



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2022 – 01:29 pm BST

PDB ID : 7QV2
EMDB ID : EMD-14158
Title : Bacillus subtilis collided disome (Collided 70S)
Authors : Filbeck, S.; Pfeffer, S.
Deposited on : 2022-01-19
Resolution : 3.50 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

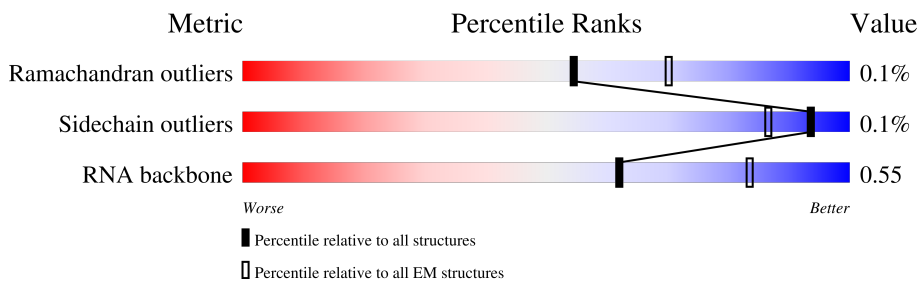
EMDB validation analysis : 0.0.0.dev97
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.27

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 3.50 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	0	59	
2	1	49	
3	2	44	
4	3	66	
5	4	37	
6	6	66	
7	A	29	
8	B	112	

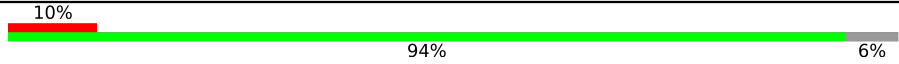
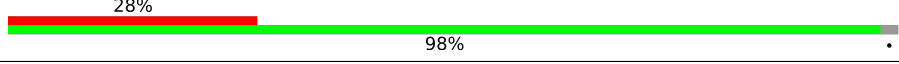
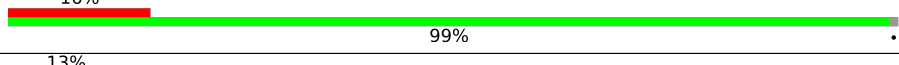
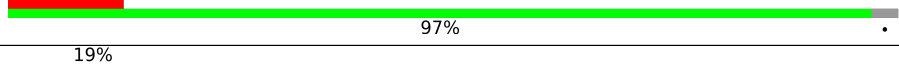
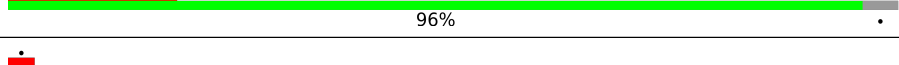
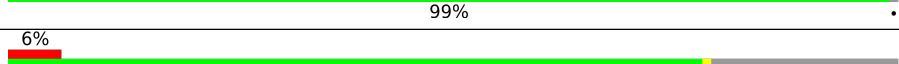
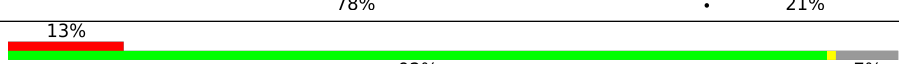
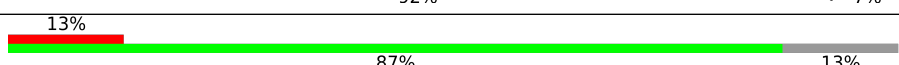
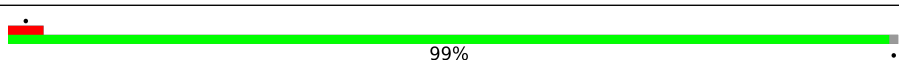
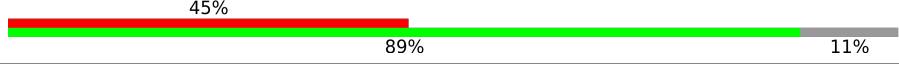
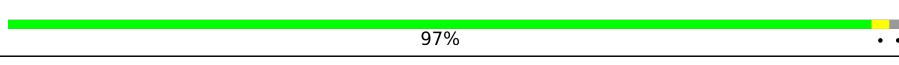
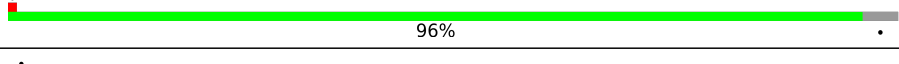
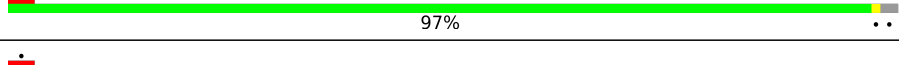
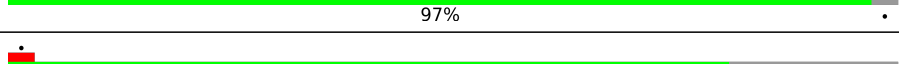
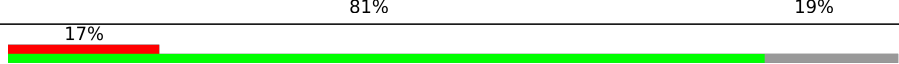
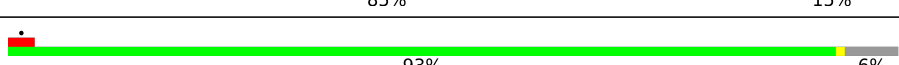
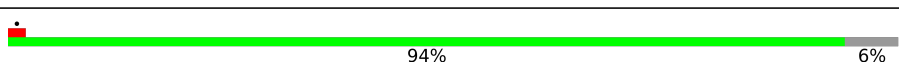



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Mol	Chain	Length	Quality of chain
9	C	277	98%
10	D	209	99%
11	E	207	99%
12	F	179	98%
13	G	179	98%
14	H	77	62%
15	I	24	100%
16	J	145	98%
17	K	122	100%
18	L	146	100%
19	M	144	94%
20	N	120	99%
21	O	120	100%
22	P	115	100%
23	Q	119	98%
24	R	102	99%
25	S	113	96%
26	T	95	95%
27	U	103	98%
28	V	2928	76%
29	W	94	87%
30	Y	66	98%
31	Z	59	98%
32	a	1545	82%
33	b	246	87%

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Mol	Chain	Length	Quality of chain
34	c	218	
35	d	200	
36	e	166	
37	f	95	
38	g	156	
39	h	132	
40	i	130	
41	j	102	
42	k	131	
43	l	138	
44	m	121	
45	n	61	
46	o	89	
47	p	90	
48	q	87	
49	r	79	
50	s	92	
51	t	88	
52	u	62	
53	x	76	

2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 142856 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 L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	0	54	426	262	86	71	7	0	0

- Molecule 2 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	1	48	401	244	80	73	4	0	0

- Molecule 3 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	2	44	368	222	89	55	2	0	0

- Molecule 4 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	3	64	512	321	107	82	2	0	0

- Molecule 5 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	4	37	297	186	60	46	5	0	0

- Molecule 6 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	6	54	413	257	73	78	5	0	0

- Molecule 7 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	29	Total	C	N	O	P	0	0
			630	282	124	195	29		

- Molecule 8 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	112	Total	C	N	O	P	0	0
			2392	1068	435	778	111		

- Molecule 9 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	272	Total	C	N	O	S	0	0
			2083	1296	408	373	6		

- Molecule 10 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	206	Total	C	N	O	S	0	0
			1569	985	289	290	5		

- Molecule 11 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	205	Total	C	N	O	S	0	0
			1561	980	289	290	2		

- Molecule 12 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	176	Total	C	N	O	S	0	0
			1386	882	241	256	7		

- Molecule 13 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G	175	Total	C	N	O	S	0	0
			1342	835	248	257	2		

- Molecule 14 is a RNA chain called A/P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
14	H	77	1643	731	290	545	77	0	0

- Molecule 15 is a protein called Nascent chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
15	I	24	121	72	24	25	0	0

- Molecule 16 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	J	142	1124	710	206	203	5	0	0

- Molecule 17 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	K	122	921	571	173	173	4	0	0

- Molecule 18 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	L	146	1082	671	207	202	2	0	0

- Molecule 19 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	M	135	1076	690	205	176	5	0	0

- Molecule 20 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	N	119	954	583	186	181	4	0	0

- Molecule 21 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	O	120	Total	C	N	O	S	0	0
			913	564	176	172	1		

- Molecule 22 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	P	115	Total	C	N	O	S	0	0
			945	600	185	159	1		

- Molecule 23 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Q	117	Total	C	N	O	S	0	0
			940	591	189	156	4		

- Molecule 24 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	R	101	Total	C	N	O	0	0
			787	501	139	147		

- Molecule 25 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	S	109	Total	C	N	O	S	0	0
			842	525	164	150	3		

- Molecule 26 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	T	90	Total	C	N	O	S	0	0
			725	452	134	136	3		

- Molecule 27 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	U	101	Total	C	N	O	S	0	0
			762	478	142	138	4		

- Molecule 28 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
28	V	2887	61999	27661	11460	19994	2884	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
V	243	G	A	conflict	GB 1491848961
V	325	A	-	insertion	GB 1491848961
V	326	A	-	insertion	GB 1491848961
V	327	G	-	insertion	GB 1491848961
V	328	G	-	insertion	GB 1491848961
V	640	U	C	conflict	GB 1491848961

- Molecule 29 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
29	W	82	630	390	123	117	0	0

- Molecule 30 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	Y	65	530	328	102	98	2	0	0

- Molecule 31 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	Z	58	456	281	89	85	1	0	0

- Molecule 32 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
32	a	1545	33138	14778	6072	10743	1545	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	1541	G	-	insertion	GB 225184640

- Molecule 33 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	b	218	1757	1119	309	323	6	0	0

