



wwPDB EM Validation Summary Report ⓘ

Jun 21, 2026 – 07:53 am BST

PDB ID : 8PHJ / pdb_00008phj
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 ⓘ symbol.

The types of validation reports are described at

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

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

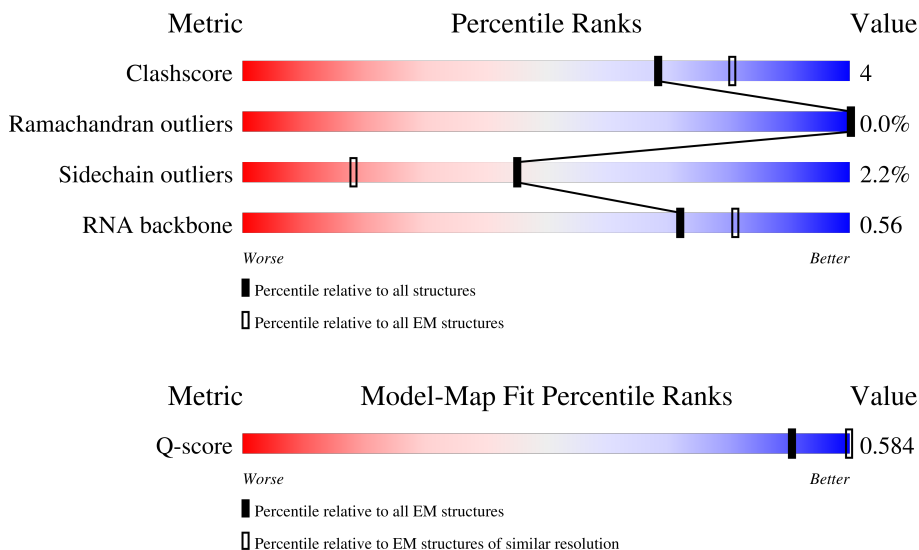
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.67 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11424 (3.17 - 4.17)

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	55	80% (green), 13% (yellow), 7% (grey)
2	1	46	91% (green), 9% (yellow), 0% (red), 0% (grey)
3	2	65	89% (green), 9% (yellow), 0% (red), 2% (grey)

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Mol	Chain	Length	Quality of chain
4	3	38	79% 21%
5	4	70	63% 21% 14%
6	5	165	7% 62% 11% 27%
7	6	142	5% 69% 24% 6%
8	7	77	16% 55% 34% 9%
8	8	77	9% 51% 36% 12%
9	9	31	6% 90%
10	A	1542	77% 19%
11	B	241	81% 11% 7%
12	C	233	76% 12% 12%
13	D	206	92% 8%
14	E	167	81% 11% 7%
15	F	135	63% 13% 24%
16	G	179	72% 13% 15%
17	H	130	92% 8%
18	I	130	78% 20%
19	J	103	80% 16% 5%
20	K	129	77% 13% 9%
21	L	124	87% 10%
22	M	118	82% 14%
23	N	101	90% 9%
24	O	89	90% 9%
25	P	82	91% 7%
26	Q	84	82% 10% 6%
27	R	75	81% 5% 13%









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Mol	Chain	Length	Quality of chain
28	S	92	82% 8% 10%
29	T	87	90% 7% ..
30	U	71	86% 13% .
31	W	120	36% 15% 49%
32	X	406	73% 21% . 5%
32	Y	406	76% 16% 8%
33	a	2904	79% 18% ..
34	b	120	85% 12% ..
35	c	273	91% 8% .
36	d	209	85% 14% .
37	e	201	90% 9% .
38	f	179	80% 18% ..
39	g	177	84% 14% ..
40	h	149	11% 71% 26% .
41	i	142	92% 7% .
42	j	123	89% 11%
43	k	144	85% 14% .
44	l	136	79% 21%
45	m	127	83% 9% . 7%
46	n	117	88% 10% ..
47	o	115	90% 9% .
48	p	118	98% ..
49	q	103	92% 6% .
50	r	110	93% 6% .
51	s	100	84% 9% 7%

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Mol	Chain	Length	Quality of chain
52	t	104	 78% 15% 7%
53	u	94	 84% 16%
54	v	85	 87% 9%
55	w	78	 90% 8% ..
56	x	63	 81% 14% 5%
57	y	59	 85% 8% . . .
58	z	57	 77% 19% .
59	Z	4	 25% 25% 50%

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
			Total	C	N	O		
1	0	51	417	269	76	72	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 9 is a RNA chain called mRNA.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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
			Total	C	N	O	S		
21	L	123	949	585	195	165	4	0	0

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

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

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

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

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

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

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

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

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

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

- 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
			Total	C	N	O	P		
33	a	2862	61456	27423	11310	19861	2862	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 60 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

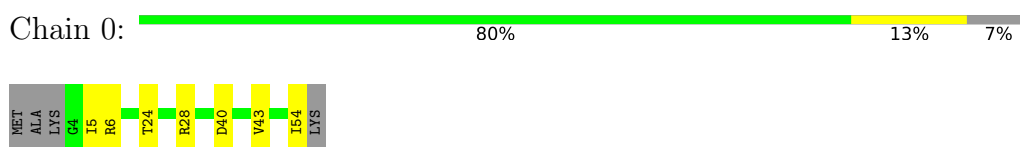
- Molecule 61 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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	

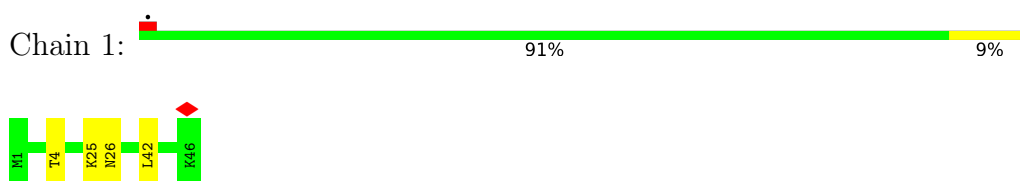
3 Residue-property plots [i](#)

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.

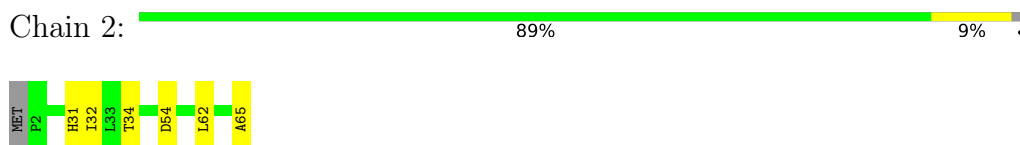
- Molecule 1: Large ribosomal subunit protein bL33



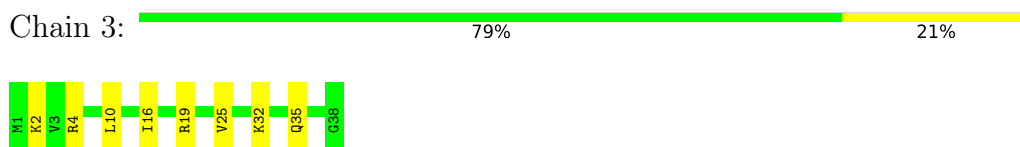
- Molecule 2: Large ribosomal subunit protein bL34



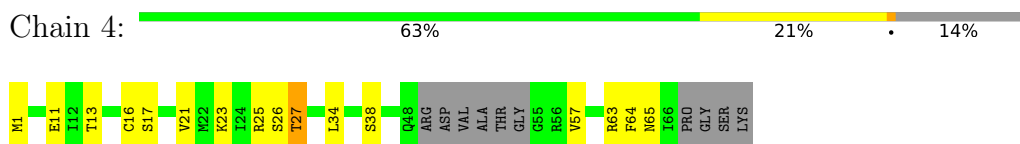
- Molecule 3: Large ribosomal subunit protein bL35



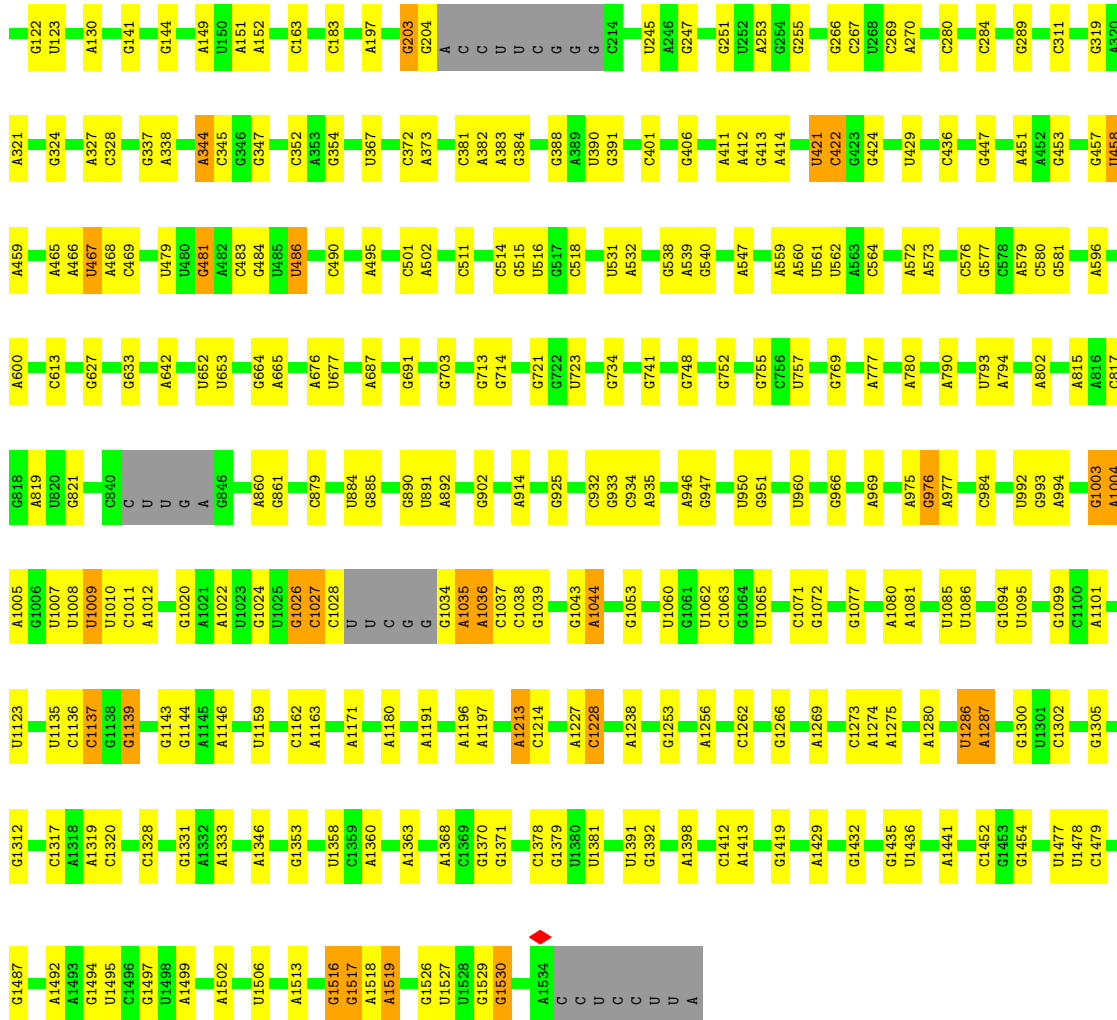
- Molecule 4: Large ribosomal subunit protein bL36A



