



wwPDB EM Validation Summary Report ⓘ

Mar 17, 2026 – 09:31 PM UTC

PDB ID : 6WD0 / pdb_00006wd0
EMDB ID : EMD-21619
Title : Cryo-EM of elongating ribosome with EF-Tu*GTP elucidates tRNA proof-reading (Cognate Structure I-A)
Authors : Loveland, A.B.; Demo, G.; Korostelev, A.A.
Deposited on : 2020-03-31
Resolution : 3.00 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

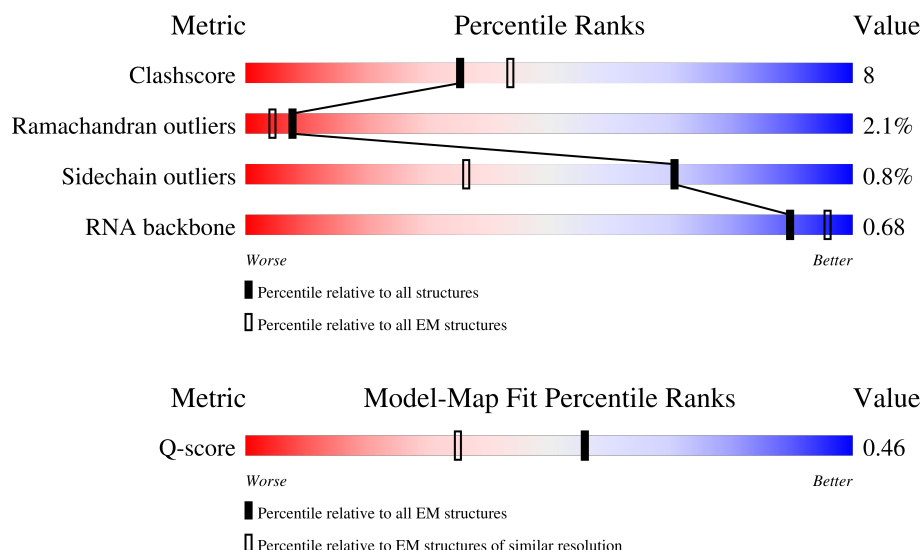
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14081 (2.50 - 3.50)

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	b	271	
2	c	209	
3	d	201	

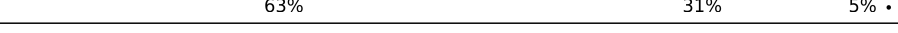
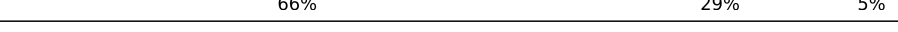
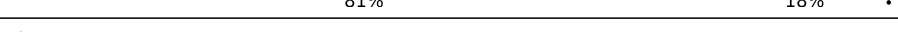
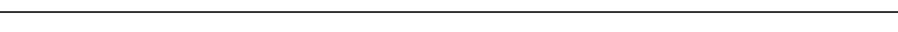
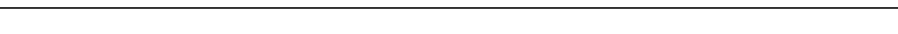
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Mol	Chain	Length	Quality of chain
4	e	177	
5	f	176	
6	g	149	
7	h	131	
8	i	141	
9	j	142	
10	k	122	
11	l	143	
12	m	136	
13	n	120	
14	o	116	
15	p	114	
16	q	117	
17	r	103	
18	s	110	
19	t	93	
20	u	102	
21	v	94	
22	w	75	
23	x	77	
24	y	63	
25	z	58	
26	B	56	
27	C	50	
28	D	46	

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Mol	Chain	Length	Quality of chain
29	E	64	 80% 19% .
30	F	38	 74% 24% .
31	G	225	 78% 21%
32	H	206	 68% 30% .
33	I	205	 65% 32% .
34	J	157	 62% 35% ..
35	K	100	 49% 48% .
36	L	151	 77% 21% .
37	M	129	 67% 32% .
38	N	127	 59% 37% ..
39	O	98	 56% 38% 5% .
40	P	116	 63% 34% .
41	Q	123	 63% 31% 5% .
42	R	114	 66% 29% 5%
43	S	100	 66% 31% .
44	T	88	 81% 18% .
45	U	82	 66% 33% .
46	V	80	 75% 22% ..
47	W	65	 80% 18% .
48	X	79	 59% 39% .
49	Y	85	 65% 32% .
50	Z	65	 48% 40% 9% .
51	a	223	 37% 20% . 40%
52	3	1539	 66% 31% .
53	1	2903	 67% 29% .

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Mol	Chain	Length	Quality of chain
54	2	120	66%28%7%
55	5	77	78%21%
55	6	77	62%34%
56	4	18	11%50%50%

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 148592 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	b	271	Total	C	N	O	S	0	0
			2083	1288	423	365	7		

- Molecule 2 is a protein called 50S ribosomal protein L3.

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

- Molecule 3 is a protein called 50S ribosomal protein L4.

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

- Molecule 4 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	e	177	Total	C	N	O	S	0	0
			1411	899	249	257	6		

- Molecule 5 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	f	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 6 is a protein called 50S ribosomal protein L9.

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

- Molecule 7 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	h	131	Total	C	N	O	S	0	0
			989	625	175	184	5		

- Molecule 8 is a protein called 50S ribosomal protein L11.

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

- Molecule 9 is a protein called 50S ribosomal protein L13.

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

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	k	122	Total	C	N	O	S	0	0
			939	587	180	166	6		

- Molecule 11 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	l	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 12 is a protein called 50S ribosomal protein L16.

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

- Molecule 13 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	n	120	Total	C	N	O	S	0	0
			961	593	196	167	5		

- Molecule 14 is a protein called 50S ribosomal protein L18.

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

- Molecule 15 is a protein called 50S ribosomal protein L19.

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

- Molecule 16 is a protein called 50S ribosomal protein L20.

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

- Molecule 17 is a protein called 50S ribosomal protein L21.

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

- Molecule 18 is a protein called 50S ribosomal protein L22.

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

- Molecule 19 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	t	93	Total	C	N	O	S	0
			739	466	139	132	2	0

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	u	102	Total	C	N	O		0
			780	492	146	142		0

- Molecule 21 is a protein called 50S ribosomal protein L25.

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

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	w	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 23 is a protein called 50S ribosomal protein L28.

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

- Molecule 24 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 25 is a protein called 50S ribosomal protein L30.

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

- Molecule 26 is a protein called 50S ribosomal protein L32.

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

- Molecule 27 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	C	50	Total	C	N	O	0	0
			410	263	75	72		

- Molecule 28 is a protein called 50S ribosomal protein L34.

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

- Molecule 29 is a protein called 50S ribosomal protein L35.

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

- Molecule 30 is a protein called 50S ribosomal protein L36.

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

- Molecule 31 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	G	225	Total	C	N	O	S	0	0
			1757	1111	315	323	8		

- Molecule 32 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	H	206	Total	C	N	O	S	0	0
			1625	1028	305	289	3		

- Molecule 33 is a protein called 30S ribosomal protein S4.

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

- Molecule 34 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	J	157	Total	C	N	O	S	0	0
			1157	719	218	214	6		

- Molecule 35 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	K	100	Total	C	N	O	S	0	0
			818	515	148	149	6		

- Molecule 36 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	L	151	Total	C	N	O	S	0	0
			1182	735	227	216	4		

- Molecule 37 is a protein called 30S ribosomal protein S8.

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

- Molecule 38 is a protein called 30S ribosomal protein S9.

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

- Molecule 39 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	O	98	Total	C	N	O	S	0	0
			787	493	150	143	1		

- Molecule 40 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	P	116	Total	C	N	O	S	0	0
			870	535	173	159	3		

- Molecule 41 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Q	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 42 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	R	114	Total	C	N	O	S	0	0
			884	546	178	157	3		

- Molecule 43 is a protein called 30S ribosomal protein S14.

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

- Molecule 44 is a protein called 30S ribosomal protein S15.

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

- Molecule 45 is a protein called 30S ribosomal protein S16.

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

- Molecule 46 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	V	80	Total	C	N	O	S	0	0
			649	411	121	114	3		

- Molecule 47 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	W	65	Total	C	N	O	S	0	0
			536	339	100	96	1		

- Molecule 48 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	X	79	Total	C	N	O	S	0	0
			638	408	120	108	2		

- Molecule 49 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Y	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 50 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Z	65	Total	C	N	O	S	0	0
			545	335	117	92	1		

- Molecule 51 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	a	134	Total	C	N	O	S	0	0
			1027	645	186	194	2		

- Molecule 52 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	3	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 53 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	1	2903	Total	C	N	O	P	0	0
			62317	27801	11468	20146	2902		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	747	C	U	conflict	GB 1036415628

- Molecule 54 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	2	120	Total	C	N	O	P	0	0
			2568	1145	471	833	119		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	120	A	-	insertion	GB 1370526515

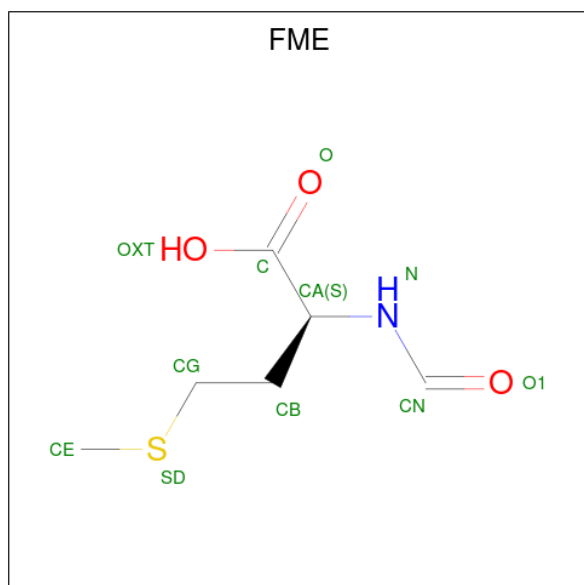
- Molecule 55 is a RNA chain called tRNAfMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	5	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		
55	6	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 56 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	4	18	Total	C	N	O	P	0	0
			388	175	76	120	17		

- Molecule 57 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: C₆H₁₁NO₃S).

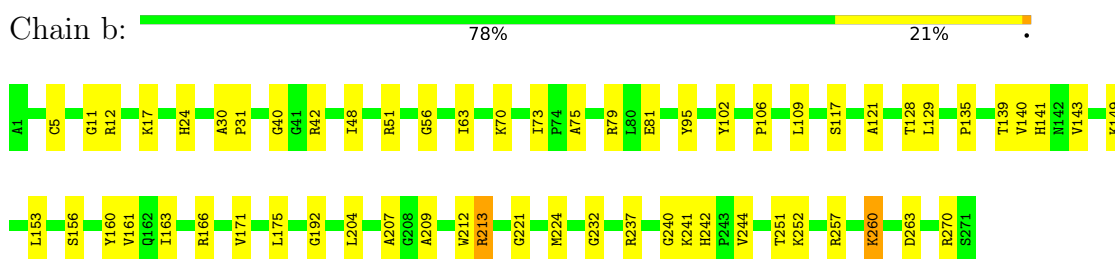


Mol	Chain	Residues	Atoms					AltConf
57	5	1	Total	C	N	O	S	0
			10	6	1	2	1	

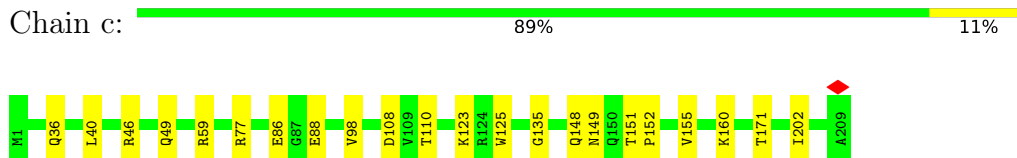
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

