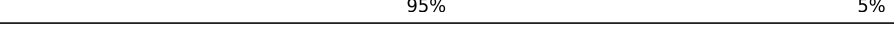
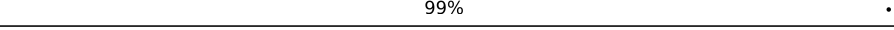
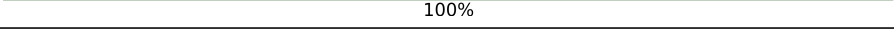
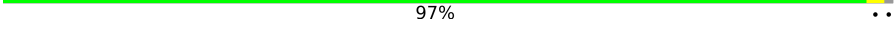
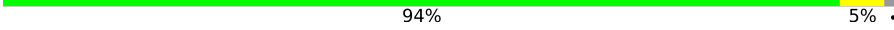
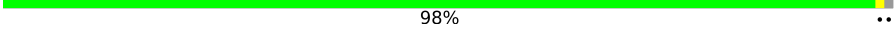

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Mol	Chain	Length	Quality of chain
9	9	165	
10	A	76	
10	B	76	
11	AA	1342	
12	AB	162	
13	AC	329	
13	AD	329	
14	AE	1407	
15	C	75	
16	D	1542	
17	E	87	
18	F	71	
19	G	241	
20	H	557	
21	I	233	
22	J	206	
23	K	167	
24	L	135	
25	M	179	
26	N	130	
27	O	130	
28	P	103	
29	Q	129	
30	R	124	
31	S	101	

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Mol	Chain	Length	Quality of chain
32	T	89	 98% ..
33	U	82	 98% .
34	V	84	 94% • 5%
35	W	92	 87% • 10%
36	X	118	 95% ..
37	Y	142	 7% 98% ...
38	Z	121	 25% 75%
39	a	2904	 80% 18% ..
40	b	85	 89% 11%
41	c	78	 96% ..
42	d	120	 88% 12%
43	e	63	 95% ..
44	f	59	 97% ..
45	g	70	 93% • 6%
46	h	273	 98% ..
47	i	57	 96% ..
48	j	209	 99% .
49	k	55	 95% 5%
50	l	201	 99% .
51	m	46	 100%
52	n	179	 97% ..
53	o	65	 94% 5% .
54	p	177	 98% ..
55	q	38	 100%
56	r	149	 100%

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

## 2 Entry composition [i](#)

There are 66 unique types of molecules in this entry. The entry contains 274307 atoms, of which 98638 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
1	0	103	Total	C	H	N	O	S	0	0
			1655	516	839	153	145	2		

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms						AltConf	Trace
6	5	26	Total	C	N	O	P		0	0
			543	254	109	154	26			

- Molecule 7 is a DNA chain called T DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	26	Total	C	N	O	P	0	0
			517	247	83	161	26		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	28	Total	C	N	O	P	0	0
			592	264	92	208	28		

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

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

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

Mol	Chain	Residues	Atoms						AltConf	Trace
10	A	76	Total 2446	C 723	H 826	N 295	O 527	P 75	0	0
10	B	76	Total 2433	C 723	H 813	N 295	O 527	P 75	0	0

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AB	94	Total	C	N	O	S	0	0
			754	484	136	131	3		

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

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

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

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

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

- Molecule 15 is a protein called 30S ribosomal protein S18.

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

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

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

- Molecule 17 is a protein called 30S ribosomal protein S20.

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

- Molecule 18 is a protein called 30S ribosomal protein S21.

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

- Molecule 19 is a protein called 30S ribosomal protein S2.

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

- Molecule 20 is a protein called 30S ribosomal protein S1.



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

- Molecule 21 is a protein called 30S ribosomal protein S3.

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

- Molecule 22 is a protein called 30S ribosomal protein S4.

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

- Molecule 23 is a protein called 30S ribosomal protein S5.

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

- Molecule 24 is a protein called 30S ribosomal protein S6.

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

- Molecule 25 is a protein called 30S ribosomal protein S7.

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

- Molecule 26 is a protein called 30S ribosomal protein S8.

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

- Molecule 27 is a protein called 30S ribosomal protein S9.

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

- Molecule 28 is a protein called 30S ribosomal protein S10.

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

- Molecule 29 is a protein called 30S ribosomal protein S11.

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

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

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

- Molecule 31 is a protein called 30S ribosomal protein S14.

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

- Molecule 32 is a protein called 30S ribosomal protein S15.

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

- Molecule 33 is a protein called 30S ribosomal protein S16.

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

- Molecule 34 is a protein called 30S ribosomal protein S17.

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

- Molecule 35 is a protein called 30S ribosomal protein S19.

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

- Molecule 36 is a protein called 30S ribosomal protein S13.

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

- Molecule 37 is a protein called 50S ribosomal protein L11.

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

- Molecule 38 is a protein called 50S ribosomal protein L7/L12.

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

- Molecule 39 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	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 40 is a protein called 50S ribosomal protein L27.

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

- Molecule 41 is a protein called 50S ribosomal protein L28.

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

- Molecule 42 is a RNA chain called 5S rRNA.

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

- Molecule 43 is a protein called 50S ribosomal protein L29.

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

- Molecule 44 is a protein called 50S ribosomal protein L30.

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

- Molecule 45 is a protein called 50S ribosomal protein L31.

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

- Molecule 46 is a protein called 50S ribosomal protein L2.

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

- Molecule 47 is a protein called 50S ribosomal protein L32.

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

- Molecule 48 is a protein called 50S ribosomal protein L3.

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

- Molecule 49 is a protein called 50S ribosomal protein L33.

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

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

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

- Molecule 51 is a protein called 50S ribosomal protein L34.

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

- Molecule 52 is a protein called 50S ribosomal protein L5.

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

- Molecule 53 is a protein called 50S ribosomal protein L35.

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

- Molecule 54 is a protein called 50S ribosomal protein L6.

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

- Molecule 55 is a protein called 50S ribosomal protein L36.

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

- Molecule 56 is a protein called 50S ribosomal protein L9.

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

- Molecule 57 is a protein called 50S ribosomal protein L13.

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

- Molecule 58 is a protein called 50S ribosomal protein L14.

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

- Molecule 59 is a protein called 50S ribosomal protein L15.

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

- Molecule 60 is a protein called 50S ribosomal protein L16.

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

- Molecule 61 is a protein called 50S ribosomal protein L17.

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

- Molecule 62 is a protein called 50S ribosomal protein L18.

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

- Molecule 63 is a protein called 50S ribosomal protein L19.

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

- Molecule 64 is a protein called 50S ribosomal protein L20.

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

- Molecule 65 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

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

- Molecule 66 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

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

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

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

- Molecule 1: Ribosomal protein L21

Chain 0:  100%


There are no outlier residues recorded for this chain.

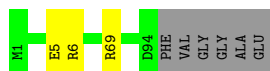
- Molecule 2: 50S ribosomal protein L22

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

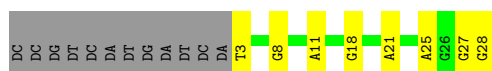
Chain 4:  98%



- Molecule 6: NT DNA with ops signal

Chain 5:  47% 21% 32%

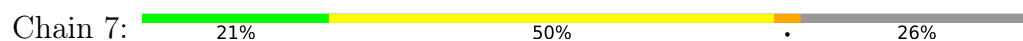




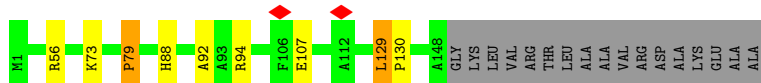
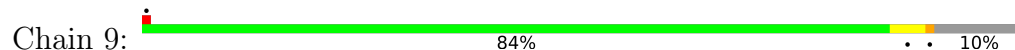
- Molecule 7: T DNA



- Molecule 8: mRNA with 21 nt long spacer



- Molecule 9: 50S ribosomal protein L10



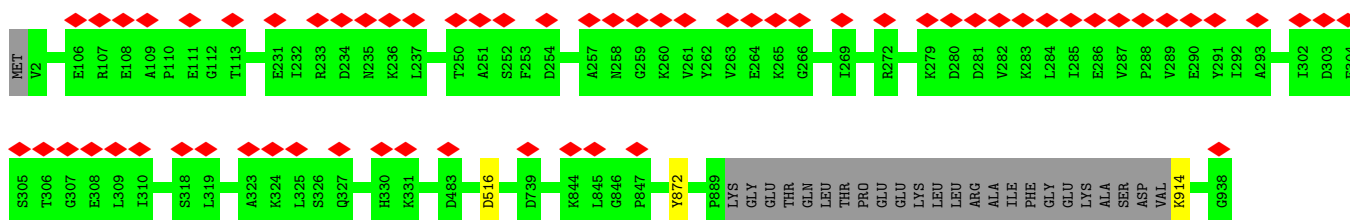
- Molecule 10: E-site and P-site tRNA (fMet)

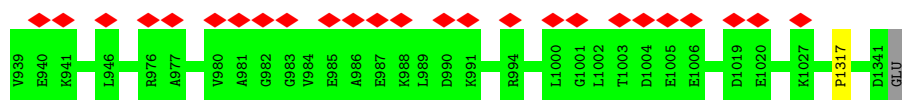


- Molecule 10: E-site and P-site tRNA (fMet)

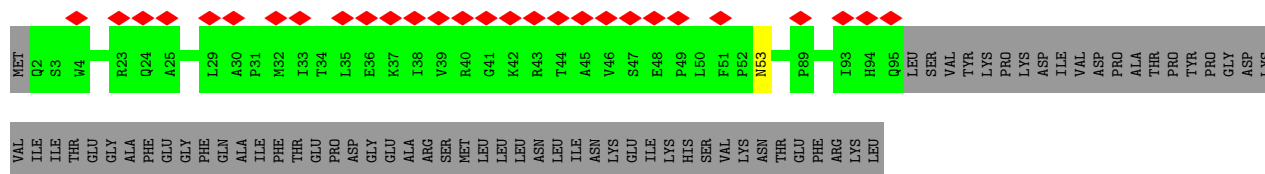


- Molecule 11: DNA-directed RNA polymerase subunit beta

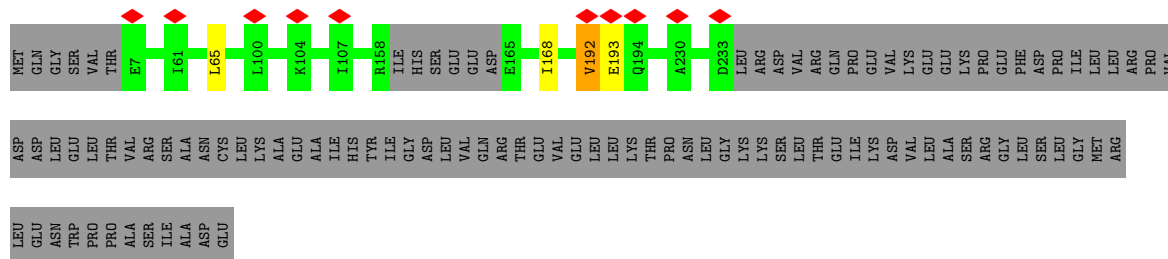




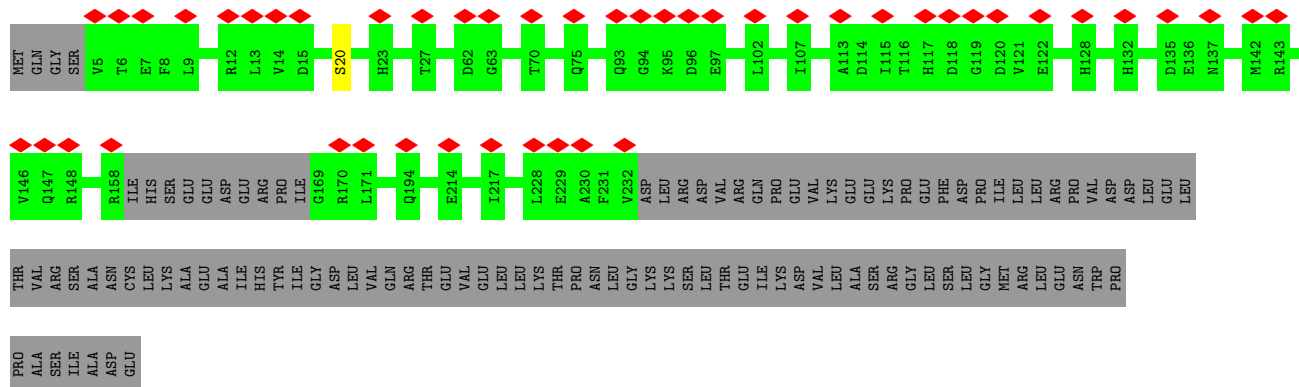
• Molecule 12: Transcription antitermination protein RfaH