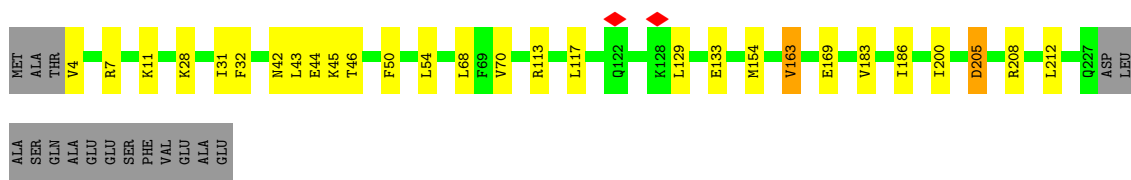
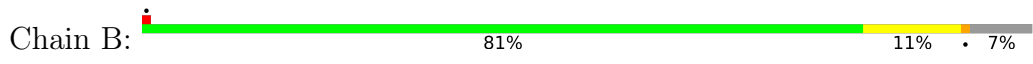
- Molecule 5: Large ribosomal subunit protein bL31A



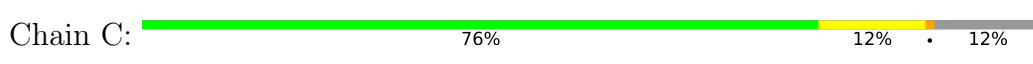
- Molecule 6: Large ribosomal subunit protein uL10



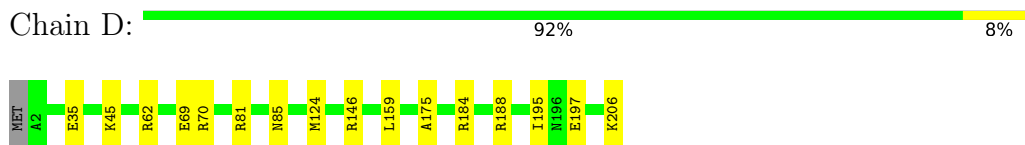
• Molecule 11: Small ribosomal subunit protein uS2



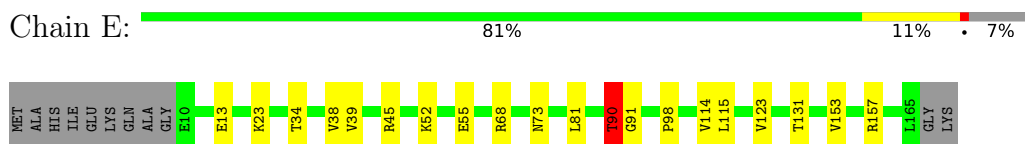
• Molecule 12: Small ribosomal subunit protein uS3



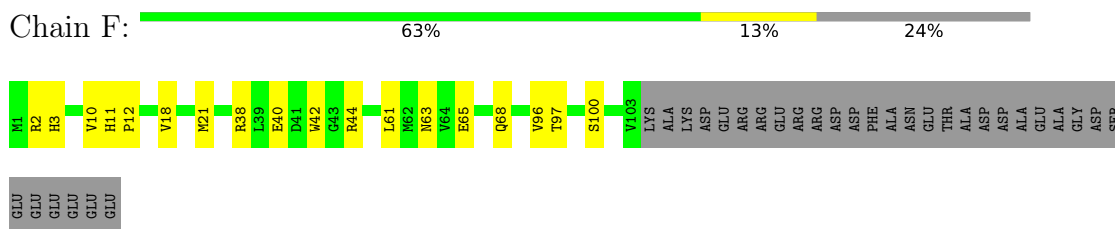
- Molecule 13: Small ribosomal subunit protein uS4



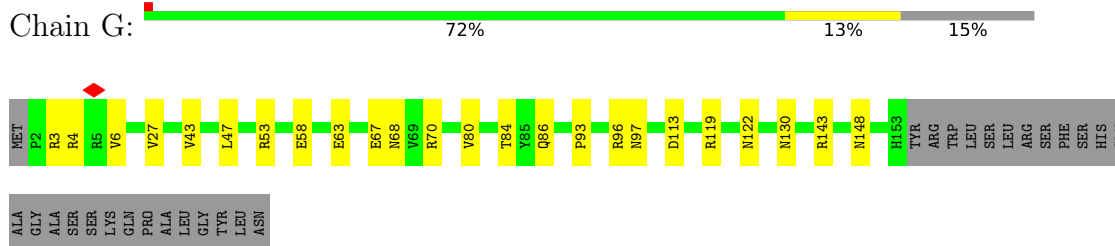
- Molecule 14: Small ribosomal subunit protein uS5



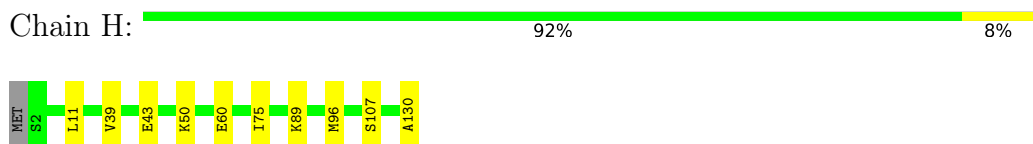
- Molecule 15: Small ribosomal subunit protein bS6, fully modified isoform



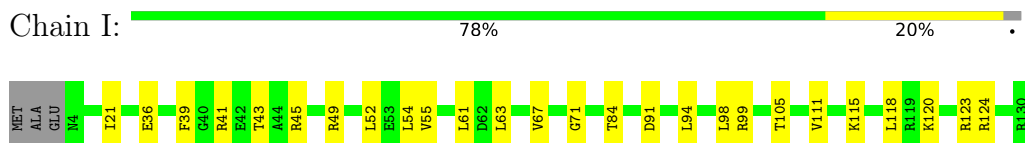
- Molecule 16: Small ribosomal subunit protein uS7




- Molecule 17: Small ribosomal subunit protein uS8



- Molecule 18: Small ribosomal subunit protein uS9



- Molecule 19: Small ribosomal subunit protein uS10

Chain J:  80% 16% 5%




- Molecule 20: Small ribosomal subunit protein uS11

Chain K:  77% 13% 9%




- Molecule 21: Small ribosomal subunit protein uS12

Chain L:  87% 10% 3%




- Molecule 22: Small ribosomal subunit protein uS13

Chain M:  82% 14% 4%




- Molecule 23: Small ribosomal subunit protein uS14

Chain N:  90% 9% 1%




- Molecule 24: Small ribosomal subunit protein uS15

Chain O:  90% 9% 1%

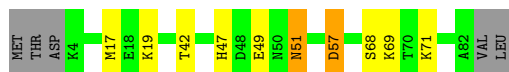
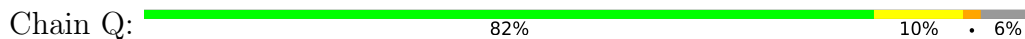


- Molecule 25: Small ribosomal subunit protein bS16

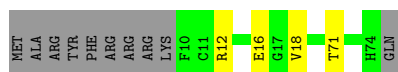
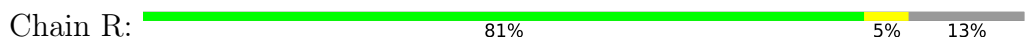
Chain P:  91% 7% 2%



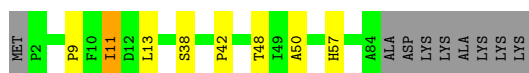
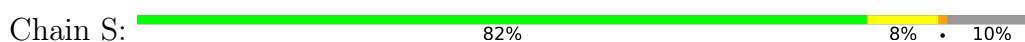
- Molecule 26: Small ribosomal subunit protein uS17



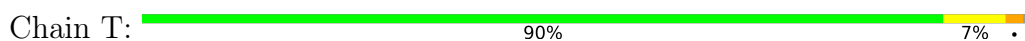
• Molecule 27: Small ribosomal subunit protein bS18



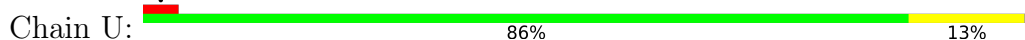
• Molecule 28: Small ribosomal subunit protein uS19