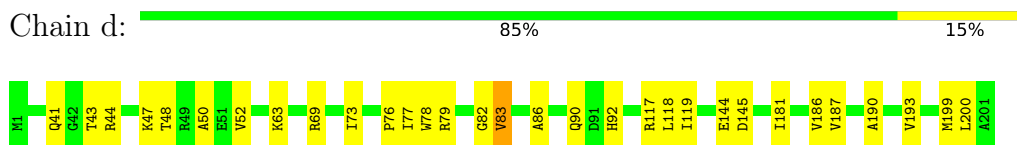
- Molecule 1: 50S ribosomal protein L2



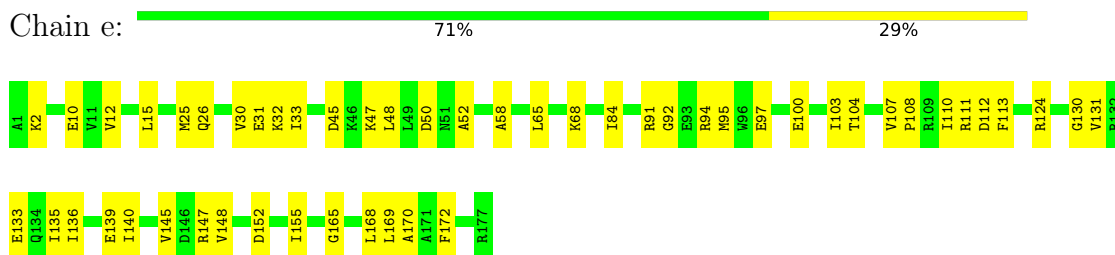
- Molecule 2: 50S ribosomal protein L3



- Molecule 3: 50S ribosomal protein L4

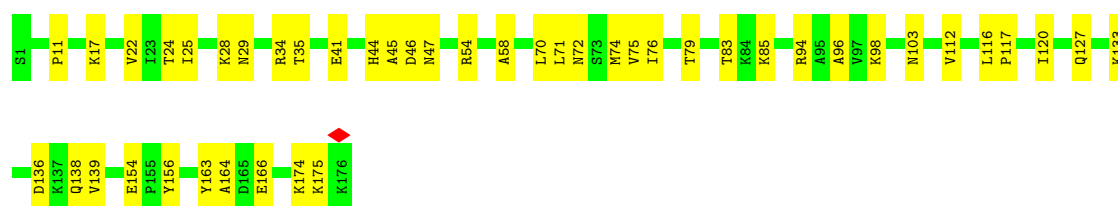


- Molecule 4: 50S ribosomal protein L5



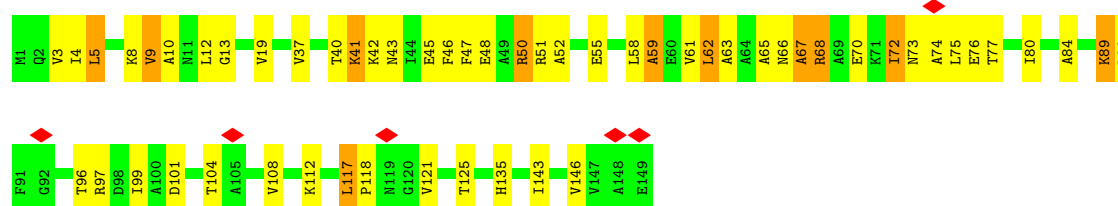
- Molecule 5: 50S ribosomal protein L6

Chain f:  74% 26%



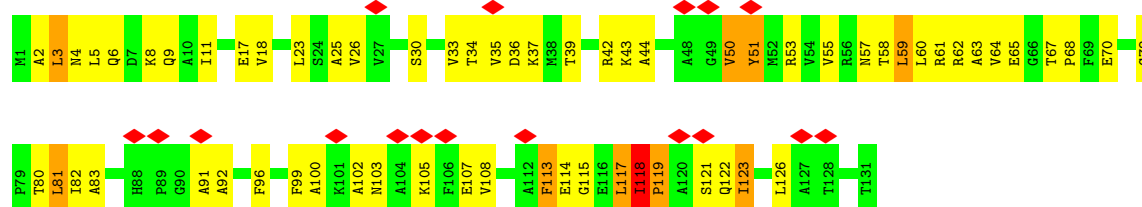
• Molecule 6: 50S ribosomal protein L9

Chain g:  62% 30% 7%



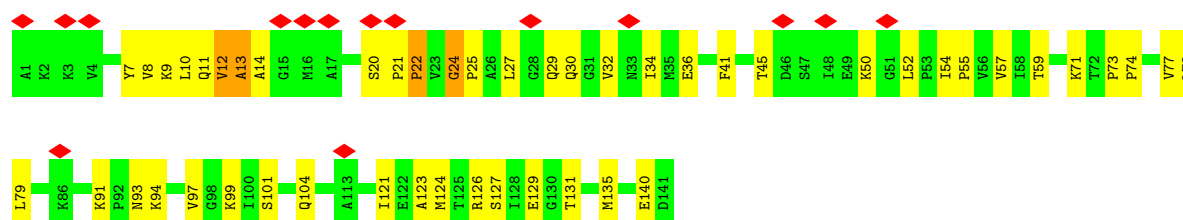
• Molecule 7: 50S ribosomal protein L10

Chain h:  13% 51% 41% 7%



• Molecule 8: 50S ribosomal protein L11

Chain i:  11% 65% 32%



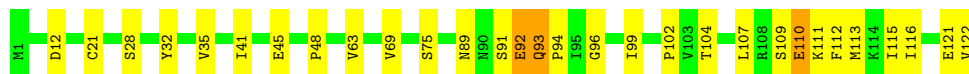
• Molecule 9: 50S ribosomal protein L13

Chain j:  77% 22%



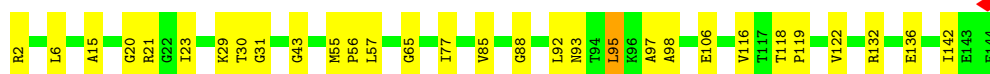
- Molecule 10: 50S ribosomal protein L14

Chain k:  75% 22%



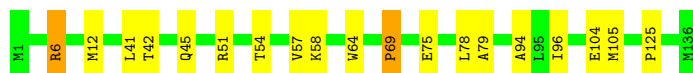
- Molecule 11: 50S ribosomal protein L15

Chain l:  79% 20%



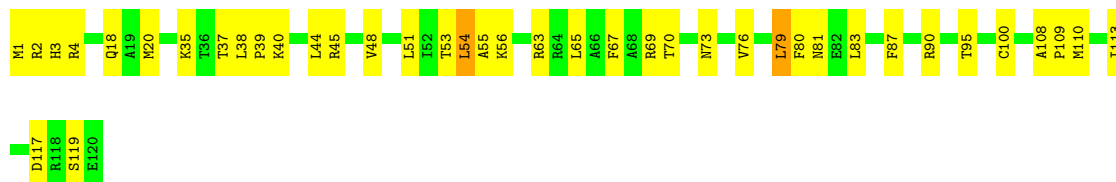
- Molecule 12: 50S ribosomal protein L16

Chain m:  86% 12%



- Molecule 13: 50S ribosomal protein L17

Chain n:  67% 32%



- Molecule 14: 50S ribosomal protein L18

Chain o:  84% 15%



- Molecule 15: 50S ribosomal protein L19

Chain p:  78% 22%



- Molecule 16: 50S ribosomal protein L20

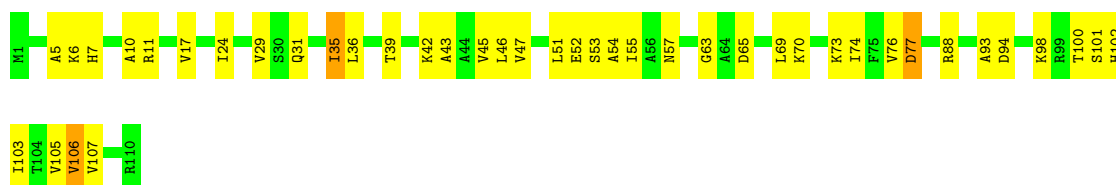
Chain q:  83% 17%



- Molecule 17: 50S ribosomal protein L21



- Molecule 18: 50S ribosomal protein L22



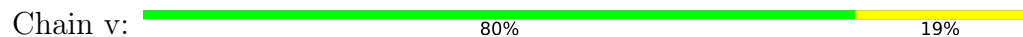
- Molecule 19: 50S ribosomal protein L23



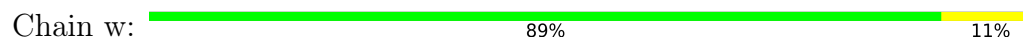
- Molecule 20: 50S ribosomal protein L24



- Molecule 21: 50S ribosomal protein L25



- Molecule 22: 50S ribosomal protein L27



- Molecule 23: 50S ribosomal protein L28

Chain x:  82% 18%



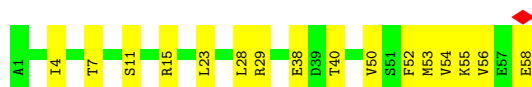
- Molecule 24: 50S ribosomal protein L29

Chain y:  60% 40%



- Molecule 25: 50S ribosomal protein L30

Chain z:  72% 28%



- Molecule 26: 50S ribosomal protein L32

Chain B:  88% 12%



- Molecule 27: 50S ribosomal protein L33

Chain C:  76% 24%



- Molecule 28: 50S ribosomal protein L34

Chain D:  72% 26%



- Molecule 29: 50S ribosomal protein L35

Chain E:  80% 19%



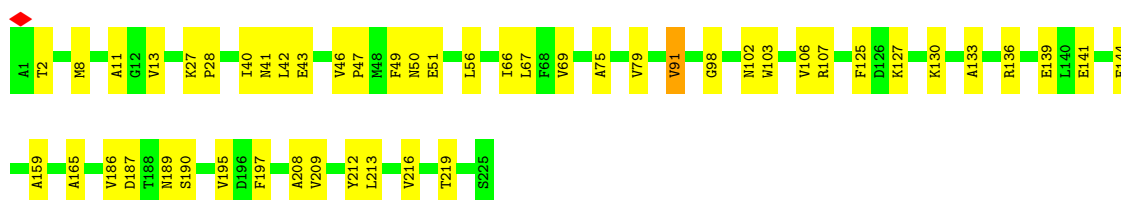
- Molecule 30: 50S ribosomal protein L36

Chain F:  74% 24% .



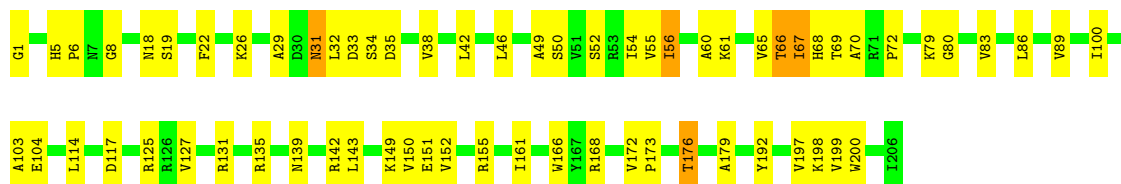
- Molecule 31: 30S ribosomal protein S2

Chain G:  78% 21%



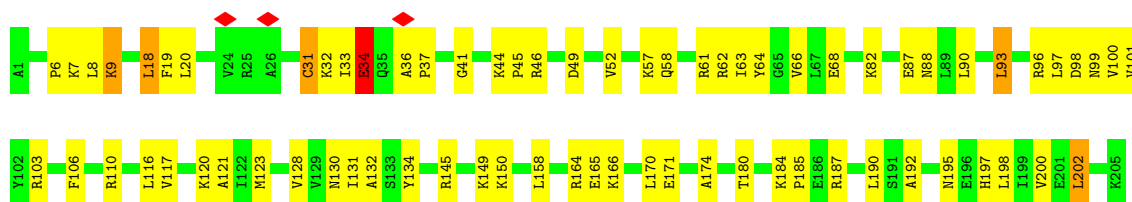
- Molecule 32: 30S ribosomal protein S3

Chain H:  68% 30% .



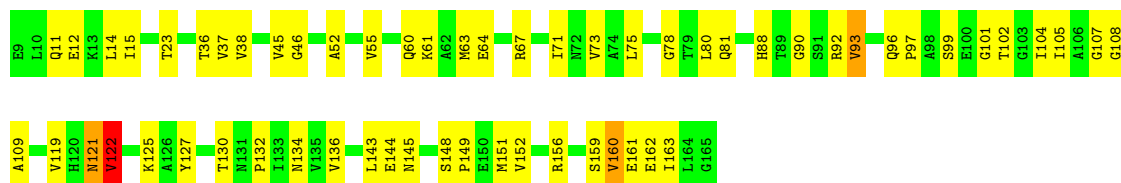
- Molecule 33: 30S ribosomal protein S4

Chain I:  65% 32% .



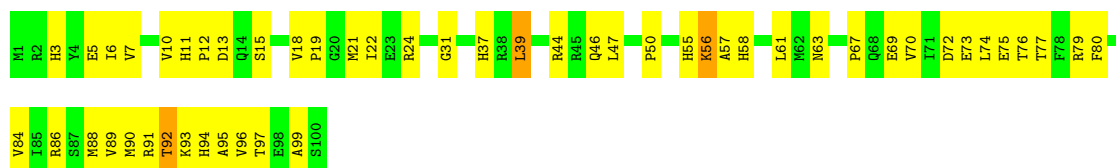
- Molecule 34: 30S ribosomal protein S5

Chain J:  62% 35% ..



- Molecule 35: 30S ribosomal protein S6

Chain K:  49% 48% .



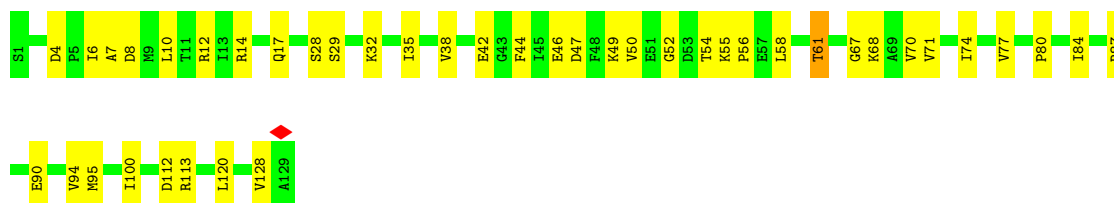
- Molecule 36: 30S ribosomal protein S7

Chain L: 77% 21% .



- Molecule 37: 30S ribosomal protein S8

Chain M: 67% 32% .



