wwPDB EM Validation Summary Report ⓘ

Nov 9, 2022 – 02:24 PM EST

PDB ID	:	6OT3
EMDB ID	:	EMD-20193
Title	:	RF2 accommodated state bound Release complex 70S at 24 ms
Authors	:	Fu, Z.; Indrisiunaite, G.; Kaledhonkar, S.; Shah, B.; Sun, M.; Chen, B.; Grassucci, R.A.; Ehrenberg, M.; Frank, J.
Deposited on	:	2019-05-02
Resolution	:	3.90 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:

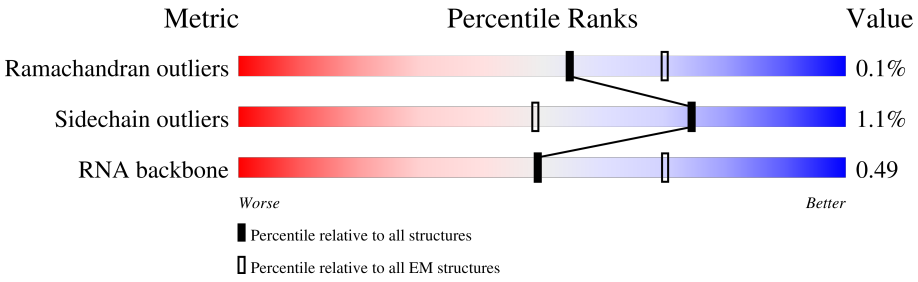
EMDB validation analysis	:	0.0.1.dev43
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

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 3.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1	2903	73% 26%
2	2	1534	72% 27%
3	3	120	81% 19%
4	4	9	78% 22%
5	B	271	99% .
6	C	209	99% .
7	D	201	99% .
8	E	177	99% .

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Mol	Chain	Length	Quality of chain
9	F	175	99%
10	G	149	99%
11	J	142	99%
12	K	123	98%
13	L	144	100%
14	M	136	100%
15	N	119	99%
16	O	116	97%
17	P	114	99%
18	Q	117	99%
19	R	103	98%
20	S	110	100%
21	T	94	100%
22	U	103	100%
23	V	94	99%
24	W	76	100%
25	X	77	99%
26	Y	62	100%
27	Z	58	98%
28	a	66	97%
29	b	56	100%
30	c	52	98%
31	d	46	98%
32	e	64	98%
33	f	38	100%

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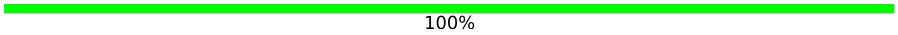
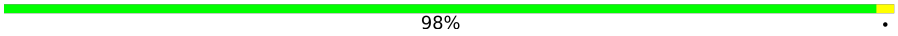
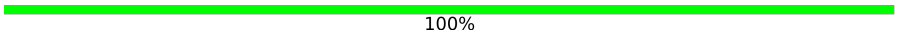
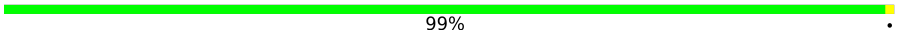
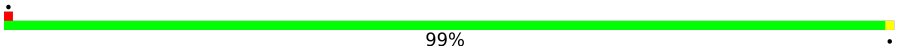
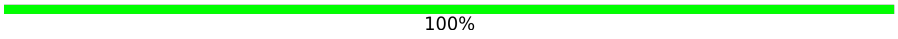
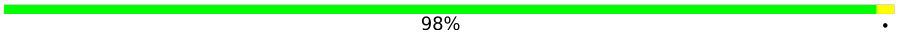
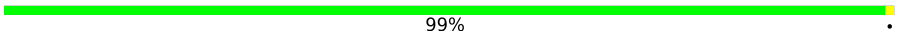
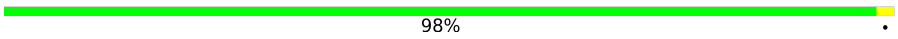
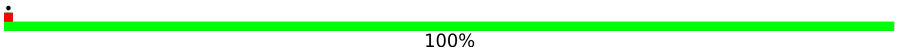
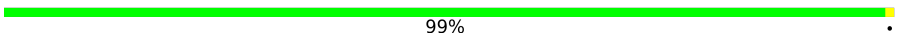
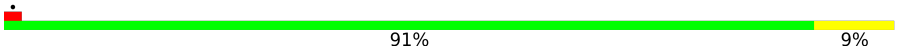
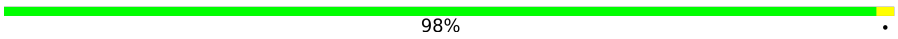
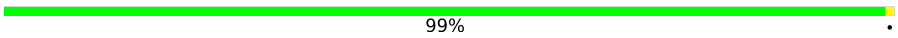
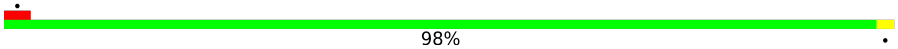
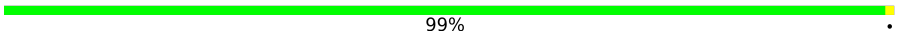
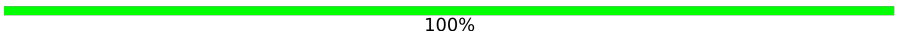
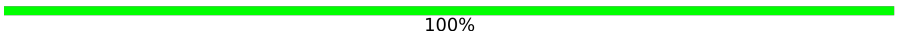
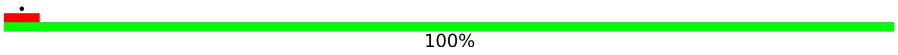
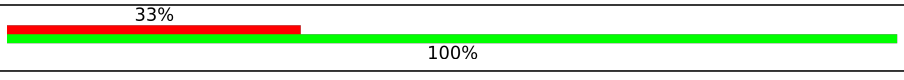
Mol	Chain	Length	Quality of chain
34	g	225	
35	h	208	
36	i	205	
37	j	156	
38	k	104	
39	l	151	
40	m	129	
41	n	127	
42	o	99	
43	p	117	
44	q	87	
45	r	116	
46	s	100	
47	t	88	
48	u	82	
49	v	80	
50	w	66	
51	x	83	
52	y	86	
53	z	70	
54	5	76	
55	A	357	
56	6	3	

2 Entry composition (i)

There are 58 unique types of molecules in this entry. The entry contains 146899 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 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	2903	62336	27816	11470	20147	2903	0	0

- Molecule 2 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	2	1534	32929	14693	6041	10661	1534	0	0

- Molecule 3 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	3	120	2569	1144	468	837	120	0	0

- Molecule 4 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	4	9	184	83	26	66	9	0	0

- Molecule 5 is a protein called 50S ribosomal protein L2.

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

- Molecule 6 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	C	209	1565	979	288	294	4	0	0

- Molecule 7 is a protein called 50S ribosomal protein L4.

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

- Molecule 8 is a protein called 50S ribosomal protein L5.

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

- Molecule 9 is a protein called 50S ribosomal protein L6.

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

- Molecule 10 is a protein called 50S ribosomal protein L9.

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

- Molecule 11 is a protein called 50S ribosomal protein L13.

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

- Molecule 12 is a protein called 50S ribosomal protein L14.

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

- Molecule 13 is a protein called 50S ribosomal protein L15.

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

- Molecule 14 is a protein called 50S ribosomal protein L16.

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

- Molecule 15 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	119	Total	C	N	O	S	0	0
			951	588	195	163	5		

- Molecule 16 is a protein called 50S ribosomal protein L18.

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

- Molecule 17 is a protein called 50S ribosomal protein L19.

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

- Molecule 18 is a protein called 50S ribosomal protein L20.

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

- Molecule 19 is a protein called 50S ribosomal protein L21.

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

- Molecule 20 is a protein called 50S ribosomal protein L22.

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

- Molecule 21 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	T	94	Total	C	N	O	S	0	0
			746	470	140	134	2		

- Molecule 22 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	U	103	Total	C	N	O	0	0
			788	498	148	142		

- Molecule 23 is a protein called 50S ribosomal protein L25.

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

- Molecule 24 is a protein called 50S ribosomal protein L27.

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

- Molecule 25 is a protein called 50S ribosomal protein L28.

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

- Molecule 26 is a protein called 50S ribosomal protein L29.

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

- Molecule 27 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Z	58	Total	C	N	O	S	0	0
			448	281	87	78	2		

- Molecule 28 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	a	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 29 is a protein called 50S ribosomal protein L32.

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

- Molecule 30 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	c	52	Total	C	N	O	0	0
			426	275	78	73		

- Molecule 31 is a protein called 50S ribosomal protein L34.

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

- Molecule 32 is a protein called 50S ribosomal protein L35.

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

- Molecule 33 is a protein called 50S ribosomal protein L36.

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

- Molecule 34 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	225	Total	C	N	O	S	0	0
			1760	1113	316	323	8		

- Molecule 35 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	h	208	Total	C	N	O	S	0	0
			1636	1036	307	290	3		

- Molecule 36 is a protein called 30S ribosomal protein S4.

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

- Molecule 37 is a protein called 30S ribosomal protein S5.

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

- Molecule 38 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	k	104	Total	C	N	O	S	0	0
			848	536	153	152	7		

- Molecule 39 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	l	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 40 is a protein called 30S ribosomal protein S8.

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

- Molecule 41 is a protein called 30S ribosomal protein S9.

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

- Molecule 42 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	o	99	Total 790	C 495	N 151	O 143	S 1	0	0

- Molecule 43 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	p	117	Total 877	C 540	N 174	O 160	S 3	0	0

- Molecule 44 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	q	87	Total 673	C 417	N 137	O 116	S 3	0	0

- Molecule 45 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	r	116	Total 900	C 558	N 181	O 158	S 3	0	0

- Molecule 46 is a protein called 30S ribosomal protein S14.

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

- Molecule 47 is a protein called 30S ribosomal protein S15.

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

- Molecule 48 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	u	82	Total 649	C 406	N 128	O 114	S 1	0	0

- Molecule 49 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	v	80	Total 648	C 411	N 121	O 113	S 3	0	0

- Molecule 50 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	w	66	Total 544	C 344	N 102	O 97	S 1	0	0

- Molecule 51 is a protein called 30S ribosomal protein S19.

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

- Molecule 52 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	y	86	Total 669	C 414	N 138	O 114	S 3	0	0

- Molecule 53 is a protein called 30S ribosomal protein S21.

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

- Molecule 54 is a RNA chain called P-tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	5	76	Total 1627	C 727	N 296	O 527	P 76	S 1	0	0

- Molecule 55 is a protein called Peptide chain release factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	A	357	Total 2833	C 1742	N 498	O 583	S 10	0	0

- Molecule 56 is a protein called FME-PHE-PHE.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	6	3	Total	C	N	O	S	0	0
			32	24	3	4	1		

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

Mol	Chain	Residues	Atoms		AltConf
57	1	2	Total	Mg	0
			2	2	
57	2	1	Total	Mg	0
			1	1	
57	3	8	Total	Mg	0
			8	8	
57	i	1	Total	Mg	0
			1	1	

- Molecule 58 is ZINC ION (three-letter code: ZN) (formula: Zn).

