



wwPDB EM Validation Summary Report ⓘ

Nov 20, 2022 – 12:45 pm GMT

PDB ID : 6Q95
EMDB ID : EMD-4475
Title : Structure of tmRNA SmpB bound in A site of T. thermophilus 70S ribosome
Authors : Rae, C.D.
Deposited on : 2018-12-17
Resolution : 3.70 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:

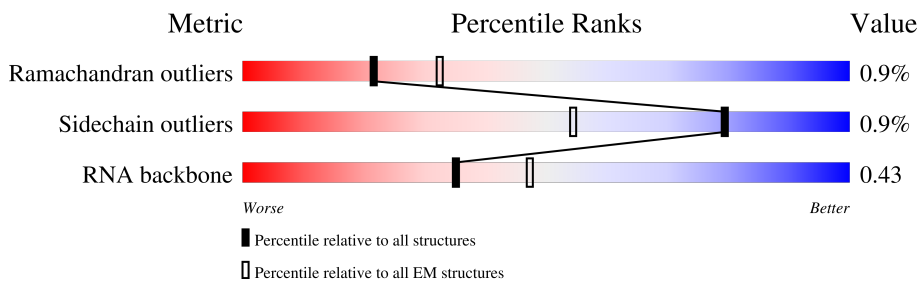
EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

1 Overall quality at a glance

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

The reported resolution of this entry is 3.70 Å.

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



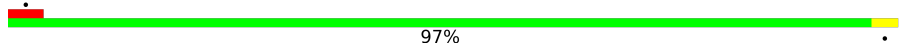
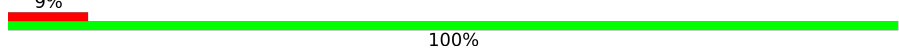
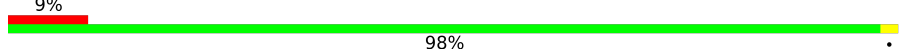
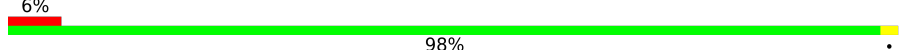

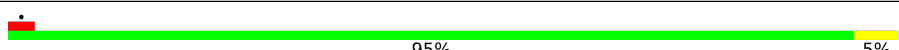
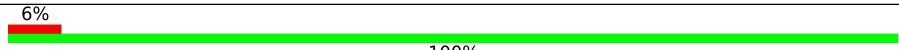
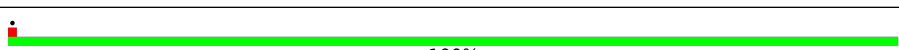
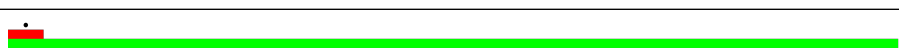
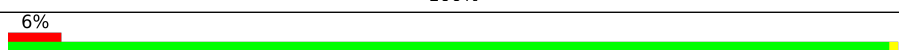
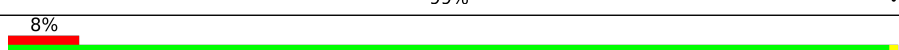
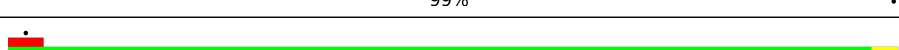
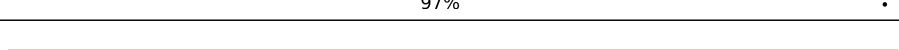
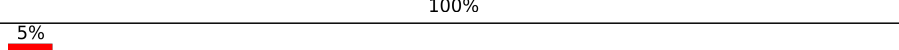
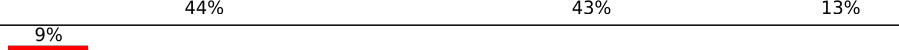
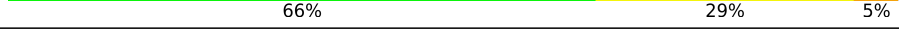

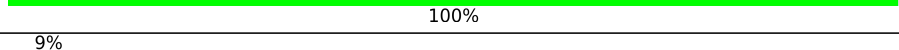
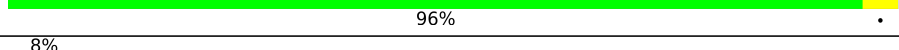
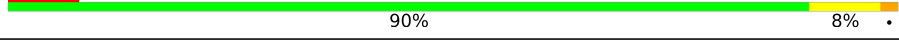
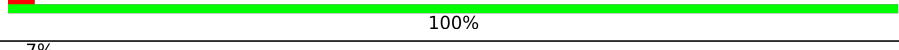
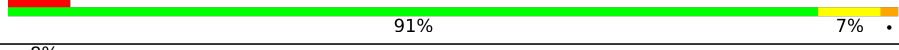
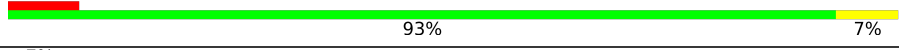

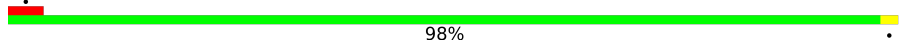
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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

Mol	Chain	Length	Quality of chain
1	2	1522	
2	g	235	
3	h	207	
4	i	208	
5	j	151	
6	k	101	
7	l	155	
8	m	138	




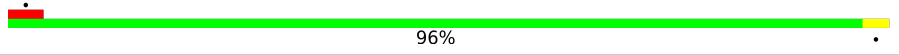
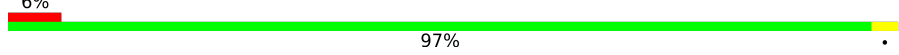
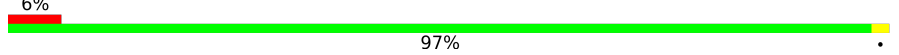
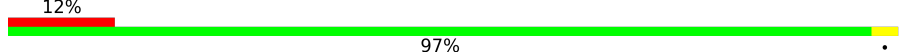
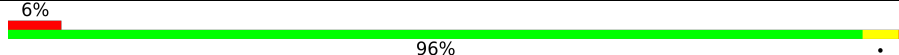
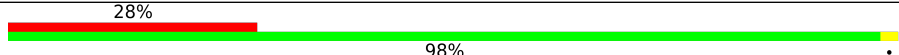
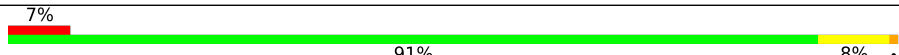
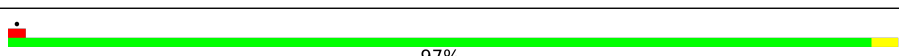

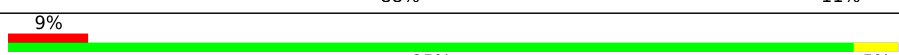
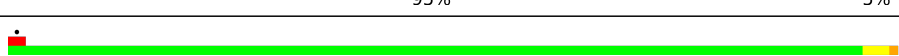
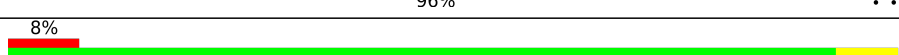
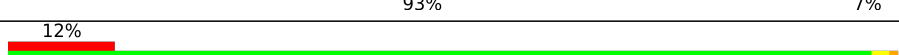
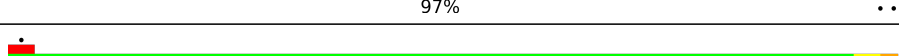
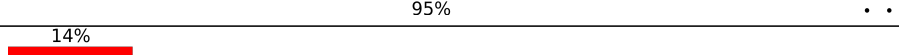
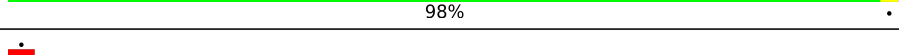
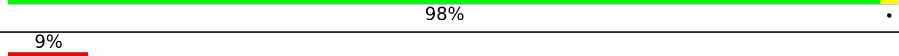
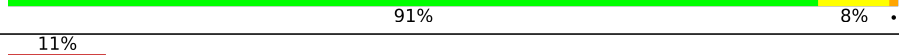
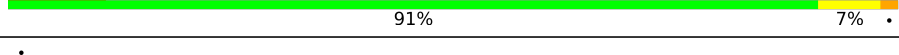
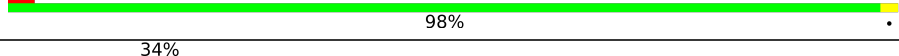
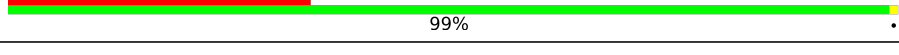
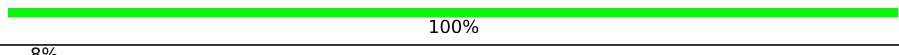
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Mol	Chain	Length	Quality of chain
9	n	127	 97%
10	o	99	 9% 100%
11	p	119	 9% 98%
12	q	125	 6% 98%
13	r	120	 8% 97%
14	s	60	 95% 5%
15	t	88	 6% 100%
16	u	84	 100%
17	v	100	 100%
18	w	70	 6% 99%
19	x	79	 8% 99%
20	y	99	 97%
21	z	25	 100%
22	7	77	 5% 44% 43% 13%
23	8	76	 9% 66% 29% 5%
24	9	6	 33% 17% 50%
25	W	85	 5% 100%
26	X	89	 9% 96%
27	Y	51	 8% 90% 8%
28	Z	60	 100%
29	a	58	 7% 91% 7%
30	b	59	 8% 93% 7%
31	c	45	 7% 84% 9%
32	d	49	 98%
33	e	64	 8% 97%

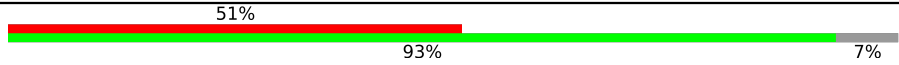
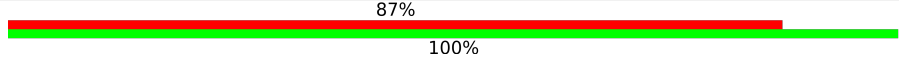
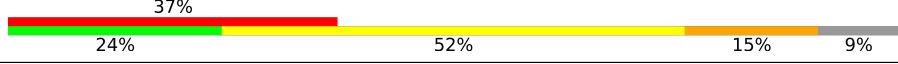
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Mol	Chain	Length	Quality of chain
34	1	2915	 51% 37% 10%
35	3	119	 55% 36% 8%
36	A	229	 53% 83% 17%
37	B	272	 96%
38	C	205	 6% 97%
39	D	208	 6% 97%
40	E	181	 12% 97%
41	F	160	 6% 96%
42	G	60	 28% 98%
43	J	139	 7% 91% 8%
44	K	122	 97%
45	L	146	 10% 88% 11%
46	M	136	 9% 95% 5%
47	N	117	 96%
48	O	99	 8% 93% 7%
49	P	138	 12% 97%
50	Q	117	 95%
51	R	101	 14% 98%
52	S	113	 98%
53	T	93	 9% 91% 8%
54	U	101	 11% 91% 7%
55	V	92	 98%
56	5	144	 34% 99%
57	6	2	 100%
58	f	37	 8% 100%

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Mol	Chain	Length	Quality of chain
59	H	140	
59	I	140	
60	4	349	

2 Entry composition [i](#)

There are 62 unique types of molecules in this entry. The entry contains 154751 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 16S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	2	1504	32329	14390	5992	10444	1503	0	0

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	g	235	1901	1213	342	341	5	0	1

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	h	207	1613	1016	315	281	1	0	1

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	i	208	1703	1066	339	291	7	0	0

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	j	151	1147	724	218	201	4	0	1

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	k	101	843	531	155	154	3	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	l	155	1257	781	252	218	6	0	0

- Molecule 8 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	m	138	1116	705	215	193	3	0	0

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
9	n	127	1011	639	198	174	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
n	58	ARG	HIS	conflict	UNP P80374

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	o	99	795	499	157	138	1	0	1

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	p	119	885	549	168	165	3	0	0

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	q	125	971	611	196	163	1	0	1

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	r	120	Total	C	N	O	S	0	0
			955	591	197	165	2		

- Molecule 14 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	s	60	Total	C	N	O	S	0	0
			492	312	104	72	4		

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	t	88	Total	C	N	O	S	0	0
			734	459	147	126	2		

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	u	84	Total	C	N	O	S	0	1
			701	443	140	117	1		

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	v	100	Total	C	N	O	S	0	1
			824	528	152	142	2		

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	w	70	Total	C	N	O	0	0
			574	367	112	95		

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	x	79	Total	C	N	O	S	0	1
			630	403	115	110	2		

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	y	99	763	470	162	129	2	0	0

- Molecule 21 is a protein called 30S ribosomal protein Thx.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
21	z	25	209	128	51	30	0	1

- Molecule 22 is a RNA chain called tRNA-fMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
22	7	77	1645	733	297	538	77	0	0

- Molecule 23 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
23	8	76	1616	720	281	539	76	0	0

- Molecule 24 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
24	9	6	125	56	19	44	6	0	0

- Molecule 25 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	W	85	650	401	137	111	1	0	0

- Molecule 26 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
26	X	89	693	435	140	118	0	1

- Molecule 27 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Y	51	Total	C	N	O	S	0	1
			421	263	85	72	1		

- Molecule 28 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Z	60	Total	C	N	O	S	0	1
			468	298	91	78	1		

- Molecule 29 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	a	58	Total	C	N	O	S	0	0
			464	295	81	84	4		