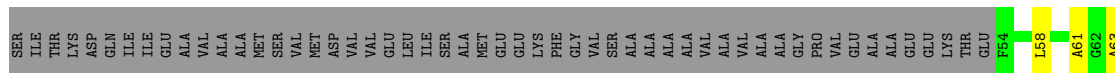
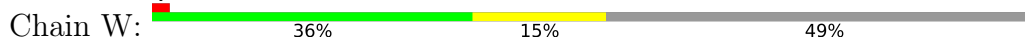
• Molecule 29: Small ribosomal subunit protein bS20



• Molecule 30: Small ribosomal subunit protein bS21

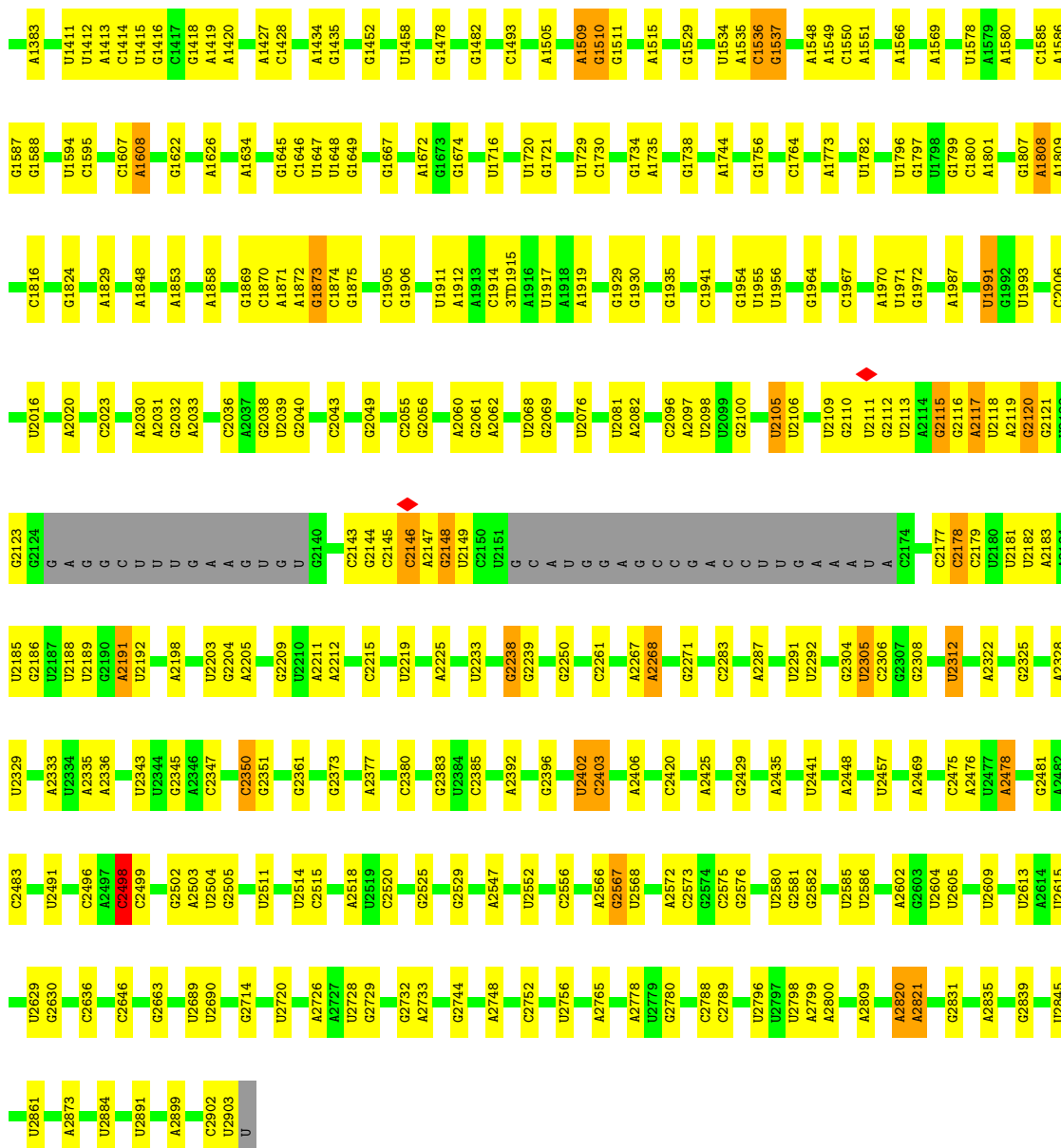


• Molecule 31: Large ribosomal subunit protein bL12

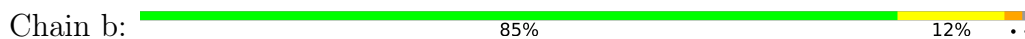


• Molecule 32: CRISPR-associated protein, APE2256 family

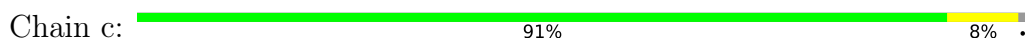





• Molecule 34: 5S rRNA



• Molecule 35: Large ribosomal subunit protein uL2




• Molecule 36: Large ribosomal subunit protein uL3

Chain d:  85% 14%




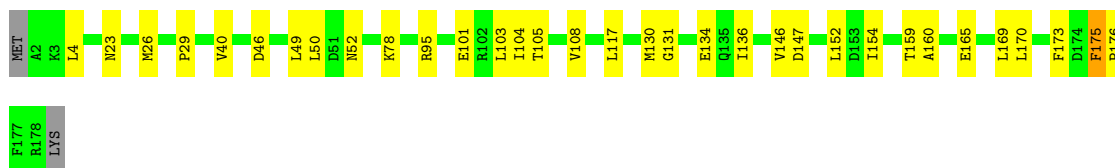
- Molecule 37: Large ribosomal subunit protein uL4

Chain e:  90% 9%




- Molecule 38: Large ribosomal subunit protein uL5

Chain f:  80% 18%



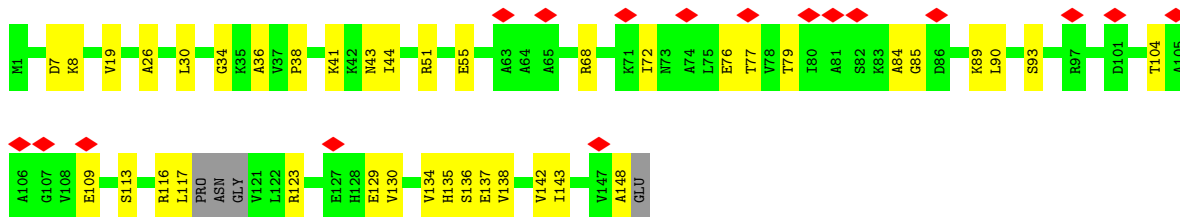
- Molecule 39: Large ribosomal subunit protein uL6

Chain g:  84% 14%




- Molecule 40: Large ribosomal subunit protein bL9

Chain h:  11% 71% 26%




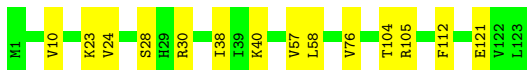
- Molecule 41: Large ribosomal subunit protein uL13

Chain i:  92% 7%




- Molecule 42: Large ribosomal subunit protein uL14

Chain j:  89% 11%




- Molecule 43: Large ribosomal subunit protein uL15

Chain k:  85% 14%




- Molecule 44: Large ribosomal subunit protein uL16

Chain l:  79% 21%




- Molecule 45: Large ribosomal subunit protein bL17

Chain m:  83% 9% 7%




- Molecule 46: Large ribosomal subunit protein uL18

Chain n:  88% 10%



- Molecule 47: Large ribosomal subunit protein bL19

Chain o:  90% 9%



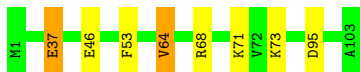
- Molecule 48: Large ribosomal subunit protein bL20

Chain p:  98%



- Molecule 49: Large ribosomal subunit protein bL21

Chain q:  92% 6%




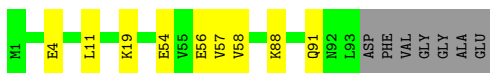
- Molecule 50: Large ribosomal subunit protein uL22

Chain r:  93% 6%



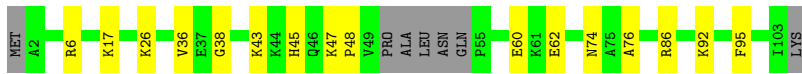
- Molecule 51: Large ribosomal subunit protein uL23

Chain s:  84% 9% 7%




- Molecule 52: Large ribosomal subunit protein uL24

Chain t:  78% 15% 7%



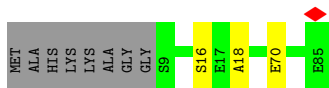
- Molecule 53: Large ribosomal subunit protein bL25

Chain u:  84% 16%



- Molecule 54: Large ribosomal subunit protein bL27

Chain v:  87% 9%




- Molecule 55: Large ribosomal subunit protein bL28

Chain w:  90% 8%




- Molecule 56: Large ribosomal subunit protein uL29

Chain x:  81% 14% 5%




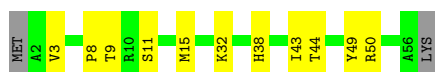
- Molecule 57: Large ribosomal subunit protein uL30

Chain y:  85% 8% . .




- Molecule 58: Large ribosomal subunit protein bL32

Chain z:  77% 19% .