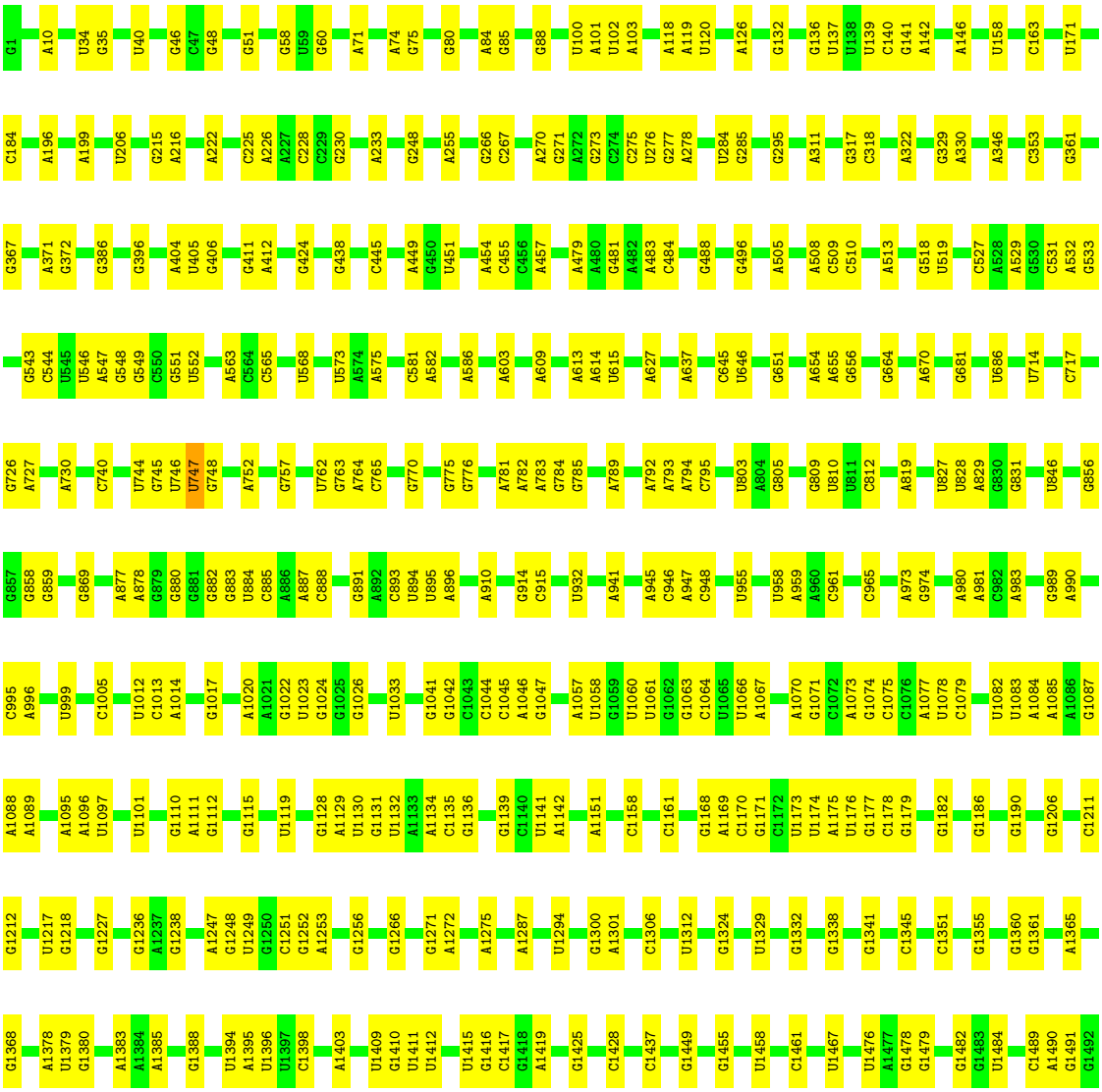
Mol	Chain	Residues	Atoms		AltConf
58	a	1	Total	Zn	0
			1	1	
58	f	1	Total	Zn	0
			1	1	

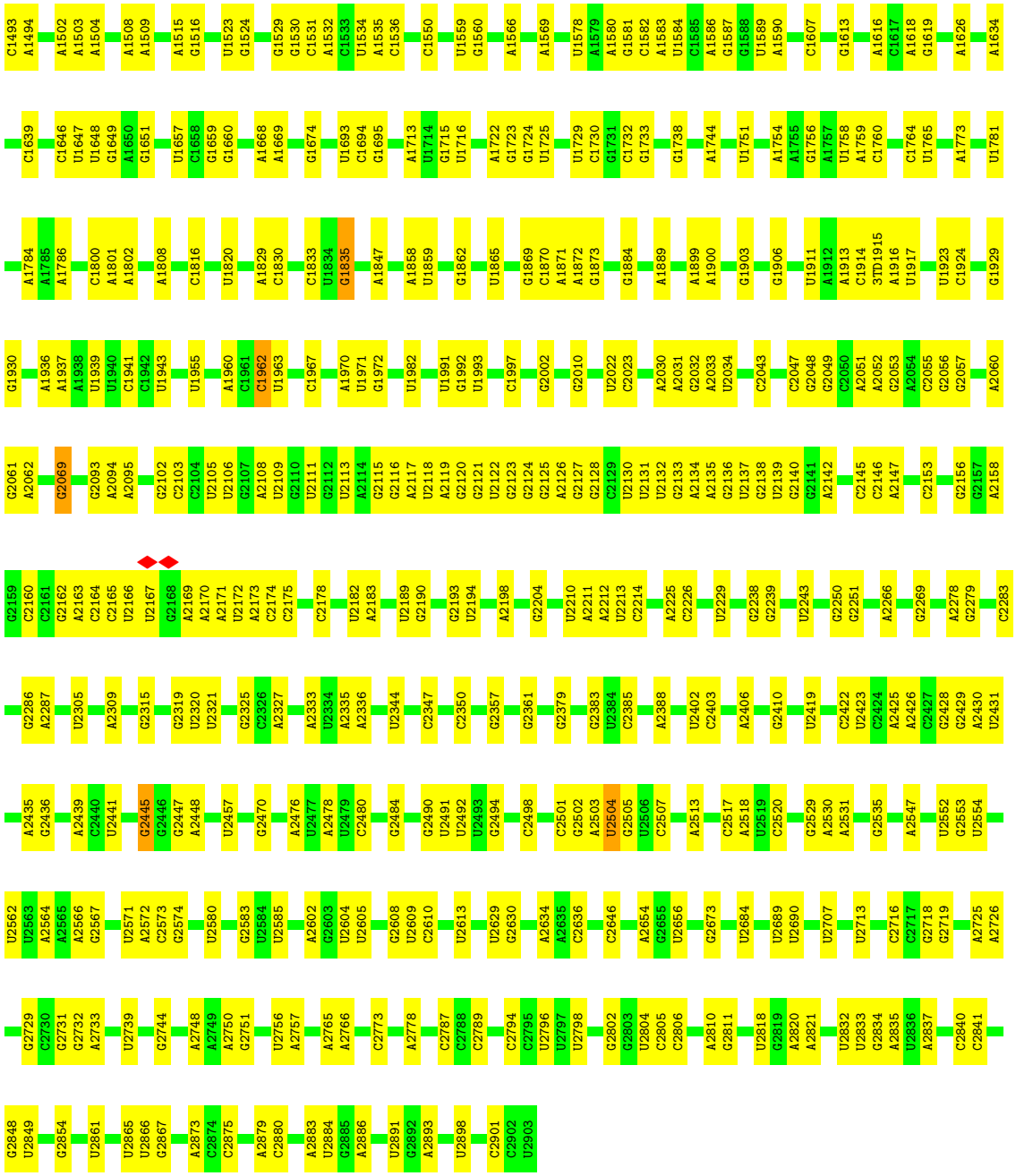
3 Residue-property plots (i)

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: 23S ribosomal RNA

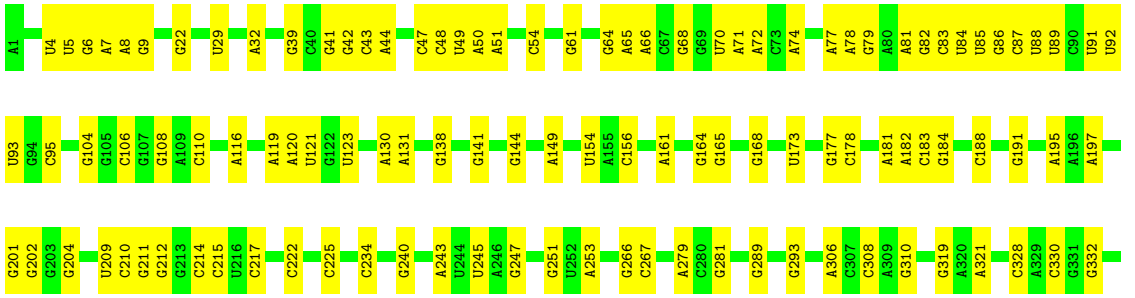
Chain 1:

