



wwPDB EM Validation Summary Report ⓘ

Dec 29, 2024 – 11:51 AM EST

PDB ID : 7P6Z
EMDB ID : EMD-13234
Title : Mycoplasma pneumoniae 70S ribosome in untreated cells
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.
Deposited on : 2021-07-18
Resolution : 3.50 Å(reported)
Based on initial models : 7OOD, 4V7C, 3J9W, 7OOC

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.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.40

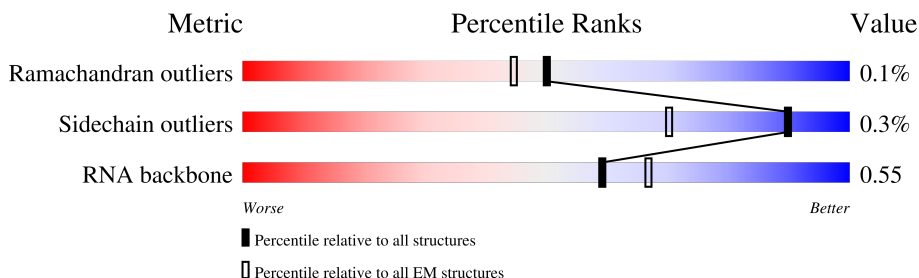
1 Overall quality at a glance

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	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	3	2907	
2	4	108	
3	w	111	
4	a	287	
5	c	212	
6	e	184	
7	k	151	
8	i	146	

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Mol	Chain	Length	Quality of chain
9	m	124	
10	q	100	
11	u	104	
12	y	57	
13	0	48	
14	2	37	
15	1	59	
16	o	119	
17	s	237	
18	v	65	
19	x	97	
20	z	53	
21	d	180	
22	b	287	
23	l	139	
24	p	127	
25	j	122	
26	n	116	
27	t	111	
28	r	159	
29	B	273	
30	D	219	
31	F	155	
32	A	294	
33	H	132	

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Mol	Chain	Length	Quality of chain
34	J	121	<div>80%</div> <div>93% 6%</div>
35	C	205	<div>84%</div> <div>99%</div>
36	S	87	<div>64%</div> <div>87% 11%</div>
37	O	94	<div>77%</div> <div>91% 7%</div>
38	K	139	<div>50%</div> <div>97% ..</div>
39	M	61	<div>77%</div> <div>98% .</div>
40	I	108	<div>80%</div> <div>93% 6%</div>
41	L	124	<div>90%</div> <div>94% 5%</div>
42	N	86	<div>58%</div> <div>97% .</div>
43	R	87	<div>97%</div> <div>97% .</div>
44	T	60	<div>67%</div> <div>87% 12%</div>
45	G	142	<div>72%</div> <div>99% ..</div>
46	Q	104	<div>46%</div> <div>62% 38%</div>
47	E	215	<div>71%</div> <div>77% 22%</div>
48	P	85	<div>79%</div> <div>96% ..</div>
49	5	1520	<div>16%</div> <div>80% 18% .</div>
50	Z	5	<div>40%</div> <div>100%</div>
51	7	76	<div>55%</div> <div>72% 26% .</div>
52	Y	9	<div>67%</div> <div>33%</div>
53	f	149	<div>85%</div> <div>96% ..</div>
54	h	137	<div>93%</div> <div>92% 7% ..</div>
55	g	161	<div>77%</div> <div>75% 22% .</div>

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 142534 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	3	2879	Total	C	N	O	P	0	0
			61690	27566	11236	20009	2879		

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	4	105	Total	C	N	O	P	0	0
			2245	1003	409	728	105		

- Molecule 3 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	w	99	Total	C	N	O	0	0
			798	505	149	144		

- Molecule 4 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	a	285	Total	C	N	O	S	0	0
			2199	1370	433	390	6		

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	c	210	Total	C	N	O	S	0	0
			1613	1026	294	290	3		

- Molecule 6 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	e	176	Total	C	N	O	0	0
			1349	867	240	242		

- Molecule 7 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	k	148	Total	C	N	O	0	0
			1138	722	223	193		

- Molecule 8 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	i	144	Total	C	N	O	S	0	0
			1158	733	212	208	5		

- Molecule 9 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	m	119	Total	C	N	O	S	0	0
			957	609	175	170	3		

