wwPDB EM Validation Summary Report

Apr 17, 2024 – 02:29 am BST

PDB ID	:	8PHJ
EMDB ID	:	EMD-17667
Title	:	cA4-bound Cami1 in complex with 70S ribosome
Authors	:	Tamulaitiene, G.; Mogila, I.; Sasnauskas, G.; Tamulaitis, G.
Deposited on	:	2023-06-20
Resolution	:	3.67 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 (i) 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 (i)) were used in the production of this report:

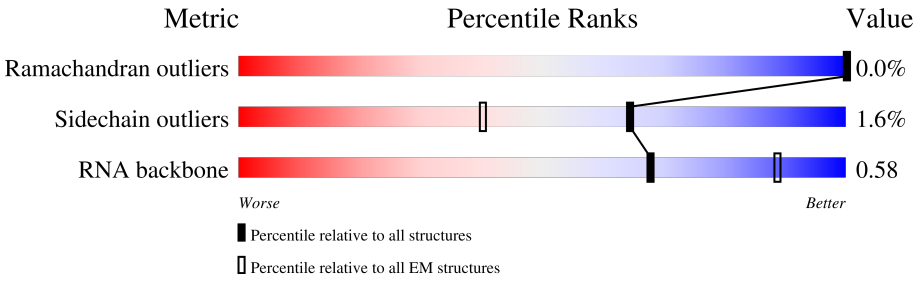
EMDB validation analysis	:	0.0.1.dev92
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.67 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 >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	55	91% · 7%
2	1	46	· 100%
3	2	65	97% · ·
4	3	38	100%
5	4	70	86% 14%
6	5	165	7% 73% 27%
7	6	142	5% 94% · 6%
8	7	77	14% 70% 25% · ·

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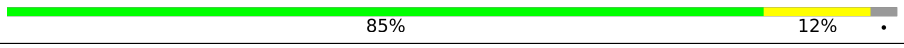
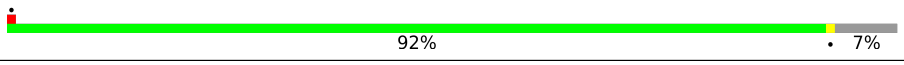
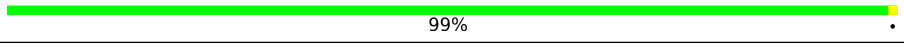
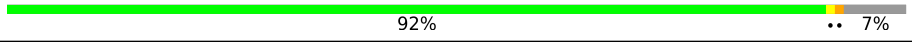
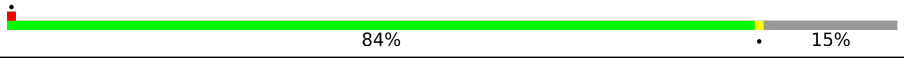
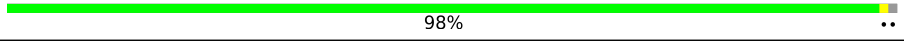
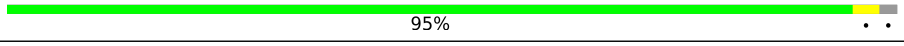
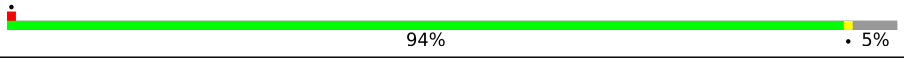
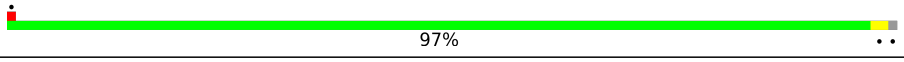
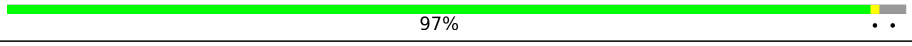
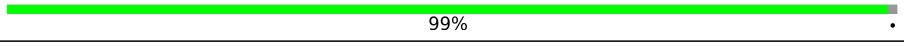
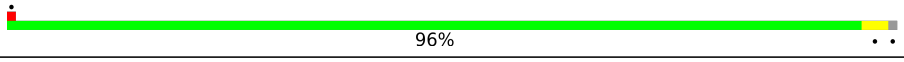
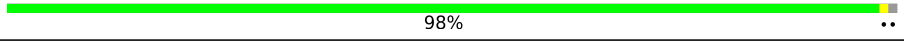
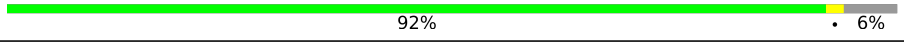
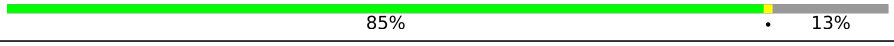
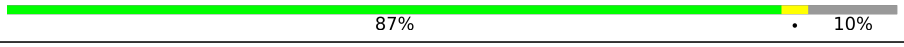
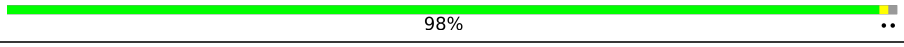
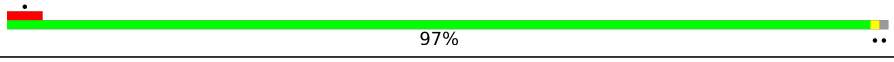
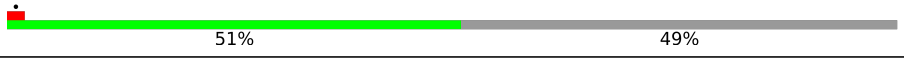
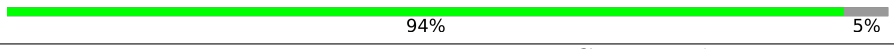
Mol	Chain	Length	Quality of chain
8	8	77	
9	9	31	
10	A	1542	
11	B	241	
12	C	233	
13	D	206	
14	E	167	
15	F	135	
16	G	179	
17	H	130	
18	I	130	
19	J	103	
20	K	129	
21	L	124	
22	M	118	
23	N	101	
24	O	89	
25	P	82	
26	Q	84	
27	R	75	
28	S	92	
29	T	87	
30	U	71	
31	W	120	
32	X	406	

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Mol	Chain	Length	Quality of chain
32	Y	406	92% 8%
33	a	2904	87% 12%
34	b	120	91% 8%
35	c	273	99%
36	d	209	98%
37	e	201	99%
38	f	179	97%
39	g	177	95%
40	h	149	11% 97%
41	i	142	99%
42	j	123	98%
43	k	144	97%
44	l	136	99%
45	m	127	91% 7%
46	n	117	97%
47	o	115	99%
48	p	118	98%
49	q	103	99%
50	r	110	98%
51	s	100	92% 7%
52	t	104	92% 7%
53	u	94	98%
54	v	85	89% 9%
55	w	78	97%
56	x	63	94% 5%

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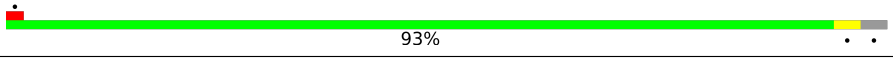
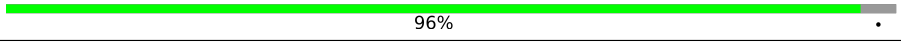
Mol	Chain	Length	Quality of chain
57	y	59	
58	z	57	
59	Z	4	

2 Entry composition (i)

There are 61 unique types of molecules in this entry. The entry contains 152518 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	0	51	Total	C	N	O	0	0
			417	269	76	72		

- Molecule 2 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 3 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 4 is a protein called Large ribosomal subunit protein bL36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 5 is a protein called Large ribosomal subunit protein bL31A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	60	Total	C	N	O	S	0	0
			480	299	90	85	6		

- Molecule 6 is a protein called Large ribosomal subunit protein uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	121	Total	C	N	O	S	0	0
			907	577	161	166	3		

- Molecule 7 is a protein called Large ribosomal subunit protein uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	134	Total	C	N	O	S	0	0
			968	613	167	182	6		

- Molecule 8 is a RNA chain called fMet-tRNA(fMet).

Mol	Chain	Residues	Atoms						AltConf	Trace
8	7	76	Total	C	N	O	P	S	0	0
			1625	726	294	528	76	1		
8	8	77	Total	C	N	O	P	S	0	0
			1642	735	297	533	76	1		

- Molecule 9 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	9	3	Total	C	N	O	P	0	0
			65	29	12	21	3		

- Molecule 10 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	A	1503	Total	C	N	O	P	0	0
			32276	14402	5932	10439	1503		

- Molecule 11 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	B	224	Total	C	N	O	S	0	0
			1753	1109	315	321	8		

- Molecule 12 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	C	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 13 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	D	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 14 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	E	156	Total	C	N	O	S	0	0
			1152	717	217	212	6		

- Molecule 15 is a protein called Small ribosomal subunit protein bS6, fully modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	F	103	Total	C	N	O	S	0	0
			839	530	151	151	7		

- Molecule 16 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	G	152	Total	C	N	O	S	0	0
			1185	738	227	216	4		

- Molecule 17 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	H	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 18 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	I	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 19 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	J	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 20 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	K	117	Total	C	N	O	S	0	0
			877	540	173	161	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	119	IAS	ASN	modified residue	UNP P0A7R9

- Molecule 21 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	L	123	Total	C	N	O	S	0	0
			949	585	195	165	4		

- Molecule 22 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	M	115	Total	C	N	O	S	0	0
			891	552	179	157	3		

- Molecule 23 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	N	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 24 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	O	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 25 is a protein called Small ribosomal subunit protein bS16.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	P	81	Total	C	N	O	S	0	0
			643	403	127	112	1		

- Molecule 26 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Q	79	Total	C	N	O	S	0	0
			641	406	120	112	3		

- Molecule 27 is a protein called Small ribosomal subunit protein bS18.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	R	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 28 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	S	83	Total	C	N	O	S	0	0
			663	424	126	111	2		

- Molecule 29 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	T	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

- Molecule 30 is a protein called Small ribosomal subunit protein bS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	U	70	Total	C	N	O	S	0	0
			589	366	125	97	1		

- Molecule 31 is a protein called Large ribosomal subunit protein bL12.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	W	61	Total	C	N	O	0	0
			402	251	71	80		

- Molecule 32 is a protein called CRISPR-associated protein, APE2256 family.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	X	384	Total	C	N	O	S	0	0
			2984	1905	531	538	10		
32	Y	375	Total	C	N	O	S	0	0
			2912	1852	517	533	10		

There are 56 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	2	ALA	PRO	engineered mutation	UNP D3RW14
X	11	ALA	SER	engineered mutation	UNP D3RW14
X	343	ALA	HIS	engineered mutation	UNP D3RW14
X	382	GLY	-	expression tag	UNP D3RW14