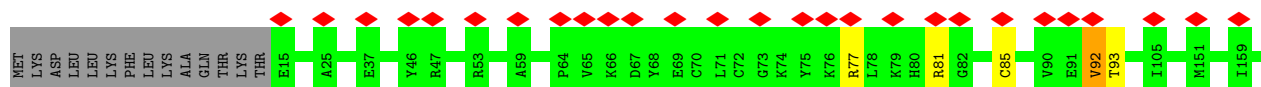
• Molecule 13: DNA-directed RNA polymerase subunit alpha

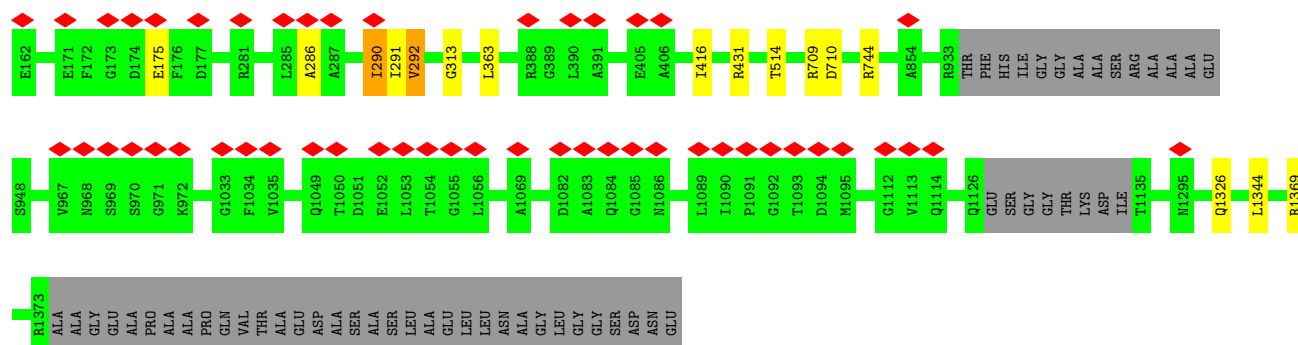


• Molecule 13: DNA-directed RNA polymerase subunit alpha



• Molecule 14: DNA-directed RNA polymerase subunit beta'





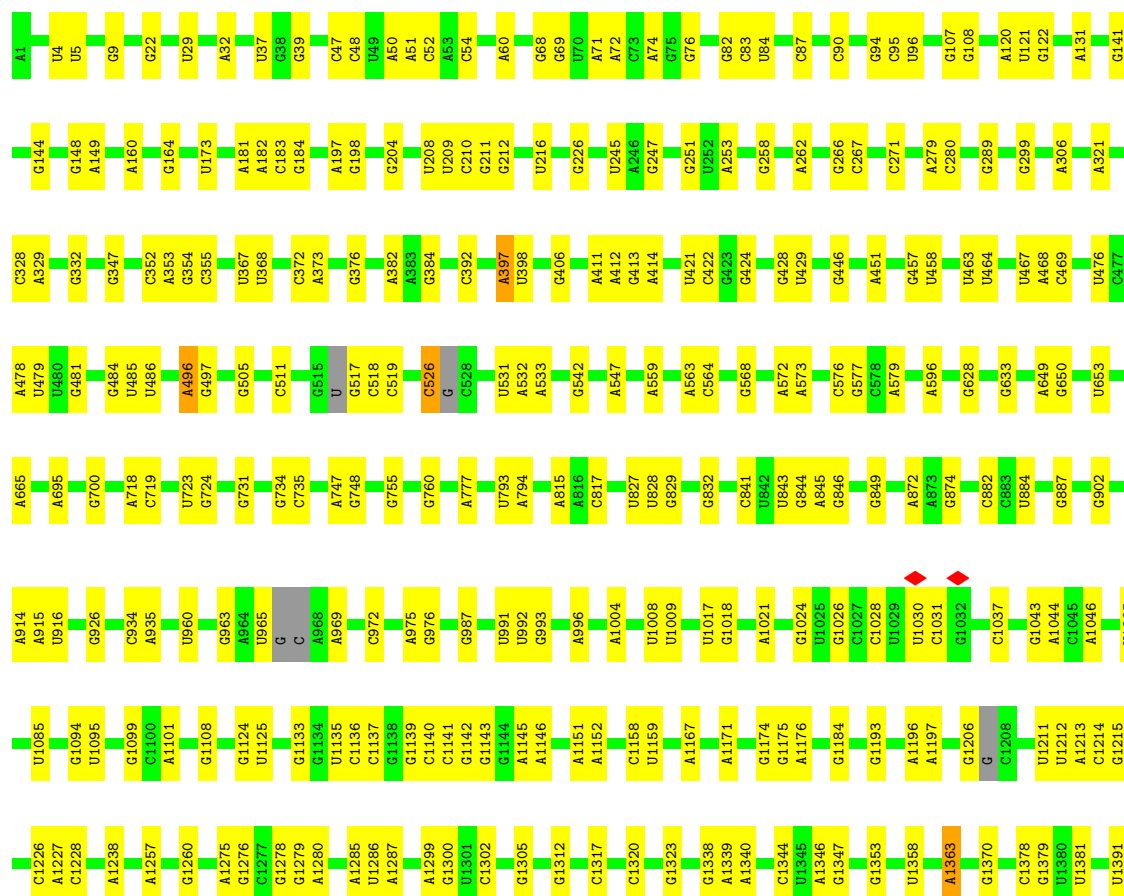
• Molecule 15: 30S ribosomal protein S18

Chain C: 84% 12%



• Molecule 16: 16S rRNA

Chain D: 79% 20%



- Molecule 17: 30S ribosomal protein S20

Chain E: 



- Molecule 18: 30S ribosomal protein S21

Chain F:  99%



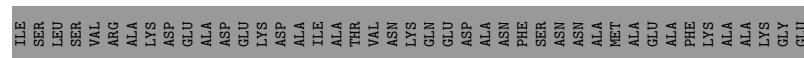
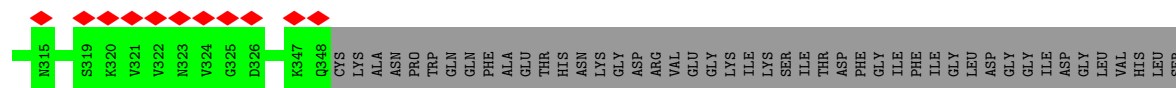
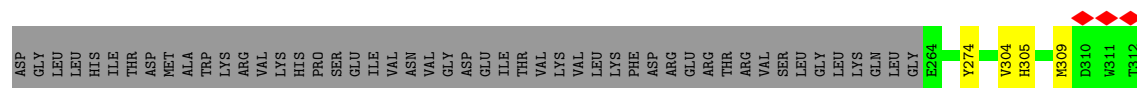
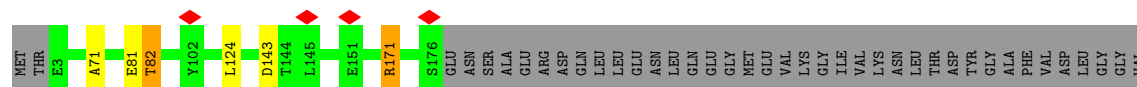
- Molecule 19: 30S ribosomal protein S2

Chain G:  90% • 7%




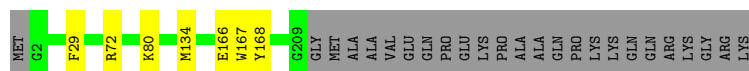
- Molecule 20: 30S ribosomal protein S1

Chain H:  45% 54%



- Molecule 21: 30S ribosomal protein S3

Chain I:  86% 11%




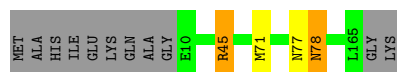
- Molecule 22: 30S ribosomal protein S4

Chain J:  98%



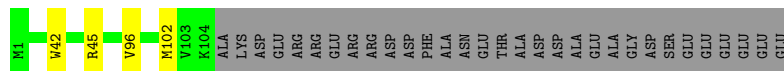
- Molecule 23: 30S ribosomal protein S5

Chain K:  91% 7%




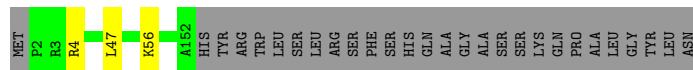
- Molecule 24: 30S ribosomal protein S6

Chain L:  74% 23%



- Molecule 25: 30S ribosomal protein S7

Chain M:  83% 16%



- Molecule 26: 30S ribosomal protein S8

Chain N:  98%



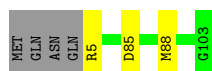
- Molecule 27: 30S ribosomal protein S9

Chain O:  94%




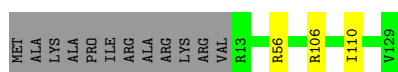
- Molecule 28: 30S ribosomal protein S10

Chain P:  93% . .



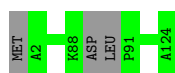
- Molecule 29: 30S ribosomal protein S11

Chain Q:  88% . 9%



- Molecule 30: 30S ribosomal protein S12

Chain R:  98% .



- Molecule 31: 30S ribosomal protein S14

Chain S:  98% ..



- Molecule 32: 30S ribosomal protein S15

Chain T:  98% ..



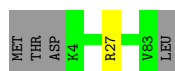
- Molecule 33: 30S ribosomal protein S16

Chain U:  98% .



- Molecule 34: 30S ribosomal protein S17

Chain V:  94% . 5%



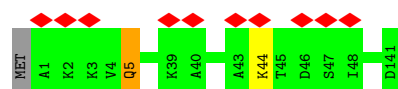
- Molecule 35: 30S ribosomal protein S19

Sequence logo for the 1000bp upstream region of the P2 promoter. The y-axis represents information content in bits, ranging from 0.00 to 0.12. The x-axis shows positions from -1000 to +1000. The sequence logo shows a strong consensus for the P2 promoter sequence: MET (position -1000), P2 (position -900), I40 (position -800), V62 (position -700), M66 (position -600), A84 (position -500), and a series of LYS residues (positions -400 to +100). The P2, I40, and A84 motifs are highlighted in yellow, while the LYS residues are highlighted in green.