- Molecule 30 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	b	59	Total	C	N	O	S	0	0
			459	288	90	76	5		

- Molecule 31 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	c	45	Total	C	N	O	S	0	1
			381	235	78	64	4		

- Molecule 32 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	d	49	Total	C	N	O	S	0	1
			419	257	105	55	2		

- Molecule 33 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	e	64	Total	C	N	O	S	0	1
			508	326	102	78	2		

- Molecule 34 is a RNA chain called 23S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
34	1	2831	60977	27139	11405	19603	2830	0	0

- Molecule 35 is a RNA chain called 5S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
35	3	119	2551	1136	471	826	118	0	0

- Molecule 36 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
36	A	191	1142	691	221	230	0	1

- Molecule 37 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	B	272	2105	1329	417	356	3	0	1

- Molecule 38 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	C	205	1564	988	300	270	6	0	1

- Molecule 39 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	D	208	1624	1035	304	282	3	0	1

- Molecule 40 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	E	181	1474	942	268	260	4	0	0

- Molecule 41 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	F	160	Total	C	N	O	S	0	1
			1223	773	229	220	1		

- Molecule 42 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	G	60	Total	C	N	O	S	0	1
			454	289	84	80	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	146	ALA	GLU	conflict	UNP Q5SLQ1

- Molecule 43 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	J	139	Total	C	N	O	S	0	1
			1105	712	207	182	4		

- Molecule 44 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	K	122	Total	C	N	O	S	0	0
			933	588	171	170	4		

- Molecule 45 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	L	146	Total	C	N	O	S	0	0
			1114	692	227	193	2		

- Molecule 46 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	M	136	Total	C	N	O	S	0	0
			1080	688	204	183	5		

- Molecule 47 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	N	117	Total	C	N	O	0	0
			960	599	202	159		

- Molecule 48 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	O	99	Total	C	N	O	0	1
			771	486	155	130		

- Molecule 49 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	P	138	Total	C	N	O	S	0	1
			1142	710	235	196	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Q	117	Total	C	N	O	S	0	0
			958	604	202	151	1		

- Molecule 51 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	R	101	Total	C	N	O	S	0	0
			779	501	142	135	1		

- Molecule 52 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	S	113	Total	C	N	O	S	0	0
			896	563	176	155	2		

- Molecule 53 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	T	93	Total	C	N	O	0	1
			726	471	132	123		

- Molecule 54 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	U	101	Total	C	N	O	S	0	1
			776	500	149	123	4		

- Molecule 55 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	V	92	Total	C	N	O	S	0	1
			766	488	148	129	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
V	179	ASP	GLU	conflict	UNP Q5SHZ1

- Molecule 56 is a protein called SsrA-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	5	144	Total	C	N	O	S	0	0
			1184	754	219	210	1		

- Molecule 57 is a protein called Nascent peptide MET-ALA.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	6	2	Total	C	N	O	S	0	0
			13	8	2	2	1		

- Molecule 58 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	f	37	Total	C	N	O	S	0	0
			307	188	68	47	4		

- Molecule 59 is a protein called 50S RIBOSOMAL PROTEIN L10 AND L11.

Mol	Chain	Residues	Atoms				AltConf	Trace
59	H	130	Total	C	N	O	0	0
			650	390	130	130		
59	I	140	Total	C	N	O	0	0
			701	420	140	141		

- Molecule 60 is a RNA chain called transfer-messenger RNA (tmRNA).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
60	4	319	6834	3040	1259	2216	319	0	0

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

Mol	Chain	Residues	Atoms		AltConf
61	2	189	Total	Mg	0
			189	189	
61	k	1	Total	Mg	0
			1	1	
61	l	2	Total	Mg	0
			2	2	
61	m	1	Total	Mg	0
			1	1	
61	q	1	Total	Mg	0
			1	1	
61	r	1	Total	Mg	0
			1	1	
61	7	4	Total	Mg	0
			4	4	
61	8	12	Total	Mg	0
			12	12	
61	9	3	Total	Mg	0
			3	3	
61	b	3	Total	Mg	0
			3	3	
61	1	397	Total	Mg	0
			397	397	
61	3	13	Total	Mg	0
			13	13	
61	C	1	Total	Mg	0
			1	1	
61	D	1	Total	Mg	0
			1	1	
61	J	2	Total	Mg	0
			2	2	
61	K	1	Total	Mg	0
			1	1	
61	L	2	Total	Mg	0
			2	2	
61	N	1	Total	Mg	0
			1	1	
61	O	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
61	5	1	Total 1	Mg 1	0

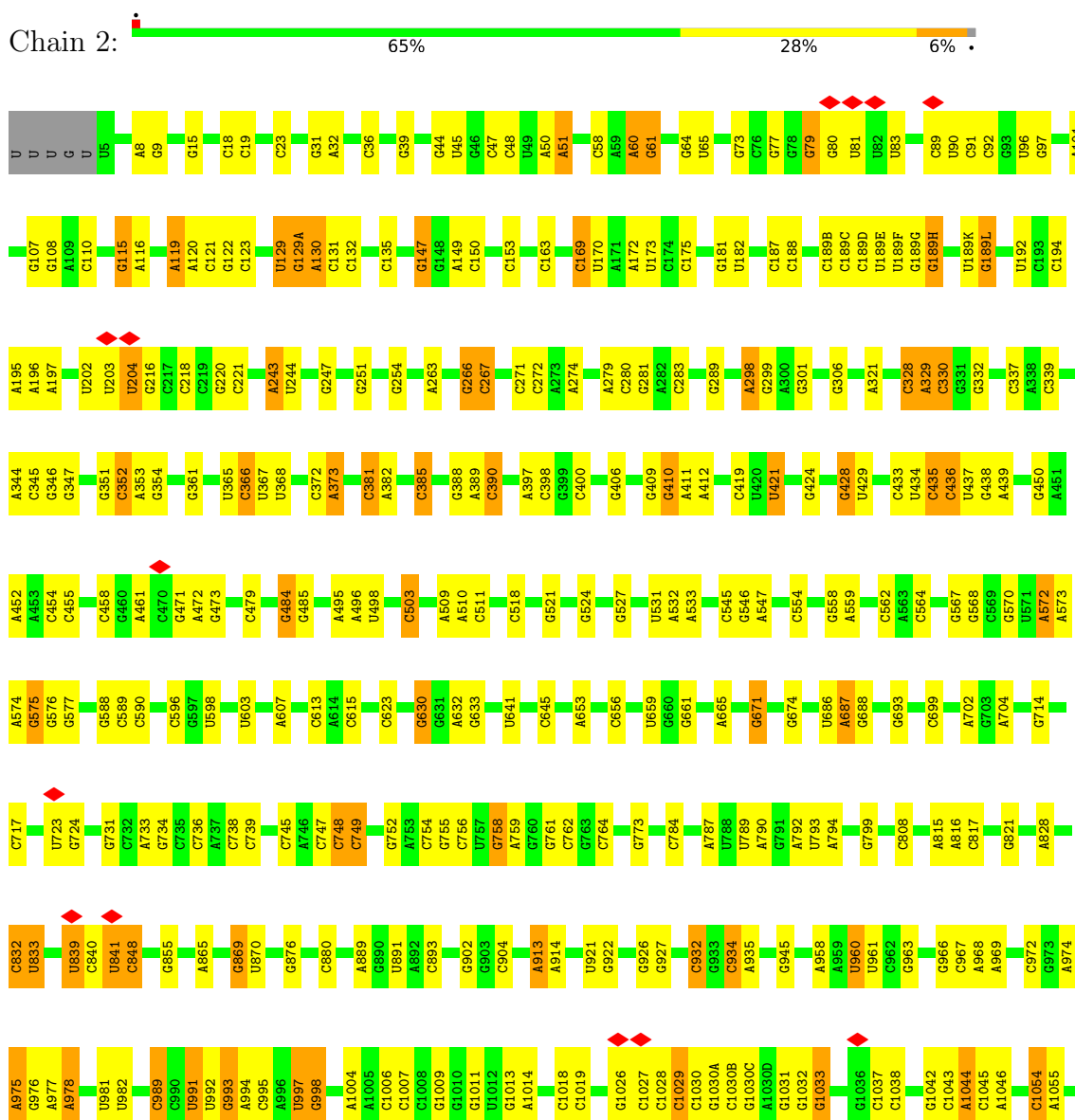
- Molecule 62 is ZINC ION (three-letter code: ZN) (formula: Zn).

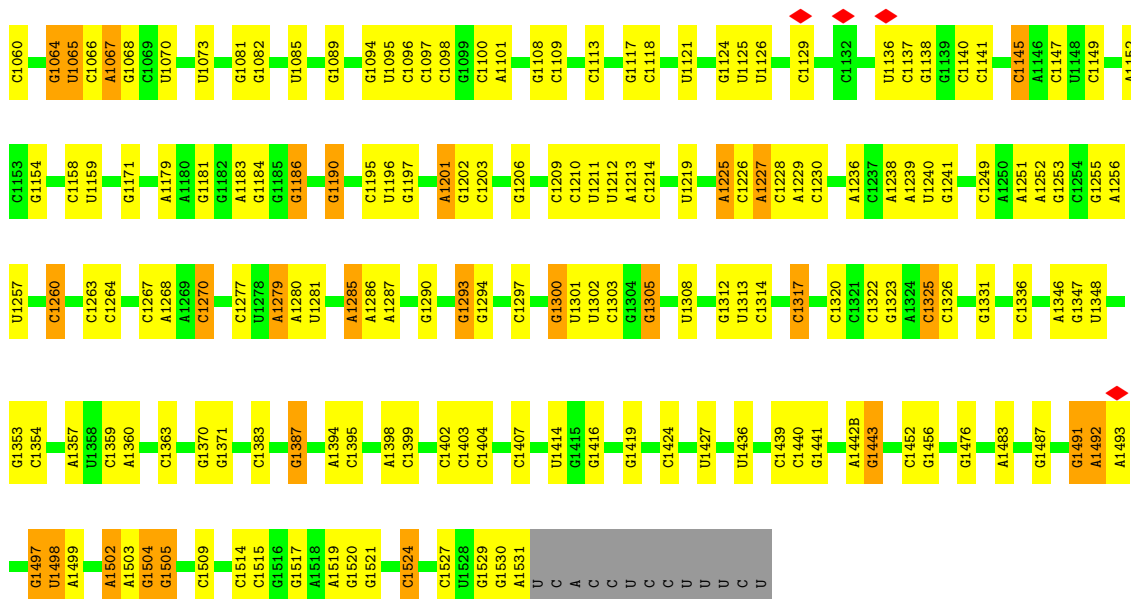
Mol	Chain	Residues	Atoms		AltConf
62	i	1	Total 1	Zn 1	0
62	s	1	Total 1	Zn 1	0
62	f	1	Total 1	Zn 1	0

3 Residue-property plots i

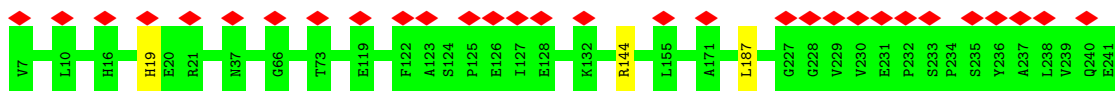
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 16S RIBOSOMAL RNA

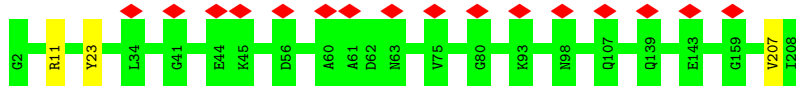




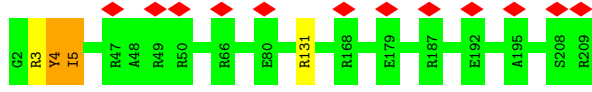
• Molecule 2: 30S ribosomal protein S2



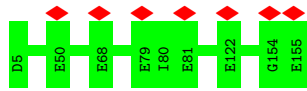
• Molecule 3: 30S ribosomal protein S3



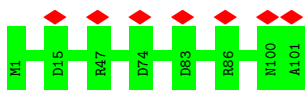
• Molecule 4: 30S ribosomal protein S4



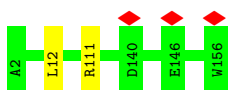
• Molecule 5: 30S ribosomal protein S5



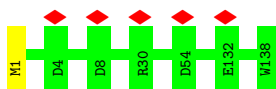
• Molecule 6: 30S ribosomal protein S6



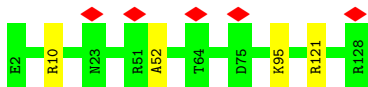
- Molecule 7: 30S ribosomal protein S7



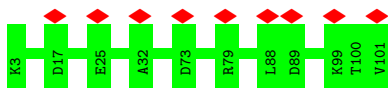
- Molecule 8: 30S ribosomal protein S8



- Molecule 9: 30S ribosomal protein S9



- Molecule 10: 30S ribosomal protein S10

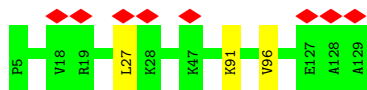


- Molecule 11: 30S ribosomal protein S11

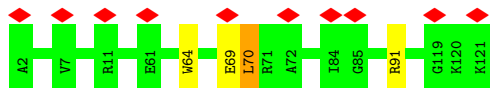


- Molecule 12: 30S ribosomal protein S12

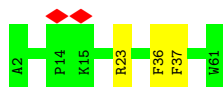




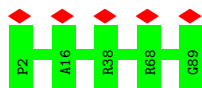
- Molecule 13: 30S ribosomal protein S13



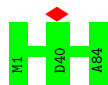
- Molecule 14: 30S ribosomal protein S14 type Z



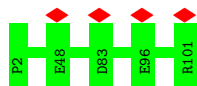
- Molecule 15: 30S ribosomal protein S15



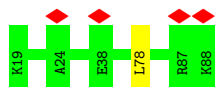
- Molecule 16: 30S ribosomal protein S16



- Molecule 17: 30S ribosomal protein S17



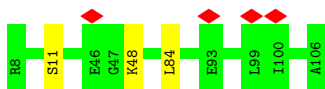
- Molecule 18: 30S ribosomal protein S18



- Molecule 19: 30S ribosomal protein S19



- Molecule 20: 30S ribosomal protein S20

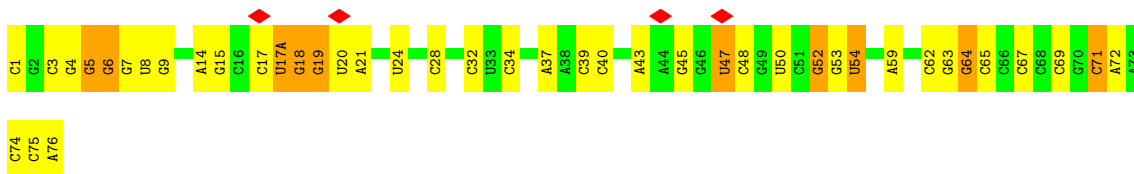
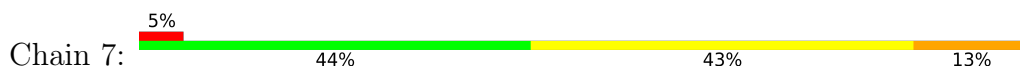


- Molecule 21: 30S ribosomal protein Thx



There are no outlier residues recorded for this chain.