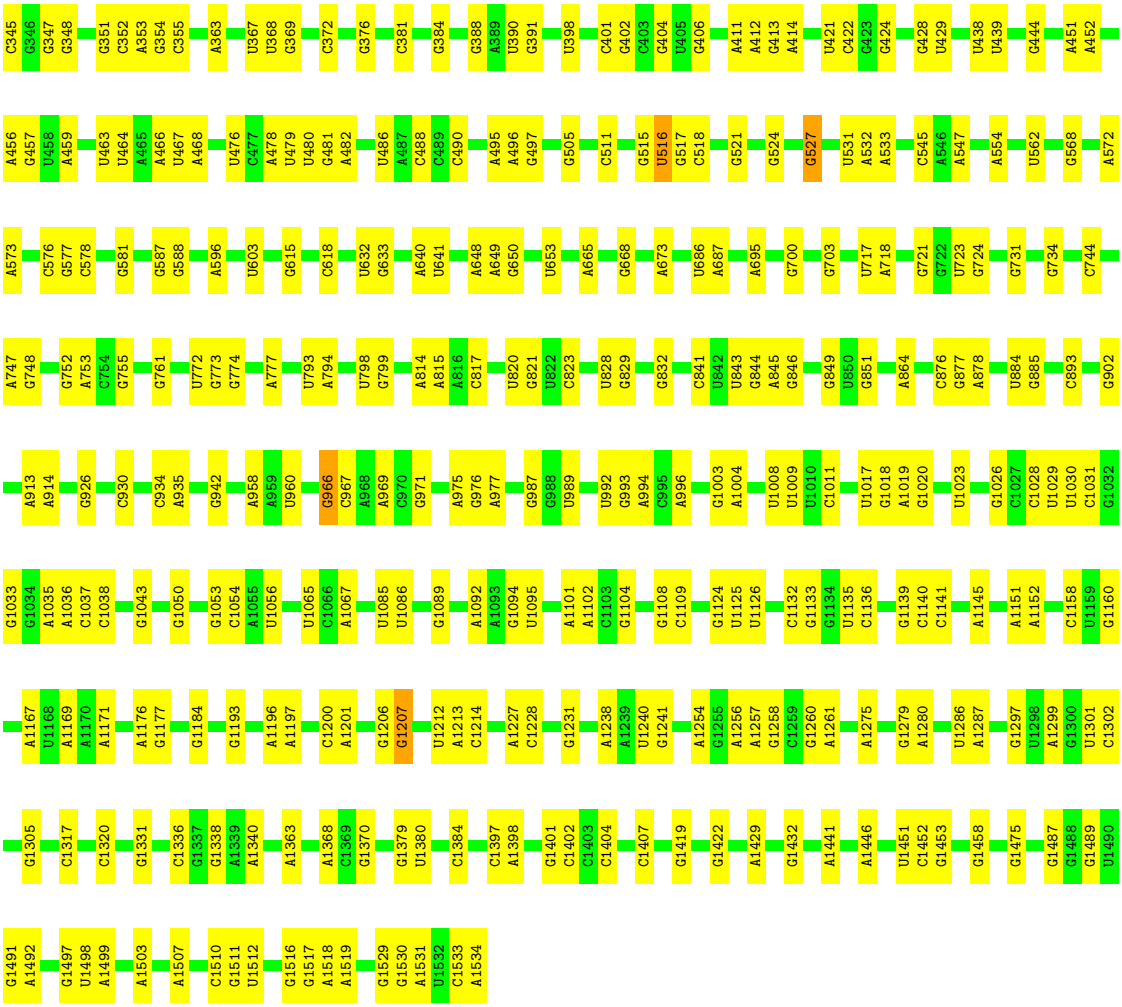




• Molecule 2: 16S ribosomal RNA

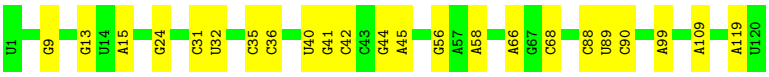
Chain 2:





• Molecule 3: 5S ribosomal RNA

Chain 3:

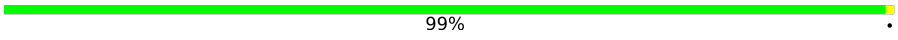


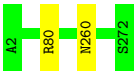
• Molecule 4: mRNA

Chain 4:

• Molecule 5: 50S ribosomal protein L2

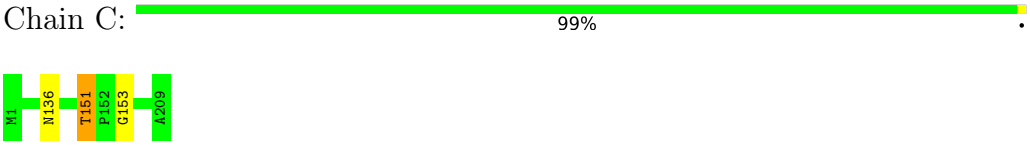
Chain B:





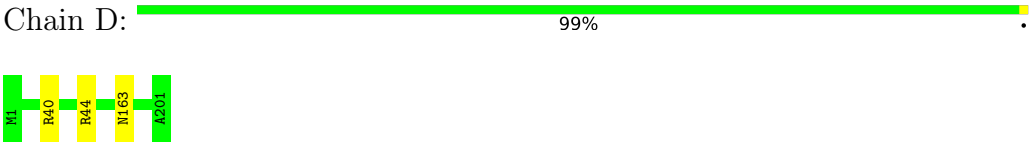
• Molecule 6: 50S ribosomal protein L3

Chain C:



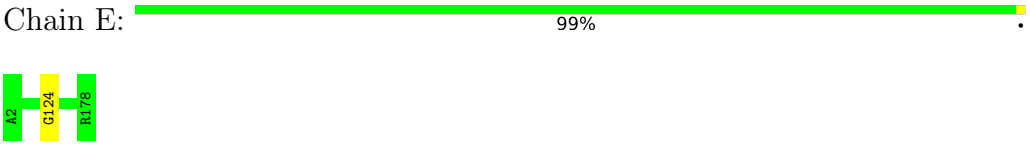
• Molecule 7: 50S ribosomal protein L4

Chain D:



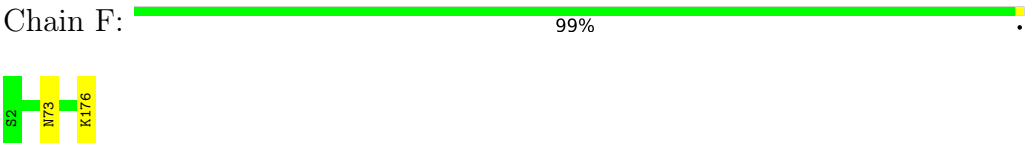
• Molecule 8: 50S ribosomal protein L5

Chain E:



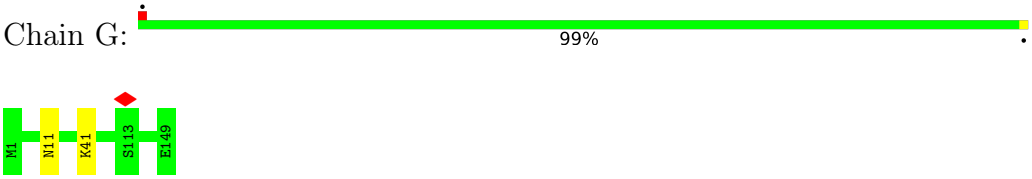
• Molecule 9: 50S ribosomal protein L6

Chain F:



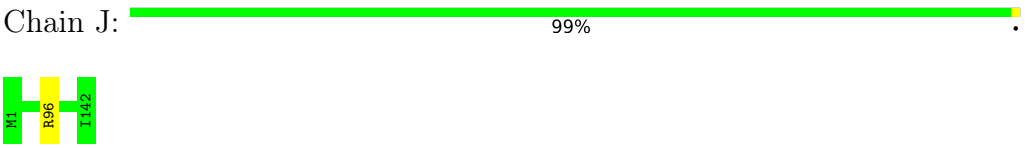
• Molecule 10: 50S ribosomal protein L9

Chain G:



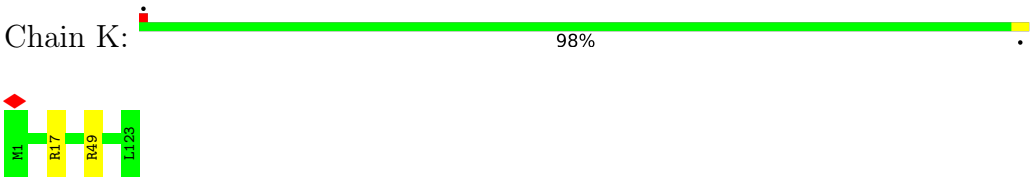
• Molecule 11: 50S ribosomal protein L13

Chain J:



• Molecule 12: 50S ribosomal protein L14

Chain K:



• Molecule 13: 50S ribosomal protein L15

Chain L: 

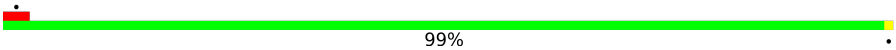
There are no outlier residues recorded for this chain.

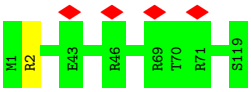
• Molecule 14: 50S ribosomal protein L16

Chain M: 

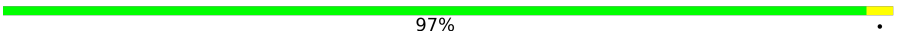
There are no outlier residues recorded for this chain.

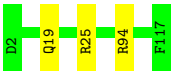
• Molecule 15: 50S ribosomal protein L17

Chain N: 

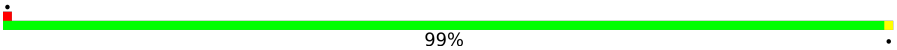


• Molecule 16: 50S ribosomal protein L18

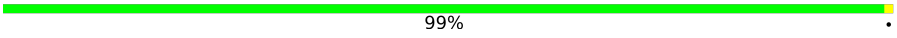
Chain O: 



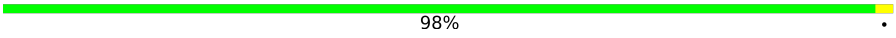
• Molecule 17: 50S ribosomal protein L19

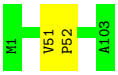
Chain P: 

• Molecule 18: 50S ribosomal protein L20

Chain Q: 

• Molecule 19: 50S ribosomal protein L21

Chain R: 

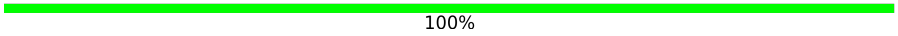


• Molecule 20: 50S ribosomal protein L22

Chain S: 

There are no outlier residues recorded for this chain.

• Molecule 21: 50S ribosomal protein L23

Chain T: 

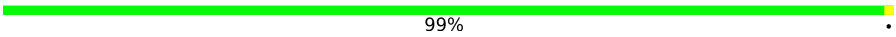
There are no outlier residues recorded for this chain.

• Molecule 22: 50S ribosomal protein L24

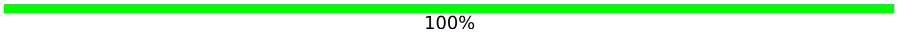
Chain U: 

There are no outlier residues recorded for this chain.

• Molecule 23: 50S ribosomal protein L25

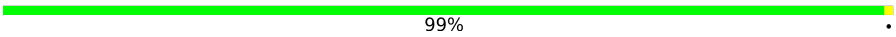
Chain V: 

• Molecule 24: 50S ribosomal protein L27

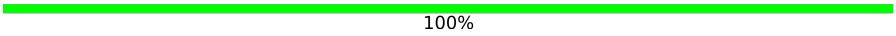
Chain W: 

There are no outlier residues recorded for this chain.

• Molecule 25: 50S ribosomal protein L28

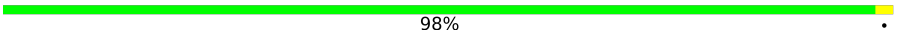
Chain X: 

• Molecule 26: 50S ribosomal protein L29

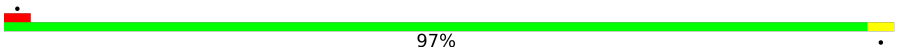
Chain Y: 

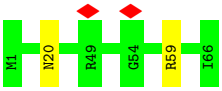
There are no outlier residues recorded for this chain.

• Molecule 27: 50S ribosomal protein L30

Chain Z: 

• Molecule 28: 50S ribosomal protein L31

Chain a: 

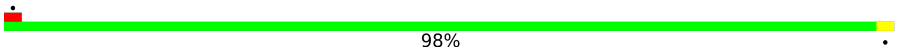


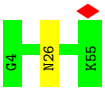
• Molecule 29: 50S ribosomal protein L32

Chain b: 

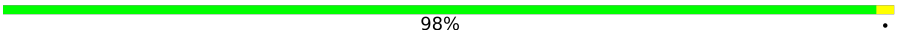
There are no outlier residues recorded for this chain.

