



wwPDB EM Validation Summary Report ⓘ

May 19, 2024 – 08:00 am BST

PDB ID : 8P16
EMDB ID : EMD-17346
Title : E167K RF2 on E. coli 70S release complex with UGG (Structure I)
Authors : Pundir, S.; Larsson, D.S.D.; Selmer, M.; Sanyal, S.
Deposited on : 2023-05-11
Resolution : 2.77 Å (reported)
Based on initial models : 8B0X, 7K00, 5MDV, 1GQE

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:

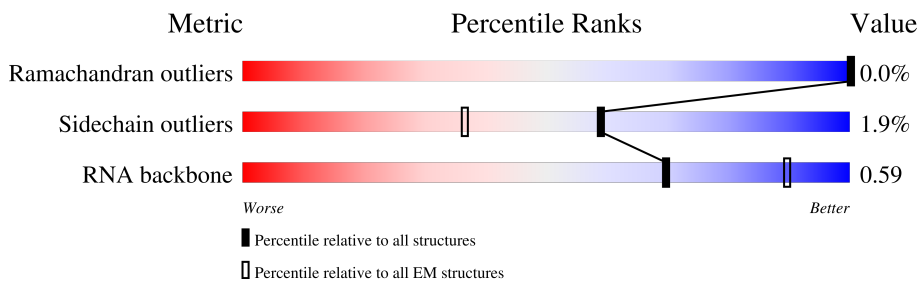
EMDB validation analysis : 0.0.1.dev92
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

1 Overall quality at a glance

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

The reported resolution of this entry is 2.77 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.



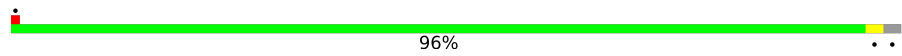
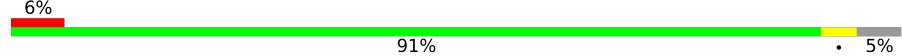

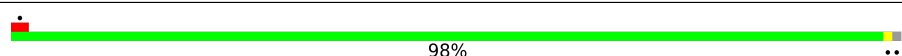
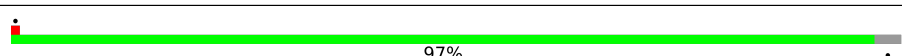
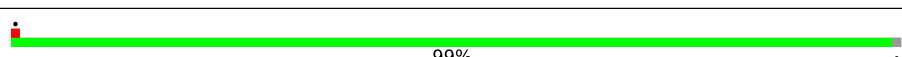
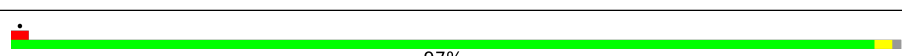
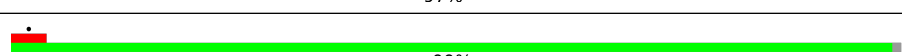
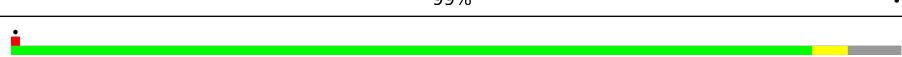
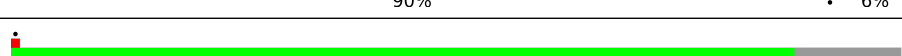
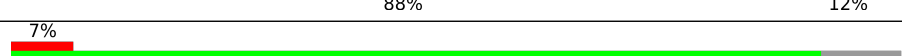
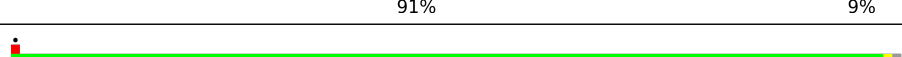
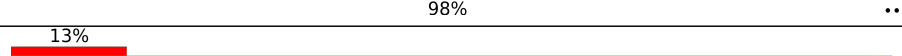
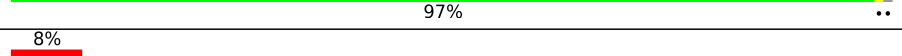
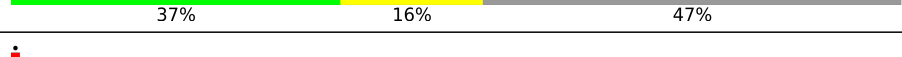



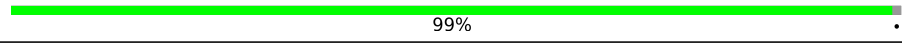
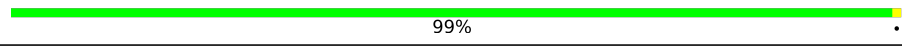
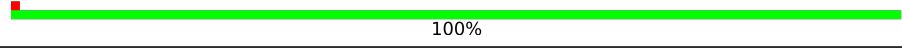
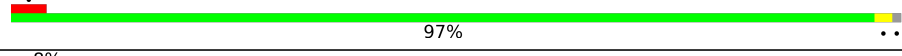
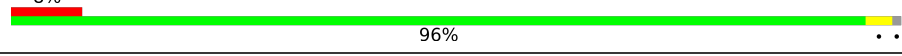
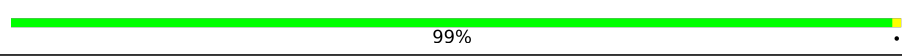
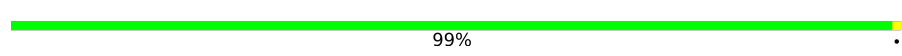
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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 $\leq 5\%$. 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	2	1542	
2	g	241	
3	h	233	
4	i	206	
5	j	167	
6	k	135	
7	l	179	
8	m	130	

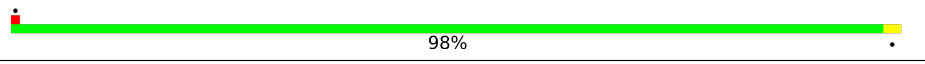
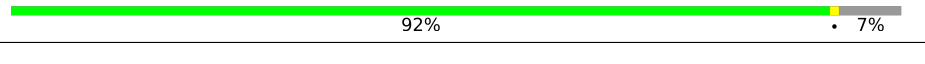
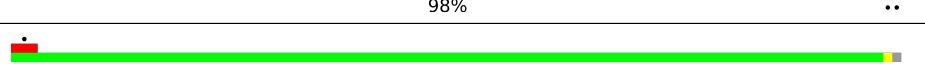
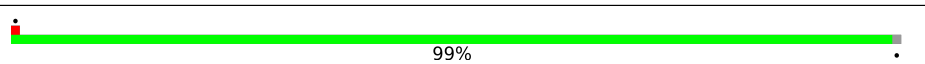
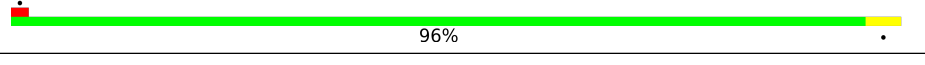
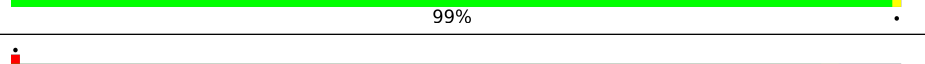
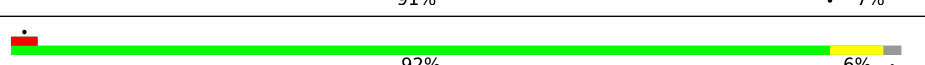
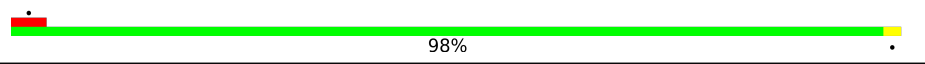
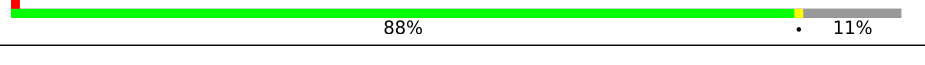
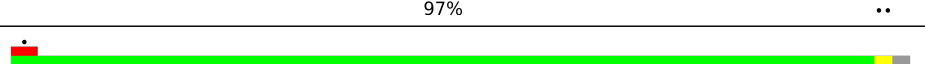
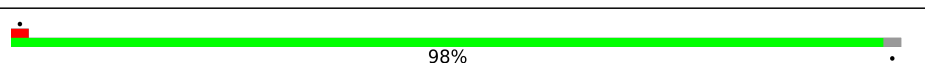
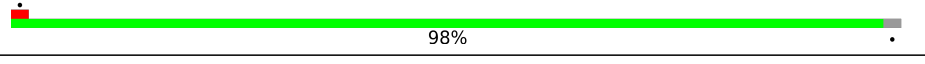

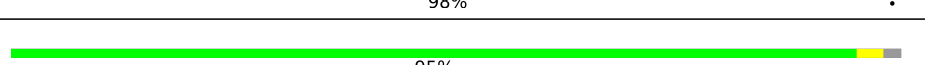
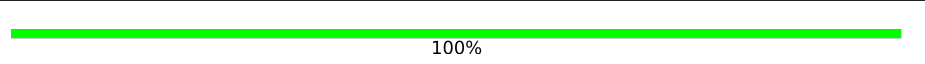
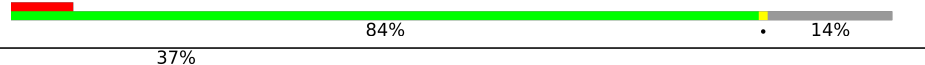

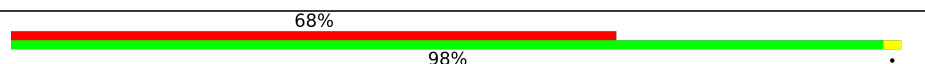





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Mol	Chain	Length	Quality of chain
9	n	130	 96%
10	o	103	 91% 6% 5%
11	p	129	 89% 9%
12	q	124	 98%
13	r	118	 97%
14	s	101	 99%
15	t	89	 97%
16	u	82	 99%
17	v	84	 90% 6%
18	w	75	 88% 12%
19	x	92	 91% 7% 9%
20	y	87	 98%
21	z	71	 97% 13%
22	4	49	 37% 16% 47% 8%
23	5	76	 59% 41%
24	1	2904	 84% 16%
25	3	120	 87% 12%
26	B	273	 99%
27	C	209	 99%
28	D	201	 100%
29	E	179	 97%
30	F	177	 96% 8%
31	J	142	 99%
32	K	123	 99%
33	L	144	 99%

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Mol	Chain	Length	Quality of chain
34	M	136	 98%
35	N	127	 92% 7%
36	O	117	 98%
37	P	115	 98%
38	Q	118	 99%
39	R	103	 96%
40	S	110	 99%
41	T	100	 91% 7%
42	U	104	 92% 6%
43	V	94	 98%
44	W	85	 88% 11%
45	X	78	 97%
46	Y	63	 97%
47	Z	59	 98%
48	b	57	 98%
49	c	55	 89% 7%
50	d	46	 98%
51	e	65	 95%
52	f	38	 100%
53	a	70	 7% 84% 14%
54	I	142	 37% 46% 52%
55	6	365	 35% 96%
56	G	149	 68% 98%

2 Entry composition

There are 62 unique types of molecules in this entry. The entry contains 148578 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 RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	2	1536	32966	14711	6044	10675	1536	0	0

- Molecule 2 is a protein called Small ribosomal subunit protein uS2.

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

- Molecule 3 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	h	210	1648	1043	309	292	4	0	0

- Molecule 4 is a protein called Small ribosomal subunit protein uS4.

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

- Molecule 5 is a protein called Small ribosomal subunit protein uS5.

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

- Molecule 6 is a protein called 30S ribosomal protein S6.

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

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	l	154	Total	C	N	O	S	0	0
			1214	756	235	219	4		

- Molecule 8 is a protein called Small ribosomal subunit protein uS8.

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

- Molecule 9 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 10 is a protein called Small ribosomal subunit protein uS10.

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

- Molecule 11 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	p	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
p	119	IAS	ASN	variant	UNP P0A7R9

- Molecule 12 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	q	123	Total	C	N	O	S	0	0
			957	591	196	165	5		

- Molecule 13 is a protein called Small ribosomal subunit protein uS13.

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

- Molecule 14 is a protein called Small ribosomal subunit protein uS14.

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

- Molecule 15 is a protein called Small ribosomal subunit protein uS15.

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

- Molecule 16 is a protein called Small ribosomal subunit protein bS16.

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

- Molecule 17 is a protein called Small ribosomal subunit protein uS17.

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

- Molecule 18 is a protein called Small ribosomal subunit protein bS18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	w	66	Total	C	N	O	S	0	0
			544	345	102	96	1		

- Molecule 19 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	x	84	Total	C	N	O	S	0	0
			668	427	127	112	2		

- Molecule 20 is a protein called Small ribosomal subunit protein bS20.

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

- Molecule 21 is a protein called Small ribosomal subunit protein bS21.

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

- Molecule 22 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	4	26	Total	C	N	O	P	0	0
			562	251	104	181	26		

- Molecule 23 is a RNA chain called tRNA(fMet).

Mol	Chain	Residues	Atoms					AltConf	Trace
23	5	76	Total	C	N	O	P	0	0
			1623	723	294	530	76		

- Molecule 24 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	1	2899	Total	C	N	O	P	0	0
			62252	27778	11456	20119	2899		

- Molecule 25 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	3	119	Total	C	N	O	P	0	0
			2549	1135	466	829	119		

- Molecule 26 is a protein called 50S ribosomal protein L2.

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

- Molecule 27 is a protein called 50S ribosomal protein L3.

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

- Molecule 28 is a protein called 50S ribosomal protein L4.

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

- Molecule 29 is a protein called 50S ribosomal protein L5.

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

- Molecule 30 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	F	175	Total	C	N	O	S	0	0
			1313	826	241	244	2		

- Molecule 31 is a protein called 50S ribosomal protein L13.

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

- Molecule 32 is a protein called 50S ribosomal protein L14.

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

- Molecule 33 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	L	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 34 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	M	136	1075	686	205	177	7	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	82	MS6	MET	variant	UNP P0ADY7

- Molecule 35 is a protein called 50S ribosomal protein L17.

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

- Molecule 36 is a protein called 50S ribosomal protein L18.

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

- Molecule 37 is a protein called 50S ribosomal protein L19.

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

- Molecule 38 is a protein called 50S ribosomal protein L20.

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

- Molecule 39 is a protein called 50S ribosomal protein L21.