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Chain	Residue	Modelled	Actual	Comment	Reference
X	383	GLU	-	expression tag	UNP D3RW14
X	384	GLY	-	expression tag	UNP D3RW14
X	385	TRP	-	expression tag	UNP D3RW14
X	386	SER	-	expression tag	UNP D3RW14
X	387	HIS	-	expression tag	UNP D3RW14
X	388	PRO	-	expression tag	UNP D3RW14
X	389	GLN	-	expression tag	UNP D3RW14
X	390	PHE	-	expression tag	UNP D3RW14
X	391	GLU	-	expression tag	UNP D3RW14
X	392	LYS	-	expression tag	UNP D3RW14
X	393	GLY	-	expression tag	UNP D3RW14
X	394	VAL	-	expression tag	UNP D3RW14
X	395	GLU	-	expression tag	UNP D3RW14
X	396	GLY	-	expression tag	UNP D3RW14
X	397	HIS	-	expression tag	UNP D3RW14
X	398	HIS	-	expression tag	UNP D3RW14
X	399	HIS	-	expression tag	UNP D3RW14
X	400	HIS	-	expression tag	UNP D3RW14
X	401	HIS	-	expression tag	UNP D3RW14
X	402	HIS	-	expression tag	UNP D3RW14
X	403	HIS	-	expression tag	UNP D3RW14
X	404	HIS	-	expression tag	UNP D3RW14
X	405	HIS	-	expression tag	UNP D3RW14
X	406	HIS	-	expression tag	UNP D3RW14
Y	2	ALA	PRO	engineered mutation	UNP D3RW14
Y	11	ALA	SER	engineered mutation	UNP D3RW14
Y	343	ALA	HIS	engineered mutation	UNP D3RW14
Y	382	GLY	-	expression tag	UNP D3RW14
Y	383	GLU	-	expression tag	UNP D3RW14
Y	384	GLY	-	expression tag	UNP D3RW14
Y	385	TRP	-	expression tag	UNP D3RW14
Y	386	SER	-	expression tag	UNP D3RW14
Y	387	HIS	-	expression tag	UNP D3RW14
Y	388	PRO	-	expression tag	UNP D3RW14
Y	389	GLN	-	expression tag	UNP D3RW14
Y	390	PHE	-	expression tag	UNP D3RW14
Y	391	GLU	-	expression tag	UNP D3RW14
Y	392	LYS	-	expression tag	UNP D3RW14
Y	393	GLY	-	expression tag	UNP D3RW14
Y	394	VAL	-	expression tag	UNP D3RW14
Y	395	GLU	-	expression tag	UNP D3RW14
Y	396	GLY	-	expression tag	UNP D3RW14

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Chain	Residue	Modelled	Actual	Comment	Reference
Y	397	HIS	-	expression tag	UNP D3RW14
Y	398	HIS	-	expression tag	UNP D3RW14
Y	399	HIS	-	expression tag	UNP D3RW14
Y	400	HIS	-	expression tag	UNP D3RW14
Y	401	HIS	-	expression tag	UNP D3RW14
Y	402	HIS	-	expression tag	UNP D3RW14
Y	403	HIS	-	expression tag	UNP D3RW14
Y	404	HIS	-	expression tag	UNP D3RW14
Y	405	HIS	-	expression tag	UNP D3RW14
Y	406	HIS	-	expression tag	UNP D3RW14

- Molecule 33 is a RNA chain called 23S rRNA (2862-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
33	a	2862	Total	C	N	O	P	0	0
			61456	27423	11310	19861	2862		

- Molecule 34 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	b	119	Total	C	N	O	P	0	0
			2549	1135	466	829	119		

- Molecule 35 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	c	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 36 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	d	209	Total	C	N	O	S	0	0
			1566	980	288	294	4		

- Molecule 37 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	e	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 38 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	f	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 39 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	g	174	Total	C	N	O	S	0	0
			1301	819	239	241	2		

- Molecule 40 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	h	145	Total	C	N	O	S	0	0
			1079	682	192	204	1		

- Molecule 41 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	i	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 42 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	j	123	Total	C	N	O	S	0	0
			946	593	181	166	6		

- Molecule 43 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	k	143	Total	C	N	O	S	0	0
			1043	649	206	186	2		

- Molecule 44 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	l	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 45 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	m	118	Total 945	C 585	N 194	O 161	S 5	0	0

- Molecule 46 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	n	116	Total 892	C 552	N 178	O 162	0	0

- Molecule 47 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	o	114	Total 917	C 574	N 179	O 163	S 1	0	0

- Molecule 48 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	p	117	Total 947	C 604	N 192	O 151	0	0

- Molecule 49 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	q	103	Total 816	C 516	N 153	O 145	S 2	0	0

- Molecule 50 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	r	110	Total 857	C 532	N 166	O 156	S 3	0	0

- Molecule 51 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	s	93	Total 738	C 466	N 139	O 131	S 2	0	0

- Molecule 52 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	t	97	Total 742	C 469	N 139	O 134	0	0

- Molecule 53 is a protein called Large ribosomal subunit protein bL25.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	u	94	Total 753	C 479	N 137	O 134	S 3	0	0

- Molecule 54 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	v	77	Total 582	C 360	N 115	O 106	S 1	0	0

- Molecule 55 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	w	77	Total 625	C 388	N 129	O 106	S 2	0	0

- Molecule 56 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	x	60	Total 491	C 303	N 96	O 91	S 1	0	0

- Molecule 57 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	y	57	Total 440	C 275	N 85	O 78	S 2	0	0

- Molecule 58 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	z	55	Total 434	C 263	N 92	O 78	S 1	0	0

- Molecule 59 is a RNA chain called Cyclic tetraadenosine monophosphate (cA4).

Mol	Chain	Residues	Atoms					AltConf	Trace
59	Z	4	Total	C	N	O	P	0	0
			88	40	20	24	4		

- Molecule 60 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
60	3	1	Total	Zn	0
			1	1	
60	4	1	Total	Zn	0
			1	1	

- Molecule 61 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

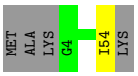
Mol	Chain	Residues	Atoms		AltConf
61	A	79	Total	Mg	0
			79	79	
61	a	156	Total	Mg	0
			156	156	
61	b	4	Total	Mg	0
			4	4	
61	c	1	Total	Mg	0
			1	1	
61	z	1	Total	Mg	0
			1	1	

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.

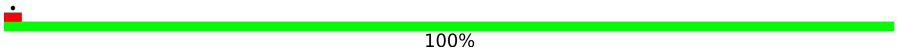
• Molecule 1: Large ribosomal subunit protein bL33

Chain 0:



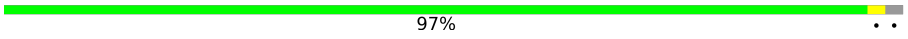
• Molecule 2: Large ribosomal subunit protein bL34

Chain 1:



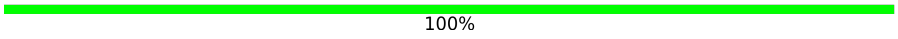
• Molecule 3: Large ribosomal subunit protein bL35

Chain 2:



• Molecule 4: Large ribosomal subunit protein bL36A

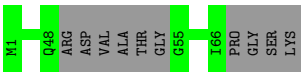
Chain 3:



There are no outlier residues recorded for this chain.

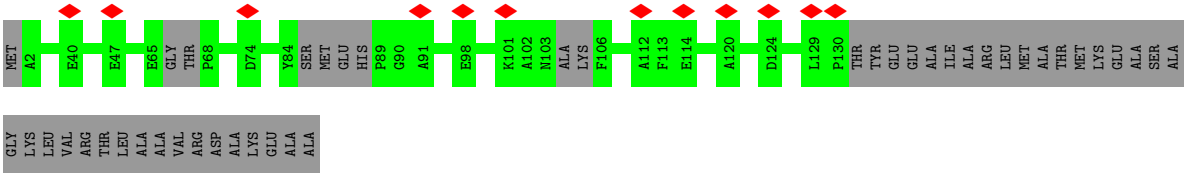
• Molecule 5: Large ribosomal subunit protein bL31A

Chain 4:

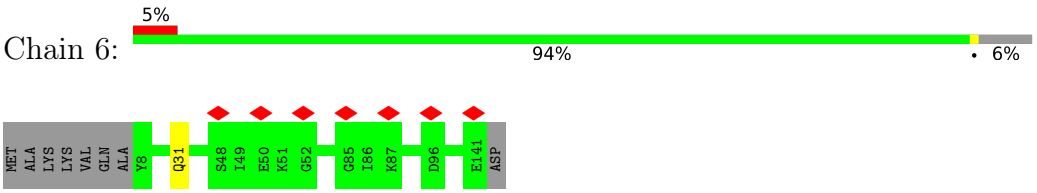


• Molecule 6: Large ribosomal subunit protein uL10

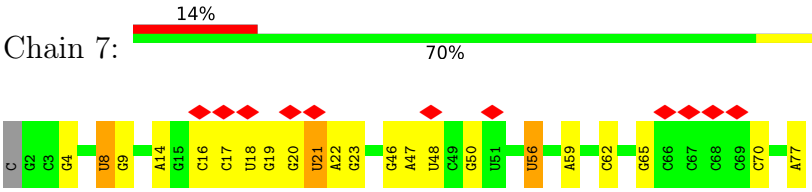
Chain 5:



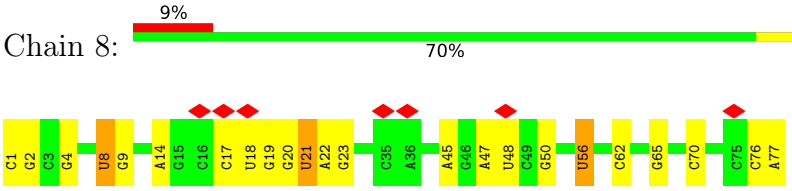
• Molecule 7: Large ribosomal subunit protein uL11



• Molecule 8: fMet-tRNA(fMet)

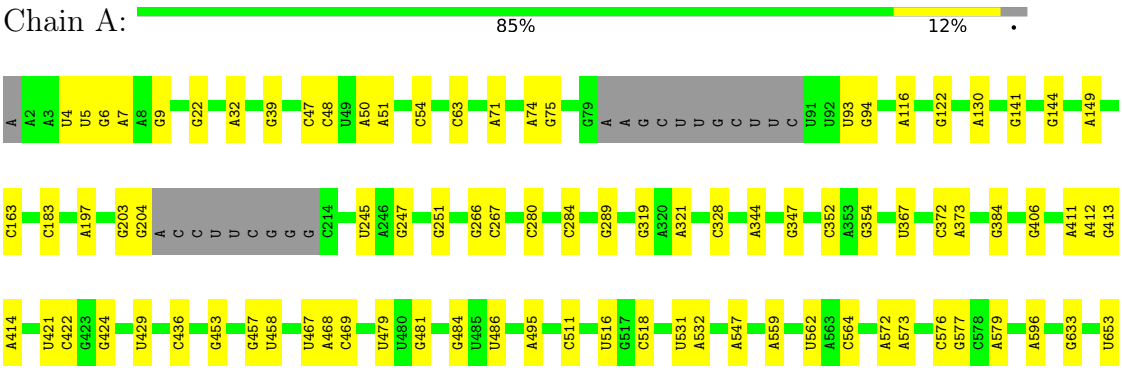


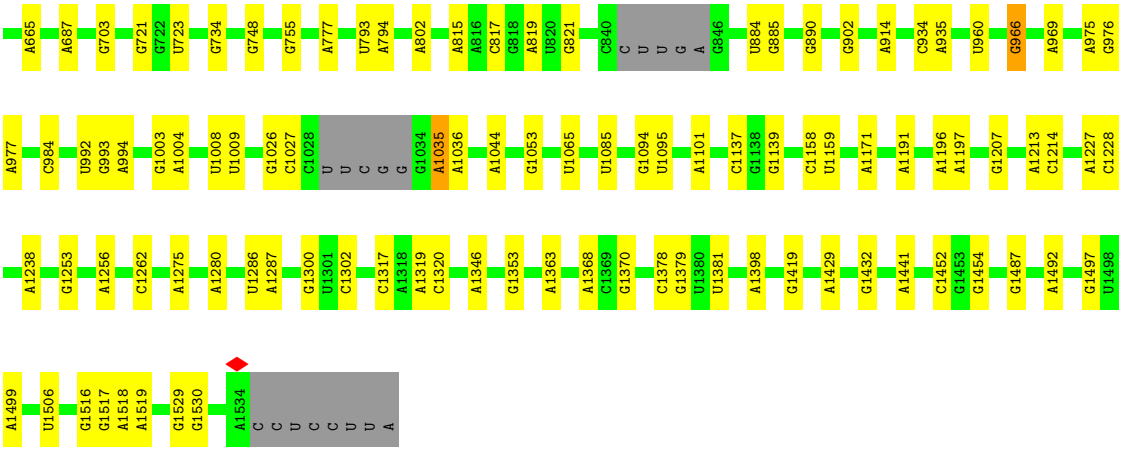
• Molecule 8: fMet-tRNA(fMet)