- Molecule 34 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	c	206	1619	1011	304	301	3	0	0

- Molecule 35 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	d	195	1569	991	291	285	2	0	0

- Molecule 36 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	e	164	1219	767	225	225	2	0	0

- Molecule 37 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	f	92	755	476	132	146	1	0	0

- Molecule 38 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	g	149	1181	740	220	215	6	0	0

- Molecule 39 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	h	131	1037	655	191	188	3	0	0

- Molecule 40 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	i	103	Total	C	N	O	0	0
			784	485	151	148		

- Molecule 41 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	j	95	Total	C	N	O	S	0	0
			761	479	139	141	2		

- Molecule 42 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	k	114	Total	C	N	O	S	0	0
			839	516	164	157	2		

- Molecule 43 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	l	136	Total	C	N	O	S	0	0
			1052	653	211	186	2		

- Molecule 44 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	m	108	Total	C	N	O	0	0
			868	534	176	158		

- Molecule 45 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	n	60	Total	C	N	O	S	0	0
			498	317	98	78	5		

- Molecule 46 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	o	85	Total	C	N	O	S	0	0
			710	436	144	129	1		

- Molecule 47 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	p	88	Total	C	N	O	S	0	0
			695	441	128	124	2		

- Molecule 48 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	q	84	Total	C	N	O	S	0	0
			691	435	128	126	2		

- Molecule 49 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	r	64	Total	C	N	O	S	0	0
			518	332	96	88	2		

- Molecule 50 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	s	78	Total	C	N	O	S	0	0
			633	409	112	110	2		

- Molecule 51 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	t	83	Total	C	N	O	S	0	0
			637	390	130	116	1		

- Molecule 52 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	u	58	Total	C	N	O	S	0	0
			444	275	92	75	2		

- Molecule 53 is a RNA chain called P/E-site tRNA.

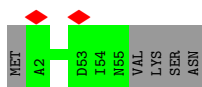
Mol	Chain	Residues	Atoms					AltConf	Trace
53	x	76	Total	C	N	O	P	0	0
			1621	721	285	539	76		

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.

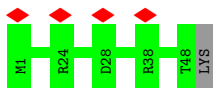
- Molecule 1: 50S ribosomal protein L32

Chain 0:  92% 8%



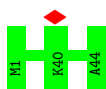
- Molecule 2: 50S ribosomal protein L33 1

Chain 1:  8% 98%



- Molecule 3: 50S ribosomal protein L34

Chain 2:  100%



- Molecule 4: 50S ribosomal protein L35

Chain 3:  97%

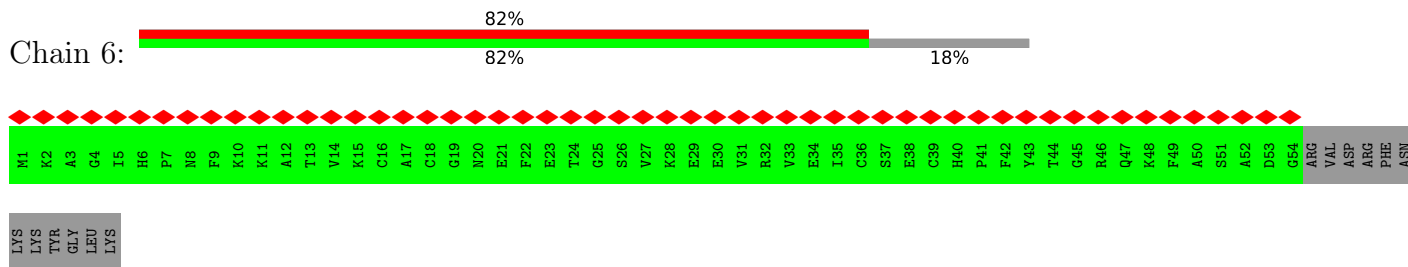


- Molecule 5: 50S ribosomal protein L36

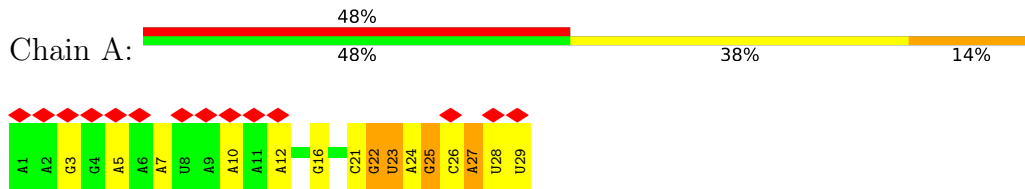
Chain 4:  100%



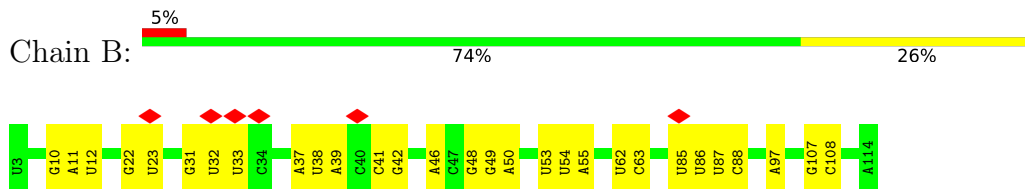
• Molecule 6: 50S ribosomal protein L31



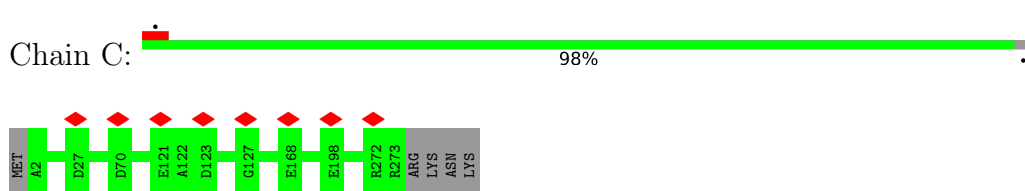
• Molecule 7: mRNA



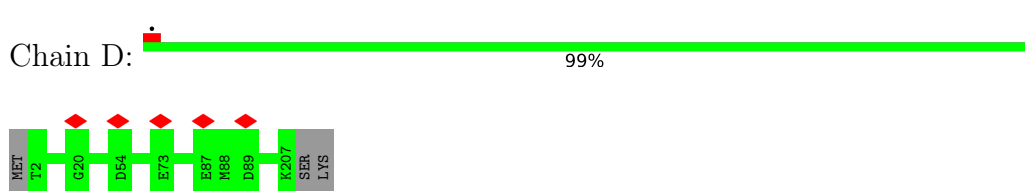
• Molecule 8: 5S ribosomal RNA



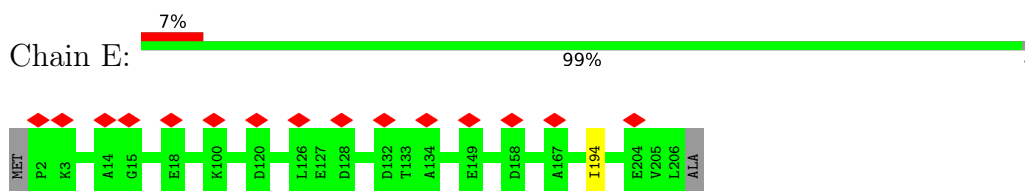
• Molecule 9: 50S ribosomal protein L2



• Molecule 10: 50S ribosomal protein L3

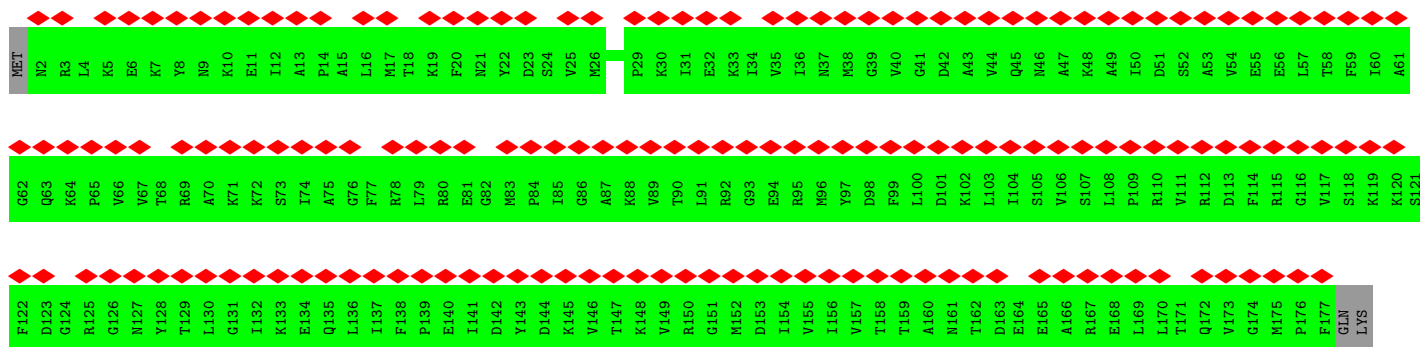


• Molecule 11: 50S ribosomal protein L4

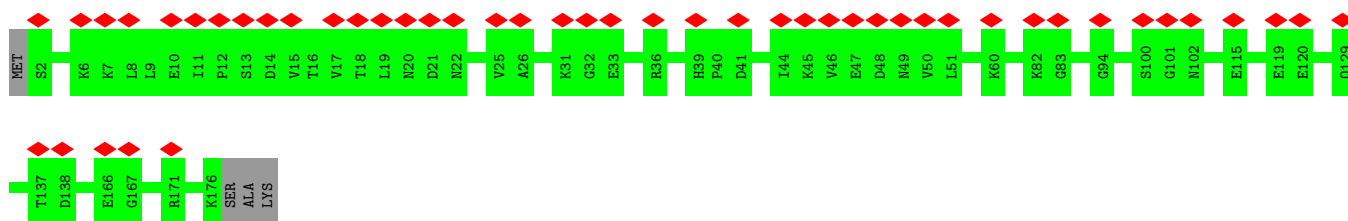


• Molecule 12: 50S ribosomal protein L5





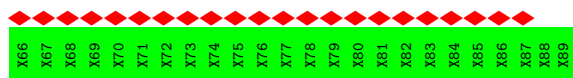
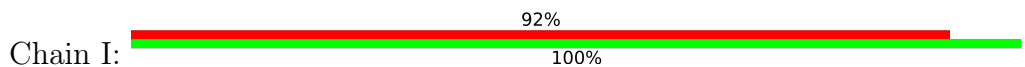
• Molecule 13: 50S ribosomal protein L6