• Molecule 30: 50S ribosomal protein L33

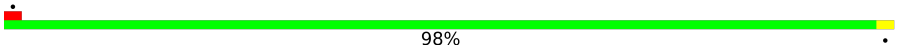
Chain c: 

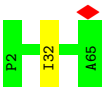


• Molecule 31: 50S ribosomal protein L34

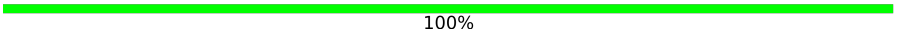
Chain d: 

• Molecule 32: 50S ribosomal protein L35

Chain e: 

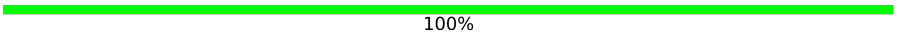


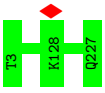
• Molecule 33: 50S ribosomal protein L36

Chain f: 

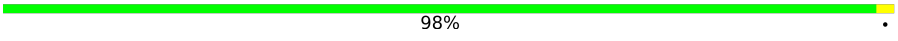
There are no outlier residues recorded for this chain.

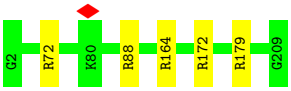
• Molecule 34: 30S ribosomal protein S2

Chain g: 

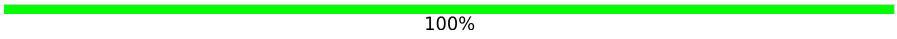


• Molecule 35: 30S ribosomal protein S3

Chain h: 

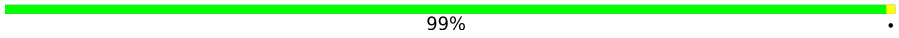


• Molecule 36: 30S ribosomal protein S4

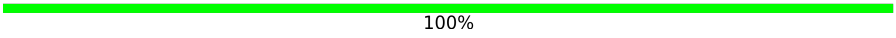
Chain i: 

There are no outlier residues recorded for this chain.

• Molecule 37: 30S ribosomal protein S5

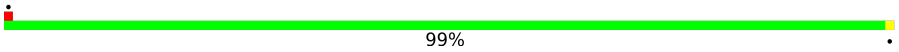
Chain j: 

• Molecule 38: 30S ribosomal protein S6

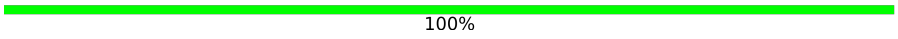
Chain k: 

There are no outlier residues recorded for this chain.

• Molecule 39: 30S ribosomal protein S7

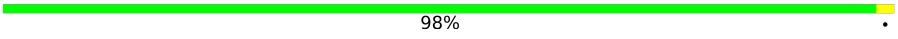
Chain l: 

• Molecule 40: 30S ribosomal protein S8

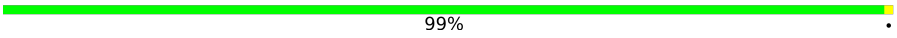
Chain m: 

There are no outlier residues recorded for this chain.

• Molecule 41: 30S ribosomal protein S9

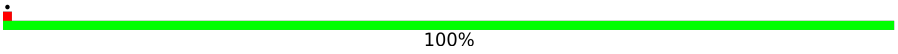
Chain n: 

• Molecule 42: 30S ribosomal protein S10

Chain o: 

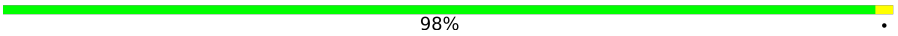
• Molecule 43: 30S ribosomal protein S11

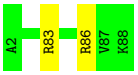
Chain p:



• Molecule 44: 30S ribosomal protein S12

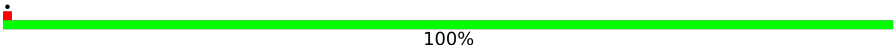
Chain q:





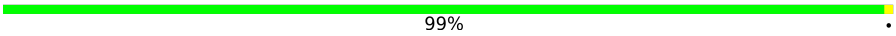
• Molecule 45: 30S ribosomal protein S13

Chain r:



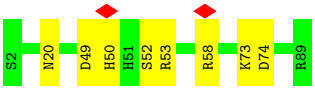
• Molecule 46: 30S ribosomal protein S14

Chain s:



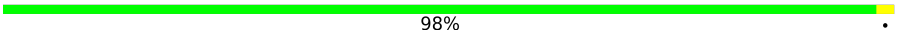
• Molecule 47: 30S ribosomal protein S15

Chain t:



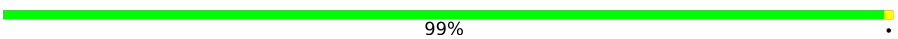
• Molecule 48: 30S ribosomal protein S16

Chain u:



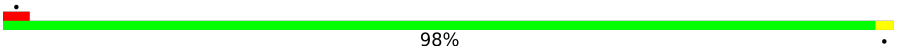
• Molecule 49: 30S ribosomal protein S17

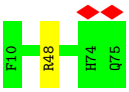
Chain v:



• Molecule 50: 30S ribosomal protein S18

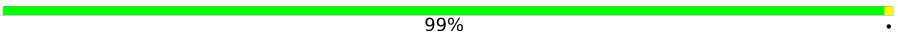
Chain w:





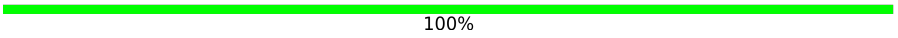
• Molecule 51: 30S ribosomal protein S19

Chain x:



• Molecule 52: 30S ribosomal protein S20

Chain y:



There are no outlier residues recorded for this chain.

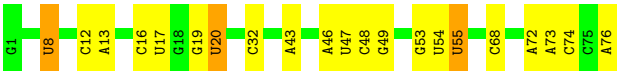
• Molecule 53: 30S ribosomal protein S21

Chain z:

There are no outlier residues recorded for this chain.

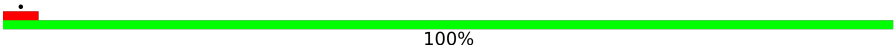
• Molecule 54: P-tRNA

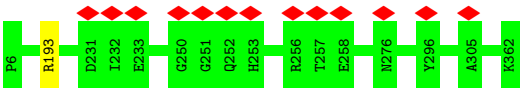
Chain 5:



• Molecule 55: Peptide chain release factor 2

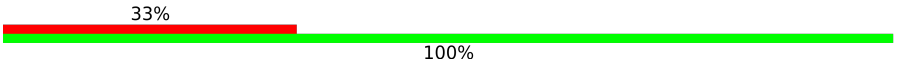
Chain A:





• Molecule 56: FME-PHE-PHE

Chain 6:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	193636	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	41.6	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.066	Depositor
Minimum map value	-0.024	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	424.96, 424.96, 424.96	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.66, 1.66, 1.66	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: PSU, 2MG, G7M, OMG, MA6, OMU, 5MU, FME, 4OC, 1MG, 2MA, 6MZ, H2U, 4SU, OMC, 3TD, ZN, 5MC, UR3, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
1	1	0.75	0/69286	0.99	0/108087
2	2	0.72	1/36590 (0.0%)	1.00	0/57074
3	3	0.67	0/2872	0.98	0/4478
4	4	0.56	0/203	1.03	0/312
5	B	0.39	0/2121	0.56	0/2852
6	C	0.40	0/1586	0.59	0/2134
7	D	0.37	0/1571	0.51	0/2113
8	E	0.39	0/1434	0.55	0/1926
9	F	0.38	0/1333	0.52	0/1805
10	G	0.33	0/1122	0.56	0/1515
11	J	0.40	0/1152	0.51	0/1551
12	K	0.37	0/955	0.57	0/1279
13	L	0.37	0/1062	0.58	0/1413
14	M	0.38	0/1093	0.55	0/1460
15	N	0.40	0/964	0.66	0/1289
16	O	0.34	0/902	0.52	0/1209
17	P	0.41	0/929	0.56	0/1242
18	Q	0.38	0/960	0.50	0/1278
19	R	0.45	0/829	0.60	0/1107
20	S	0.36	0/864	0.54	0/1156
21	T	0.36	0/752	0.52	0/1005
22	U	0.41	0/796	0.55	0/1062
23	V	0.37	0/766	0.49	0/1025
24	W	0.38	0/589	0.52	0/779
25	X	0.40	0/635	0.53	0/848
26	Y	0.33	0/502	0.47	0/667
27	Z	0.32	0/452	0.56	0/605
28	a	0.37	0/531	0.52	0/709
29	b	0.35	0/450	0.55	0/599
30	c	0.36	0/433	0.54	0/576
31	d	0.37	0/380	0.56	0/498

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
32	e	0.38	0/513	0.61	0/676
33	f	0.35	0/303	0.53	0/397
34	g	0.36	0/1791	0.54	0/2413
35	h	0.37	0/1663	0.53	0/2241
36	i	0.35	0/1665	0.50	0/2227
37	j	0.37	0/1165	0.57	0/1568
38	k	0.36	0/867	0.56	0/1171
39	l	0.33	0/1195	0.51	0/1602
40	m	0.37	0/989	0.54	0/1326
41	n	0.35	0/1034	0.55	0/1375
42	o	0.33	0/800	0.58	0/1082
43	p	0.34	0/893	0.49	0/1205
44	q	0.38	0/682	0.56	0/918
45	r	0.34	0/909	0.55	0/1215
46	s	0.33	0/817	0.50	0/1088
47	t	0.36	0/722	0.65	0/964
48	u	0.37	0/659	0.61	0/884
49	v	0.38	0/657	0.63	0/881
50	w	0.34	0/553	0.51	0/743
51	x	0.36	0/680	0.52	0/915
52	y	0.35	0/675	0.46	0/895
53	z	0.34	0/597	0.50	0/792
54	5	0.65	0/1704	1.00	0/2654
55	A	0.37	0/2873	0.57	0/3870
56	6	0.63	0/23	0.45	0/29
All	All	0.65	1/158543 (0.0%)	0.90	0/236784

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	1158	C	O3'-P	-5.15	1.54	1.61

There are no bond angle outliers.

