



wwPDB EM Validation Summary Report ⓘ

Dec 14, 2024 – 06:26 PM EST

PDB ID : 8UQP
EMDB ID : EMD-42477
Title : Escherichia coli transcription-translation coupled complex class B (TTC-B) containing RfaH bound to ops signal, mRNA with a 24 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 : 2023-10-24
Resolution : 3.80 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

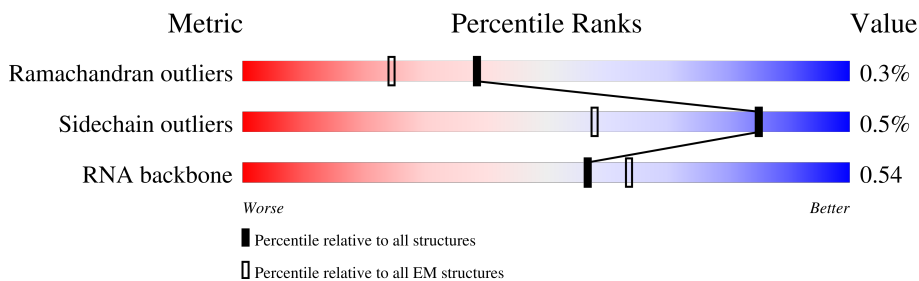
EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.40

1 Overall quality at a glance

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

The reported resolution of this entry is 3.80 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.



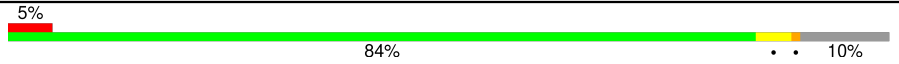


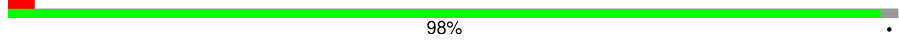








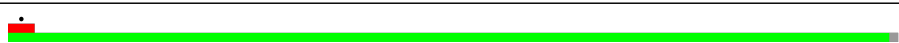




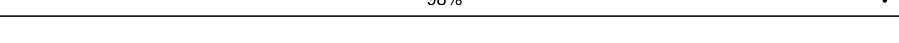
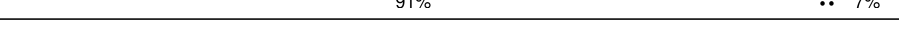
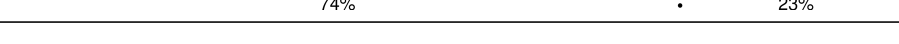
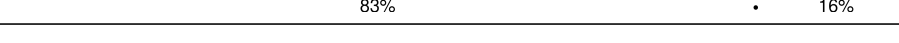
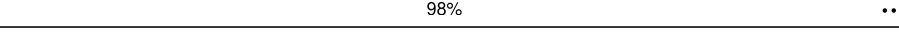
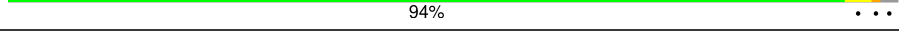
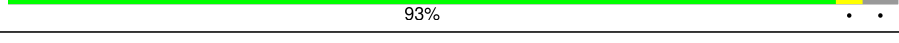

Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 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	41	

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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	AF	91	
16	C	75	
17	D	1542	
18	E	87	
19	F	71	
20	G	241	
21	H	557	
22	I	233	
23	J	206	
24	K	167	
25	L	135	
26	M	179	
27	N	130	
28	O	130	
29	P	103	
30	Q	129	
31	R	124	

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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	20% 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	<p>9% 100%</p>
58	s	142	<p>97%</p>
59	t	123	<p>97%</p>
60	u	144	<p>98%</p>
61	v	136	<p>99%</p>
62	w	127	<p>89% 5% 6%</p>
63	x	117	<p>99%</p>
64	y	115	<p>97%</p>
65	z	118	<p>97%</p>

2 Entry composition [i](#)

There are 67 unique types of molecules in this entry. The entry contains 276039 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 24 nt long spacer.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
8	7	37	772	345	110	280	37	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 fMet-tRNA.

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
27	N	129	Total	C	H	N	O	S	0	0
			2010	616	1031	173	184	6		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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.

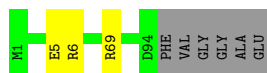
- Molecule 2: 50S ribosomal protein L22

Chain 1:  100%

There are no outlier residues recorded for this chain.

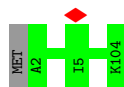
- Molecule 3: 50S ribosomal protein L23

Chain 2:  91% 6%



- Molecule 4: 50S ribosomal protein L24

Chain 3:  99%



- Molecule 5: 50S ribosomal protein L25

Chain 4:  98%

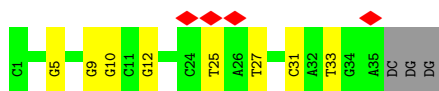


- Molecule 6: NT DNA ops

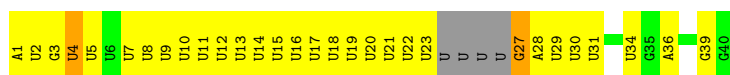
Chain 5:  5% 58% 34% 8%



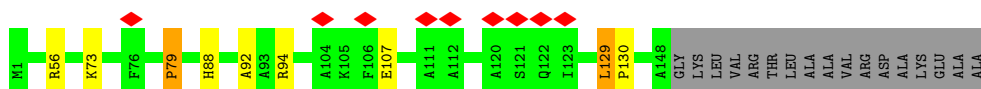
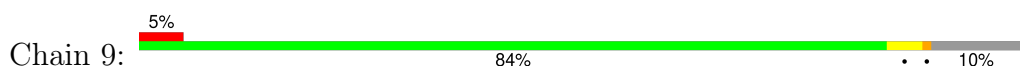
• Molecule 7: T DNA ops



• Molecule 8: mRNA with 24 nt long spacer



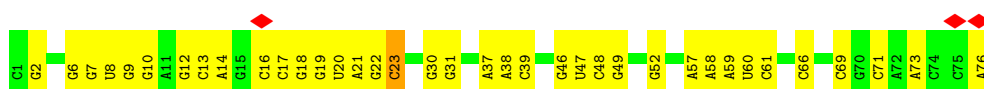
• Molecule 9: 50S ribosomal protein L10



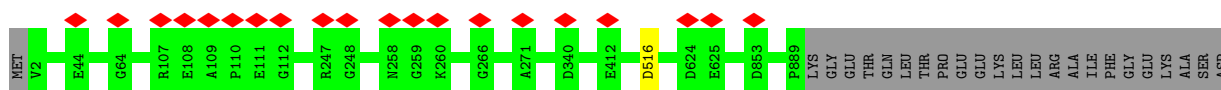
• Molecule 10: E-site and P-site fMet-tRNA

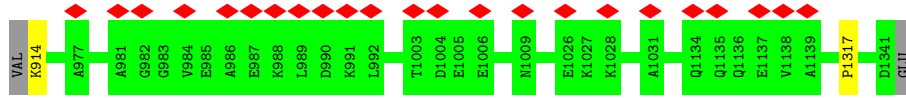


• Molecule 10: E-site and P-site fMet-tRNA

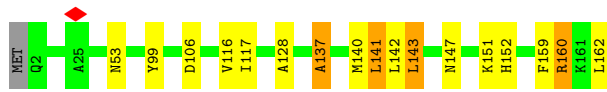
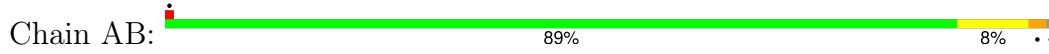


• Molecule 11: DNA-directed RNA polymerase subunit beta

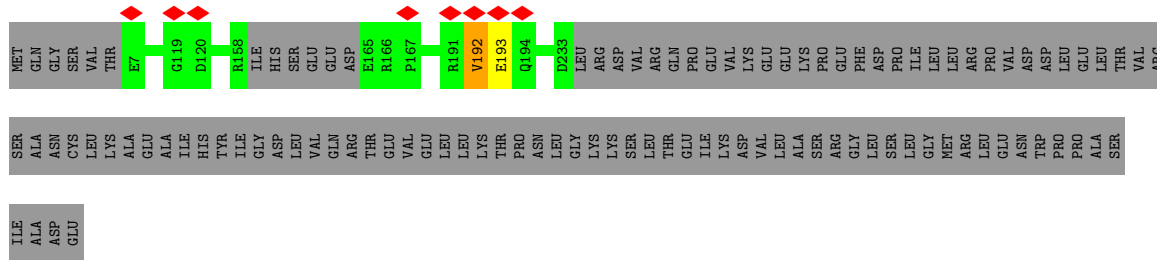




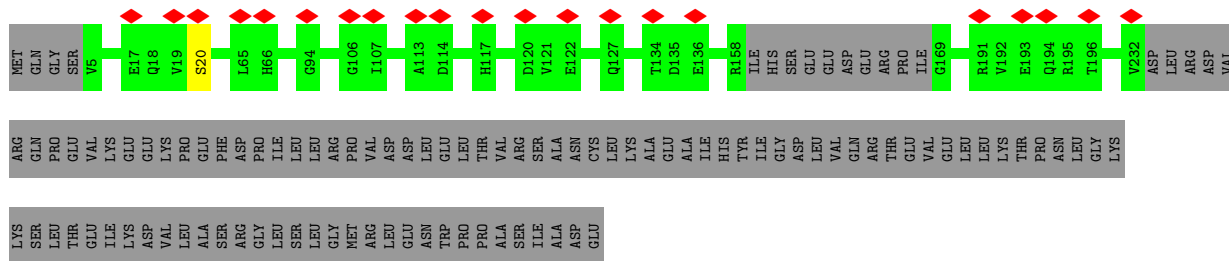
• Molecule 12: Transcription antitermination protein RfaH