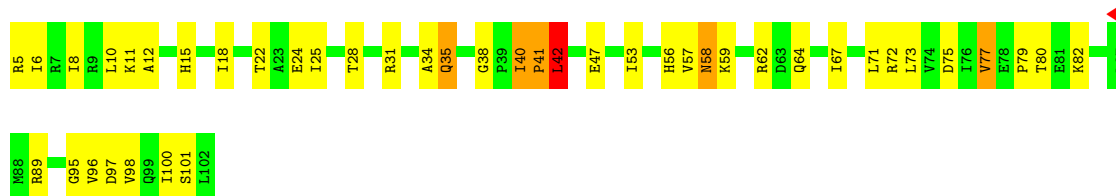
- Molecule 38: 30S ribosomal protein S9

Chain N: 59% 37% .



- Molecule 39: 30S ribosomal protein S10

Chain O: 56% 38% 5% .

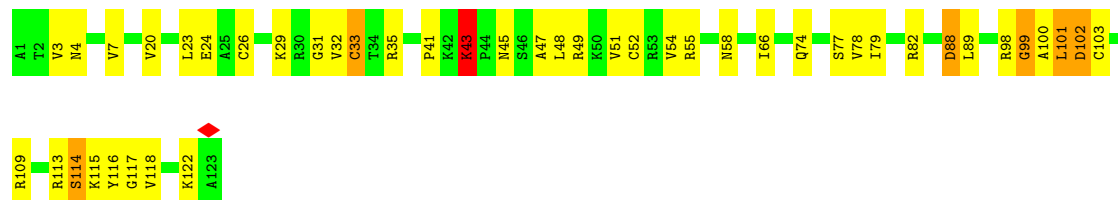


- Molecule 40: 30S ribosomal protein S11

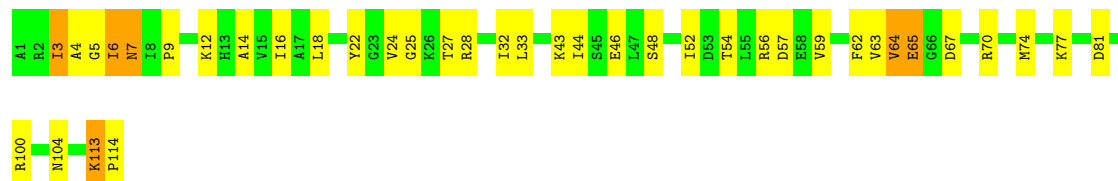
Chain P: 63% 34% .



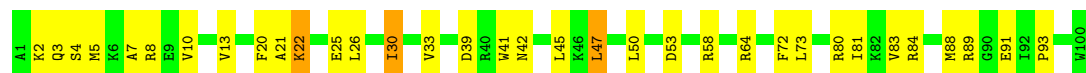
- Molecule 41: 30S ribosomal protein S12



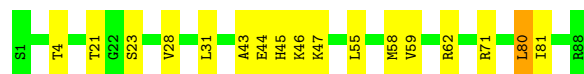
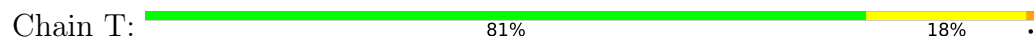
- Molecule 42: 30S ribosomal protein S13



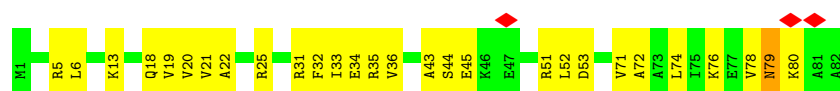
- Molecule 43: 30S ribosomal protein S14



- Molecule 44: 30S ribosomal protein S15



- Molecule 45: 30S ribosomal protein S16



- Molecule 46: 30S ribosomal protein S17

Chain V:  75% 22% ..



- Molecule 47: 30S ribosomal protein S18

Chain W:  80% 18% .



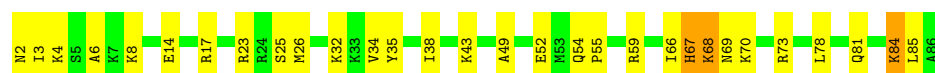
- Molecule 48: 30S ribosomal protein S19

Chain X:  59% 39% .

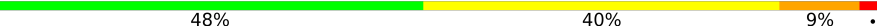


- Molecule 49: 30S ribosomal protein S20

Chain Y:  65% 32% .

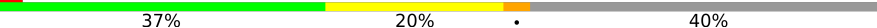


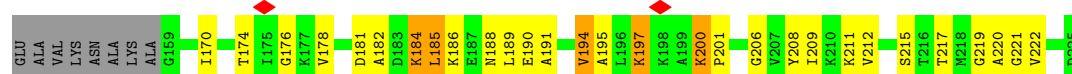
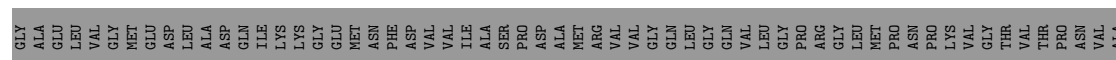
- Molecule 50: 30S ribosomal protein S21

Chain Z:  48% 40% 9% .



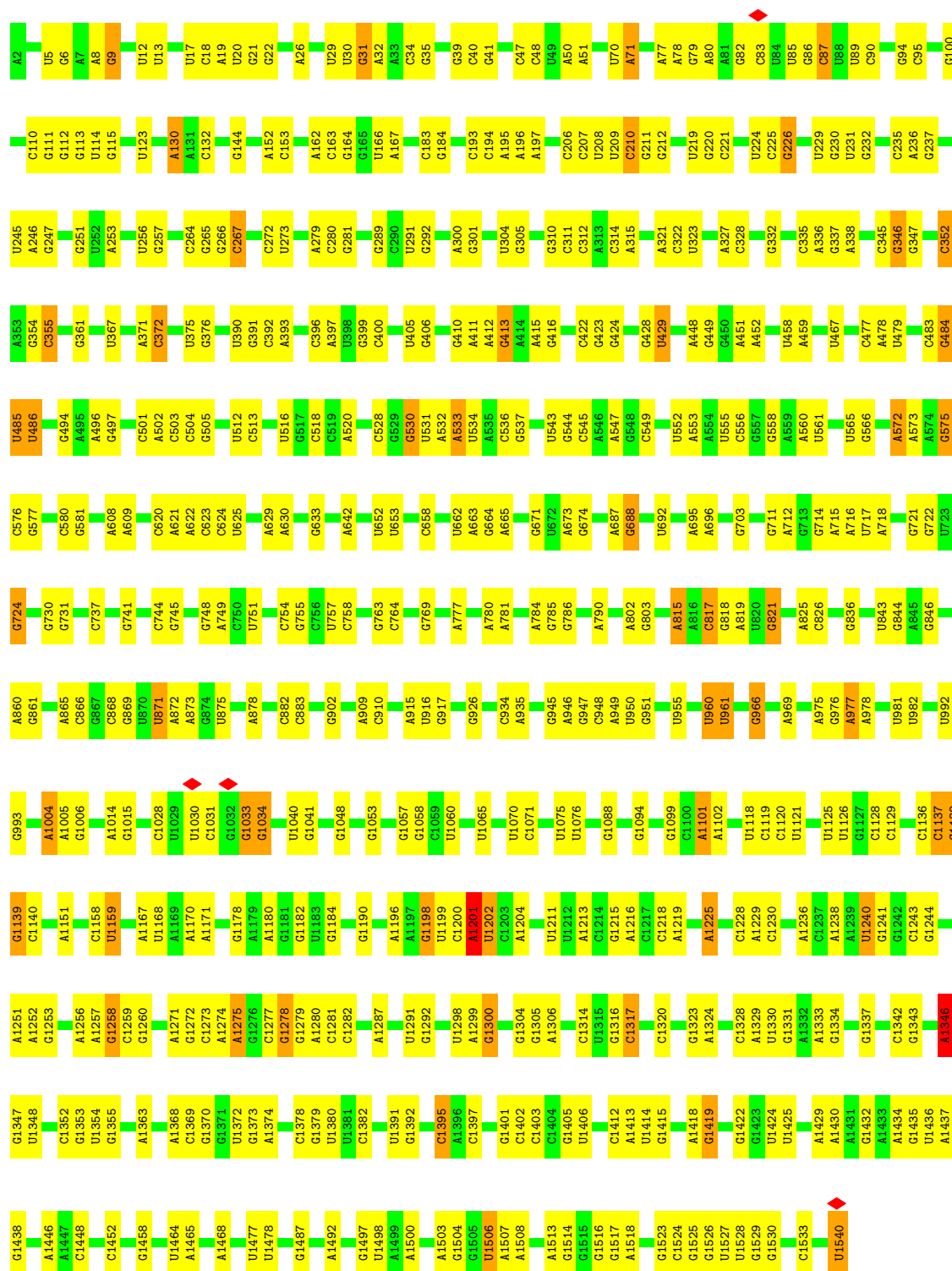
- Molecule 51: 50S ribosomal protein L1

Chain a:  37% 20% 40% .



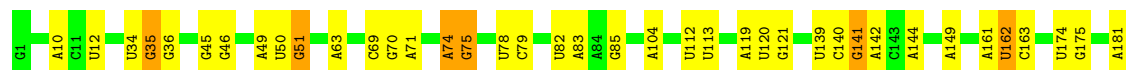
- Molecule 52: 16S ribosomal RNA

Chain 3:  66% 31% .