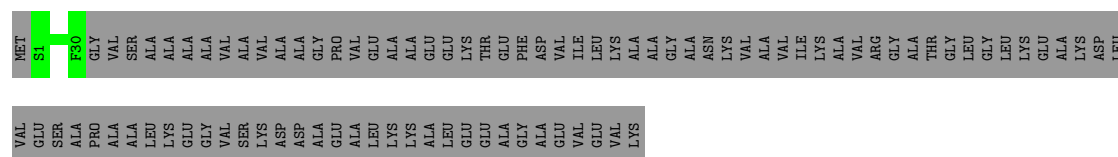
- Chain X:  95%



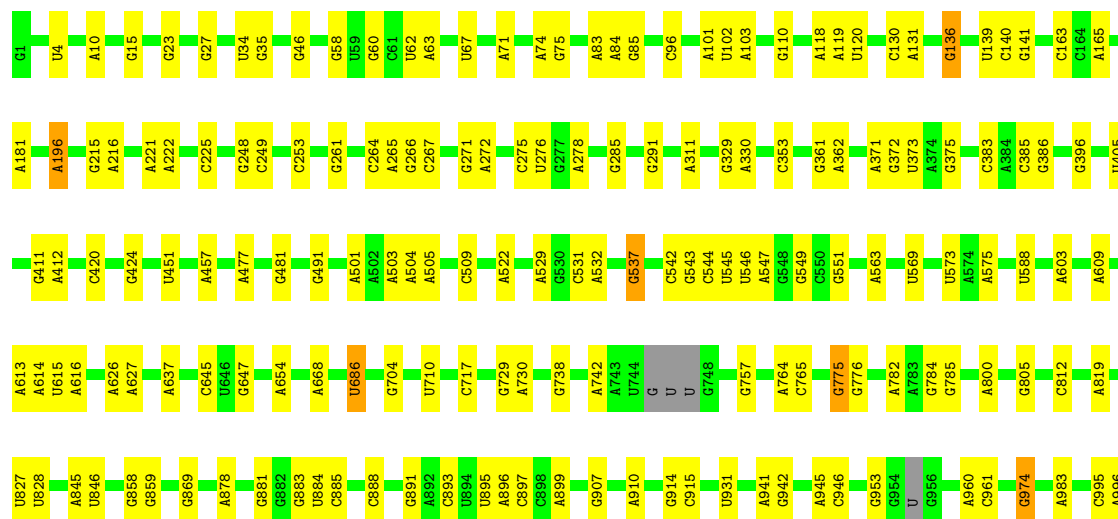
- Chain Y:  7% 98%

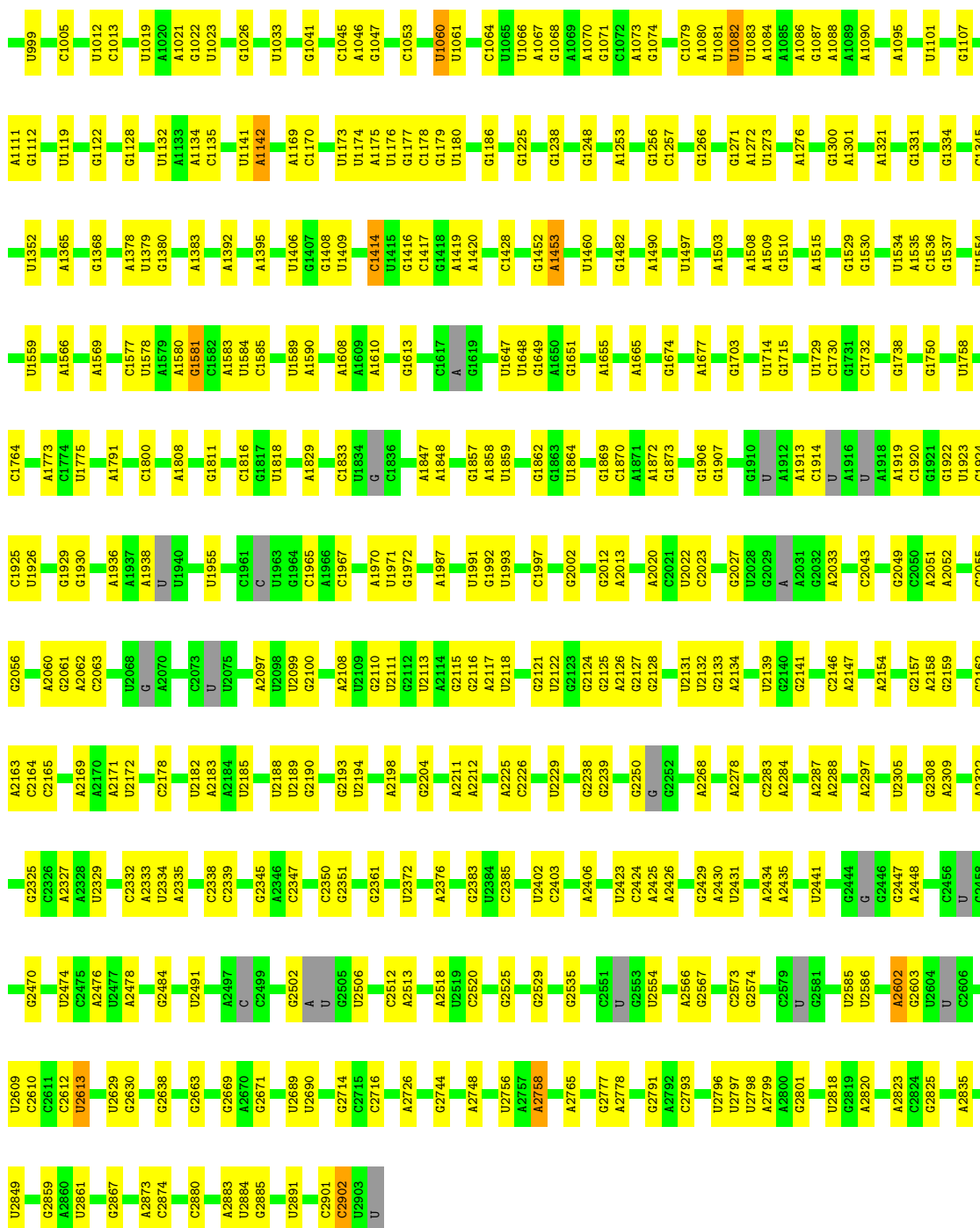


- Chain Z:  25% 75%



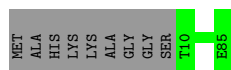
- Chain a:  80% 18% ..





- Molecule 40: 50S ribosomal protein L27

Chain b:




- Molecule 41: 50S ribosomal protein L28



Chain c:  96% ..



- Molecule 42: 5S rRNA

Chain d:  88% 12%



- Molecule 43: 50S ribosomal protein L29

Chain e:  95% ..



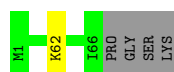
- Molecule 44: 50S ribosomal protein L30

Chain f:  97% ..



- Molecule 45: 50S ribosomal protein L31

Chain g:  93% 6%



- Molecule 46: 50S ribosomal protein L2

Chain h:  98% ..



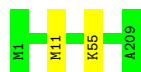
- Molecule 47: 50S ribosomal protein L32

Chain i:  96% ..



- Molecule 48: 50S ribosomal protein L3

Chain j:  99% .



- Molecule 49: 50S ribosomal protein L33

Chain k:  95% 5%



- Molecule 50: 50S ribosomal protein L4

Chain l:  99% .



- Molecule 51: 50S ribosomal protein L34

Chain m:  100%

There are no outlier residues recorded for this chain.

- Molecule 52: 50S ribosomal protein L5

Chain n:  97% ..



- Molecule 53: 50S ribosomal protein L35

Chain o:  94% 5% .



- Molecule 54: 50S ribosomal protein L6

Chain p:  98% ..



- Molecule 55: 50S ribosomal protein L36

Chain q:  100%

There are no outlier residues recorded for this chain.

- Molecule 56: 50S ribosomal protein L9

Chain r:  100%

There are no outlier residues recorded for this chain.

- Molecule 57: 50S ribosomal protein L13

Chain s:  97% ..



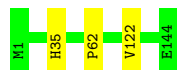
- Molecule 58: 50S ribosomal protein L14

Chain t:  97% .



- Molecule 59: 50S ribosomal protein L15

Chain u:  98% .

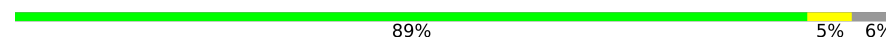


- Molecule 60: 50S ribosomal protein L16

Chain v:  99% .



- Molecule 61: 50S ribosomal protein L17

Chain w:  89% 5% 6%



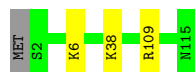
- Molecule 62: 50S ribosomal protein L18

Chain x:  99% .



- Molecule 63: 50S ribosomal protein L19

Chain y:  97% ..



- Molecule 64: 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	1720	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	0.033	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 (Å)	531.968, 531.968, 531.968	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.039, 1.039, 1.039	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, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	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	6/611 (1.0%)	1.07	2/943 (0.2%)
7	6	1.17	5/574 (0.9%)	1.02	0/880
8	7	0.39	1/658 (0.2%)	0.83	3/1020 (0.3%)
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	0.57	2/1810 (0.1%)	1.27	14/2821 (0.5%)
11	AA	0.43	0/10547	0.60	1/14232 (0.0%)
12	AB	0.33	0/773	0.64	0/1051
13	AC	0.41	0/1718	0.62	0/2328
13	AD	0.36	0/1696	0.62	0/2298
14	AE	0.41	0/10561	0.63	3/14258 (0.0%)
15	C	0.70	0/553	0.92	4/743 (0.5%)
16	D	0.59	14/36610 (0.0%)	1.03	67/57091 (0.1%)
17	E	0.57	0/675	0.71	0/895
18	F	0.62	0/597	0.59	0/792
19	G	0.66	2/1791 (0.1%)	0.83	7/2413 (0.3%)
20	H	0.43	0/1746	0.70	0/2382
21	I	0.62	2/1663 (0.1%)	0.71	4/2241 (0.2%)
22	J	0.54	2/1665 (0.1%)	0.59	0/2227
23	K	0.69	1/1165 (0.1%)	0.86	5/1568 (0.3%)
24	L	0.79	3/867 (0.3%)	0.82	3/1171 (0.3%)
25	M	0.54	0/1195	0.70	2/1602 (0.1%)
26	N	0.52	0/989	0.63	1/1326 (0.1%)
27	O	0.67	4/1034 (0.4%)	0.82	4/1375 (0.3%)
28	P	0.52	0/800	0.70	2/1082 (0.2%)
29	Q	0.71	1/893 (0.1%)	0.82	4/1205 (0.3%)
30	R	0.56	0/952	0.65	0/1274