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

- Molecule 40 is a protein called 50S ribosomal protein L22.

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

- Molecule 41 is a protein called 50S ribosomal protein L23.

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

- Molecule 42 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
42	U	102	779	492	146	141	0	0

- Molecule 43 is a protein called 50S ribosomal protein L25.

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

- Molecule 44 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	W	76	582	360	117	104	1	0	0

- Molecule 45 is a protein called 50S ribosomal protein L28.

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

- Molecule 46 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	Y	62	501	308	98	94	1	0	0

- Molecule 47 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Z	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
48	b	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

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

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

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

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

- Molecule 51 is a protein called 50S ribosomal protein L35.

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

- Molecule 52 is a protein called 50S ribosomal protein L36.

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

- Molecule 53 is a protein called Large ribosomal subunit protein bL31A.

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

- Molecule 54 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	I	68	Total	C	N	O	S	0	0
			484	298	89	94	3		

- Molecule 55 is a protein called Peptide chain release factor RF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	6	361	Total	C	N	O	S	1	0
			2863	1762	504	587	10		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
6	167	LYS	GLU	engineered mutation	UNP P07012

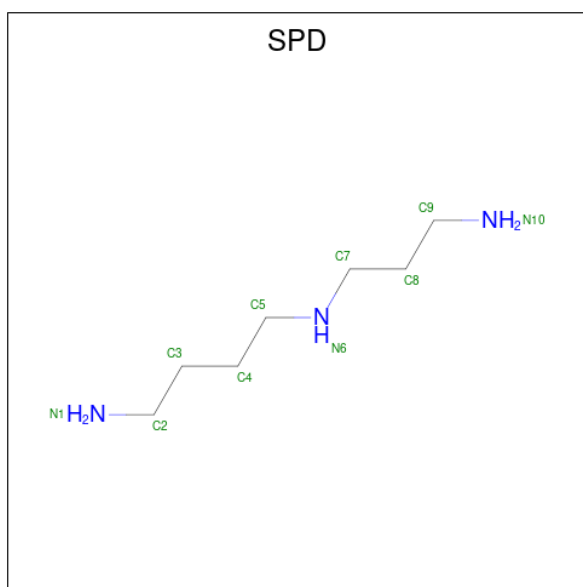
- Molecule 56 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	G	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 57 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
57	2	95	Total	Mg	0
			95	95	
57	s	1	Total	Mg	0
			1	1	
57	5	2	Total	Mg	0
			2	2	
57	1	223	Total	Mg	0
			223	223	
57	3	5	Total	Mg	0
			5	5	
57	B	1	Total	Mg	0
			1	1	
57	C	1	Total	Mg	0
			1	1	
57	Q	1	Total	Mg	0
			1	1	
57	b	1	Total	Mg	0
			1	1	

- Molecule 58 is SPERMIDINE (three-letter code: SPD) (formula: C₇H₁₉N₃).

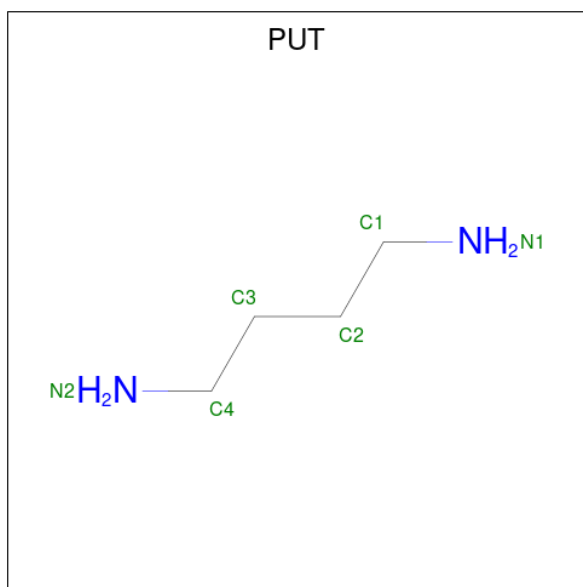


Mol	Chain	Residues	Atoms			AltConf
58	2	1	Total	C	N	0
			10	7	3	
58	2	1	Total	C	N	0
			10	7	3	
58	1	1	Total	C	N	0
			10	7	3	
58	1	1	Total	C	N	0
			10	7	3	
58	1	1	Total	C	N	0
			10	7	3	
58	1	1	Total	C	N	0
			10	7	3	
58	1	1	Total	C	N	0
			10	7	3	
58	1	1	Total	C	N	0
			10	7	3	
58	1	1	Total	C	N	0
			10	7	3	
58	1	1	Total	C	N	0
			10	7	3	

- Molecule 59 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	AltConf
59	2	35	Total K 35 35	0
59	1	93	Total K 93 93	0

- Molecule 60 is 1,4-DIAMINOBTUTANE (three-letter code: PUT) (formula: C₄H₁₂N₂).



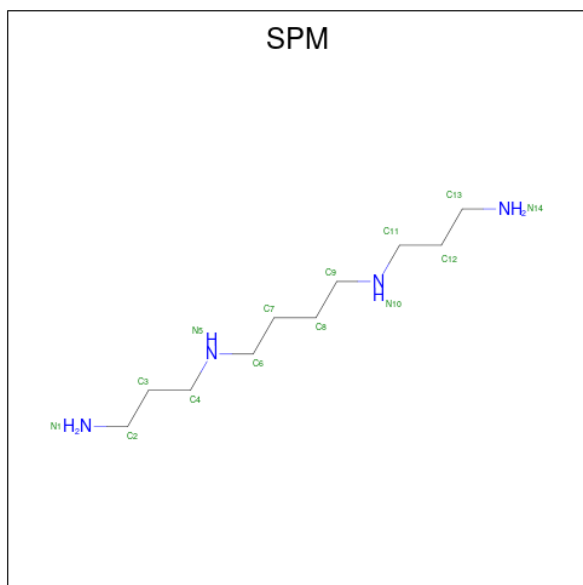
Mol	Chain	Residues	Atoms	AltConf
60	2	1	Total C N 6 4 2	0
60	2	1	Total C N 6 4 2	0
60	1	1	Total C N 6 4 2	0
60	1	1	Total C N 6 4 2	0
60	1	1	Total C N 6 4 2	0
60	1	1	Total C N 6 4 2	0
60	1	1	Total C N 6 4 2	0
60	1	1	Total C N 6 4 2	0
60	1	1	Total C N 6 4 2	0
60	1	1	Total C N 6 4 2	0

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Mol	Chain	Residues	Atoms			AltConf
			Total	C	N	
60	1	1	6	4	2	0
60	1	1	6	4	2	0
60	1	1	6	4	2	0

- Molecule 61 is SPERMINE (three-letter code: SPM) (formula: $C_{10}H_{26}N_4$).



Mol	Chain	Residues	Atoms			AltConf
			Total	C	N	
61	1	1	14	10	4	0

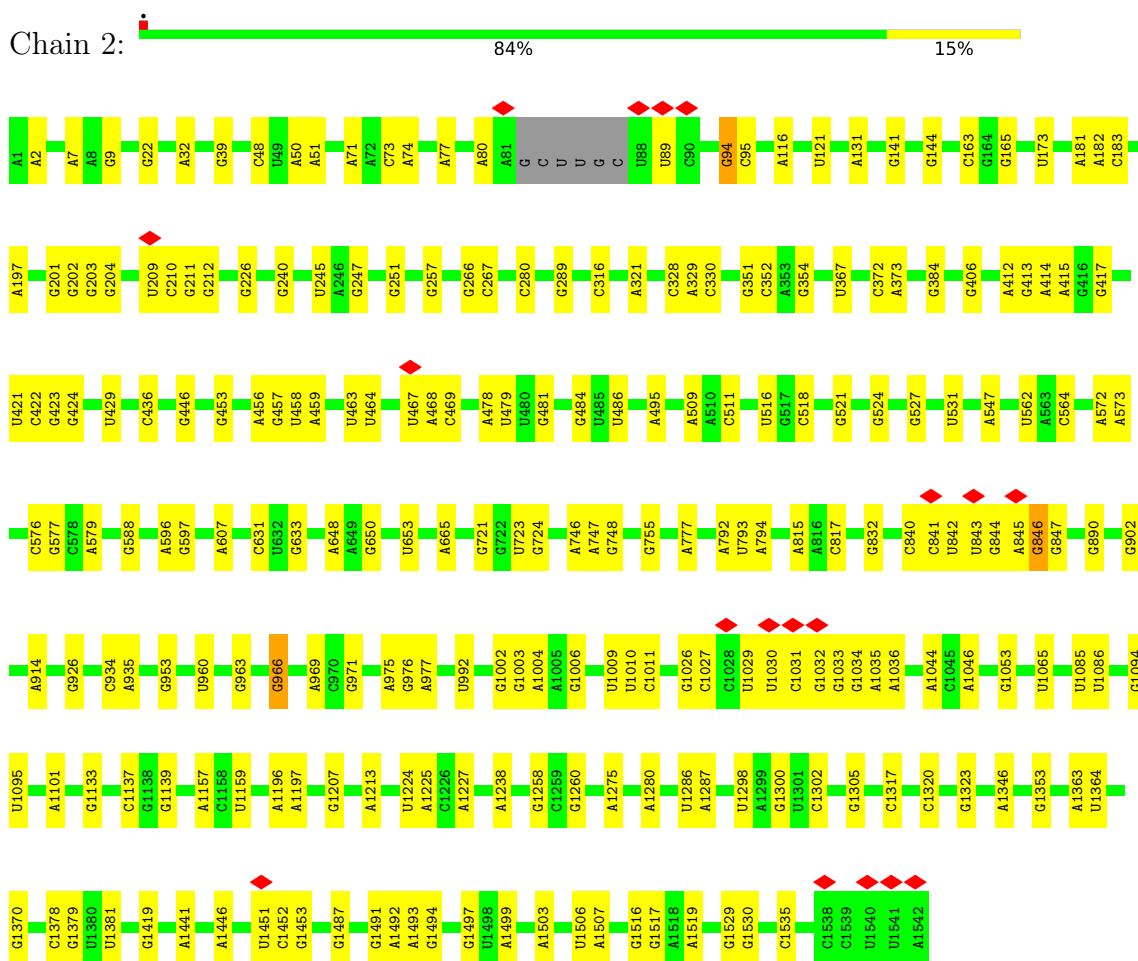
- Molecule 62 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
62	f	1	1	1	0
62	a	1	1	1	0

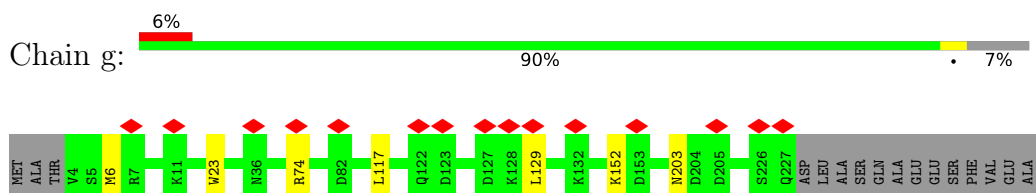
3 Residue-property plots [i](#)

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: 16S rRNA

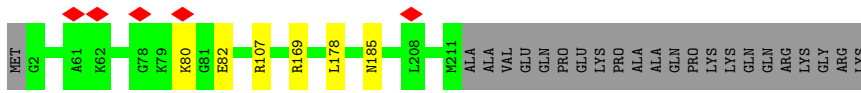


- Molecule 2: Small ribosomal subunit protein uS2



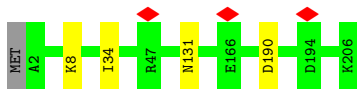
- Molecule 3: Small ribosomal subunit protein uS3

Chain h:  88% 10%




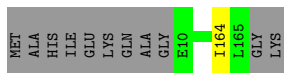
- Molecule 4: Small ribosomal subunit protein uS4

Chain i:  98%



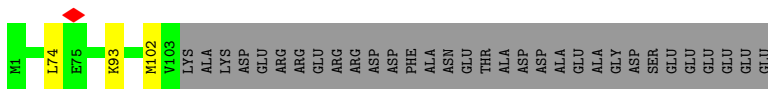
- Molecule 5: Small ribosomal subunit protein uS5

Chain j:  93% 7%




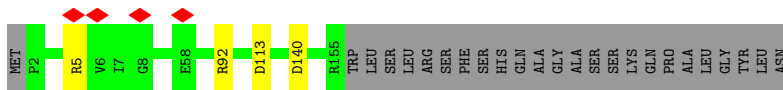
- Molecule 6: 30S ribosomal protein S6

Chain k:  74% 24%



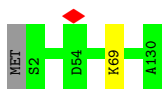
- Molecule 7: 30S ribosomal protein S7

Chain l:  84% 14%



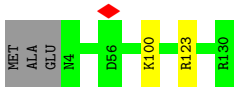
- Molecule 8: Small ribosomal subunit protein uS8

Chain m:  98%

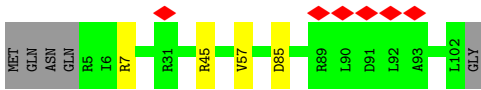
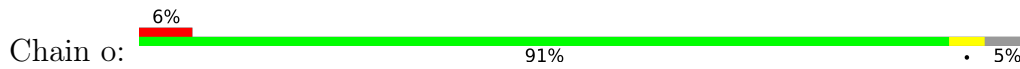


- Molecule 9: Small ribosomal subunit protein uS9

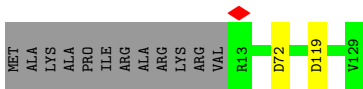
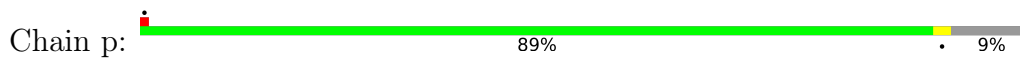
Chain n:  96%



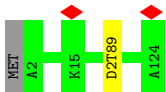
- Molecule 10: Small ribosomal subunit protein uS10



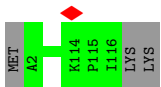
- Molecule 11: Small ribosomal subunit protein uS11



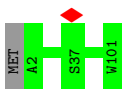
- Molecule 12: Small ribosomal subunit protein uS12



- Molecule 13: Small ribosomal subunit protein uS13



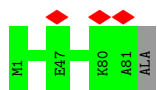
- Molecule 14: Small ribosomal subunit protein uS14