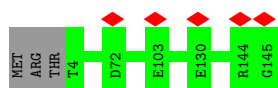
• Molecule 14: A/P-site tRNA



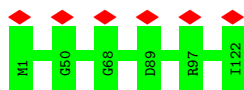
• Molecule 15: Nascent chain



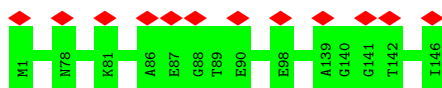
• Molecule 16: 50S ribosomal protein L13



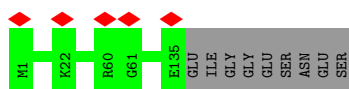
• Molecule 17: 50S ribosomal protein L14



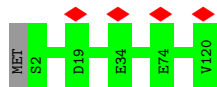
- Molecule 18: 50S ribosomal protein L15



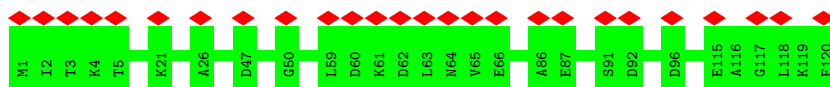
- Molecule 19: 50S ribosomal protein L16



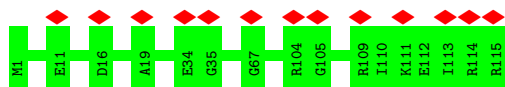
- Molecule 20: 50S ribosomal protein L17



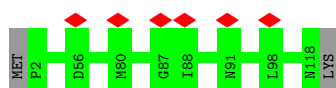
- Molecule 21: 50S ribosomal protein L18

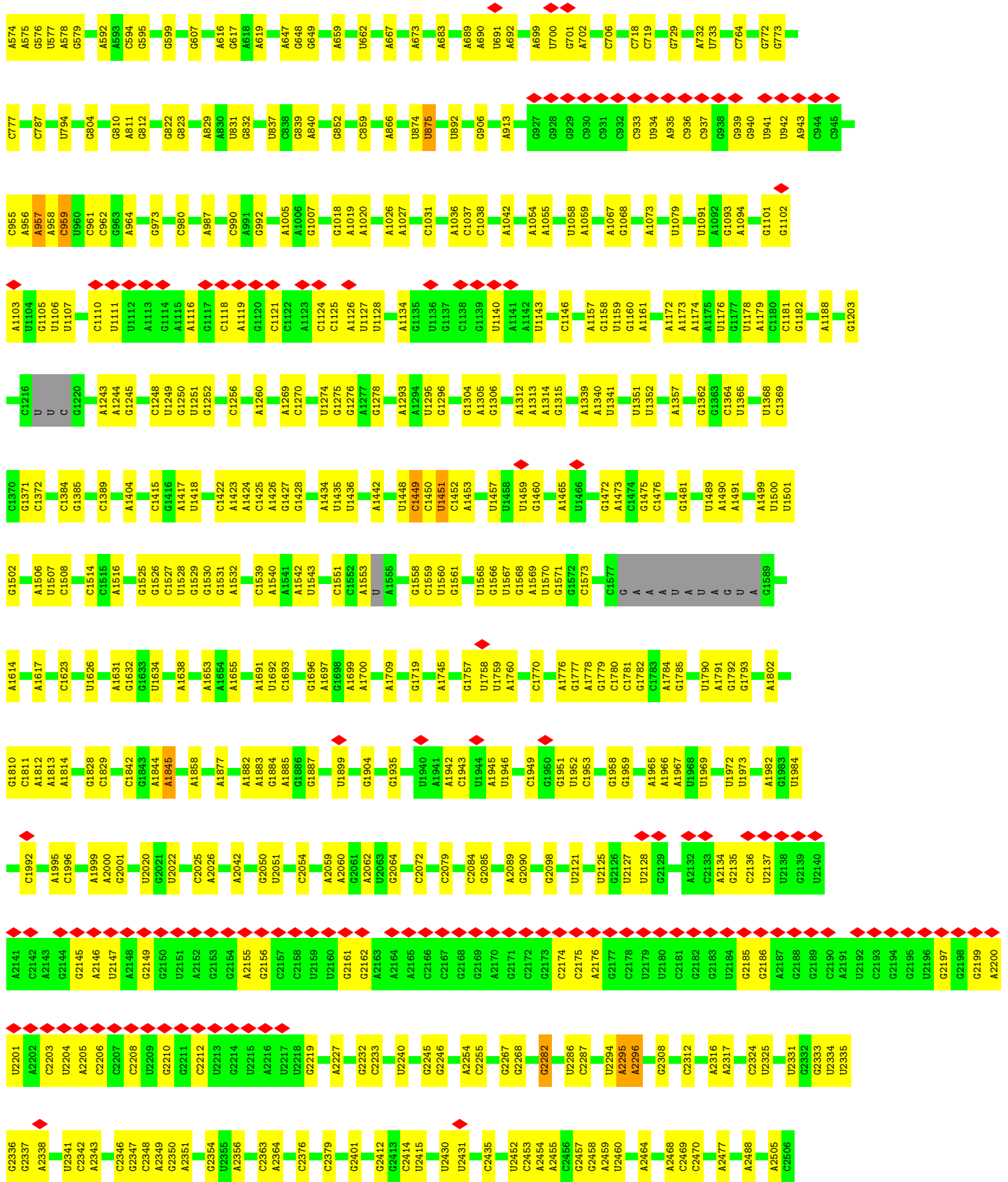


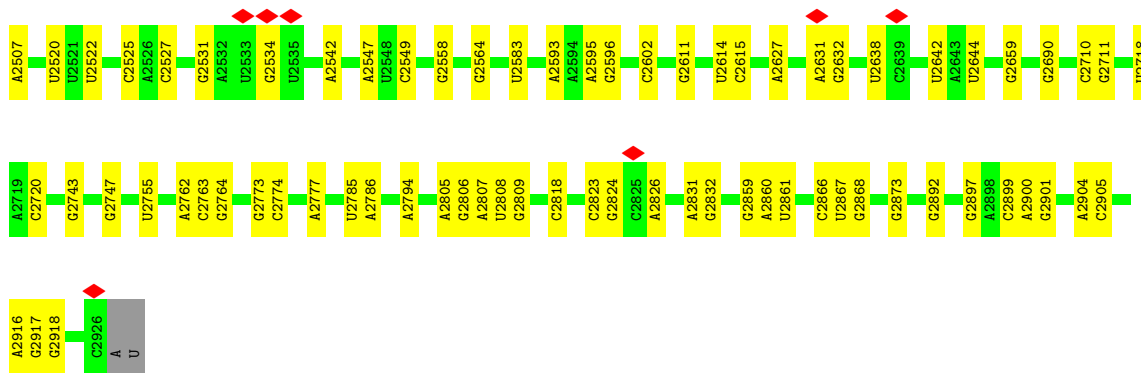
- Molecule 22: 50S ribosomal protein L19



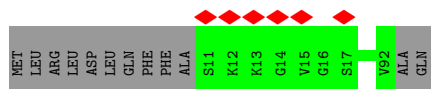
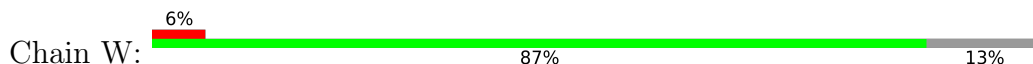
- Molecule 23: 50S ribosomal protein L20



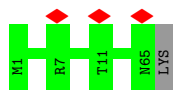




• Molecule 29: 50S ribosomal protein L27



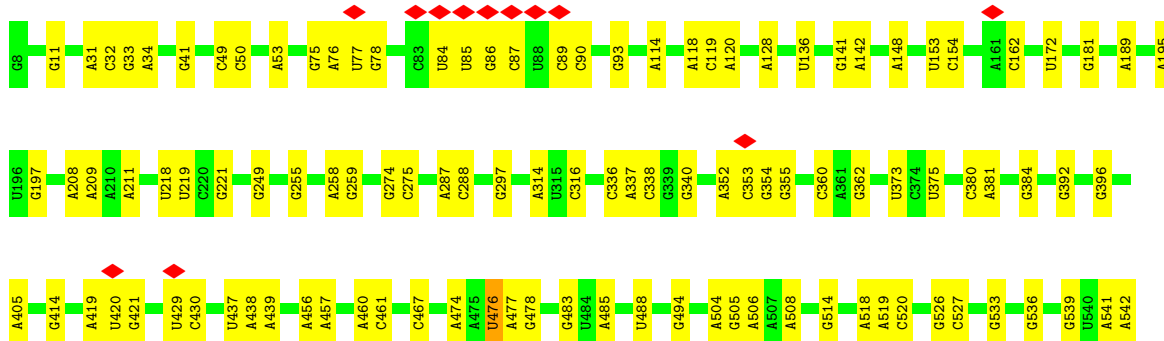
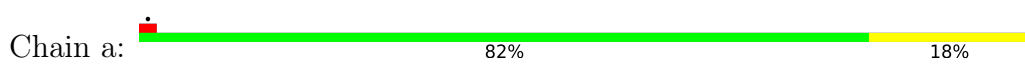
• Molecule 30: 50S ribosomal protein L29