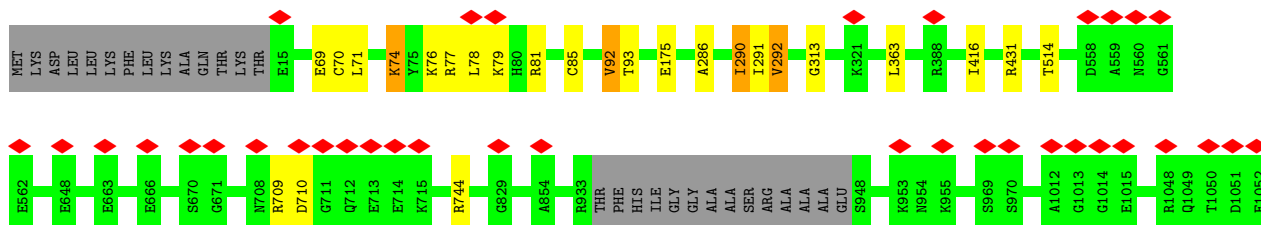
• Molecule 13: DNA-directed RNA polymerase subunit alpha

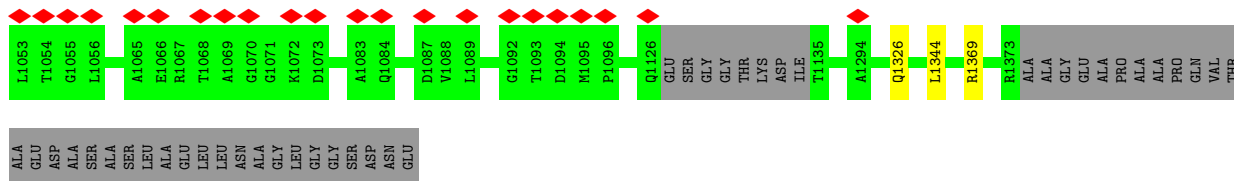


• Molecule 13: DNA-directed RNA polymerase subunit alpha

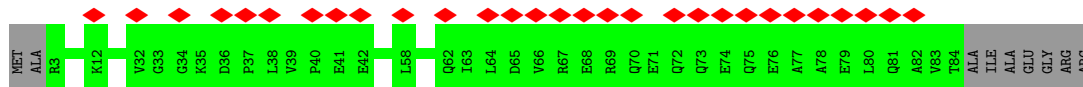
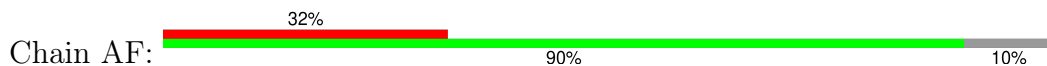


• Molecule 14: DNA-directed RNA polymerase subunit beta'

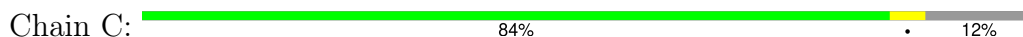




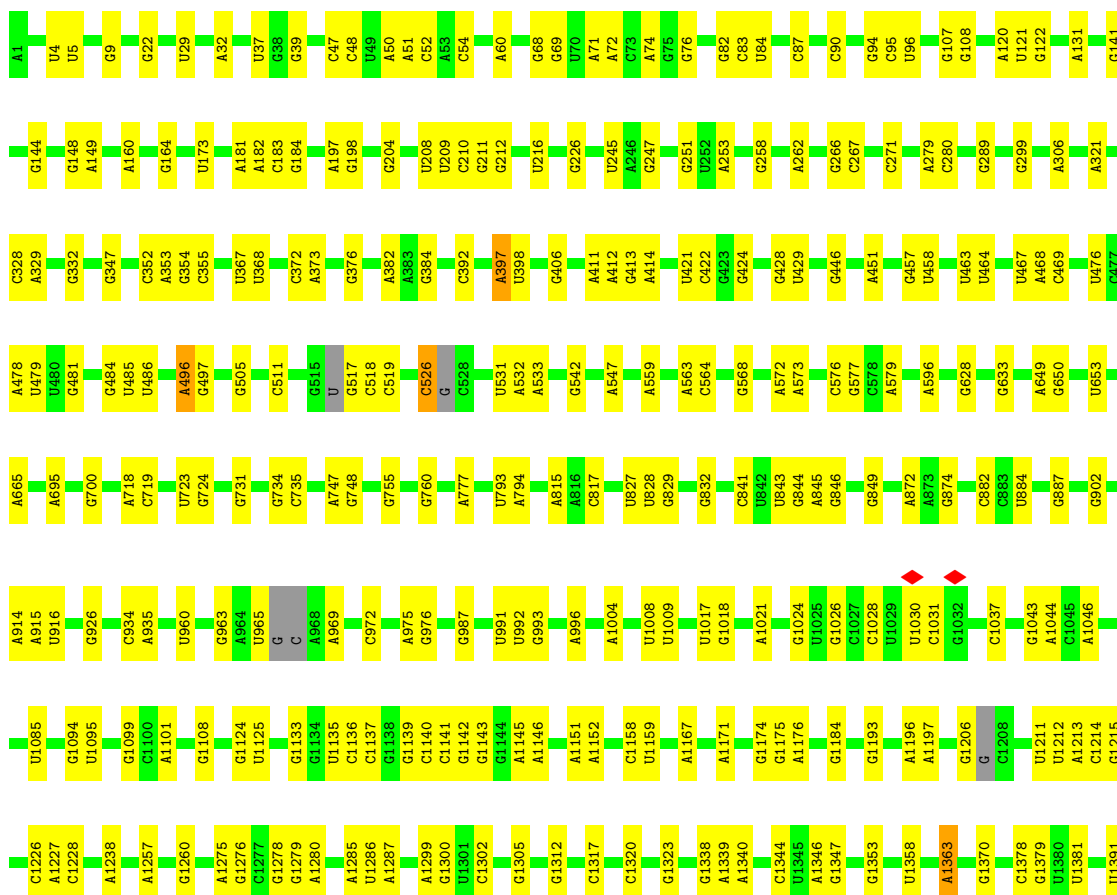
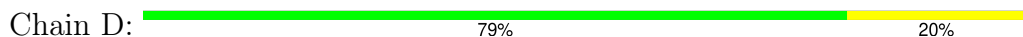
• Molecule 15: DNA-directed RNA polymerase subunit omega



• Molecule 16: 30S ribosomal protein S18

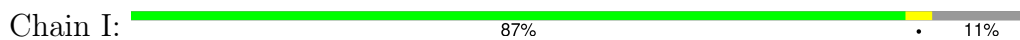


• Molecule 17: 16S rRNA



GLU
LYS
ASP
ALA
ILE
ALA
THR
VAL
ASN
LYS
GLN
GLU
ASP
ALA
ASN
PHE
SER
ASN
ASN
ALA
MET
ALA
GLU
GLU
ALA
PHE
LYS
LYS
GLY
GLU

• Molecule 22: 30S ribosomal protein S3



MET
G2
F29
R72
M134
E166
W167
Y168
G209
GLY
MET
ALA
ALA
VAL
GLU
PRO
GLU
LYS
PRO
ALA
ALA
GLN
PRO
LYS
LYS
GLN
GLN
ARG
LYS
GLY
ARG
LYS

• Molecule 23: 30S ribosomal protein S4



MET
A2
R47
F72
F182
R206

• Molecule 24: 30S ribosomal protein S5



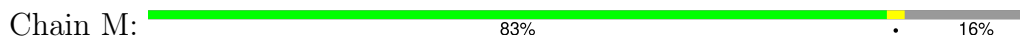
MET
ALA
HIS
ILE
GLU
LYS
GLN
ALA
GLY
E10
R45
M71
N77
N78
L165
GLY
LYS

• Molecule 25: 30S ribosomal protein S6



M1
W42
R45
V96
M102
K104
ALA
LYS
ASP
GLU
ARG
GLU
ARG
ARG
ARG
ASP
ASP
PHE
GLN
ALA
ASN
GLU
THR
ALA
ASP
ASP
ALA
GLU
ALA
GLY
ASP
SER
SER
GLU
GLU
GLU
GLU
GLU

• Molecule 26: 30S ribosomal protein S7



MET
F2
R3
R4
L47
K56
A152
HIS
TYR
ARG
TRP
LEU
SER
LEU
LEU
ARG
SER
PHE
SER
SER
HIS
GLN
ALA
GLY
ALA
SER
SER
LYS
GLN
PRO
ALA
LEU
LEU
GLY
TYR
LEU
LEU
ASN