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	
5	B	269/271 (99%)	254 (94%)	15 (6%)	0	100	100
6	C	207/209 (99%)	198 (96%)	7 (3%)	2 (1%)	15	52
7	D	199/201 (99%)	191 (96%)	8 (4%)	0	100	100
8	E	175/177 (99%)	160 (91%)	14 (8%)	1 (1%)	25	63
9	F	173/175 (99%)	164 (95%)	9 (5%)	0	100	100
10	G	147/149 (99%)	135 (92%)	12 (8%)	0	100	100
11	J	140/142 (99%)	134 (96%)	6 (4%)	0	100	100
12	K	121/123 (98%)	117 (97%)	4 (3%)	0	100	100
13	L	142/144 (99%)	139 (98%)	3 (2%)	0	100	100
14	M	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
15	N	117/119 (98%)	106 (91%)	11 (9%)	0	100	100
16	O	114/116 (98%)	110 (96%)	4 (4%)	0	100	100
17	P	112/114 (98%)	107 (96%)	5 (4%)	0	100	100
18	Q	115/117 (98%)	114 (99%)	1 (1%)	0	100	100
19	R	101/103 (98%)	90 (89%)	10 (10%)	1 (1%)	15	52
20	S	108/110 (98%)	105 (97%)	3 (3%)	0	100	100
21	T	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
22	U	101/103 (98%)	92 (91%)	9 (9%)	0	100	100
23	V	92/94 (98%)	88 (96%)	4 (4%)	0	100	100
24	W	74/76 (97%)	68 (92%)	6 (8%)	0	100	100
25	X	75/77 (97%)	74 (99%)	1 (1%)	0	100	100
26	Y	60/62 (97%)	59 (98%)	1 (2%)	0	100	100
27	Z	56/58 (97%)	53 (95%)	3 (5%)	0	100	100
28	a	64/66 (97%)	56 (88%)	8 (12%)	0	100	100
29	b	54/56 (96%)	51 (94%)	3 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
30	c	50/52 (96%)	49 (98%)	1 (2%)	0	100 100
31	d	44/46 (96%)	44 (100%)	0	0	100 100
32	e	62/64 (97%)	57 (92%)	4 (6%)	1 (2%)	9 44
33	f	36/38 (95%)	36 (100%)	0	0	100 100
34	g	223/225 (99%)	214 (96%)	9 (4%)	0	100 100
35	h	206/208 (99%)	189 (92%)	17 (8%)	0	100 100
36	i	203/205 (99%)	197 (97%)	6 (3%)	0	100 100
37	j	154/156 (99%)	142 (92%)	12 (8%)	0	100 100
38	k	102/104 (98%)	99 (97%)	3 (3%)	0	100 100
39	l	149/151 (99%)	147 (99%)	2 (1%)	0	100 100
40	m	127/129 (98%)	124 (98%)	3 (2%)	0	100 100
41	n	125/127 (98%)	115 (92%)	10 (8%)	0	100 100
42	o	97/99 (98%)	90 (93%)	7 (7%)	0	100 100
43	p	115/117 (98%)	108 (94%)	7 (6%)	0	100 100
44	q	85/87 (98%)	80 (94%)	5 (6%)	0	100 100
45	r	114/116 (98%)	110 (96%)	4 (4%)	0	100 100
46	s	98/100 (98%)	97 (99%)	1 (1%)	0	100 100
47	t	86/88 (98%)	79 (92%)	5 (6%)	2 (2%)	6 38
48	u	80/82 (98%)	74 (92%)	6 (8%)	0	100 100
49	v	78/80 (98%)	73 (94%)	5 (6%)	0	100 100
50	w	64/66 (97%)	63 (98%)	1 (2%)	0	100 100
51	x	81/83 (98%)	77 (95%)	4 (5%)	0	100 100
52	y	84/86 (98%)	84 (100%)	0	0	100 100
53	z	68/70 (97%)	66 (97%)	2 (3%)	0	100 100
55	A	355/357 (99%)	331 (93%)	24 (7%)	0	100 100
56	6	1/3 (33%)	1 (100%)	0	0	100 100
All	All	5929/6031 (98%)	5627 (95%)	295 (5%)	7 (0%)	54 84

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	C	151	THR
47	t	50	HIS

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Mol	Chain	Res	Type
47	t	74	ASP
19	R	52	PRO
32	e	32	ILE

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
5	B	216/216 (100%)	214 (99%)	2 (1%)	78 87
6	C	164/164 (100%)	162 (99%)	2 (1%)	71 83
7	D	165/165 (100%)	162 (98%)	3 (2%)	59 77
8	E	148/148 (100%)	148 (100%)	0	100 100
9	F	136/136 (100%)	134 (98%)	2 (2%)	65 80
10	G	114/114 (100%)	112 (98%)	2 (2%)	59 77
11	J	116/116 (100%)	115 (99%)	1 (1%)	78 87
12	K	104/104 (100%)	102 (98%)	2 (2%)	57 75
13	L	103/103 (100%)	103 (100%)	0	100 100
14	M	109/109 (100%)	109 (100%)	0	100 100
15	N	99/99 (100%)	98 (99%)	1 (1%)	76 86
16	O	86/86 (100%)	83 (96%)	3 (4%)	36 62
17	P	99/99 (100%)	98 (99%)	1 (1%)	76 86
18	Q	89/89 (100%)	88 (99%)	1 (1%)	73 84
19	R	84/84 (100%)	83 (99%)	1 (1%)	71 83
20	S	93/93 (100%)	93 (100%)	0	100 100
21	T	81/81 (100%)	81 (100%)	0	100 100
22	U	84/84 (100%)	84 (100%)	0	100 100
23	V	78/78 (100%)	77 (99%)	1 (1%)	69 82
24	W	58/58 (100%)	58 (100%)	0	100 100
25	X	67/67 (100%)	66 (98%)	1 (2%)	65 80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
26	Y	54/54 (100%)	54 (100%)	0	100 100
27	Z	48/48 (100%)	47 (98%)	1 (2%)	53 73
28	a	59/59 (100%)	57 (97%)	2 (3%)	37 62
29	b	47/47 (100%)	47 (100%)	0	100 100
30	c	47/47 (100%)	46 (98%)	1 (2%)	53 73
31	d	38/38 (100%)	37 (97%)	1 (3%)	46 68
32	e	51/51 (100%)	51 (100%)	0	100 100
33	f	34/34 (100%)	34 (100%)	0	100 100
34	g	187/187 (100%)	187 (100%)	0	100 100
35	h	171/171 (100%)	166 (97%)	5 (3%)	42 65
36	i	172/172 (100%)	172 (100%)	0	100 100
37	j	119/119 (100%)	118 (99%)	1 (1%)	81 89
38	k	91/91 (100%)	91 (100%)	0	100 100
39	l	124/124 (100%)	123 (99%)	1 (1%)	81 89
40	m	104/104 (100%)	104 (100%)	0	100 100
41	n	105/105 (100%)	103 (98%)	2 (2%)	57 75
42	o	86/86 (100%)	85 (99%)	1 (1%)	71 83
43	p	90/90 (100%)	90 (100%)	0	100 100
44	q	74/74 (100%)	72 (97%)	2 (3%)	44 67
45	r	94/94 (100%)	94 (100%)	0	100 100
46	s	83/83 (100%)	82 (99%)	1 (1%)	71 83
47	t	76/76 (100%)	70 (92%)	6 (8%)	12 41
48	u	65/65 (100%)	63 (97%)	2 (3%)	40 64
49	v	74/74 (100%)	73 (99%)	1 (1%)	67 81
50	w	57/57 (100%)	56 (98%)	1 (2%)	59 77
51	x	72/72 (100%)	71 (99%)	1 (1%)	67 81
52	y	65/65 (100%)	65 (100%)	0	100 100
53	z	60/60 (100%)	60 (100%)	0	100 100
55	A	304/305 (100%)	303 (100%)	1 (0%)	92 95
56	6	2/2 (100%)	2 (100%)	0	100 100
All	All	4946/4947 (100%)	4893 (99%)	53 (1%)	74 84

5 of 53 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
35	h	72	ARG
41	n	106	ARG
49	v	81	LYS
35	h	88	ARG
35	h	179	ARG

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

Mol	Chain	Res	Type
26	Y	20	ASN
55	A	276	ASN
34	g	51	ASN
55	A	43	GLN
48	u	26	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2898/2903 (99%)	755 (26%)	16 (0%)
2	2	1529/1534 (99%)	412 (26%)	5 (0%)
3	3	119/120 (99%)	23 (19%)	0
4	4	8/9 (88%)	2 (25%)	0
54	5	74/76 (97%)	19 (25%)	0
All	All	4628/4642 (99%)	1211 (26%)	21 (0%)

5 of 1211 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	10	A
1	1	34	U
1	1	35	G
1	1	40	U
1	1	46	G

5 of 21 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	2425	A
2	2	210	C

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Mol	Chain	Res	Type
2	2	1109	C
2	2	496	A
2	2	83	C

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

39 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	$\#\|Z\|>2$
1	PSU	1	1917	1	18,21,22	1.07	1 (5%)	22,30,33	1.73	4 (18%)
2	PSU	2	516	2	18,21,22	1.00	1 (5%)	22,30,33	1.82	5 (22%)
2	UR3	2	1498	2	19,22,23	2.50	7 (36%)	26,32,35	1.26	2 (7%)
1	2MG	1	1835	1	18,26,27	2.48	7 (38%)	16,38,41	1.42	4 (25%)
1	2MG	1	2445	1	18,26,27	2.48	7 (38%)	16,38,41	1.43	3 (18%)
1	OMU	1	2552	1	19,22,23	2.84	8 (42%)	26,31,34	1.81	5 (19%)
1	6MZ	1	2030	1	18,25,26	2.15	3 (16%)	16,36,39	2.01	3 (18%)
54	5MU	5	54	54	19,22,23	4.76	7 (36%)	28,32,35	3.52	8 (28%)
1	2MA	1	2503	1	17,25,26	2.36	5 (29%)	17,37,40	1.34	2 (11%)
54	H2U	5	20	54	18,21,22	3.29	5 (27%)	21,30,33	1.86	5 (23%)
1	1MG	1	745	1	18,26,27	2.63	5 (27%)	19,39,42	1.40	3 (15%)
56	FME	6	77	56	8,9,10	0.88	0	7,9,11	0.59	0
2	G7M	2	527	2	20,26,27	3.92	10 (50%)	17,39,42	1.08	2 (11%)
1	3TD	1	1915	1	18,22,23	4.16	5 (27%)	22,32,35	1.58	3 (13%)
1	5MC	1	1962	1	18,22,23	3.55	7 (38%)	26,32,35	1.04	2 (7%)
1	6MZ	1	1618	1	18,25,26	2.08	3 (16%)	16,36,39	2.33	3 (18%)
1	PSU	1	955	1	18,21,22	1.01	1 (5%)	22,30,33	1.67	2 (9%)
2	MA6	2	1518	2	19,26,27	1.04	1 (5%)	18,38,41	2.75	2 (11%)
2	2MG	2	966	2	18,26,27	2.58	7 (38%)	16,38,41	1.43	3 (18%)
1	PSU	1	1911	1	18,21,22	1.10	1 (5%)	22,30,33	2.00	5 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	2MG	2	1207	2	18,26,27	2.49	7 (38%)	16,38,41	1.45	4 (25%)
2	4OC	2	1402	2	20,23,24	2.97	8 (40%)	26,32,35	1.23	3 (11%)
54	4SU	5	8	54	18,21,22	3.57	7 (38%)	26,30,33	2.15	5 (19%)
1	PSU	1	746	1	18,21,22	1.04	1 (5%)	22,30,33	1.69	3 (13%)
54	4OC	5	32	54	20,23,24	2.98	8 (40%)	26,32,35	1.00	1 (3%)
1	5MU	1	747	1	19,22,23	4.76	7 (36%)	28,32,35	3.94	9 (32%)
1	PSU	1	2605	1	18,21,22	1.09	1 (5%)	22,30,33	1.95	5 (22%)
1	PSU	1	2580	1	18,21,22	1.08	2 (11%)	22,30,33	1.92	5 (22%)
1	5MU	1	1939	1	19,22,23	4.72	7 (36%)	28,32,35	3.84	10 (35%)
2	5MC	2	967	2	18,22,23	3.60	7 (38%)	26,32,35	1.01	1 (3%)
2	2MG	2	1516	2	18,26,27	2.56	7 (38%)	16,38,41	1.32	3 (18%)
1	G7M	1	2069	1	20,26,27	2.35	7 (35%)	17,39,42	1.33	2 (11%)
1	PSU	1	2504	1	18,21,22	1.18	1 (5%)	22,30,33	1.78	4 (18%)
1	OMG	1	2251	54,1	18,26,27	2.47	8 (44%)	19,38,41	1.58	4 (21%)
54	PSU	5	55	54	18,21,22	1.07	1 (5%)	22,30,33	1.74	4 (18%)
1	PSU	1	2457	1	18,21,22	1.14	3 (16%)	22,30,33	1.87	6 (27%)
2	5MC	2	1407	2	18,22,23	3.58	7 (38%)	26,32,35	1.11	2 (7%)
2	MA6	2	1519	2	19,26,27	1.02	1 (5%)	18,38,41	2.85	2 (11%)
1	OMC	1	2498	1	19,22,23	2.89	7 (36%)	26,31,34	0.89	1 (3%)