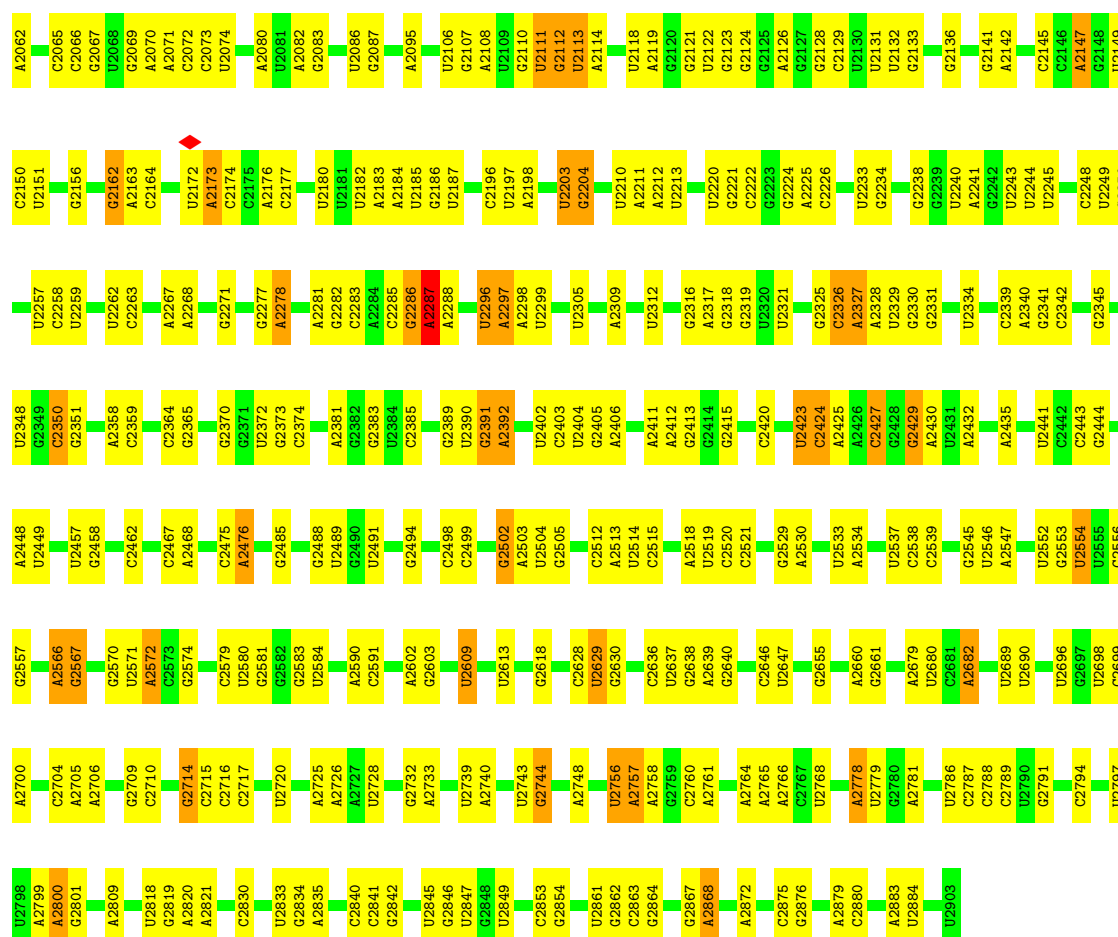


• Molecule 53: 23S ribosomal RNA

Chain 1: 67% 29%

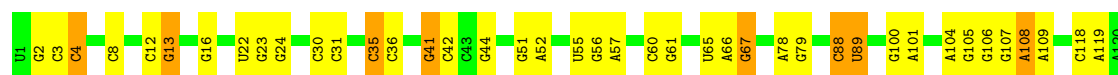


U1943	G1816	G1715	A1569	G1430	G1300	G1138	G1056	G942	U807	U688	U573	G467	A311	G189
U1944	U1818	G1720	A1570	A1431	A1301	G1139	A1057	C946	G808	C692	A574	G468	G312	A190
U1955	U1827	G1721	A1571	G1432	A1302	G1140	U1058	A947	G809	A693	U575	G469	C323	A191
U1956	G1828	U1729	G1581	A1433	C1306	U1141	G1059	C948	U810	U694	U576	G473	G329	C192
C1957	A1829	C1730	U1584	A1434	A1307	U1142	U1060	G949	C812	G695	G577	G474	A330	U193
U1963	G1830	G1731	U1584	G1435	A1308	A1143	U1061	C957	A819	A699	G579	A477	A331	A196
G1964	G1831	G1732	A1603	U1437	A1309	C1152	U1065	C961	A820	G700	U580	A477	C340	A197
C1965	C1837	A1735	A1603	U1438	C1320	G1153	U1066	G962	G822	U703	C581	G481	C341	C198
A1966	G1846	U1736	C1606	G1444	A1321	A1155	A1070	C967	U827	G704	G585	G481	A342	A199
C1967	A1847	U1739	C1607	G1445	U1326	A1156	G1071	C968	U828	G713	U588	C490	G205	G206
A1970	U1856	G1740	A1608	C1454	A1327	A1175	G1072	C968	A829	G713	U589	C491	G361	U207
U1971	G1857	A1744	A1609	A1461	A1328	U1176	A1073	G971	G830	A718	U590	G494	A362	A208
G1972	A1858	A1745	C1611	U1468	U1329	G1177	G1074	A972	G831	U499	U594	U499	A371	G215
U1979	U1859	G1763	A1614	U1468	G1331	C1178	A1077	A973	U832	C723	C595	U503	G372	A216
G1980	G1860	A1754	C1615	G1475	G1332	G1179	C1078	A975	A833	G725	C595	A503	A371	A216
U1991	A1871	A1758	A1616	U1476	U1344	U1183	C1079	A979	A845	G726	U598	A504	G386	A221
G1992	G1872	A1759	C1625	U1476	U1345	G1186	A1080	A982	U846	A727	A599	A505	U387	A222
U1993	C1874	C1760	A1626	G1482	C1352	U1188	U1082	A983	U847	G729	A603	U511	U395	U224
C1996	G1875	G1761	A1637	A1490	A1353	U1188	A1083	A983	G858	G730	A613	G512	G396	A226
C1997	A1876	A1762	G1642	G1491	A1354	U1189	A1084	C987	G859	C740	A614	A528	A404	A227
G2004	G1877	C1764	G1643	C1498	G1355	A1189	A1085	A988	U860	U741	U615	A529	U405	C228
A2005	G1878	C1764	G1644	C1498	G1356	G1191	A1088	G989	A861	A742	A616	G530	G406	C229
G2010	G1884	A1773	G1645	C1507	C1357	G1210	G1092	C995	G863	C747	G617	A532	G411	G230
U2011	A1885	G1774	C1646	A1508	A1358	C1211	G1093	A996	G864	C747	A627	A533	A414	A231
G2012	A1889	G1776	U1647	A1509	G1360	G1212	A1095	A997	C865	A752	G628	U534	C414	G242
A2019	A1890	G1779	U1648	G1510	G1361	A1213	A1096	C1005	C873	G760	G629	G535	A415	G248
A2020	G1893	A1780	G1651	A1515	A1365	G1236	U1097	C1006	G874	A761	A637	A538	C420	C249
C2021	C1894	A1784	U1657	A1522	A1366	G1239	C1102	C1007	A878	U762	G638	C542	G254	G254
C2023	A1899	A1785	C1658	G1523	A1367	U1240	A1103	U1012	C885	G763	U639	G543	A256	A256
G2029	A1900	A1786	U1662	A1524	G1368	C1251	U1105	C1013	A886	A764	C640	C544	C433	A265
A2030	A1901	G1790	G1663	A1525	C1370	G1252	G1106	U1019	U887	G770	C644	U545	U434	A265
A2031	C1902	A1791	A1664	A1528	G1371	A1253	G1107	A1020	C888	C772	U646	A547	C435	G266
G2032	C1905	A1794	G1674	G1529	A1373	G1256	A1021	A1021	C889	U773	C650	G548	C436	C275
G2035	G1906	A1795	U1678	A1535	A1378	U1257	G1110	G1022	C890	U773	A654	G549	U437	U276
C2036	A1907	U1796	A1678	C1536	A1379	U1258	G1111	U1023	G891	G776	A654	U554	G438	U276
A2042	A1913	G1797	A1679	G1537	U1383	A1268	U1113	G1026	A892	U776	A654	G555	A277	A277
C2043	G1929	U1798	U1680	G1538	A1383	A1268	C1114	A1027	C893	U776	A654	G555	C440	A279
G2048	G1930	C1800	G1681	U1539	U1394	A1269	G1115	A1028	U895	A782	G669	U558	U441	U280
C2049	A1931	A1801	C1685	G1540	U1405	C1270	G1122	U1028	A896	A783	A670	G559	G442	C281
G2055	A1932	G1807	C1686	G1540	U1406	A1271	G1125	U1033	C897	G785	A677	U562	C444	C281
C2056	C1933	A1808	A1701	G1555	U1406	A1272	G1125	C1045	A910	U785	A677	U562	U448	U290
A1936	G1935	A1809	G1702	U1559	U1415	C1278	U1130	A1046	A917	G799	A677	C564	A457	A294
A1937	A1936	G1810	G1703	G1560	G1416	G1279	U1132	G1047	A917	A800	G682	C565	G458	A294
A1938	A1937	G1811	A1705	C1564	A1419	C1289	U1133	C1053	U932	G805	U686	U571	U459	G301
G2061	A1938	G1811	A1705	C1565	A1419	C1289	A1134	A1054	A941	C806	C687	A572	A459	A310



• Molecule 54: 5S ribosomal RNA

Chain 2: 66% 28% 7%



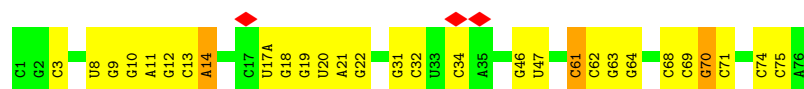
• Molecule 55: tRNA^{fMet}

Chain 5: 78% 21%

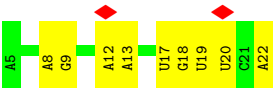


• Molecule 55: tRNA^{fMet}

Chain 6: 62% 34%



• Molecule 56: mRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	115115	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	35	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	27.527	Depositor
Minimum map value	-12.932	Depositor
Average map value	0.110	Depositor
Map value standard deviation	1.011	Depositor
Recommended contour level	1	Depositor
Map size (Å)	383.904, 383.904, 383.904	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.333, 1.333, 1.333	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FME

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	b	0.30	0/2122	0.91	6/2852 (0.2%)
2	c	0.28	0/1586	0.80	0/2134
3	d	0.28	0/1571	0.81	1/2113 (0.0%)
4	e	0.29	0/1435	0.91	5/1926 (0.3%)
5	f	0.29	0/1343	0.87	2/1816 (0.1%)
6	g	0.33	0/1122	1.11	10/1515 (0.7%)
7	h	0.35	0/1002	1.15	11/1350 (0.8%)
8	i	0.37	0/1046	0.98	6/1410 (0.4%)
9	j	0.28	0/1152	0.79	0/1551
10	k	0.28	0/948	0.89	1/1268 (0.1%)
11	l	0.30	0/1054	0.95	4/1403 (0.3%)
12	m	0.29	0/1093	0.76	0/1460
13	n	0.29	0/974	0.92	4/1301 (0.3%)
14	o	0.29	0/902	0.85	3/1209 (0.2%)
15	p	0.29	0/929	0.79	1/1242 (0.1%)
16	q	0.30	0/960	0.86	2/1278 (0.2%)
17	r	0.28	0/829	0.81	0/1107
18	s	0.27	0/864	0.89	1/1156 (0.1%)
19	t	0.28	0/745	0.82	1/994 (0.1%)
20	u	0.29	0/788	0.88	1/1051 (0.1%)
21	v	0.29	0/766	0.83	1/1025 (0.1%)
22	w	0.26	0/582	0.73	0/769
23	x	0.29	0/635	0.85	0/848
24	y	0.28	0/510	0.90	1/677 (0.1%)
25	z	0.28	0/453	0.79	1/605 (0.2%)
26	B	0.27	0/450	0.80	0/599
27	C	0.33	0/417	0.81	0/554
28	D	0.32	0/380	0.93	1/498 (0.2%)
29	E	0.28	0/513	0.83	0/676
30	F	0.32	0/303	0.86	0/397
31	G	0.29	0/1788	0.93	5/2408 (0.2%)
32	H	0.31	0/1652	0.88	5/2225 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	I	0.31	0/1665	0.99	7/2227 (0.3%)
34	J	0.33	0/1170	0.96	7/1573 (0.4%)
35	K	0.31	0/836	0.85	1/1128 (0.1%)
36	L	0.29	0/1196	0.90	3/1602 (0.2%)
37	M	0.30	0/989	0.92	1/1326 (0.1%)
38	N	0.32	0/1034	0.96	4/1375 (0.3%)
39	O	0.35	0/797	0.89	5/1077 (0.5%)
40	P	0.30	0/886	0.90	2/1195 (0.2%)
41	Q	0.32	0/969	0.97	6/1300 (0.5%)
42	R	0.31	0/893	0.91	2/1193 (0.2%)
43	S	0.30	0/817	0.93	3/1088 (0.3%)
44	T	0.29	0/722	0.87	4/964 (0.4%)
45	U	0.33	0/659	1.05	4/884 (0.5%)
46	V	0.28	0/658	0.89	1/881 (0.1%)
47	W	0.31	0/545	0.83	2/731 (0.3%)
48	X	0.33	0/653	0.96	5/877 (0.6%)
49	Y	0.30	0/671	0.89	2/888 (0.2%)
50	Z	0.34	0/551	1.10	6/728 (0.8%)
51	a	0.34	0/1034	1.01	10/1387 (0.7%)
52	3	0.41	0/36963	0.51	3/57662 (0.0%)
53	1	0.39	0/69796	0.51	4/108888 (0.0%)
54	2	0.40	0/2872	0.50	0/4479
55	5	0.40	0/1832	0.47	0/2855
55	6	0.41	0/1832	0.52	0/2855
56	4	0.43	0/436	0.50	0/679
All	All	0.37	0/161390	0.64	155/241259 (0.1%)

There are no bond length outliers.

The worst 5 of 155 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	I	9	LYS	N-CA-C	-11.47	97.78	112.23
6	g	67	ALA	N-CA-C	-11.06	98.30	112.23
37	M	67	GLY	N-CA-C	-10.62	101.31	114.16
34	J	161	GLU	N-CA-C	8.48	120.14	111.07
51	a	178	VAL	N-CA-C	8.25	118.34	110.42

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	b	2083	0	2157	35	0
2	c	1565	0	1616	16	0
3	d	1552	0	1619	24	0
4	e	1411	0	1447	29	0
5	f	1323	0	1374	25	0
6	g	1111	0	1148	48	0
7	h	989	0	1025	47	0
8	i	1032	0	1088	42	0
9	j	1129	0	1162	29	0
10	k	939	0	1012	20	0
11	l	1045	0	1117	16	0
12	m	1074	0	1157	12	0
13	n	961	0	1000	27	0
14	o	892	0	923	11	0
15	p	917	0	965	19	0
16	q	947	0	1022	15	0
17	r	816	0	839	26	0
18	s	857	0	922	25	0
19	t	739	0	807	23	0
20	u	780	0	834	21	0
21	v	753	0	780	13	0
22	w	575	0	592	5	0
23	x	625	0	655	8	0
24	y	509	0	543	19	0
25	z	449	0	491	10	0
26	B	444	0	461	6	0
27	C	410	0	440	8	0
28	D	377	0	418	11	0
29	E	504	0	574	9	0
30	F	302	0	343	12	0
31	G	1757	0	1787	29	0
32	H	1625	0	1699	44	0
33	I	1643	0	1710	52	0
34	J	1157	0	1199	35	0
35	K	818	0	808	39	0
36	L	1182	0	1240	26	0
37	M	979	0	1034	33	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	N	1022	0	1070	35	0
39	O	787	0	828	31	0
40	P	870	0	878	35	0
41	Q	955	0	1019	39	0
42	R	884	0	944	30	0
43	S	805	0	847	25	0
44	T	714	0	737	9	0
45	U	649	0	666	22	0
46	V	649	0	691	16	0
47	W	536	0	552	6	0
48	X	638	0	665	17	0
49	Y	665	0	714	25	0
50	Z	545	0	579	34	0
51	a	1027	0	1092	42	0
52	3	33012	0	16618	347	0
53	1	62317	0	31346	579	0
54	2	2568	0	1303	31	0
55	5	1640	0	836	8	0
55	6	1640	0	837	17	0
56	4	388	0	196	5	0
57	5	10	0	10	0	0
All	All	148592	0	100436	1975	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

The worst 5 of 1975 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:P:118:ASN:HD21	52:3:718:A:H5'	1.00	1.12
53:1:45:G:H5''	53:1:46:G:H5'	1.31	1.12
52:3:405:U:H3'	52:3:406:G:H5'	1.42	1.01
53:1:821:A:H5''	53:1:822:G:H5''	1.41	1.01
53:1:1906:G:H2'	53:1:1907:G:H5''	1.44	0.98