- Molecule 10 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	q	99	Total	C	N	O	S	0	0
			809	525	148	133	3		

- Molecule 11 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	u	86	Total	C	N	O	S	0	0
			641	397	127	116	1		

- Molecule 12 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	y	56	Total	C	N	O	S	0	0
			436	262	96	73	5		

- Molecule 13 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	0	47	Total	C	N	O	S	0	0
			377	234	81	61	1		

- Molecule 14 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	2	37	Total	C	N	O	S	0	0
			303	189	65	45	4		

- Molecule 15 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	1	59	Total	C	N	O	S	0	0
			477	300	99	77	1		

- Molecule 16 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	o	115	Total	C	N	O	S	0	0
			895	568	169	157	1		

- Molecule 17 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	s	92	Total	C	N	O	S	0	0
			714	470	121	122	1		

- Molecule 18 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	v	63	Total	C	N	O	S	0	0
			504	312	107	84	1		

- Molecule 19 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	x	44	Total	C	N	O	0	0
			218	130	44	44		

- Molecule 20 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	z	50	Total	C	N	O	S	0	0
			408	255	81	68	4		

- Molecule 21 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	d	175	Total	C	N	O	S	0	0
			1244	797	214	229	4		

- Molecule 22 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	b	229	Total	C	N	O	S	0	0
			1758	1116	317	318	7		

- Molecule 23 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	l	136	Total	C	N	O	S	0	0
			1057	680	193	177	7		

- Molecule 24 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	p	114	Total	C	N	O	S	0	0
			941	600	185	154	2		

- Molecule 25 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	j	122	Total	C	N	O	S	0	0
			944	595	178	167	4		

- Molecule 26 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	n	112	Total	C	N	O	S	0	0
			853	534	169	149	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	t	96	Total	C	N	O	S	0	0
			706	449	132	122	3		

- Molecule 28 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	r	139	Total	C	N	O	S	0	0
			1068	663	207	191	7		

- Molecule 29 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	B	215	Total	C	N	O	S	0	0
			1682	1063	308	306	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
30	D	153	Total	C	N	O	S	0	0
			1153	731	222	197	3		

- Molecule 31 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	F	154	Total	C	N	O	S	0	0
			1231	777	234	215	5		

- Molecule 32 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	A	249	Total	C	N	O	S	0	0
			1917	1224	331	355	7		

- Molecule 33 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	H	128	Total	C	N	O	S	0	0
			993	634	184	174	1		

- Molecule 34 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	J	114	Total	C	N	O	S	0	0
			828	514	153	155	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
35	C	203	Total	C	N	O	S	0	0
			1605	1015	306	280	4		

- Molecule 36 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	S	77	Total	C	N	O		0	0
			629	383	135	111			

- Molecule 37 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	O	87	Total	C	N	O	S	0	0
			690	445	128	115	2		

- Molecule 38 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	K	136	Total	C	N	O	S	0	0
			1055	667	209	177	2		

- Molecule 39 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	M	60	Total	C	N	O	S	0	0
			473	302	96	71	4		

- Molecule 40 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	I	101	Total	C	N	O	S	0	0
			803	518	141	143	1		

- Molecule 41 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	L	118	Total	C	N	O		0	0
			922	576	186	160			

- Molecule 42 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	N	83	Total	C	N	O	0	0
			673	428	125	120		

- Molecule 43 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	R	84	Total	C	N	O	S	0
			654	419	119	114	2	0

- Molecule 44 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	T	53	Total	C	N	O	S	0
			439	275	93	70	1	0

- Molecule 45 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	G	141	Total	C	N	O	S	0
			1103	720	192	189	2	0

- Molecule 46 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	Q	65	Total	C	N	O	S	0
			535	342	103	86	4	0

- Molecule 47 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	E	167	Total	C	N	O	S	0
			1211	762	219	229	1	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
48	P	83	Total	C	N	O	0	0
			675	425	135	115		

- Molecule 49 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	5	1493	Total	C	N	O	P	0	0
			31952	14279	5792	10388	1493		

- Molecule 50 is a protein called nascent peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	Z	5	Total	C	N	O	0	0
			26	15	5	6		

- Molecule 51 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	7	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		

- Molecule 52 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Y	9	Total	C	N	O	P	0	0
			177	81	18	70	8		