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
1	PSU	1	1917	1	-	0/7/25/26	0/2/2/2
2	PSU	2	516	2	-	2/7/25/26	0/2/2/2
2	UR3	2	1498	2	-	0/7/25/26	0/2/2/2
1	2MG	1	1835	1	-	2/5/27/28	0/3/3/3
1	2MG	1	2445	1	-	2/5/27/28	0/3/3/3
1	OMU	1	2552	1	-	1/9/27/28	0/2/2/2
1	6MZ	1	2030	1	-	3/5/27/28	0/3/3/3
54	5MU	5	54	54	-	0/7/25/26	0/2/2/2
1	2MA	1	2503	1	-	3/3/25/26	0/3/3/3
54	H2U	5	20	54	-	4/7/38/39	0/2/2/2
1	1MG	1	745	1	-	0/3/25/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
56	FME	6	77	56	-	3/7/9/11	-
2	G7M	2	527	2	-	2/3/25/26	0/3/3/3
1	3TD	1	1915	1	-	4/7/25/26	0/2/2/2
1	5MC	1	1962	1	-	2/7/25/26	0/2/2/2
1	6MZ	1	1618	1	-	4/5/27/28	0/3/3/3
1	PSU	1	955	1	-	0/7/25/26	0/2/2/2
2	MA6	2	1518	2	-	0/7/29/30	0/3/3/3
2	2MG	2	966	2	-	0/5/27/28	0/3/3/3
1	PSU	1	1911	1	-	0/7/25/26	0/2/2/2
2	2MG	2	1207	2	-	2/5/27/28	0/3/3/3
2	4OC	2	1402	2	-	2/9/29/30	0/2/2/2
54	4SU	5	8	54	-	3/7/25/26	0/2/2/2
1	PSU	1	746	1	-	1/7/25/26	0/2/2/2
54	4OC	5	32	54	-	0/9/29/30	0/2/2/2
1	5MU	1	747	1	-	1/7/25/26	0/2/2/2
1	PSU	1	2605	1	-	0/7/25/26	0/2/2/2
1	PSU	1	2580	1	-	0/7/25/26	0/2/2/2
1	5MU	1	1939	1	-	0/7/25/26	0/2/2/2
2	5MC	2	967	2	-	0/7/25/26	0/2/2/2
2	2MG	2	1516	2	-	0/5/27/28	0/3/3/3
1	G7M	1	2069	1	-	1/3/25/26	0/3/3/3
1	PSU	1	2504	1	-	2/7/25/26	0/2/2/2
1	OMG	1	2251	54,1	-	0/5/27/28	0/3/3/3
54	PSU	5	55	54	-	1/7/25/26	0/2/2/2
1	PSU	1	2457	1	-	0/7/25/26	0/2/2/2
2	5MC	2	1407	2	-	0/7/25/26	0/2/2/2
2	MA6	2	1519	2	-	3/7/29/30	0/3/3/3
1	OMC	1	2498	1	-	0/9/27/28	0/2/2/2

The worst 5 of 188 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	1915	3TD	C6-C5	12.48	1.49	1.35
1	1	747	5MU	C2-N1	11.02	1.56	1.38
54	5	20	H2U	C2-N1	10.80	1.51	1.35
54	5	54	5MU	C2-N1	10.70	1.55	1.38
1	1	1939	5MU	C2-N1	10.57	1.55	1.38

The worst 5 of 140 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1	747	5MU	C5-C4-N3	13.13	126.52	115.31
1	1	1939	5MU	C5-C4-N3	12.75	126.19	115.31
54	5	54	5MU	C5-C4-N3	12.22	125.74	115.31
1	1	747	5MU	C5-C6-N1	-11.30	111.72	123.34
1	1	1939	5MU	C5-C6-N1	-11.03	112.00	123.34

There are no chirality outliers.

5 of 48 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	1	1618	6MZ	C5-C6-N6-C9
1	1	1618	6MZ	N1-C6-N6-C9
1	1	1915	3TD	O4'-C1'-C5-C4
1	1	1915	3TD	O4'-C1'-C5-C6
1	1	2030	6MZ	C3'-C4'-C5'-O5'

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 14 ligands modelled in this entry, 14 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

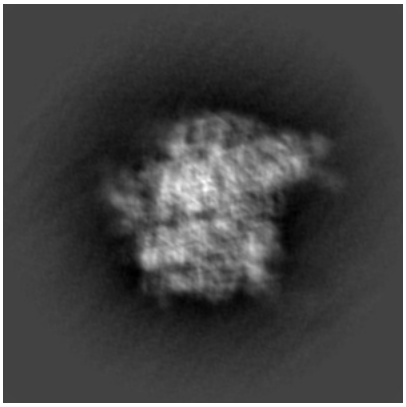
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-20193. These allow visual inspection of the internal detail of the map and identification of artifacts.

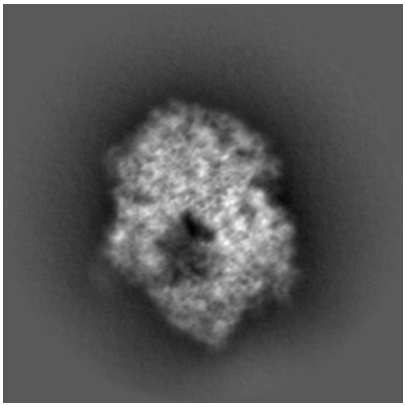
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

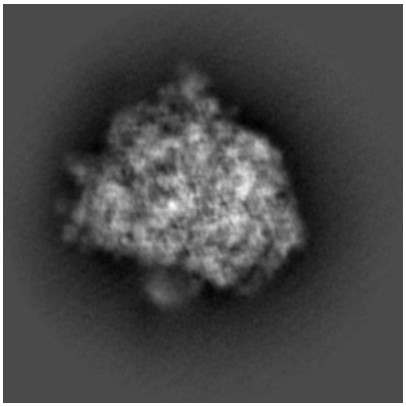
6.1.1 Primary map



X



Y

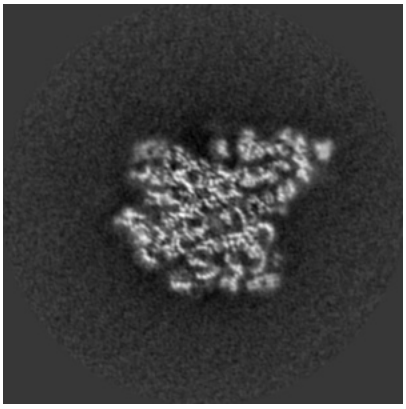


Z

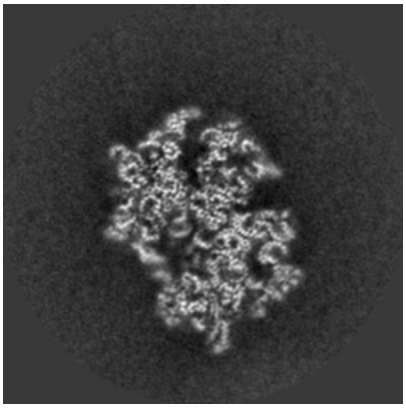
The images above show the map projected in three orthogonal directions.

6.2 Central slices

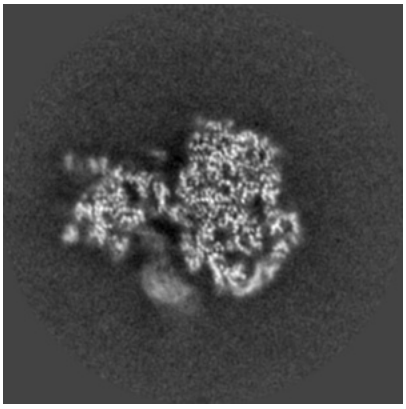
6.2.1 Primary map



X Index: 128



Y Index: 128

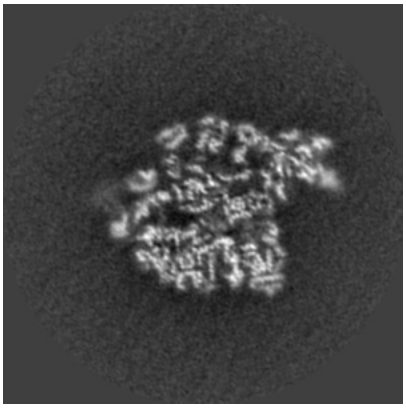


Z Index: 128

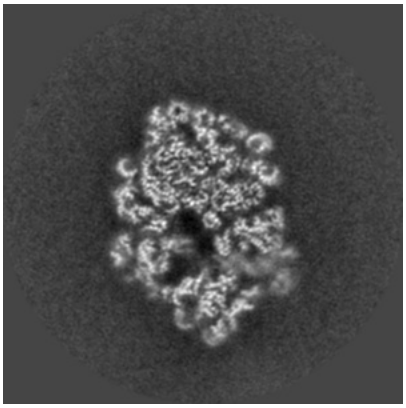
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