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	b	269/271 (99%)	239 (89%)	25 (9%)	5 (2%)	6	30
2	c	207/209 (99%)	194 (94%)	12 (6%)	1 (0%)	24	60
3	d	199/201 (99%)	184 (92%)	14 (7%)	1 (0%)	24	60
4	e	175/177 (99%)	151 (86%)	24 (14%)	0	100	100
5	f	174/176 (99%)	159 (91%)	13 (8%)	2 (1%)	11	43
6	g	147/149 (99%)	121 (82%)	21 (14%)	5 (3%)	3	17
7	h	129/131 (98%)	92 (71%)	30 (23%)	7 (5%)	1	9
8	i	139/141 (99%)	118 (85%)	16 (12%)	5 (4%)	2	16
9	j	140/142 (99%)	134 (96%)	5 (4%)	1 (1%)	18	53
10	k	120/122 (98%)	99 (82%)	17 (14%)	4 (3%)	3	17
11	l	141/143 (99%)	118 (84%)	18 (13%)	5 (4%)	3	16
12	m	134/136 (98%)	125 (93%)	6 (4%)	3 (2%)	5	26
13	n	118/120 (98%)	103 (87%)	14 (12%)	1 (1%)	16	50
14	o	114/116 (98%)	105 (92%)	8 (7%)	1 (1%)	14	48
15	p	112/114 (98%)	99 (88%)	13 (12%)	0	100	100
16	q	115/117 (98%)	111 (96%)	4 (4%)	0	100	100
17	r	101/103 (98%)	89 (88%)	9 (9%)	3 (3%)	3	19
18	s	108/110 (98%)	97 (90%)	9 (8%)	2 (2%)	6	30
19	t	91/93 (98%)	83 (91%)	7 (8%)	1 (1%)	11	43
20	u	100/102 (98%)	86 (86%)	12 (12%)	2 (2%)	6	28
21	v	92/94 (98%)	85 (92%)	6 (6%)	1 (1%)	11	43
22	w	73/75 (97%)	67 (92%)	6 (8%)	0	100	100
23	x	75/77 (97%)	68 (91%)	7 (9%)	0	100	100
24	y	61/63 (97%)	60 (98%)	1 (2%)	0	100	100
25	z	56/58 (97%)	50 (89%)	6 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	B	54/56 (96%)	50 (93%)	4 (7%)	0	100	100
27	C	48/50 (96%)	43 (90%)	4 (8%)	1 (2%)	5	27
28	D	44/46 (96%)	39 (89%)	5 (11%)	0	100	100
29	E	62/64 (97%)	55 (89%)	6 (10%)	1 (2%)	7	34
30	F	36/38 (95%)	30 (83%)	5 (14%)	1 (3%)	4	21
31	G	223/225 (99%)	208 (93%)	15 (7%)	0	100	100
32	H	204/206 (99%)	189 (93%)	13 (6%)	2 (1%)	12	45
33	I	203/205 (99%)	178 (88%)	23 (11%)	2 (1%)	12	45
34	J	155/157 (99%)	127 (82%)	20 (13%)	8 (5%)	1	9
35	K	98/100 (98%)	79 (81%)	13 (13%)	6 (6%)	1	7
36	L	149/151 (99%)	133 (89%)	16 (11%)	0	100	100
37	M	127/129 (98%)	116 (91%)	10 (8%)	1 (1%)	16	50
38	N	125/127 (98%)	101 (81%)	20 (16%)	4 (3%)	3	18
39	O	96/98 (98%)	75 (78%)	14 (15%)	7 (7%)	1	4
40	P	114/116 (98%)	96 (84%)	14 (12%)	4 (4%)	3	16
41	Q	121/123 (98%)	93 (77%)	22 (18%)	6 (5%)	1	10
42	R	112/114 (98%)	94 (84%)	12 (11%)	6 (5%)	1	9
43	S	98/100 (98%)	84 (86%)	12 (12%)	2 (2%)	6	28
44	T	86/88 (98%)	79 (92%)	6 (7%)	1 (1%)	10	40
45	U	80/82 (98%)	69 (86%)	9 (11%)	2 (2%)	4	23
46	V	78/80 (98%)	66 (85%)	10 (13%)	2 (3%)	4	23
47	W	63/65 (97%)	57 (90%)	5 (8%)	1 (2%)	7	34
48	X	77/79 (98%)	64 (83%)	9 (12%)	4 (5%)	1	9
49	Y	83/85 (98%)	78 (94%)	3 (4%)	2 (2%)	4	24
50	Z	63/65 (97%)	42 (67%)	15 (24%)	6 (10%)	0	2
51	a	130/223 (58%)	120 (92%)	7 (5%)	3 (2%)	5	25
All	All	5919/6112 (97%)	5202 (88%)	595 (10%)	122 (2%)	8	27

5 of 122 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	b	232	GLY
5	f	45	ALA

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Mol	Chain	Res	Type
7	h	81	LEU
7	h	108	VAL
7	h	118	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	
1	b	216/216 (100%)	216 (100%)	0	100	100
2	c	164/164 (100%)	164 (100%)	0	100	100
3	d	165/165 (100%)	165 (100%)	0	100	100
4	e	148/148 (100%)	148 (100%)	0	100	100
5	f	137/137 (100%)	137 (100%)	0	100	100
6	g	114/114 (100%)	113 (99%)	1 (1%)	70	85
7	h	100/100 (100%)	97 (97%)	3 (3%)	36	69
8	i	109/109 (100%)	109 (100%)	0	100	100
9	j	116/116 (100%)	116 (100%)	0	100	100
10	k	103/103 (100%)	101 (98%)	2 (2%)	50	76
11	l	102/102 (100%)	102 (100%)	0	100	100
12	m	109/109 (100%)	109 (100%)	0	100	100
13	n	100/100 (100%)	100 (100%)	0	100	100
14	o	86/86 (100%)	86 (100%)	0	100	100
15	p	99/99 (100%)	99 (100%)	0	100	100
16	q	89/89 (100%)	88 (99%)	1 (1%)	65	83
17	r	84/84 (100%)	83 (99%)	1 (1%)	63	82
18	s	93/93 (100%)	91 (98%)	2 (2%)	45	74
19	t	80/80 (100%)	79 (99%)	1 (1%)	61	81
20	u	83/83 (100%)	83 (100%)	0	100	100
21	v	78/78 (100%)	78 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	w	57/57 (100%)	56 (98%)	1 (2%)	51	77
23	x	67/67 (100%)	66 (98%)	1 (2%)	57	80
24	y	55/55 (100%)	55 (100%)	0	100	100
25	z	48/48 (100%)	48 (100%)	0	100	100
26	B	47/47 (100%)	47 (100%)	0	100	100
27	C	45/45 (100%)	45 (100%)	0	100	100
28	D	38/38 (100%)	37 (97%)	1 (3%)	40	72
29	E	51/51 (100%)	50 (98%)	1 (2%)	48	76
30	F	34/34 (100%)	34 (100%)	0	100	100
31	G	186/186 (100%)	186 (100%)	0	100	100
32	H	170/170 (100%)	166 (98%)	4 (2%)	43	73
33	I	172/172 (100%)	169 (98%)	3 (2%)	53	78
34	J	119/119 (100%)	117 (98%)	2 (2%)	53	78
35	K	87/87 (100%)	86 (99%)	1 (1%)	65	83
36	L	124/124 (100%)	123 (99%)	1 (1%)	73	86
37	M	104/104 (100%)	103 (99%)	1 (1%)	68	84
38	N	105/105 (100%)	103 (98%)	2 (2%)	50	76
39	O	86/86 (100%)	86 (100%)	0	100	100
40	P	89/89 (100%)	89 (100%)	0	100	100
41	Q	103/103 (100%)	103 (100%)	0	100	100
42	R	92/92 (100%)	91 (99%)	1 (1%)	65	83
43	S	83/83 (100%)	82 (99%)	1 (1%)	63	82
44	T	76/76 (100%)	76 (100%)	0	100	100
45	U	65/65 (100%)	64 (98%)	1 (2%)	57	80
46	V	74/74 (100%)	73 (99%)	1 (1%)	59	80
47	W	56/56 (100%)	56 (100%)	0	100	100
48	X	70/70 (100%)	69 (99%)	1 (1%)	59	80
49	Y	65/65 (100%)	65 (100%)	0	100	100
50	Z	55/55 (100%)	54 (98%)	1 (2%)	51	77
51	a	110/174 (63%)	108 (98%)	2 (2%)	51	77
All	All	4908/4972 (99%)	4871 (99%)	37 (1%)	70	86

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
38	N	60	LEU
51	a	53	ARG
42	R	64	VAL
46	V	59	GLU
23	x	33	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 104 such sidechains are listed below:

Mol	Chain	Res	Type
31	G	167	HIS
33	I	99	ASN
49	Y	2	ASN
31	G	177	ASN
32	H	31	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	1538/1539 (99%)	142 (9%)	2 (0%)
53	1	2902/2903 (99%)	322 (11%)	11 (0%)
54	2	119/120 (99%)	11 (9%)	1 (0%)
55	5	76/77 (98%)	7 (9%)	0
55	6	76/77 (98%)	16 (21%)	0
56	4	17/18 (94%)	2 (11%)	0
All	All	4728/4734 (99%)	500 (10%)	14 (0%)

5 of 500 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	3	6	G
52	3	9	G
52	3	22	G
52	3	31	G
52	3	32	A

5 of 14 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	1	1475	G

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Mol	Chain	Res	Type
53	1	2286	G
54	2	88	C
53	1	2391	G
53	1	2756	U

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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	$\# Z > 2$
57	FME	5	101	55	8,9,10	0.51	0	8,9,11	0.92	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
57	FME	5	101	55	-	1/7/9/11	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
57	5	101	FME	CB-CA-N-CN

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.

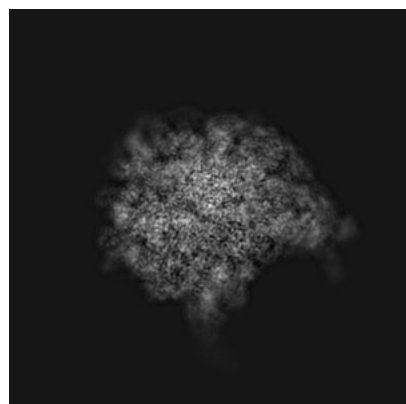
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21619. These allow visual inspection of the internal detail of the map and identification of artifacts.

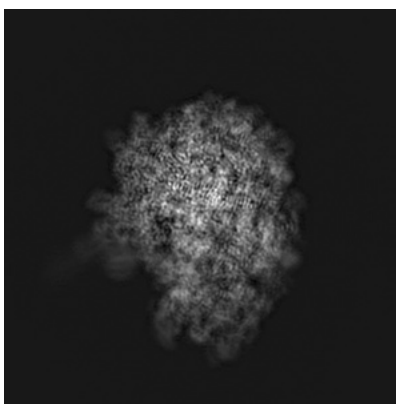
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

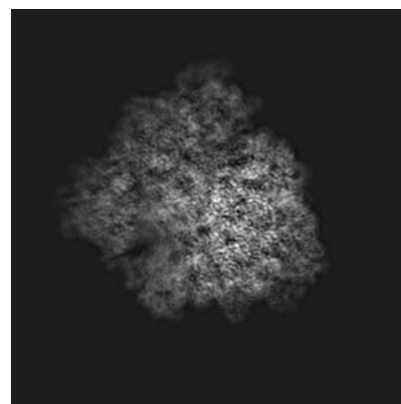
6.1.1 Primary map



X

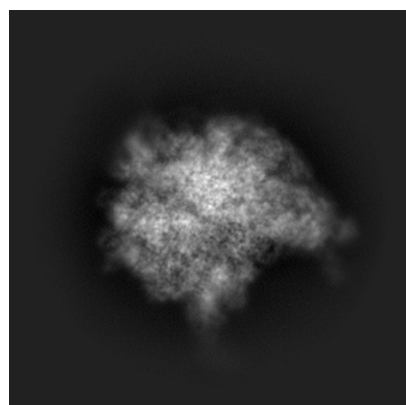


Y

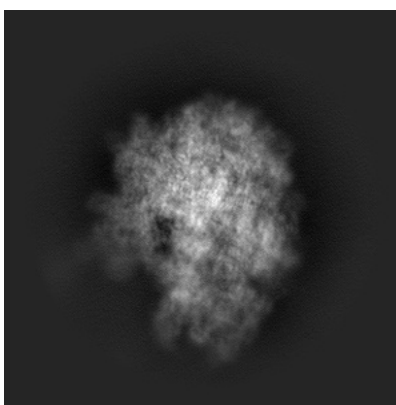


Z

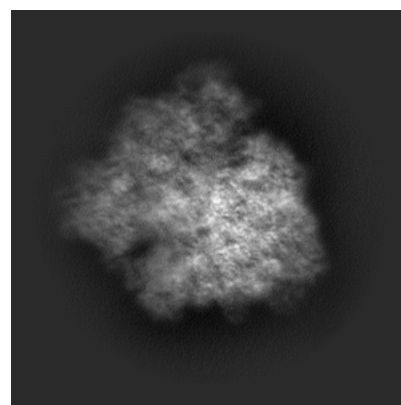
6.1.2 Raw map



X



Y

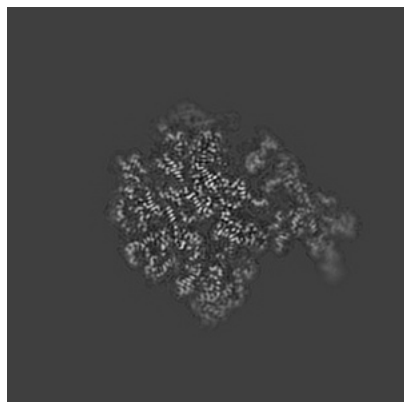


Z

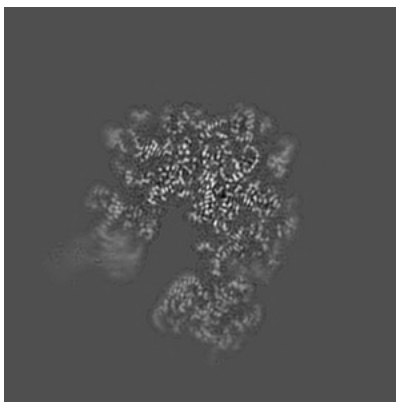
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