- Molecule 59: Cyclic tetraadenosine monophosphate (cA4)

Chain Z:  25% 25% 50%



4 Experimental information

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 ($e^-/\text{\AA}^2$)	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	Depositor
Map size (\AA)	448.0, 448.0, 448.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.12, 1.12, 1.12	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: OMU, 3TD, 4SU, 5MC, 6MZ, IAS, G7M, 2MG, MEQ, OMC, UR3, H2U, PSU, 1MG, MG, 2MA, ZN, MA6, 4OC, OMG, 5MU

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	0.23	0/424	0.28	0/565
2	1	0.27	0/380	0.30	0/498
3	2	0.25	0/513	0.30	0/676
4	3	0.25	0/303	0.27	0/397
5	4	0.12	0/488	0.24	0/649
6	5	0.10	0/916	0.24	0/1232
7	6	0.11	0/982	0.32	0/1328
8	7	0.16	0/1701	0.20	0/2649
8	8	0.15	0/1720	0.23	0/2679
9	9	0.17	0/72	0.18	0/110
10	A	0.25	0/35860	0.24	0/55930
11	B	0.14	0/1784	0.27	0/2403
12	C	0.20	0/1651	0.26	0/2225
13	D	0.19	0/1665	0.23	0/2227
14	E	0.22	0/1165	0.28	0/1568
15	F	0.17	0/858	0.27	0/1160
16	G	0.15	0/1200	0.25	0/1610
17	H	0.21	0/989	0.29	0/1326
18	I	0.17	0/1034	0.26	0/1375
19	J	0.18	0/796	0.31	0/1077
20	K	0.18	0/884	0.25	0/1191
21	L	0.21	0/963	0.27	0/1293
22	M	0.16	0/900	0.23	0/1204
23	N	0.19	0/817	0.22	0/1088
24	O	0.18	0/722	0.22	0/964
25	P	0.22	0/653	0.30	0/877
26	Q	0.19	0/650	0.26	0/871
27	R	0.19	0/544	0.23	0/731
28	S	0.16	0/680	0.25	0/915
29	T	0.19	0/676	0.21	0/895
30	U	0.14	0/597	0.22	0/792

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	W	0.11	0/401	0.25	0/541
32	X	0.23	0/3049	0.30	0/4143
32	Y	0.24	0/2972	0.30	0/4039
33	a	0.29	0/68253	0.27	0/106469
34	b	0.23	0/2850	0.22	0/4444
35	c	0.25	0/2121	0.31	0/2852
36	d	0.25	0/1576	0.30	0/2119
37	e	0.21	0/1571	0.29	0/2113
38	f	0.15	0/1434	0.24	0/1926
39	g	0.18	0/1321	0.26	0/1790
40	h	0.12	0/1088	0.29	0/1468
41	i	0.24	0/1152	0.27	0/1551
42	j	0.24	0/955	0.31	0/1279
43	k	0.23	0/1052	0.28	0/1401
44	l	0.24	0/1093	0.31	0/1460
45	m	0.25	0/958	0.31	0/1281
46	n	0.19	0/902	0.28	0/1209
47	o	0.23	0/929	0.26	0/1242
48	p	0.26	0/960	0.28	0/1278
49	q	0.21	0/829	0.30	0/1107
50	r	0.23	0/864	0.27	0/1156
51	s	0.21	0/744	0.29	0/994
52	t	0.18	0/748	0.27	0/994
53	u	0.21	0/766	0.26	0/1025
54	v	0.24	0/589	0.31	0/780
55	w	0.24	0/635	0.27	0/848
56	x	0.17	0/492	0.25	0/655
57	y	0.22	0/444	0.26	0/594
58	z	0.25	0/440	0.31	0/588
59	Z	0.38	0/99	0.41	0/152
All	All	0.25	0/163874	0.27	0/244003

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	417	0	451	4	0
2	1	377	0	418	3	0
3	2	504	0	572	4	0
4	3	302	0	340	7	0
5	4	480	0	478	11	0
6	5	907	0	935	14	0
7	6	968	0	1009	28	0
8	7	1625	0	833	12	0
8	8	1642	0	845	15	0
9	9	65	0	33	1	0
10	A	32276	0	16264	113	0
11	B	1753	0	1780	16	0
12	C	1624	0	1696	18	0
13	D	1643	0	1707	10	0
14	E	1152	0	1196	11	0
15	F	839	0	833	11	0
16	G	1185	0	1234	15	0
17	H	979	0	1031	6	0
18	I	1022	0	1070	13	0
19	J	786	0	828	9	0
20	K	877	0	884	16	0
21	L	949	0	998	9	0
22	M	891	0	952	12	0
23	N	805	0	844	7	0
24	O	714	0	734	4	0
25	P	643	0	661	3	0
26	Q	641	0	682	8	0
27	R	535	0	552	2	0
28	S	663	0	688	5	0
29	T	670	0	719	6	0
30	U	589	0	629	8	0
31	W	402	0	402	13	0
32	X	2984	0	2973	65	0
32	Y	2912	0	2886	44	0
33	a	61456	0	30938	213	0
34	b	2549	0	1291	8	0
35	c	2082	0	2154	13	0
36	d	1566	0	1618	26	0
37	e	1552	0	1619	12	0
38	f	1410	0	1444	23	0
39	g	1301	0	1343	12	0

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Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
40	h	1079	0	1123	31	0
41	i	1129	0	1162	9	0
42	j	946	0	1023	7	0
43	k	1043	0	1123	12	0
44	l	1074	0	1157	19	0
45	m	945	0	989	7	0
46	n	892	0	923	10	0
47	o	917	0	962	10	0
48	p	947	0	1019	0	0
49	q	816	0	839	5	0
50	r	857	0	922	5	0
51	s	738	0	807	6	0
52	t	742	0	794	10	0
53	u	753	0	780	7	0
54	v	582	0	593	2	0
55	w	625	0	652	5	0
56	x	491	0	523	4	0
57	y	440	0	472	4	0
58	z	434	0	445	7	0
59	Z	88	0	44	2	0
60	3	1	0	0	0	0
60	4	1	0	0	0	0
61	A	79	0	0	0	0
61	a	156	0	0	0	0
61	b	4	0	0	0	0
61	c	1	0	0	0	0
61	z	1	0	0	0	0
All	All	152518	0	104916	855	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 855 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:a:1047:G:HO2'	33:a:1110:G:H1	1.03	0.95
40:h:117:LEU:HD23	40:h:130:VAL:HG23	1.48	0.94
10:A:1009:U:H3	10:A:1020:G:H1	1.22	0.83
51:s:56:GLU:HG3	51:s:57:VAL:HG23	1.66	0.78
20:K:74:VAL:HG12	20:K:74:VAL:O	1.81	0.78

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	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%)	21	52
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
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	45	62
2	1	38/38 (100%)	37 (97%)	1 (3%)	40	59
3	2	51/52 (98%)	51 (100%)	0	100	100
4	3	34/34 (100%)	34 (100%)	0	100	100
5	4	55/62 (89%)	53 (96%)	2 (4%)	31	54
6	5	90/123 (73%)	89 (99%)	1 (1%)	65	72
7	6	101/110 (92%)	99 (98%)	2 (2%)	48	64
11	B	186/199 (94%)	183 (98%)	3 (2%)	55	67
12	C	170/190 (90%)	166 (98%)	4 (2%)	43	61
13	D	172/173 (99%)	170 (99%)	2 (1%)	63	71
14	E	119/126 (94%)	117 (98%)	2 (2%)	53	67
15	F	90/116 (78%)	87 (97%)	3 (3%)	33	55
16	G	124/147 (84%)	122 (98%)	2 (2%)	55	67
17	H	104/105 (99%)	104 (100%)	0	100	100
18	I	105/107 (98%)	101 (96%)	4 (4%)	29	52
19	J	86/90 (96%)	85 (99%)	1 (1%)	63	71
20	K	89/98 (91%)	87 (98%)	2 (2%)	45	62

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	L	101/104 (97%)	98 (97%)	3 (3%)	36	57
22	M	93/96 (97%)	91 (98%)	2 (2%)	45	62
23	N	83/84 (99%)	83 (100%)	0	100	100
24	O	76/77 (99%)	75 (99%)	1 (1%)	61	70
25	P	65/65 (100%)	64 (98%)	1 (2%)	57	68
26	Q	73/78 (94%)	70 (96%)	3 (4%)	27	51
27	R	56/65 (86%)	55 (98%)	1 (2%)	51	66
28	S	72/79 (91%)	70 (97%)	2 (3%)	38	58
29	T	65/66 (98%)	63 (97%)	2 (3%)	35	56
30	U	60/61 (98%)	59 (98%)	1 (2%)	53	67
31	W	33/84 (39%)	33 (100%)	0	100	100
32	X	305/339 (90%)	301 (99%)	4 (1%)	61	70
32	Y	299/339 (88%)	294 (98%)	5 (2%)	53	67
35	c	216/218 (99%)	212 (98%)	4 (2%)	50	65
36	d	163/163 (100%)	157 (96%)	6 (4%)	30	53
37	e	165/165 (100%)	161 (98%)	4 (2%)	43	61
38	f	148/150 (99%)	144 (97%)	4 (3%)	39	58
39	g	134/138 (97%)	128 (96%)	6 (4%)	24	49
40	h	110/114 (96%)	108 (98%)	2 (2%)	51	66
41	i	116/116 (100%)	114 (98%)	2 (2%)	53	67
42	j	104/104 (100%)	99 (95%)	5 (5%)	23	48
43	k	102/103 (99%)	98 (96%)	4 (4%)	28	52
44	l	109/109 (100%)	106 (97%)	3 (3%)	38	58
45	m	98/103 (95%)	95 (97%)	3 (3%)	35	56
46	n	86/87 (99%)	83 (96%)	3 (4%)	32	54
47	o	99/100 (99%)	99 (100%)	0	100	100
48	p	89/90 (99%)	88 (99%)	1 (1%)	65	72
49	q	84/84 (100%)	82 (98%)	2 (2%)	43	61
50	r	93/93 (100%)	91 (98%)	2 (2%)	45	62
51	s	80/84 (95%)	79 (99%)	1 (1%)	61	70
52	t	79/85 (93%)	78 (99%)	1 (1%)	61	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
53	u	78/78 (100%)	75 (96%)	3 (4%)	29	52
54	v	58/63 (92%)	57 (98%)	1 (2%)	53	67
55	w	67/68 (98%)	66 (98%)	1 (2%)	57	68
56	x	54/55 (98%)	51 (94%)	3 (6%)	19	45
57	y	47/49 (96%)	45 (96%)	2 (4%)	26	50
58	z	46/48 (96%)	46 (100%)	0	100	100
All	All	5466/5823 (94%)	5348 (98%)	118 (2%)	45	62