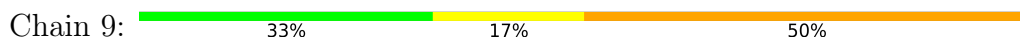
- Molecule 22: tRNA-fMet



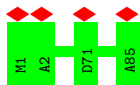
- Molecule 23: tRNA-Phe



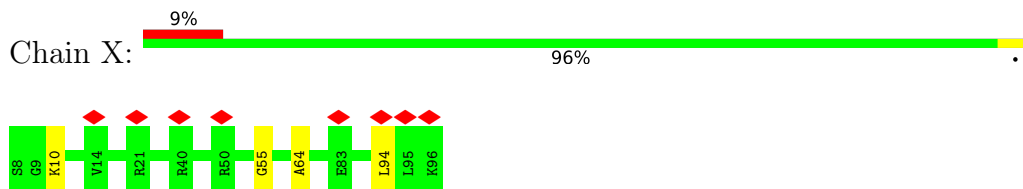
- Molecule 24: mRNA



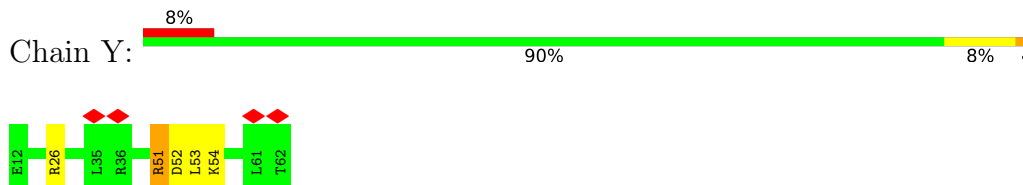
- Molecule 25: 50S ribosomal protein L27



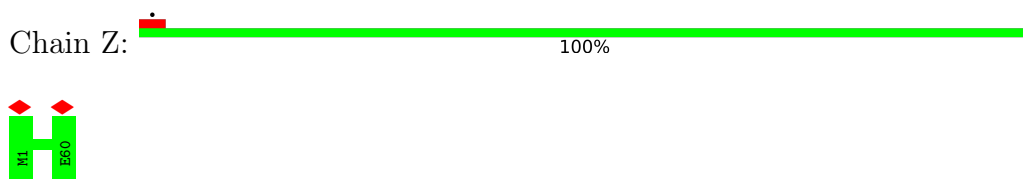
- Molecule 26: 50S ribosomal protein L28



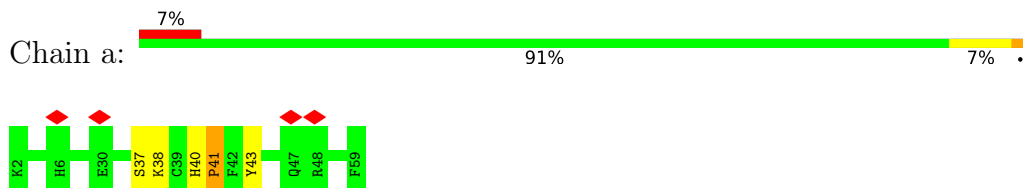
- Molecule 27: 50S ribosomal protein L29



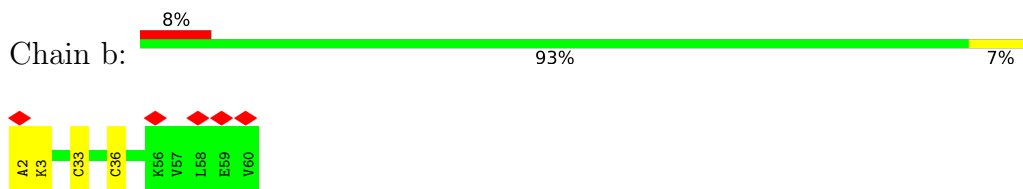
- Molecule 28: 50S ribosomal protein L30



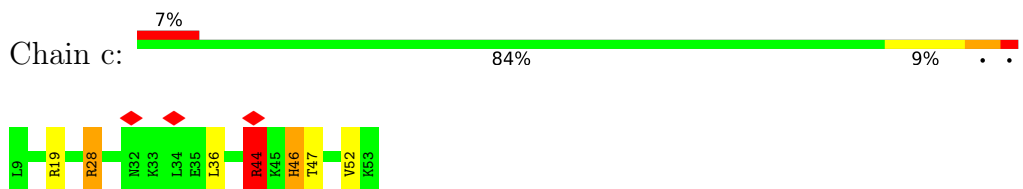
- Molecule 29: 50S ribosomal protein L31