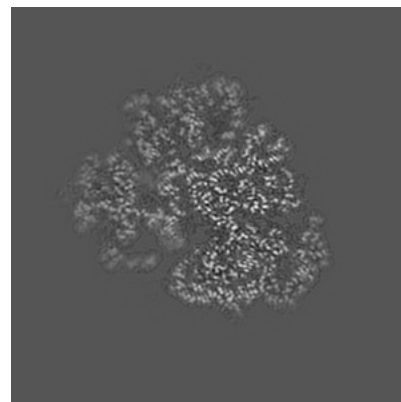
6.2.1 Primary map



X Index: 144

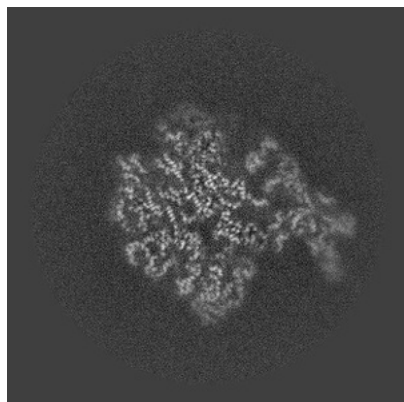


Y Index: 144

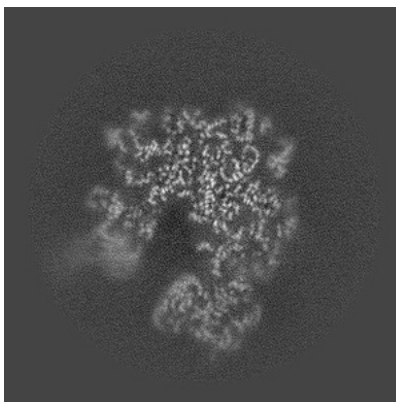


Z Index: 144

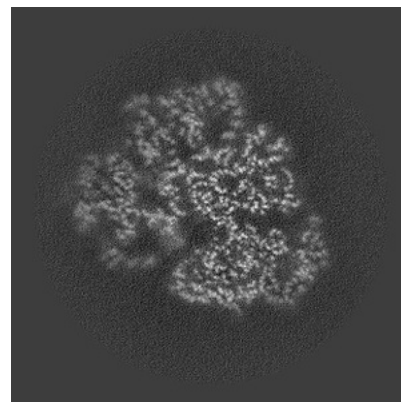
6.2.2 Raw map



X Index: 144



Y Index: 144

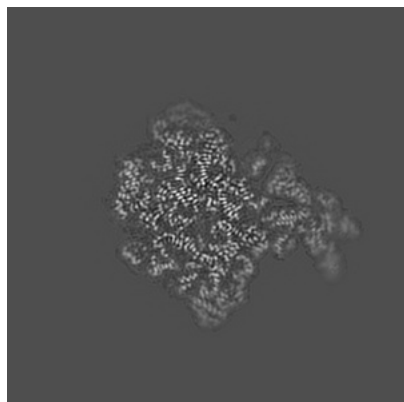


Z Index: 144

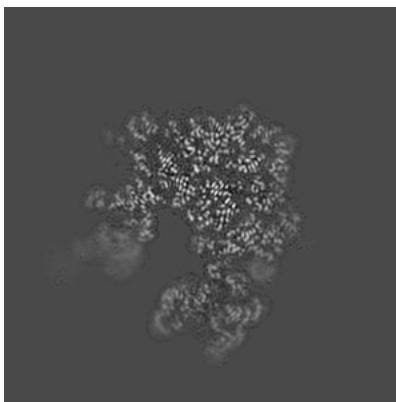
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

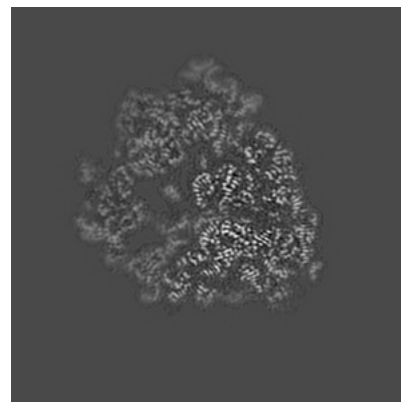
6.3.1 Primary map



X Index: 147

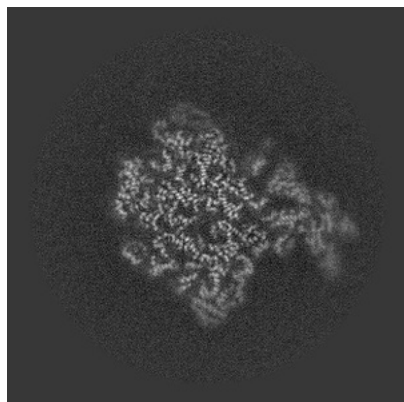


Y Index: 149

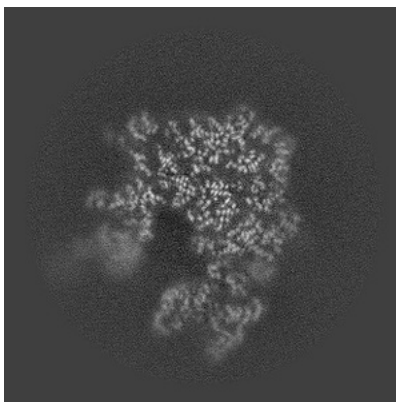


Z Index: 135

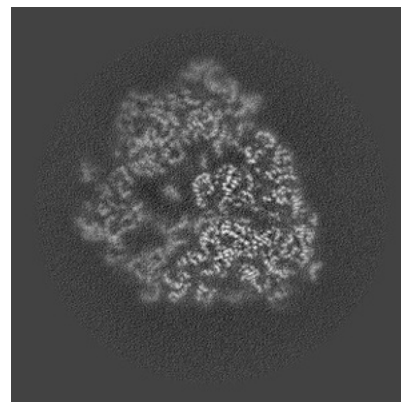
6.3.2 Raw map



X Index: 147



Y Index: 149

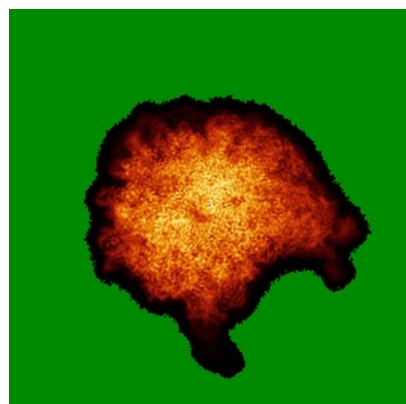


Z Index: 135

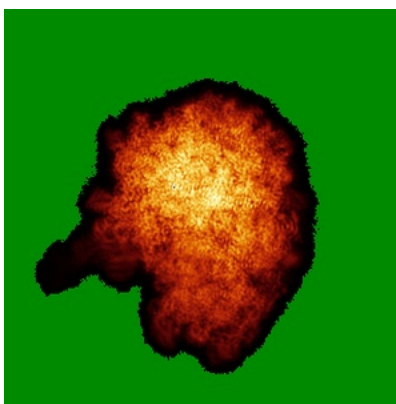
The images above show the largest variance slices of the map in three orthogonal directions.

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

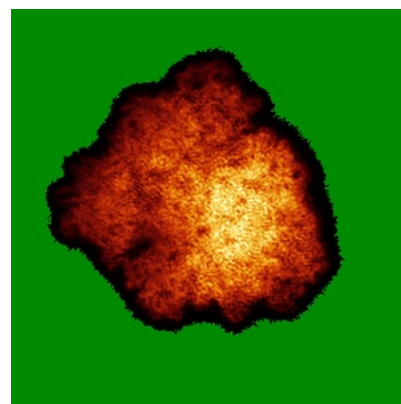
6.4.1 Primary map



X

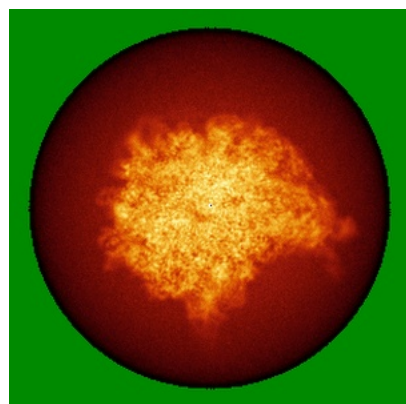


Y

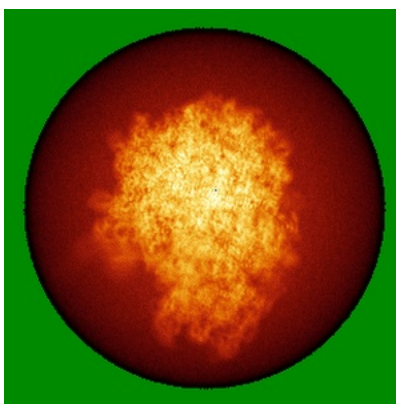


Z

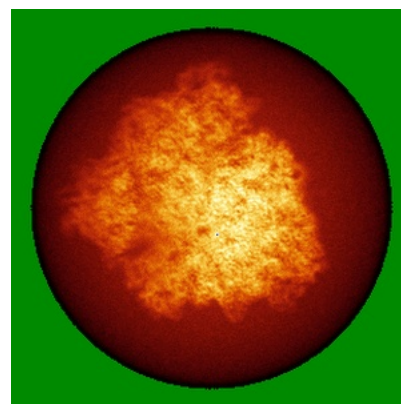
6.4.2 Raw map



X



Y

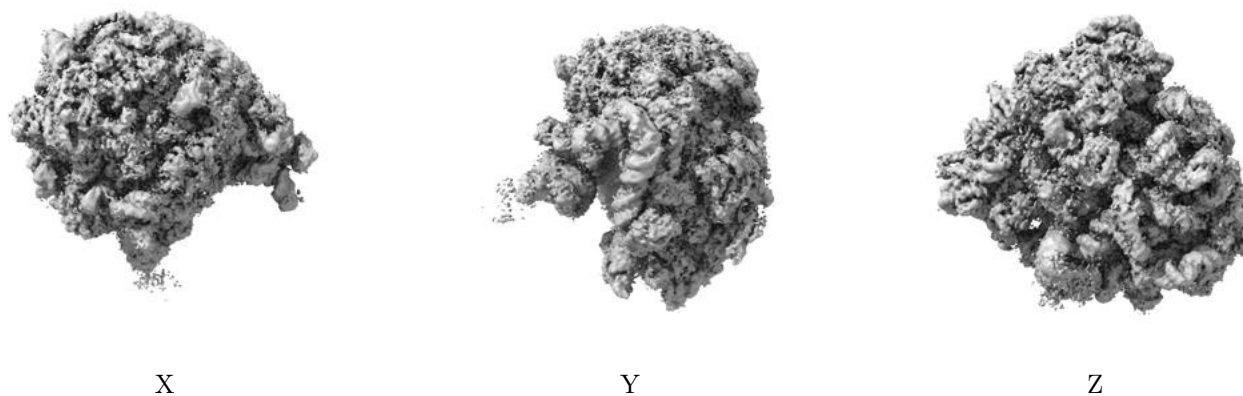


Z

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

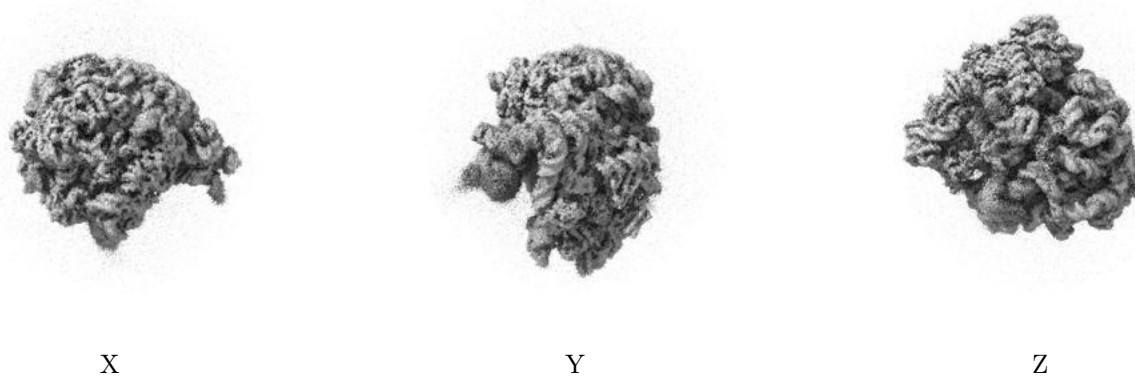
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