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
31	S	0.63	1/817 (0.1%)	0.64	0/1088
32	T	0.56	0/722	0.72	1/964 (0.1%)
33	U	0.45	0/659	0.65	1/884 (0.1%)
34	V	0.57	0/657	0.70	0/881
35	W	0.56	1/680 (0.1%)	0.69	3/915 (0.3%)
36	X	0.48	0/909	0.72	1/1215 (0.1%)
37	Y	0.42	1/1046 (0.1%)	0.57	1/1410 (0.1%)
38	Z	0.23	0/227	0.38	0/304
39	a	0.61	14/69247 (0.0%)	1.03	129/107985 (0.1%)
40	b	0.47	0/589	0.57	0/779
41	c	0.56	1/635 (0.2%)	0.66	1/848 (0.1%)
42	d	0.50	0/2872	0.95	0/4478
43	e	0.81	2/502 (0.4%)	0.66	0/667
44	f	0.53	0/452	0.72	2/605 (0.3%)
45	g	0.50	1/531 (0.2%)	0.67	1/709 (0.1%)
46	h	0.53	2/2121 (0.1%)	0.67	6/2852 (0.2%)
47	i	0.42	0/450	0.64	1/599 (0.2%)
48	j	0.53	0/1586	0.64	2/2134 (0.1%)
49	k	0.51	0/433	0.68	0/576
50	l	0.54	1/1571 (0.1%)	0.64	1/2113 (0.0%)
51	m	0.43	0/380	0.60	0/498
52	n	0.51	0/1434	0.68	2/1926 (0.1%)
53	o	0.51	0/513	0.85	1/676 (0.1%)
54	p	0.50	0/1333	0.68	3/1805 (0.2%)
55	q	0.46	0/303	0.61	0/397
56	r	0.34	0/1122	0.52	0/1515
57	s	0.83	5/1152 (0.4%)	0.81	4/1551 (0.3%)
58	t	0.55	1/955 (0.1%)	0.89	5/1279 (0.4%)
59	u	0.47	1/1062 (0.1%)	0.63	0/1413
60	v	0.61	1/1093 (0.1%)	0.75	1/1460 (0.1%)
61	w	0.90	5/964 (0.5%)	0.95	9/1289 (0.7%)
62	x	0.42	0/902	0.57	0/1209
63	y	0.46	0/929	0.59	1/1242 (0.1%)
64	z	0.63	1/960 (0.1%)	0.60	0/1278
All	All	0.58	85/188899 (0.0%)	0.92	317/278462 (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

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	#Chirality outliers	#Planarity outliers
13	AC	0	1
13	AD	0	1
14	AE	0	4
19	G	0	1
20	H	0	5
21	I	0	1
23	K	0	2
27	O	0	1
36	X	0	1
37	Y	0	1
52	n	0	1
53	o	0	1
57	s	0	1
59	u	0	2
All	All	0	26

The worst 5 of 85 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
61	w	35	LYS	CE-NZ	-15.23	1.10	1.49
24	L	42	TRP	CB-CG	-12.39	1.27	1.50
3	2	5	GLU	CG-CD	-11.56	1.34	1.51
43	e	46	VAL	CB-CG1	-11.29	1.29	1.52
61	w	42	LYS	CD-CE	-10.81	1.24	1.51

The worst 5 of 317 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	a	1019	U	C5-C4-O4	30.76	144.35	125.90
39	a	1141	U	C5-C4-O4	29.53	143.62	125.90
16	D	37	U	C5-C4-O4	29.49	143.59	125.90
16	D	1358	U	C5-C4-O4	29.24	143.44	125.90
16	D	827	U	C5-C4-O4	28.63	143.08	125.90

There are no chirality outliers.

5 of 26 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	9	107	GLU	Peptide
9	9	79	PRO	Peptide
9	9	92	ALA	Peptide

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Mol	Chain	Res	Type	Group
13	AC	192	VAL	Peptide
13	AD	20	SER	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	36
11	AA	1312/1342 (98%)	1198 (91%)	113 (9%)	1 (0%)	51	85
12	AB	92/162 (57%)	70 (76%)	21 (23%)	1 (1%)	14	51
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%)	1212 (91%)	114 (9%)	5 (0%)	34	72
15	C	64/75 (85%)	63 (98%)	1 (2%)	0	100	100
17	E	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
18	F	68/71 (96%)	68 (100%)	0	0	100	100
19	G	223/241 (92%)	213 (96%)	9 (4%)	1 (0%)	34	72
20	H	255/557 (46%)	182 (71%)	66 (26%)	7 (3%)	5	31
21	I	206/233 (88%)	193 (94%)	12 (6%)	1 (0%)	29	69

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	J	203/206 (98%)	201 (99%)	2 (1%)	0	100	100
23	K	154/167 (92%)	145 (94%)	8 (5%)	1 (1%)	25	65
24	L	102/135 (76%)	97 (95%)	4 (4%)	1 (1%)	15	53
25	M	149/179 (83%)	140 (94%)	8 (5%)	1 (1%)	22	62
26	N	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
27	O	125/130 (96%)	116 (93%)	8 (6%)	1 (1%)	19	59
28	P	97/103 (94%)	89 (92%)	8 (8%)	0	100	100
29	Q	115/129 (89%)	107 (93%)	8 (7%)	0	100	100
30	R	117/124 (94%)	112 (96%)	5 (4%)	0	100	100
31	S	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
32	T	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
33	U	80/82 (98%)	76 (95%)	4 (5%)	0	100	100
34	V	78/84 (93%)	74 (95%)	4 (5%)	0	100	100
35	W	81/92 (88%)	80 (99%)	1 (1%)	0	100	100
36	X	114/118 (97%)	103 (90%)	9 (8%)	2 (2%)	8	40
37	Y	139/142 (98%)	101 (73%)	38 (27%)	0	100	100
38	Z	28/121 (23%)	22 (79%)	6 (21%)	0	100	100
40	b	74/85 (87%)	73 (99%)	1 (1%)	0	100	100
41	c	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
43	e	60/63 (95%)	57 (95%)	3 (5%)	0	100	100
44	f	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
45	g	64/70 (91%)	62 (97%)	2 (3%)	0	100	100
46	h	269/273 (98%)	254 (94%)	15 (6%)	0	100	100
47	i	54/57 (95%)	49 (91%)	5 (9%)	0	100	100
48	j	207/209 (99%)	198 (96%)	9 (4%)	0	100	100
49	k	50/55 (91%)	50 (100%)	0	0	100	100
50	l	199/201 (99%)	188 (94%)	11 (6%)	0	100	100
51	m	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
52	n	175/179 (98%)	161 (92%)	13 (7%)	1 (1%)	25	65
53	o	62/65 (95%)	57 (92%)	4 (6%)	1 (2%)	9	43
54	p	173/177 (98%)	162 (94%)	11 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
55	q	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
56	r	147/149 (99%)	139 (95%)	8 (5%)	0	100	100
57	s	140/142 (99%)	133 (95%)	7 (5%)	0	100	100
58	t	121/123 (98%)	114 (94%)	7 (6%)	0	100	100
59	u	142/144 (99%)	134 (94%)	8 (6%)	0	100	100
60	v	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
61	w	117/127 (92%)	112 (96%)	5 (4%)	0	100	100
62	x	114/117 (97%)	107 (94%)	7 (6%)	0	100	100
63	y	112/115 (97%)	105 (94%)	7 (6%)	0	100	100
64	z	115/118 (98%)	111 (96%)	4 (4%)	0	100	100
All	All	9339/10467 (89%)	8625 (92%)	685 (7%)	29 (0%)	44	76

5 of 29 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
19	G	127	ASP
20	H	304	VAL
25	M	56	LYS
53	o	32	ILE
14	AE	92	VAL

### 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	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
5	4	78/78 (100%)	78 (100%)	0	100	100
9	9	112/123 (91%)	109 (97%)	3 (3%)	44	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	AA	1135/1157 (98%)	1133 (100%)	2 (0%)	93	96
12	AB	82/142 (58%)	82 (100%)	0	100	100
13	AC	186/286 (65%)	184 (99%)	2 (1%)	73	84
13	AD	185/286 (65%)	185 (100%)	0	100	100
14	AE	1122/1168 (96%)	1110 (99%)	12 (1%)	73	84
15	C	57/65 (88%)	57 (100%)	0	100	100
17	E	65/66 (98%)	65 (100%)	0	100	100
18	F	60/61 (98%)	60 (100%)	0	100	100
19	G	187/199 (94%)	186 (100%)	1 (0%)	88	93
20	H	137/461 (30%)	137 (100%)	0	100	100
21	I	171/190 (90%)	170 (99%)	1 (1%)	86	91
22	J	172/173 (99%)	171 (99%)	1 (1%)	86	91
23	K	119/126 (94%)	119 (100%)	0	100	100
24	L	91/116 (78%)	91 (100%)	0	100	100
25	M	124/147 (84%)	124 (100%)	0	100	100
26	N	104/105 (99%)	104 (100%)	0	100	100
27	O	105/107 (98%)	104 (99%)	1 (1%)	76	86
28	P	86/90 (96%)	85 (99%)	1 (1%)	71	84
29	Q	90/99 (91%)	90 (100%)	0	100	100
30	R	101/104 (97%)	101 (100%)	0	100	100
31	S	83/84 (99%)	83 (100%)	0	100	100
32	T	76/77 (99%)	76 (100%)	0	100	100
33	U	65/65 (100%)	64 (98%)	1 (2%)	65	80
34	V	74/78 (95%)	73 (99%)	1 (1%)	67	80
35	W	72/79 (91%)	72 (100%)	0	100	100
36	X	94/96 (98%)	94 (100%)	0	100	100
37	Y	109/110 (99%)	108 (99%)	1 (1%)	78	88
38	Z	26/85 (31%)	26 (100%)	0	100	100
40	b	58/63 (92%)	58 (100%)	0	100	100
41	c	67/68 (98%)	67 (100%)	0	100	100
43	e	54/55 (98%)	54 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
44	f	48/49 (98%)	48 (100%)	0	100	100
45	g	59/62 (95%)	59 (100%)	0	100	100
46	h	216/218 (99%)	216 (100%)	0	100	100
47	i	47/48 (98%)	47 (100%)	0	100	100
48	j	164/164 (100%)	164 (100%)	0	100	100
49	k	47/49 (96%)	47 (100%)	0	100	100
50	l	165/165 (100%)	164 (99%)	1 (1%)	86	91
51	m	38/38 (100%)	38 (100%)	0	100	100
52	n	148/150 (99%)	148 (100%)	0	100	100
53	o	51/52 (98%)	51 (100%)	0	100	100
54	p	136/138 (99%)	136 (100%)	0	100	100
55	q	34/34 (100%)	34 (100%)	0	100	100
56	r	114/114 (100%)	114 (100%)	0	100	100
57	s	116/116 (100%)	115 (99%)	1 (1%)	78	88
58	t	104/104 (100%)	103 (99%)	1 (1%)	76	86
59	u	103/103 (100%)	103 (100%)	0	100	100
60	v	109/109 (100%)	109 (100%)	0	100	100
61	w	99/103 (96%)	98 (99%)	1 (1%)	76	86
62	x	86/87 (99%)	86 (100%)	0	100	100
63	y	99/100 (99%)	97 (98%)	2 (2%)	55	73
64	z	89/90 (99%)	88 (99%)	1 (1%)	73	84
All	All	7761/8648 (90%)	7726 (100%)	35 (0%)	89	93

5 of 35 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
50	l	57	LYS
57	s	86	GLN
63	y	6	LYS
14	AE	93	THR
14	AE	92	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 71 such sidechains are listed below:

Mol	Chain	Res	Type
51	m	29	GLN
53	o	24	HIS
62	x	19	GLN
14	AE	805	GLN
14	AE	777	HIS

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	A	75/76 (98%)	29 (38%)	8 (10%)
10	B	75/76 (98%)	30 (40%)	9 (12%)
16	D	1514/1542 (98%)	290 (19%)	20 (1%)
39	a	2859/2904 (98%)	507 (17%)	0
42	d	119/120 (99%)	15 (12%)	0
8	7	26/38 (68%)	18 (69%)	3 (11%)
All	All	4668/4756 (98%)	889 (19%)	40 (0%)

5 of 889 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 40 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
16	D	991	U
16	D	1214	C
16	D	992	U
16	D	1211	U
16	D	1491	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 [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.