- Molecule 30: 50S ribosomal protein L32

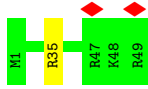


- Molecule 31: 50S ribosomal protein L33

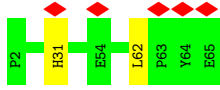


- Molecule 32: 50S ribosomal protein L34

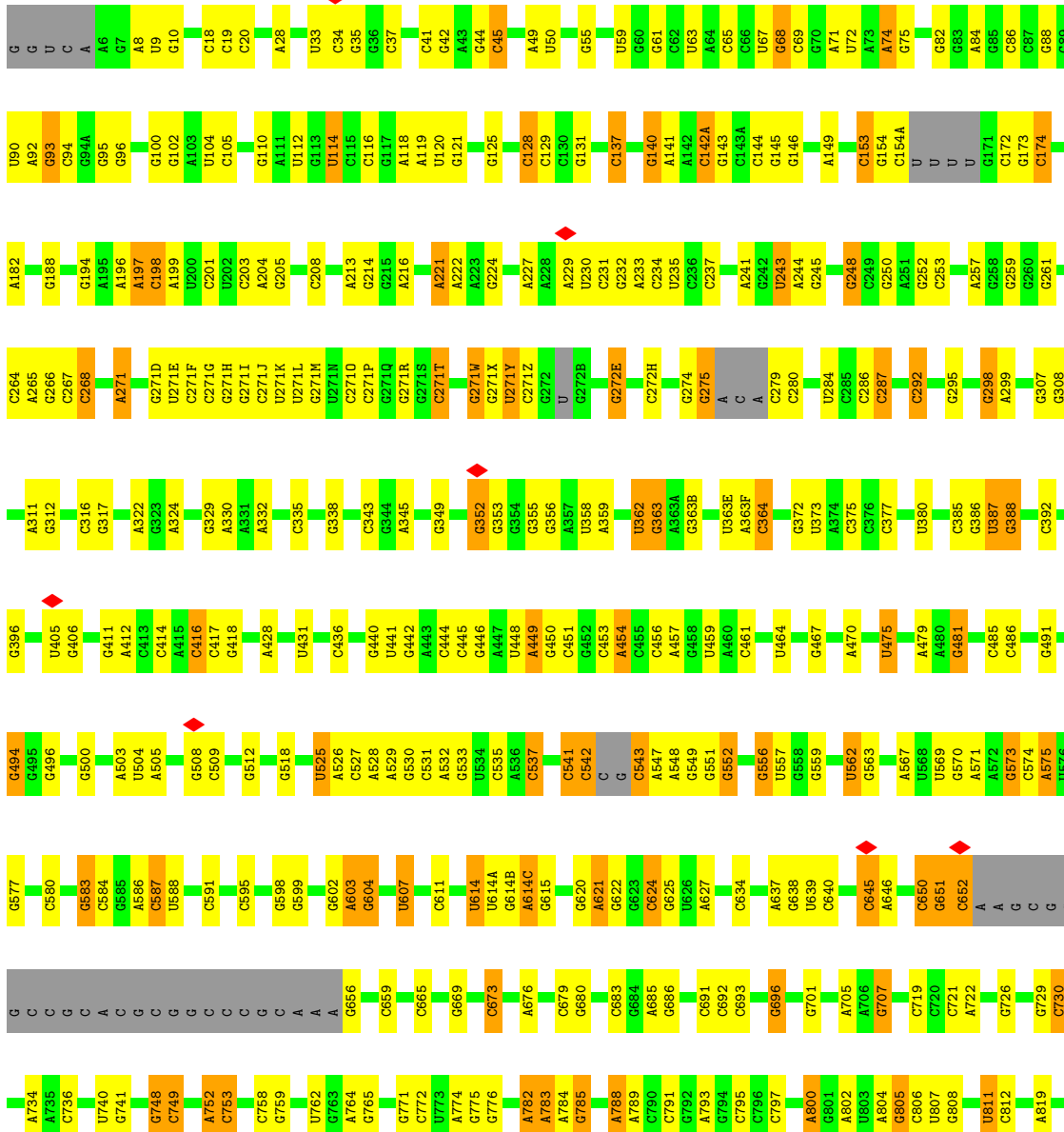


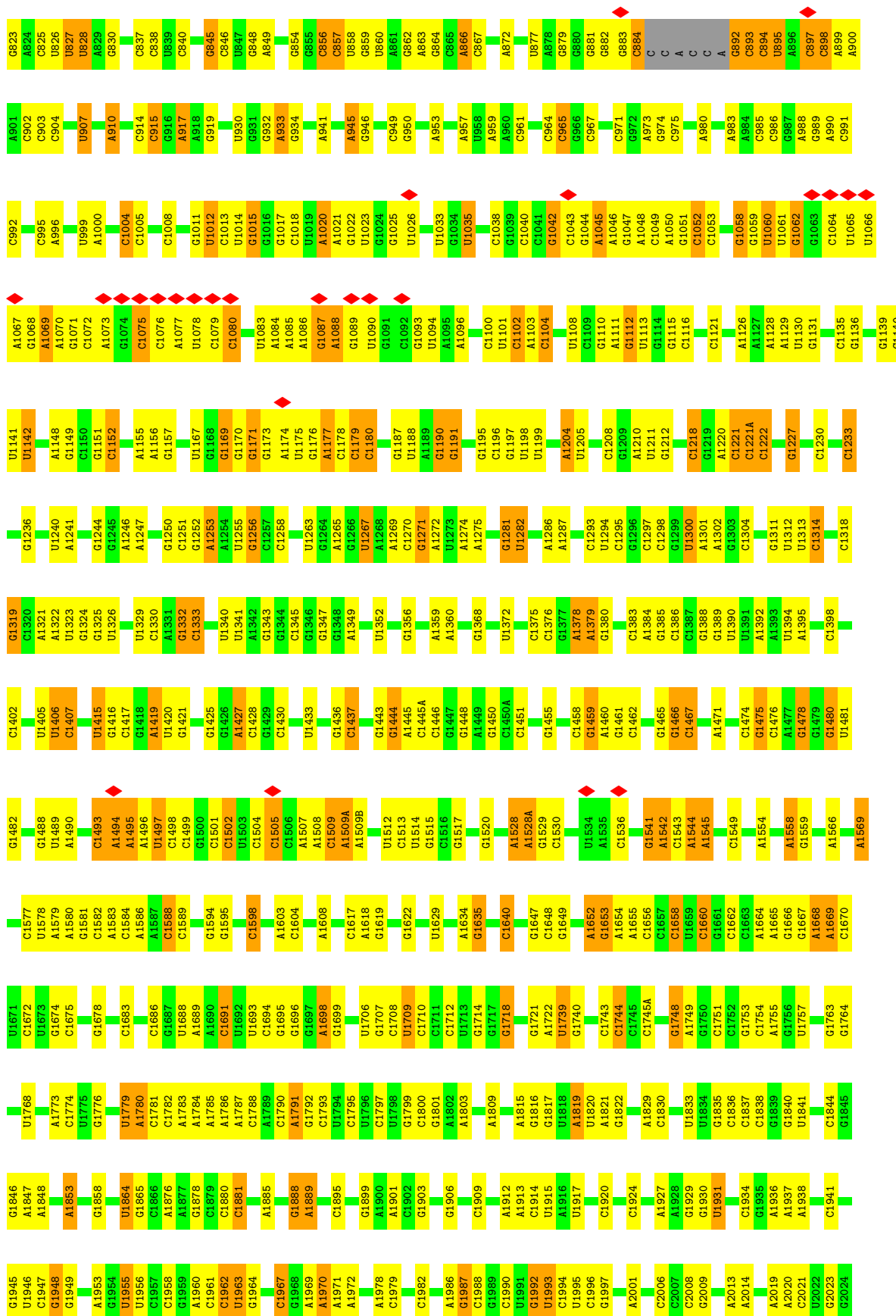


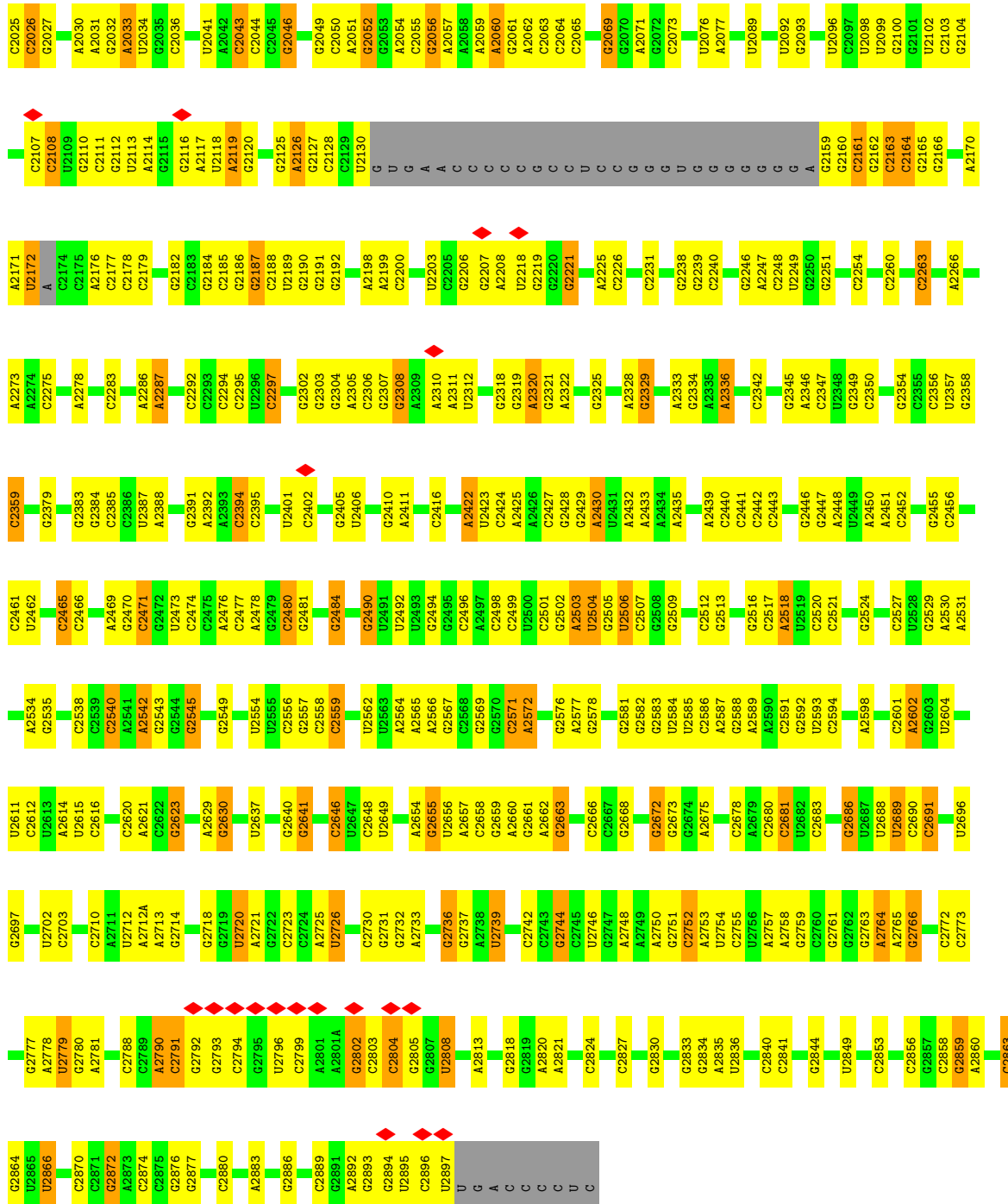
- Molecule 33: 50S ribosomal protein L35



- Molecule 34: 23S RIBOSOMAL RNA





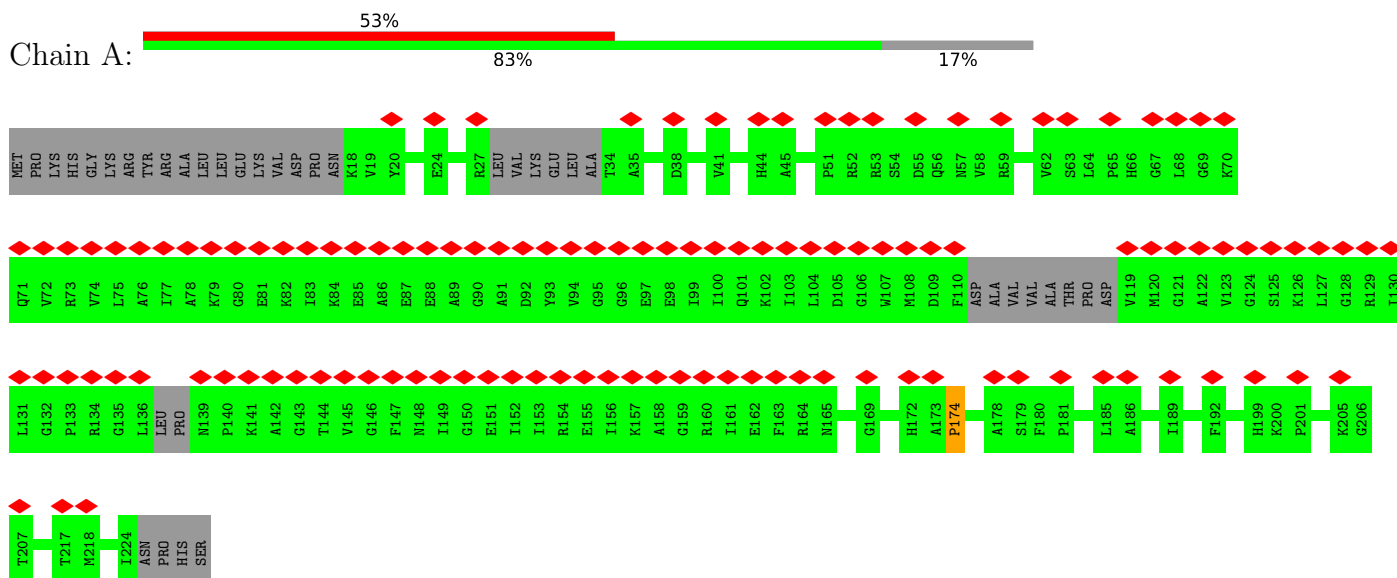


• Molecule 35: 5S RIBOSOMAL RNA

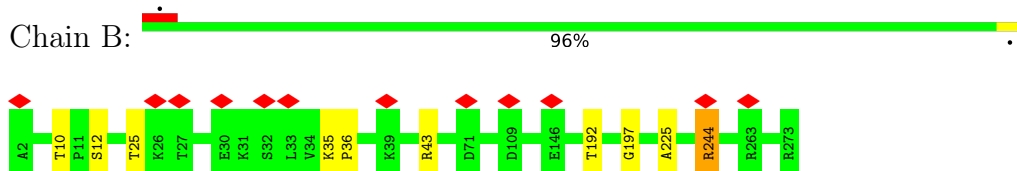
Chain 3: 55% 36% 8%



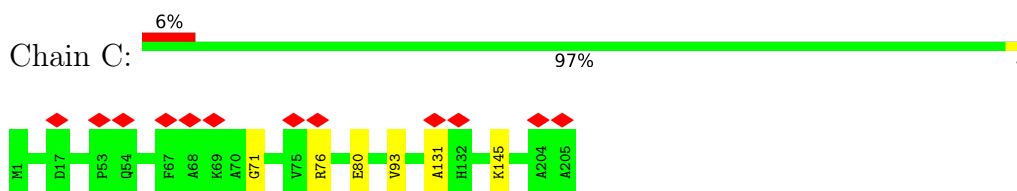
• Molecule 36: 50S ribosomal protein L1



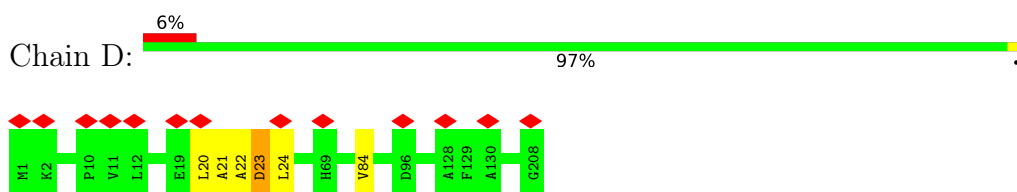
• Molecule 37: 50S ribosomal protein L2



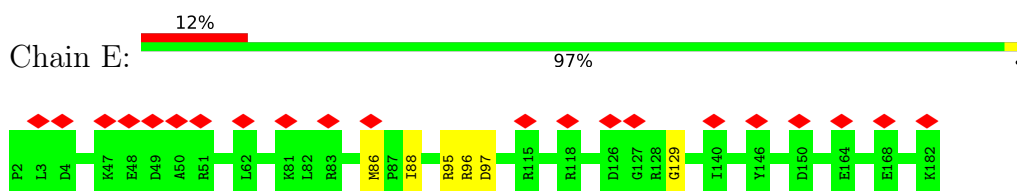
• Molecule 38: 50S ribosomal protein L3



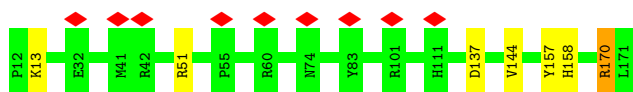
• Molecule 39: 50S ribosomal protein L4



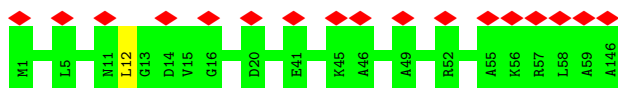
• Molecule 40: 50S ribosomal protein L5



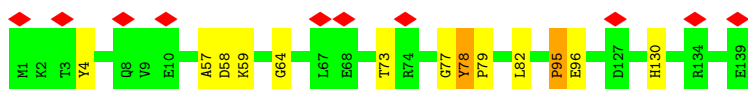
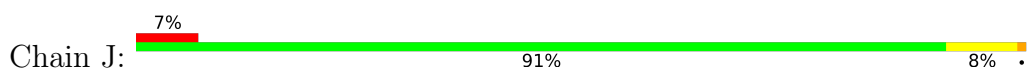
• Molecule 41: 50S ribosomal protein L6



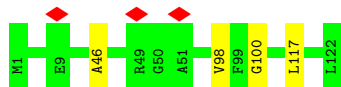
- Molecule 42: 50S ribosomal protein L9



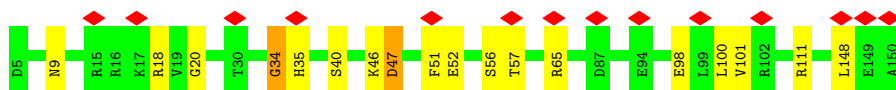
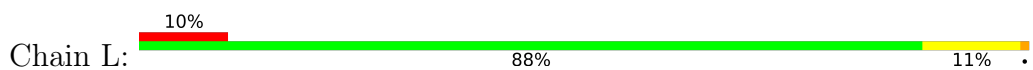
- Molecule 43: 50S ribosomal protein L13



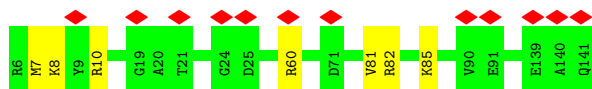
- Molecule 44: 50S ribosomal protein L14



- Molecule 45: 50S ribosomal protein L15



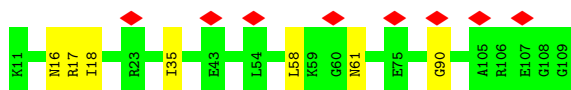
- Molecule 46: 50S ribosomal protein L16



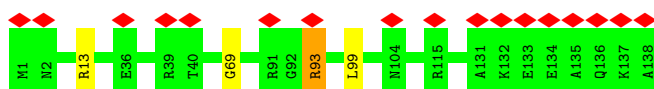
- Molecule 47: 50S ribosomal protein L17



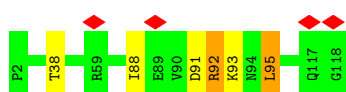
- Molecule 48: 50S ribosomal protein L18



- Molecule 49: 50S ribosomal protein L19



- Molecule 50: 50S ribosomal protein L20



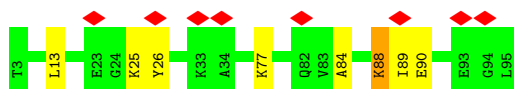
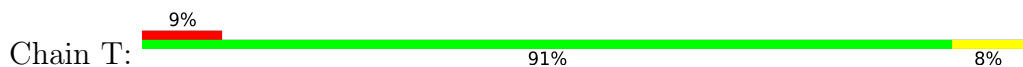
- Molecule 51: 50S ribosomal protein L21