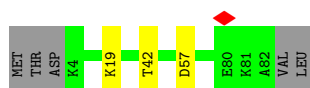
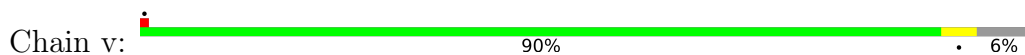
- Molecule 15: Small ribosomal subunit protein uS15



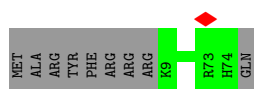
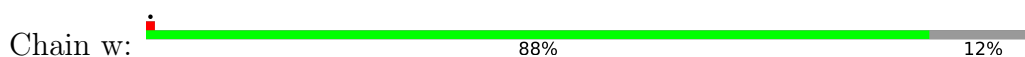
- Molecule 16: Small ribosomal subunit protein bS16



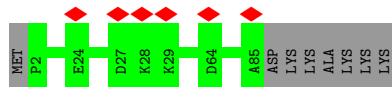
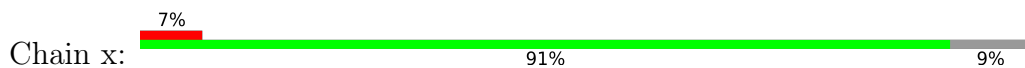
- Molecule 17: Small ribosomal subunit protein uS17



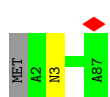
- Molecule 18: Small ribosomal subunit protein bS18



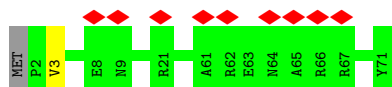
- Molecule 19: Small ribosomal subunit protein uS19



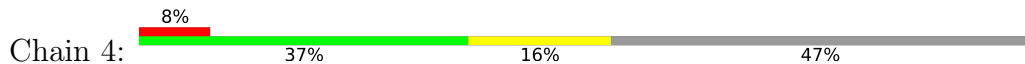
- Molecule 20: Small ribosomal subunit protein bS20



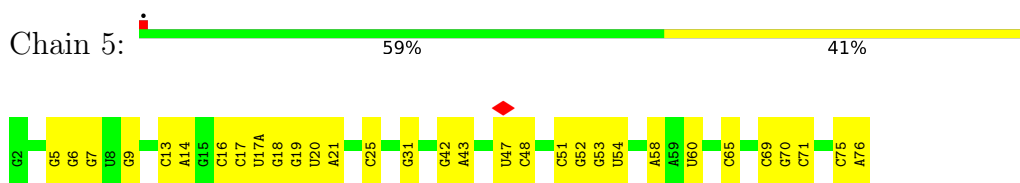
- Molecule 21: Small ribosomal subunit protein bS21



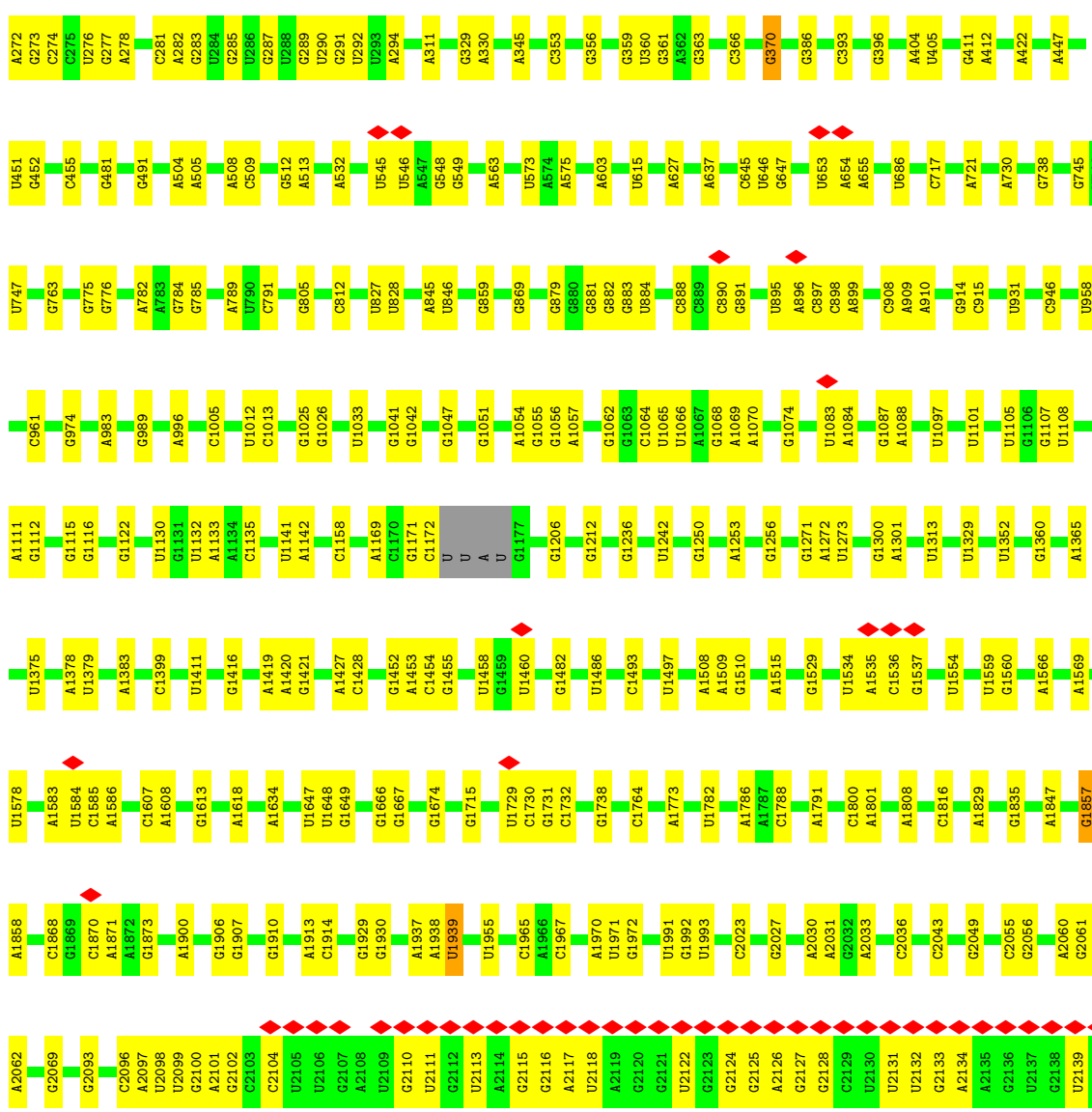
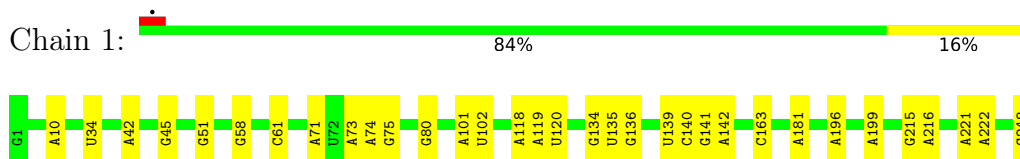
- Molecule 22: mRNA

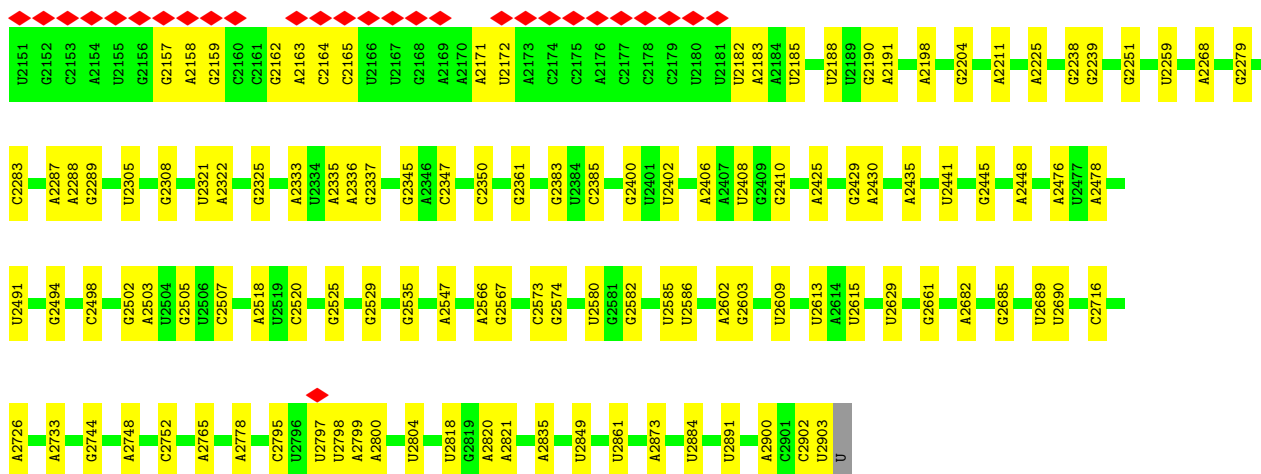


• Molecule 23: tRNA(fMet)

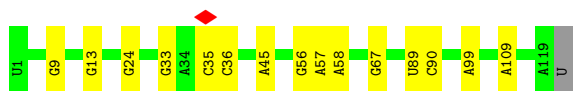
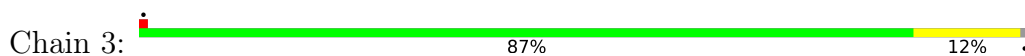


• Molecule 24: 23S rRNA

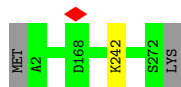




• Molecule 25: 5S rRNA



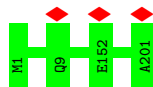
• Molecule 26: 50S ribosomal protein L2



• Molecule 27: 50S ribosomal protein L3

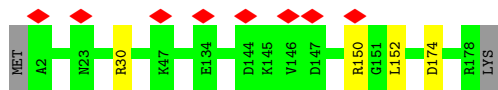


• Molecule 28: 50S ribosomal protein L4

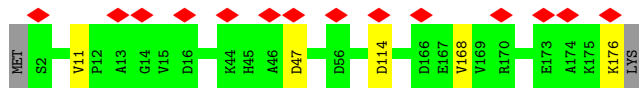


• Molecule 29: 50S ribosomal protein L5

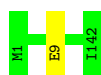




- Molecule 30: 50S ribosomal protein L6



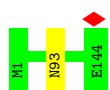
- Molecule 31: 50S ribosomal protein L13



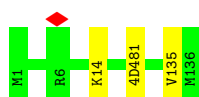
- Molecule 32: 50S ribosomal protein L14



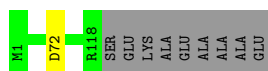
- Molecule 33: 50S ribosomal protein L15



- Molecule 34: Large ribosomal subunit protein uL16



- Molecule 35: 50S ribosomal protein L17



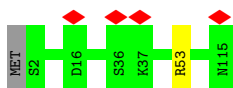
- Molecule 36: 50S ribosomal protein L18

Chain O:  98% ..



- Molecule 37: 50S ribosomal protein L19

Chain P:  98% ..



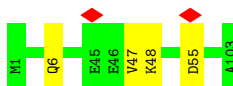
- Molecule 38: 50S ribosomal protein L20

Chain Q:  99% .



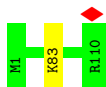
- Molecule 39: 50S ribosomal protein L21

Chain R:  96% .




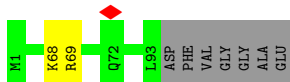
- Molecule 40: 50S ribosomal protein L22

Chain S:  99% .



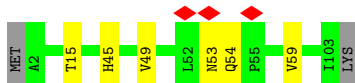
- Molecule 41: 50S ribosomal protein L23

Chain T:  91% . 7%

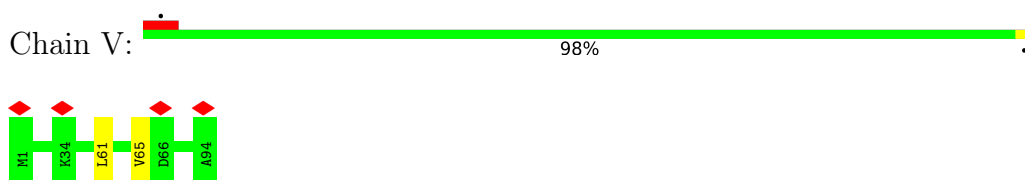


- Molecule 42: 50S ribosomal protein L24

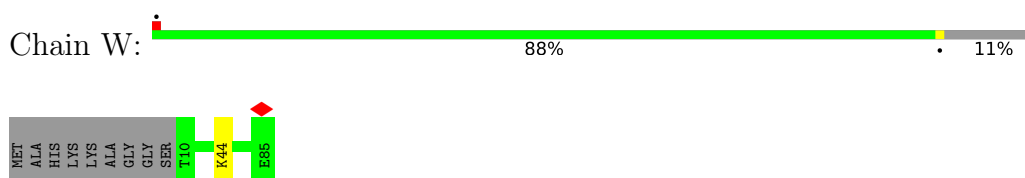
Chain U:  92% . 6%



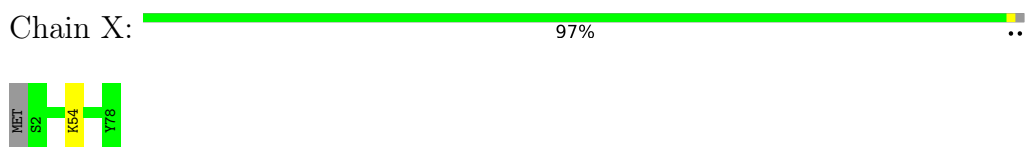
- Molecule 43: 50S ribosomal protein L25



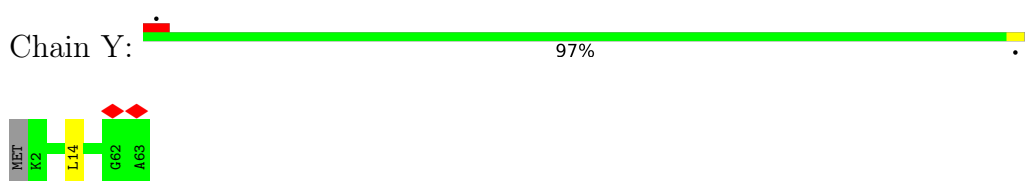
- Molecule 44: 50S ribosomal protein L27