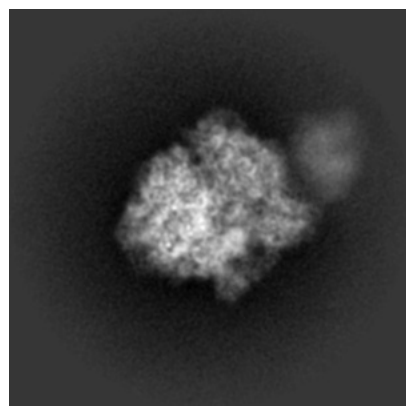
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42453. These allow visual inspection of the internal detail of the map and identification of artifacts.

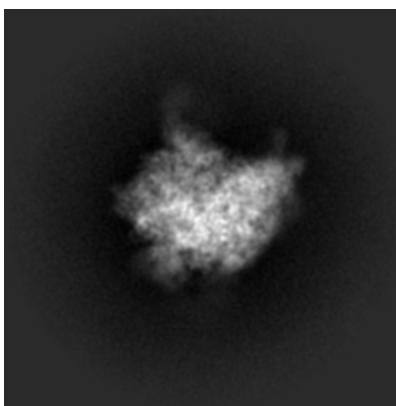
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

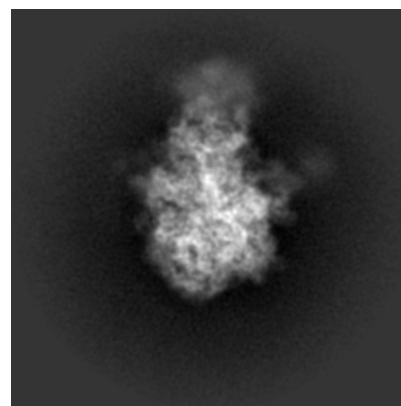
#### 6.1.1 Primary map



X

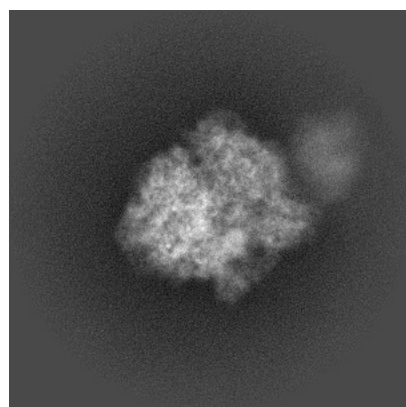


Y

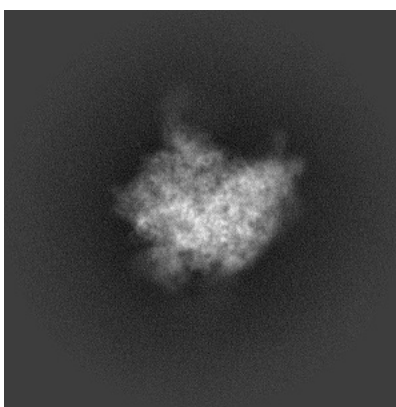


Z

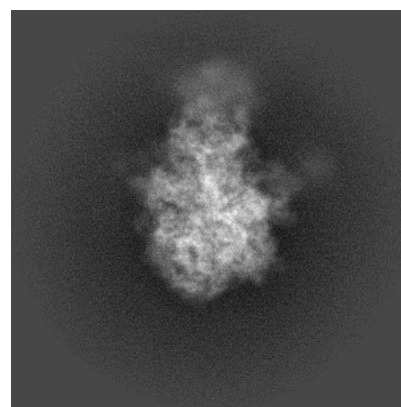
#### 6.1.2 Raw map



X



Y



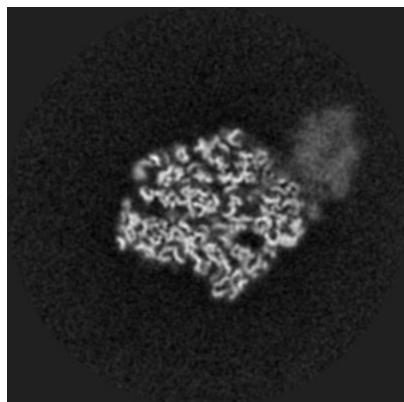
Z

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

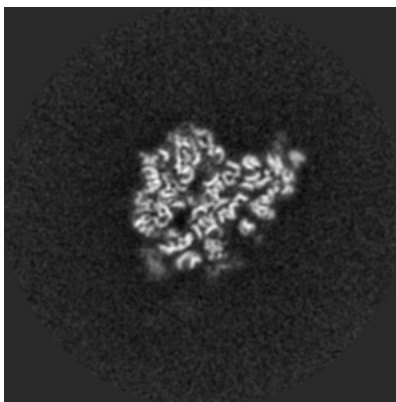


## 6.2 Central slices [i](#)

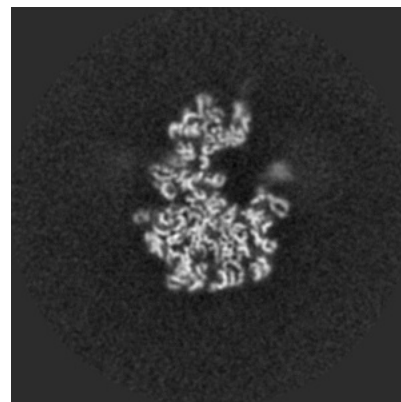
### 6.2.1 Primary map



X Index: 256

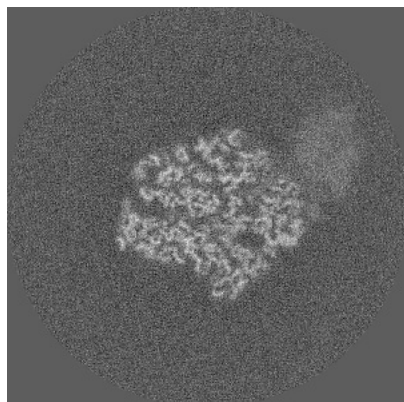


Y Index: 256

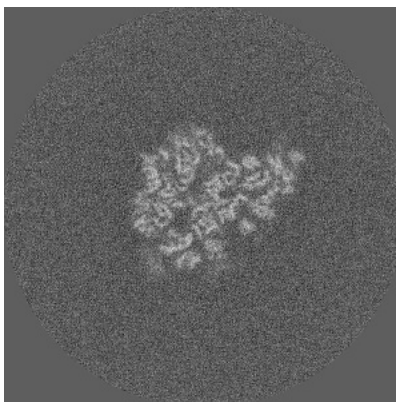


Z Index: 256

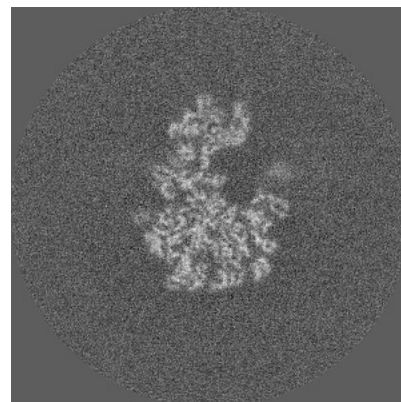
### 6.2.2 Raw map



X Index: 256



Y Index: 256

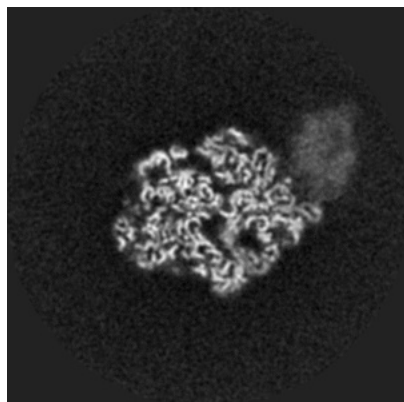


Z Index: 256

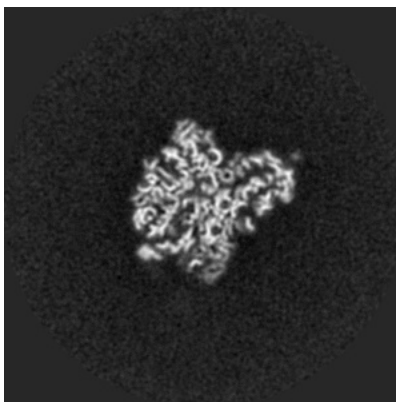
The images above show central slices of the map in three orthogonal directions.

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

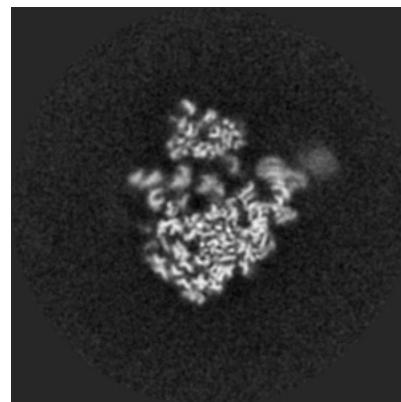
### 6.3.1 Primary map



X Index: 249

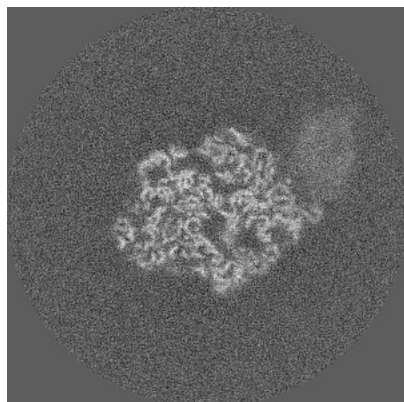


Y Index: 249

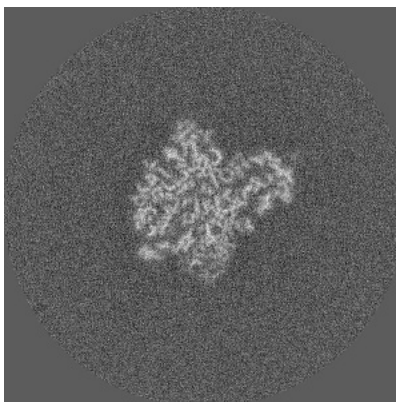


Z Index: 222

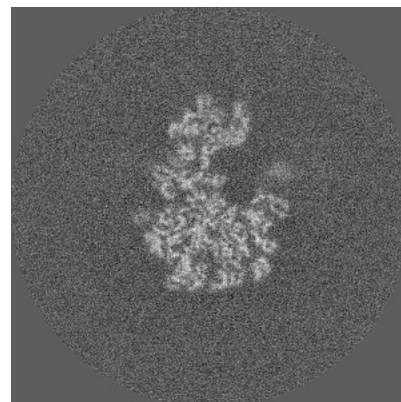
### 6.3.2 Raw map



X Index: 248



Y Index: 248

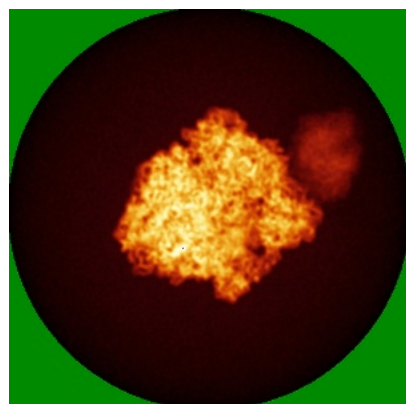


Z Index: 256

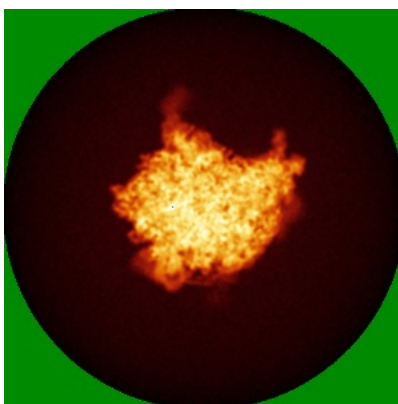
The images above show the largest variance slices of the map in three orthogonal directions.