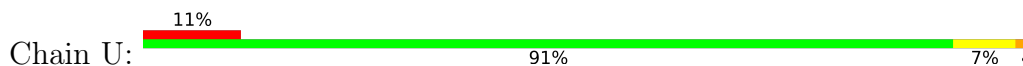
- Molecule 52: 50S ribosomal protein L22

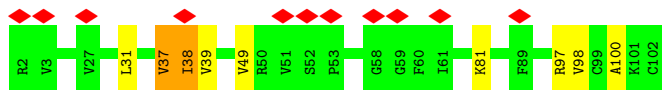


- Molecule 53: 50S ribosomal protein L23



- Molecule 54: 50S ribosomal protein L24

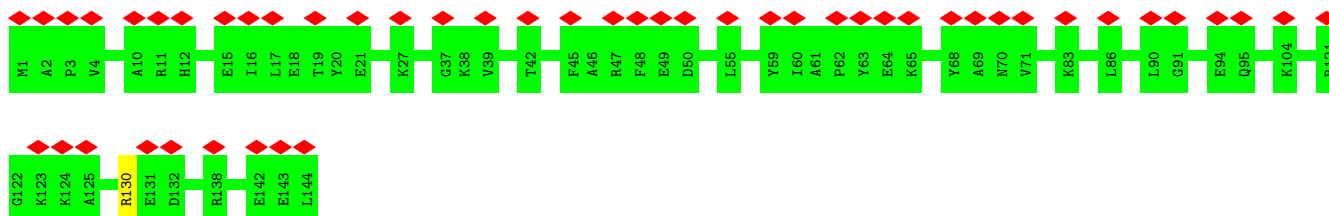




- Molecule 55: 50S ribosomal protein L25



- Molecule 56: SsrA-binding protein

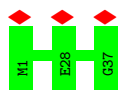


- Molecule 57: Nascent peptide MET-ALA

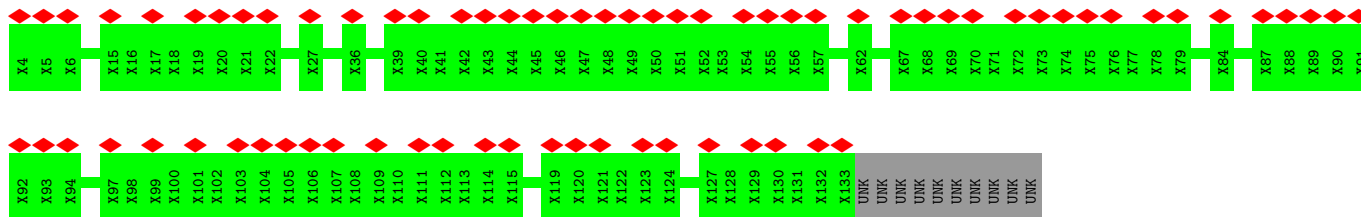
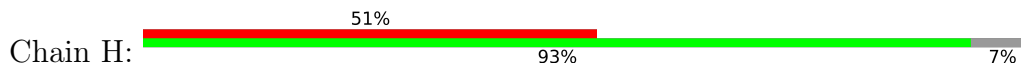


There are no outlier residues recorded for this chain.

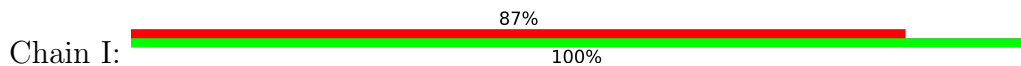
- Molecule 58: 50S ribosomal protein L36

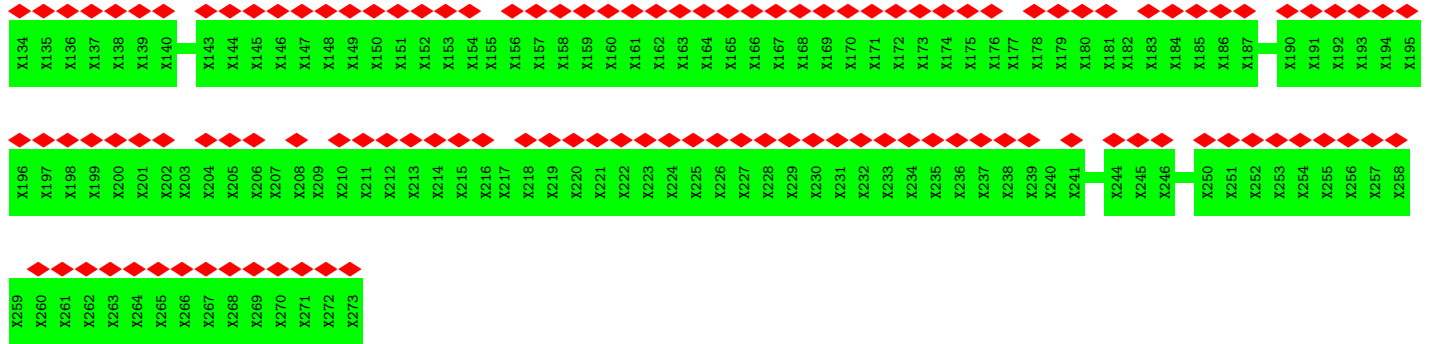


- Molecule 59: 50S RIBOSOMAL PROTEIN L10 AND L11

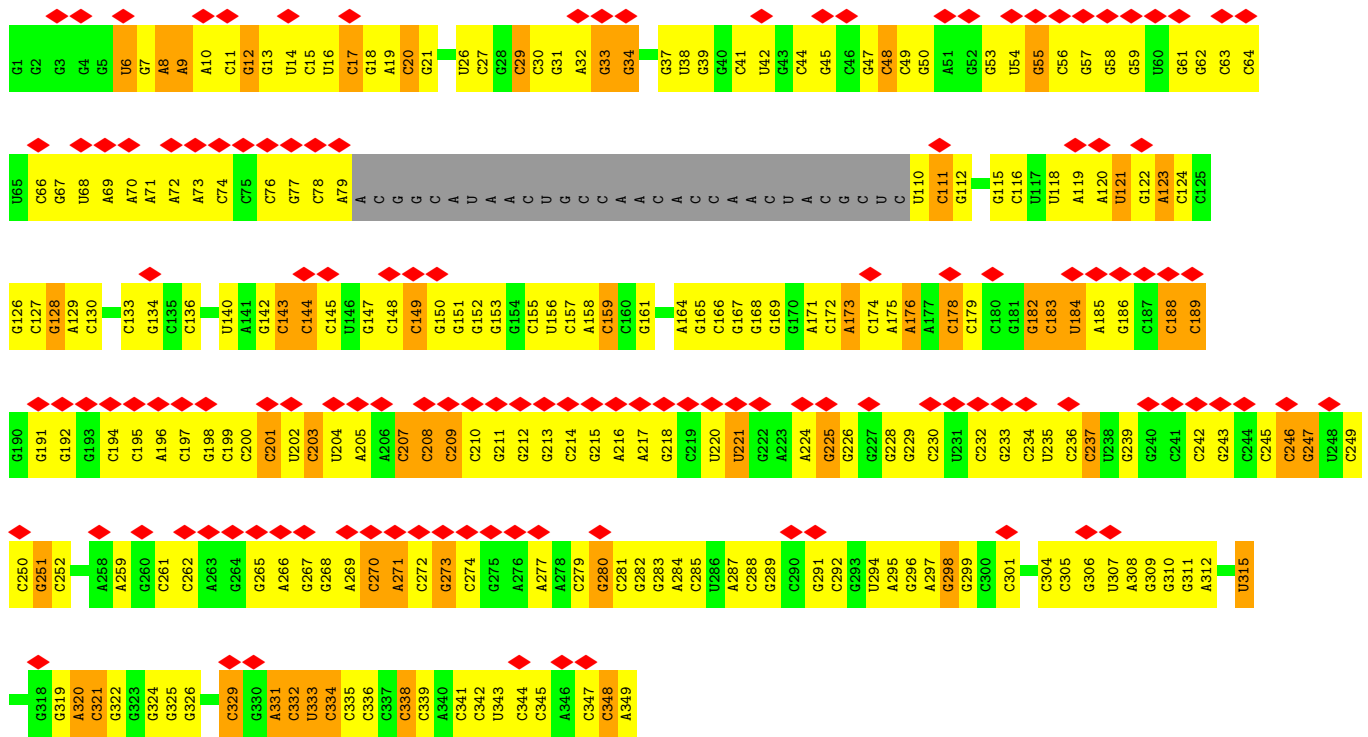


- Molecule 59: 50S RIBOSOMAL PROTEIN L10 AND L11





• Molecule 60: transfer-messenger RNA (tmRNA)



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	24400	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 ($e^-/\text{\AA}^2$)	42	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.420	Depositor
Minimum map value	-0.202	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.012	Depositor
Recommended contour level	0.05	Depositor
Map size (\AA)	482.40002, 482.40002, 482.40002	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.34, 1.34, 1.34	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: 5MU, MG, ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	2	1.29	17/36183 (0.0%)	1.36	436/56458 (0.8%)
2	g	0.48	0/1935	0.63	0/2609
3	h	0.55	0/1637	0.68	0/2207
4	i	0.54	0/1733	0.69	3/2318 (0.1%)
5	j	0.60	0/1163	0.66	0/1566
6	k	0.50	0/856	0.63	0/1154
7	l	0.53	1/1276 (0.1%)	0.59	0/1709
8	m	0.57	0/1136	0.66	0/1527
9	n	0.54	0/1029	0.72	0/1378
10	o	0.50	0/808	0.66	0/1087
11	p	0.55	0/900	0.62	0/1213
12	q	0.67	0/987	0.72	1/1322 (0.1%)
13	r	0.57	0/963	0.74	0/1285
14	s	0.67	0/501	0.65	0/664
15	t	0.50	0/745	0.60	0/992
16	u	0.59	0/717	0.63	0/965
17	v	0.61	0/837	0.63	0/1119
18	w	0.52	1/579 (0.2%)	0.61	0/768
19	x	0.51	0/643	0.66	0/867
20	y	0.44	0/765	0.62	0/1007
21	z	0.65	0/213	0.63	0/279
22	7	1.11	1/1814 (0.1%)	1.53	37/2825 (1.3%)
23	8	0.86	3/1803 (0.2%)	1.39	25/2806 (0.9%)
24	9	1.31	2/138 (1.4%)	1.49	3/212 (1.4%)
25	W	0.75	0/658	0.74	0/878
26	X	0.57	0/700	0.83	1/931 (0.1%)
27	Y	0.50	0/423	0.90	2/560 (0.4%)
28	Z	0.63	0/473	0.67	0/636
29	a	0.46	0/475	0.70	0/641
30	b	0.64	0/473	0.77	0/639
31	c	0.57	0/388	1.02	3/520 (0.6%)
32	d	0.67	0/427	0.63	0/563

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	e	0.60	0/516	0.88	1/681 (0.1%)
34	1	1.67	170/68276 (0.2%)	2.06	1235/106538 (1.2%)
35	3	1.14	0/2853	1.43	46/4451 (1.0%)
36	A	0.32	0/1145	0.63	0/1556
37	B	0.69	0/2155	0.77	2/2907 (0.1%)
38	C	0.71	0/1597	0.78	0/2155
39	D	0.65	0/1659	0.71	1/2246 (0.0%)
40	E	0.47	0/1498	0.70	0/2013
41	F	0.46	0/1246	0.69	0/1684
42	G	0.41	0/457	0.67	0/617
43	J	0.62	0/1132	0.80	1/1527 (0.1%)
44	K	0.77	1/943 (0.1%)	0.76	1/1269 (0.1%)
45	L	0.55	0/1131	1.02	4/1504 (0.3%)
46	M	0.71	0/1100	0.73	0/1470
47	N	0.64	0/974	0.81	1/1302 (0.1%)
48	O	0.52	0/779	0.85	0/1038
49	P	0.54	0/1156	0.74	1/1544 (0.1%)
50	Q	0.72	0/975	0.69	1/1297 (0.1%)
51	R	0.57	0/789	0.87	2/1054 (0.2%)
52	S	0.64	0/907	0.70	0/1216
53	T	0.61	0/740	0.93	2/995 (0.2%)
54	U	0.49	0/789	0.90	2/1053 (0.2%)
55	V	0.53	0/782	0.63	0/1053
56	5	0.43	0/1203	0.68	0/1606
57	6	1.13	0/12	0.48	0/14
58	f	0.72	0/310	0.73	0/407
60	4	0.67	5/7639 (0.1%)	1.58	203/11915 (1.7%)
All	All	1.29	201/166141 (0.1%)	1.61	2014/248817 (0.8%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	g	0	1
3	h	0	2
4	i	0	2
9	n	0	1
12	q	0	1
13	r	0	1
20	y	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
26	X	0	3
27	Y	0	4
29	a	0	5
30	b	0	3
33	e	0	1
34	1	0	3
36	A	0	1
37	B	0	5
38	C	0	4
39	D	0	1
40	E	0	4
41	F	0	3
43	J	0	9
44	K	0	2
45	L	0	10
46	M	0	2
47	N	0	2
48	O	0	2
49	P	0	1
50	Q	0	5
52	S	0	1
53	T	0	4
54	U	0	5
All	All	0	90

The worst 5 of 201 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	1	271	A	C6-N1	112.45	2.14	1.35
34	1	271	A	C6-N6	76.24	1.95	1.33
34	1	1142	U	C4-C5	75.31	2.11	1.43
34	1	271	A	N9-C8	73.54	1.96	1.37
34	1	1142	U	N1-C2	54.45	1.87	1.38

The worst 5 of 2014 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	1	363	G	C4-C5-N7	-192.01	34.00	110.80
34	1	271	A	C8-N9-C4	-187.56	30.78	105.80
34	1	1142	U	C2-N3-C4	-156.84	32.90	127.00
34	1	363	G	N7-C8-N9	-145.54	40.33	113.10
34	1	271	A	C4-C5-C6	-125.57	54.21	117.00

There are no chirality outliers.