5 of 118 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
35	c	162	VAL
53	u	66	ASP
38	f	159	THR
53	u	65	VAL
46	n	28	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 57 such sidechains are listed below:

Mol	Chain	Res	Type
32	Y	321	HIS
55	w	34	HIS
37	e	165	HIS
54	v	76	ASN
47	o	66	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	A	1498/1542 (97%)	180 (12%)	3 (0%)
33	a	2858/2904 (98%)	326 (11%)	0
34	b	118/120 (98%)	10 (8%)	0
59	Z	3/4 (75%)	3 (100%)	0
8	7	75/77 (97%)	22 (29%)	0
8	8	77/77 (100%)	22 (28%)	1 (1%)
9	9	2/31 (6%)	0	0
All	All	4631/4755 (97%)	563 (12%)	4 (0%)

5 of 563 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	$\# Z > 2$
8	4OC	8	33	8	20,23,24	0.36	0	26,32,35	0.66	0
10	PSU	A	516	10	18,21,22	0.65	0	22,30,33	0.93	1 (4%)
33	2MG	a	1835	33	23,26,27	0.44	0	32,38,41	0.48	0
33	PSU	a	2504	33	18,21,22	0.65	0	22,30,33	1.00	1 (4%)
10	4OC	A	1402	10	20,23,24	0.34	0	26,32,35	0.58	0
33	PSU	a	746	61,33	18,21,22	0.77	0	22,30,33	0.82	1 (4%)
10	2MG	A	1516	10	23,26,27	1.33	4 (17%)	32,38,41	2.36	9 (28%)
10	G7M	A	527	10	23,26,27	0.44	0	35,39,42	0.66	0
8	4SU	8	8	8	18,21,22	0.36	0	26,30,33	1.16	2 (7%)
8	5MU	7	55	8	19,22,23	0.36	0	28,32,35	0.52	0
33	5MC	a	1962	33	18,22,23	0.37	0	26,32,35	0.75	0
33	6MZ	a	1618	33	22,25,26	0.37	0	30,36,39	0.57	0
33	OMC	a	2498	61,33	19,22,23	0.64	0	26,31,34	0.83	1 (3%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
10	MA6	A	1519	10	23,26,27	0.39	0	34,38,41	0.82	1 (2%)
33	PSU	a	955	33	18,21,22	0.69	0	22,30,33	1.03	1 (4%)
33	PSU	a	2605	33	18,21,22	0.68	0	22,30,33	1.04	1 (4%)
33	H2U	a	2449	33	18,21,22	0.41	0	21,30,33	0.57	0
8	H2U	8	21	8	18,21,22	0.58	0	21,30,33	0.81	1 (4%)
8	PSU	7	56	8	18,21,22	0.60	0	22,30,33	0.98	1 (4%)
33	PSU	a	2580	33	18,21,22	0.72	0	22,30,33	0.93	1 (4%)
33	PSU	a	2457	33	18,21,22	0.70	0	22,30,33	0.98	1 (4%)
33	6MZ	a	2030	33	22,25,26	0.38	0	30,36,39	0.55	0
8	H2U	7	21	8	18,21,22	0.58	0	21,30,33	0.82	1 (4%)
36	MEQ	d	150	36	8,9,10	0.82	0	5,10,12	0.41	0
33	OMU	a	2552	33	19,22,23	0.39	0	26,31,34	0.46	0
10	5MC	A	1407	10	18,22,23	0.36	0	26,32,35	0.78	0
33	2MG	a	2445	33	23,26,27	0.49	0	32,38,41	0.46	0
33	PSU	a	1911	33	18,21,22	0.62	0	22,30,33	0.95	1 (4%)
8	4OC	7	33	8	20,23,24	0.34	0	26,32,35	0.54	0
33	5MU	a	1939	33	19,22,23	0.40	0	28,32,35	0.57	0
33	G7M	a	2069	33	23,26,27	0.44	0	35,39,42	0.60	0
33	5MU	a	747	33	19,22,23	0.36	0	28,32,35	0.45	0
10	2MG	A	966	10	23,26,27	0.47	0	32,38,41	0.49	0
10	MA6	A	1518	10	23,26,27	0.38	0	34,38,41	0.79	1 (2%)
8	PSU	8	56	8	18,21,22	0.60	0	22,30,33	0.98	1 (4%)
33	3TD	a	1915	33	19,22,23	0.58	0	21,32,35	0.86	0
10	2MG	A	1207	10	23,26,27	0.48	0	32,38,41	0.51	0
8	4SU	7	8	8	18,21,22	0.37	0	26,30,33	1.19	2 (7%)
33	OMG	a	2251	8,33	23,26,27	0.60	0	33,38,41	0.45	0
33	PSU	a	1917	33	18,21,22	0.65	0	22,30,33	0.96	1 (4%)
33	PSU	a	2604	33	18,21,22	0.67	0	22,30,33	1.08	1 (4%)
10	5MC	A	967	10	18,22,23	0.37	0	26,32,35	0.70	0
33	1MG	a	745	33	22,26,27	0.56	0	33,39,42	0.59	0
8	5MU	8	55	8	19,22,23	0.37	0	28,32,35	0.51	0
20	IAS	K	119	20	6,7,8	1.03	0	6,8,10	1.31	1 (16%)
33	2MA	a	2503	61,33	22,25,26	1.29	3 (13%)	33,37,40	0.98	1 (3%)
10	UR3	A	1498	10	19,22,23	0.39	0	26,32,35	0.63	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	4OC	8	33	8	-	0/9/29/30	0/2/2/2
10	PSU	A	516	10	-	0/7/25/26	0/2/2/2
33	2MG	a	1835	33	-	0/9/27/28	0/3/3/3
33	PSU	a	2504	33	-	2/7/25/26	0/2/2/2
10	4OC	A	1402	10	-	0/9/29/30	0/2/2/2
33	PSU	a	746	61,33	-	4/7/25/26	0/2/2/2
10	2MG	A	1516	10	-	0/9/27/28	0/3/3/3
10	G7M	A	527	10	-	0/7/25/26	0/3/3/3
8	4SU	8	8	8	-	0/7/25/26	0/2/2/2
8	5MU	7	55	8	-	0/7/25/26	0/2/2/2
33	5MC	a	1962	33	-	4/7/25/26	0/2/2/2
33	6MZ	a	1618	33	-	0/9/27/28	0/3/3/3
33	OMC	a	2498	61,33	-	2/9/27/28	0/2/2/2
10	MA6	A	1519	10	-	0/11/29/30	0/3/3/3
33	PSU	a	955	33	-	0/7/25/26	0/2/2/2
33	PSU	a	2605	33	-	0/7/25/26	0/2/2/2
33	H2U	a	2449	33	-	0/7/38/39	0/2/2/2
8	H2U	8	21	8	-	5/7/38/39	0/2/2/2
8	PSU	7	56	8	-	1/7/25/26	0/2/2/2
33	PSU	a	2580	33	-	0/7/25/26	0/2/2/2
33	PSU	a	2457	33	-	0/7/25/26	0/2/2/2
33	6MZ	a	2030	33	-	2/9/27/28	0/3/3/3
8	H2U	7	21	8	-	5/7/38/39	0/2/2/2
36	MEQ	d	150	36	-	3/8/9/11	-
33	OMU	a	2552	33	-	0/9/27/28	0/2/2/2
10	5MC	A	1407	10	-	0/7/25/26	0/2/2/2
33	2MG	a	2445	33	-	0/9/27/28	0/3/3/3
33	PSU	a	1911	33	-	0/7/25/26	0/2/2/2
8	4OC	7	33	8	-	0/9/29/30	0/2/2/2
33	5MU	a	1939	33	-	0/7/25/26	0/2/2/2
33	G7M	a	2069	33	-	2/7/25/26	0/3/3/3
33	5MU	a	747	33	-	0/7/25/26	0/2/2/2
10	2MG	A	966	10	-	2/9/27/28	0/3/3/3
10	MA6	A	1518	10	-	0/11/29/30	0/3/3/3
8	PSU	8	56	8	-	1/7/25/26	0/2/2/2
33	3TD	a	1915	33	-	0/7/25/26	0/2/2/2
10	2MG	A	1207	10	-	0/9/27/28	0/3/3/3
8	4SU	7	8	8	-	0/7/25/26	0/2/2/2
33	OMG	a	2251	8,33	-	1/9/27/28	0/3/3/3
33	PSU	a	1917	33	-	0/7/25/26	0/2/2/2
33	PSU	a	2604	33	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
10	5MC	A	967	10	-	0/7/25/26	0/2/2/2
33	1MG	a	745	33	-	0/7/25/26	0/3/3/3
8	5MU	8	55	8	-	0/7/25/26	0/2/2/2
20	IAS	K	119	20	-	1/7/7/8	-
33	2MA	a	2503	61,33	-	2/7/25/26	0/3/3/3
10	UR3	A	1498	10	-	0/7/25/26	0/2/2/2

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
33	a	2503	2MA	C2-N1	3.70	1.40	1.34
33	a	2503	2MA	C6-N1	3.18	1.39	1.35
10	A	1516	2MG	C6-N1	-2.96	1.33	1.38
33	a	2503	2MA	C6-N6	-2.67	1.27	1.34
10	A	1516	2MG	C5-C4	2.50	1.45	1.38

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	A	1516	2MG	C2-N3-C4	7.41	121.23	112.04
10	A	1516	2MG	C5-C4-N3	-5.80	119.05	128.46
10	A	1516	2MG	N9-C4-N3	4.08	134.13	125.94
10	A	1516	2MG	C2'-C1'-N9	-3.93	102.08	113.22
8	7	8	4SU	C4-N3-C2	-3.72	123.73	127.34

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.