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

### 6.4.1 Primary map



X

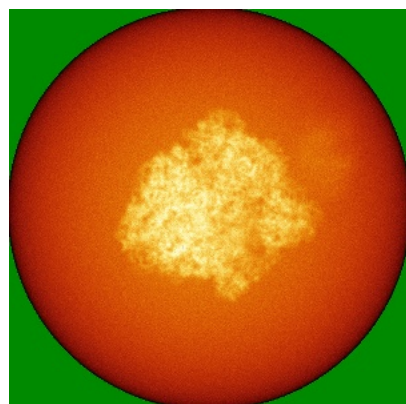


Y

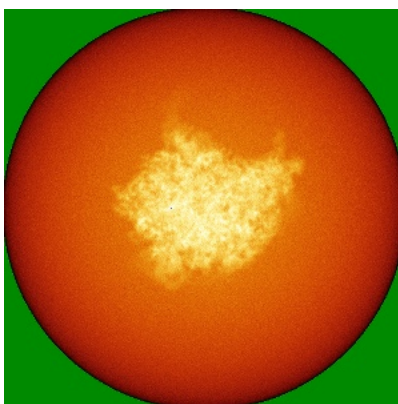


Z

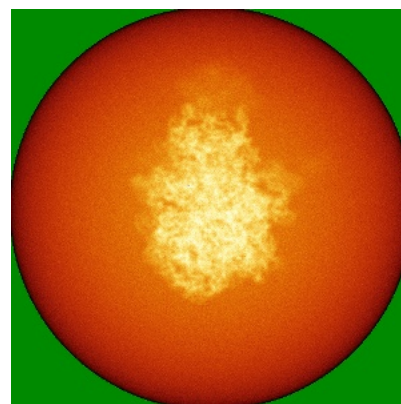
### 6.4.2 Raw map



X



Y

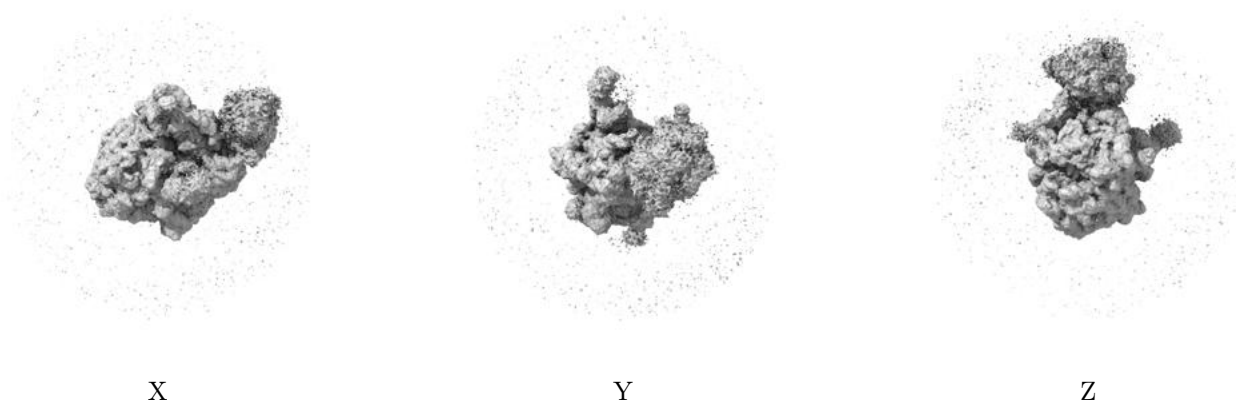


Z

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.

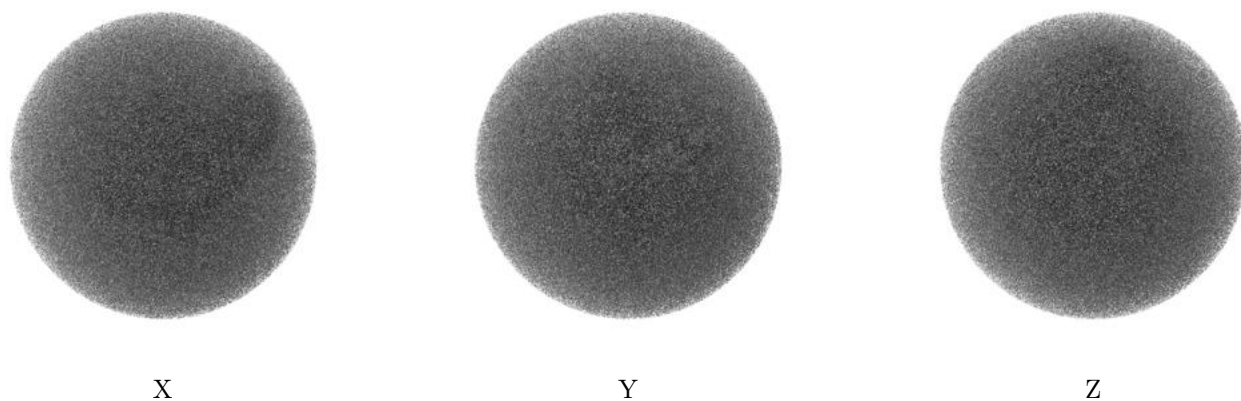
## 6.5 Orthogonal surface views [i](#)

### 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](#)

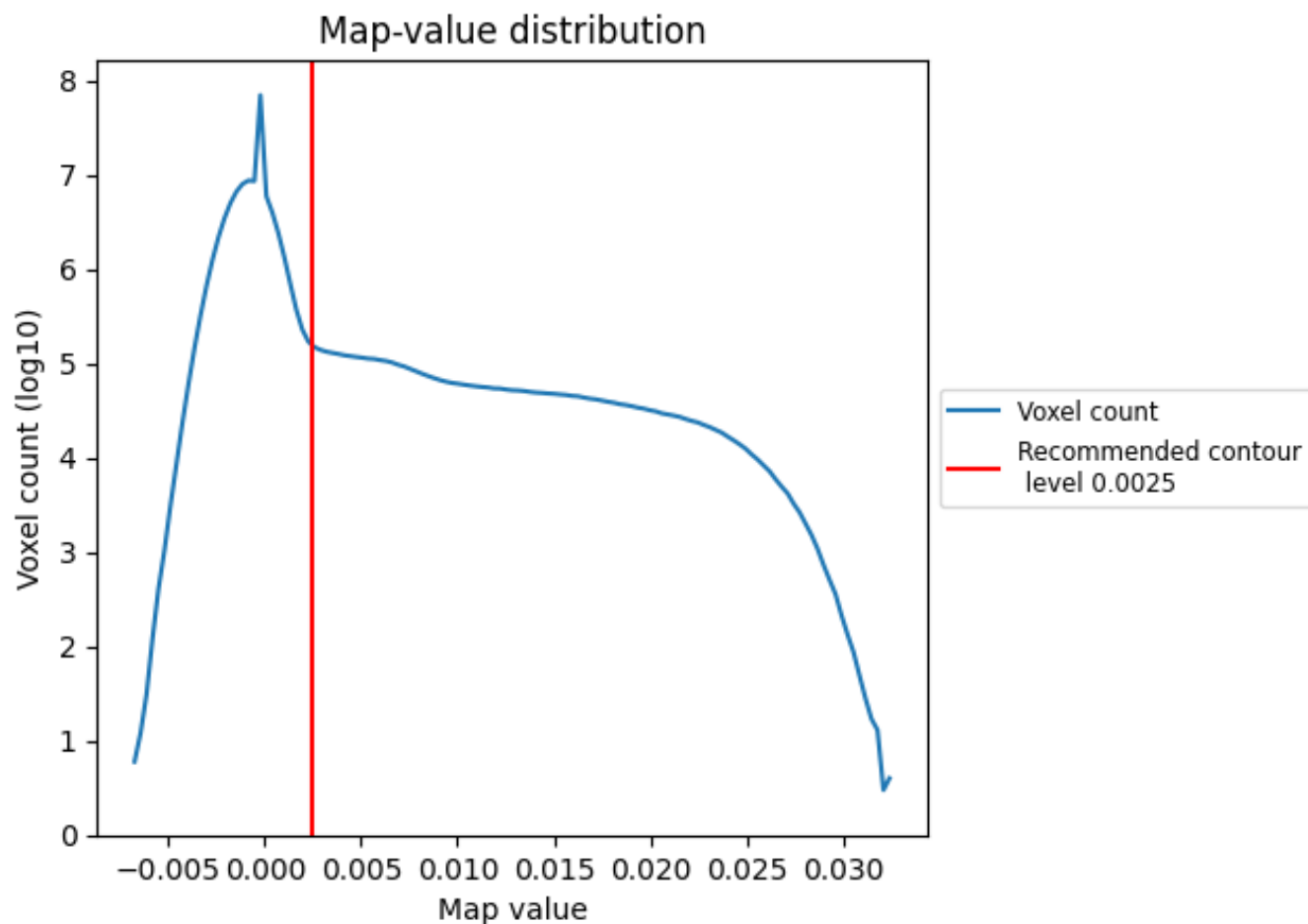
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