5 of 90 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	g	19	HIS	Peptide
3	h	11	ARG	Peptide
3	h	23	TYR	Peptide
4	i	4	TYR	Peptide
4	i	5	ILE	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	g	232/235 (99%)	206 (89%)	26 (11%)	0	100	100
3	h	205/207 (99%)	182 (89%)	22 (11%)	1 (0%)	29	66
4	i	206/208 (99%)	189 (92%)	16 (8%)	1 (0%)	29	66
5	j	149/151 (99%)	137 (92%)	12 (8%)	0	100	100
6	k	99/101 (98%)	91 (92%)	8 (8%)	0	100	100
7	l	153/155 (99%)	143 (94%)	10 (6%)	0	100	100
8	m	136/138 (99%)	124 (91%)	12 (9%)	0	100	100
9	n	125/127 (98%)	103 (82%)	22 (18%)	0	100	100
10	o	97/99 (98%)	85 (88%)	12 (12%)	0	100	100
11	p	117/119 (98%)	104 (89%)	12 (10%)	1 (1%)	17	54
12	q	123/125 (98%)	89 (72%)	33 (27%)	1 (1%)	19	56
13	r	114/120 (95%)	91 (80%)	21 (18%)	2 (2%)	8	41
14	s	58/60 (97%)	50 (86%)	6 (10%)	2 (3%)	3	30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	t	86/88 (98%)	81 (94%)	5 (6%)	0	100	100
16	u	82/84 (98%)	76 (93%)	6 (7%)	0	100	100
17	v	98/100 (98%)	85 (87%)	13 (13%)	0	100	100
18	w	68/70 (97%)	66 (97%)	2 (3%)	0	100	100
19	x	77/79 (98%)	64 (83%)	13 (17%)	0	100	100
20	y	97/99 (98%)	87 (90%)	10 (10%)	0	100	100
21	z	23/25 (92%)	19 (83%)	4 (17%)	0	100	100
25	W	83/85 (98%)	72 (87%)	11 (13%)	0	100	100
26	X	87/89 (98%)	61 (70%)	26 (30%)	0	100	100
27	Y	49/51 (96%)	40 (82%)	9 (18%)	0	100	100
28	Z	58/60 (97%)	52 (90%)	6 (10%)	0	100	100
29	a	56/58 (97%)	41 (73%)	14 (25%)	1 (2%)	8	41
30	b	57/59 (97%)	42 (74%)	14 (25%)	1 (2%)	8	41
31	c	43/45 (96%)	27 (63%)	12 (28%)	4 (9%)	0	9
32	d	47/49 (96%)	46 (98%)	1 (2%)	0	100	100
33	e	62/64 (97%)	42 (68%)	20 (32%)	0	100	100
36	A	183/229 (80%)	120 (66%)	62 (34%)	1 (0%)	29	66
37	B	270/272 (99%)	227 (84%)	41 (15%)	2 (1%)	22	59
38	C	203/205 (99%)	168 (83%)	33 (16%)	2 (1%)	15	51
39	D	206/208 (99%)	184 (89%)	20 (10%)	2 (1%)	15	51
40	E	177/181 (98%)	145 (82%)	30 (17%)	2 (1%)	14	50
41	F	158/160 (99%)	131 (83%)	25 (16%)	2 (1%)	12	47
42	G	57/60 (95%)	55 (96%)	2 (4%)	0	100	100
43	J	137/139 (99%)	104 (76%)	28 (20%)	5 (4%)	3	29
44	K	120/122 (98%)	103 (86%)	17 (14%)	0	100	100
45	L	144/146 (99%)	88 (61%)	51 (35%)	5 (4%)	3	30
46	M	134/136 (98%)	111 (83%)	21 (16%)	2 (2%)	10	44
47	N	115/117 (98%)	92 (80%)	22 (19%)	1 (1%)	17	54
48	O	97/99 (98%)	64 (66%)	29 (30%)	4 (4%)	3	26
49	P	136/138 (99%)	95 (70%)	40 (29%)	1 (1%)	22	59
50	Q	115/117 (98%)	102 (89%)	11 (10%)	2 (2%)	9	42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	R	97/101 (96%)	67 (69%)	30 (31%)	0	100	100
52	S	111/113 (98%)	97 (87%)	14 (13%)	0	100	100
53	T	91/93 (98%)	58 (64%)	31 (34%)	2 (2%)	6	37
54	U	99/101 (98%)	55 (56%)	39 (39%)	5 (5%)	2	21
55	V	89/92 (97%)	75 (84%)	14 (16%)	0	100	100
56	5	142/144 (99%)	121 (85%)	21 (15%)	0	100	100
58	f	35/37 (95%)	24 (69%)	11 (31%)	0	100	100
All	All	5803/5960 (97%)	4781 (82%)	970 (17%)	52 (1%)	21	54

5 of 52 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	i	5	ILE
13	r	69	GLU
13	r	70	LEU
40	E	96	ARG
41	F	170	ARG

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	g	202/203 (100%)	200 (99%)	2 (1%)	76	86
3	h	160/161 (99%)	160 (100%)	0	100	100
4	i	180/180 (100%)	179 (99%)	1 (1%)	86	93
5	j	115/116 (99%)	115 (100%)	0	100	100
6	k	90/90 (100%)	90 (100%)	0	100	100
7	l	126/126 (100%)	125 (99%)	1 (1%)	81	89
8	m	119/119 (100%)	118 (99%)	1 (1%)	81	89
9	n	98/98 (100%)	95 (97%)	3 (3%)	40	65
10	o	88/89 (99%)	88 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	p	90/90 (100%)	89 (99%)	1 (1%)	73	85
12	q	104/104 (100%)	104 (100%)	0	100	100
13	r	96/96 (100%)	94 (98%)	2 (2%)	53	74
14	s	49/49 (100%)	48 (98%)	1 (2%)	55	74
15	t	79/79 (100%)	79 (100%)	0	100	100
16	u	72/72 (100%)	72 (100%)	0	100	100
17	v	94/95 (99%)	94 (100%)	0	100	100
18	w	61/61 (100%)	61 (100%)	0	100	100
19	x	69/69 (100%)	68 (99%)	1 (1%)	67	82
20	y	76/76 (100%)	75 (99%)	1 (1%)	69	83
21	z	19/20 (95%)	19 (100%)	0	100	100
25	W	61/67 (91%)	61 (100%)	0	100	100
26	X	73/74 (99%)	73 (100%)	0	100	100
27	Y	46/47 (98%)	46 (100%)	0	100	100
28	Z	51/52 (98%)	51 (100%)	0	100	100
29	a	52/52 (100%)	52 (100%)	0	100	100
30	b	51/51 (100%)	51 (100%)	0	100	100
31	c	43/44 (98%)	38 (88%)	5 (12%)	5	27
32	d	41/42 (98%)	40 (98%)	1 (2%)	49	71
33	e	53/54 (98%)	53 (100%)	0	100	100
36	A	61/181 (34%)	61 (100%)	0	100	100
37	B	213/214 (100%)	210 (99%)	3 (1%)	67	82
38	C	165/165 (100%)	165 (100%)	0	100	100
39	D	165/165 (100%)	162 (98%)	3 (2%)	59	77
40	E	155/155 (100%)	155 (100%)	0	100	100
41	F	132/133 (99%)	129 (98%)	3 (2%)	50	71
42	G	47/47 (100%)	46 (98%)	1 (2%)	53	74
43	J	117/118 (99%)	117 (100%)	0	100	100
44	K	100/100 (100%)	100 (100%)	0	100	100
45	L	112/112 (100%)	111 (99%)	1 (1%)	78	88
46	M	106/106 (100%)	103 (97%)	3 (3%)	43	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
47	N	100/100 (100%)	98 (98%)	2 (2%)	55	74
48	O	77/77 (100%)	76 (99%)	1 (1%)	69	83
49	P	120/120 (100%)	118 (98%)	2 (2%)	60	79
50	Q	92/93 (99%)	92 (100%)	0	100	100
51	R	82/82 (100%)	82 (100%)	0	100	100
52	S	91/92 (99%)	90 (99%)	1 (1%)	73	85
53	T	74/75 (99%)	73 (99%)	1 (1%)	67	82
54	U	84/85 (99%)	84 (100%)	0	100	100
55	V	83/84 (99%)	81 (98%)	2 (2%)	49	71
56	5	120/120 (100%)	119 (99%)	1 (1%)	81	89
57	6	1/1 (100%)	1 (100%)	0	100	100
58	f	34/34 (100%)	34 (100%)	0	100	100
All	All	4789/4935 (97%)	4745 (99%)	44 (1%)	79	88

5 of 44 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
41	F	170	ARG
47	N	117	VAL
42	G	12	LEU
46	M	82	ARG
49	P	13	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 60 such sidechains are listed below:

Mol	Chain	Res	Type
36	A	56	GLN
52	S	102	HIS
38	C	137	HIS
52	S	61	ASN
55	V	73	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1496/1522 (98%)	353 (23%)	29 (1%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
22	7	76/77 (98%)	32 (42%)	1 (1%)
23	8	75/76 (98%)	16 (21%)	2 (2%)
24	9	6/6 (100%)	3 (50%)	1 (16%)
34	1	2809/2915 (96%)	952 (33%)	35 (1%)
35	3	118/119 (99%)	39 (33%)	1 (0%)
60	4	317/349 (90%)	203 (64%)	11 (3%)
All	All	4897/5064 (96%)	1598 (32%)	80 (1%)

5 of 1598 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	8	A
1	2	9	G
1	2	31	G
1	2	32	A
1	2	39	G

5 of 80 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
34	1	1558	A
60	4	29	C
34	1	1653	G
34	1	2506	U
60	4	183	C

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

1 non-standard protein/DNA/RNA residue 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
22	5MU	7	54	22	19,22,23	1.43	6 (31%)	28,32,35	2.23	6 (21%)

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
22	5MU	7	54	22	-	2/7/25/26	0/2/2/2

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	7	54	5MU	C4-N3	-2.75	1.33	1.38
22	7	54	5MU	C6-C5	2.67	1.39	1.34
22	7	54	5MU	C4-C5	2.37	1.48	1.44
22	7	54	5MU	C6-N1	-2.25	1.34	1.38
22	7	54	5MU	C2-N3	-2.18	1.34	1.38

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	7	54	5MU	C4-N3-C2	-5.47	120.27	127.35
22	7	54	5MU	C5-C4-N3	5.14	119.69	115.31
22	7	54	5MU	N3-C2-N1	4.80	121.26	114.89
22	7	54	5MU	C5-C6-N1	-4.25	118.96	123.34
22	7	54	5MU	O4-C4-C5	-3.85	120.44	124.90

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
22	7	54	5MU	C3'-C4'-C5'-O5'
22	7	54	5MU	O4'-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 640 ligands modelled in this entry, 640 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
34	1	20
1	2	7
13	r	2
55	V	1
42	G	1
2	g	1
40	E	1
51	R	1
18	w	1

The worst 5 of 35 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	V	93:ASP	C	179:ASP	N	55.01
1	G	59:ALA	C	146:ALA	N	44.80
1	1	271(Z):C	O3'	272:G	P	25.34
1	1	362:U	O3'	363:G	P	24.58
1	1	363:G	O3'	363(A):A	P	17.94

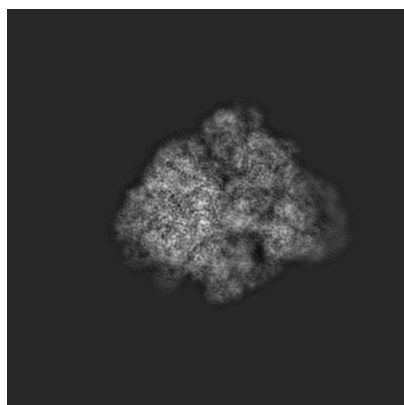
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4475. These allow visual inspection of the internal detail of the map and identification of artifacts.