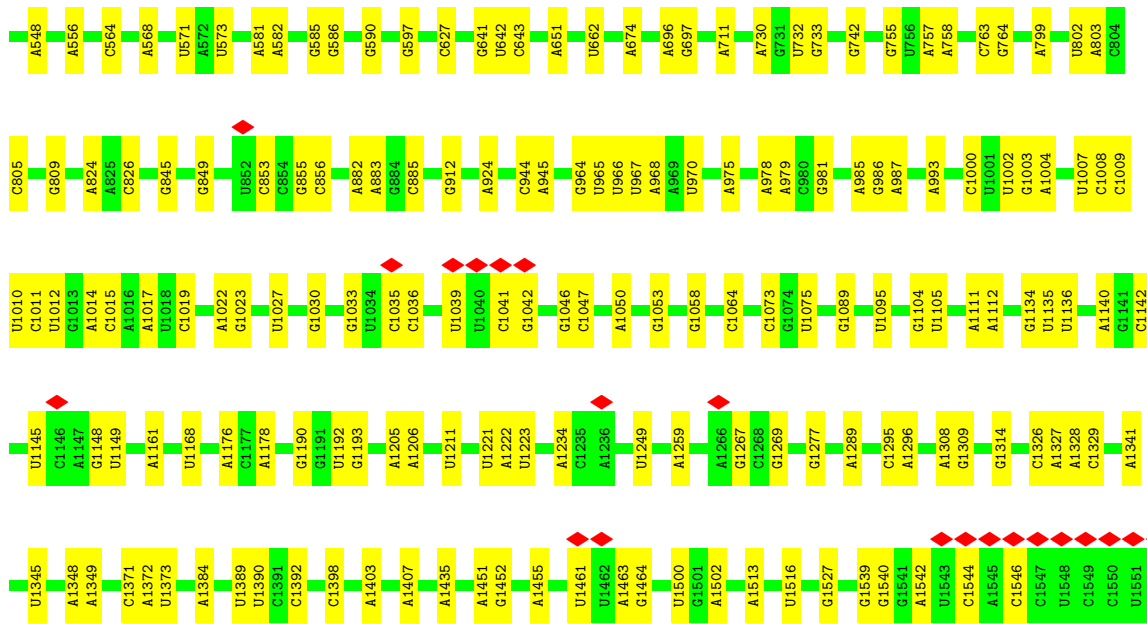


• Molecule 31: 50S ribosomal protein L30

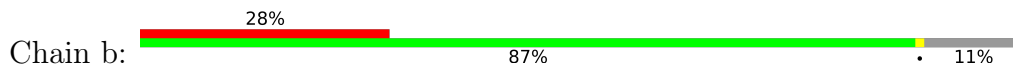


• Molecule 32: 16S ribosomal RNA

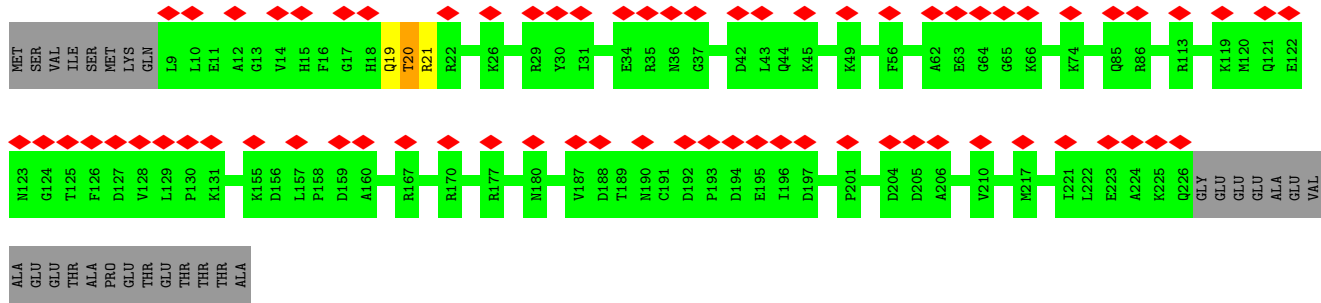




• Molecule 33: 30S ribosomal protein S2



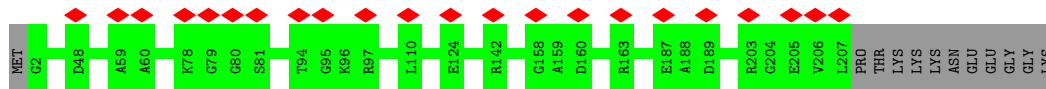
Chain b:



• Molecule 34: 30S ribosomal protein S3



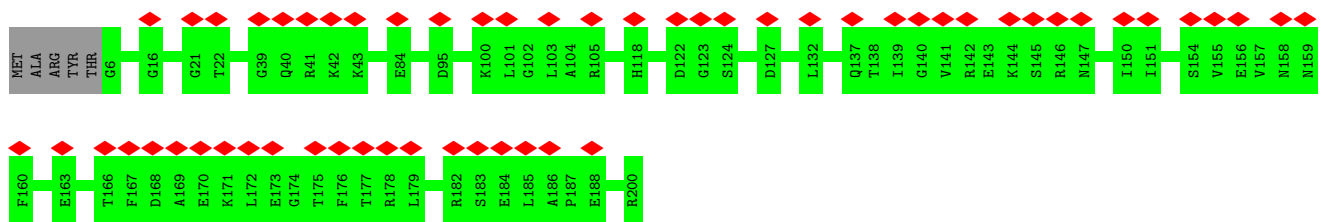
Chain c:



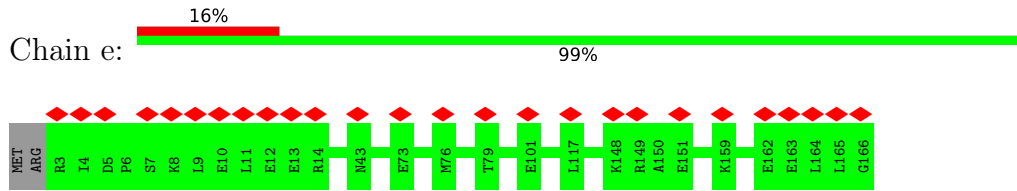
• Molecule 35: 30S ribosomal protein S4



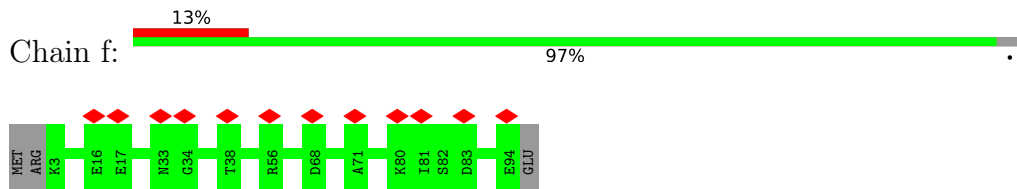
Chain d:



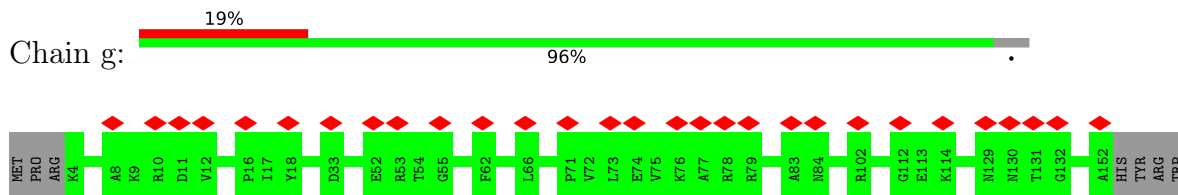
- Molecule 36: 30S ribosomal protein S5



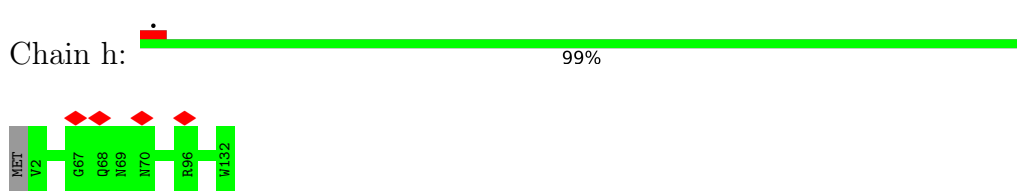
- Molecule 37: 30S ribosomal protein S6



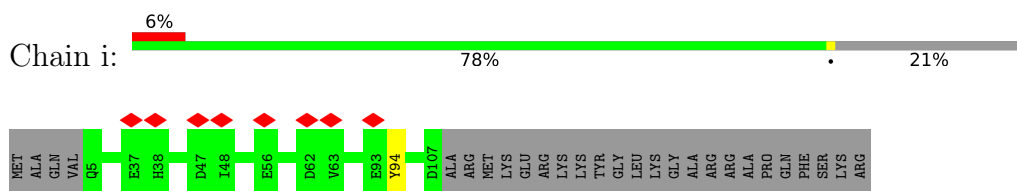
- Molecule 38: 30S ribosomal protein S7



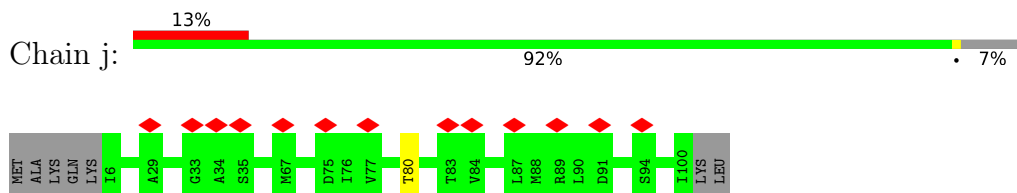
- Molecule 39: 30S ribosomal protein S8



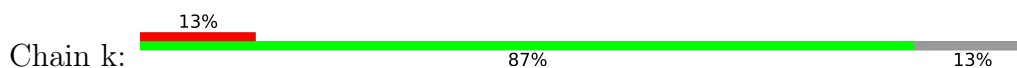
- Molecule 40: 30S ribosomal protein S9

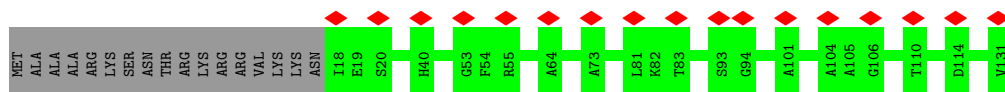


- Molecule 41: 30S ribosomal protein S10

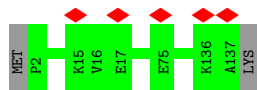


- Molecule 42: 30S ribosomal protein S11

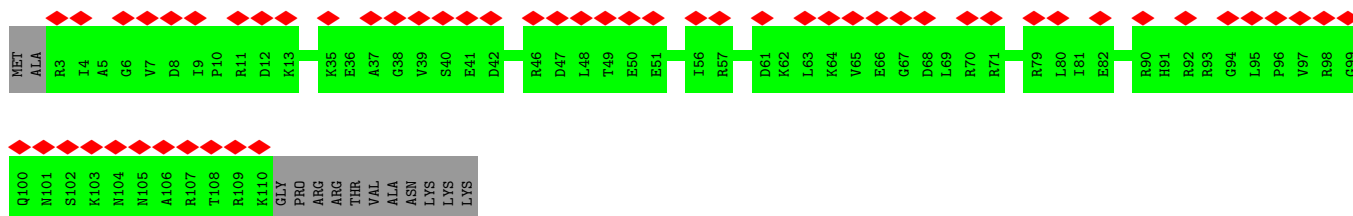
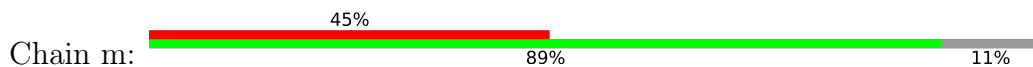




• Molecule 43: 30S ribosomal protein S12



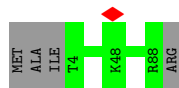
• Molecule 44: 30S ribosomal protein S13



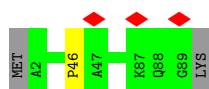
• Molecule 45: 30S ribosomal protein S14



• Molecule 46: 30S ribosomal protein S15

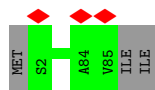


• Molecule 47: 30S ribosomal protein S16

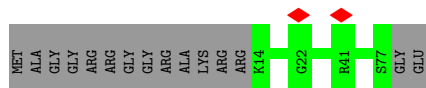
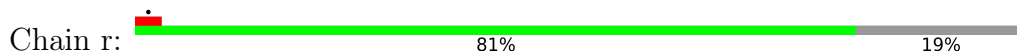


• Molecule 48: 30S ribosomal protein S17

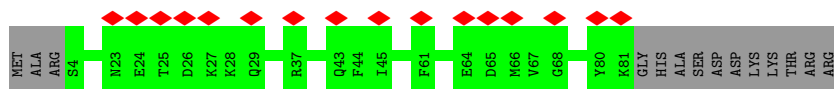
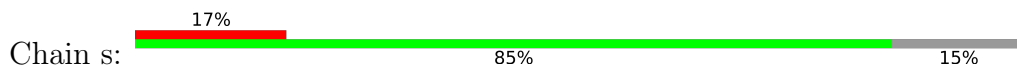




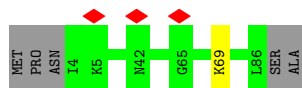
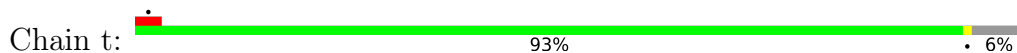
• Molecule 49: 30S ribosomal protein S18



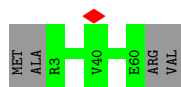
• Molecule 50: 30S ribosomal protein S19



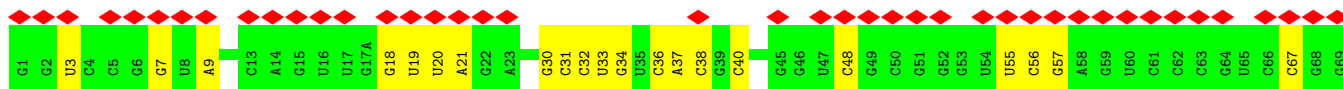
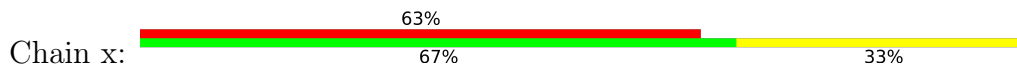
• Molecule 51: 30S ribosomal protein S20



• Molecule 52: 50S ribosomal protein L28



• Molecule 53: P/E-site tRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	27833	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 ($e^-/\text{\AA}^2$)	46.5	Depositor
Minimum defocus (nm)	750	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	43.238	Depositor
Minimum map value	-15.141	Depositor
Average map value	-0.028	Depositor
Map value standard deviation	1.347	Depositor
Recommended contour level	5.0	Depositor
Map size (\AA)	590.64, 590.64, 590.64	wwPDB
Map dimensions	368, 368, 368	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.605, 1.605, 1.605	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	0	0.26	0/433	0.40	0/574
2	1	0.25	0/406	0.40	0/540
3	2	0.25	0/371	0.42	0/483
4	3	0.25	0/519	0.44	0/680
5	4	0.26	0/300	0.38	0/393
6	6	0.26	0/421	0.40	0/562
7	A	0.49	0/708	1.09	5/1103 (0.5%)
8	B	0.17	0/2675	0.74	0/4170
9	C	0.25	0/2120	0.42	0/2845
10	D	0.29	0/1591	0.46	0/2132
11	E	0.24	0/1580	0.40	0/2132
12	F	0.25	0/1405	0.42	0/1887
13	G	0.23	0/1360	0.41	0/1832
14	H	0.21	0/1834	0.83	1/2858 (0.0%)
16	J	0.24	0/1147	0.41	0/1542
17	K	0.26	0/928	0.44	0/1245
18	L	0.26	0/1094	0.44	0/1457
19	M	0.25	0/1099	0.41	0/1468
20	N	0.24	0/961	0.42	0/1284
21	O	0.24	0/922	0.41	0/1236
22	P	0.25	0/958	0.44	0/1279
23	Q	0.24	0/952	0.39	0/1266
24	R	0.26	0/798	0.46	0/1070
25	S	0.24	0/851	0.43	0/1146
26	T	0.25	0/731	0.42	0/974
27	U	0.26	0/772	0.42	0/1032
28	V	0.22	0/69445	0.76	38/108336 (0.0%)
29	W	0.30	0/638	0.50	0/847
30	Y	0.24	0/531	0.37	0/707
31	Z	0.23	0/458	0.44	0/613
32	a	0.20	0/37100	0.73	2/57875 (0.0%)
33	b	0.25	0/1782	0.41	0/2392
34	c	0.24	0/1641	0.43	0/2208
35	d	0.25	0/1599	0.39	0/2147

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
36	e	0.25	0/1231	0.44	0/1655
37	f	0.24	0/766	0.40	0/1031
38	g	0.23	0/1196	0.38	0/1604
39	h	0.24	0/1049	0.43	0/1407
40	i	0.24	0/794	0.41	0/1074
41	j	0.24	0/773	0.41	0/1044
42	k	0.24	0/853	0.45	0/1153
43	l	0.24	0/1069	0.42	0/1435
44	m	0.23	0/873	0.42	0/1166
45	n	0.26	0/508	0.41	0/672
46	o	0.23	0/718	0.38	0/960
47	p	0.25	0/708	0.40	0/950
48	q	0.24	0/699	0.43	0/933
49	r	0.24	0/526	0.41	0/705
50	s	0.24	0/649	0.40	0/872
51	t	0.23	0/639	0.38	0/852
52	u	0.23	0/448	0.44	0/596
53	x	0.18	0/1809	0.74	0/2819
All	All	0.22	0/155438	0.69	46/233243 (0.0%)

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
33	b	0	1

There are no bond length outliers.