- Molecule 53 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	f	144	Total	C	N	O	0	0
			713	425	144	144		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
54	h	128	Total	C	N	O	0	0
			630	374	128	128		

- Molecule 55 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	g	125	Total	C	N	O	0	0
			617	367	125	125		

- Molecule 56 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
56	3	24	Total 24	Mg 24	0
56	y	1	Total 1	Mg 1	0

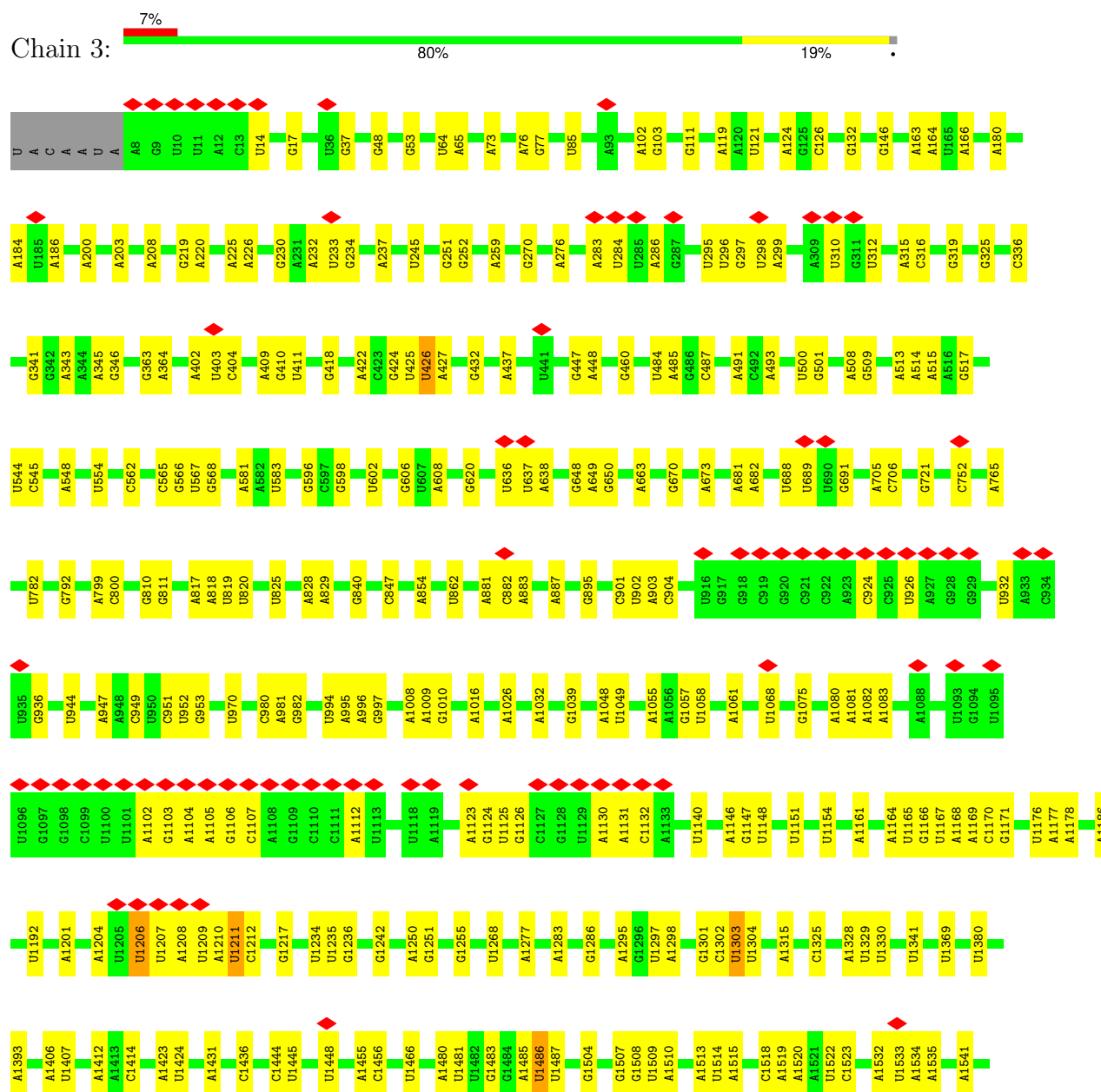
- Molecule 57 is ZINC ION (three-letter code: ZN) (formula: Zn).