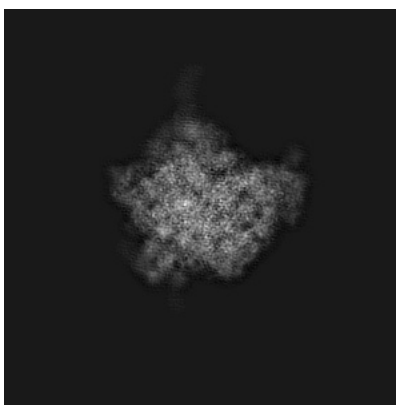
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

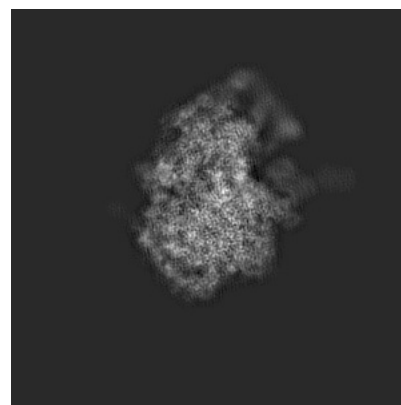
6.1.1 Primary map



X



Y

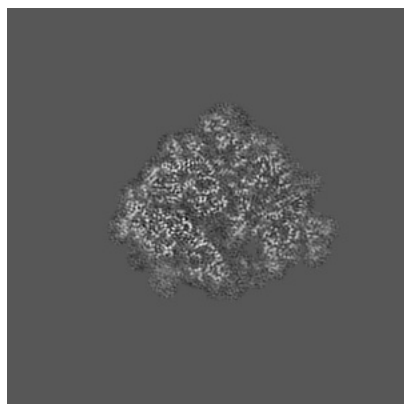


Z

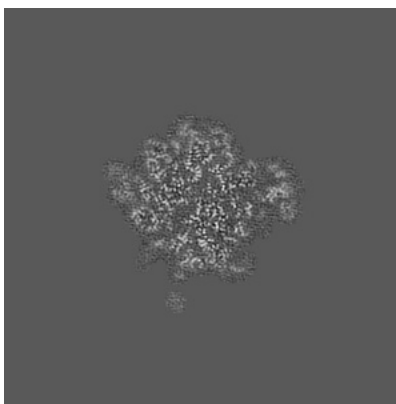
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

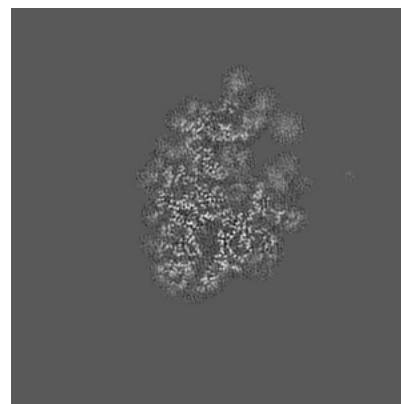
6.2.1 Primary map



X Index: 180



Y Index: 180

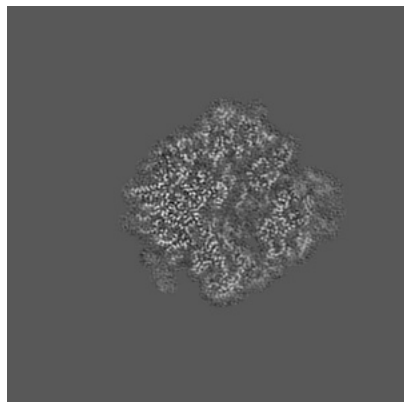


Z Index: 180

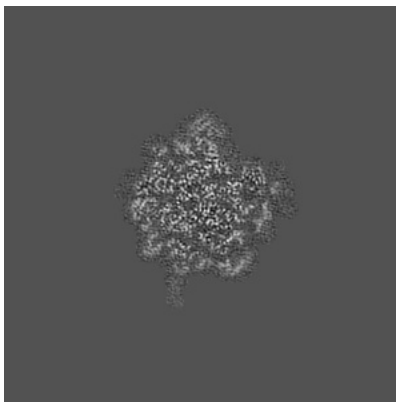
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

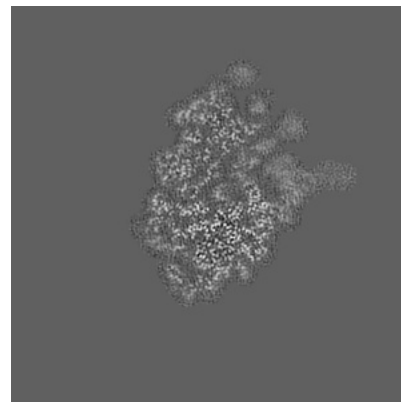
6.3.1 Primary map



X Index: 191



Y Index: 173



Z Index: 167

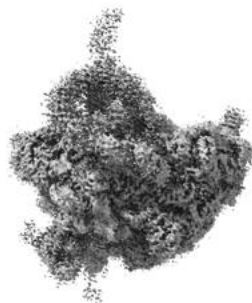
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

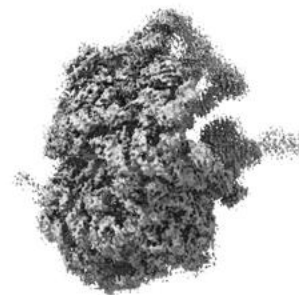
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

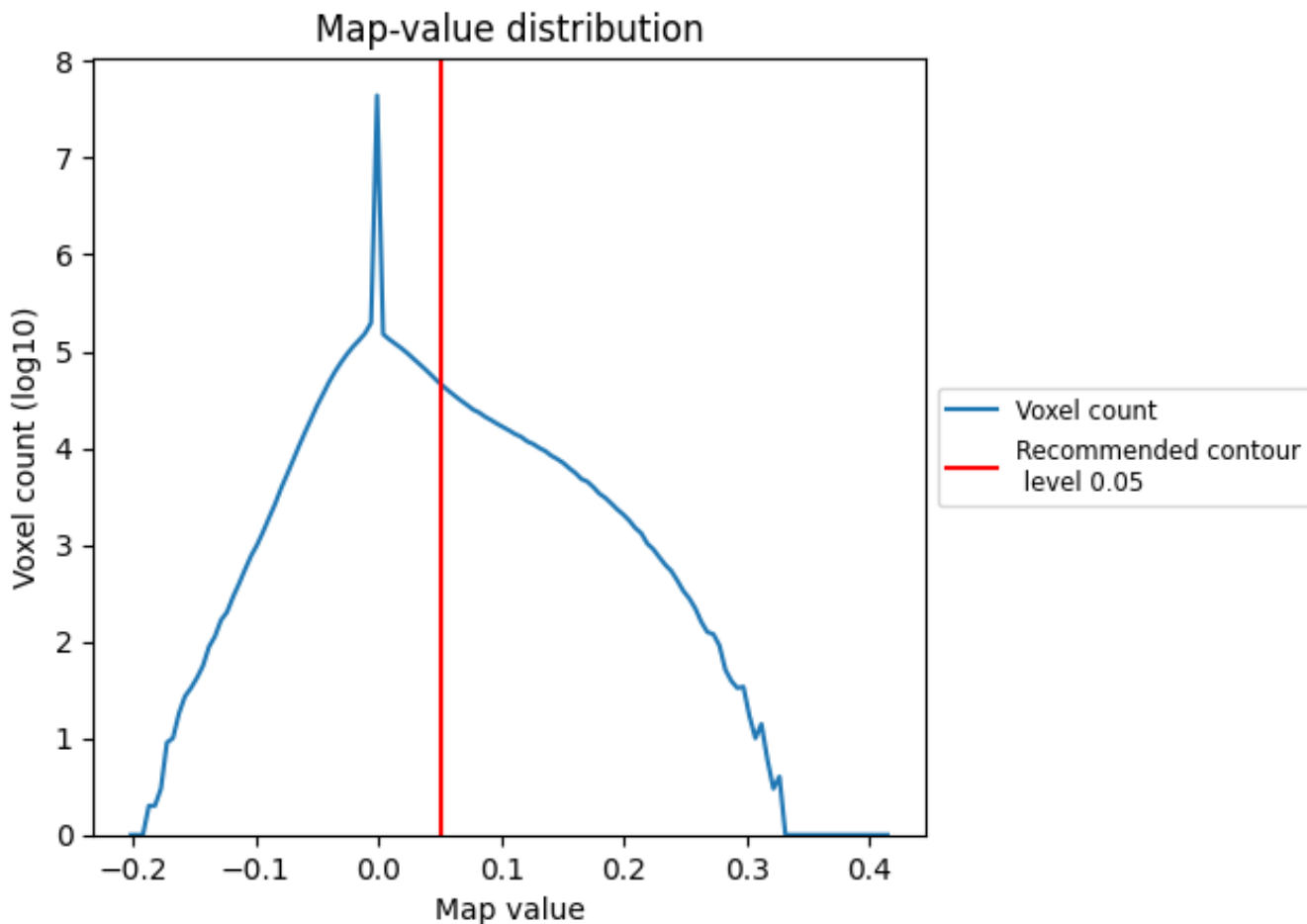
6.5 Mask visualisation

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

7 Map analysis [i](#)

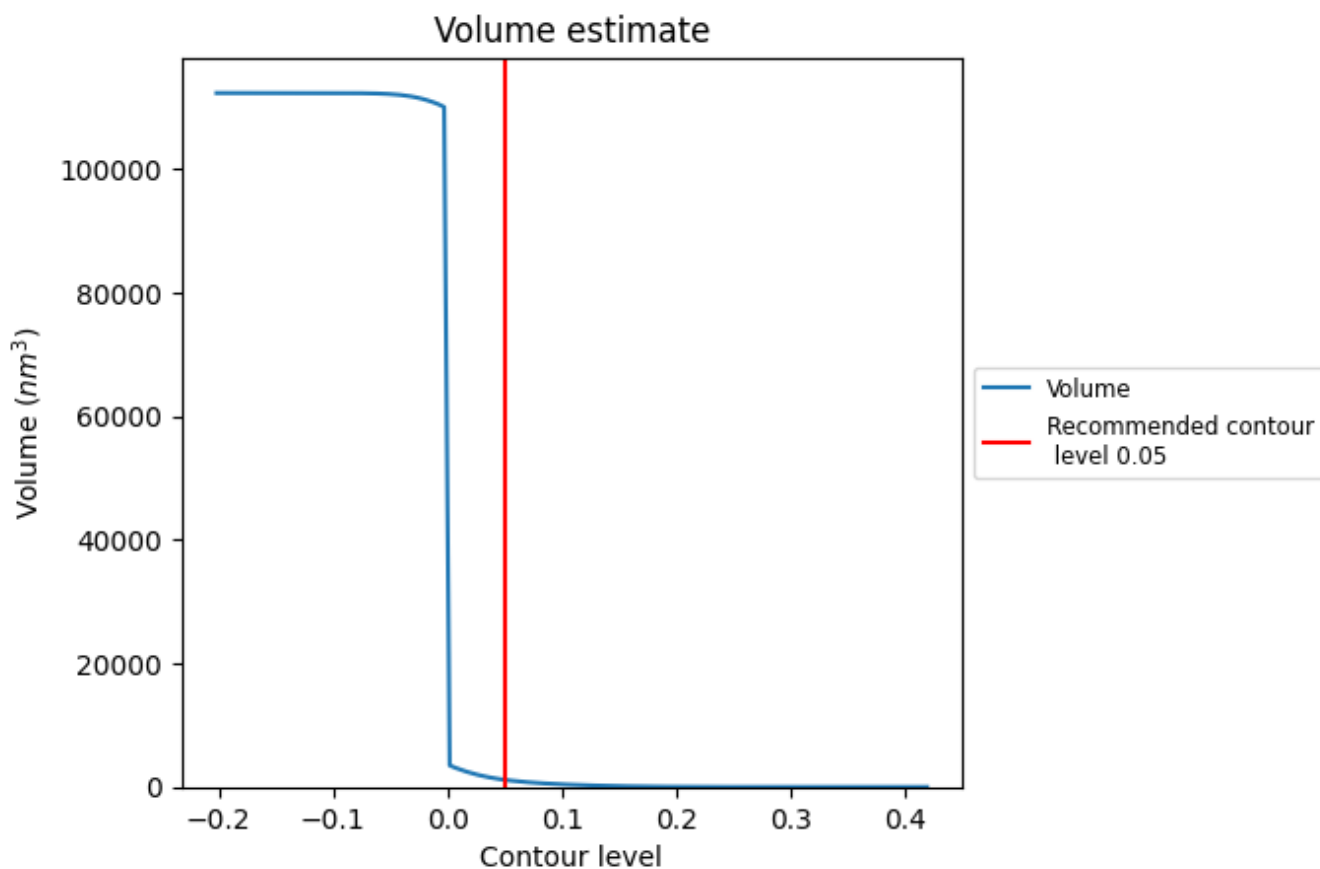
This section contains the results of statistical analysis of the map.

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.