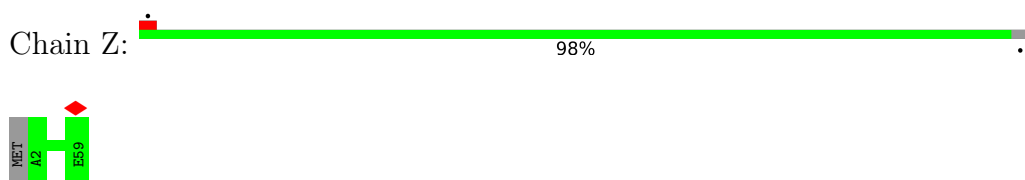
- Molecule 45: 50S ribosomal protein L28



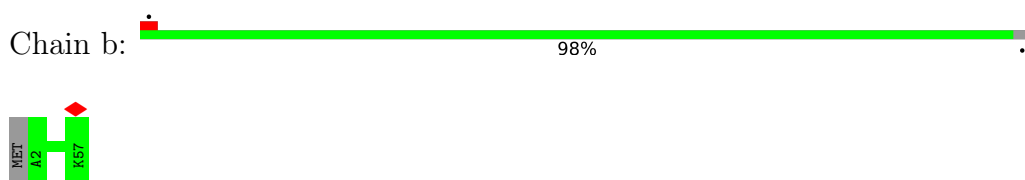
- Molecule 46: 50S ribosomal protein L29



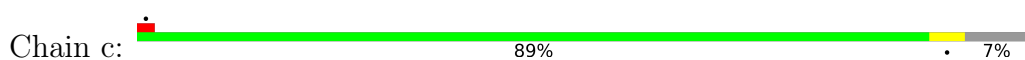
- Molecule 47: 50S ribosomal protein L30

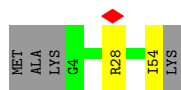


- Molecule 48: 50S ribosomal protein L32

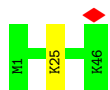


- Molecule 49: 50S ribosomal protein L33





• Molecule 50: 50S ribosomal protein L34



• Molecule 51: 50S ribosomal protein L35

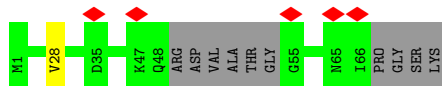
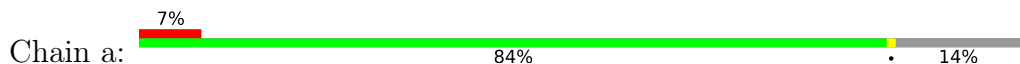


• Molecule 52: 50S ribosomal protein L36

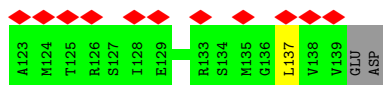
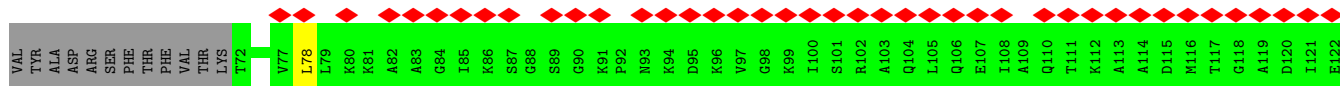
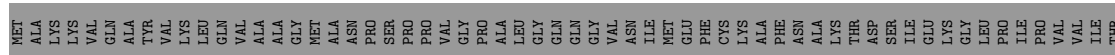
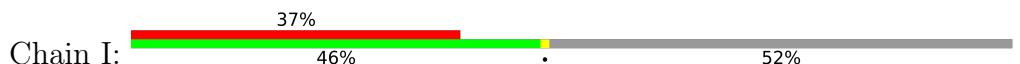


There are no outlier residues recorded for this chain.

• Molecule 53: Large ribosomal subunit protein bL31A

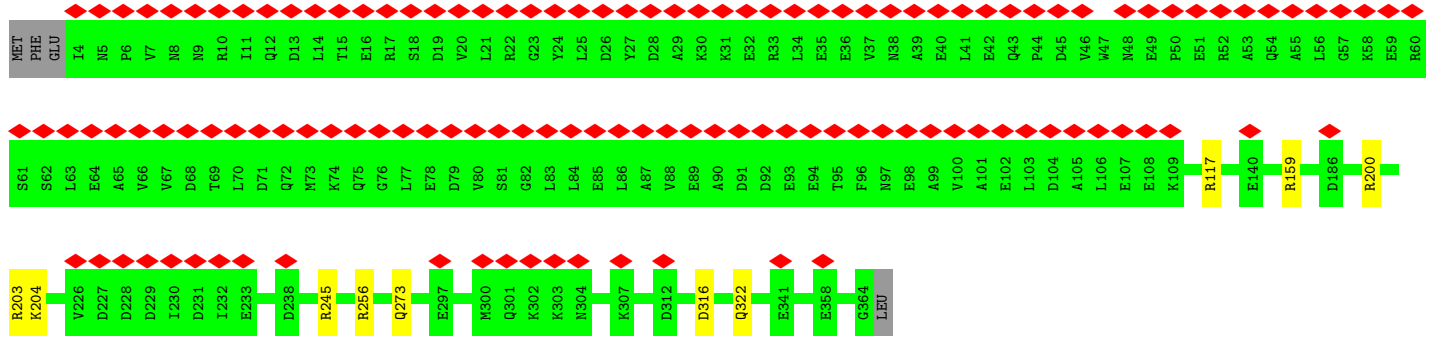


• Molecule 54: 50S ribosomal protein L11



• Molecule 55: Peptide chain release factor RF2





• Molecule 56: 50S ribosomal protein L9



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	21843	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	38.14	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1300	Depositor
Magnification	105000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.263	Depositor
Minimum map value	-0.392	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.055	Depositor
Recommended contour level	0.19	Depositor
Map size (Å)	433.44598, 433.44598, 433.44598	wwPDB
Map dimensions	520, 520, 520	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83355, 0.83355, 0.83355	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: K, OMU, 1MG, MA6, MG, 5MU, OMC, 2MA, MS6, SPD, IAS, 4D4, 6MZ, D2T, OMG, 2MG, H2U, 5MC, ZN, SPM, PSU, 4OC, UR3, MEQ, G7M, PUT, 3TD

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	2	0.56	0/36631	0.82	8/57136 (0.0%)
2	g	0.28	0/1784	0.48	0/2403
3	h	0.31	0/1675	0.52	0/2256
4	i	0.31	0/1665	0.52	0/2227
5	j	0.32	0/1165	0.52	0/1568
6	k	0.32	0/858	0.51	0/1160
7	l	0.28	0/1230	0.53	0/1649
8	m	0.32	0/989	0.50	0/1326
9	n	0.30	0/1034	0.57	0/1375
10	o	0.29	0/796	0.56	0/1077
11	p	0.31	0/884	0.55	0/1191
12	q	0.34	0/960	0.59	0/1286
13	r	0.28	0/900	0.56	0/1204
14	s	0.29	0/817	0.53	0/1088
15	t	0.29	0/722	0.53	0/964
16	u	0.31	0/653	0.57	0/877
17	v	0.30	0/650	0.52	0/871
18	w	0.33	0/553	0.53	0/742
19	x	0.30	0/685	0.50	0/922
20	y	0.28	0/676	0.48	0/895
21	z	0.34	0/597	0.57	0/792
22	4	0.40	0/630	0.84	0/981
23	5	0.52	0/1813	0.85	0/2825
24	1	0.62	0/69147	0.81	9/107869 (0.0%)
25	3	0.50	0/2850	0.79	0/4444
26	B	0.36	0/2121	0.57	0/2852
27	C	0.34	0/1576	0.52	0/2119
28	D	0.32	0/1571	0.51	0/2113
29	E	0.30	0/1434	0.51	0/1926
30	F	0.30	0/1333	0.52	0/1805
31	J	0.34	0/1152	0.50	0/1551

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	K	0.35	0/955	0.57	0/1279
33	L	0.32	0/1062	0.57	0/1413
34	M	0.35	0/1073	0.55	0/1433
35	N	0.33	0/958	0.57	0/1281
36	O	0.31	0/902	0.54	0/1209
37	P	0.34	0/929	0.55	0/1242
38	Q	0.38	0/960	0.53	0/1278
39	R	0.35	0/829	0.57	0/1107
40	S	0.32	0/864	0.53	0/1156
41	T	0.30	0/744	0.51	0/994
42	U	0.31	0/787	0.51	0/1051
43	V	0.31	0/766	0.50	0/1025
44	W	0.34	0/589	0.54	0/779
45	X	0.33	0/635	0.57	0/848
46	Y	0.27	0/502	0.48	0/667
47	Z	0.29	0/453	0.57	0/605
48	b	0.33	0/450	0.57	0/599
49	c	0.33	0/424	0.51	0/565
50	d	0.32	0/380	0.64	0/498
51	e	0.33	0/513	0.54	0/676
52	f	0.34	0/303	0.56	0/397
53	a	0.30	0/488	0.50	0/649
54	I	0.25	0/486	0.49	0/650
55	6	0.28	0/2895	0.48	0/3899
56	G	0.28	0/1122	0.51	0/1515
All	All	0.53	0/159620	0.75	17/238309 (0.0%)

There are no bond length outliers.

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	1	2096	C	N1-C2-O2	-9.50	113.20	118.90
1	2	1133	G	N3-C2-N2	-8.47	113.97	119.90
24	1	2096	C	C2-N3-C4	-8.27	115.77	119.90
1	2	1535	C	N1-C2-O2	-7.08	114.65	118.90
24	1	1666	G	N3-C2-N2	-5.93	115.75	119.90

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	
2	g	222/241 (92%)	217 (98%)	5 (2%)	0	100	100
3	h	208/233 (89%)	204 (98%)	4 (2%)	0	100	100
4	i	203/206 (98%)	200 (98%)	3 (2%)	0	100	100
5	j	154/167 (92%)	150 (97%)	4 (3%)	0	100	100
6	k	101/135 (75%)	100 (99%)	1 (1%)	0	100	100
7	l	152/179 (85%)	145 (95%)	7 (5%)	0	100	100
8	m	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
9	n	125/130 (96%)	123 (98%)	2 (2%)	0	100	100
10	o	96/103 (93%)	93 (97%)	2 (2%)	1 (1%)	15	41
11	p	113/129 (88%)	110 (97%)	3 (3%)	0	100	100
12	q	120/124 (97%)	115 (96%)	5 (4%)	0	100	100
13	r	113/118 (96%)	110 (97%)	3 (3%)	0	100	100
14	s	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
15	t	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
16	u	79/82 (96%)	76 (96%)	3 (4%)	0	100	100
17	v	77/84 (92%)	76 (99%)	1 (1%)	0	100	100
18	w	64/75 (85%)	64 (100%)	0	0	100	100
19	x	82/92 (89%)	82 (100%)	0	0	100	100
20	y	84/87 (97%)	84 (100%)	0	0	100	100
21	z	68/71 (96%)	68 (100%)	0	0	100	100
26	B	269/273 (98%)	265 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	C	206/209 (99%)	199 (97%)	6 (3%)	1 (0%)	29	58
28	D	199/201 (99%)	196 (98%)	3 (2%)	0	100	100
29	E	175/179 (98%)	166 (95%)	9 (5%)	0	100	100
30	F	173/177 (98%)	166 (96%)	7 (4%)	0	100	100
31	J	140/142 (99%)	138 (99%)	2 (1%)	0	100	100
32	K	121/123 (98%)	119 (98%)	2 (2%)	0	100	100
33	L	142/144 (99%)	139 (98%)	3 (2%)	0	100	100
34	M	132/136 (97%)	130 (98%)	2 (2%)	0	100	100
35	N	116/127 (91%)	111 (96%)	5 (4%)	0	100	100
36	O	114/117 (97%)	112 (98%)	2 (2%)	0	100	100
37	P	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
38	Q	115/118 (98%)	115 (100%)	0	0	100	100
39	R	101/103 (98%)	98 (97%)	3 (3%)	0	100	100
40	S	108/110 (98%)	106 (98%)	2 (2%)	0	100	100
41	T	91/100 (91%)	87 (96%)	4 (4%)	0	100	100
42	U	100/104 (96%)	98 (98%)	2 (2%)	0	100	100
43	V	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
44	W	74/85 (87%)	73 (99%)	1 (1%)	0	100	100
45	X	75/78 (96%)	75 (100%)	0	0	100	100
46	Y	60/63 (95%)	60 (100%)	0	0	100	100
47	Z	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
48	b	54/57 (95%)	54 (100%)	0	0	100	100
49	c	49/55 (89%)	49 (100%)	0	0	100	100
50	d	44/46 (96%)	44 (100%)	0	0	100	100
51	e	62/65 (95%)	60 (97%)	2 (3%)	0	100	100
52	f	36/38 (95%)	36 (100%)	0	0	100	100
53	a	56/70 (80%)	54 (96%)	2 (4%)	0	100	100
54	I	66/142 (46%)	65 (98%)	1 (2%)	0	100	100
55	6	359/365 (98%)	356 (99%)	3 (1%)	0	100	100
56	G	147/149 (99%)	140 (95%)	6 (4%)	1 (1%)	22	50
All	All	6016/6420 (94%)	5884 (98%)	129 (2%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	o	57	VAL
27	C	149	ASN
56	G	76	GLU

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
2	g	186/199 (94%)	179 (96%)	7 (4%)	33 64
3	h	172/190 (90%)	166 (96%)	6 (4%)	36 67
4	i	172/173 (99%)	168 (98%)	4 (2%)	50 79
5	j	119/126 (94%)	118 (99%)	1 (1%)	81 93
6	k	90/116 (78%)	87 (97%)	3 (3%)	38 69
7	l	127/147 (86%)	123 (97%)	4 (3%)	40 71
8	m	104/105 (99%)	103 (99%)	1 (1%)	76 91
9	n	105/107 (98%)	103 (98%)	2 (2%)	57 83
10	o	86/90 (96%)	83 (96%)	3 (4%)	36 67
11	p	89/98 (91%)	88 (99%)	1 (1%)	73 90
12	q	102/103 (99%)	102 (100%)	0	100 100
13	r	93/96 (97%)	93 (100%)	0	100 100
14	s	83/84 (99%)	83 (100%)	0	100 100
15	t	76/77 (99%)	74 (97%)	2 (3%)	46 76
16	u	65/65 (100%)	65 (100%)	0	100 100
17	v	73/78 (94%)	70 (96%)	3 (4%)	30 61
18	w	57/65 (88%)	57 (100%)	0	100 100
19	x	72/79 (91%)	72 (100%)	0	100 100
20	y	65/66 (98%)	64 (98%)	1 (2%)	65 87
21	z	60/61 (98%)	59 (98%)	1 (2%)	60 85