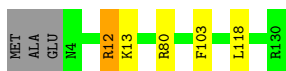
• Molecule 27: 30S ribosomal protein S8



MET
S2
M27
A130

• Molecule 28: 30S ribosomal protein S9

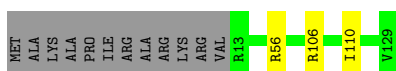
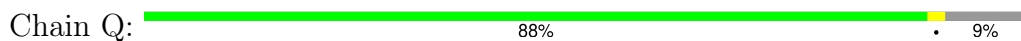




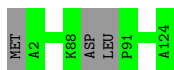
- Molecule 29: 30S ribosomal protein S10



- Molecule 30: 30S ribosomal protein S11



- Molecule 31: 30S ribosomal protein S12



- Molecule 32: 30S ribosomal protein S14



- Molecule 33: 30S ribosomal protein S15

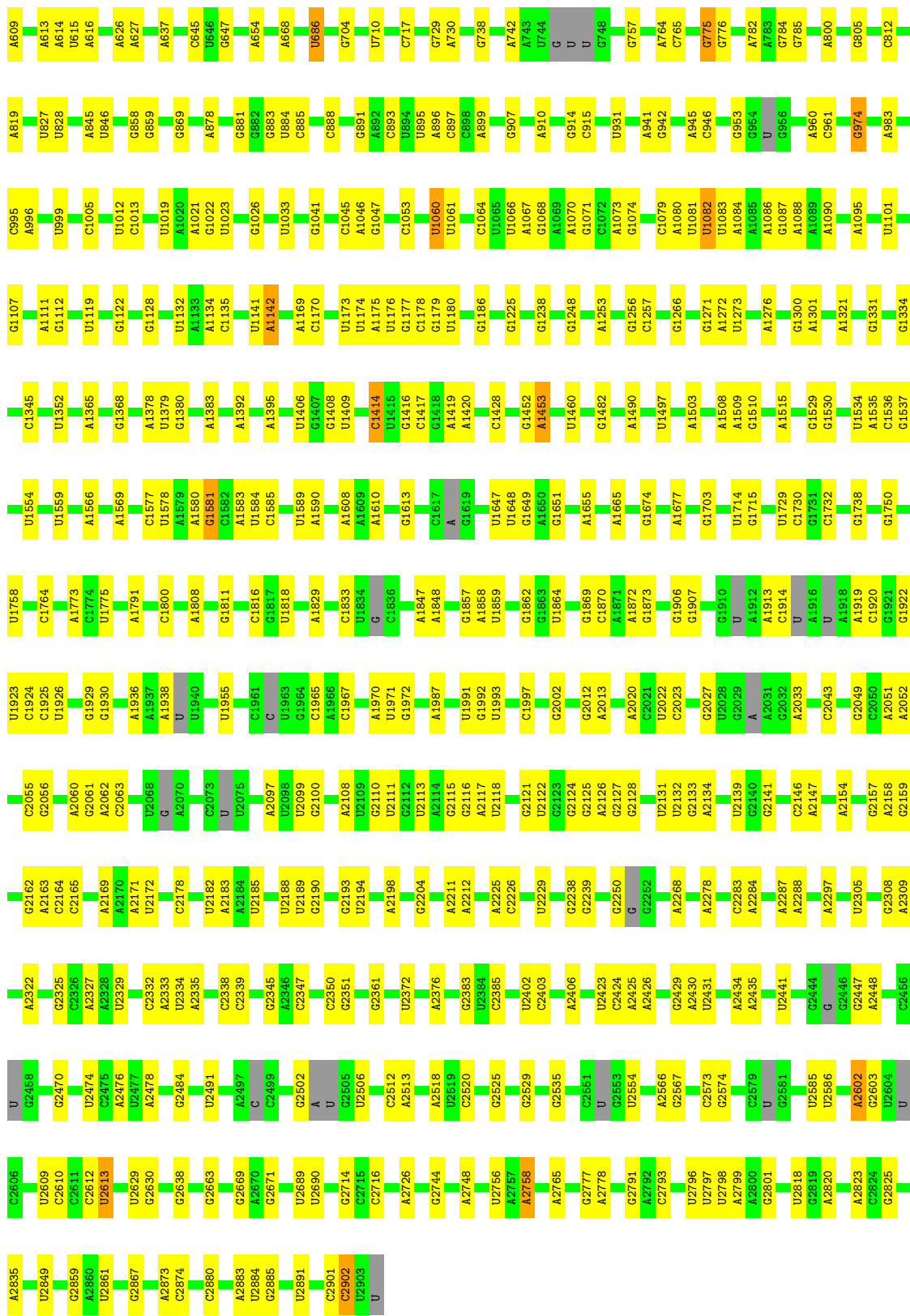


- Molecule 34: 30S ribosomal protein S16

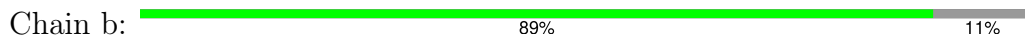


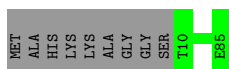
- Molecule 35: 30S ribosomal protein S17





● Molecule 41: 50S ribosomal protein L27





- 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%



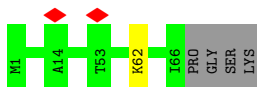
- Molecule 45: 50S ribosomal protein L30

Chain f: 97%



- Molecule 46: 50S ribosomal protein L31

Chain g: 93% 6%



- Molecule 47: 50S ribosomal protein L2

Chain h: 98%



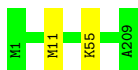
- Molecule 48: 50S ribosomal protein L32

Chain i: 96%



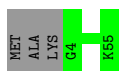
- Molecule 49: 50S ribosomal protein L3

Chain j: 99%



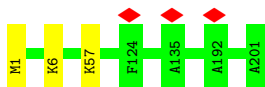
- Molecule 50: 50S ribosomal protein L33

Chain k: 95% 5%



- Molecule 51: 50S ribosomal protein L4

Chain l: 99%



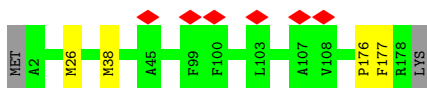
- Molecule 52: 50S ribosomal protein L34

Chain m: 100%

There are no outlier residues recorded for this chain.

- Molecule 53: 50S ribosomal protein L5

Chain n: 97%



- Molecule 54: 50S ribosomal protein L35

Chain o: 94% 5%



- Molecule 55: 50S ribosomal protein L6

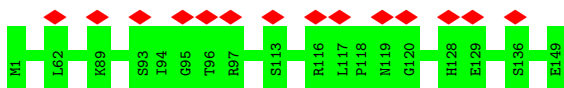
Chain p: 98%



- Molecule 56: 50S ribosomal protein L36



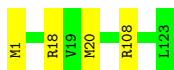
- Molecule 57: 50S ribosomal protein L9



- Molecule 58: 50S ribosomal protein L13



- Molecule 59: 50S ribosomal protein L14



- Molecule 60: 50S ribosomal protein L15



- Molecule 61: 50S ribosomal protein L16

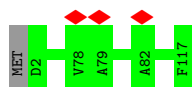


- Molecule 62: 50S ribosomal protein L17

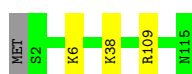




- Molecule 63: 50S ribosomal protein L18



- Molecule 64: 50S ribosomal protein L19



- Molecule 65: 50S ribosomal protein L20



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	49622	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	0.034	Depositor
Minimum map value	-0.007	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0037	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 [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	1.11	8/783 (1.0%)	1.10	0/1203
8	7	0.53	2/856 (0.2%)	0.89	4/1326 (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	0.55	1/1810 (0.1%)	1.26	11/2821 (0.4%)
11	AA	0.42	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	14/36610 (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%)	0.70	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	0.70	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%)	0.82	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	0.63	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	0.56	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	0.37	0/304
40	a	0.61	14/69247 (0.0%)	1.03	130/107985 (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	0.68	0/576
51	l	0.54	1/1571 (0.1%)	0.64	1/2113 (0.0%)
52	m	0.43	0/380	0.60	0/498
53	n	0.51	0/1434	0.68	2/1926 (0.1%)
54	o	0.51	0/513	0.85	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	4/1551 (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	0.41	0/902	0.57	0/1209
64	y	0.46	0/929	0.59	1/1242 (0.1%)
65	z	0.63	1/960 (0.1%)	0.60	0/1278
All	All	0.58	93/190707 (0.0%)	0.92	321/281021 (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 93 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
62	w	35	LYS	CE-NZ	-15.20	1.11	1.49
25	L	42	TRP	CB-CG	-12.37	1.27	1.50
3	2	5	GLU	CG-CD	-11.55	1.34	1.51
44	e	46	VAL	CB-CG1	-11.28	1.29	1.52
62	w	42	LYS	CD-CE	-10.80	1.24	1.51

The worst 5 of 321 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
40	a	1019	U	C5-C4-O4	30.70	144.32	125.90
40	a	1141	U	C5-C4-O4	29.59	143.65	125.90
17	D	37	U	C5-C4-O4	29.43	143.56	125.90
17	D	1358	U	C5-C4-O4	29.22	143.43	125.90
17	D	827	U	C5-C4-O4	28.61	143.07	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

Continued on next page...

Continued from previous page...