11 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	8	33	4OC	1	0
10	A	1516	2MG	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
33	a	2498	OMC	1	0
10	A	1519	MA6	1	0
8	8	21	H2U	1	0
33	a	2030	6MZ	3	0
8	7	21	H2U	2	0
36	d	150	MEQ	5	0
33	a	2552	OMU	1	0
8	7	33	4OC	1	0
33	a	1915	3TD	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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.

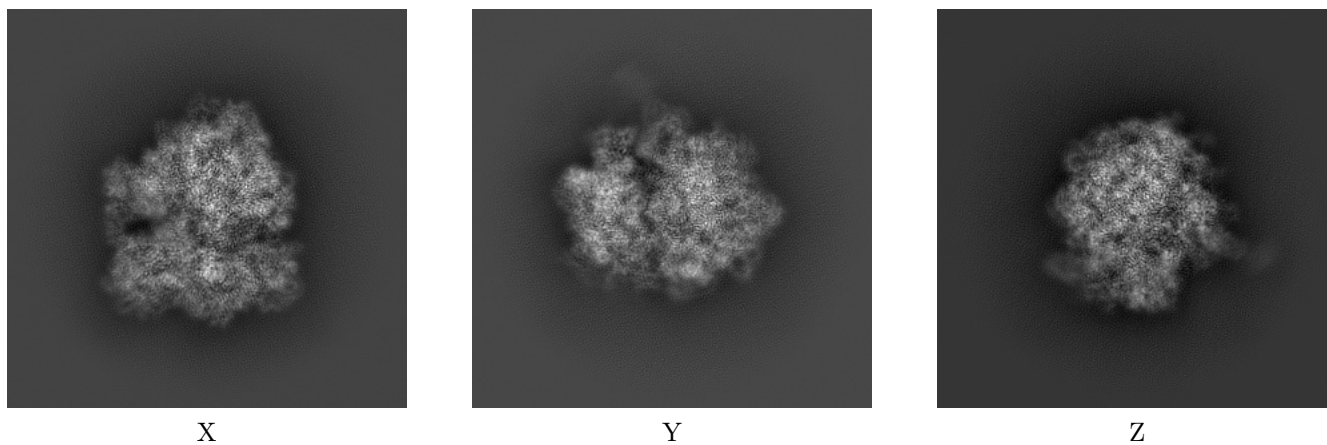
6 Map visualisation [i](#)

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 [i](#)

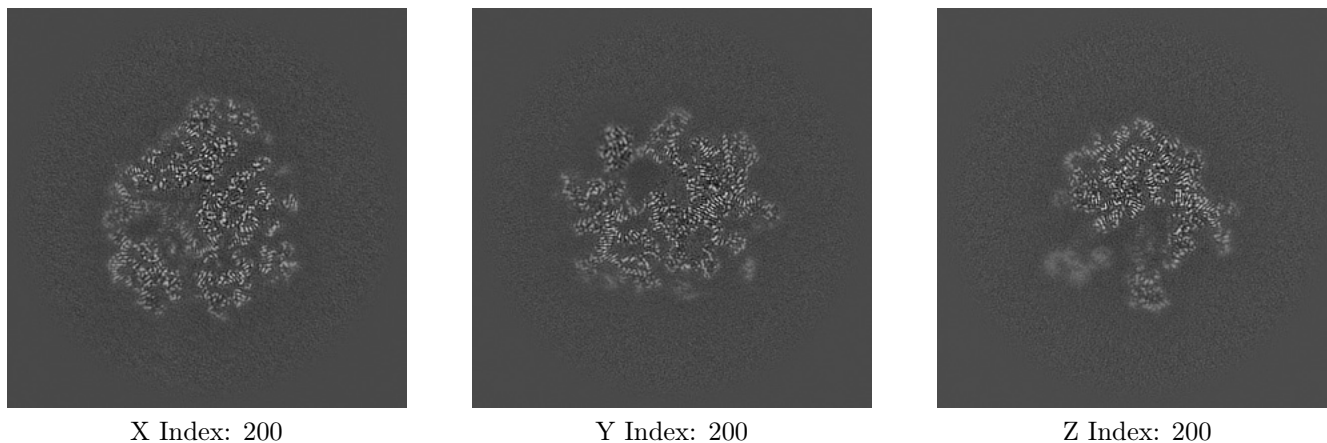
6.1.1 Primary map



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

6.2 Central slices [i](#)

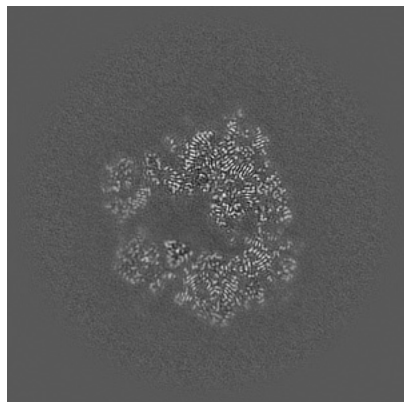
6.2.1 Primary map



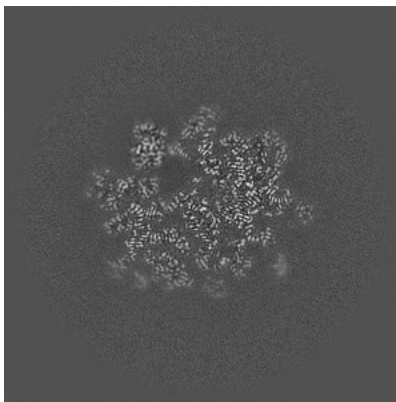
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

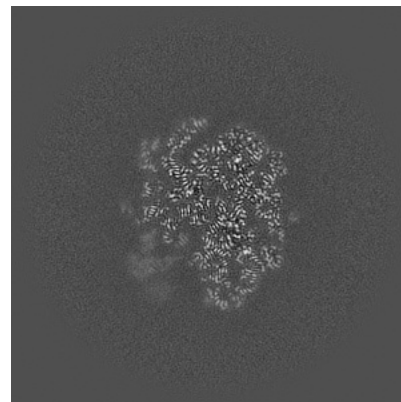
6.3.1 Primary map



X Index: 218



Y Index: 202

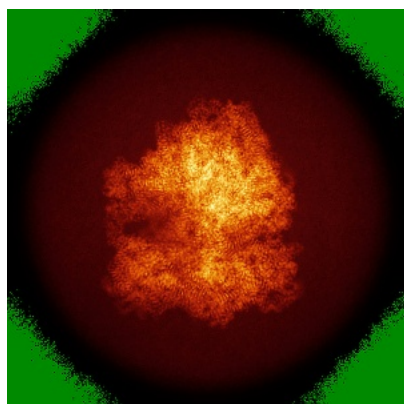


Z Index: 222

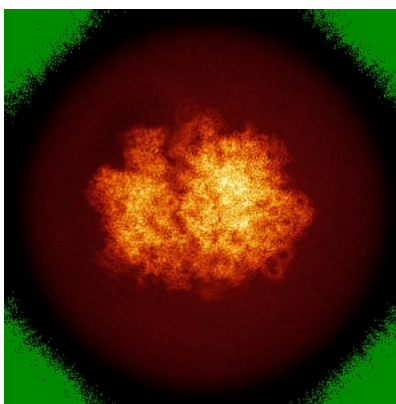
The images above show the largest variance slices of the map in three orthogonal directions.

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

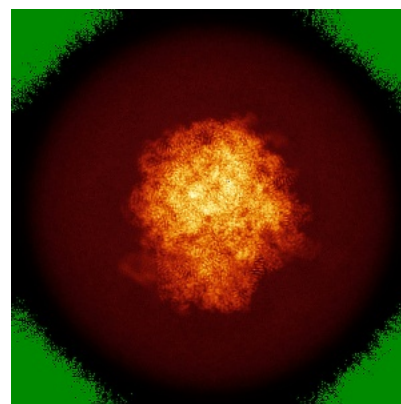
6.4.1 Primary map



X



Y

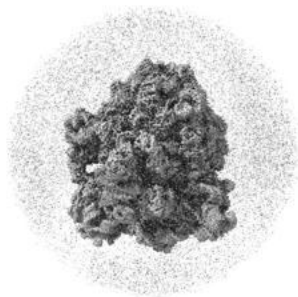


Z

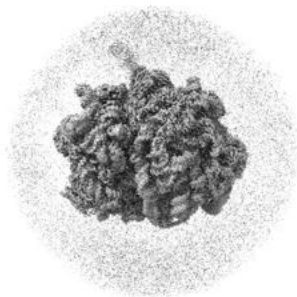
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

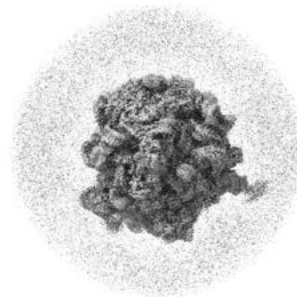
6.5.1 Primary map



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.