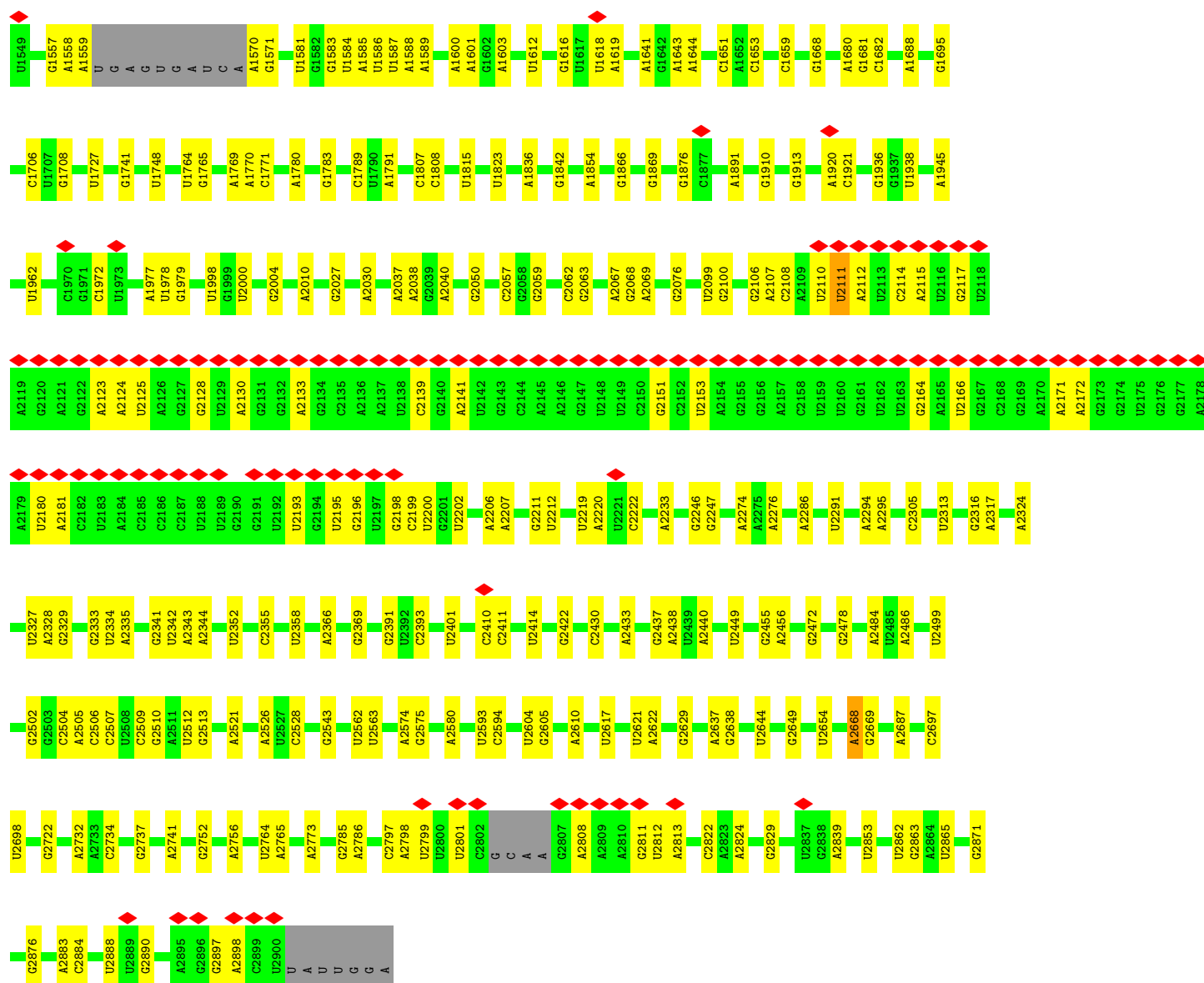
Mol	Chain	Residues	Atoms		AltConf
57	y	1	Total 1	Zn 1	0
57	2	1	Total 1	Zn 1	0
57	z	1	Total 1	Zn 1	0
57	M	1	Total 1	Zn 1	0
57	Q	1	Total 1	Zn 1	0