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%)	5	32
11	AA	1312/1342 (98%)	1198 (91%)	113 (9%)	1 (0%)	48	79
12	AB	159/162 (98%)	111 (70%)	43 (27%)	5 (3%)	3	25
13	AC	217/329 (66%)	203 (94%)	12 (6%)	2 (1%)	14	45
13	AD	214/329 (65%)	198 (92%)	16 (8%)	0	100	100
14	AE	1331/1407 (95%)	1213 (91%)	112 (8%)	6 (0%)	25	58
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%)	30	63

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	H	255/557 (46%)	182 (71%)	66 (26%)	7 (3%)	4	27
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%)	22	55
25	L	102/135 (76%)	97 (95%)	4 (4%)	1 (1%)	13	44
26	M	149/179 (83%)	140 (94%)	8 (5%)	1 (1%)	19	52
27	N	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
28	O	125/130 (96%)	116 (93%)	8 (6%)	1 (1%)	16	49
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%)	7	34
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%)	22	55

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	o	62/65 (95%)	57 (92%)	4 (6%)	1 (2%)	8	36
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%)	8744 (92%)	709 (8%)	33 (0%)	38	69

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%)	67	77
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%)	40	60
11	AA	1135/1157 (98%)	1134 (100%)	1 (0%)	92	95
12	AB	141/142 (99%)	140 (99%)	1 (1%)	81	86
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%)	56	72
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%)	86	90
21	H	137/461 (30%)	137 (100%)	0	100	100
22	I	171/190 (90%)	170 (99%)	1 (1%)	84	88
23	J	172/173 (99%)	171 (99%)	1 (1%)	84	88
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%)	73	80
29	P	86/90 (96%)	85 (99%)	1 (1%)	67	77
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%)	60	74
35	V	74/78 (95%)	73 (99%)	1 (1%)	62	75
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%)	75	82
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%)	84	88
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%)	75	82
59	t	104/104 (100%)	103 (99%)	1 (1%)	73	80
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%)	73	80
63	x	86/87 (99%)	86 (100%)	0	100	100
64	y	99/100 (99%)	97 (98%)	2 (2%)	50	68
65	z	89/90 (99%)	88 (99%)	1 (1%)	70	79
All	All	7890/8723 (90%)	7850 (100%)	40 (0%)	85	90

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 71 such sidechains are listed below:

Mol	Chain	Res	Type
52	m	29	GLN
54	o	24	HIS
63	x	19	GLN
14	AE	805	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%)	507 (17%)	0
43	d	119/120 (99%)	15 (12%)	0
8	7	36/41 (87%)	26 (72%)	5 (13%)
All	All	4678/4759 (98%)	896 (19%)	41 (0%)

5 of 896 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 oligosaccharides 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.

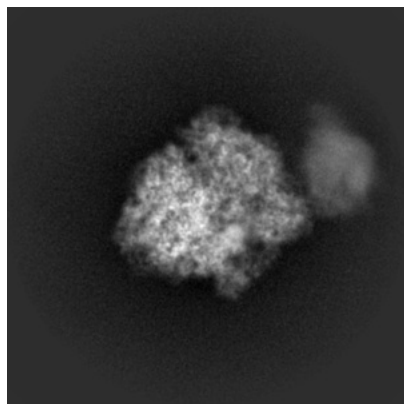
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42477. These allow visual inspection of the internal detail of the map and identification of artifacts.

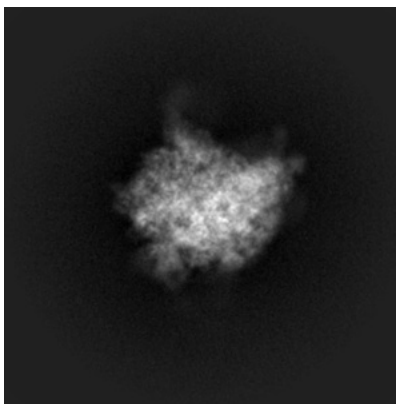
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

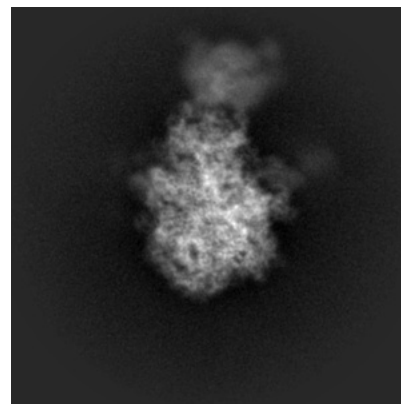
6.1.1 Primary map



X

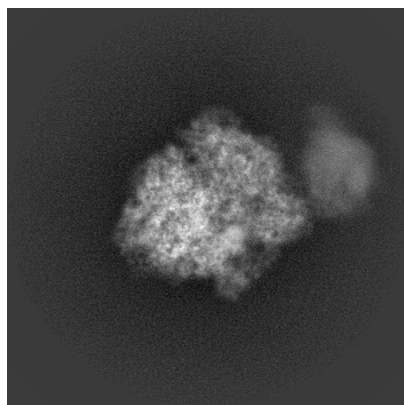


Y

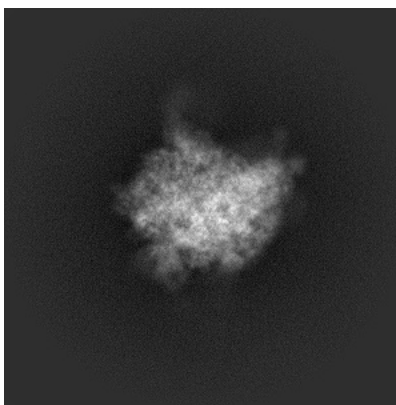


Z

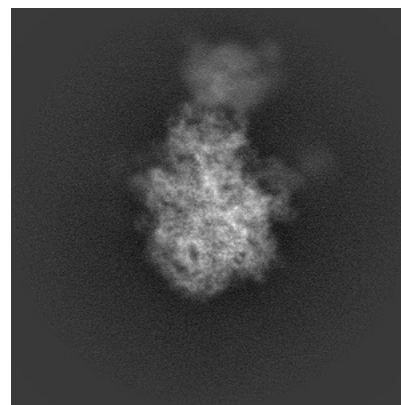
6.1.2 Raw map



X



Y

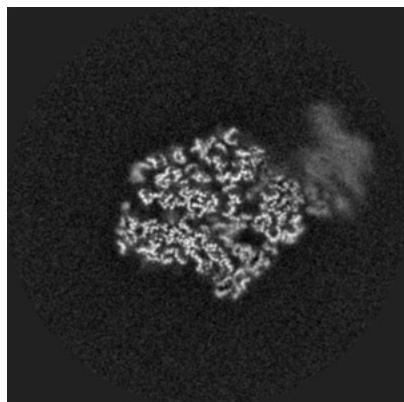


Z

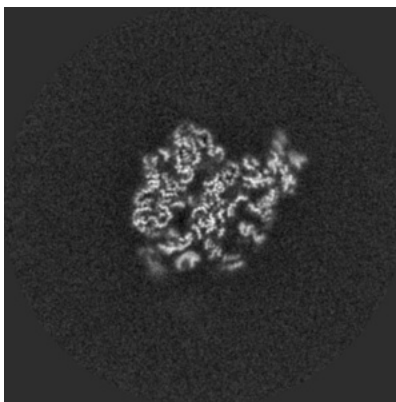
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