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
26	B	216/218 (99%)	215 (100%)	1 (0%)	88	95
27	C	163/163 (100%)	161 (99%)	2 (1%)	71	90
28	D	165/165 (100%)	165 (100%)	0	100	100
29	E	148/150 (99%)	144 (97%)	4 (3%)	44	75
30	F	136/138 (99%)	131 (96%)	5 (4%)	34	65
31	J	116/116 (100%)	115 (99%)	1 (1%)	78	92
32	K	104/104 (100%)	103 (99%)	1 (1%)	76	91
33	L	103/103 (100%)	102 (99%)	1 (1%)	76	91
34	M	107/107 (100%)	105 (98%)	2 (2%)	57	83
35	N	98/103 (95%)	97 (99%)	1 (1%)	76	91
36	O	86/87 (99%)	85 (99%)	1 (1%)	71	90
37	P	99/100 (99%)	98 (99%)	1 (1%)	76	91
38	Q	89/90 (99%)	89 (100%)	0	100	100
39	R	84/84 (100%)	80 (95%)	4 (5%)	25	55
40	S	93/93 (100%)	92 (99%)	1 (1%)	73	90
41	T	80/84 (95%)	78 (98%)	2 (2%)	47	77
42	U	83/85 (98%)	77 (93%)	6 (7%)	14	36
43	V	78/78 (100%)	76 (97%)	2 (3%)	46	76
44	W	58/63 (92%)	57 (98%)	1 (2%)	60	85
45	X	67/68 (98%)	66 (98%)	1 (2%)	65	87
46	Y	54/55 (98%)	53 (98%)	1 (2%)	57	83
47	Z	48/49 (98%)	48 (100%)	0	100	100
48	b	47/48 (98%)	47 (100%)	0	100	100
49	c	46/49 (94%)	44 (96%)	2 (4%)	29	59
50	d	38/38 (100%)	37 (97%)	1 (3%)	46	76
51	e	51/52 (98%)	49 (96%)	2 (4%)	32	63
52	f	34/34 (100%)	34 (100%)	0	100	100
53	a	55/62 (89%)	54 (98%)	1 (2%)	59	84
54	I	50/110 (46%)	48 (96%)	2 (4%)	31	62
55	6	306/310 (99%)	296 (97%)	10 (3%)	38	69
56	G	114/114 (100%)	112 (98%)	2 (2%)	59	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	5012/5245 (96%)	4915 (98%)	97 (2%)	59 83

5 of 97 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
36	O	13	ARG
42	U	59	VAL
39	R	6	GLN
41	T	69	ARG
45	X	54	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 35 such sidechains are listed below:

Mol	Chain	Res	Type
44	W	12	ASN
46	Y	39	GLN
55	6	275	GLN
19	x	14	HIS
17	v	51	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1531/1542 (99%)	225 (14%)	5 (0%)
22	4	25/49 (51%)	7 (28%)	1 (4%)
23	5	75/76 (98%)	31 (41%)	1 (1%)
24	1	2893/2904 (99%)	454 (15%)	8 (0%)
25	3	118/120 (98%)	15 (12%)	0
All	All	4642/4691 (98%)	732 (15%)	15 (0%)

5 of 732 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	7	A
1	2	9	G
1	2	22	G
1	2	32	A

5 of 15 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
24	1	277	G
24	1	2146	C
24	1	404	A
24	1	2162	G
24	1	784	G

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

40 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
24	PSU	1	2504	24,59	18,21,22	0.60	0	22,30,33	0.62	0
1	MA6	2	1519	1	18,26,27	0.77	0	19,38,41	0.82	1 (5%)
24	OMU	1	2552	24,57	19,22,23	0.34	0	26,31,34	0.42	0
24	1MG	1	745	24	18,26,27	0.99	2 (11%)	19,39,42	0.47	0
55	MEQ	6	252	55	8,9,10	0.90	0	5,10,12	0.64	0
1	5MC	2	967	1	18,22,23	0.32	0	26,32,35	0.41	0
1	2MG	2	966	1	18,26,27	0.99	3 (16%)	16,38,41	0.68	0
24	PSU	1	2580	24	18,21,22	0.64	1 (5%)	22,30,33	0.67	1 (4%)
24	6MZ	1	1618	24	18,25,26	0.76	0	16,36,39	0.80	1 (6%)
24	5MC	1	1962	24,59	18,22,23	0.33	0	26,32,35	0.44	0
24	PSU	1	1911	24	18,21,22	0.53	0	22,30,33	0.57	0
24	3TD	1	1915	24,57	19,22,23	0.53	0	21,32,35	0.78	0
24	PSU	1	2457	24	18,21,22	0.61	0	22,30,33	0.59	0
12	D2T	q	89	12	7,9,10	0.89	0	6,11,13	1.72	2 (33%)
24	PSU	1	746	24,57	18,21,22	0.60	0	22,30,33	0.37	0
24	G7M	1	2069	24,59	20,26,27	0.64	0	17,39,42	0.51	0
1	UR3	2	1498	1	19,22,23	0.33	0	26,32,35	0.35	0
24	OMG	1	2251	23,24,59	18,26,27	1.07	3 (16%)	19,38,41	0.57	0
1	G7M	2	527	1,59	20,26,27	0.61	0	17,39,42	0.50	0
24	OMC	1	2498	24,57	19,22,23	0.36	0	26,31,34	0.43	0
24	5MU	1	747	24	19,22,23	0.35	0	28,32,35	0.34	0
24	PSU	1	2605	24	18,21,22	0.56	0	22,30,33	0.67	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
24	PSU	1	955	24	18,21,22	0.60	0	22,30,33	0.59	0
24	6MZ	1	2030	24	18,25,26	0.79	0	16,36,39	0.78	1 (6%)
1	2MG	2	1516	1	18,26,27	1.05	3 (16%)	16,38,41	0.71	0
24	2MG	1	2445	24	18,26,27	1.17	3 (16%)	16,38,41	0.63	0
24	2MA	1	2503	24,57,59	17,25,26	0.88	2 (11%)	17,37,40	0.60	0
1	PSU	2	516	57,1	18,21,22	0.54	0	22,30,33	0.60	1 (4%)
24	2MG	1	1835	24	18,26,27	1.08	3 (16%)	16,38,41	0.64	0
27	MEQ	C	150	27	8,9,10	0.85	0	5,10,12	0.63	0
11	IAS	p	119	11	6,7,8	0.95	0	6,8,10	1.25	1 (16%)
24	H2U	1	2449	24	18,21,22	0.36	0	21,30,33	0.44	0
1	MA6	2	1518	1	18,26,27	0.78	0	19,38,41	0.77	0
1	2MG	2	1207	1,59	18,26,27	1.02	3 (16%)	16,38,41	0.66	0
1	4OC	2	1402	57,1	20,23,24	0.36	0	26,32,35	0.61	0
24	PSU	1	1917	24	18,21,22	0.57	0	22,30,33	0.56	0
24	5MU	1	1939	24,59	19,22,23	0.58	0	28,32,35	0.90	3 (10%)
1	5MC	2	1407	1	18,22,23	0.33	0	26,32,35	0.45	0
34	4D4	M	81	34	9,11,12	0.67	0	8,13,15	1.90	3 (37%)
24	PSU	1	2604	24	18,21,22	0.56	0	22,30,33	0.64	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
24	PSU	1	2504	24,59	-	0/7/25/26	0/2/2/2
1	MA6	2	1519	1	-	1/7/29/30	0/3/3/3
24	OMU	1	2552	24,57	-	0/9/27/28	0/2/2/2
24	1MG	1	745	24	-	0/3/25/26	0/3/3/3
55	MEQ	6	252	55	-	2/8/9/11	-
1	5MC	2	967	1	-	0/7/25/26	0/2/2/2
1	2MG	2	966	1	-	2/5/27/28	0/3/3/3
24	PSU	1	2580	24	-	0/7/25/26	0/2/2/2
24	6MZ	1	1618	24	-	0/5/27/28	0/3/3/3
24	5MC	1	1962	24,59	-	0/7/25/26	0/2/2/2
24	PSU	1	1911	24	-	0/7/25/26	0/2/2/2
24	3TD	1	1915	24,57	-	2/7/25/26	0/2/2/2
24	PSU	1	2457	24	-	0/7/25/26	0/2/2/2
12	D2T	q	89	12	-	3/7/12/14	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
24	PSU	1	746	24,57	-	1/7/25/26	0/2/2/2
24	G7M	1	2069	24,59	-	2/3/25/26	0/3/3/3
1	UR3	2	1498	1	-	0/7/25/26	0/2/2/2
24	OMG	1	2251	23,24,59	-	1/5/27/28	0/3/3/3
1	G7M	2	527	1,59	-	3/3/25/26	0/3/3/3
24	OMC	1	2498	24,57	-	0/9/27/28	0/2/2/2
24	5MU	1	747	24	-	0/7/25/26	0/2/2/2
24	PSU	1	2605	24	-	0/7/25/26	0/2/2/2
24	PSU	1	955	24	-	0/7/25/26	0/2/2/2
24	6MZ	1	2030	24	-	2/5/27/28	0/3/3/3
1	2MG	2	1516	1	-	0/5/27/28	0/3/3/3
24	2MG	1	2445	24	-	1/5/27/28	0/3/3/3
24	2MA	1	2503	24,57,59	-	2/3/25/26	0/3/3/3
1	PSU	2	516	57,1	-	0/7/25/26	0/2/2/2
24	2MG	1	1835	24	-	0/5/27/28	0/3/3/3
27	MEQ	C	150	27	-	2/8/9/11	-
11	IAS	p	119	11	-	1/7/7/8	-
24	H2U	1	2449	24	-	0/7/38/39	0/2/2/2
1	MA6	2	1518	1	-	0/7/29/30	0/3/3/3
1	2MG	2	1207	1,59	-	0/5/27/28	0/3/3/3
1	4OC	2	1402	57,1	-	3/9/29/30	0/2/2/2
24	PSU	1	1917	24	-	0/7/25/26	0/2/2/2
24	5MU	1	1939	24,59	-	2/7/25/26	0/2/2/2
1	5MC	2	1407	1	-	0/7/25/26	0/2/2/2
34	4D4	M	81	34	-	2/11/12/14	-
24	PSU	1	2604	24	-	0/7/25/26	0/2/2/2

The worst 5 of 23 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	1	2445	2MG	C5-C6	-3.13	1.41	1.47
24	1	1835	2MG	C5-C6	-2.98	1.41	1.47
24	1	2251	OMG	C5-C6	-2.80	1.41	1.47
1	2	1516	2MG	C5-C6	-2.66	1.42	1.47
24	1	745	1MG	C5-C4	-2.64	1.36	1.43

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	M	81	4D4	NE-CZ-NH2	3.56	126.95	120.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	M	81	4D4	O-C-CA	-3.04	116.80	124.78
12	q	89	D2T	O-C-CA	-2.85	117.31	124.78
24	1	1939	5MU	O4'-C1'-N1	2.55	114.18	108.36
34	M	81	4D4	NH1-CZ-NE	-2.52	113.39	119.19

There are no chirality outliers.

5 of 32 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
24	1	1915	3TD	C3'-C4'-C5'-O5'
24	1	1915	3TD	O4'-C4'-C5'-O5'
24	1	1939	5MU	O4'-C4'-C5'-O5'
24	1	2030	6MZ	O4'-C4'-C5'-O5'
24	1	2251	OMG	C1'-C2'-O2'-CM2

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 487 ligands modelled in this entry, 460 are monoatomic - leaving 27 for Mogul analysis.

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	$\# Z > 2$
60	PUT	2	1732	-	5,5,5	0.15	0	4,4,4	0.16	0
58	SPD	1	3212	-	9,9,9	0.09	0	8,8,8	0.32	0
60	PUT	1	3330	-	5,5,5	0.12	0	4,4,4	0.17	0
60	PUT	1	3336	-	5,5,5	0.15	0	4,4,4	0.15	0
58	SPD	1	3207	-	9,9,9	0.08	0	8,8,8	0.19	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
58	SPD	2	1690	-	9,9,9	0.12	0	8,8,8	0.12	0
60	PUT	1	3337	-	5,5,5	0.11	0	4,4,4	0.17	0
61	SPM	1	3216	-	13,13,13	0.36	0	12,12,12	0.95	0
58	SPD	2	1691	-	9,9,9	0.07	0	8,8,8	0.19	0
60	PUT	1	3334	-	5,5,5	0.09	0	4,4,4	0.20	0
60	PUT	1	3335	-	5,5,5	0.10	0	4,4,4	0.18	0
60	PUT	2	1731	-	5,5,5	0.13	0	4,4,4	0.16	0
58	SPD	1	3213	-	9,9,9	0.07	0	8,8,8	0.17	0
58	SPD	1	3208	-	9,9,9	0.13	0	8,8,8	0.10	0
60	PUT	1	3329	-	5,5,5	0.10	0	4,4,4	0.15	0
58	SPD	1	3210	-	9,9,9	0.11	0	8,8,8	0.16	0
58	SPD	1	3211	-	9,9,9	0.08	0	8,8,8	0.18	0
60	PUT	1	3332	-	5,5,5	0.14	0	4,4,4	0.15	0
58	SPD	1	3215	-	9,9,9	0.10	0	8,8,8	0.14	0
58	SPD	1	3209	-	9,9,9	0.10	0	8,8,8	0.14	0
60	PUT	1	3339	-	5,5,5	0.10	0	4,4,4	0.17	0
58	SPD	1	3206	-	9,9,9	0.08	0	8,8,8	0.16	0
60	PUT	1	3331	-	5,5,5	0.07	0	4,4,4	0.19	0
60	PUT	1	3333	-	5,5,5	0.09	0	4,4,4	0.18	0
58	SPD	1	3214	-	9,9,9	0.07	0	8,8,8	0.14	0
58	SPD	1	3338	-	9,9,9	0.10	0	8,8,8	0.15	0
60	PUT	1	3328	-	5,5,5	0.07	0	4,4,4	0.20	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
60	PUT	2	1732	-	-	3/3/3/3	-
58	SPD	1	3212	-	-	5/7/7/7	-
60	PUT	1	3330	-	-	2/3/3/3	-
60	PUT	1	3336	-	-	3/3/3/3	-
58	SPD	1	3207	-	-	2/7/7/7	-
58	SPD	2	1690	-	-	2/7/7/7	-
60	PUT	1	3337	-	-	1/3/3/3	-
61	SPM	1	3216	-	-	8/11/11/11	-
58	SPD	2	1691	-	-	5/7/7/7	-
60	PUT	1	3334	-	-	1/3/3/3	-
60	PUT	1	3335	-	-	3/3/3/3	-
60	PUT	2	1731	-	-	0/3/3/3	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
58	SPD	1	3213	-	-	3/7/7/7	-
58	SPD	1	3208	-	-	2/7/7/7	-
60	PUT	1	3329	-	-	2/3/3/3	-
58	SPD	1	3210	-	-	5/7/7/7	-
58	SPD	1	3211	-	-	1/7/7/7	-
60	PUT	1	3332	-	-	1/3/3/3	-
58	SPD	1	3215	-	-	5/7/7/7	-
58	SPD	1	3209	-	-	1/7/7/7	-
60	PUT	1	3339	-	-	3/3/3/3	-
58	SPD	1	3206	-	-	1/7/7/7	-
60	PUT	1	3331	-	-	1/3/3/3	-
60	PUT	1	3333	-	-	0/3/3/3	-
58	SPD	1	3214	-	-	0/7/7/7	-
58	SPD	1	3338	-	-	3/7/7/7	-
60	PUT	1	3328	-	-	1/3/3/3	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 64 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
58	2	1691	SPD	C7-C8-C9-N10
58	1	3211	SPD	N6-C7-C8-C9
60	1	3332	PUT	C1-C2-C3-C4
58	1	3212	SPD	C3-C4-C5-N6
58	2	1690	SPD	C4-C5-N6-C7

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.