• Molecule 9: mRNA

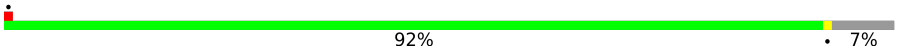
• Molecule 10: 16S rRNA

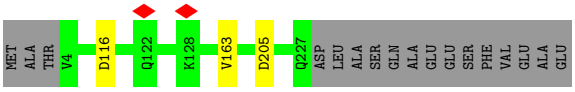




• Molecule 11: Small ribosomal subunit protein uS2

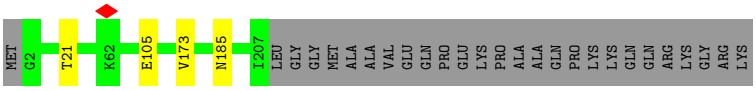
Chain B:





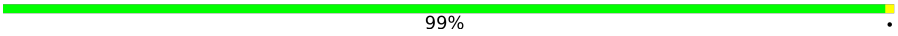
• Molecule 12: Small ribosomal subunit protein uS3

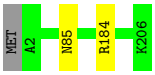
Chain C:



• Molecule 13: Small ribosomal subunit protein uS4

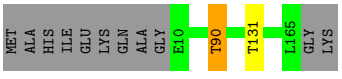
Chain D:





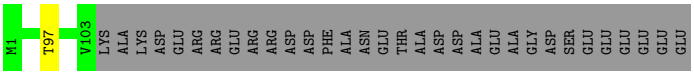
• Molecule 14: Small ribosomal subunit protein uS5

Chain E:



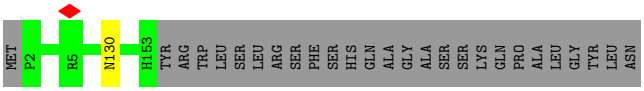
• Molecule 15: Small ribosomal subunit protein bS6, fully modified isoform

Chain F:



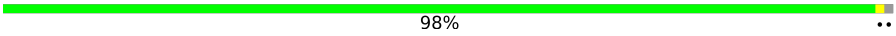
• Molecule 16: Small ribosomal subunit protein uS7

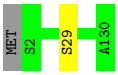
Chain G:



• Molecule 17: Small ribosomal subunit protein uS8

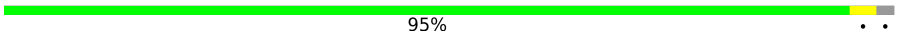
Chain H:





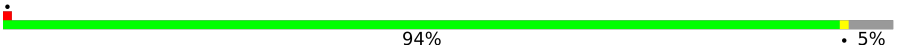
• Molecule 18: Small ribosomal subunit protein uS9

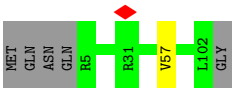
Chain I:



• Molecule 19: Small ribosomal subunit protein uS10

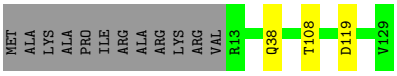
Chain J:





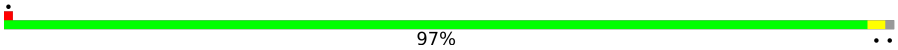
• Molecule 20: Small ribosomal subunit protein uS11

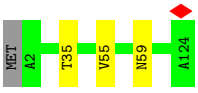
Chain K:



• Molecule 21: Small ribosomal subunit protein uS12

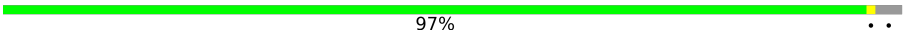
Chain L:





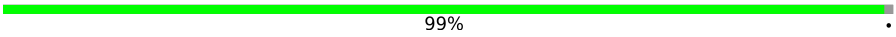
• Molecule 22: Small ribosomal subunit protein uS13

Chain M:



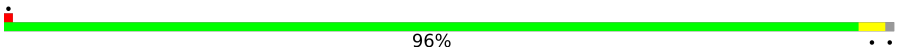
• Molecule 23: Small ribosomal subunit protein uS14

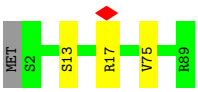
Chain N:



• Molecule 24: Small ribosomal subunit protein uS15

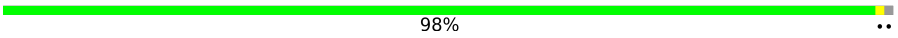
Chain O:

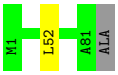




• Molecule 25: Small ribosomal subunit protein bS16

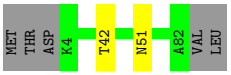
Chain P:





• Molecule 26: Small ribosomal subunit protein uS17

Chain Q:

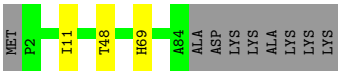


• Molecule 27: Small ribosomal subunit protein bS18

Chain R:

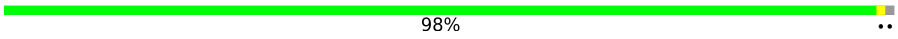
• Molecule 28: Small ribosomal subunit protein uS19

Chain S:



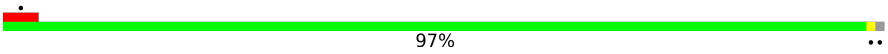
• Molecule 29: Small ribosomal subunit protein bS20

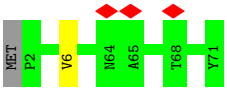
Chain T:



• Molecule 30: Small ribosomal subunit protein bS21

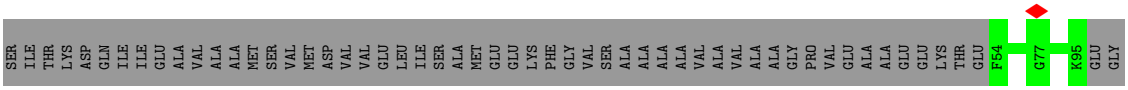
Chain U:

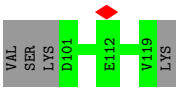




• Molecule 31: Large ribosomal subunit protein bL12

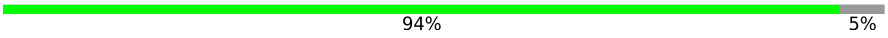
Chain W:

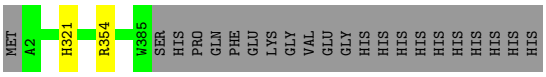




• Molecule 32: CRISPR-associated protein, APE2256 family

Chain X:



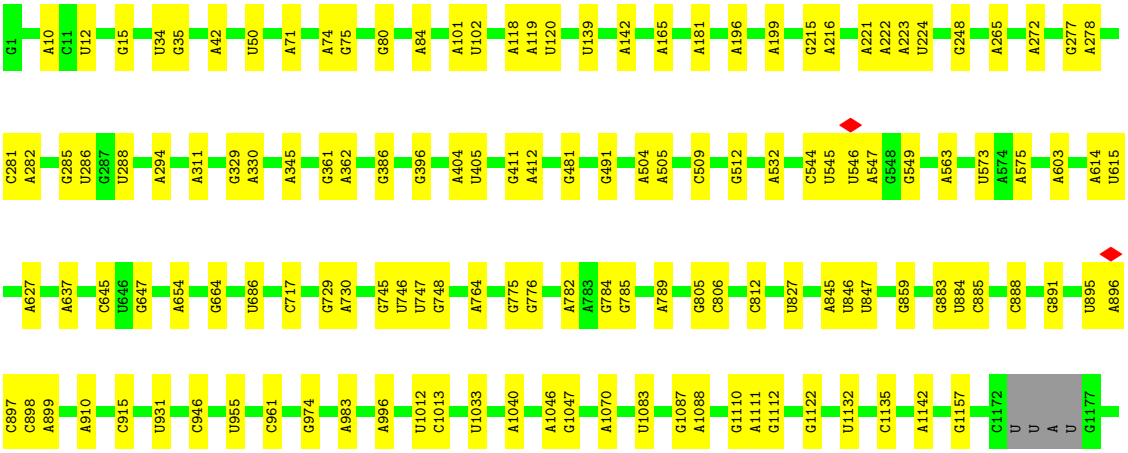


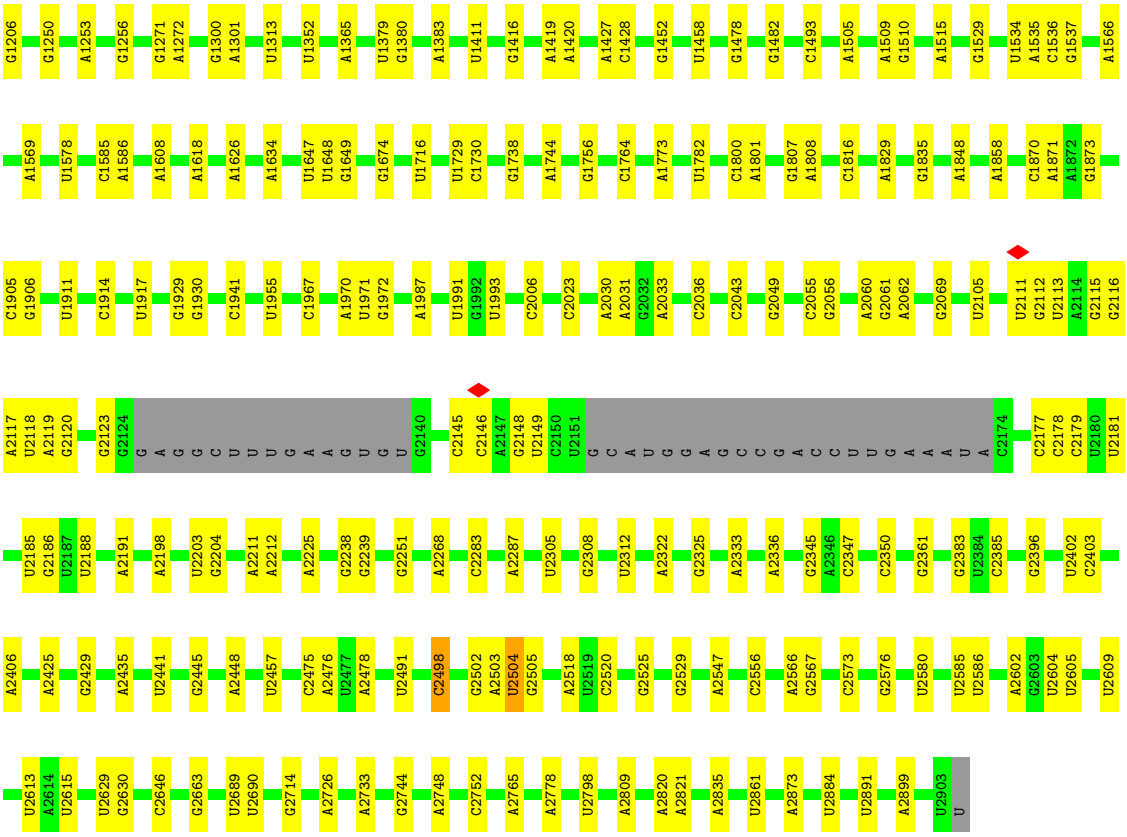
• Molecule 32: CRISPR-associated protein, APE2256 family

Chain Y:

• Molecule 33: 23S rRNA (2862-MER)

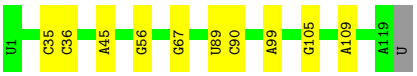
Chain a:





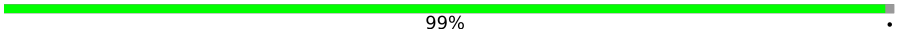
• Molecule 34: 5S rRNA

Chain b:



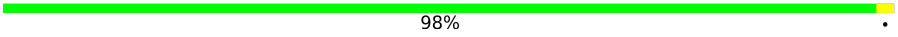
• Molecule 35: Large ribosomal subunit protein uL2

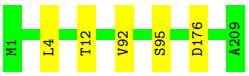
Chain c:



• Molecule 36: Large ribosomal subunit protein uL3

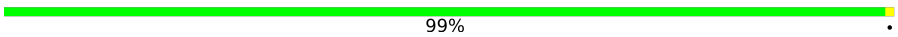
Chain d:

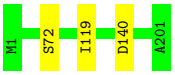




• Molecule 37: Large ribosomal subunit protein uL4

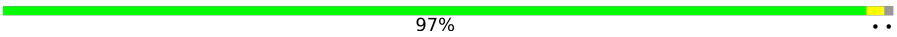
Chain e:

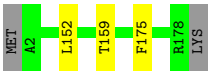




• Molecule 38: Large ribosomal subunit protein uL5

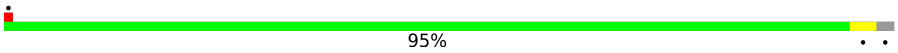
Chain f:

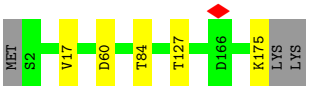




• Molecule 39: Large ribosomal subunit protein uL6

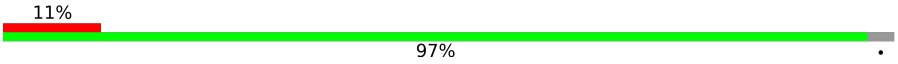
Chain g:

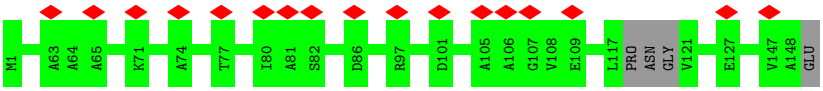




• Molecule 40: Large ribosomal subunit protein bL9

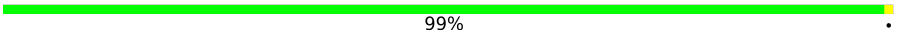
Chain h:





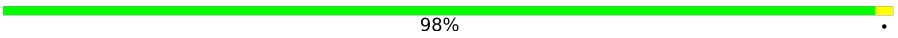
• Molecule 41: Large ribosomal subunit protein uL13

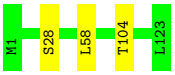
Chain i:



• Molecule 42: Large ribosomal subunit protein uL14

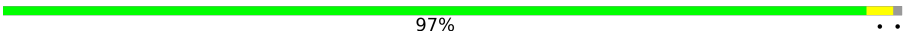
Chain j:





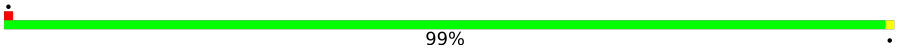
• Molecule 43: Large ribosomal subunit protein uL15

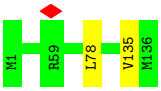
Chain k:



• Molecule 44: Large ribosomal subunit protein uL16

Chain l:



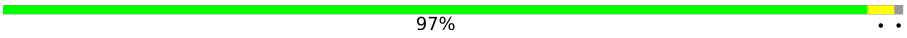


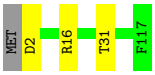
• Molecule 45: Large ribosomal subunit protein bL17

Chain m:

• Molecule 46: Large ribosomal subunit protein uL18

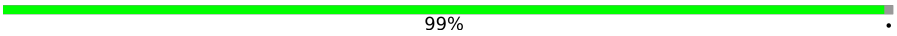
Chain n:





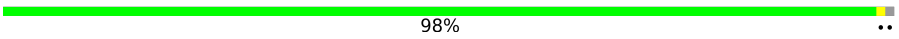
• Molecule 47: Large ribosomal subunit protein bL19

Chain o:



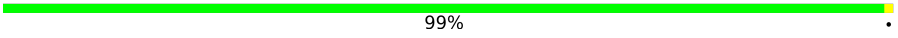
• Molecule 48: Large ribosomal subunit protein bL20

Chain p:



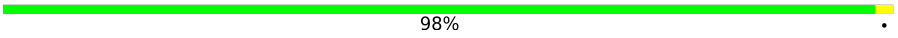
• Molecule 49: Large ribosomal subunit protein bL21

Chain q:



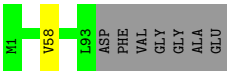
• Molecule 50: Large ribosomal subunit protein uL22

Chain r:



• Molecule 51: Large ribosomal subunit protein uL23

Chain s:

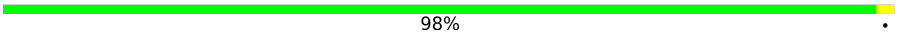


• Molecule 52: Large ribosomal subunit protein uL24

Chain t:

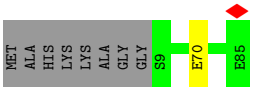
• Molecule 53: Large ribosomal subunit protein bL25

Chain u:



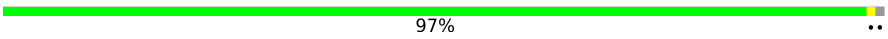
• Molecule 54: Large ribosomal subunit protein bL27

Chain v:



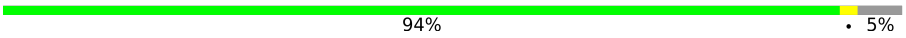
• Molecule 55: Large ribosomal subunit protein bL28

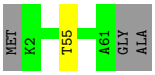
Chain w:



• Molecule 56: Large ribosomal subunit protein uL29

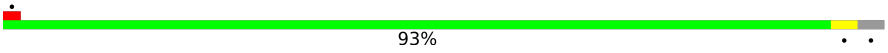
Chain x:

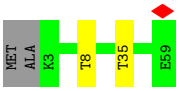




• Molecule 57: Large ribosomal subunit protein uL30

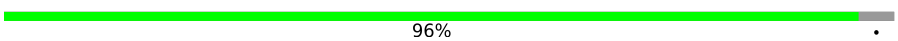
Chain y:





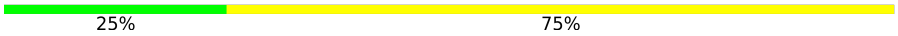
• Molecule 58: Large ribosomal subunit protein bL32

Chain z:



• Molecule 59: Cyclic tetraadenosine monophosphate (cA4)

Chain Z:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	158387	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/Å^2$)	30	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	33.264	Depositor
Minimum map value	-14.170	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2.0	Depositor
Map size (Å)	448.0, 448.0, 448.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.12, 1.12, 1.12	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 6MZ, OMG, MA6, 5MC, G7M, 1MG, PSU, UR3, 3TD, 2MG, OMU, H2U, 4SU, OMC, MG, ZN, IAS, 5MU, 4OC, MEQ, 2MA

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	0.34	0/424	0.53	0/565
2	1	0.32	0/380	0.65	0/498
3	2	0.31	0/513	0.53	0/676
4	3	0.33	0/303	0.57	0/397
5	4	0.27	0/488	0.48	0/649
6	5	0.25	0/916	0.50	0/1232
7	6	0.25	0/982	0.46	0/1328
8	7	0.25	0/1701	0.69	0/2649
8	8	0.22	0/1720	0.69	0/2679
9	9	0.33	0/72	0.63	0/110
10	A	0.54	0/35860	0.72	2/55930 (0.0%)
11	B	0.26	0/1784	0.47	0/2403
12	C	0.29	0/1651	0.52	0/2225
13	D	0.30	0/1665	0.51	0/2227
14	E	0.32	0/1165	0.51	0/1568
15	F	0.29	0/858	0.50	0/1160
16	G	0.26	0/1200	0.50	0/1610
17	H	0.31	0/989	0.51	0/1326
18	I	0.29	0/1034	0.56	0/1375
19	J	0.29	0/796	0.57	0/1077
20	K	0.29	0/884	0.54	0/1191
21	L	0.32	0/963	0.58	0/1293
22	M	0.27	0/900	0.54	0/1204
23	N	0.28	0/817	0.52	0/1088
24	O	0.27	0/722	0.52	0/964
25	P	0.32	0/653	0.56	0/877
26	Q	0.31	0/650	0.53	0/871
27	R	0.31	0/544	0.52	0/731
28	S	0.28	0/680	0.50	0/915
29	T	0.27	0/676	0.45	0/895
30	U	0.27	0/597	0.56	0/792

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
31	W	0.24	0/401	0.43	0/541
32	X	0.33	0/3049	0.51	0/4143
32	Y	0.34	0/2972	0.52	0/4039
33	a	0.63	0/68253	0.75	5/106469 (0.0%)
34	b	0.49	0/2850	0.70	0/4444
35	c	0.35	0/2121	0.57	0/2852
36	d	0.34	0/1576	0.54	0/2119
37	e	0.30	0/1571	0.52	0/2113
38	f	0.28	0/1434	0.50	0/1926
39	g	0.30	0/1321	0.51	0/1790
40	h	0.26	0/1088	0.50	0/1468
41	i	0.34	0/1152	0.51	0/1551
42	j	0.33	0/955	0.58	0/1279
43	k	0.31	0/1052	0.57	0/1401
44	l	0.33	0/1093	0.56	0/1460
45	m	0.32	0/958	0.57	0/1281
46	n	0.30	0/902	0.54	0/1209
47	o	0.33	0/929	0.54	0/1242
48	p	0.36	0/960	0.53	0/1278
49	q	0.33	0/829	0.56	0/1107
50	r	0.30	0/864	0.53	0/1156
51	s	0.30	0/744	0.51	0/994
52	t	0.29	0/748	0.50	0/994
53	u	0.31	0/766	0.50	0/1025
54	v	0.33	0/589	0.55	0/780
55	w	0.31	0/635	0.58	0/848
56	x	0.25	0/492	0.51	0/655
57	y	0.29	0/444	0.55	0/594
58	z	0.34	0/440	0.59	0/588
59	Z	0.69	0/99	0.82	0/152
All	All	0.52	0/163874	0.68	7/244003 (0.0%)

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
33	a	512	G	O4'-C1'-N9	6.07	113.06	108.20
33	a	1313	U	C2-N1-C1'	6.00	124.91	117.70
33	a	12	U	N3-C2-O2	-5.73	118.19	122.20
10	A	1158	C	C2-N1-C1'	5.58	124.93	118.80
33	a	12	U	N1-C2-O2	5.45	126.61	122.80

There are no chirality outliers.

There are no planarity outliers.