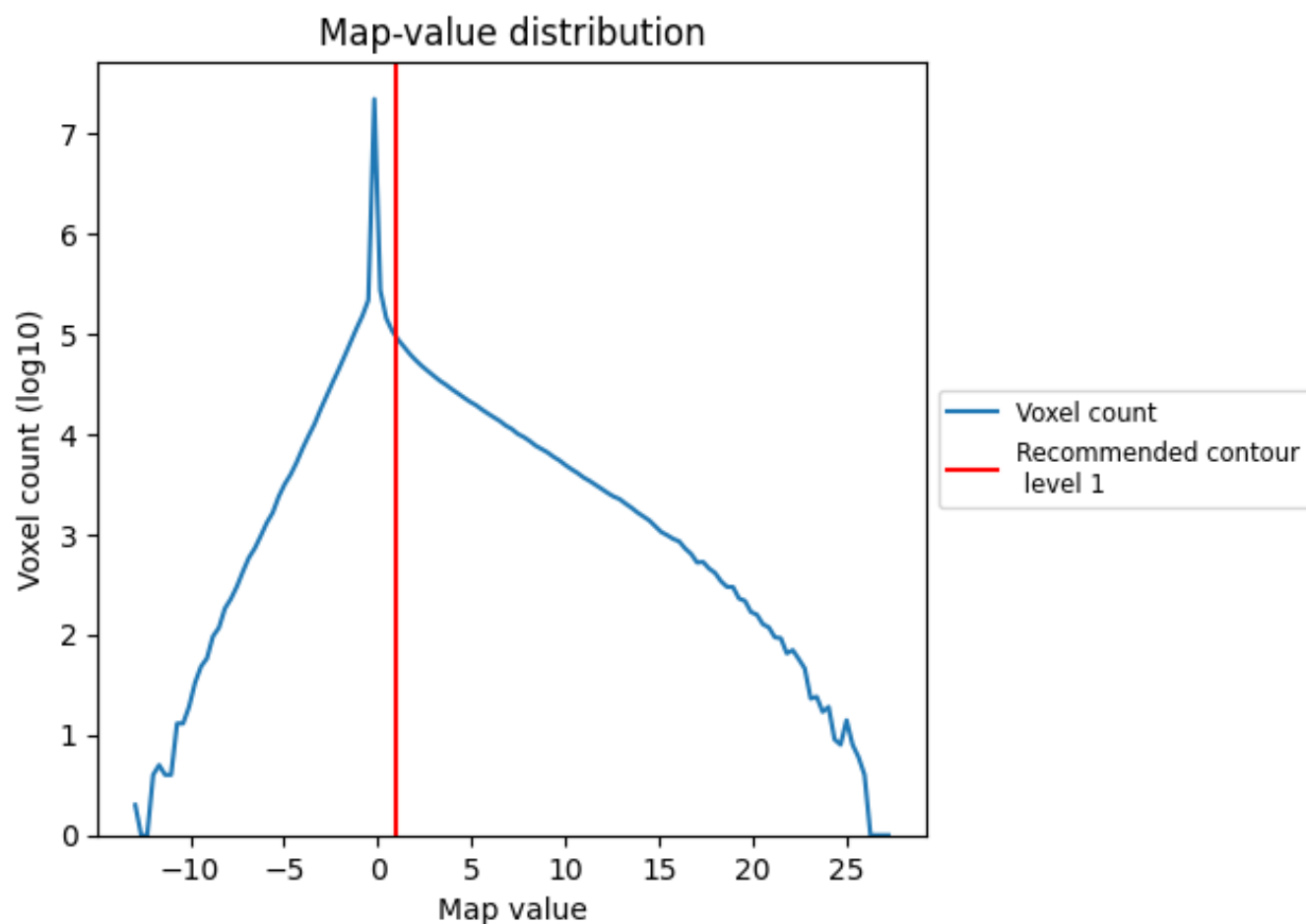
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

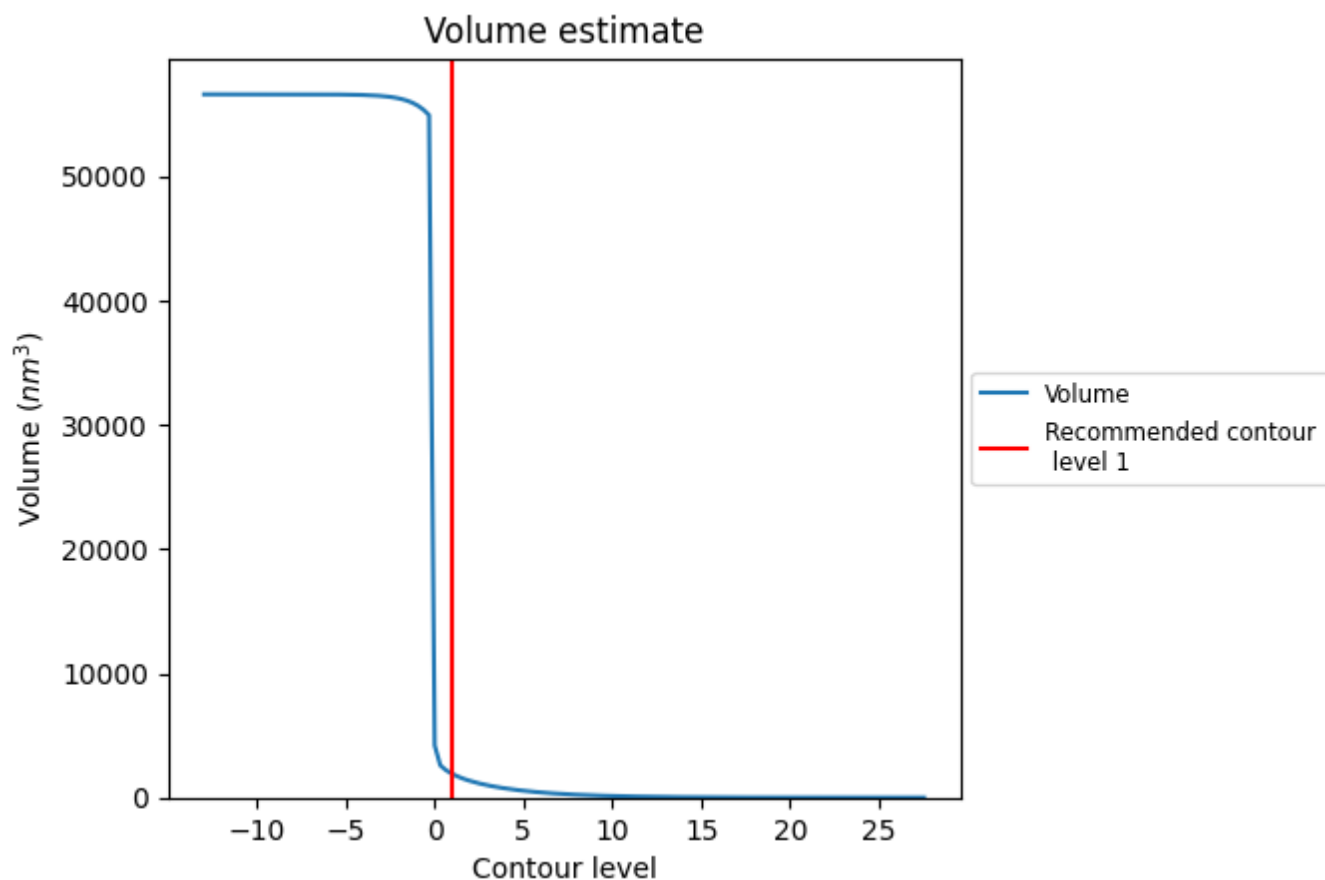
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

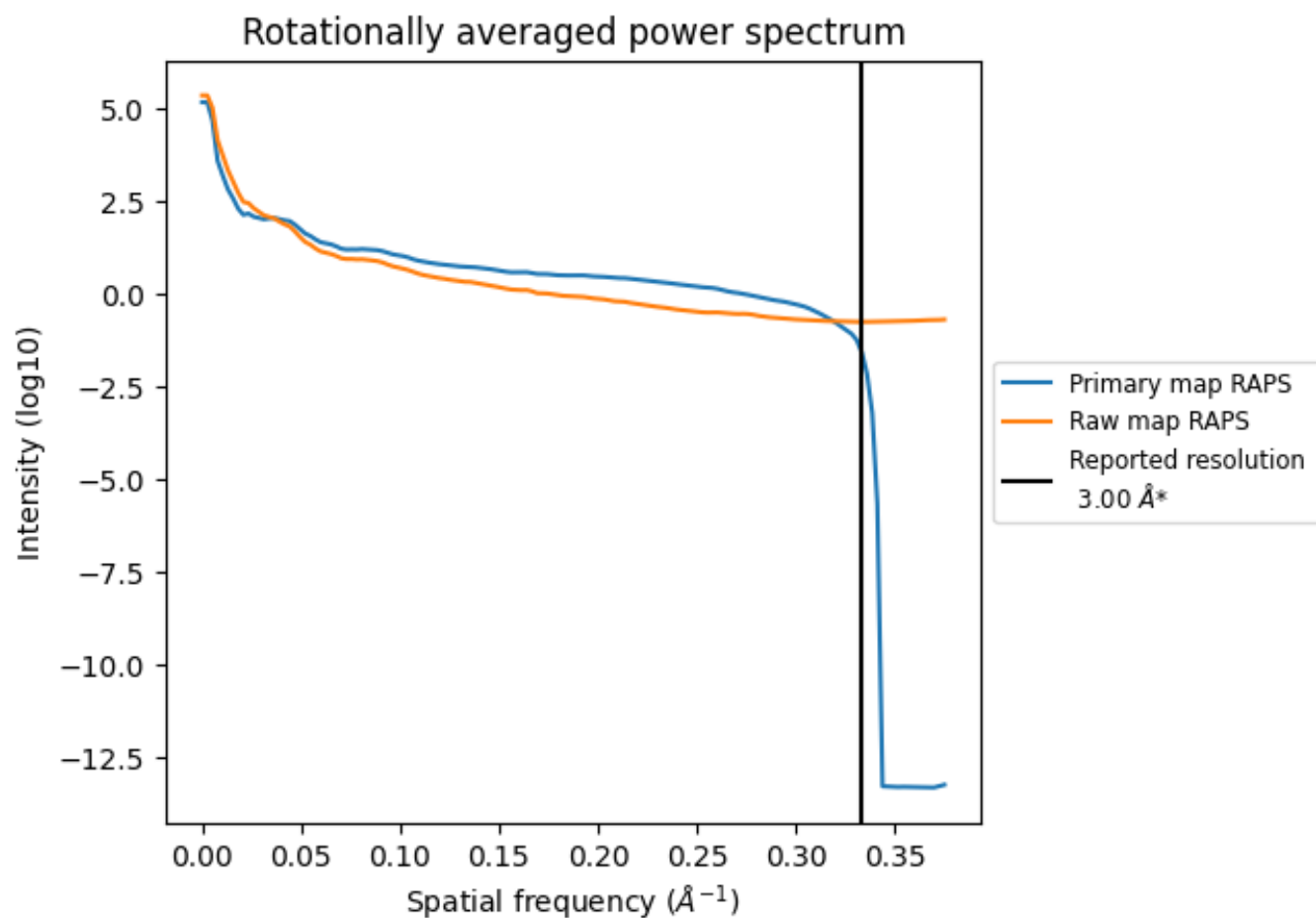
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1918 nm³; this corresponds to an approximate mass of 1732 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 ⓘ