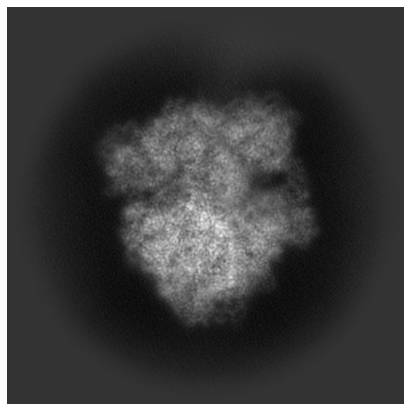
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-17346. These allow visual inspection of the internal detail of the map and identification of artifacts.

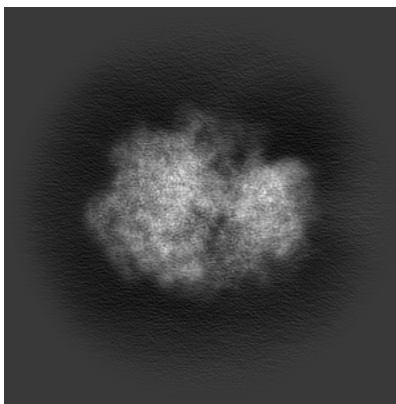
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

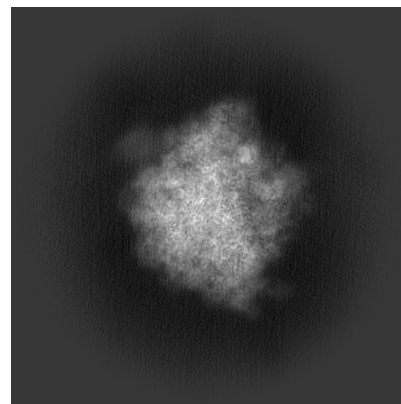
6.1.1 Primary map



X

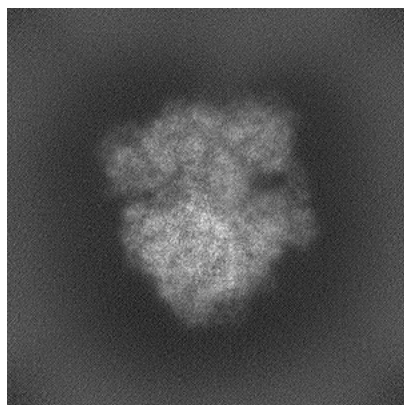


Y

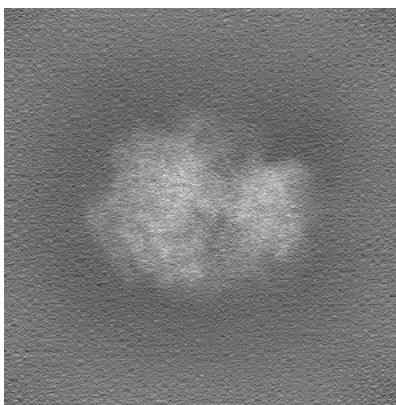


Z

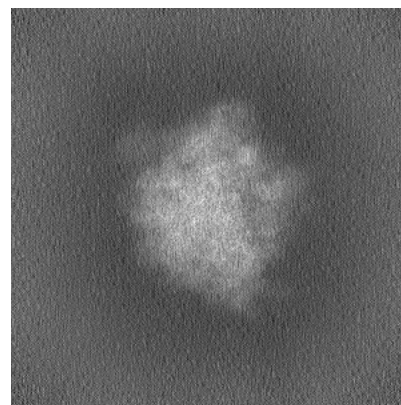
6.1.2 Raw map



X



Y

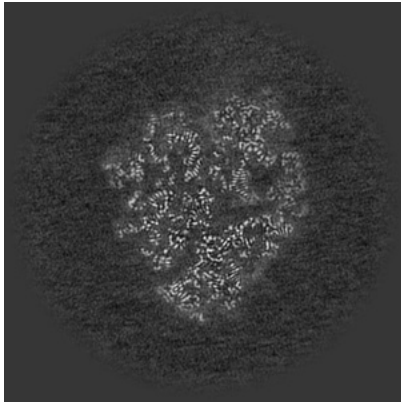


Z

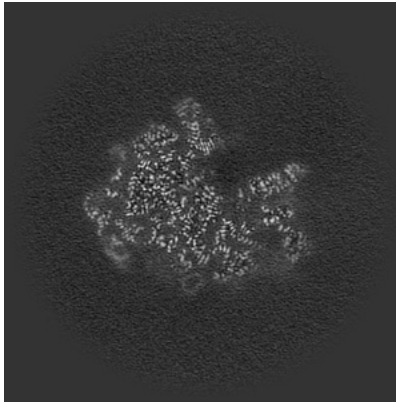
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

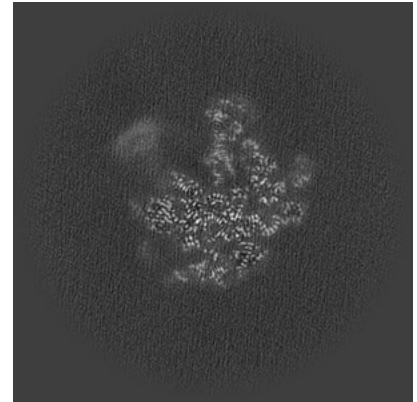
6.2.1 Primary map



X Index: 260

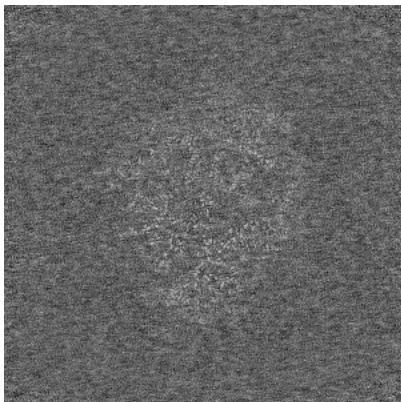


Y Index: 260

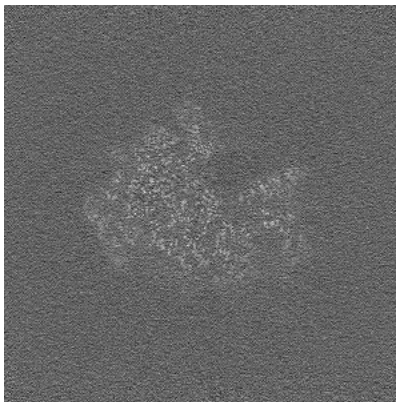


Z Index: 260

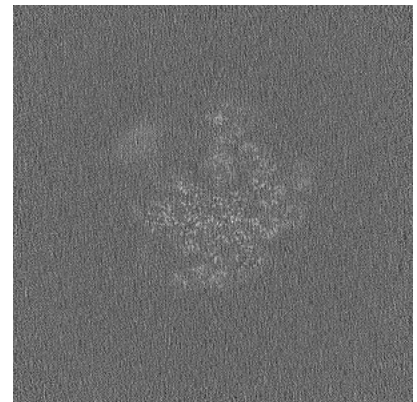
6.2.2 Raw map



X Index: 260



Y Index: 260

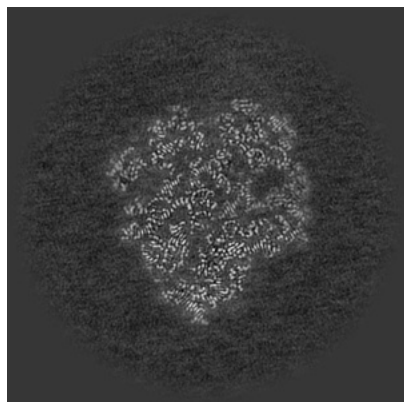


Z Index: 260

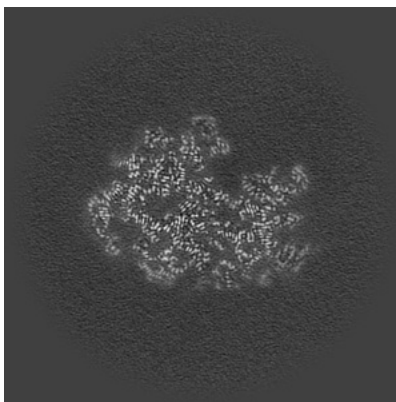
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

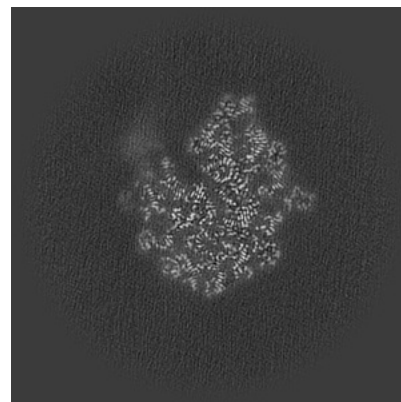
6.3.1 Primary map



X Index: 266

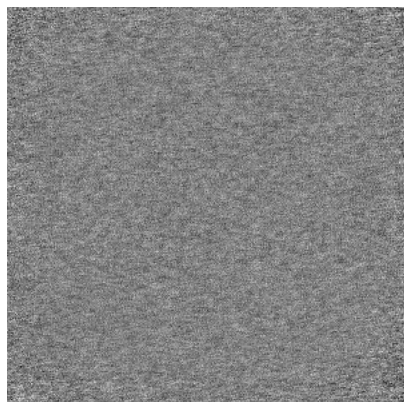


Y Index: 246

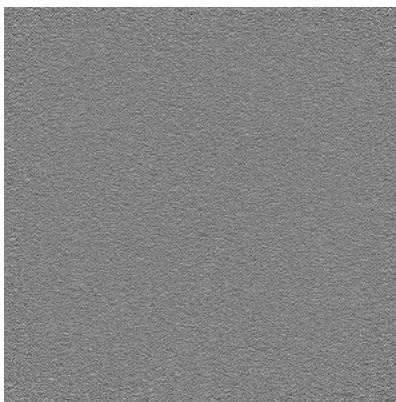


Z Index: 231

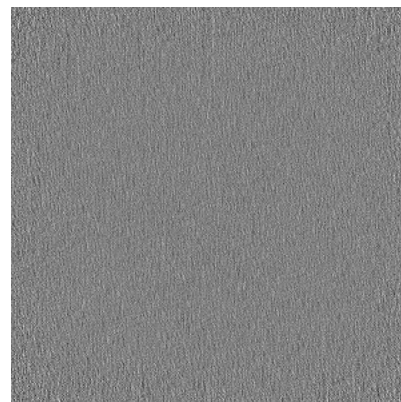
6.3.2 Raw map



X Index: 0



Y Index: 0

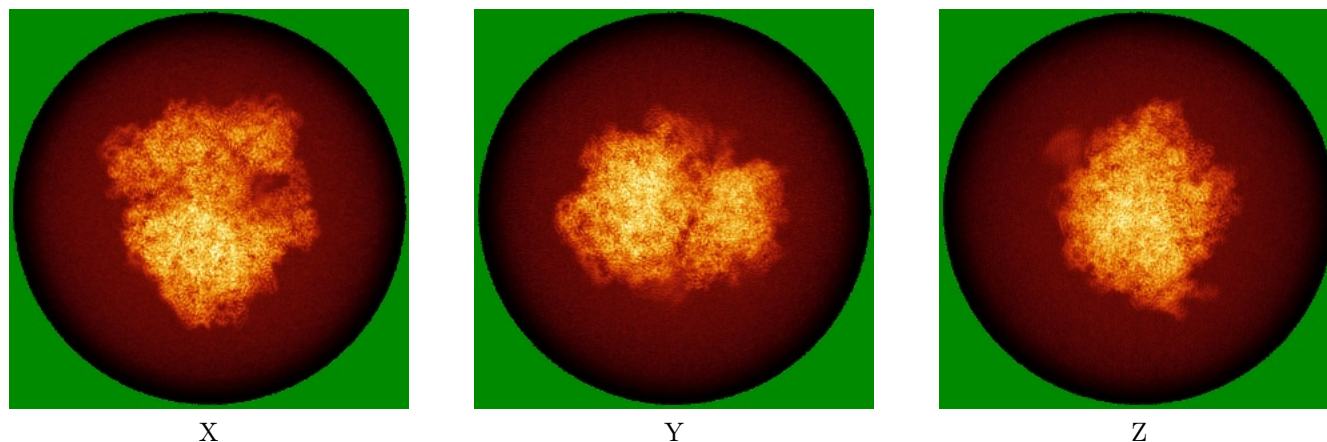


Z Index: 0

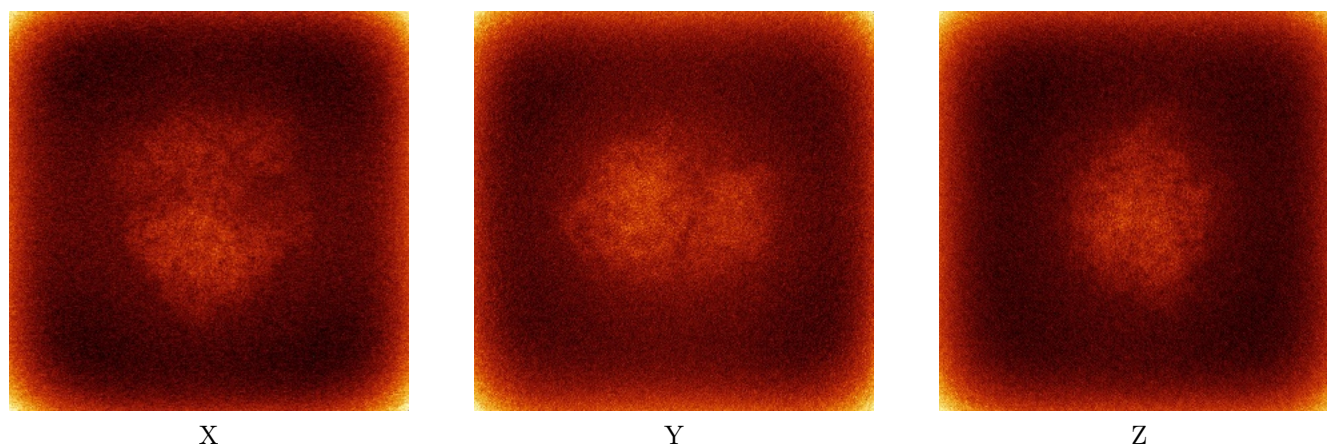
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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