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	49/55 (89%)	48 (98%)	1 (2%)	0	100	100
2	1	44/46 (96%)	44 (100%)	0	0	100	100
3	2	62/65 (95%)	57 (92%)	5 (8%)	0	100	100
4	3	36/38 (95%)	36 (100%)	0	0	100	100
5	4	56/70 (80%)	54 (96%)	2 (4%)	0	100	100
6	5	113/165 (68%)	111 (98%)	2 (2%)	0	100	100
7	6	132/142 (93%)	123 (93%)	9 (7%)	0	100	100
11	B	222/241 (92%)	211 (95%)	11 (5%)	0	100	100
12	C	204/233 (88%)	197 (97%)	7 (3%)	0	100	100
13	D	203/206 (98%)	199 (98%)	4 (2%)	0	100	100
14	E	154/167 (92%)	149 (97%)	4 (3%)	1 (1%)	25	62
15	F	101/135 (75%)	97 (96%)	4 (4%)	0	100	100
16	G	150/179 (84%)	145 (97%)	5 (3%)	0	100	100
17	H	127/130 (98%)	124 (98%)	3 (2%)	0	100	100
18	I	125/130 (96%)	120 (96%)	5 (4%)	0	100	100
19	J	96/103 (93%)	90 (94%)	6 (6%)	0	100	100
20	K	113/129 (88%)	109 (96%)	4 (4%)	0	100	100
21	L	121/124 (98%)	115 (95%)	6 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	M	113/118 (96%)	109 (96%)	4 (4%)	0	100	100
23	N	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
24	O	86/89 (97%)	84 (98%)	2 (2%)	0	100	100
25	P	79/82 (96%)	75 (95%)	4 (5%)	0	100	100
26	Q	77/84 (92%)	73 (95%)	4 (5%)	0	100	100
27	R	63/75 (84%)	62 (98%)	1 (2%)	0	100	100
28	S	81/92 (88%)	79 (98%)	2 (2%)	0	100	100
29	T	84/87 (97%)	84 (100%)	0	0	100	100
30	U	68/71 (96%)	68 (100%)	0	0	100	100
31	W	57/120 (48%)	54 (95%)	3 (5%)	0	100	100
32	X	382/406 (94%)	363 (95%)	19 (5%)	0	100	100
32	Y	371/406 (91%)	351 (95%)	20 (5%)	0	100	100
35	c	269/273 (98%)	261 (97%)	8 (3%)	0	100	100
36	d	206/209 (99%)	199 (97%)	7 (3%)	0	100	100
37	e	199/201 (99%)	195 (98%)	4 (2%)	0	100	100
38	f	175/179 (98%)	169 (97%)	6 (3%)	0	100	100
39	g	172/177 (97%)	163 (95%)	9 (5%)	0	100	100
40	h	141/149 (95%)	129 (92%)	12 (8%)	0	100	100
41	i	140/142 (99%)	139 (99%)	1 (1%)	0	100	100
42	j	121/123 (98%)	117 (97%)	4 (3%)	0	100	100
43	k	141/144 (98%)	139 (99%)	2 (1%)	0	100	100
44	l	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
45	m	116/127 (91%)	112 (97%)	4 (3%)	0	100	100
46	n	114/117 (97%)	111 (97%)	3 (3%)	0	100	100
47	o	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
48	p	115/118 (98%)	115 (100%)	0	0	100	100
49	q	101/103 (98%)	97 (96%)	4 (4%)	0	100	100
50	r	108/110 (98%)	105 (97%)	3 (3%)	0	100	100
51	s	91/100 (91%)	89 (98%)	2 (2%)	0	100	100
52	t	93/104 (89%)	88 (95%)	5 (5%)	0	100	100
53	u	92/94 (98%)	90 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	v	75/85 (88%)	74 (99%)	1 (1%)	0	100	100
55	w	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
56	x	58/63 (92%)	56 (97%)	2 (3%)	0	100	100
57	y	55/59 (93%)	54 (98%)	1 (2%)	0	100	100
58	z	53/57 (93%)	53 (100%)	0	0	100	100
All	All	6623/7152 (93%)	6396 (97%)	226 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
14	E	90	THR

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	46/49 (94%)	45 (98%)	1 (2%)	52	72
2	1	38/38 (100%)	38 (100%)	0	100	100
3	2	51/52 (98%)	50 (98%)	1 (2%)	55	74
4	3	34/34 (100%)	34 (100%)	0	100	100
5	4	55/62 (89%)	55 (100%)	0	100	100
6	5	90/123 (73%)	90 (100%)	0	100	100
7	6	101/110 (92%)	100 (99%)	1 (1%)	76	86
11	B	186/199 (94%)	183 (98%)	3 (2%)	62	79
12	C	170/190 (90%)	166 (98%)	4 (2%)	49	70
13	D	172/173 (99%)	170 (99%)	2 (1%)	71	84
14	E	119/126 (94%)	117 (98%)	2 (2%)	60	79
15	F	90/116 (78%)	89 (99%)	1 (1%)	73	85
16	G	124/147 (84%)	123 (99%)	1 (1%)	81	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	H	104/105 (99%)	103 (99%)	1 (1%)	76	86
18	I	105/107 (98%)	101 (96%)	4 (4%)	33	61
19	J	86/90 (96%)	85 (99%)	1 (1%)	71	84
20	K	89/98 (91%)	87 (98%)	2 (2%)	52	72
21	L	101/104 (97%)	98 (97%)	3 (3%)	41	66
22	M	93/96 (97%)	92 (99%)	1 (1%)	73	85
23	N	83/84 (99%)	83 (100%)	0	100	100
24	O	76/77 (99%)	73 (96%)	3 (4%)	32	60
25	P	65/65 (100%)	64 (98%)	1 (2%)	65	81
26	Q	73/78 (94%)	71 (97%)	2 (3%)	44	68
27	R	56/65 (86%)	55 (98%)	1 (2%)	59	77
28	S	72/79 (91%)	69 (96%)	3 (4%)	30	59
29	T	65/66 (98%)	64 (98%)	1 (2%)	65	81
30	U	60/61 (98%)	59 (98%)	1 (2%)	60	79
31	W	33/84 (39%)	33 (100%)	0	100	100
32	X	305/339 (90%)	303 (99%)	2 (1%)	84	91
32	Y	299/339 (88%)	298 (100%)	1 (0%)	92	96
35	c	216/218 (99%)	215 (100%)	1 (0%)	88	94
36	d	163/163 (100%)	158 (97%)	5 (3%)	40	65
37	e	165/165 (100%)	162 (98%)	3 (2%)	59	77
38	f	148/150 (99%)	145 (98%)	3 (2%)	55	74
39	g	134/138 (97%)	129 (96%)	5 (4%)	34	61
40	h	110/114 (96%)	110 (100%)	0	100	100
41	i	116/116 (100%)	114 (98%)	2 (2%)	60	79
42	j	104/104 (100%)	101 (97%)	3 (3%)	42	66
43	k	102/103 (99%)	98 (96%)	4 (4%)	32	60
44	l	109/109 (100%)	107 (98%)	2 (2%)	59	77
45	m	98/103 (95%)	95 (97%)	3 (3%)	40	65
46	n	86/87 (99%)	83 (96%)	3 (4%)	36	63
47	o	99/100 (99%)	99 (100%)	0	100	100
48	p	89/90 (99%)	88 (99%)	1 (1%)	73	85

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
49	q	84/84 (100%)	83 (99%)	1 (1%)	71 84
50	r	93/93 (100%)	91 (98%)	2 (2%)	52 72
51	s	80/84 (95%)	79 (99%)	1 (1%)	69 83
52	t	79/85 (93%)	78 (99%)	1 (1%)	69 83
53	u	78/78 (100%)	76 (97%)	2 (3%)	46 69
54	v	58/63 (92%)	57 (98%)	1 (2%)	60 79
55	w	67/68 (98%)	66 (98%)	1 (2%)	65 81
56	x	54/55 (98%)	53 (98%)	1 (2%)	57 76
57	y	47/49 (96%)	45 (96%)	2 (4%)	29 58
58	z	46/48 (96%)	46 (100%)	0	100 100
All	All	5466/5823 (94%)	5376 (98%)	90 (2%)	64 79

5 of 90 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
39	g	84	THR
45	m	15	SER
39	g	175	LYS
43	k	42	SER
46	n	16	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
38	f	135	GLN
41	i	76	HIS
40	h	135	HIS
41	i	135	GLN
16	G	52	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	A	1495/1542 (96%)	180 (12%)	3 (0%)
33	a	2854/2904 (98%)	327 (11%)	0
34	b	118/120 (98%)	10 (8%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
59	Z	3/4 (75%)	3 (100%)	0
8	7	74/77 (96%)	22 (29%)	0
8	8	76/77 (98%)	22 (28%)	1 (1%)
9	9	2/31 (6%)	0	0
All	All	4622/4755 (97%)	564 (12%)	4 (0%)

5 of 564 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	7	4	G
8	7	8	4SU
8	7	9	G
8	7	14	A
8	7	16	C

All (4) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
8	8	1	C
10	A	4	U
10	A	1026	G
10	A	1035	A

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

47 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
10	MA6	A	1519	10	18,26,27	0.75	1 (5%)	19,38,41	0.72	0
8	5MU	7	55	8	19,22,23	0.36	0	28,32,35	0.52	0
33	PSU	a	2457	33	18,21,22	0.70	0	22,30,33	0.98	1 (4%)
33	OMG	a	2251	33,8	18,26,27	1.23	3 (16%)	19,38,41	0.89	1 (5%)
36	MEQ	d	150	36	8,9,10	0.82	0	5,10,12	0.41	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
33	5MU	a	1939	33	19,22,23	0.40	0	28,32,35	0.57	0
10	2MG	A	1516	10	18,26,27	1.15	2 (11%)	16,38,41	1.18	3 (18%)
10	MA6	A	1518	10	18,26,27	0.74	1 (5%)	19,38,41	0.69	0
33	5MU	a	747	33	19,22,23	0.36	0	28,32,35	0.45	0
10	G7M	A	527	10	20,26,27	0.64	0	17,39,42	0.73	0
10	UR3	A	1498	10	19,22,23	0.39	0	26,32,35	0.63	0
33	6MZ	a	2030	33	18,25,26	0.82	1 (5%)	16,36,39	0.95	1 (6%)
8	H2U	8	21	8	18,21,22	0.58	0	21,30,33	0.81	1 (4%)
8	4OC	7	33	8	20,23,24	0.34	0	26,32,35	0.54	0
33	OMC	a	2498	61,33	19,22,23	0.64	0	26,31,34	0.83	1 (3%)
33	PSU	a	1911	33	18,21,22	0.62	0	22,30,33	0.95	1 (4%)
33	3TD	a	1915	33	19,22,23	0.58	0	21,32,35	0.86	0
33	PSU	a	2605	33	18,21,22	0.68	0	22,30,33	1.04	1 (4%)
8	4SU	7	8	8	18,21,22	0.37	0	26,30,33	1.19	2 (7%)
10	5MC	A	1407	10	18,22,23	0.36	0	26,32,35	0.78	0
8	PSU	8	56	8	18,21,22	0.60	0	22,30,33	0.98	1 (4%)
33	OMU	a	2552	33	19,22,23	0.39	0	26,31,34	0.46	0
33	6MZ	a	1618	33	18,25,26	0.79	1 (5%)	16,36,39	1.00	1 (6%)
8	PSU	7	56	8	18,21,22	0.60	0	22,30,33	0.98	1 (4%)
33	PSU	a	2604	33	18,21,22	0.68	0	22,30,33	1.08	1 (4%)
33	2MG	a	1835	33	18,26,27	1.15	3 (16%)	16,38,41	0.83	0
33	2MG	a	2445	33	18,26,27	1.19	2 (11%)	16,38,41	0.81	1 (6%)
10	5MC	A	967	10	18,22,23	0.37	0	26,32,35	0.70	0
33	H2U	a	2449	33	18,21,22	0.41	0	21,30,33	0.57	0
10	2MG	A	966	10	18,26,27	1.15	3 (16%)	16,38,41	0.80	0
8	4SU	8	8	8	18,21,22	0.36	0	26,30,33	1.16	2 (7%)
10	4OC	A	1402	10	20,23,24	0.34	0	26,32,35	0.58	0
33	2MA	a	2503	61,33	17,25,26	0.96	1 (5%)	17,37,40	0.82	0
33	PSU	a	955	33	18,21,22	0.69	0	22,30,33	1.03	1 (4%)
10	2MG	A	1207	10	18,26,27	1.17	3 (16%)	16,38,41	0.87	0
10	PSU	A	516	10	18,21,22	0.65	0	22,30,33	0.93	1 (4%)
33	PSU	a	1917	33	18,21,22	0.65	0	22,30,33	0.96	1 (4%)
33	5MC	a	1962	33	18,22,23	0.37	0	26,32,35	0.75	0
8	4OC	8	33	8	20,23,24	0.36	0	26,32,35	0.66	0
8	5MU	8	55	8	19,22,23	0.37	0	28,32,35	0.51	0
33	1MG	a	745	33	18,26,27	1.05	3 (16%)	19,39,42	0.71	0
33	PSU	a	2504	33	18,21,22	0.65	0	22,30,33	1.00	1 (4%)
33	G7M	a	2069	33	20,26,27	0.63	0	17,39,42	0.67	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
33	PSU	a	2580	33	18,21,22	0.72	0	22,30,33	0.93	1 (4%)
20	IAS	K	119	20	6,7,8	1.03	0	6,8,10	1.31	1 (16%)
8	H2U	7	21	8	18,21,22	0.58	0	21,30,33	0.82	1 (4%)
33	PSU	a	746	61,33	18,21,22	0.77	0	22,30,33	0.82	1 (4%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
10	MA6	A	1519	10	-	0/7/29/30	0/3/3/3
8	5MU	7	55	8	-	0/7/25/26	0/2/2/2
33	PSU	a	2457	33	-	0/7/25/26	0/2/2/2
33	OMG	a	2251	33,8	-	1/5/27/28	0/3/3/3
36	MEQ	d	150	36	-	3/8/9/11	-
33	5MU	a	1939	33	-	0/7/25/26	0/2/2/2
10	2MG	A	1516	10	-	0/5/27/28	0/3/3/3
10	MA6	A	1518	10	-	0/7/29/30	0/3/3/3
33	5MU	a	747	33	-	0/7/25/26	0/2/2/2
10	G7M	A	527	10	-	0/3/25/26	0/3/3/3
10	UR3	A	1498	10	-	0/7/25/26	0/2/2/2
33	6MZ	a	2030	33	-	2/5/27/28	0/3/3/3
8	H2U	8	21	8	-	5/7/38/39	0/2/2/2
8	4OC	7	33	8	-	0/9/29/30	0/2/2/2
33	OMC	a	2498	61,33	-	2/9/27/28	0/2/2/2
33	PSU	a	1911	33	-	0/7/25/26	0/2/2/2
33	3TD	a	1915	33	-	0/7/25/26	0/2/2/2
33	PSU	a	2605	33	-	0/7/25/26	0/2/2/2
8	4SU	7	8	8	-	0/7/25/26	0/2/2/2
10	5MC	A	1407	10	-	0/7/25/26	0/2/2/2
8	PSU	8	56	8	-	1/7/25/26	0/2/2/2
33	OMU	a	2552	33	-	0/9/27/28	0/2/2/2
33	6MZ	a	1618	33	-	0/5/27/28	0/3/3/3
8	PSU	7	56	8	-	1/7/25/26	0/2/2/2
33	PSU	a	2604	33	-	0/7/25/26	0/2/2/2
33	2MG	a	1835	33	-	0/5/27/28	0/3/3/3
33	2MG	a	2445	33	-	0/5/27/28	0/3/3/3
10	5MC	A	967	10	-	0/7/25/26	0/2/2/2
33	H2U	a	2449	33	-	0/7/38/39	0/2/2/2
10	2MG	A	966	10	-	2/5/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	4SU	8	8	8	-	0/7/25/26	0/2/2/2
10	4OC	A	1402	10	-	0/9/29/30	0/2/2/2
33	2MA	a	2503	61,33	-	2/3/25/26	0/3/3/3
33	PSU	a	955	33	-	0/7/25/26	0/2/2/2
10	2MG	A	1207	10	-	0/5/27/28	0/3/3/3
10	PSU	A	516	10	-	0/7/25/26	0/2/2/2
33	PSU	a	1917	33	-	0/7/25/26	0/2/2/2
33	5MC	a	1962	33	-	4/7/25/26	0/2/2/2
8	4OC	8	33	8	-	0/9/29/30	0/2/2/2
8	5MU	8	55	8	-	0/7/25/26	0/2/2/2
33	1MG	a	745	33	-	0/3/25/26	0/3/3/3
33	PSU	a	2504	33	-	2/7/25/26	0/2/2/2
33	G7M	a	2069	33	-	2/3/25/26	0/3/3/3
33	PSU	a	2580	33	-	0/7/25/26	0/2/2/2
20	IAS	K	119	20	-	1/7/7/8	-
8	H2U	7	21	8	-	5/7/38/39	0/2/2/2
33	PSU	a	746	61,33	-	4/7/25/26	0/2/2/2