3 Residue-property plots

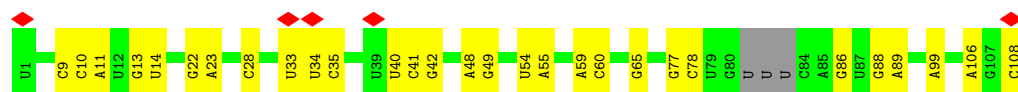
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 23S ribosomal RNA

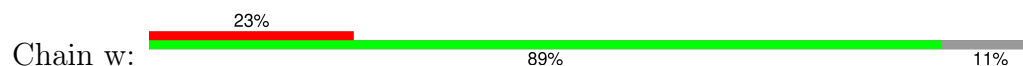




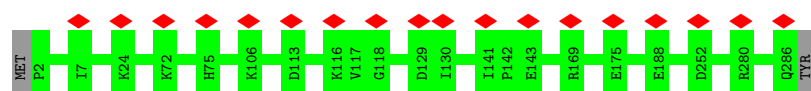
• Molecule 2: 5S ribosomal RNA



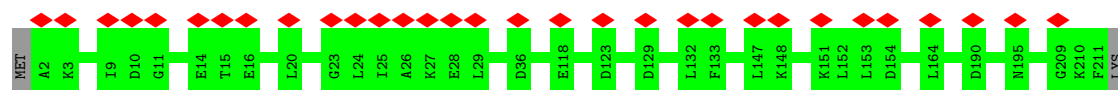
• Molecule 3: 50S ribosomal protein L29



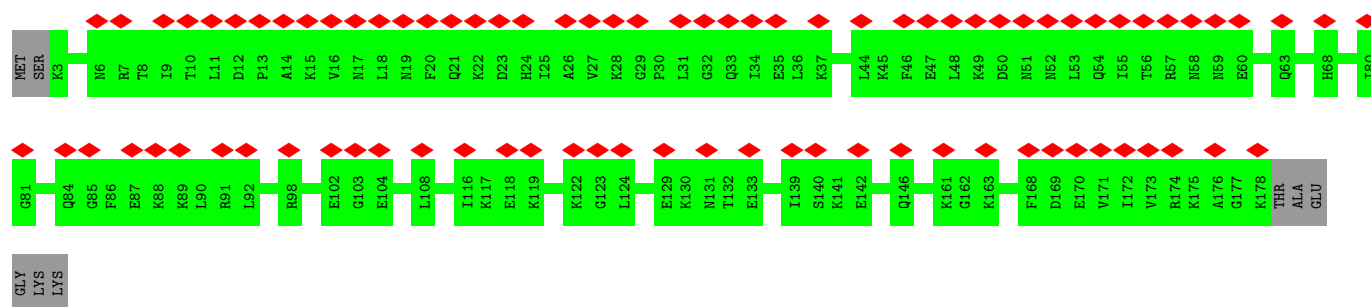
• Molecule 4: 50S ribosomal protein L2



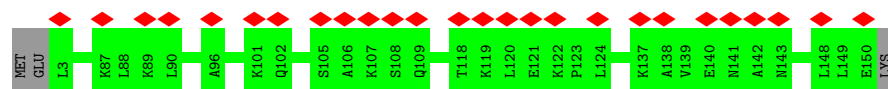
- Molecule 5: 50S ribosomal protein L4



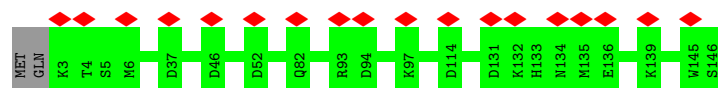
- Molecule 6: 50S ribosomal protein L6



- Molecule 7: 50S ribosomal protein L15



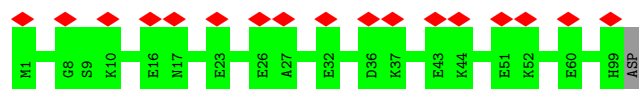
- Molecule 8: 50S ribosomal protein L13



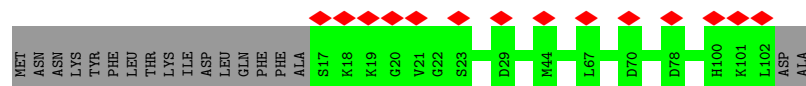
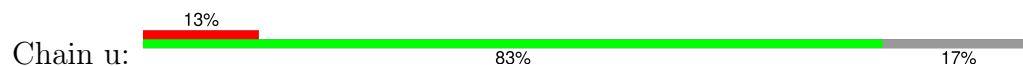
- Molecule 9: 50S ribosomal protein L17