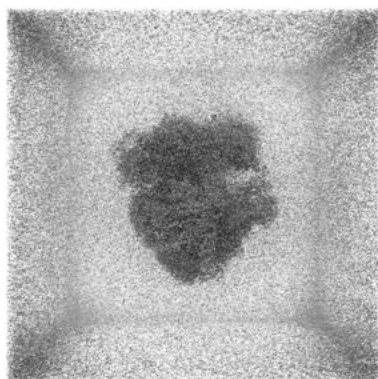
Y



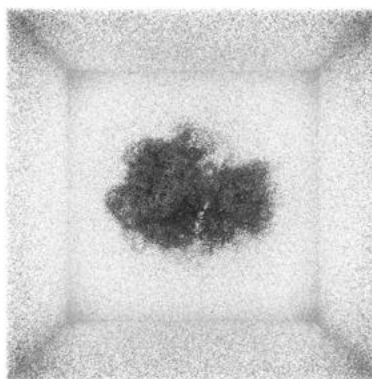
Z

The images above show the 3D surface view of the map at the recommended contour level 0.19. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

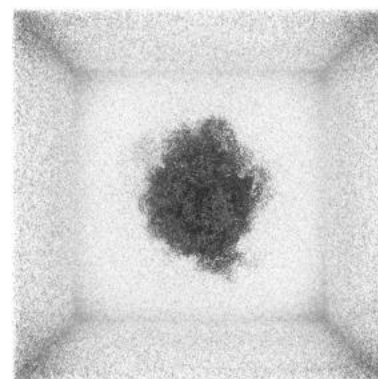
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

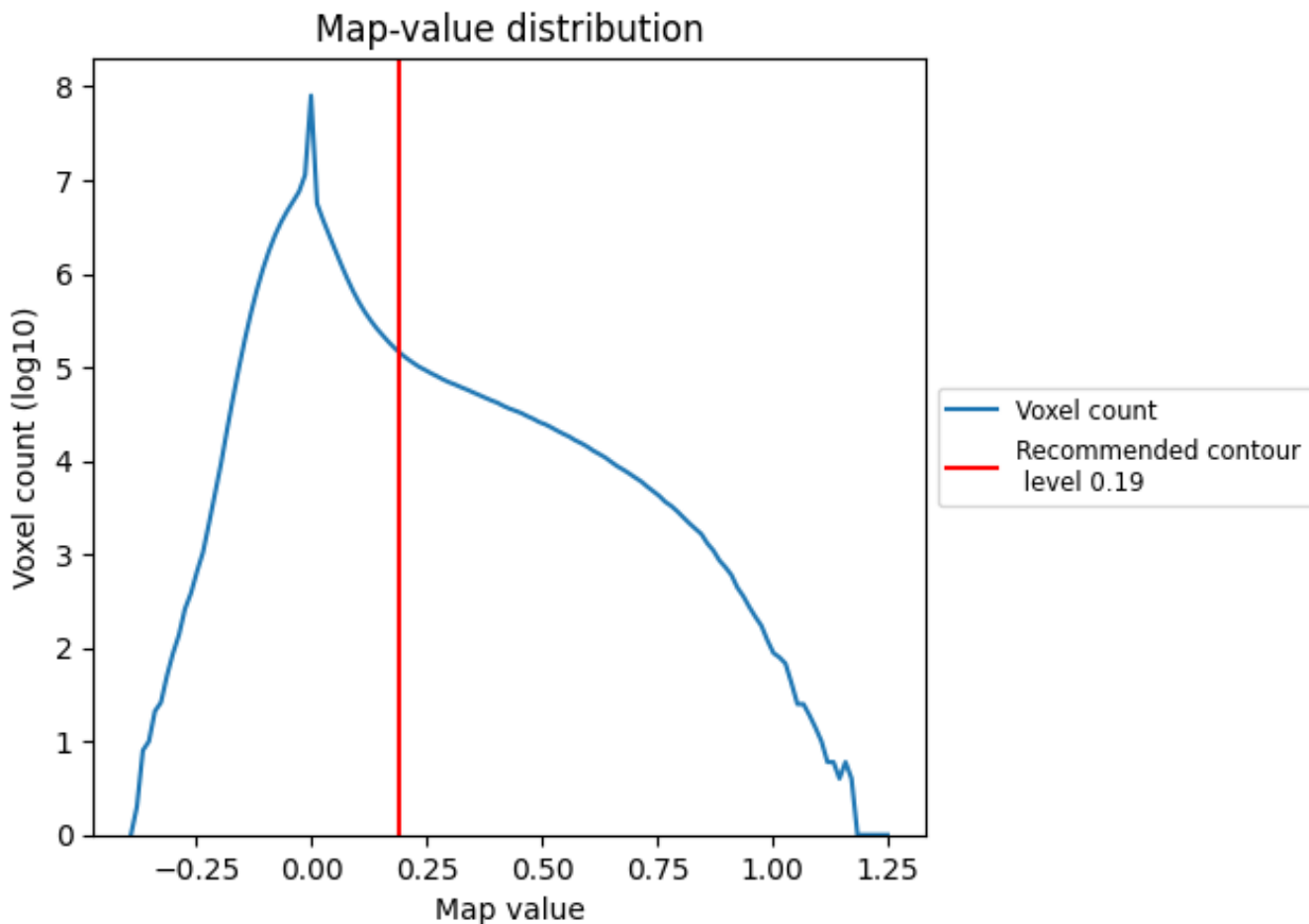
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

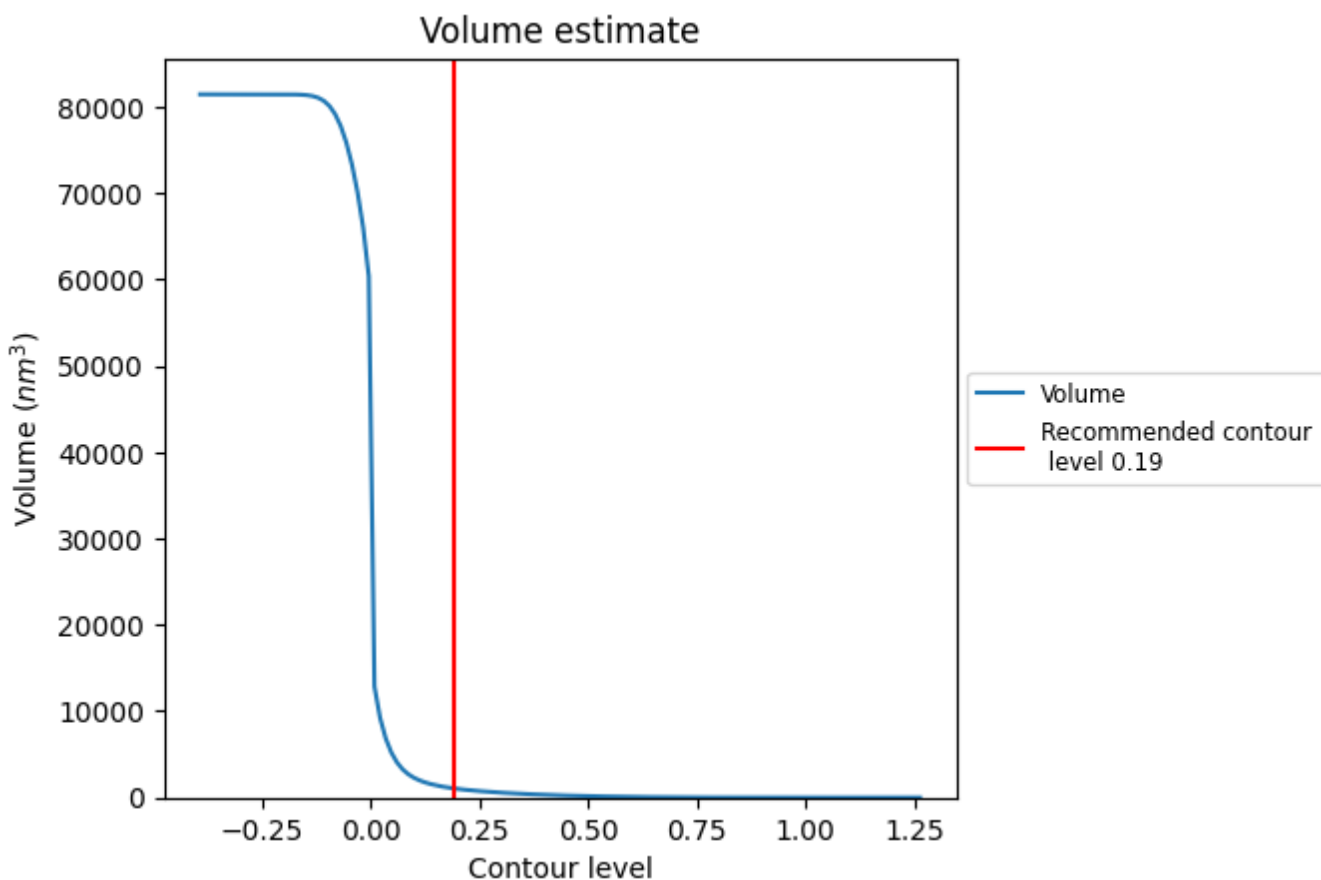
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

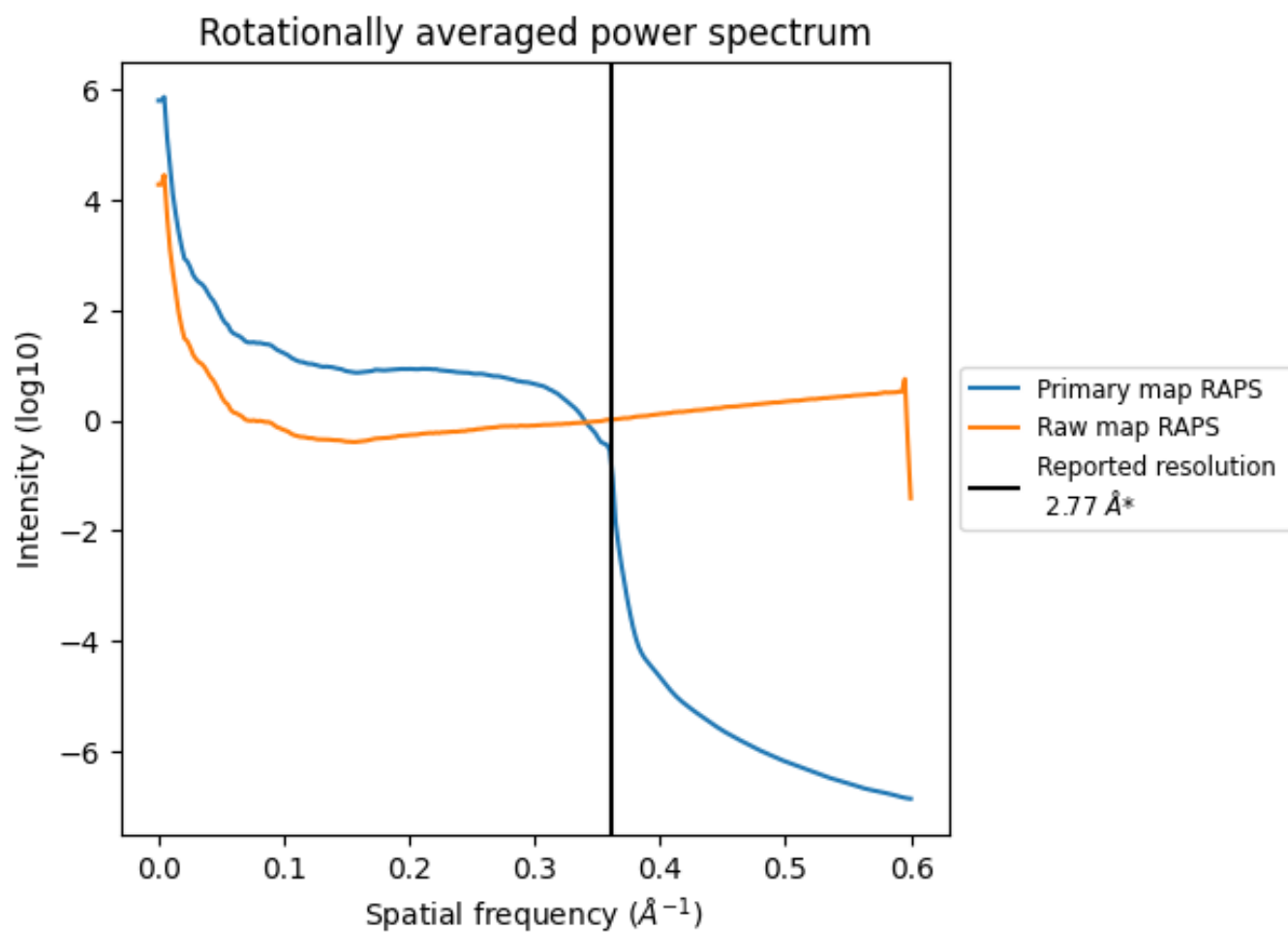
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1072 nm^3 ; this corresponds to an approximate mass of 968 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](#)