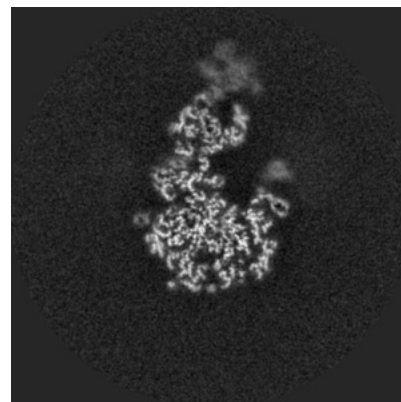
6.2.1 Primary map



X Index: 256

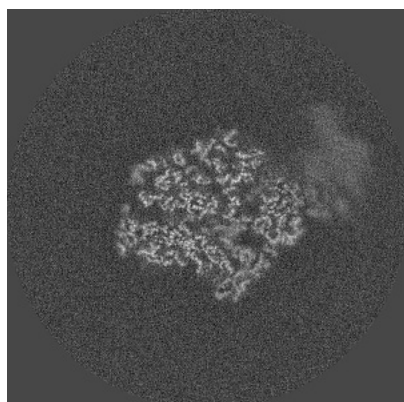


Y Index: 256

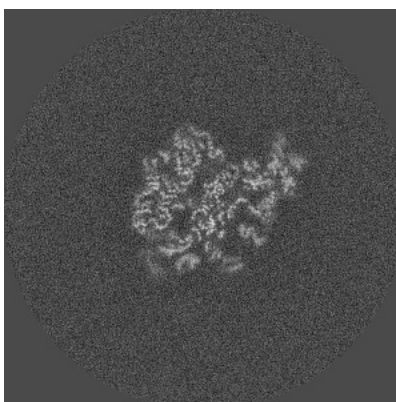


Z Index: 256

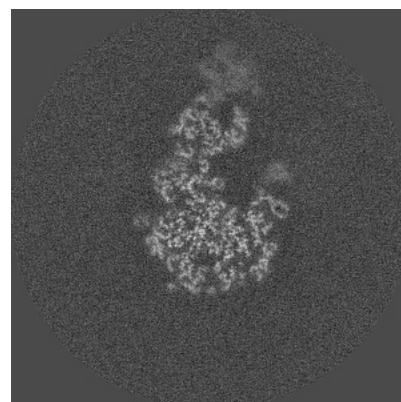
6.2.2 Raw map



X Index: 256



Y Index: 256

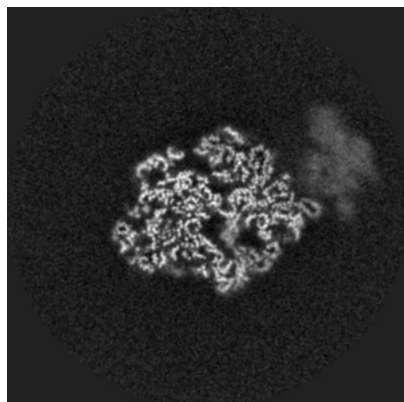


Z Index: 256

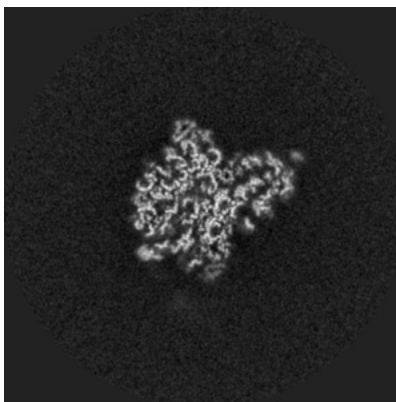
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

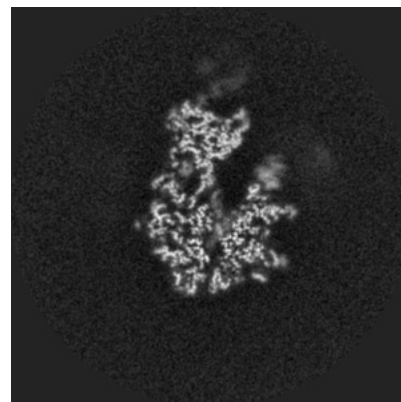
6.3.1 Primary map



X Index: 248

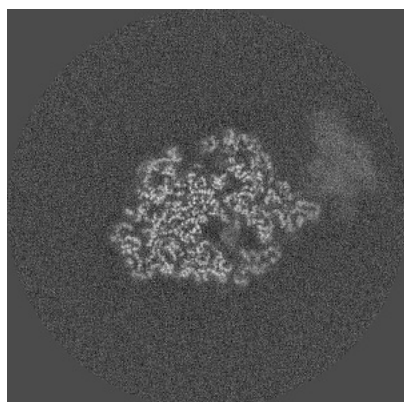


Y Index: 248

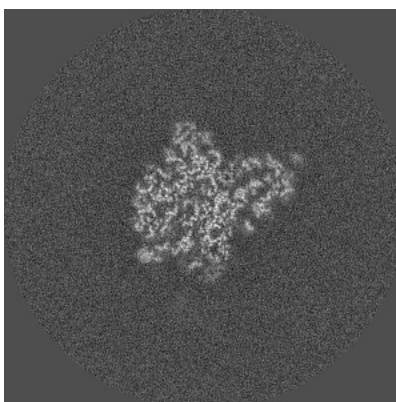


Z Index: 242

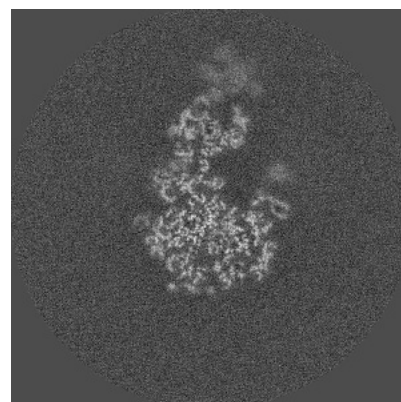
6.3.2 Raw map



X Index: 242



Y Index: 248



Z Index: 257

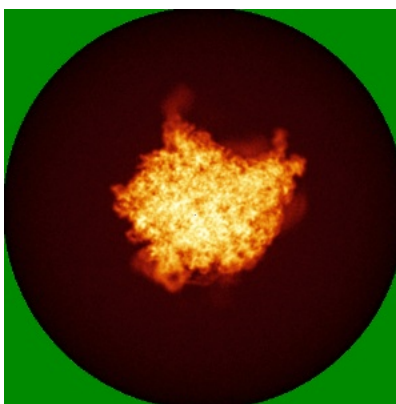
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X

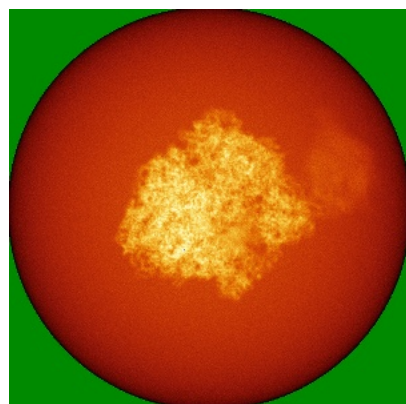


Y

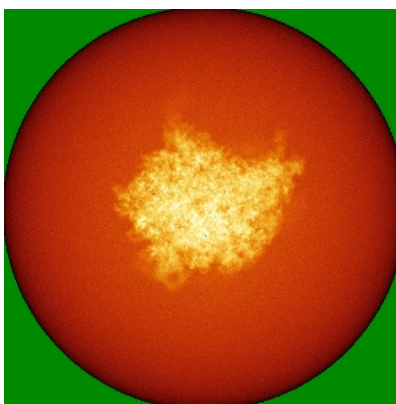


Z

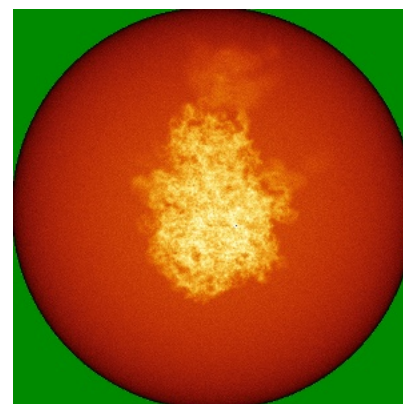
6.4.2 Raw map



X



Y

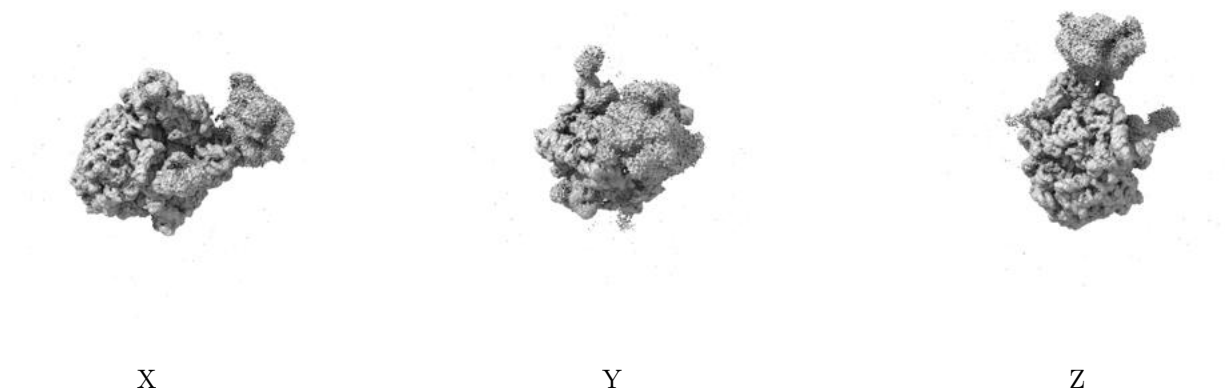


Z

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.

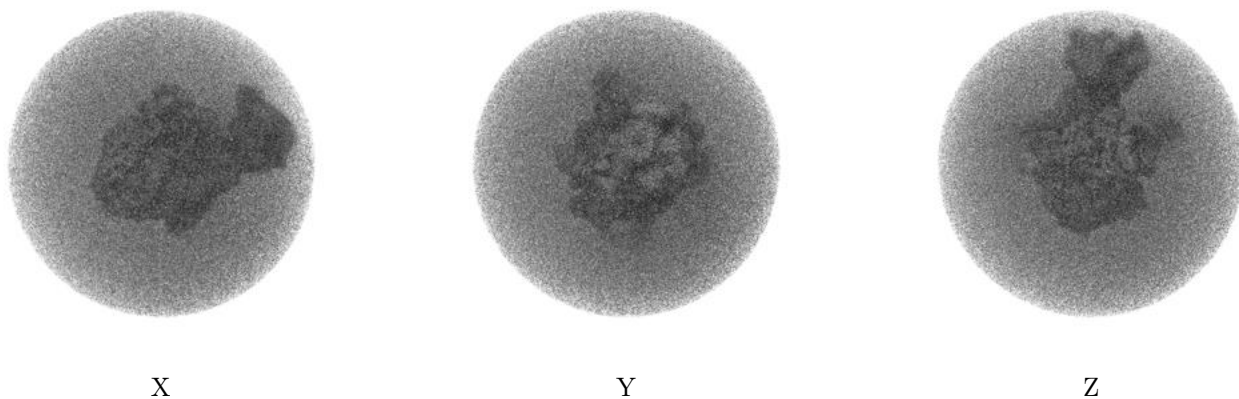
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0037. 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.