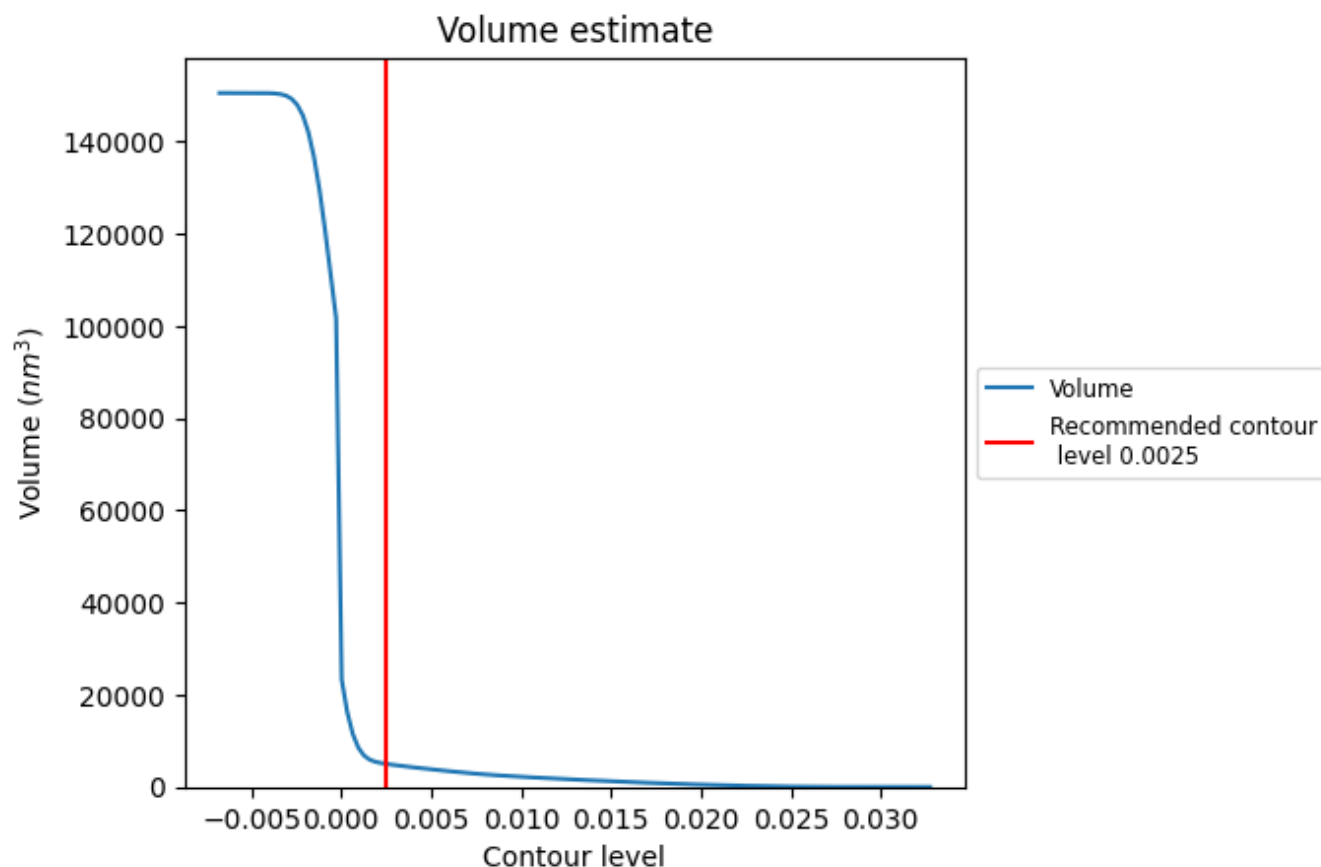
This section contains the results of statistical analysis of the map.

### 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.

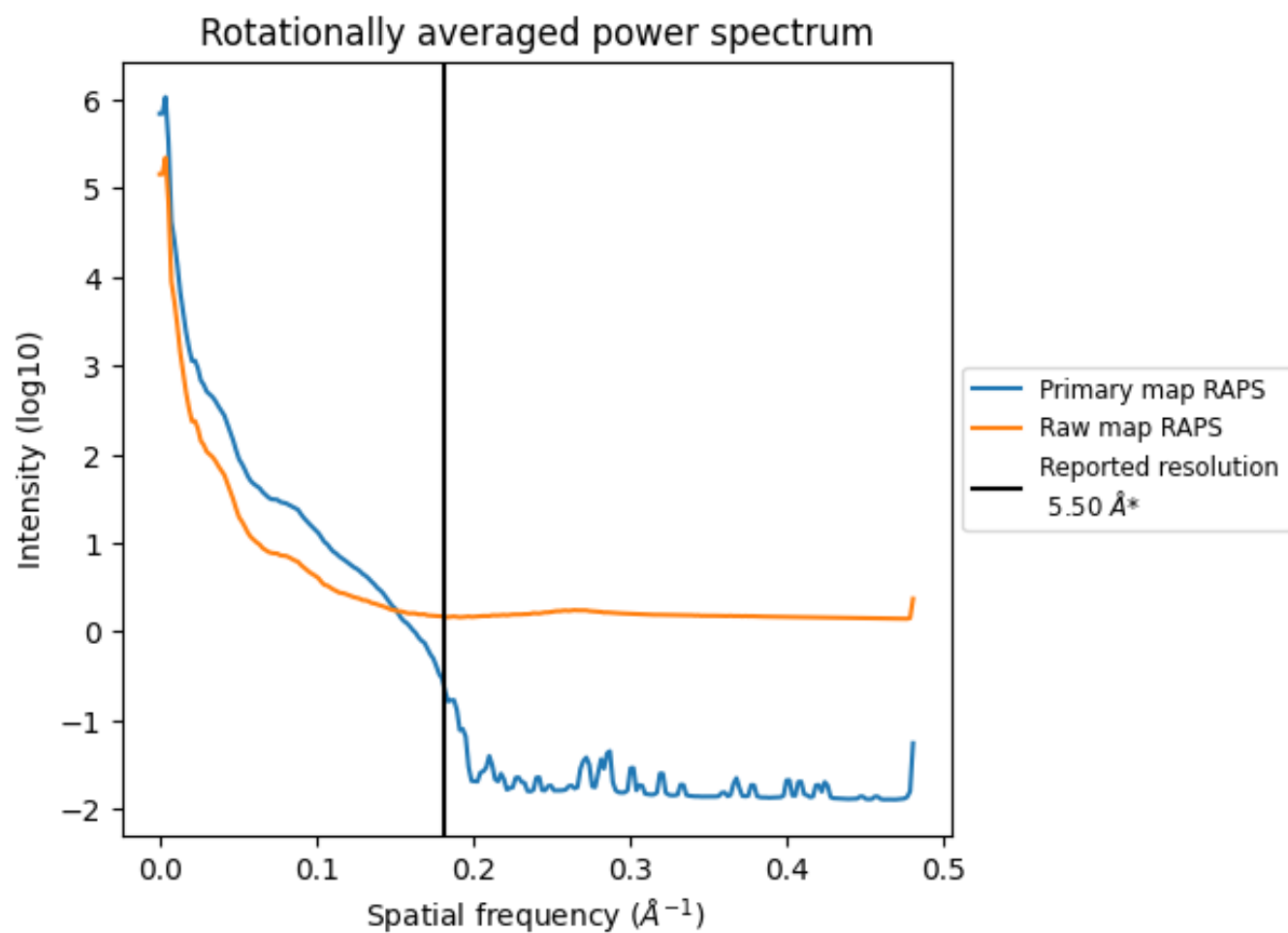
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5004  $\text{nm}^3$ ; this corresponds to an approximate mass of 4521 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 ⓘ

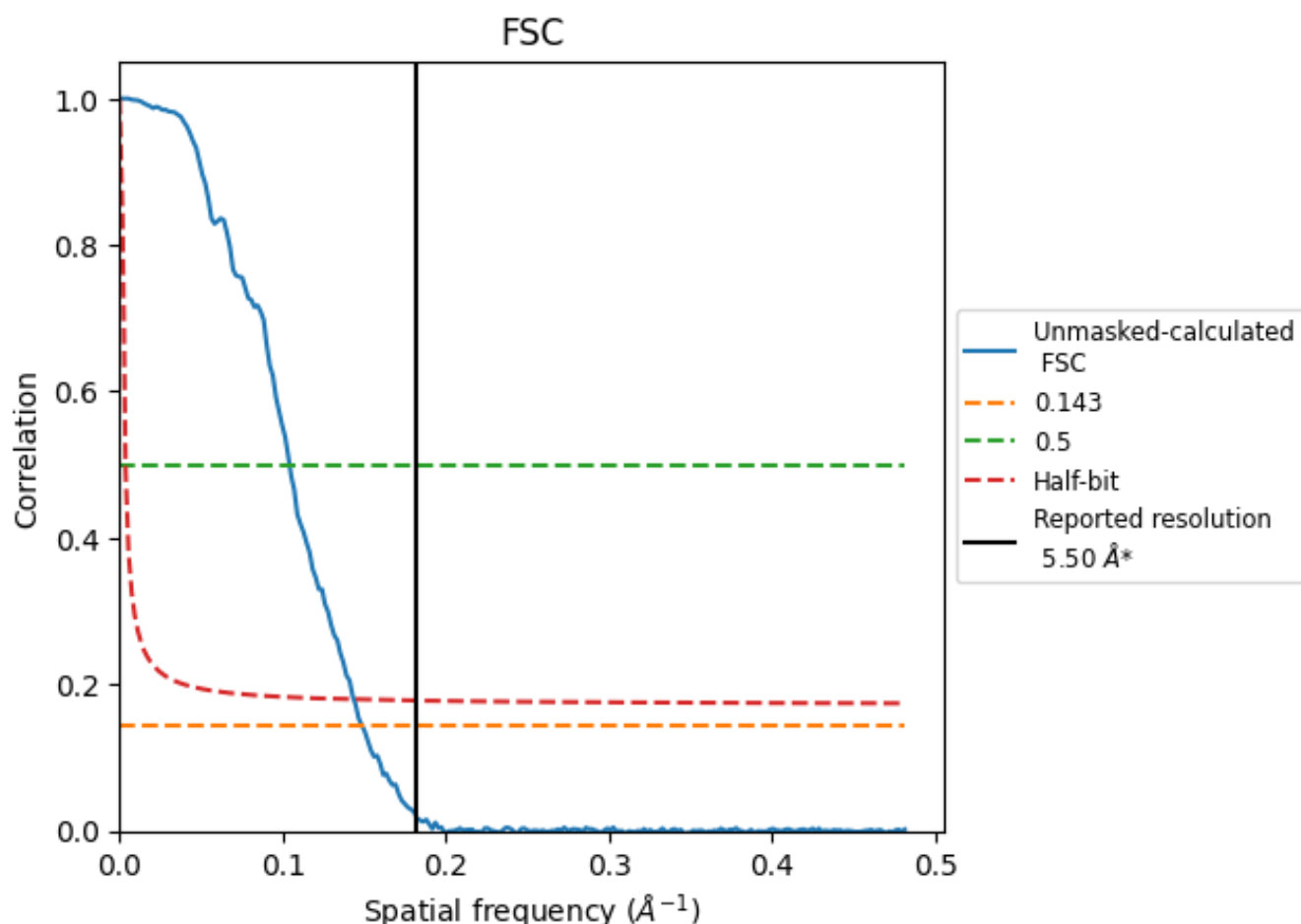


\*Reported resolution corresponds to spatial frequency of 0.182 Å<sup>-1</sup>

## 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 0.182 Å<sup>-1</sup>



## 8.2 Resolution estimates [i](#)

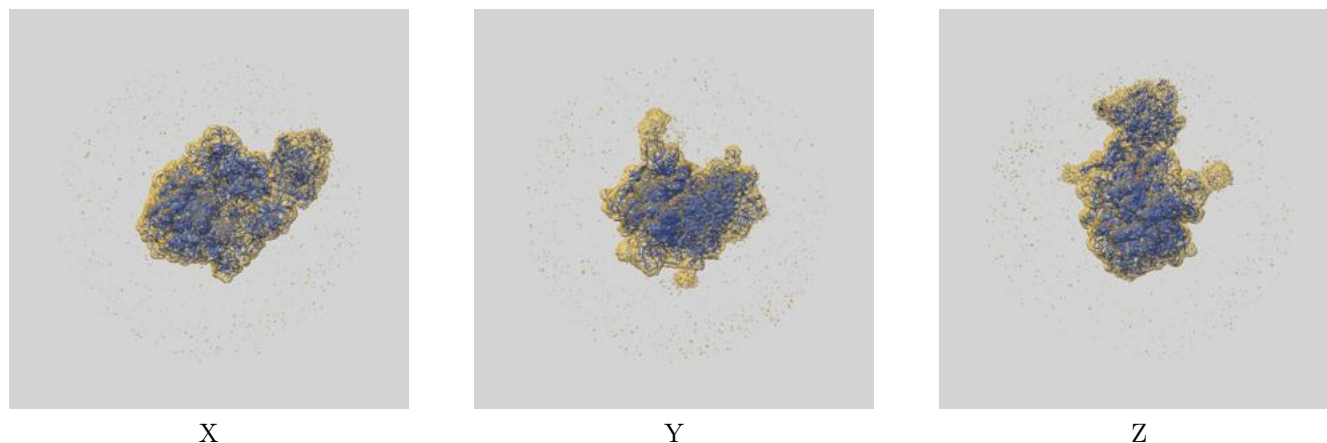
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.50	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.72	9.60	6.96