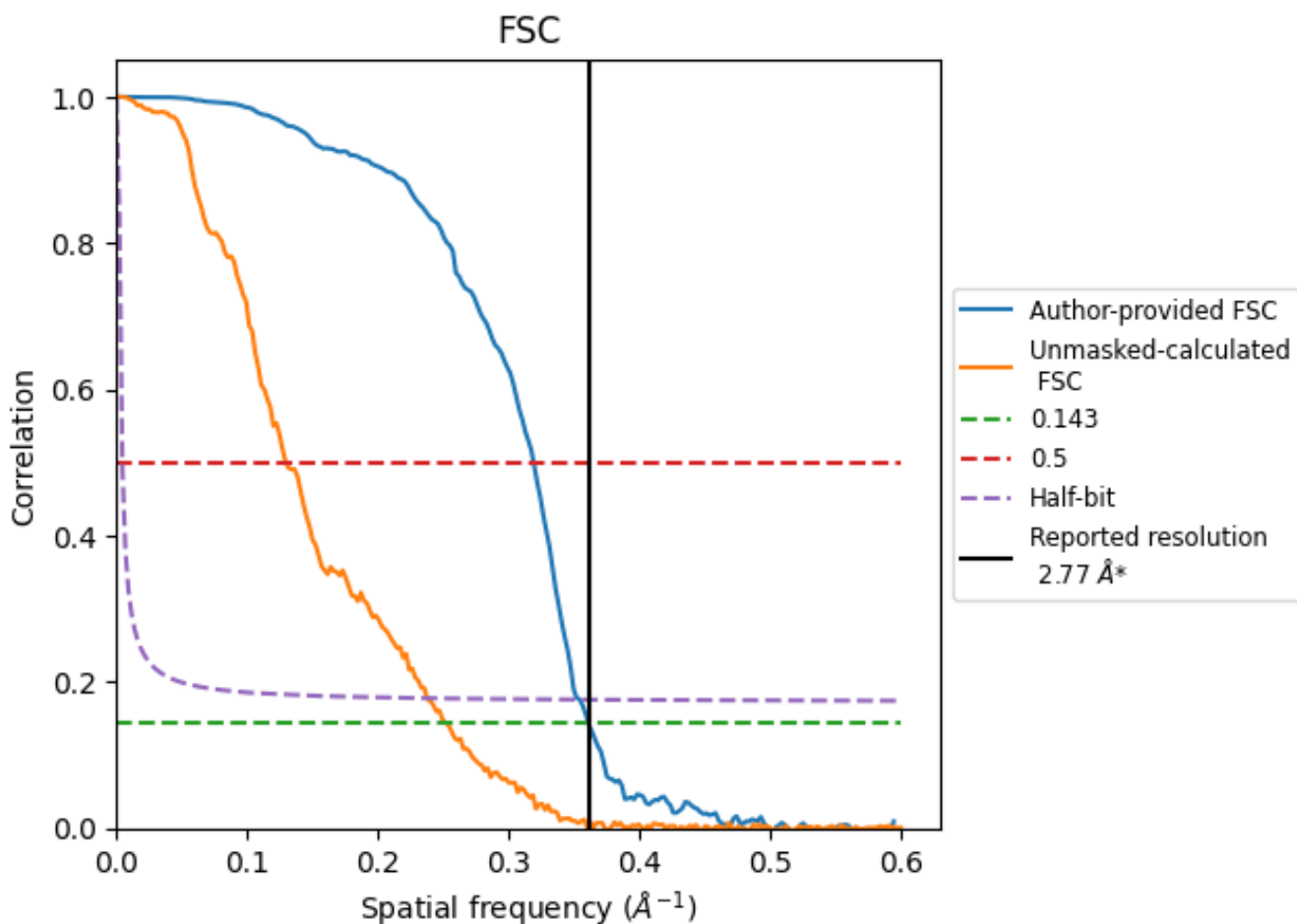


*Reported resolution corresponds to spatial frequency of 0.361 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.361 \AA^{-1}

8.2 Resolution estimates [i](#)

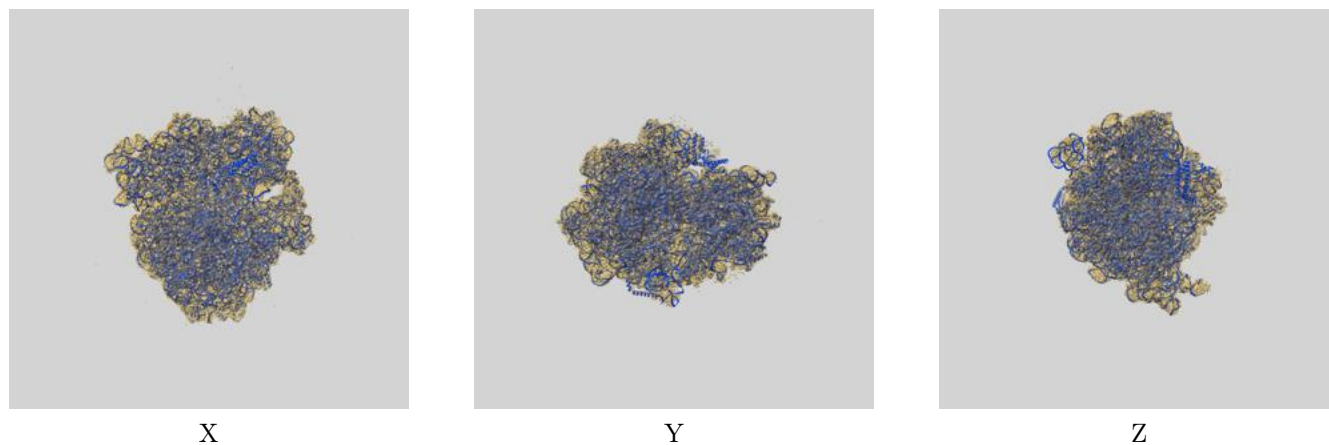
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.77	-	-
Author-provided FSC curve	2.77	3.14	2.82
Unmasked-calculated*	3.97	7.72	4.21

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.97 differs from the reported value 2.77 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-17346 and PDB model 8P16. Per-residue inclusion information can be found in section 3 on page 17.

9.1 Map-model overlay [i](#)



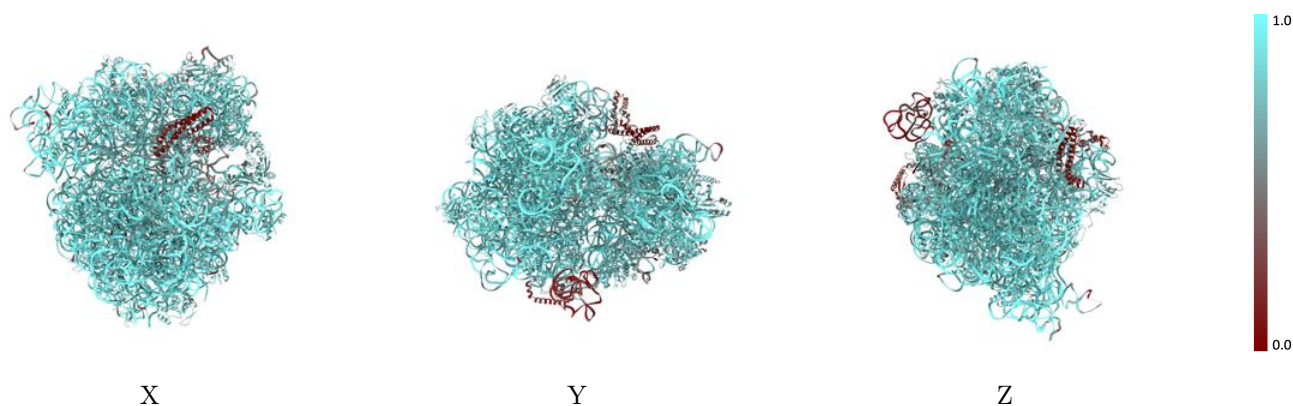
The images above show the 3D surface view of the map at the recommended contour level 0.19 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



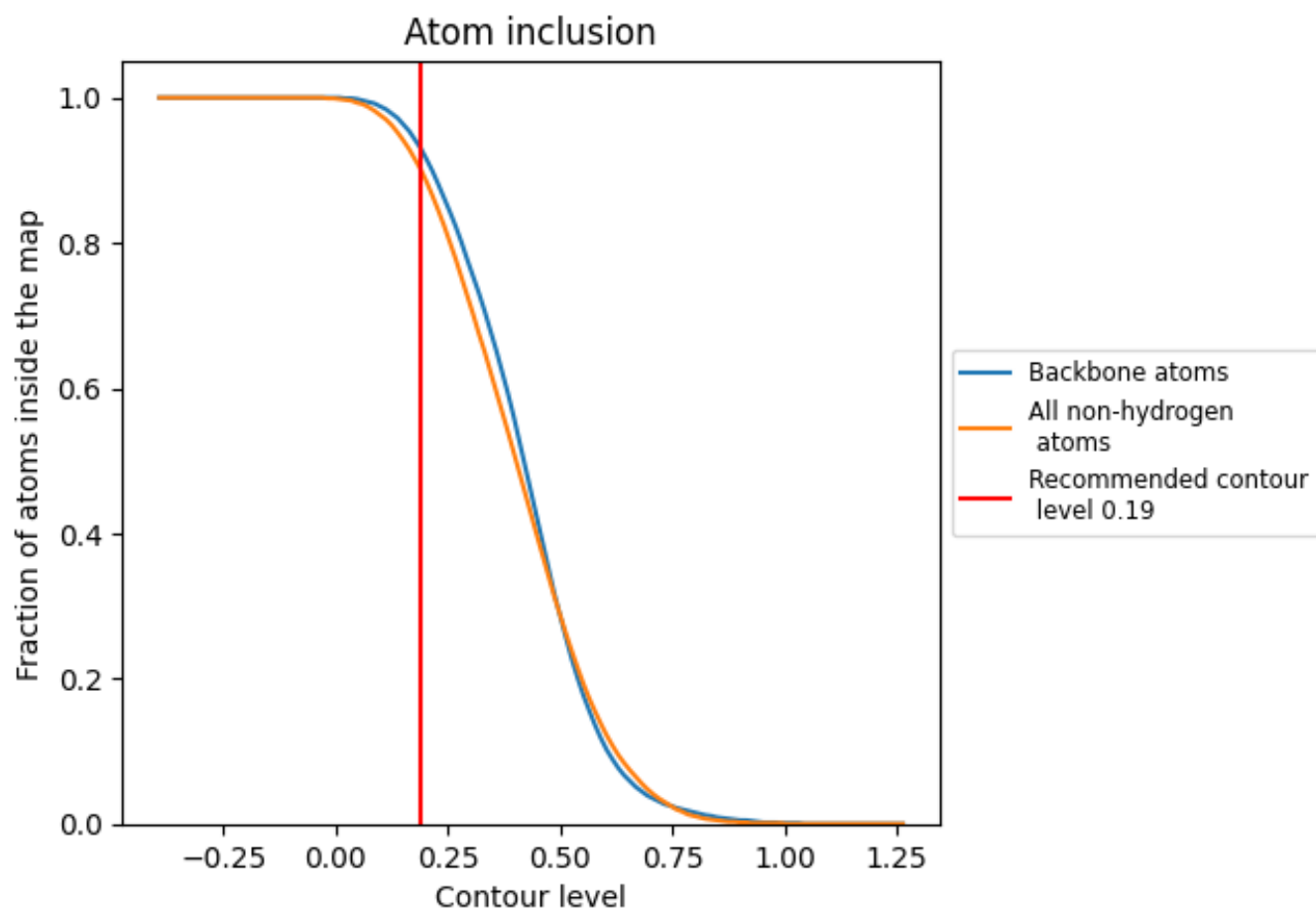
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.19).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 90% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary













































The table lists the average atom inclusion at the recommended contour level (0.19) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9010	 0.5430
1	 0.9440	 0.5610
2	 0.9510	 0.5480
3	 0.9540	 0.5490
4	 0.6390	 0.3320
5	 0.8970	 0.5380
6	 0.5370	 0.3920
B	 0.9160	 0.5940
C	 0.9070	 0.5840
D	 0.8680	 0.5560
E	 0.7640	 0.4860
F	 0.7380	 0.4700
G	 0.3150	 0.3670
I	 0.2240	 0.1340
J	 0.9170	 0.5820
K	 0.8550	 0.5750
L	 0.8910	 0.5720
M	 0.8820	 0.5730
N	 0.9450	 0.5950
O	 0.8460	 0.5310
P	 0.8450	 0.5680
Q	 0.9460	 0.5960
R	 0.8830	 0.5650
S	 0.8990	 0.5760
T	 0.8570	 0.5390
U	 0.8540	 0.5280
V	 0.8250	 0.5340
W	 0.8920	 0.5600
X	 0.8870	 0.5650
Y	 0.8020	 0.4980
Z	 0.8880	 0.5670
a	 0.6930	 0.4490
b	 0.8950	 0.5790
c	 0.8460	 0.5410
d	 0.9580	 0.6140



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Chain	Atom inclusion	Q-score
e	 0.9490	 0.6080
f	 0.9210	 0.5720
g	 0.7060	 0.4530
h	 0.8280	 0.5030
i	 0.8430	 0.5200
j	 0.8850	 0.5590
k	 0.7950	 0.5160
l	 0.7580	 0.4810
m	 0.8710	 0.5540
n	 0.8260	 0.5050
o	 0.7620	 0.4480
p	 0.8340	 0.5420
q	 0.8560	 0.5650
r	 0.8060	 0.4960
s	 0.8440	 0.5170
t	 0.8250	 0.5330
u	 0.8780	 0.5450
v	 0.8050	 0.5100
w	 0.8360	 0.5180
x	 0.7700	 0.4930
y	 0.8550	 0.5160
z	 0.7100	 0.4420