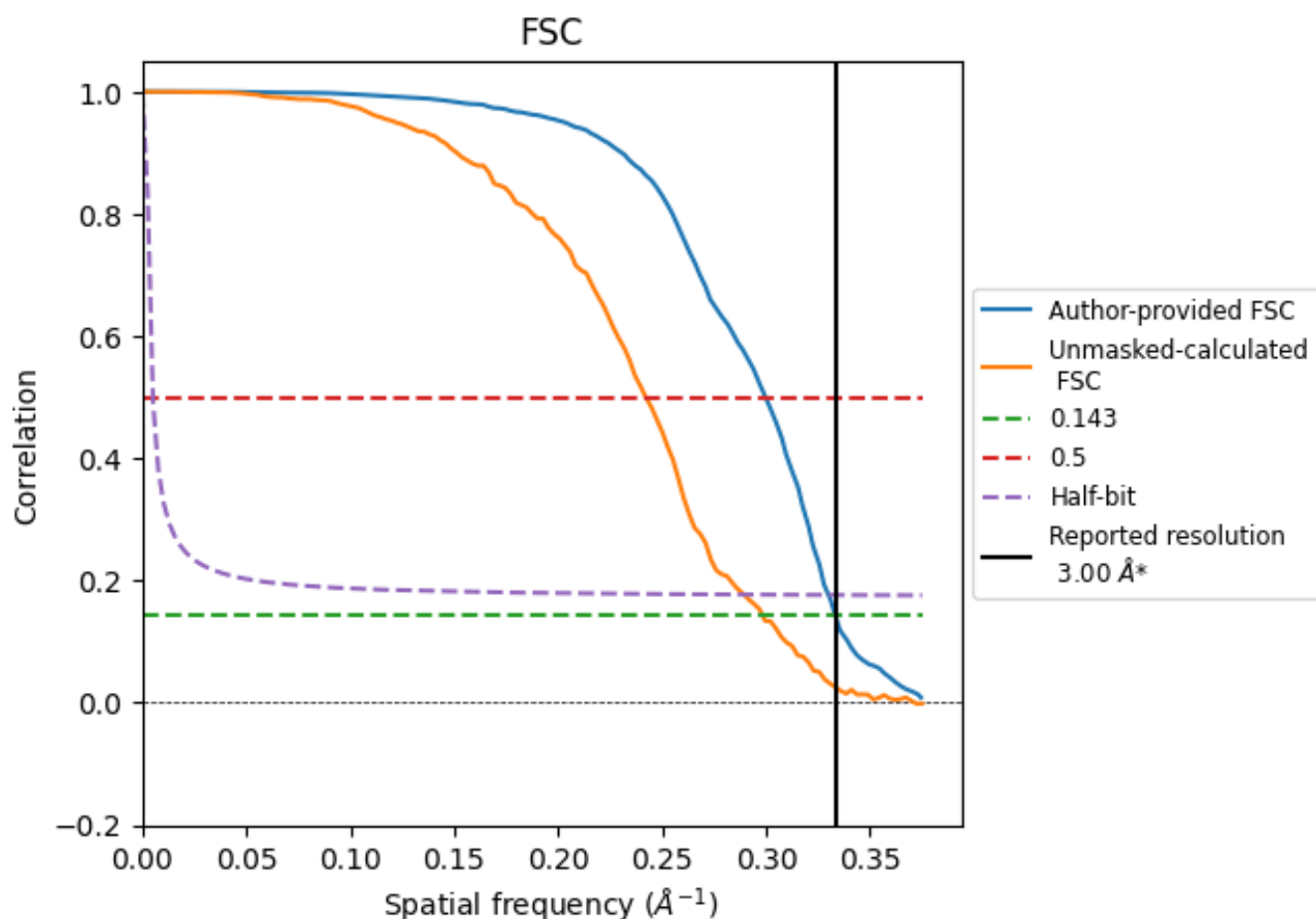


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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 0.333 Å⁻¹

8.2 Resolution estimates [i](#)

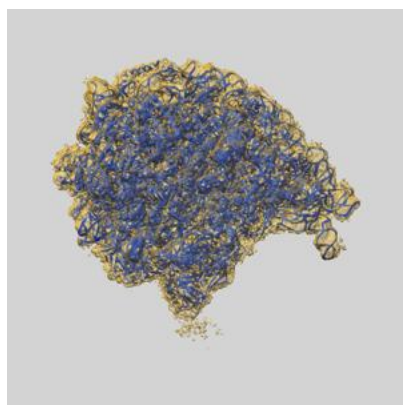
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.00	3.34	3.03
Unmasked-calculated*	3.35	4.13	3.46

*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 3.35 differs from the reported value 3.0 by more than 10 %

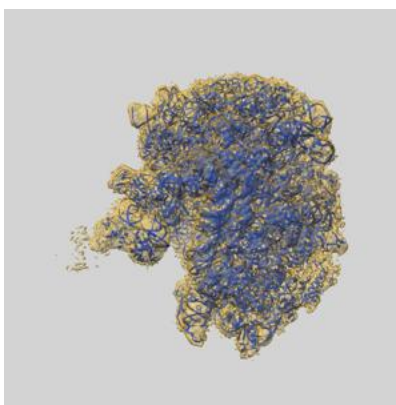
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21619 and PDB model 6WD0. Per-residue inclusion information can be found in section [3](#) on page [15](#).

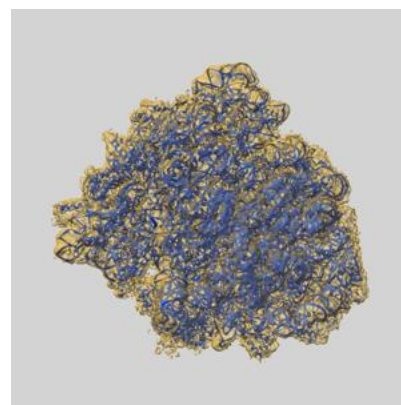
9.1 Map-model overlay [i](#)



X



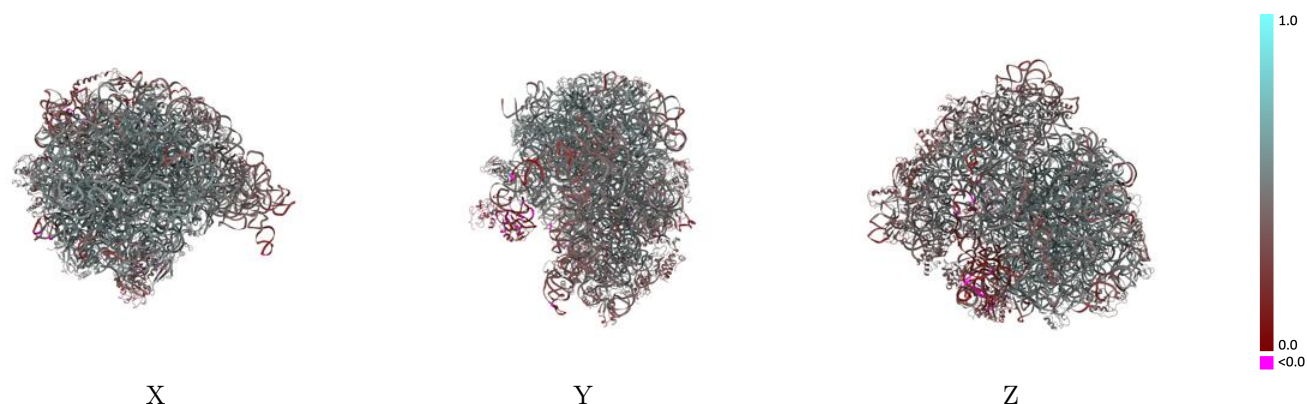
Y



Z

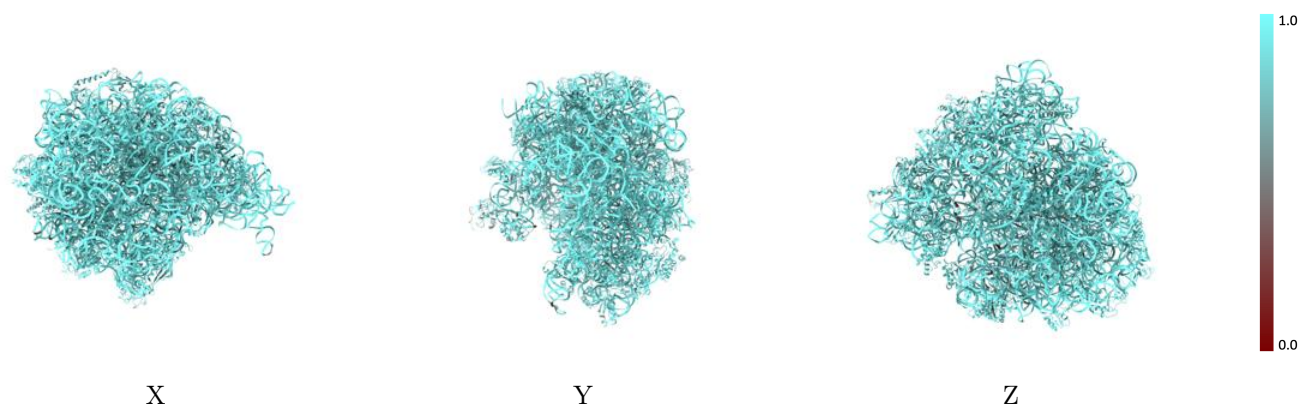
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



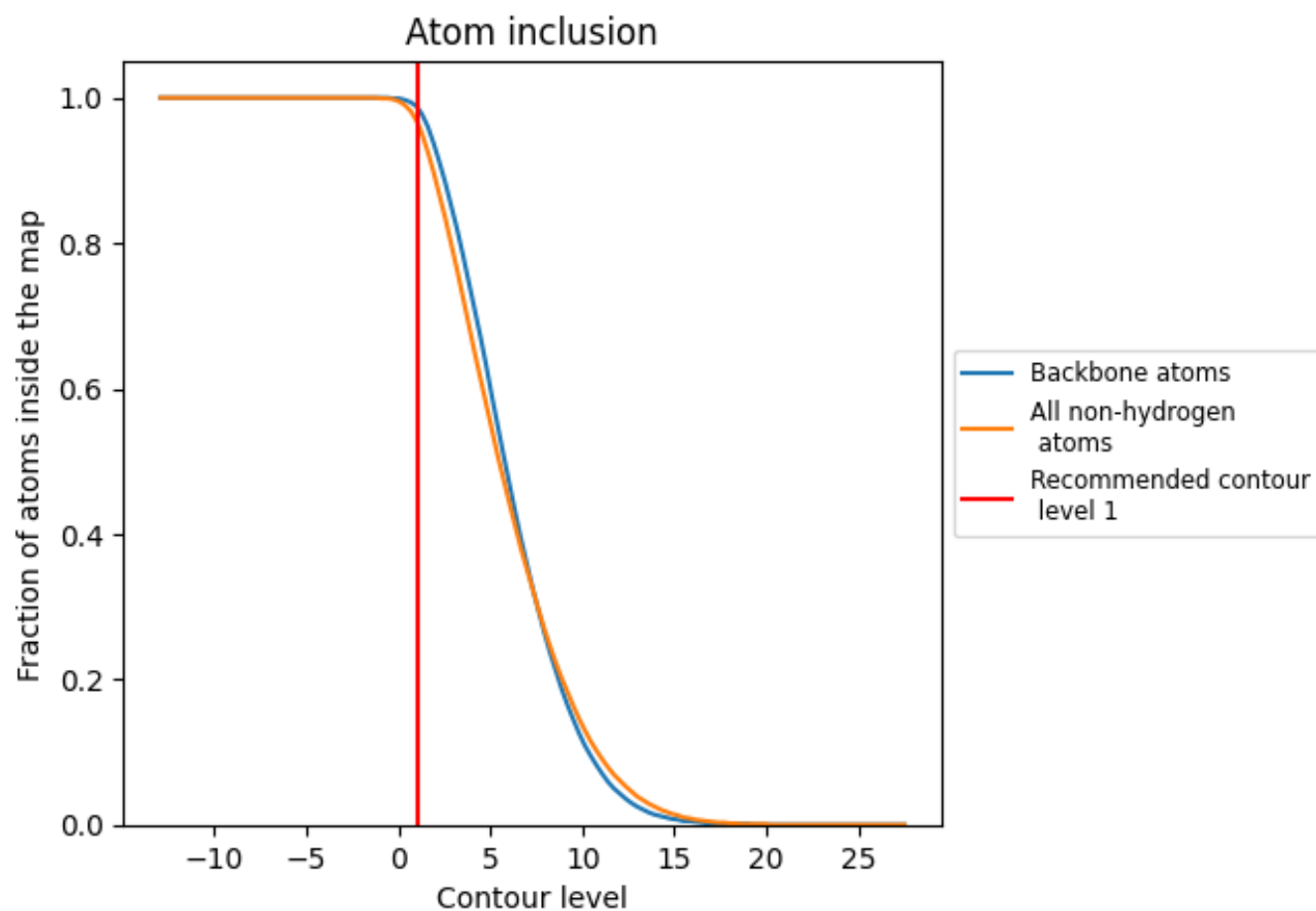
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% 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 (1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9680	 0.4600
1	 0.9890	 0.4910
2	 0.9900	 0.4520
3	 0.9850	 0.4450
4	 0.7760	 0.2400
5	 0.9810	 0.4280
6	 0.8370	 0.1630
B	 0.9560	 0.5200
C	 0.8860	 0.4770
D	 0.9610	 0.5500
E	 0.9840	 0.5510
F	 0.9140	 0.4900
G	 0.8900	 0.3890
H	 0.9130	 0.4320
I	 0.8730	 0.3930
J	 0.9330	 0.4700
K	 0.9520	 0.4190
L	 0.9400	 0.3980
M	 0.9170	 0.4680
N	 0.9330	 0.4050
O	 0.8390	 0.3810
P	 0.9630	 0.4570
Q	 0.9520	 0.4780
R	 0.9430	 0.3910
S	 0.9000	 0.4150
T	 0.9670	 0.4560
U	 0.9110	 0.4450
V	 0.9510	 0.4450
W	 0.9550	 0.4320
X	 0.9600	 0.4010
Y	 0.9120	 0.4150
Z	 0.8490	 0.3370
a	 0.8410	 0.2150
b	 0.9720	 0.5390
c	 0.9680	 0.5290



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Chain	Atom inclusion	Q-score
d	 0.9590	 0.4910
e	 0.9350	 0.3920
f	 0.9610	 0.4330
g	 0.8600	 0.3450
h	 0.7890	 0.1690
i	 0.8560	 0.1240
j	 0.9640	 0.5230
k	 0.9580	 0.5220
l	 0.9560	 0.5060
m	 0.9570	 0.5210
n	 0.9720	 0.5300
o	 0.9500	 0.4540
p	 0.9640	 0.5190
q	 0.9800	 0.5350
r	 0.9650	 0.4940
s	 0.9460	 0.5100
t	 0.9530	 0.4930
u	 0.9440	 0.4600
v	 0.9540	 0.4790
w	 0.9620	 0.5400
x	 0.9770	 0.5190
y	 0.9280	 0.4200
z	 0.9630	 0.5000