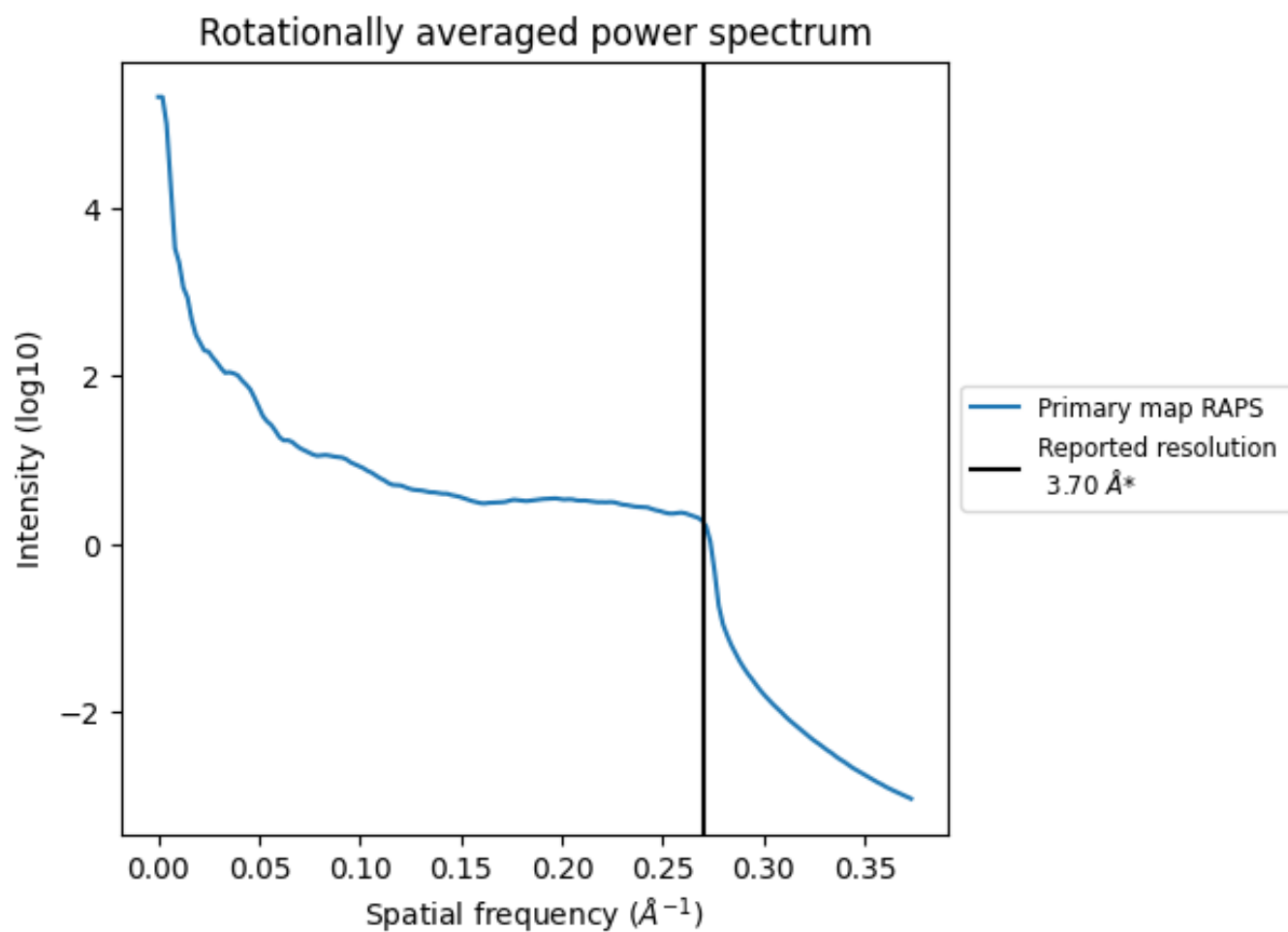
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 1158 nm³; this corresponds to an approximate mass of 1046 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 0.270 Å⁻¹

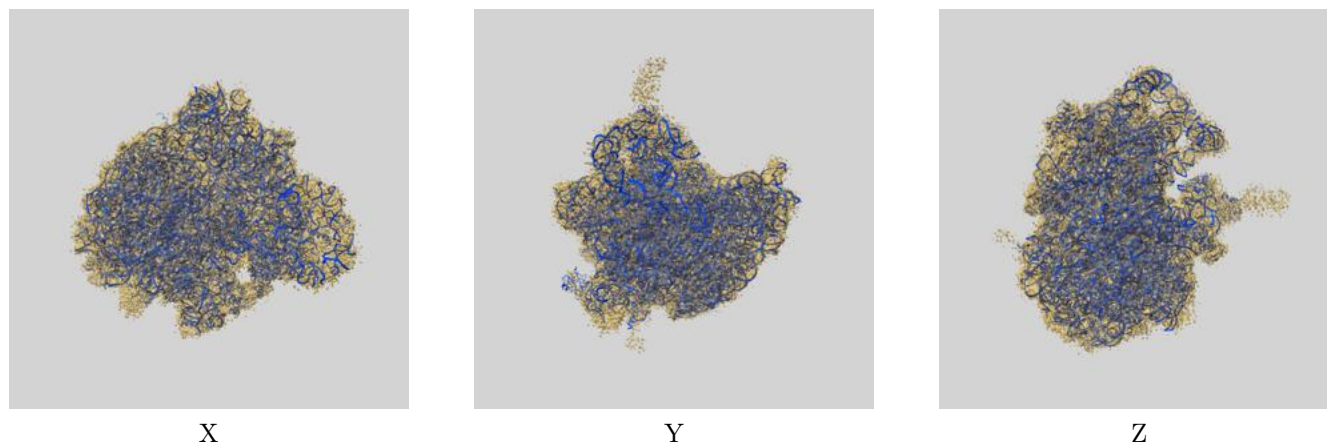
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

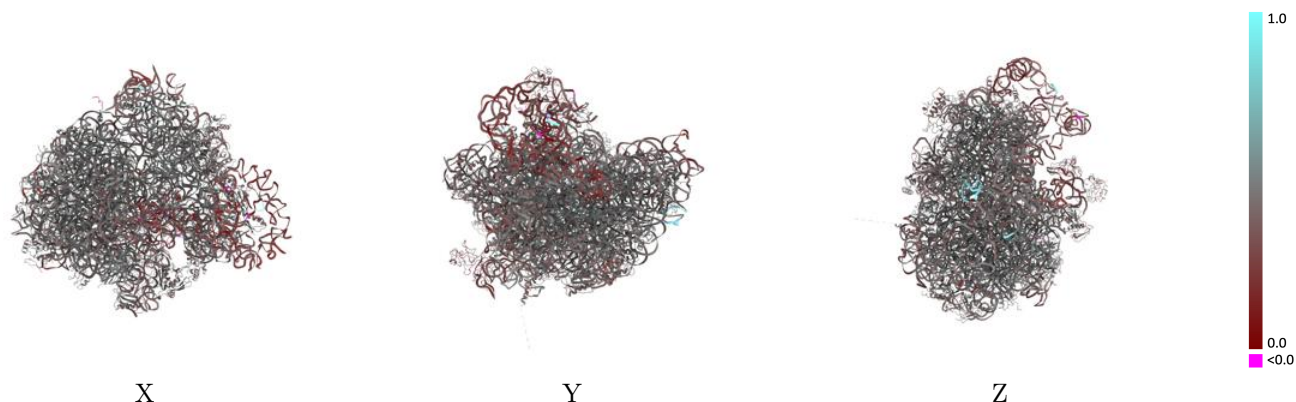
This section contains information regarding the fit between EMDB map EMD-4475 and PDB model 6Q95. Per-residue inclusion information can be found in section 3 on page 17.

9.1 Map-model overlay [i](#)



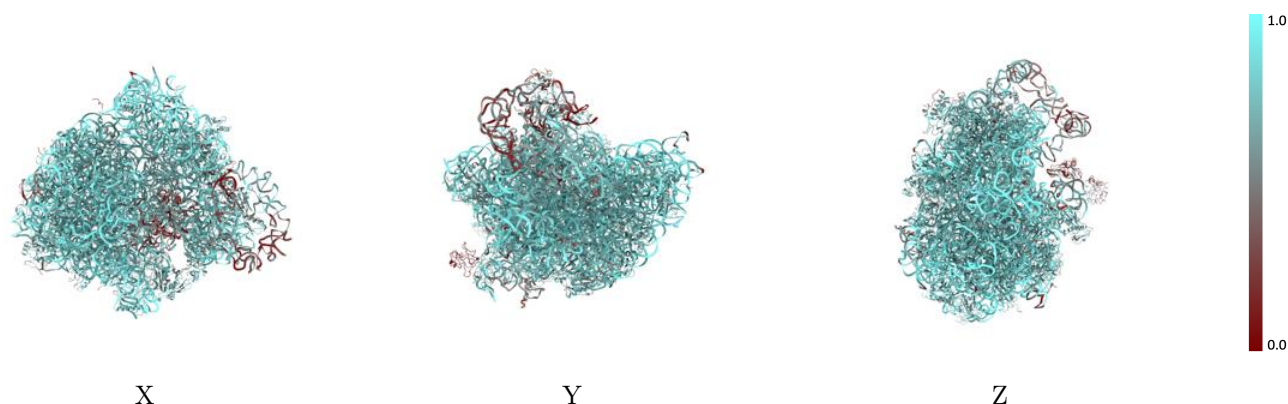
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



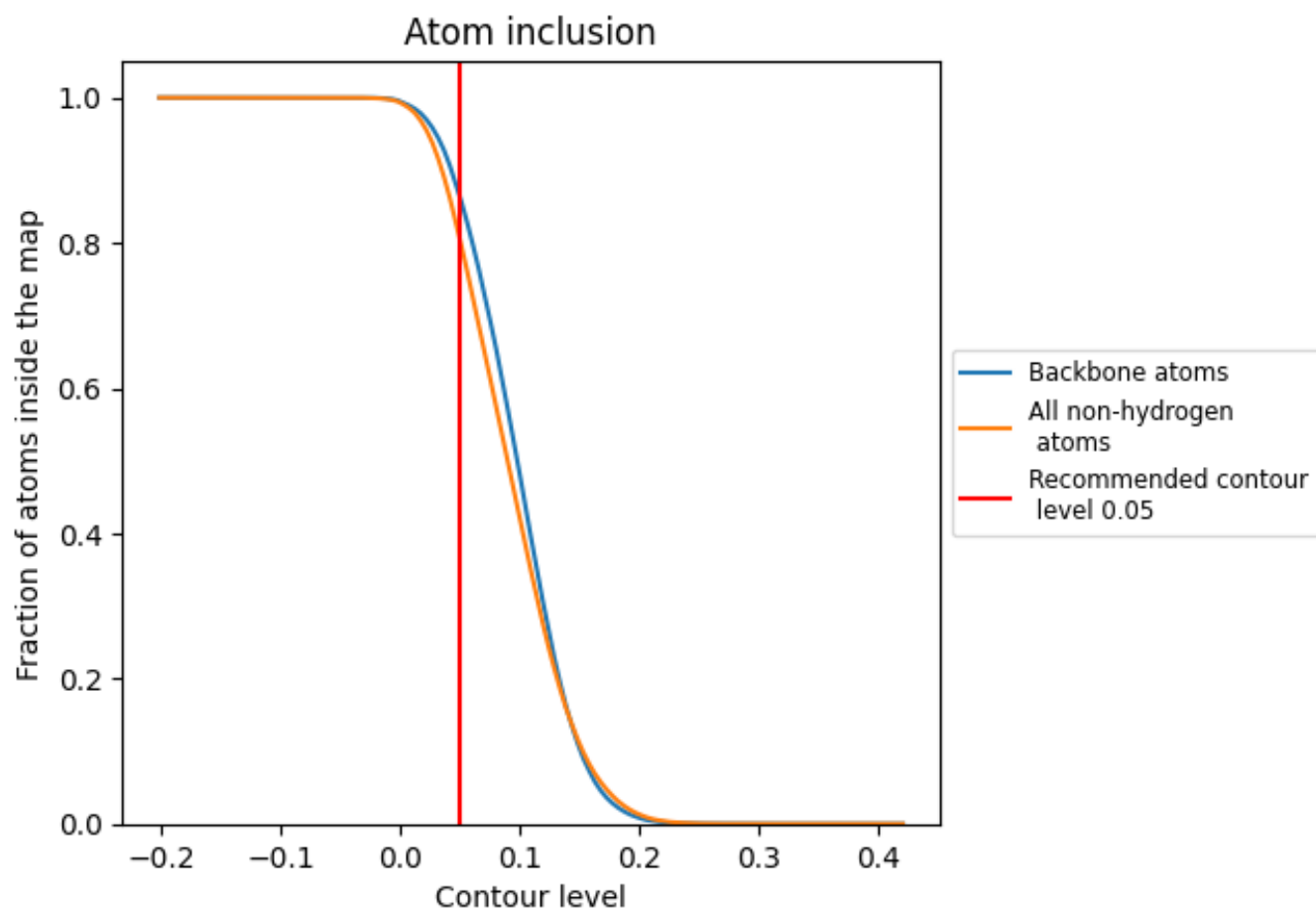
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.05).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 80% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8008	 0.4320
1	 0.8792	 0.4400
2	 0.8809	 0.4310
3	 0.9080	 0.4240
4	 0.4756	 0.2810
5	 0.4965	 0.4210
6	 0.7692	 0.4930
7	 0.7629	 0.4040
8	 0.6867	 0.3670
9	 0.7109	 0.4260
A	 0.3106	 0.3390
B	 0.7569	 0.4920
C	 0.7541	 0.4760
D	 0.7236	 0.4520
E	 0.6671	 0.4240
F	 0.7037	 0.4140
G	 0.5656	 0.4080
H	 0.4077	 0.3540
I	 0.1897	 0.3310
J	 0.7226	 0.4650
K	 0.7127	 0.5040
L	 0.6852	 0.4330
M	 0.6957	 0.4600
N	 0.7804	 0.4860
O	 0.7530	 0.4240
P	 0.6847	 0.4370
Q	 0.7773	 0.4760
R	 0.6785	 0.4370
S	 0.7613	 0.4960
T	 0.6934	 0.4180
U	 0.6825	 0.4150
V	 0.7436	 0.4630
W	 0.7605	 0.4990
X	 0.6870	 0.4520
Y	 0.6978	 0.3870



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Chain	Atom inclusion	Q-score
Z	 0.7209	 0.4800
a	 0.7174	 0.4120
b	 0.7400	 0.4690
c	 0.7268	 0.4300
d	 0.7815	 0.5110
e	 0.7097	 0.4620
f	 0.7864	 0.4860
g	 0.6312	 0.4190
h	 0.6945	 0.4640
i	 0.7301	 0.4470
j	 0.7374	 0.4730
k	 0.6843	 0.4320
l	 0.7339	 0.4470
m	 0.7393	 0.4670
n	 0.7364	 0.4290
o	 0.6991	 0.4390
p	 0.7045	 0.4520
q	 0.7220	 0.5000
r	 0.6999	 0.4360
s	 0.7393	 0.4700
t	 0.7161	 0.4510
u	 0.7740	 0.4730
v	 0.7134	 0.4840
w	 0.7034	 0.4500
x	 0.6883	 0.4330
y	 0.7145	 0.4430
z	 0.7812	 0.4670