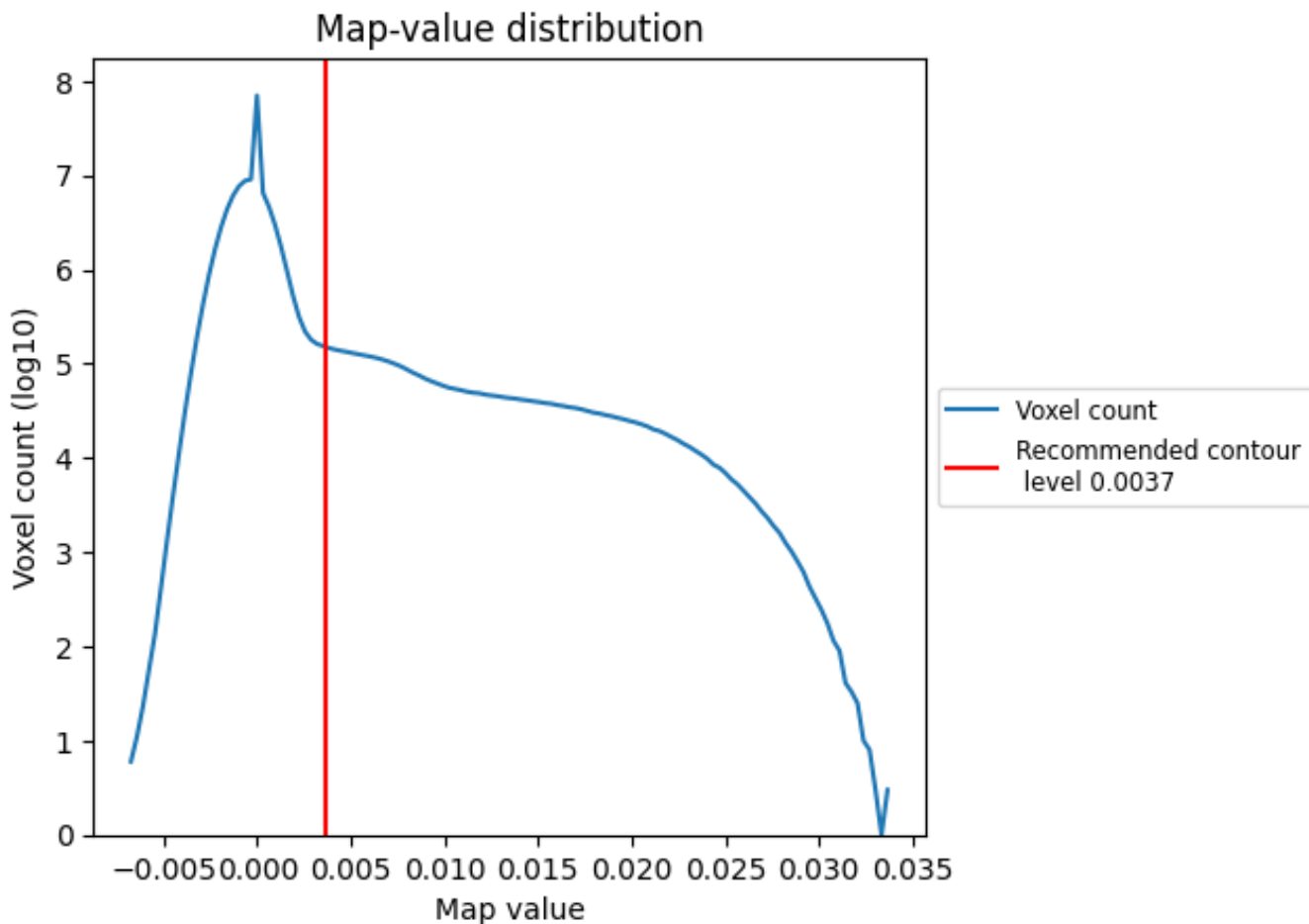
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

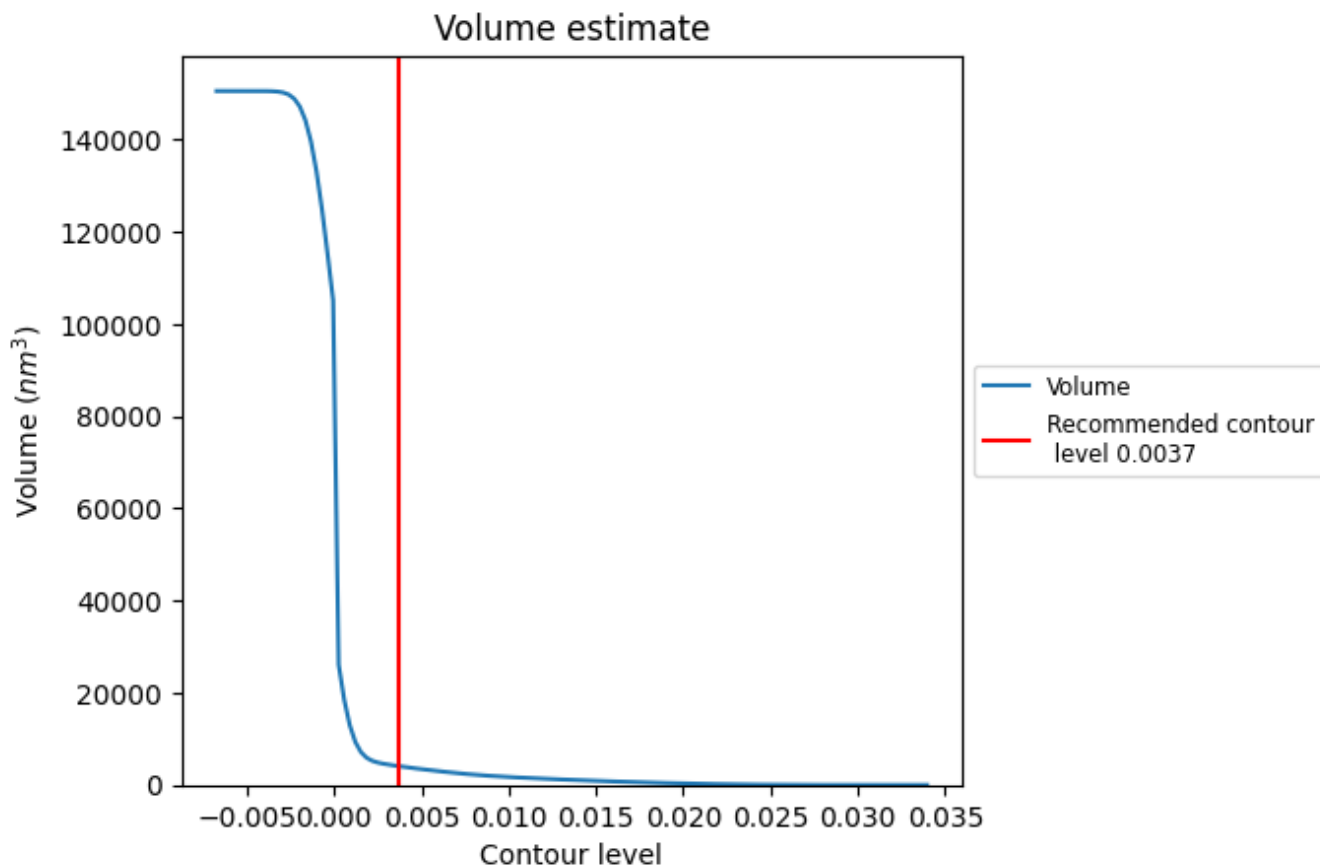
This section contains the results of statistical analysis of the map.

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.