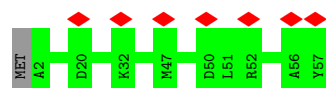
- Molecule 10: 50S ribosomal protein L21



- Molecule 11: 50S ribosomal protein L27



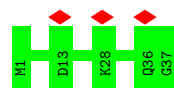
- Molecule 12: 50S ribosomal protein L32



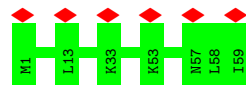
- Molecule 13: 50S ribosomal protein L34



- Molecule 14: 50S ribosomal protein L36

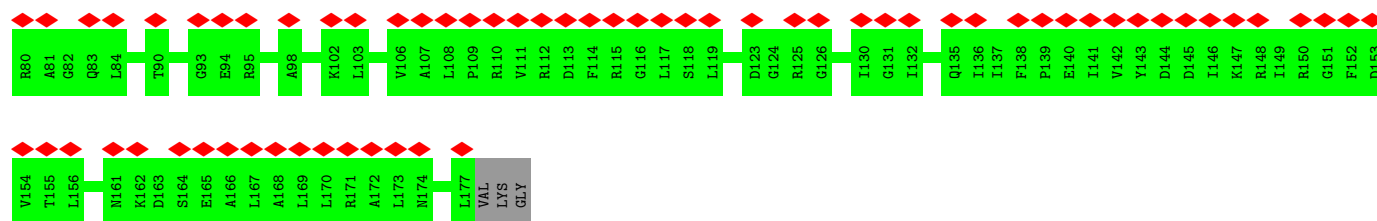


- Molecule 15: 50S ribosomal protein L35

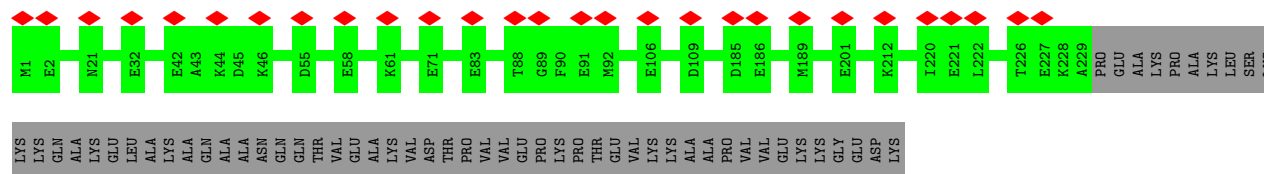
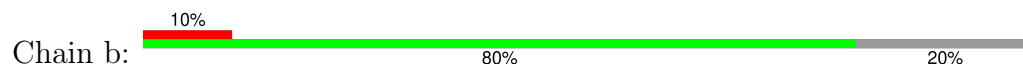


- Molecule 16: 50S ribosomal protein L19

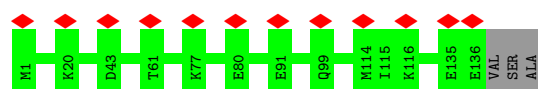




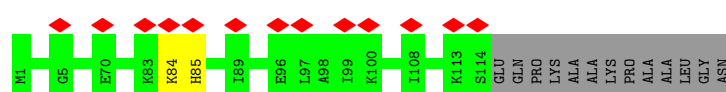
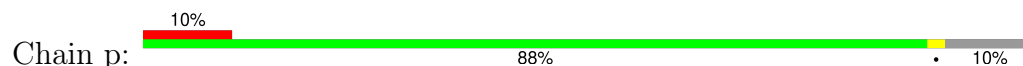
- Molecule 22: 50S ribosomal protein L3



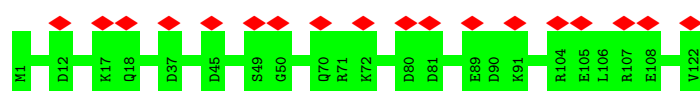
- Molecule 23: 50S ribosomal protein L16



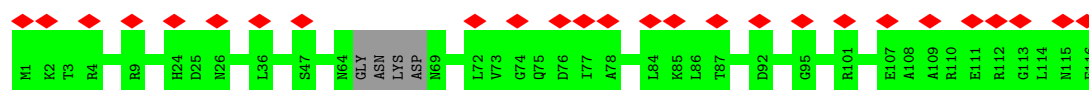
- Molecule 24: 50S ribosomal protein L20