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	21	C	P-O3'-C3'	-12.16	105.11	119.70
28	V	181	G	P-O3'-C3'	-9.75	108.00	119.70
28	V	76	C	P-O3'-C3'	-9.67	108.10	119.70
7	A	27	A	P-O3'-C3'	-8.82	109.12	119.70
28	V	1842	C	P-O3'-C3'	-8.76	109.19	119.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
33	b	20	THR	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	
1	0	52/59 (88%)	51 (98%)	1 (2%)	0	100	100
2	1	46/49 (94%)	45 (98%)	1 (2%)	0	100	100
3	2	42/44 (96%)	41 (98%)	1 (2%)	0	100	100
4	3	62/66 (94%)	58 (94%)	4 (6%)	0	100	100
5	4	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
6	6	52/66 (79%)	49 (94%)	3 (6%)	0	100	100
9	C	270/277 (98%)	258 (96%)	12 (4%)	0	100	100
10	D	204/209 (98%)	198 (97%)	6 (3%)	0	100	100
11	E	203/207 (98%)	192 (95%)	11 (5%)	0	100	100
12	F	174/179 (97%)	163 (94%)	11 (6%)	0	100	100
13	G	173/179 (97%)	170 (98%)	3 (2%)	0	100	100
16	J	140/145 (97%)	136 (97%)	4 (3%)	0	100	100
17	K	120/122 (98%)	118 (98%)	2 (2%)	0	100	100
18	L	144/146 (99%)	142 (99%)	2 (1%)	0	100	100
19	M	133/144 (92%)	128 (96%)	5 (4%)	0	100	100
20	N	117/120 (98%)	112 (96%)	5 (4%)	0	100	100
21	O	118/120 (98%)	116 (98%)	2 (2%)	0	100	100
22	P	113/115 (98%)	108 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
23	Q	115/119 (97%)	107 (93%)	8 (7%)	0	100	100
24	R	99/102 (97%)	90 (91%)	9 (9%)	0	100	100
25	S	107/113 (95%)	99 (92%)	8 (8%)	0	100	100
26	T	88/95 (93%)	85 (97%)	3 (3%)	0	100	100
27	U	99/103 (96%)	93 (94%)	6 (6%)	0	100	100
29	W	80/94 (85%)	75 (94%)	5 (6%)	0	100	100
30	Y	63/66 (96%)	62 (98%)	1 (2%)	0	100	100
31	Z	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
33	b	216/246 (88%)	195 (90%)	18 (8%)	3 (1%)	11	46
34	c	204/218 (94%)	191 (94%)	13 (6%)	0	100	100
35	d	193/200 (96%)	188 (97%)	5 (3%)	0	100	100
36	e	162/166 (98%)	156 (96%)	6 (4%)	0	100	100
37	f	90/95 (95%)	87 (97%)	3 (3%)	0	100	100
38	g	147/156 (94%)	146 (99%)	1 (1%)	0	100	100
39	h	129/132 (98%)	118 (92%)	11 (8%)	0	100	100
40	i	101/130 (78%)	97 (96%)	4 (4%)	0	100	100
41	j	93/102 (91%)	85 (91%)	8 (9%)	0	100	100
42	k	112/131 (86%)	108 (96%)	4 (4%)	0	100	100
43	l	134/138 (97%)	125 (93%)	9 (7%)	0	100	100
44	m	106/121 (88%)	98 (92%)	8 (8%)	0	100	100
45	n	58/61 (95%)	51 (88%)	6 (10%)	1 (2%)	9	42
46	o	83/89 (93%)	83 (100%)	0	0	100	100
47	p	86/90 (96%)	79 (92%)	6 (7%)	1 (1%)	13	50
48	q	82/87 (94%)	77 (94%)	5 (6%)	0	100	100
49	r	62/79 (78%)	58 (94%)	4 (6%)	0	100	100
50	s	76/92 (83%)	75 (99%)	1 (1%)	0	100	100
51	t	81/88 (92%)	78 (96%)	2 (2%)	1 (1%)	13	50
52	u	56/62 (90%)	51 (91%)	5 (9%)	0	100	100
All	All	5176/5518 (94%)	4929 (95%)	241 (5%)	6 (0%)	54	84

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
33	b	20	THR
51	t	69	LYS
33	b	21	ARG
47	p	46	PRO
33	b	19	GLN

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	48/53 (91%)	48 (100%)	0	100	100
2	1	46/47 (98%)	46 (100%)	0	100	100
3	2	39/39 (100%)	39 (100%)	0	100	100
4	3	54/56 (96%)	54 (100%)	0	100	100
5	4	35/35 (100%)	35 (100%)	0	100	100
6	6	44/55 (80%)	44 (100%)	0	100	100
9	C	220/225 (98%)	220 (100%)	0	100	100
10	D	167/170 (98%)	167 (100%)	0	100	100
11	E	169/170 (99%)	168 (99%)	1 (1%)	86	94
12	F	151/154 (98%)	151 (100%)	0	100	100
13	G	148/151 (98%)	148 (100%)	0	100	100
16	J	120/123 (98%)	120 (100%)	0	100	100
17	K	101/101 (100%)	101 (100%)	0	100	100
18	L	110/110 (100%)	110 (100%)	0	100	100
19	M	109/116 (94%)	109 (100%)	0	100	100
20	N	99/100 (99%)	99 (100%)	0	100	100
21	O	93/93 (100%)	93 (100%)	0	100	100
22	P	100/100 (100%)	100 (100%)	0	100	100
23	Q	96/98 (98%)	96 (100%)	0	100	100
24	R	83/84 (99%)	83 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	S	90/93 (97%)	90 (100%)	0	100	100
26	T	81/85 (95%)	81 (100%)	0	100	100
27	U	85/87 (98%)	85 (100%)	0	100	100
29	W	64/74 (86%)	64 (100%)	0	100	100
30	Y	56/57 (98%)	56 (100%)	0	100	100
31	Z	52/53 (98%)	52 (100%)	0	100	100
33	b	189/212 (89%)	189 (100%)	0	100	100
34	c	168/178 (94%)	168 (100%)	0	100	100
35	d	169/173 (98%)	169 (100%)	0	100	100
36	e	128/130 (98%)	128 (100%)	0	100	100
37	f	81/84 (96%)	81 (100%)	0	100	100
38	g	125/132 (95%)	125 (100%)	0	100	100
39	h	111/112 (99%)	111 (100%)	0	100	100
40	i	81/102 (79%)	80 (99%)	1 (1%)	71	87
41	j	86/92 (94%)	85 (99%)	1 (1%)	71	87
42	k	86/100 (86%)	86 (100%)	0	100	100
43	l	114/116 (98%)	114 (100%)	0	100	100
44	m	94/104 (90%)	94 (100%)	0	100	100
45	n	53/54 (98%)	53 (100%)	0	100	100
46	o	80/83 (96%)	80 (100%)	0	100	100
47	p	74/76 (97%)	74 (100%)	0	100	100
48	q	77/80 (96%)	77 (100%)	0	100	100
49	r	56/64 (88%)	56 (100%)	0	100	100
50	s	70/81 (86%)	70 (100%)	0	100	100
51	t	66/70 (94%)	66 (100%)	0	100	100
52	u	47/50 (94%)	47 (100%)	0	100	100
All	All	4415/4622 (96%)	4412 (100%)	3 (0%)	93	98

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
11	E	194	ILE
40	i	94	TYR

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Mol	Chain	Res	Type
41	j	80	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
14	H	76/77 (98%)	28 (36%)	4 (5%)
28	V	2881/2928 (98%)	627 (21%)	57 (1%)
32	a	1544/1545 (99%)	278 (18%)	0
53	x	75/76 (98%)	25 (33%)	0
7	A	28/29 (96%)	14 (50%)	5 (17%)
8	B	111/112 (99%)	27 (24%)	4 (3%)
All	All	4715/4767 (98%)	999 (21%)	70 (1%)

5 of 999 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	A	3	G
7	A	5	A
7	A	7	A
7	A	10	A
7	A	12	A

5 of 70 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
28	V	2254	A
28	V	2295	A
28	V	2468	A
28	V	554	U
28	V	549	A

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.

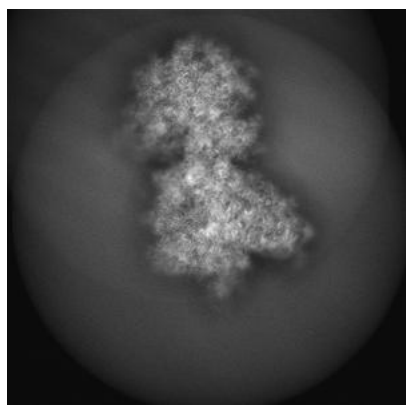
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14158. These allow visual inspection of the internal detail of the map and identification of artifacts.

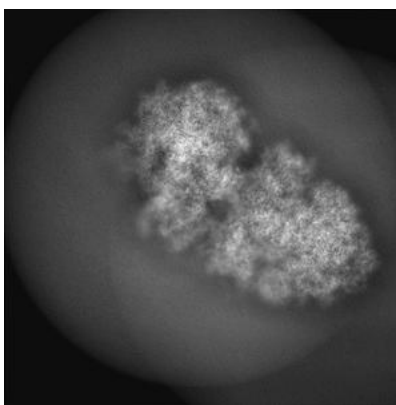
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

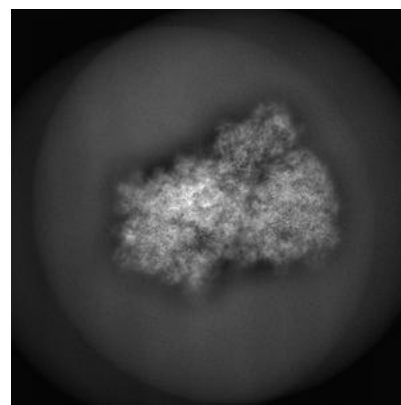
6.1.1 Primary map



X



Y

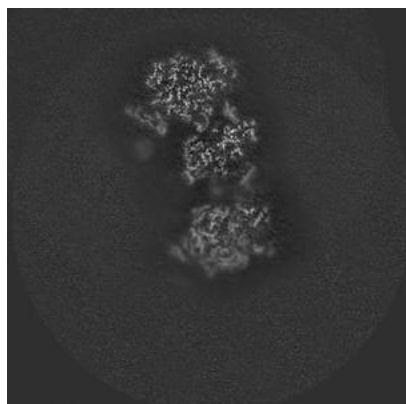


Z

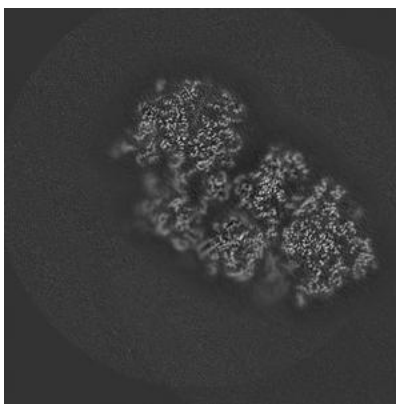
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