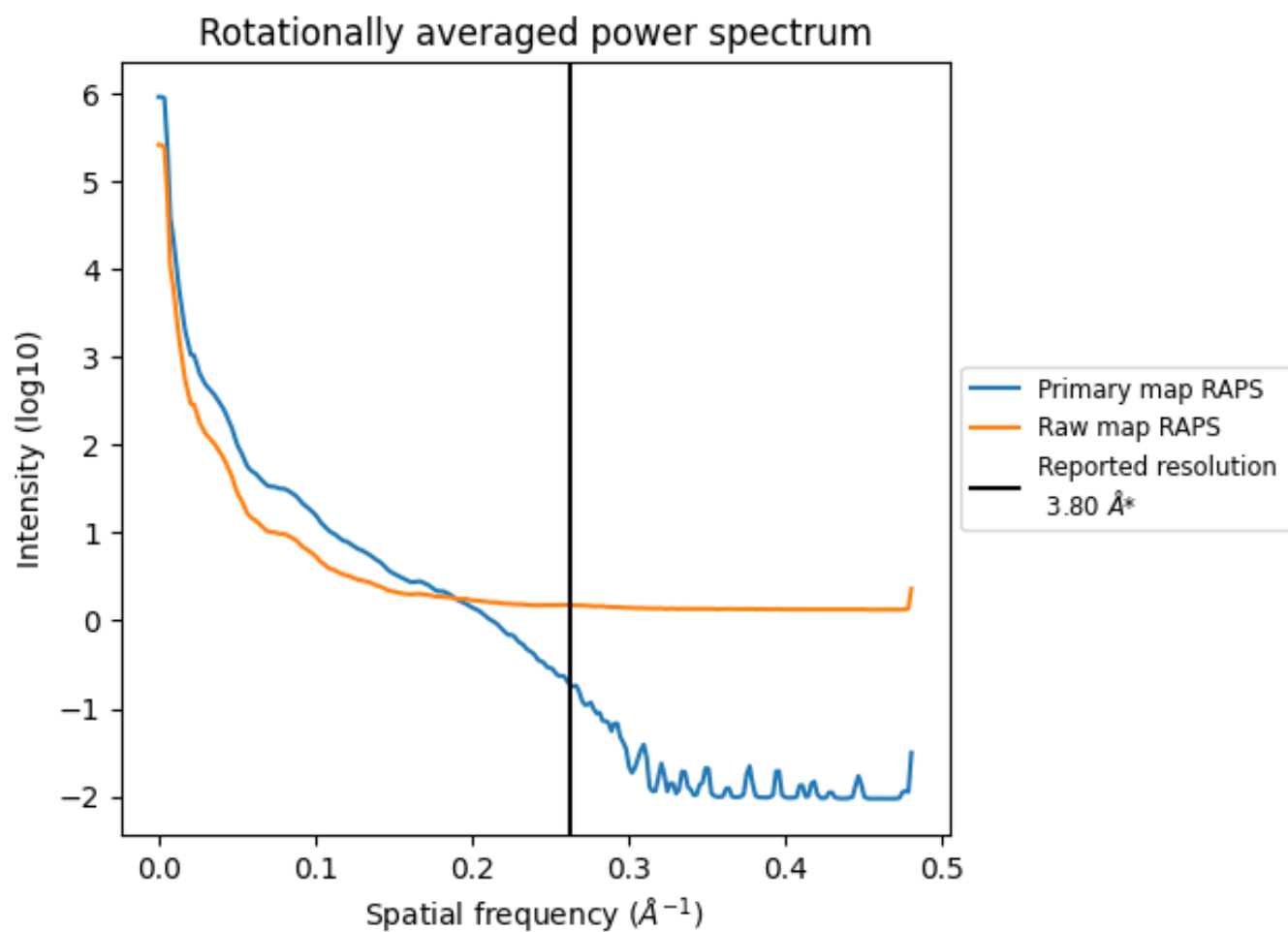
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 4079 nm^3 ; this corresponds to an approximate mass of 3685 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

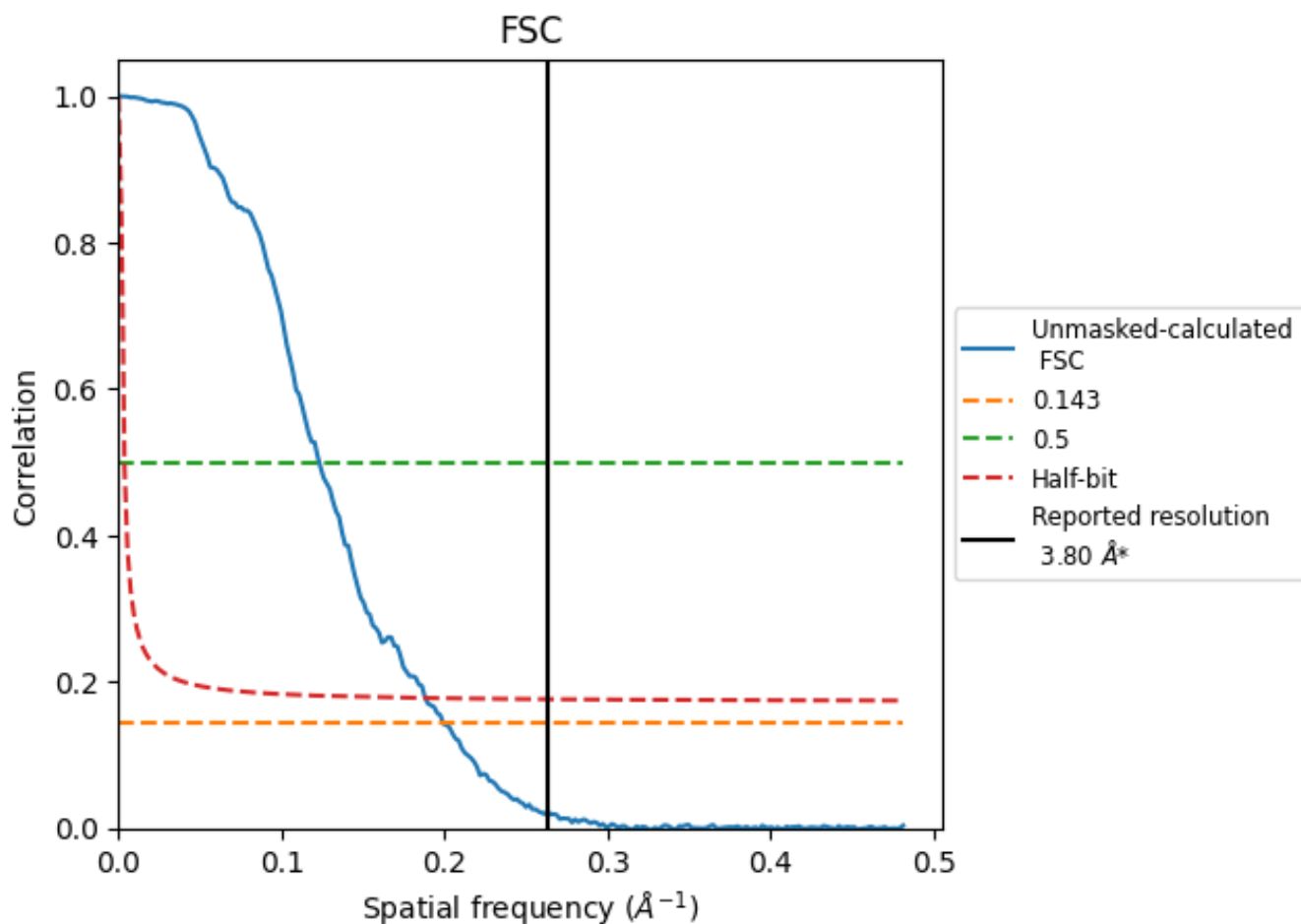


*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

8.2 Resolution estimates [i](#)

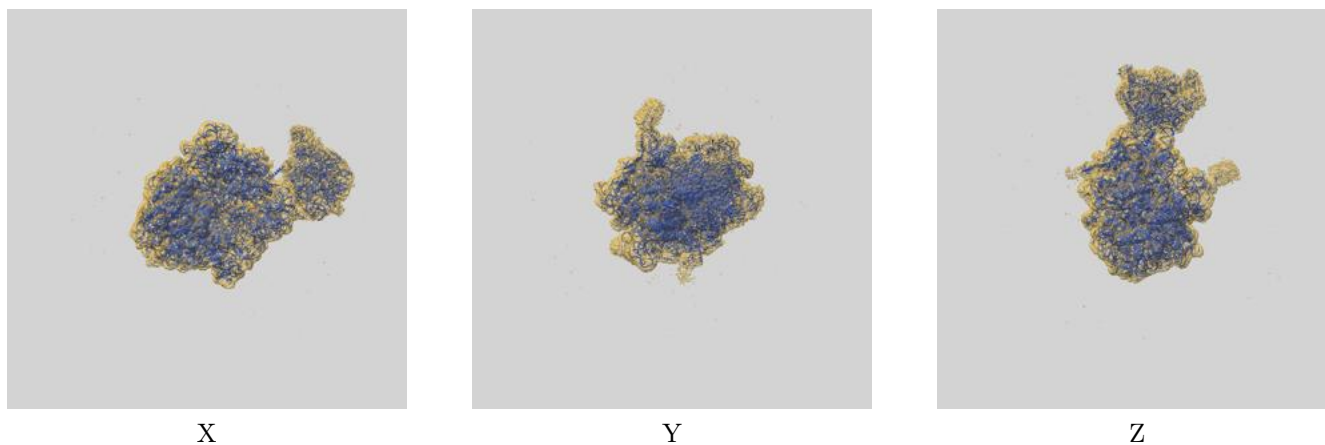
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	5.02	8.12	5.31

*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 5.02 differs from the reported value 3.8 by more than 10 %