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	A	1516	2MG	C6-N1	-3.04	1.33	1.37
33	a	2251	OMG	C8-N7	-3.00	1.29	1.35
33	a	2445	2MG	C5-C6	-2.58	1.42	1.47
33	a	1835	2MG	C5-C6	-2.57	1.42	1.47
10	A	966	2MG	C5-C6	-2.54	1.42	1.47

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	7	8	4SU	C4-N3-C2	-3.72	123.73	127.34
8	8	8	4SU	C4-N3-C2	-3.67	123.77	127.34
10	A	1516	2MG	C5-C6-N1	2.73	118.77	113.95
33	a	2251	OMG	O6-C6-C5	2.61	129.48	124.37
33	a	2030	6MZ	C2-N1-C6	2.59	118.81	116.59

There are no chirality outliers.

5 of 37 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	7	21	H2U	O4'-C1'-N1-C2
8	7	21	H2U	O4'-C1'-N1-C6
8	8	21	H2U	O4'-C1'-N1-C2
8	8	21	H2U	O4'-C1'-N1-C6
36	d	150	MEQ	N-CA-CB-CG

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 243 ligands modelled in this entry, 243 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.

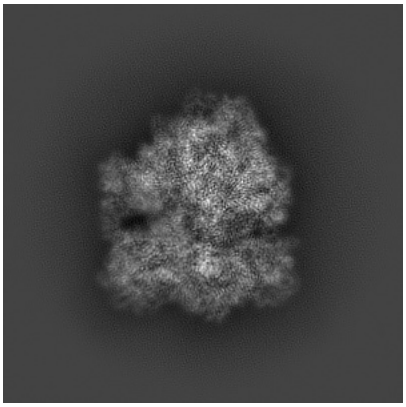
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-17667. These allow visual inspection of the internal detail of the map and identification of artifacts.

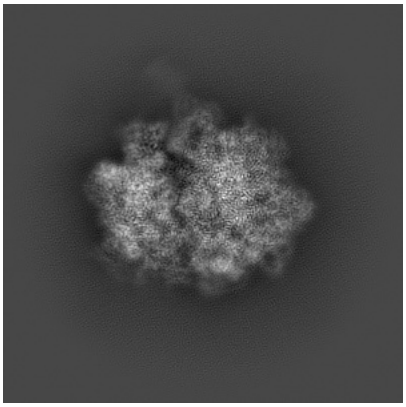
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

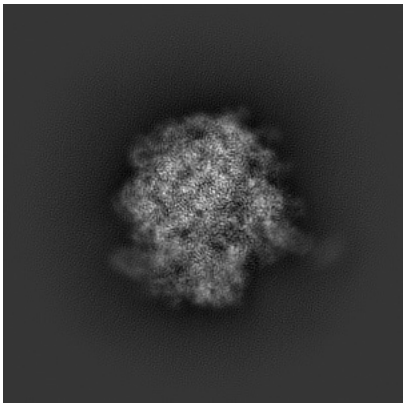
6.1.1 Primary map



X



Y

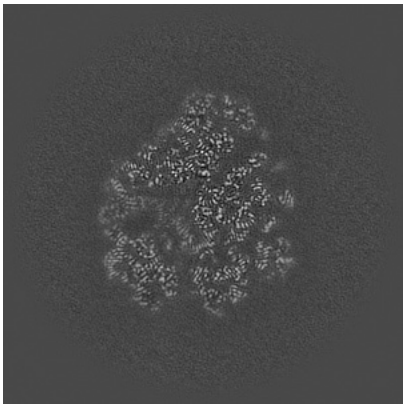


Z

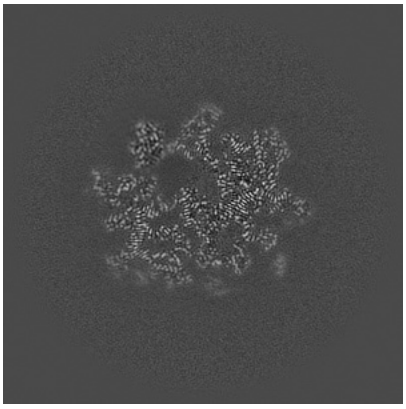
The images above show the map projected in three orthogonal directions.

6.2 Central slices

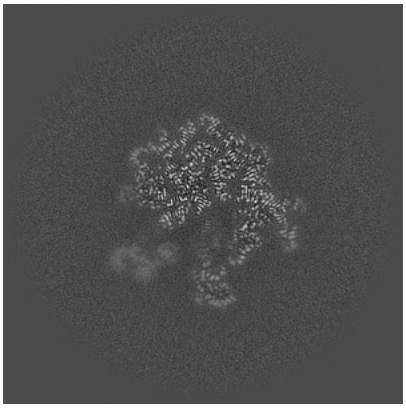
6.2.1 Primary map



X Index: 200



Y Index: 200

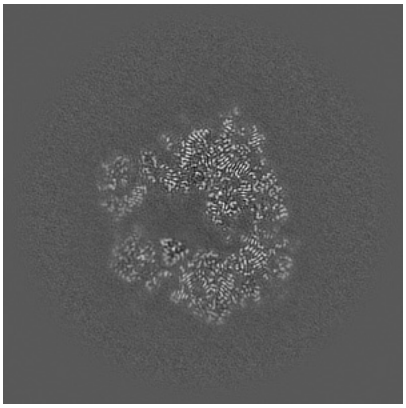


Z Index: 200

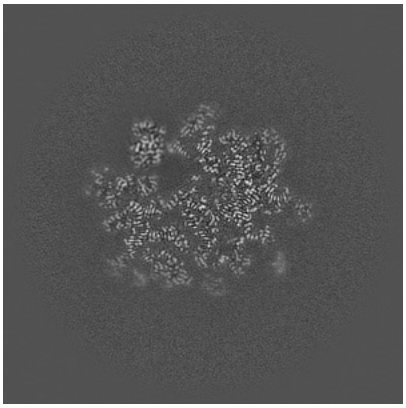
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

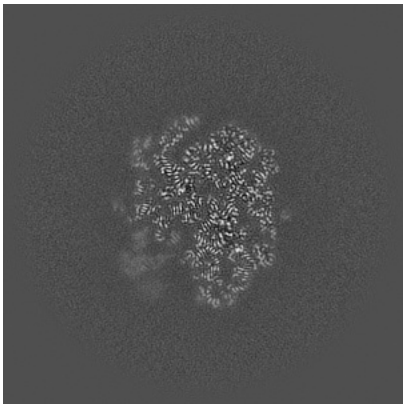
6.3.1 Primary map



X Index: 218



Y Index: 202

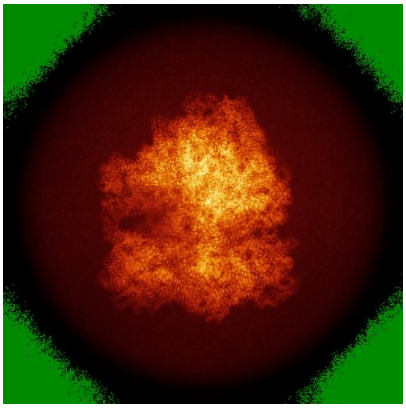


Z Index: 222

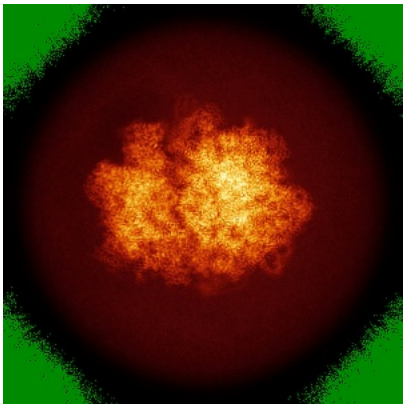
The images above show the largest variance slices of the map in three orthogonal directions.