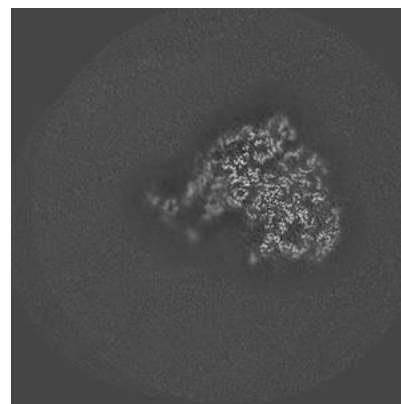
6.2.1 Primary map



X Index: 184



Y Index: 184

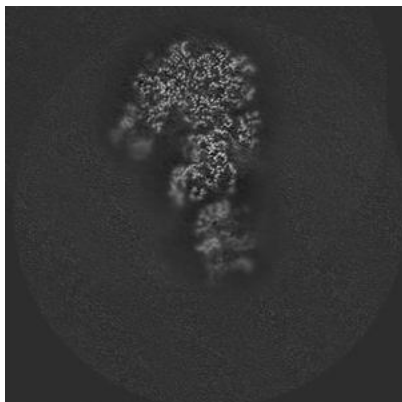


Z Index: 184

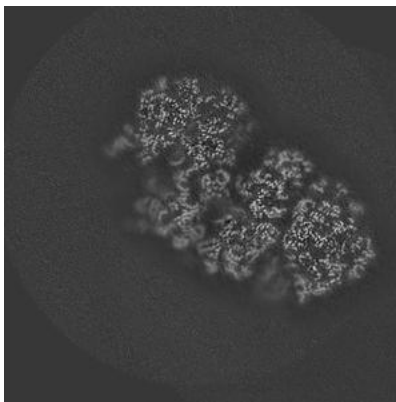
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

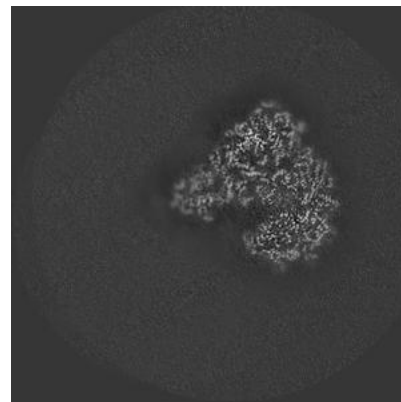
6.3.1 Primary map



X Index: 163



Y Index: 187



Z Index: 169

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 5.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

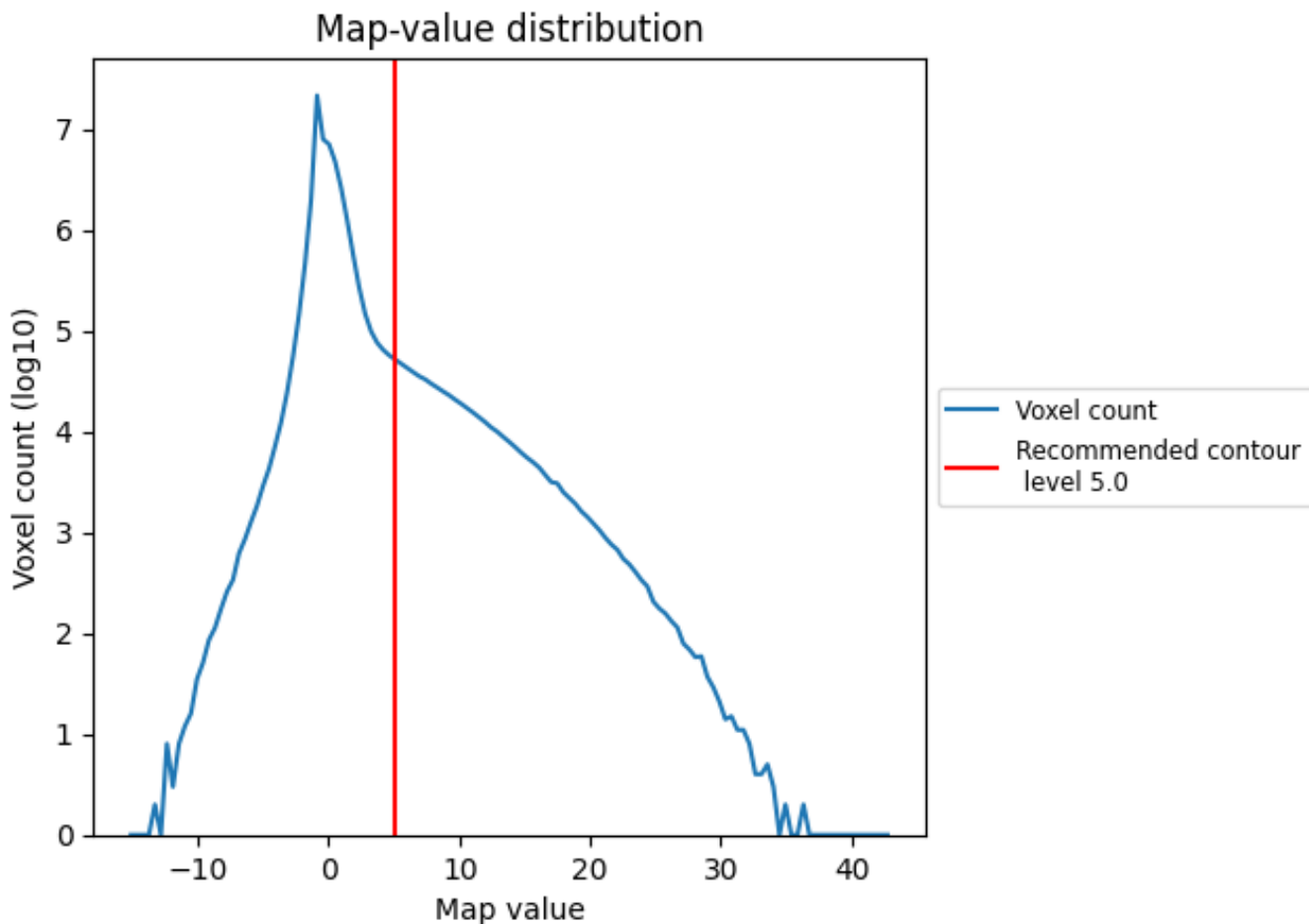
6.5 Mask visualisation

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

7 Map analysis [i](#)

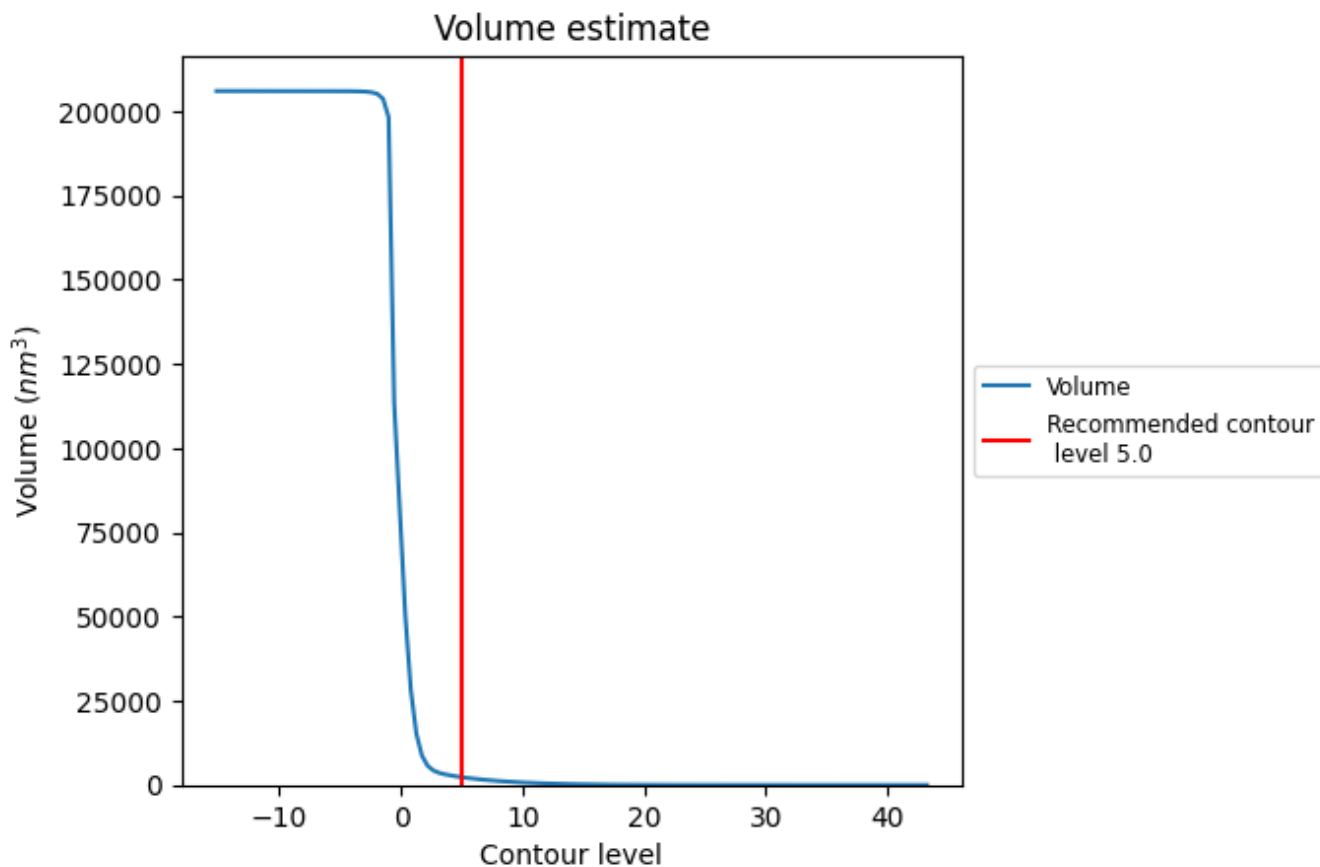
This section contains the results of statistical analysis of the map.

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.