\*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 6.72 differs from the reported value 5.5 by more than 10 %

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

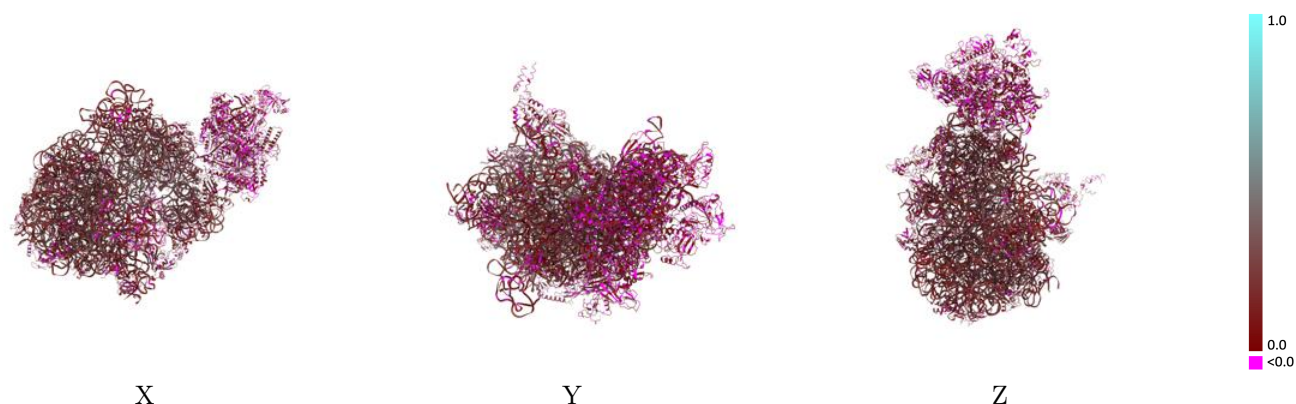
This section contains information regarding the fit between EMDB map EMD-42453 and PDB model 8UPO. Per-residue inclusion information can be found in section [3](#) on page [16](#).

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



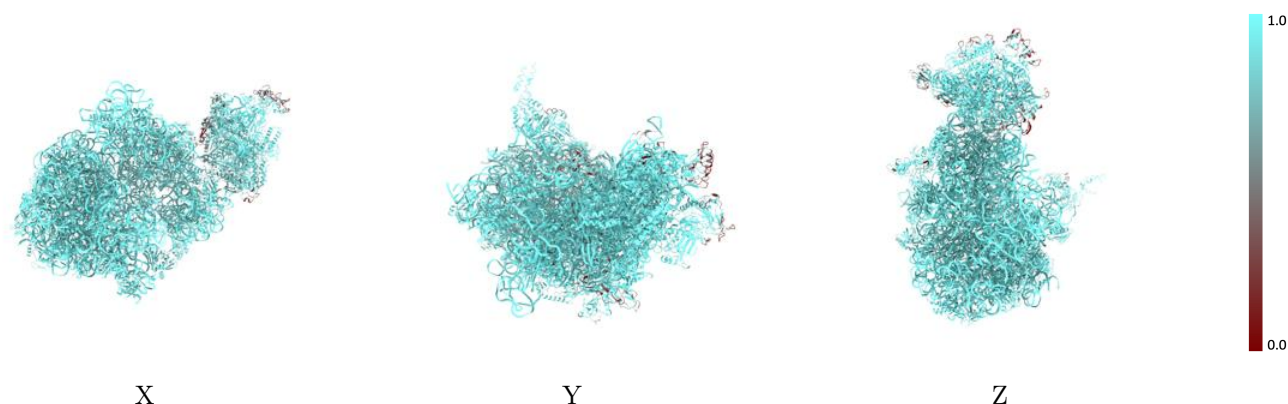
The images above show the 3D surface view of the map at the recommended contour level 0.0025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



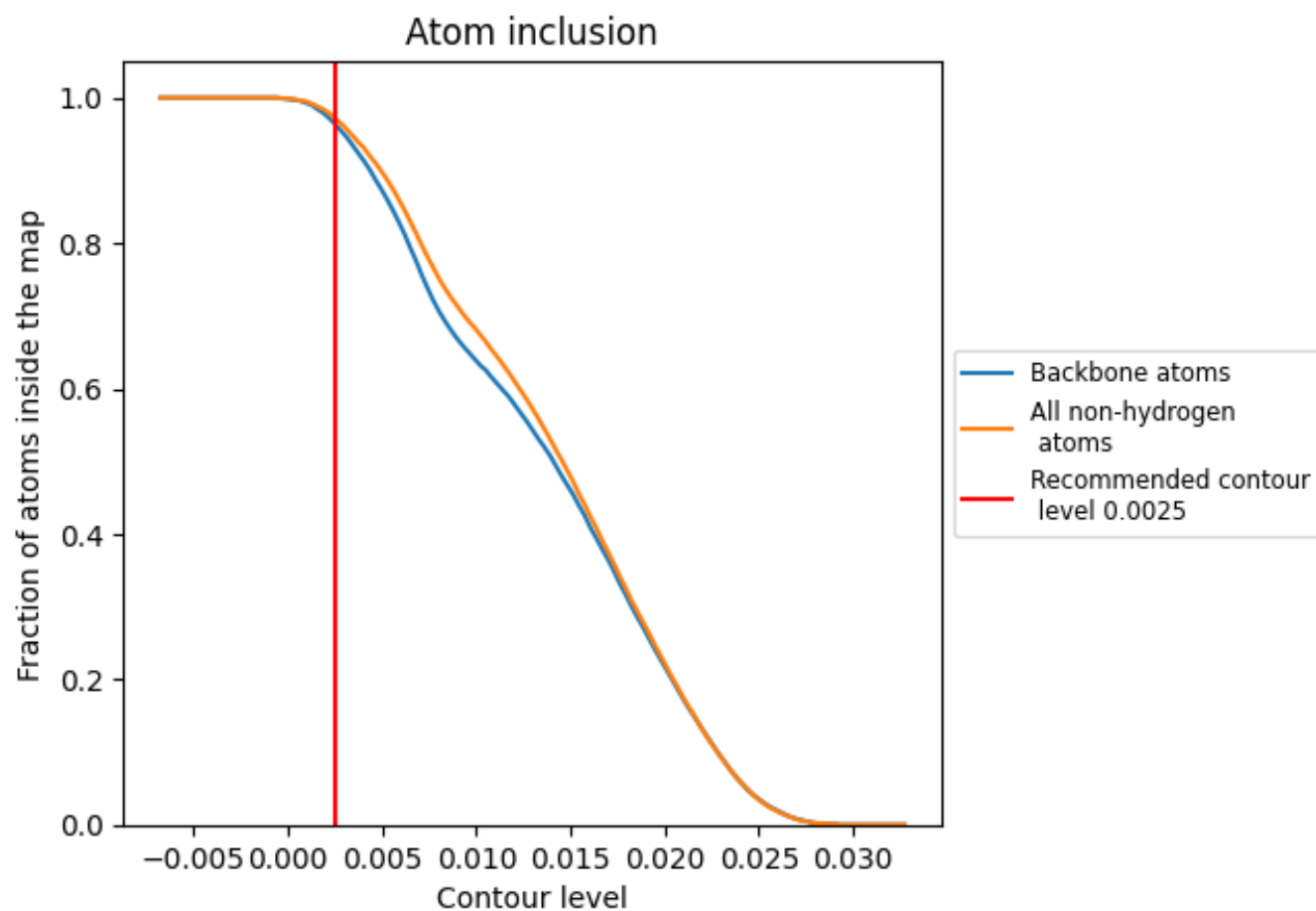
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	 0.9720	 0.1740
0	 0.9940	 0.1550
1	 0.9960	 0.1780
2	 0.9900	 0.1570
3	 0.9920	 0.1300
4	 0.9960	 0.1560
5	 0.9800	 0.1320
6	 0.9750	 0.1300
7	 0.9880	 0.1180
9	 0.9750	 0.0980
A	 1.0000	 0.1700
AA	 0.9090	 0.0700
AB	 0.6880	 0.0650
AC	 0.8870	 0.0820
AD	 0.7090	 0.0450
AE	 0.9100	 0.0770
B	 0.9760	 0.1080
C	 0.9960	 0.1510
D	 0.9980	 0.2230
E	 0.9950	 0.1520
F	 0.9840	 0.1780
G	 0.9900	 0.1600
H	 0.9090	 0.0730
I	 0.9910	 0.1900
J	 0.9960	 0.1750
K	 0.9970	 0.2140
L	 0.9990	 0.1540
M	 0.9970	 0.1500
N	 0.9850	 0.1750
O	 0.9900	 0.1290
P	 0.9990	 0.1590
Q	 0.9970	 0.1560
R	 0.9990	 0.2050
S	 0.9950	 0.1600
T	 0.9970	 0.1560



*Continued on next page...*

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Chain	Atom inclusion	Q-score
U	 0.9980	 0.1540
V	 0.9910	 0.1750
W	 0.9770	 0.1210
X	 0.9910	 0.1390
Y	 0.9040	 0.0660
Z	 0.9910	 0.0450
a	 0.9990	 0.2120
b	 0.9950	 0.1290
c	 0.9870	 0.1560
d	 1.0000	 0.1830
e	 0.9900	 0.1360
f	 0.9980	 0.1730
g	 0.9820	 0.1140
h	 0.9960	 0.1560
i	 0.9910	 0.1850
j	 0.9970	 0.1630
k	 0.9980	 0.1330
l	 0.9890	 0.1310
m	 0.9940	 0.1750
n	 0.9850	 0.1260
o	 0.9940	 0.1270
p	 0.9970	 0.1560
q	 1.0000	 0.1460
r	 0.9760	 0.1150
s	 0.9900	 0.1790
t	 0.9880	 0.1730
u	 0.9910	 0.1380
v	 0.9930	 0.1810
w	 0.9910	 0.1580
x	 0.9920	 0.0970
y	 0.9930	 0.1600
z	 0.9960	 0.1440