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

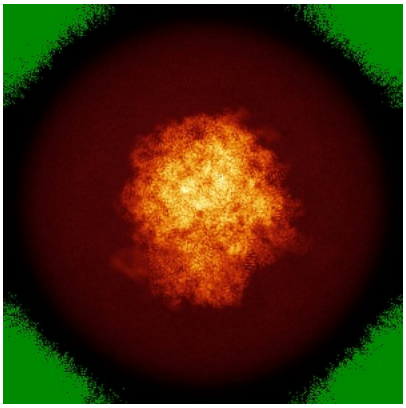
6.4.1 Primary map



X



Y

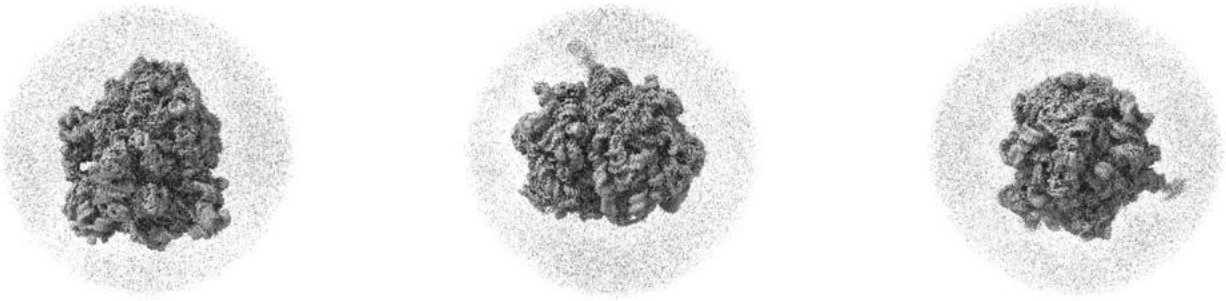


Z

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



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 2.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

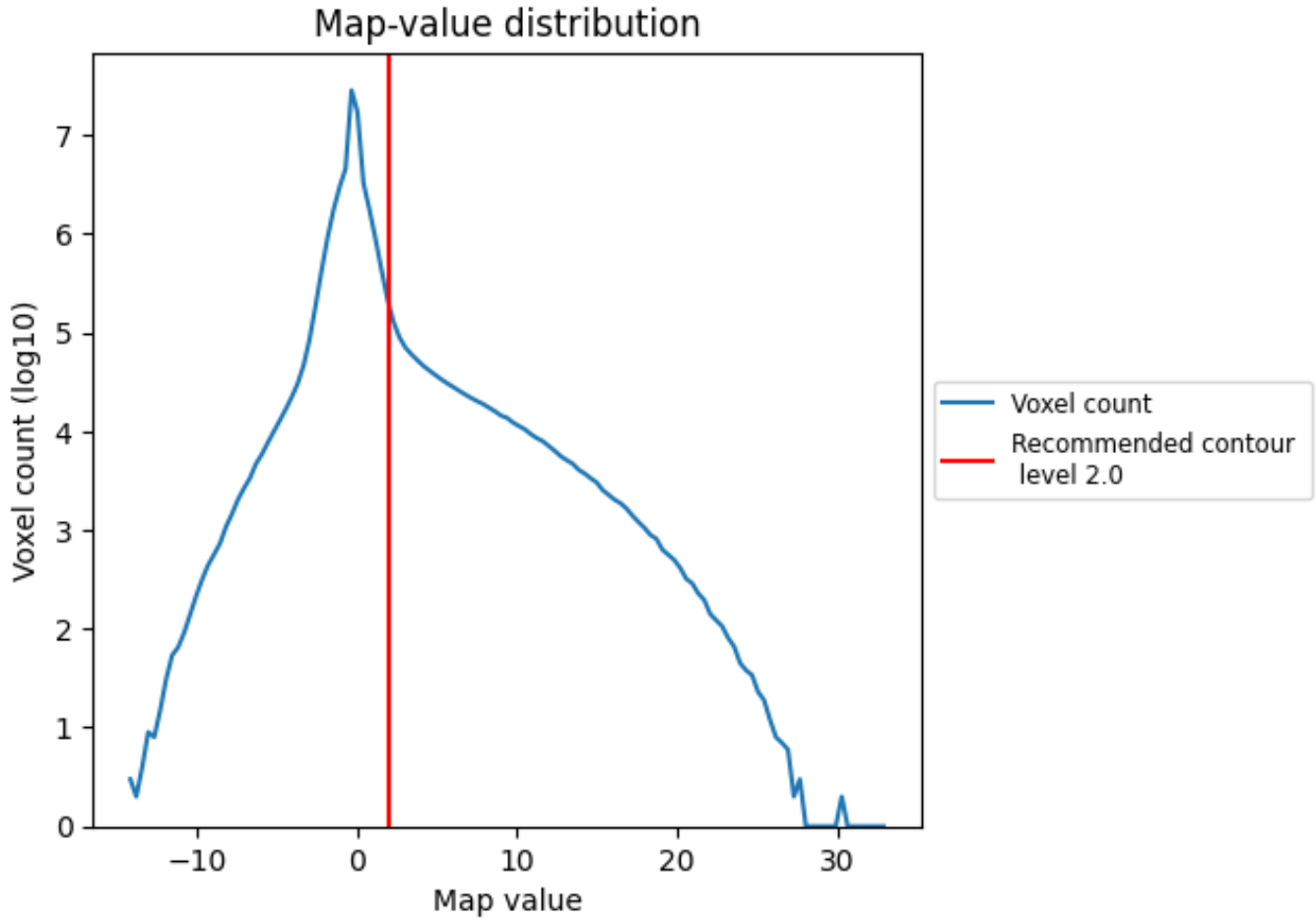
6.6 Mask visualisation (i)

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

7 Map analysis

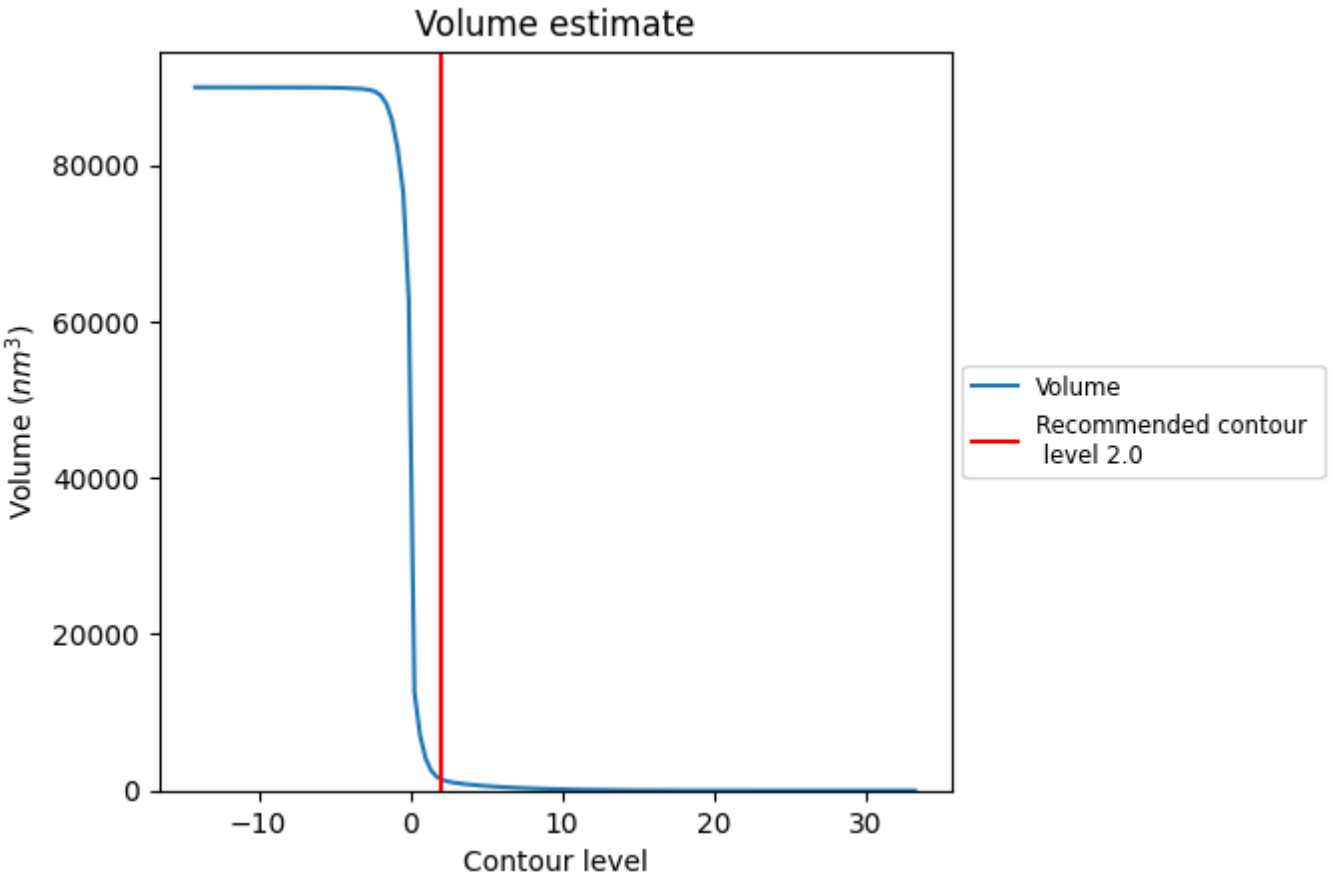
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

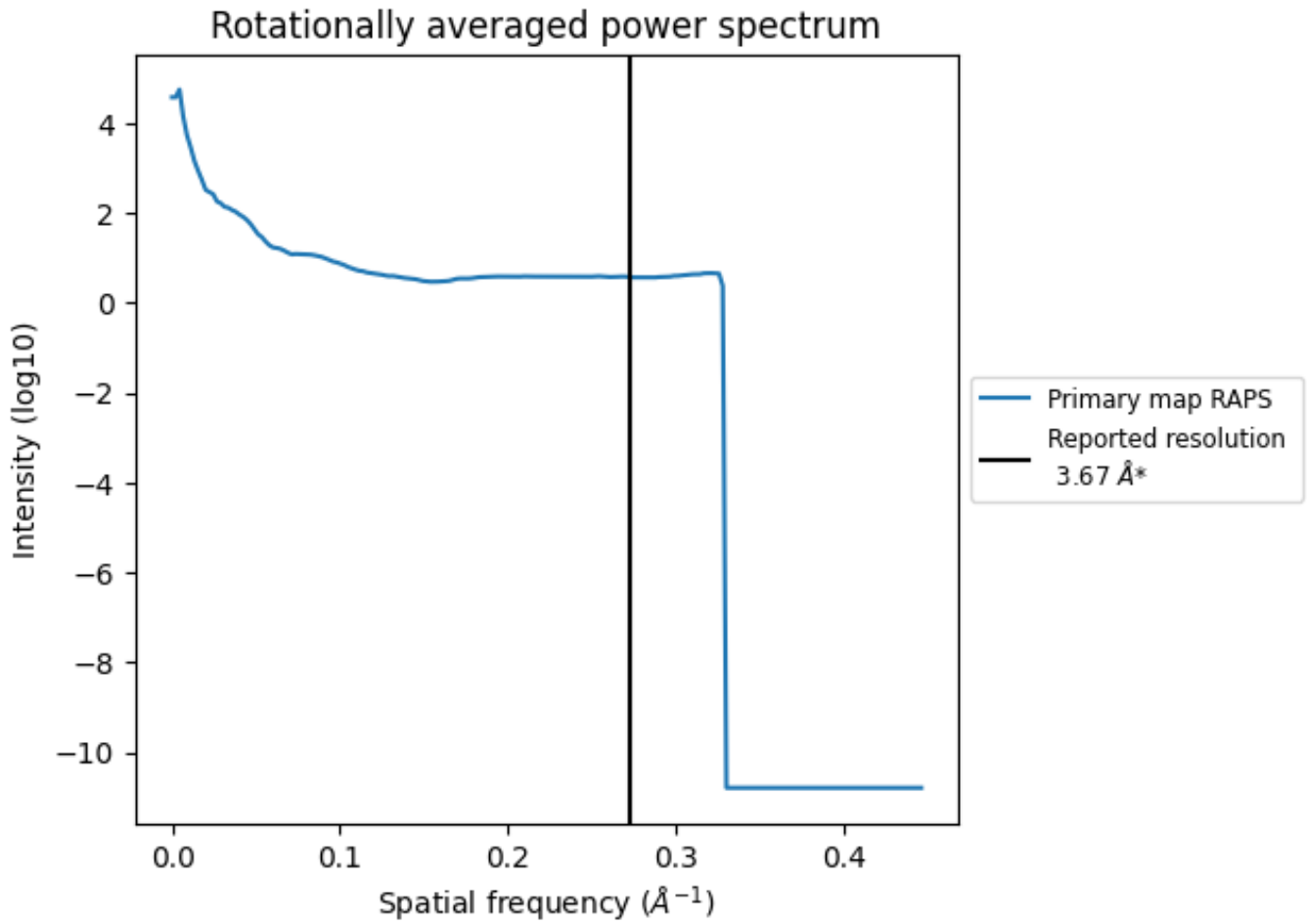
7.2 Volume estimate (i)