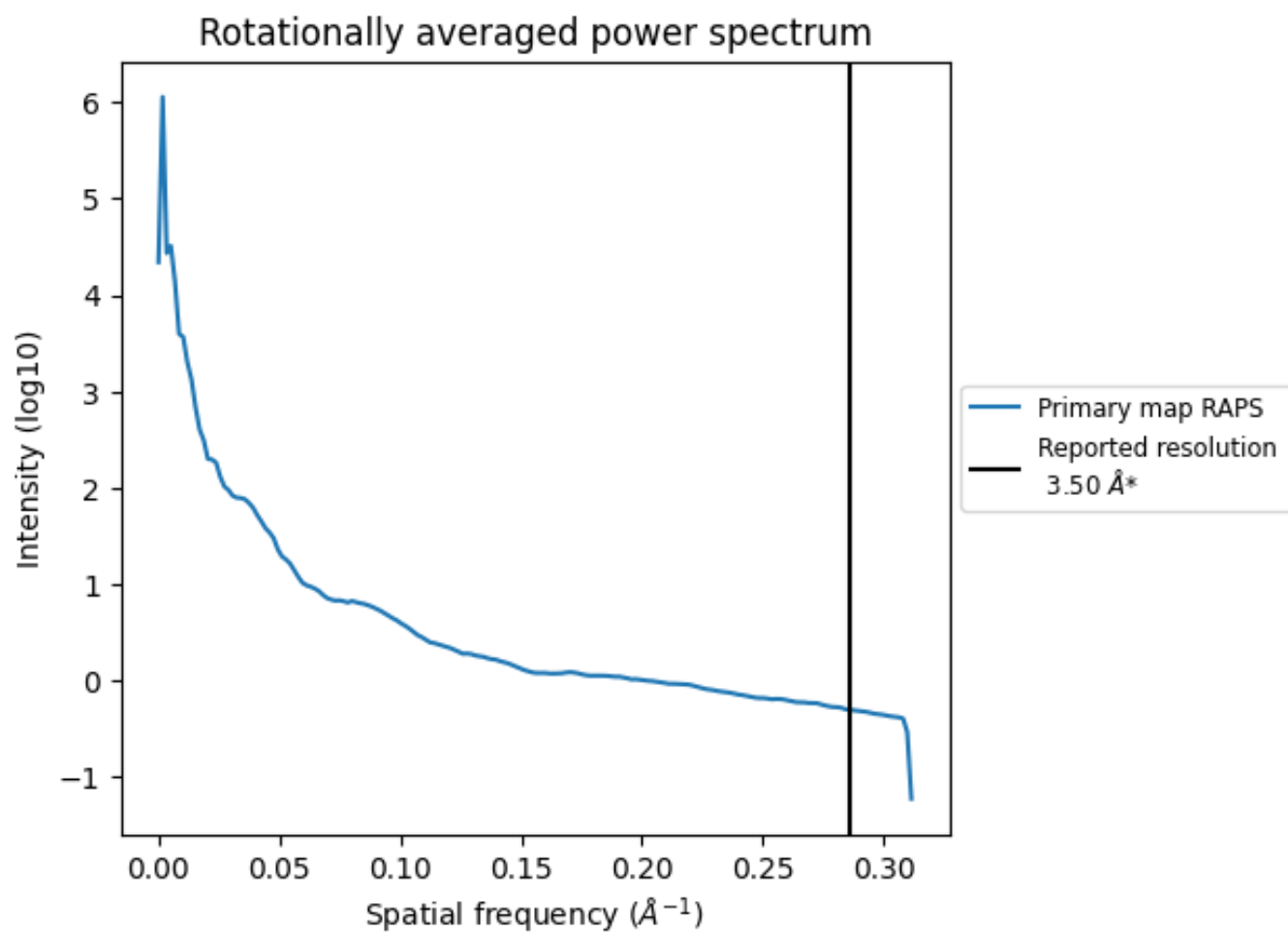
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 2302 nm^3 ; this corresponds to an approximate mass of 2079 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 0.286 Å⁻¹

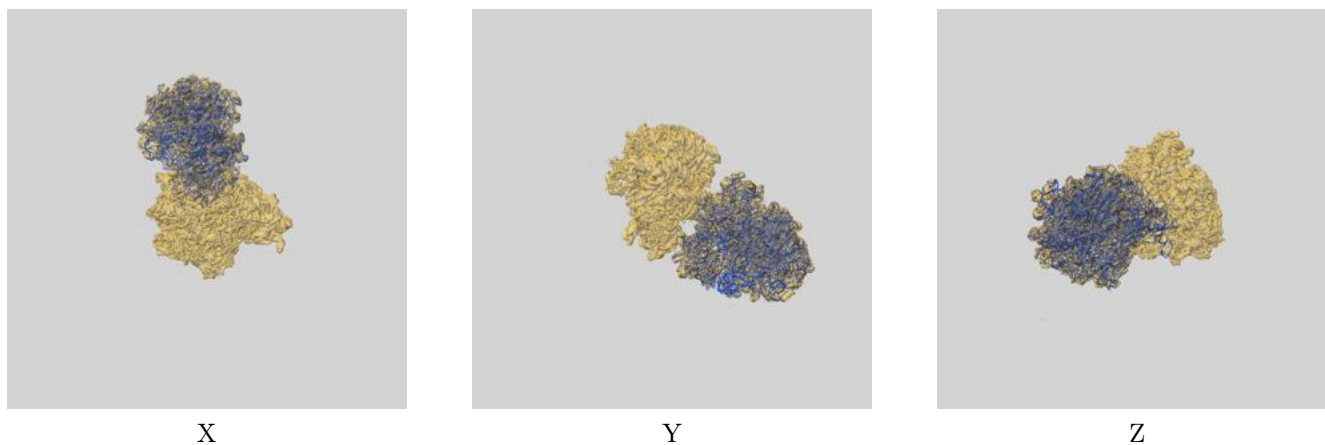
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

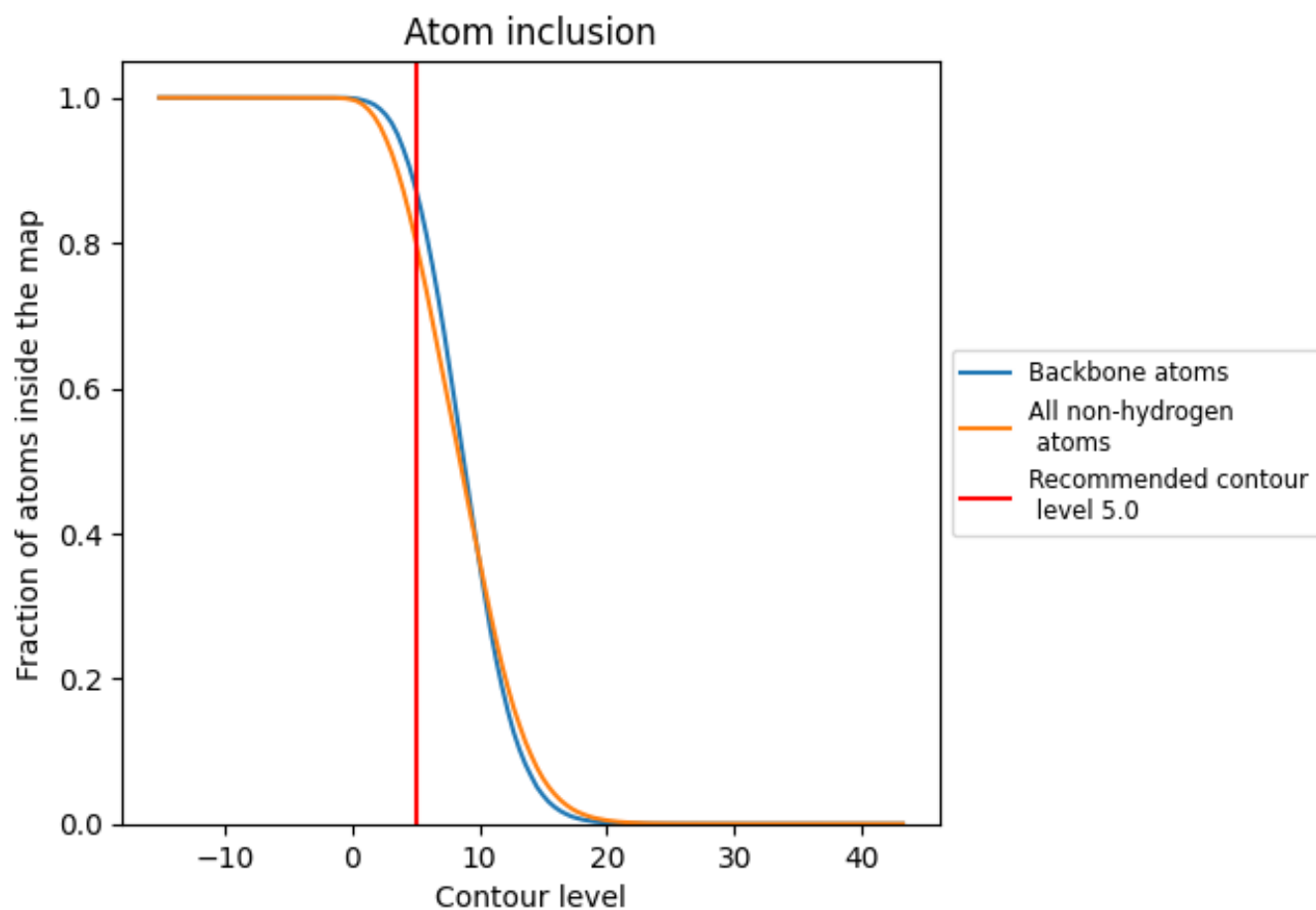
This section contains information regarding the fit between EMDB map EMD-14158 and PDB model 7QV2. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 5.0 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 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 80% of all non-hydrogen atoms, are inside the map.