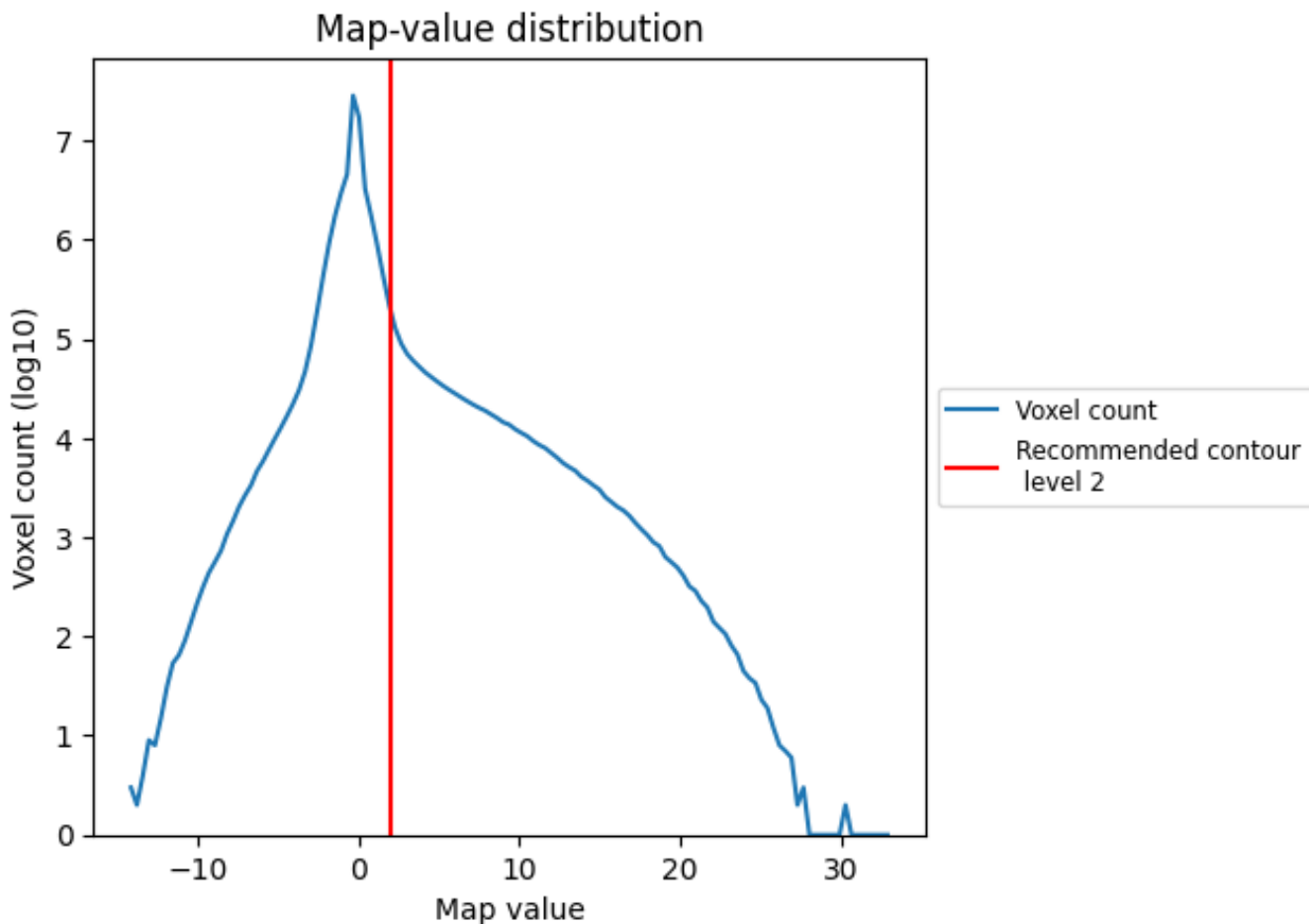
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

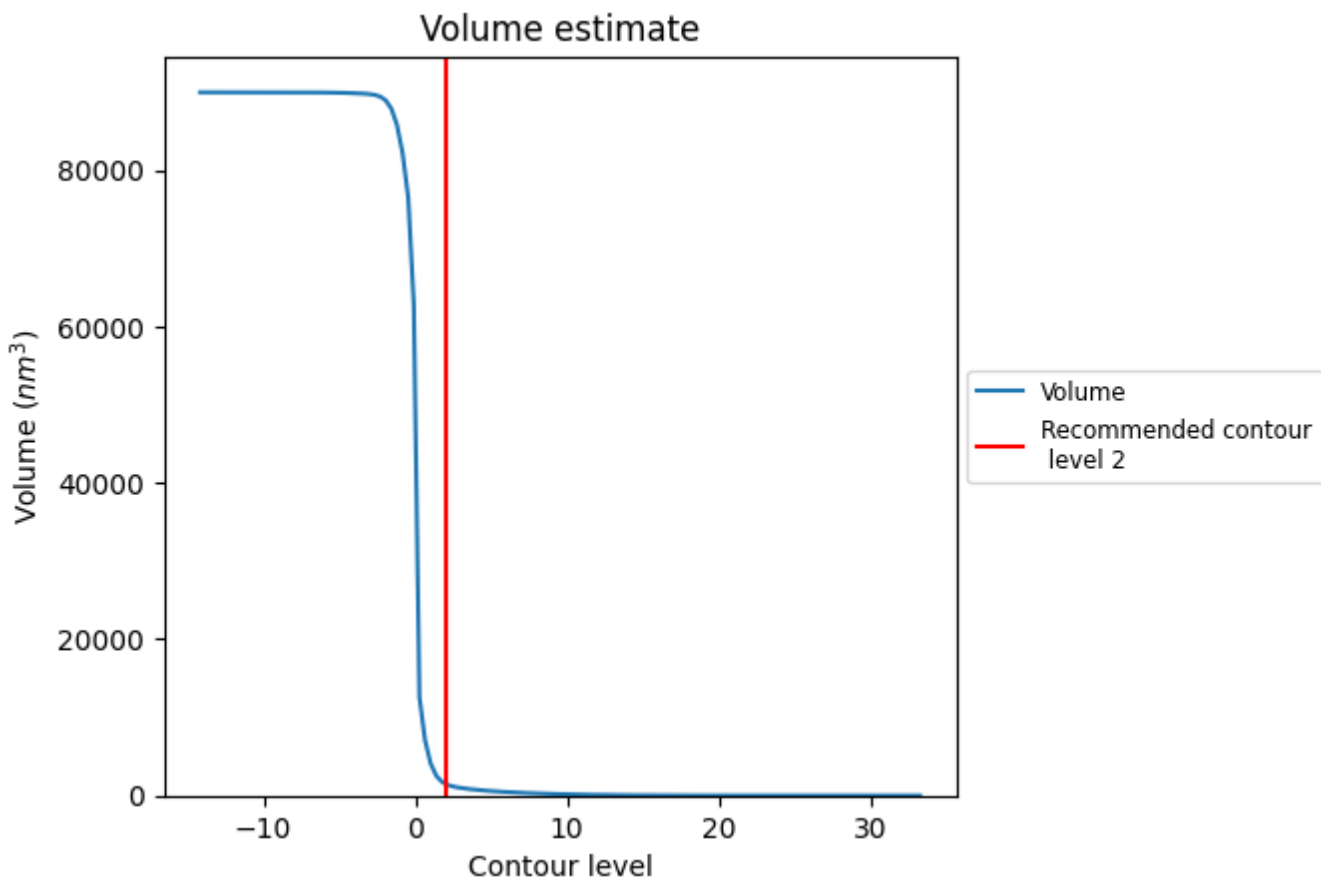
This section contains the results of statistical analysis of the map.

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.

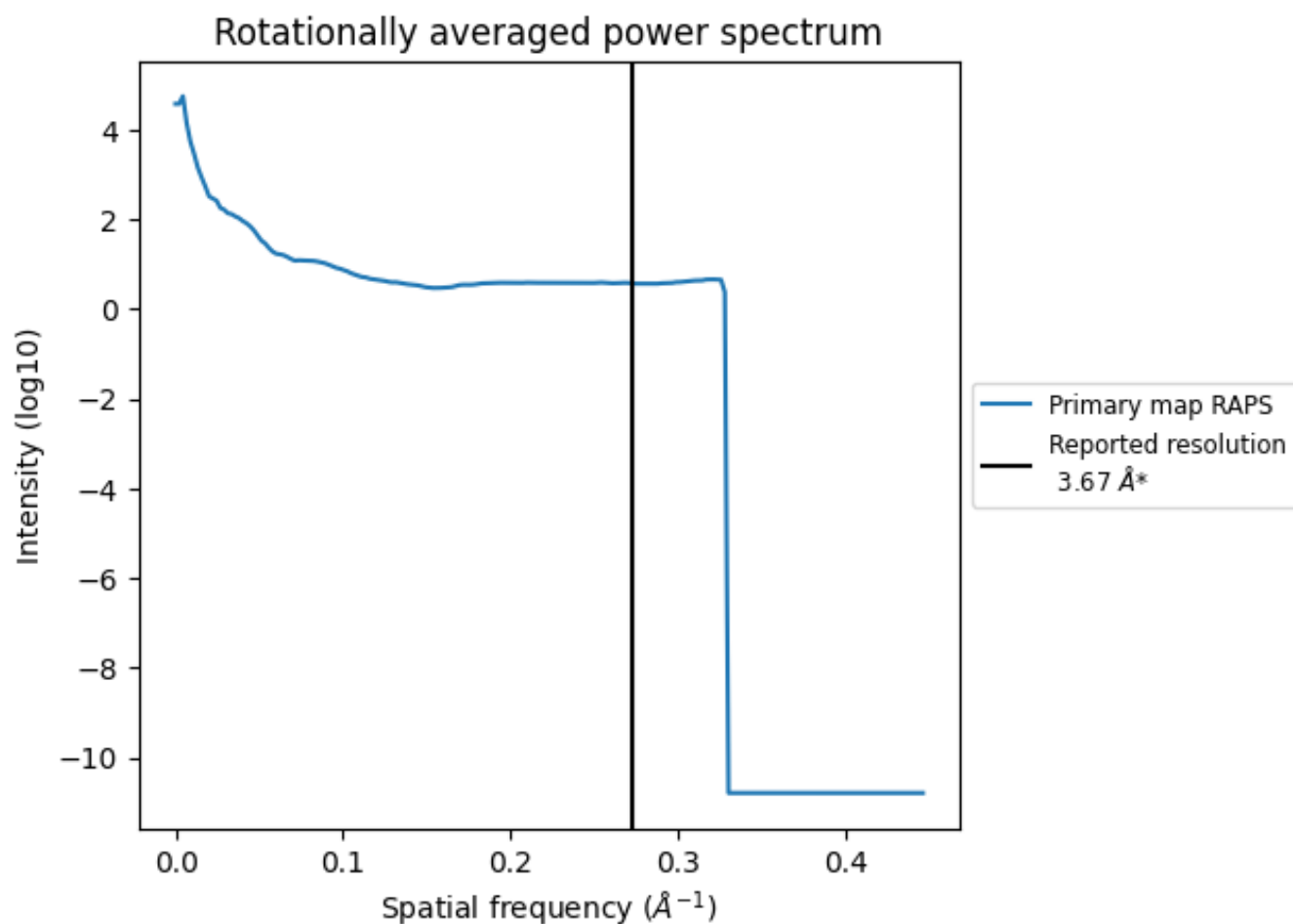
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 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