The volume at the recommended contour level is 1507 nm^3; this corresponds to an approximate mass of 1361 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 0.272 Å^{-1}

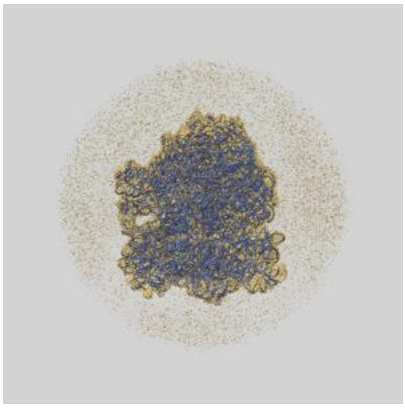
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

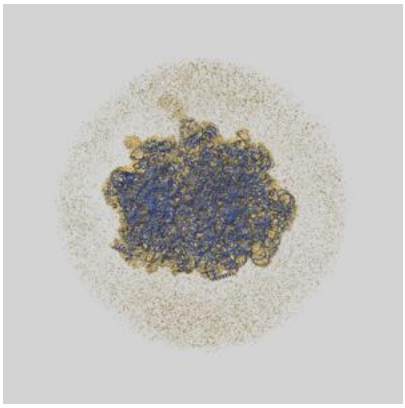
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-17667 and PDB model 8PHJ. Per-residue inclusion information can be found in section 3 on page 17.

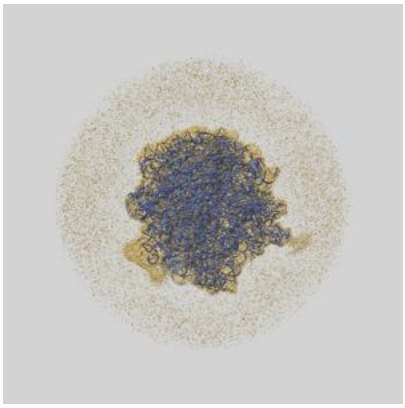
9.1 Map-model overlay



X



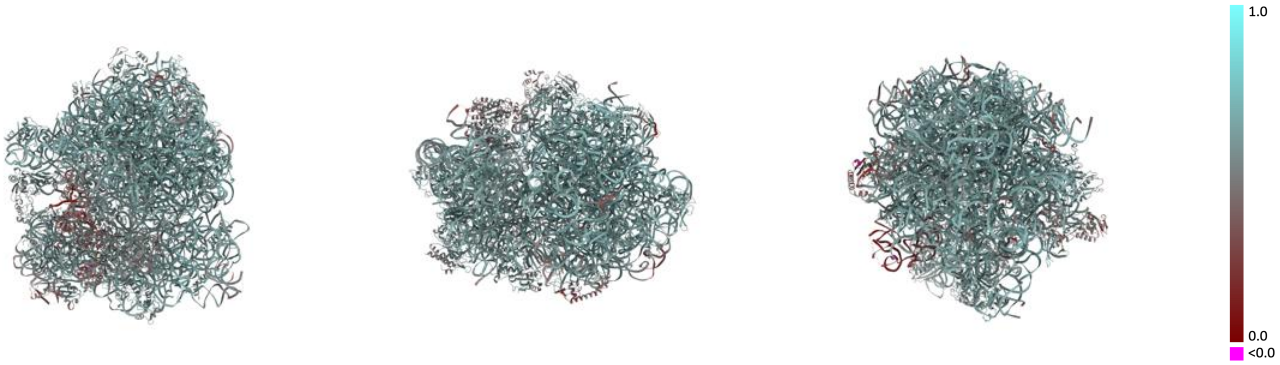
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 2.0 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.

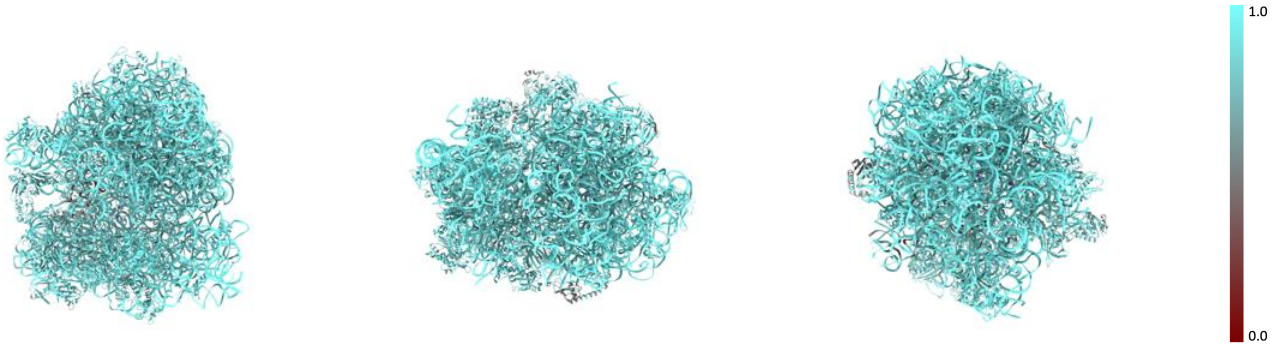
9.2 Q-score mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according 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.

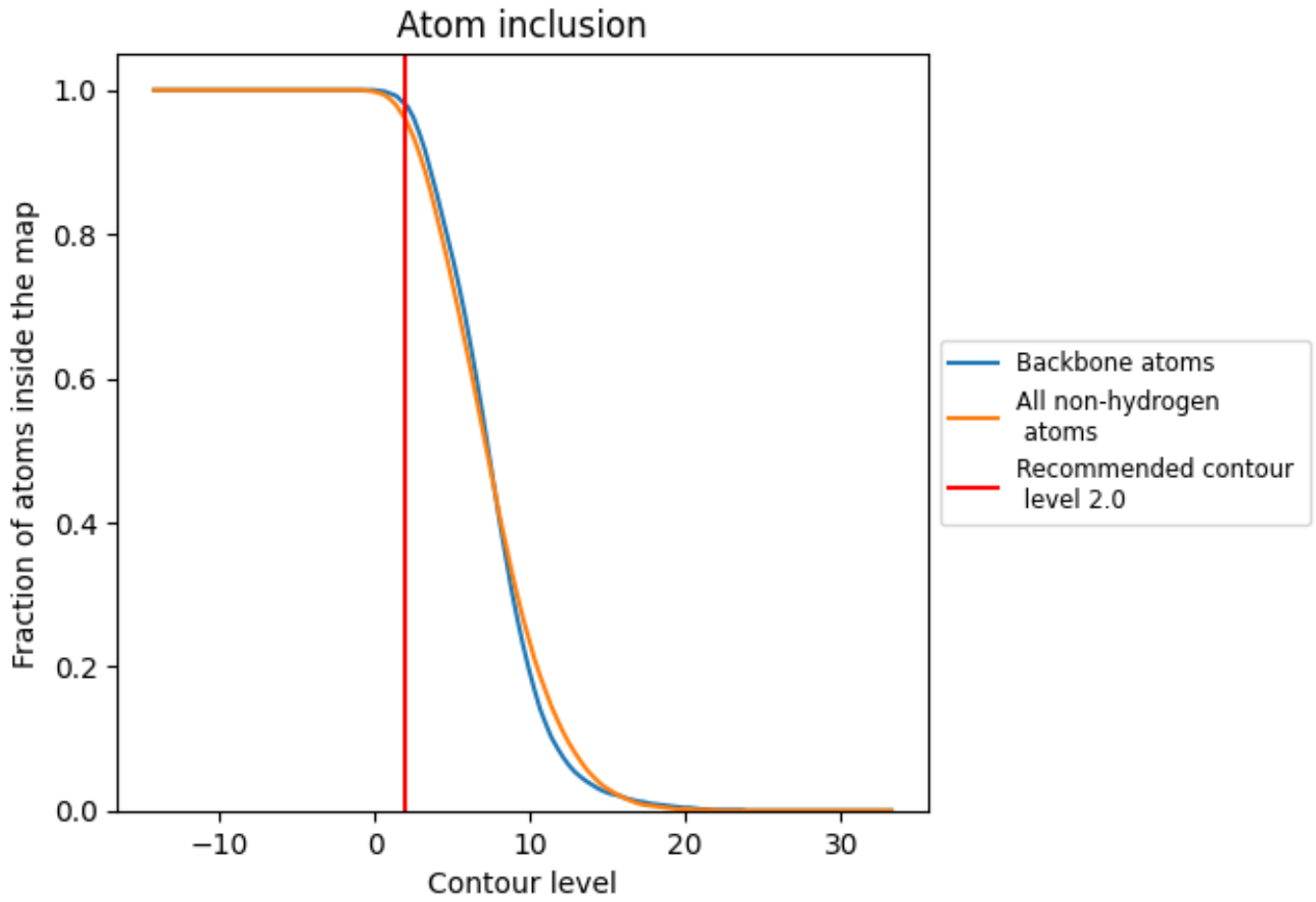
9.3 Atom inclusion mapped to coordinate model



X Y Z

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 (2.0).

9.4 Atom inclusion (i)



At the recommended contour level, 98% 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 (2.0) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9590	0.5840
0	0.9310	0.5990
1	0.9690	0.6370
2	0.9900	0.6380
3	0.9630	0.6130
4	0.8920	0.5190
5	0.7130	0.3780
6	0.7240	0.3250
7	0.6370	0.4920
8	0.7150	0.2620
9	0.9690	0.6100
A	0.9930	0.6020
B	0.8570	0.5190
C	0.9260	0.5740
D	0.9360	0.5740
E	0.9500	0.5960
F	0.9120	0.5440
G	0.8830	0.5330
H	0.9500	0.5980
I	0.9380	0.5710
J	0.8700	0.5200
K	0.9320	0.5790
L	0.9390	0.6010
M	0.9200	0.5630
N	0.9560	0.5860
O	0.9320	0.5770
P	0.9500	0.5940
Q	0.9340	0.5770
R	0.9320	0.5720
S	0.9370	0.5720
T	0.9470	0.5820
U	0.7870	0.5150
W	0.8450	0.3380
X	0.8920	0.4820
Y	0.9270	0.4780

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Continued from previous page...

Chain	Atom inclusion	Q-score
Z	0.9660	0.5170
a	0.9880	0.6050
b	0.9920	0.5990
c	0.9700	0.6280
d	0.9600	0.6160
e	0.9470	0.5880
f	0.8910	0.5390
g	0.9230	0.5530
h	0.6830	0.4230
i	0.9660	0.6160
j	0.9520	0.6170
k	0.9670	0.6080
l	0.9560	0.6220
m	0.9810	0.6280
n	0.9550	0.5820
o	0.9390	0.6070
p	0.9850	0.6330
q	0.9510	0.6080
r	0.9510	0.6130
s	0.9280	0.5830
t	0.9450	0.5810
u	0.9400	0.5960
v	0.9560	0.6200
w	0.9670	0.6180
x	0.9270	0.5570
y	0.9440	0.6070
z	0.9740	0.6220