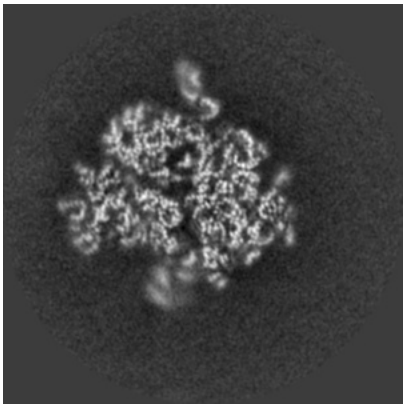
6.3.1 Primary map



X Index: 122



Y Index: 114

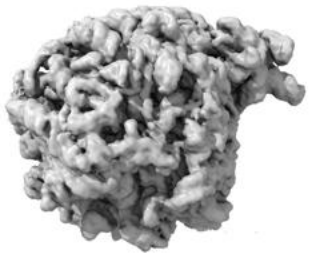


Z Index: 143

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

6.4 Orthogonal surface views (i)

6.4.1 Primary map



X

Y

Z

The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

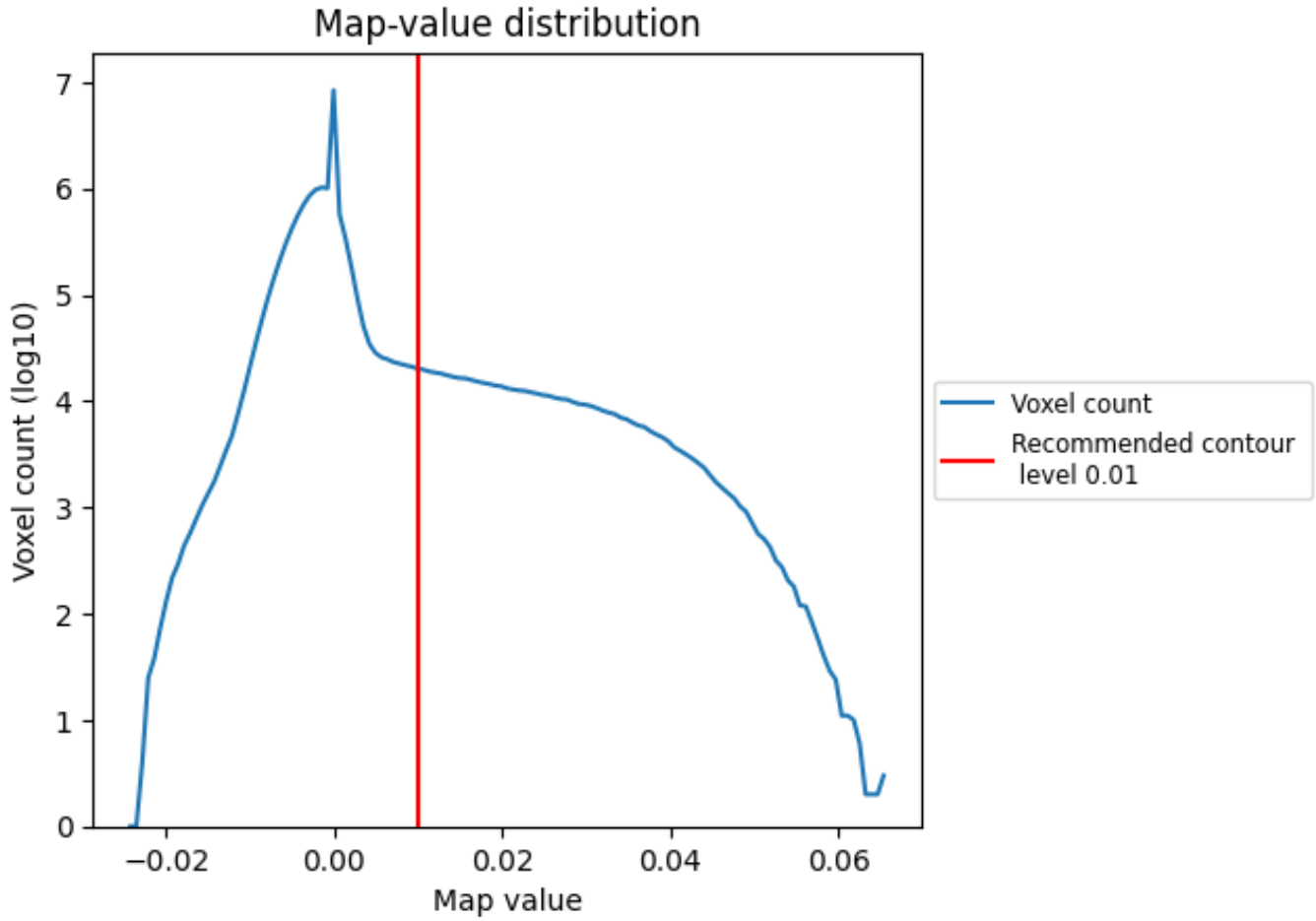
6.5 Mask visualisation (i)

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

7 Map analysis

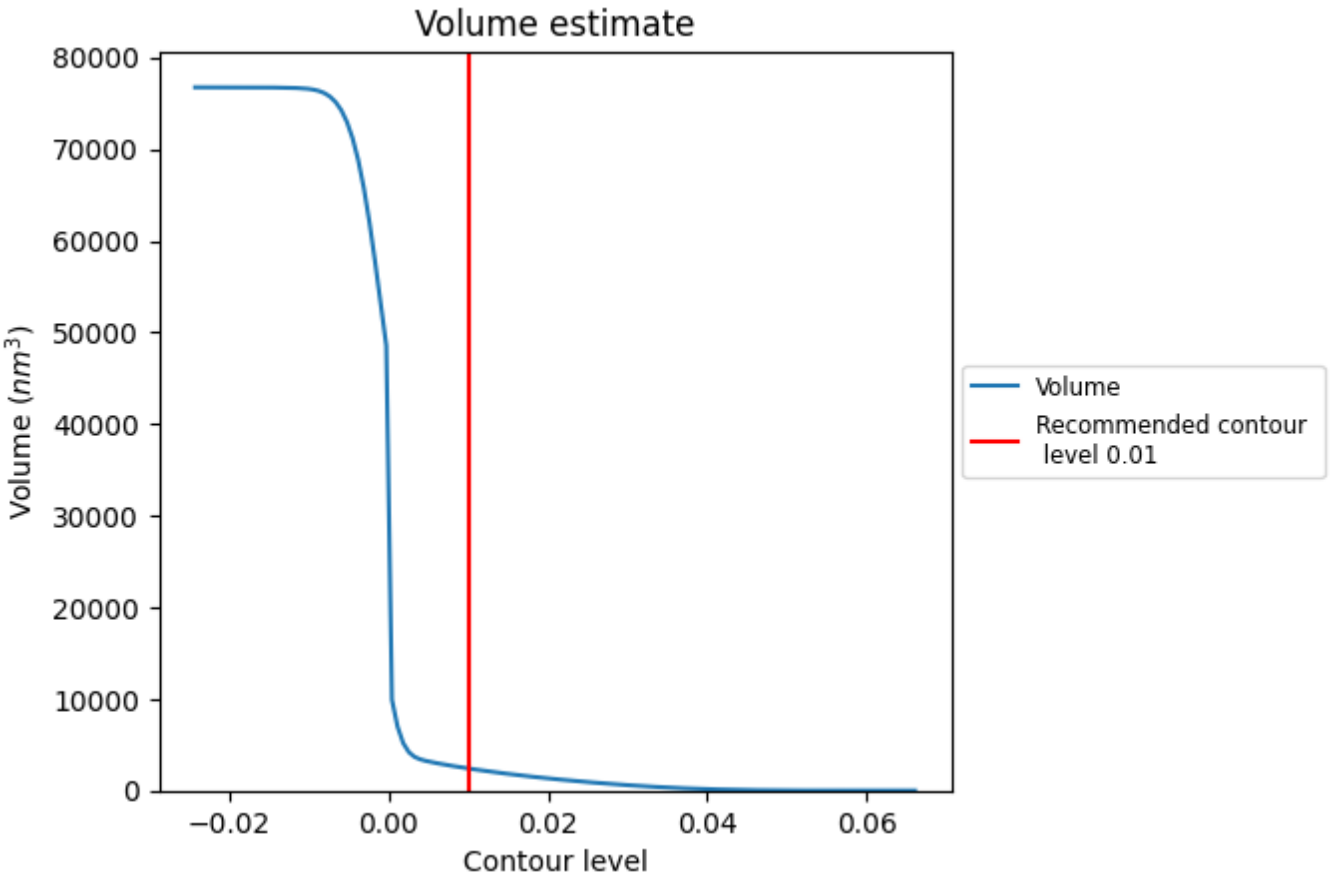
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

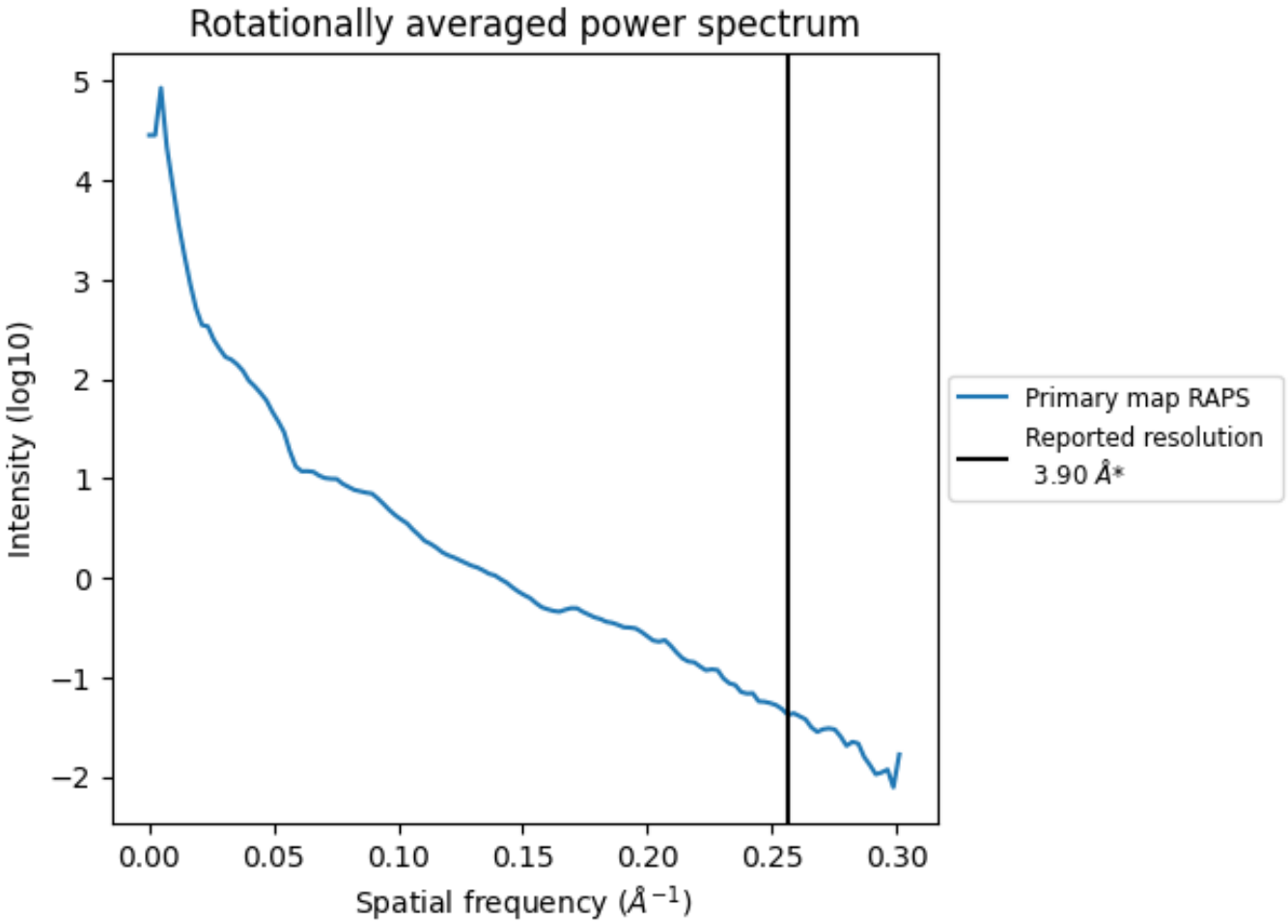
7.2 Volume estimate (i)



The volume at the recommended contour level is 2414 nm^3; this corresponds to an approximate mass of 2180 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 0.256 Å^{-1}

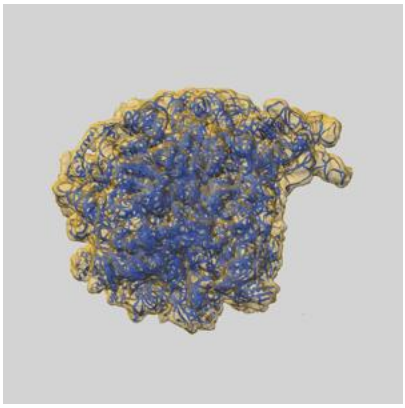
8 Fourier-Shell correlation (i)

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

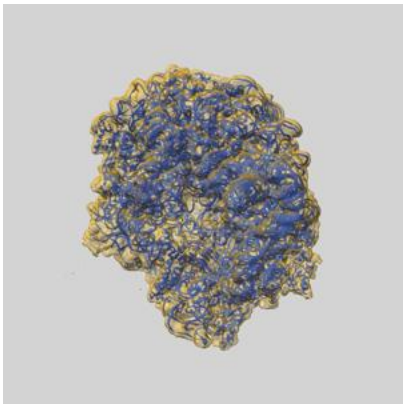
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-20193 and PDB model 6OT3. Per-residue inclusion information can be found in section 3 on page 14.