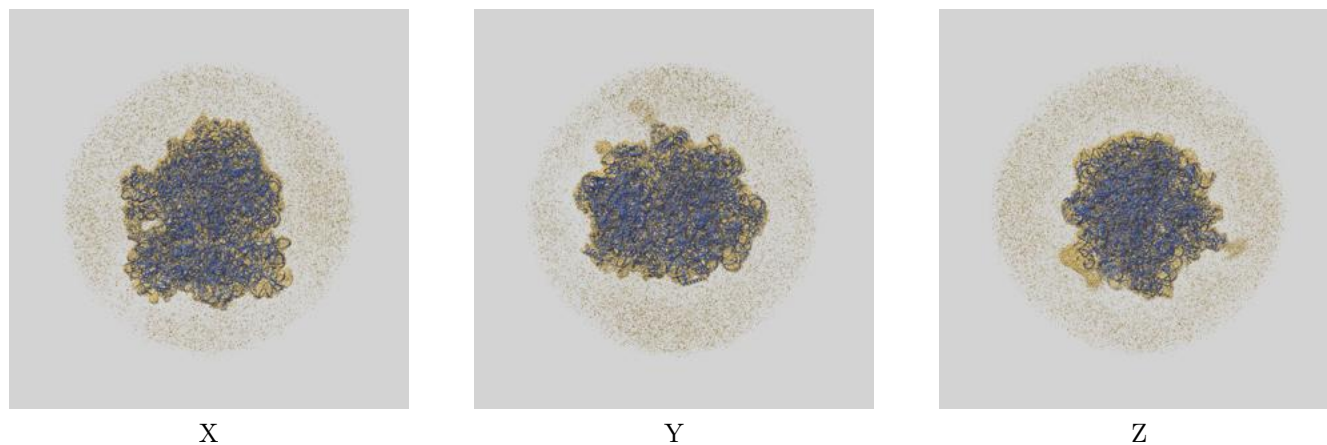
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

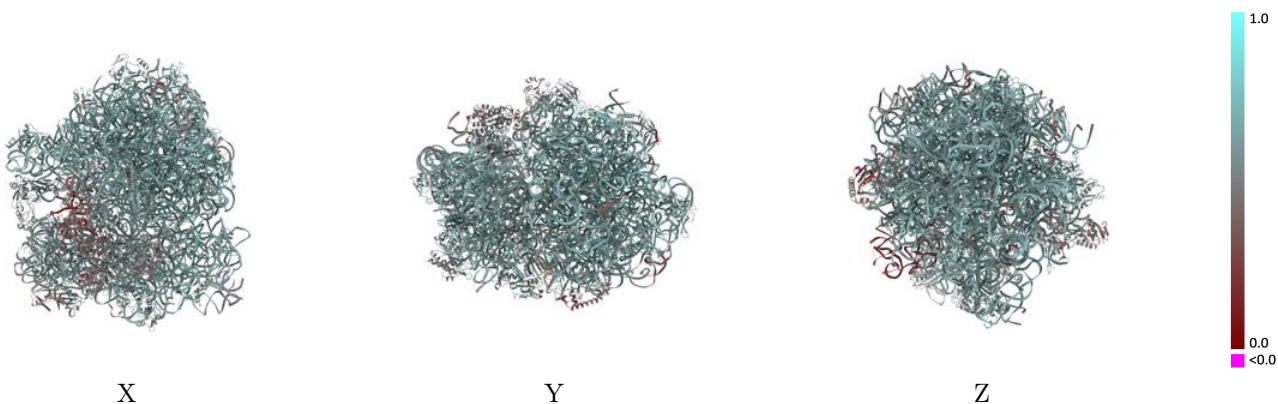
This section contains information regarding the fit between EMDB map EMD-17667 and PDB model 8PHJ. Per-residue inclusion information can be found in section 3 on page 17.

9.1 Map-model overlay [i](#)



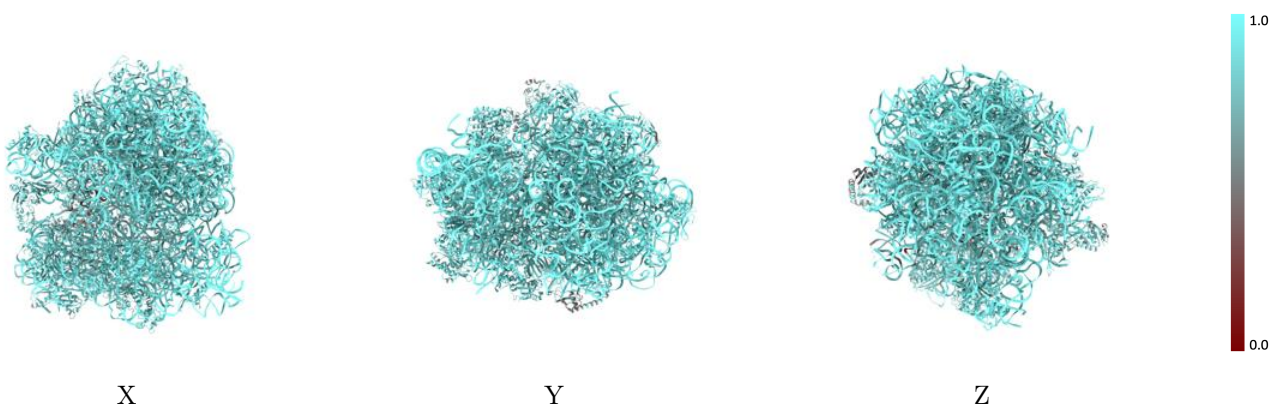
The images above show the 3D surface view of the map at the recommended contour level 2.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



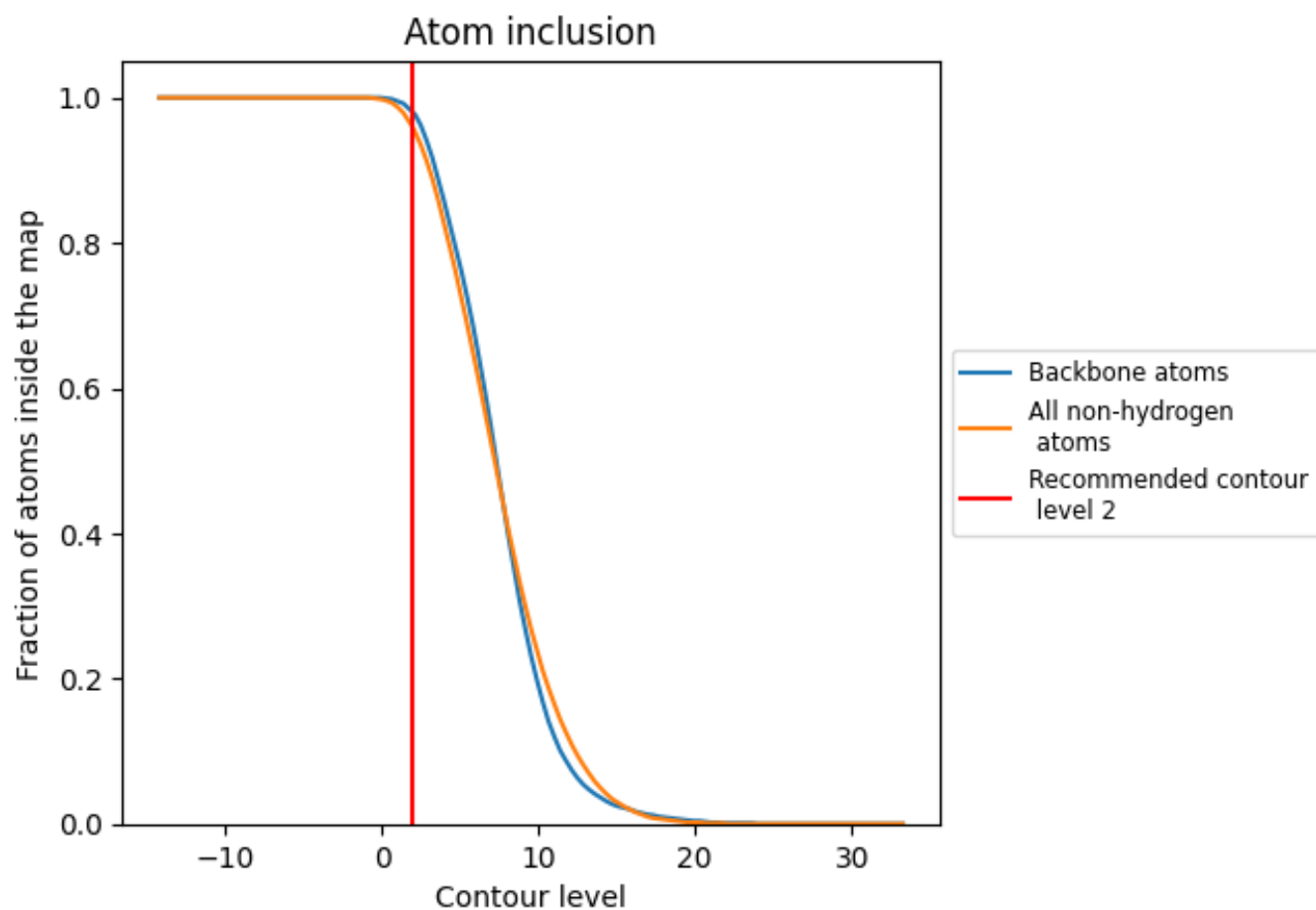
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2).







































































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) 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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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