9 Map-model fit [i](#)

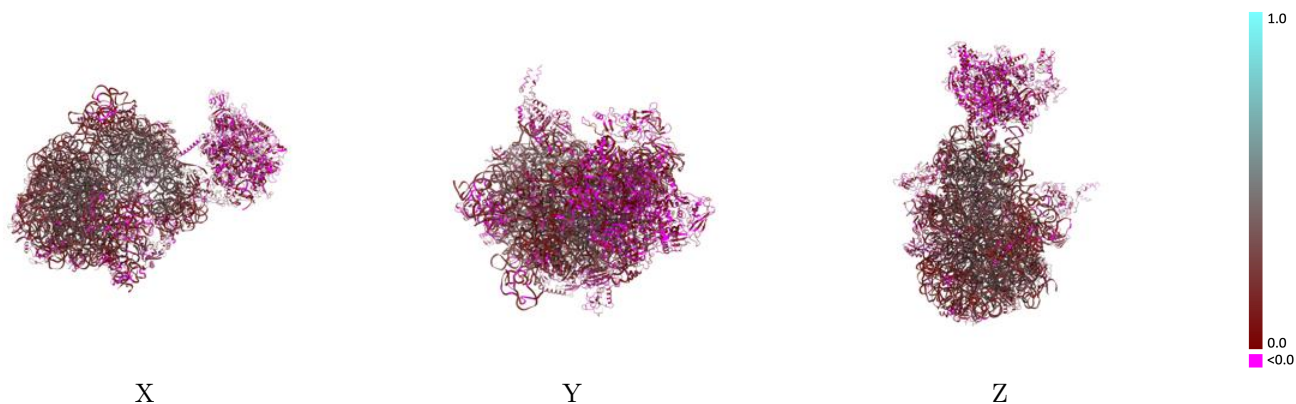
This section contains information regarding the fit between EMDB map EMD-42477 and PDB model 8UQP. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)



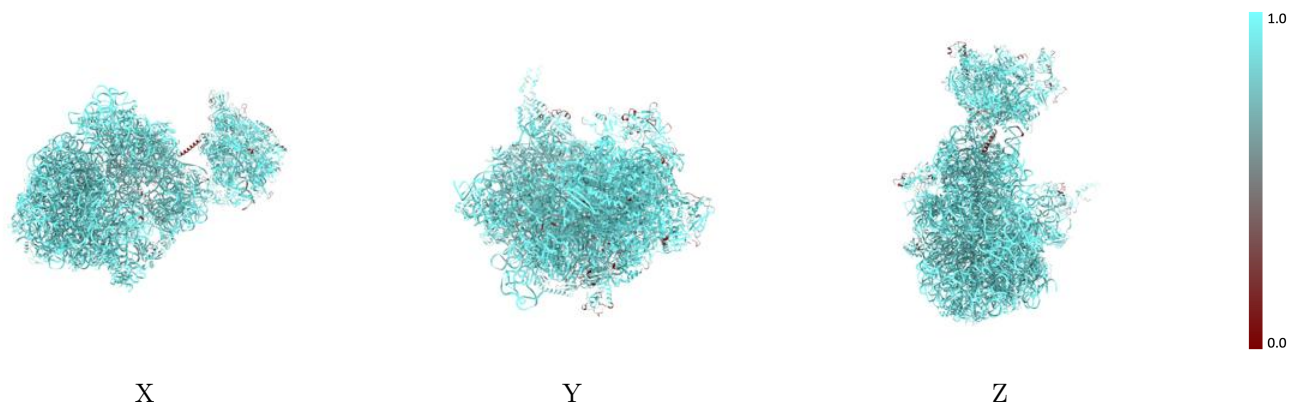
The images above show the 3D surface view of the map at the recommended contour level 0.0037 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



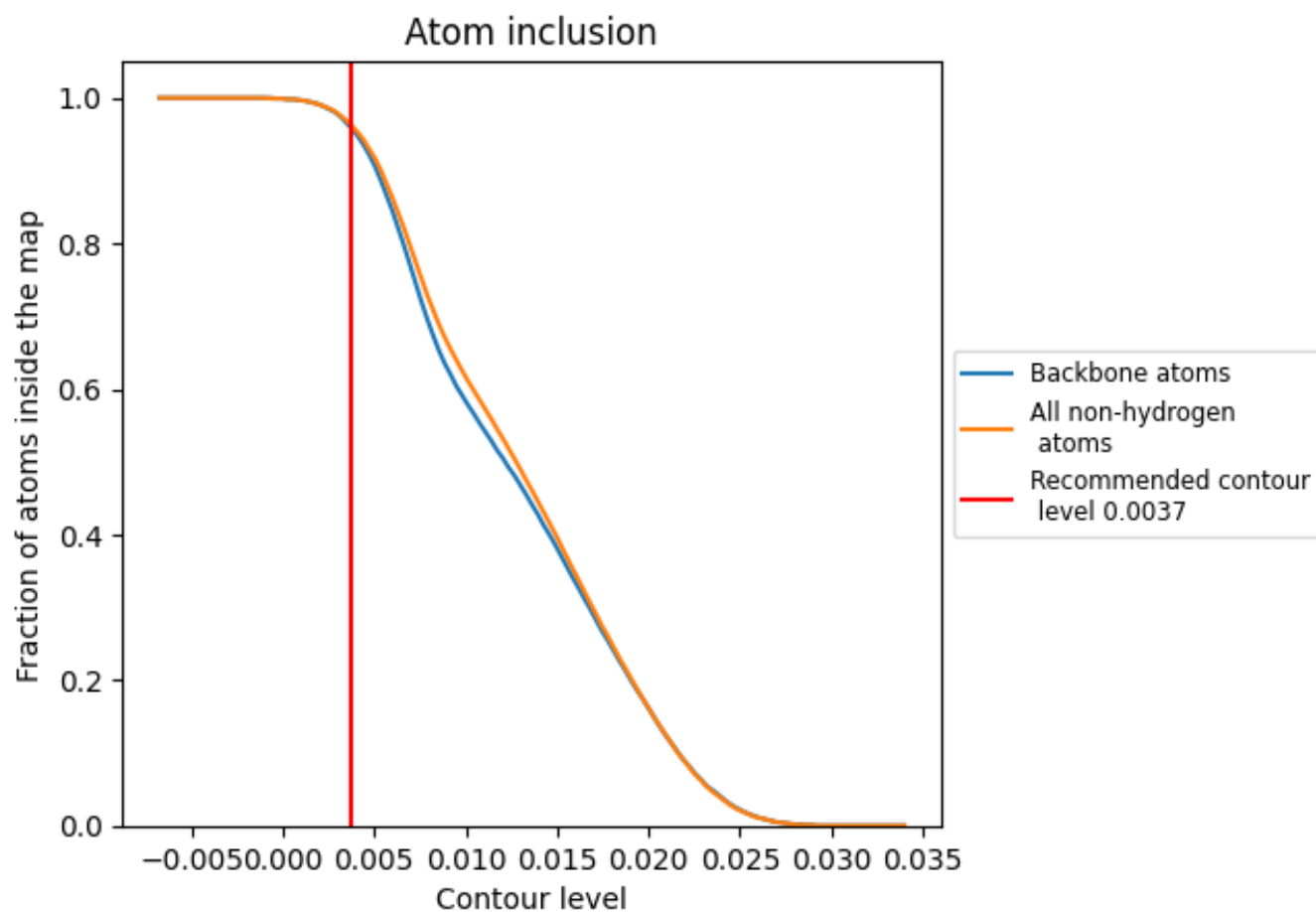
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0037).






































































9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 96% 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 (0.0037) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9640	 0.1970
0	 0.9620	 0.1700
1	 0.9580	 0.2760
2	 0.9490	 0.1540
3	 0.9550	 0.1090
4	 0.9730	 0.1470
5	 0.9020	 0.0740
6	 0.8790	 0.1000
7	 0.9260	 0.1100
9	 0.9120	 0.0720
A	 0.9880	 0.1760
AA	 0.9380	 0.0470
AB	 0.9750	 0.1520
AC	 0.9330	 0.0440
AD	 0.8380	 0.0120
AE	 0.9330	 0.0610
AF	 0.5600	 0.0210
B	 0.9200	 0.0920
C	 0.9730	 0.1770
D	 0.9940	 0.2680
E	 0.9790	 0.1620
F	 0.9590	 0.2180
G	 0.9560	 0.2080
H	 0.7420	 0.0610
I	 0.9620	 0.2700
J	 0.9800	 0.2420
K	 0.9830	 0.3380
L	 0.9540	 0.1120
M	 0.9650	 0.1790
N	 0.9710	 0.2650
O	 0.9720	 0.1620
P	 0.9600	 0.2040
Q	 0.9580	 0.1750
R	 0.9890	 0.3460
S	 0.9730	 0.1960



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Chain	Atom inclusion	Q-score
T	 0.9710	 0.2030
U	 0.9670	 0.1880
V	 0.9650	 0.2250
W	 0.9120	 0.1020
X	 0.9370	 0.1280
Y	 0.7780	 0.0690
Z	 0.8850	 0.0720
a	 0.9920	 0.2390
b	 0.9470	 0.1440
c	 0.9530	 0.1960
d	 0.9860	 0.1490
e	 0.9450	 0.1240
f	 0.9660	 0.1780
g	 0.9370	 0.0700
h	 0.9680	 0.2090
i	 0.9700	 0.2910
j	 0.9770	 0.2520
k	 0.9710	 0.1310
l	 0.9260	 0.1280
m	 0.9800	 0.2970
n	 0.9310	 0.1110
o	 0.9470	 0.1670
p	 0.9680	 0.1270
q	 0.9560	 0.1680
r	 0.8130	 0.0960
s	 0.9670	 0.2210
t	 0.9590	 0.2830
u	 0.9530	 0.1440
v	 0.9710	 0.2290
w	 0.9720	 0.2430
x	 0.9490	 0.0410
y	 0.9620	 0.2170
z	 0.9710	 0.2310