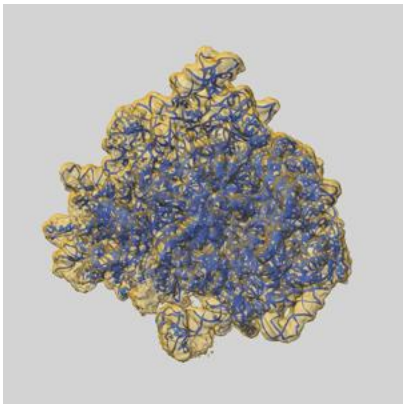
9.1 Map-model overlay



X



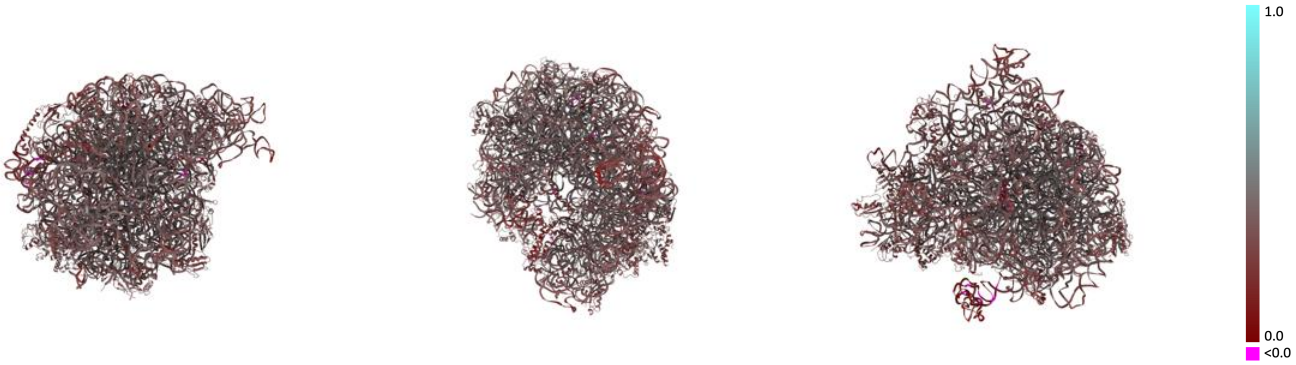
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

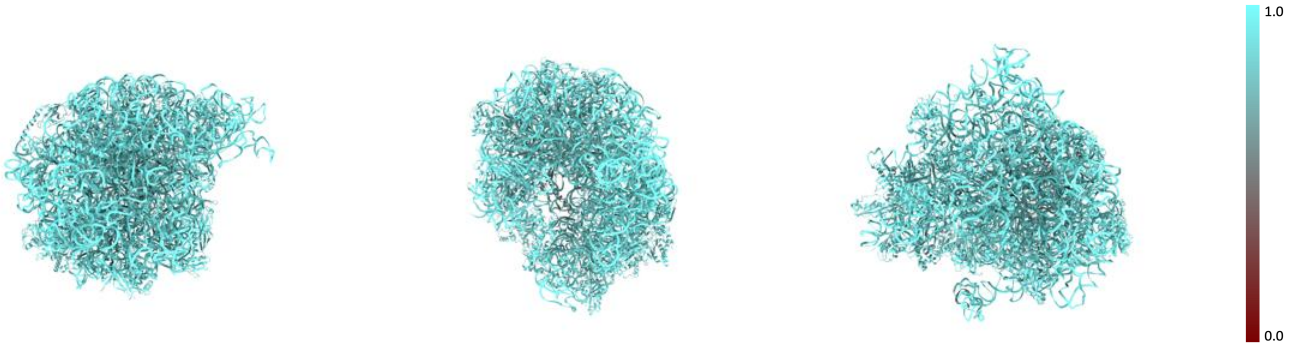
9.2 Q-score mapped to coordinate model



X Y Z

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

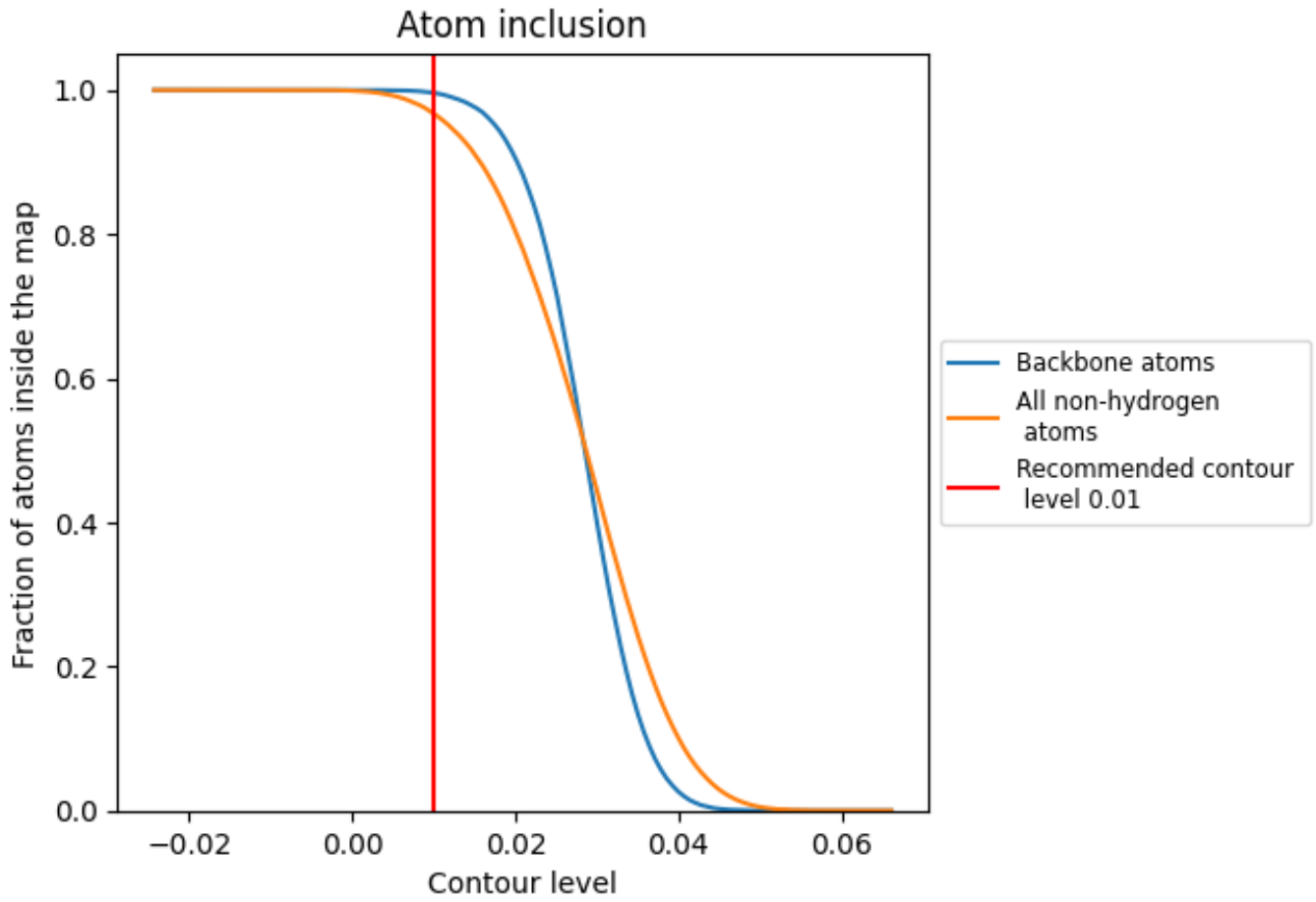
9.3 Atom inclusion mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.01).

9.4 Atom inclusion (i)



At the recommended contour level, 100% of all backbone atoms, 97% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9672	0.3480
1	0.9957	0.3640
2	0.9982	0.3560
3	0.9992	0.3490
4	0.9946	0.3690
5	0.9742	0.3360
6	0.7188	0.2220
A	0.8142	0.2480
B	0.8934	0.3790
C	0.9181	0.3550
D	0.9158	0.3480
E	0.9162	0.2980
F	0.9441	0.3200
G	0.8458	0.2660
J	0.9136	0.3540
K	0.8350	0.3410
L	0.9238	0.3660
M	0.8973	0.3630
N	0.9069	0.2820
O	0.9594	0.3270
P	0.8964	0.3220
Q	0.9218	0.3150
R	0.9285	0.3610
S	0.8744	0.3610
T	0.8986	0.3340
U	0.9497	0.3290
V	0.9553	0.3380
W	0.9134	0.3650
X	0.9002	0.3440
Y	0.9489	0.2730
Z	0.9128	0.3570
a	0.8984	0.2840
b	0.9252	0.3540
c	0.9282	0.3520
d	0.8930	0.3530

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Chain	Atom inclusion	Q-score
e	0.8839	0.3580
f	0.9249	0.3470
g	0.9023	0.2960
h	0.8912	0.3320
i	0.9353	0.3090
j	0.9204	0.3470
k	0.8984	0.3010
l	0.9082	0.2950
m	0.9271	0.3470
n	0.9346	0.3150
o	0.9046	0.3120
p	0.9074	0.3450
q	0.8618	0.3460
r	0.9171	0.2960
s	0.9328	0.3170
t	0.8971	0.2190
u	0.9522	0.3230
v	0.9288	0.3360
w	0.8719	0.3110
x	0.9304	0.3120
y	0.9251	0.2880
z	0.8301	0.2790