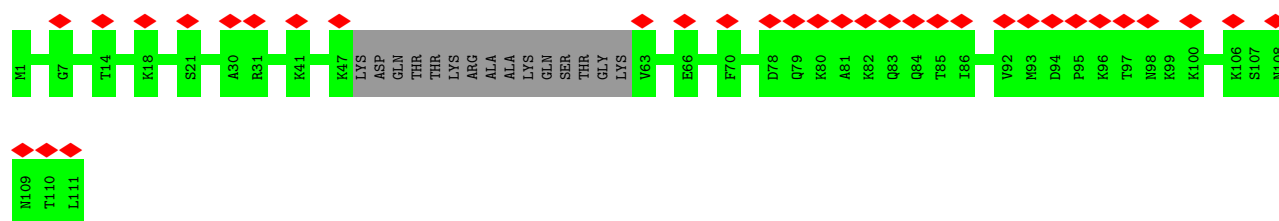
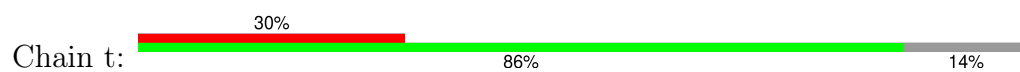
- Molecule 25: 50S ribosomal protein L14



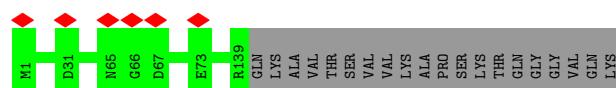
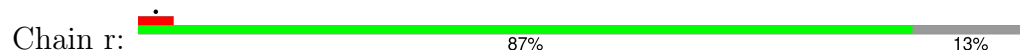
- Molecule 26: 50S ribosomal protein L18



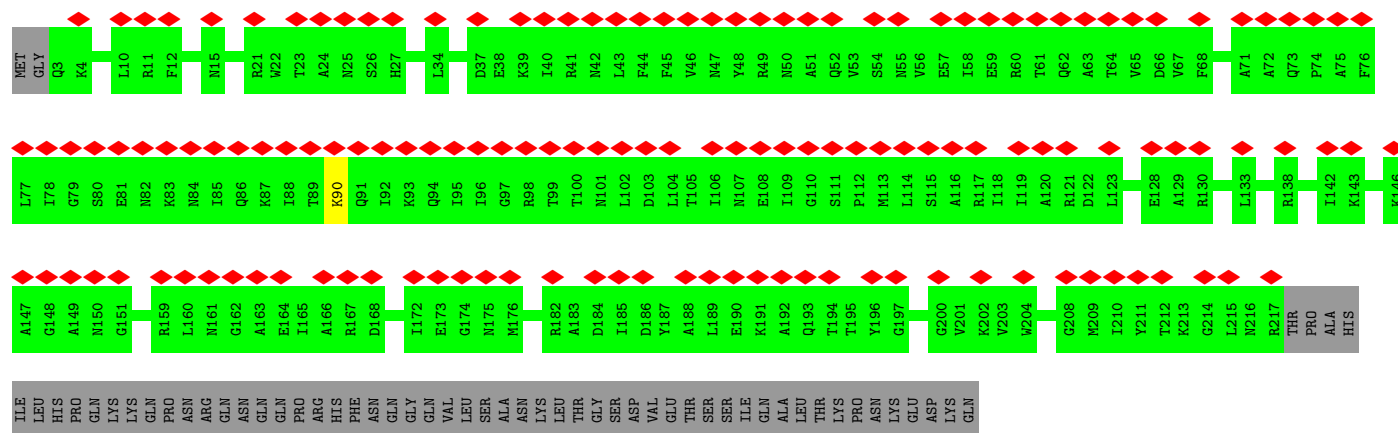
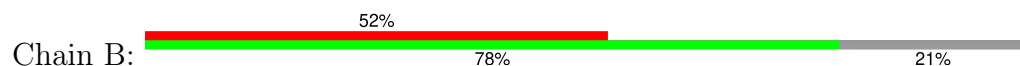
- Molecule 27: 50S ribosomal protein L24



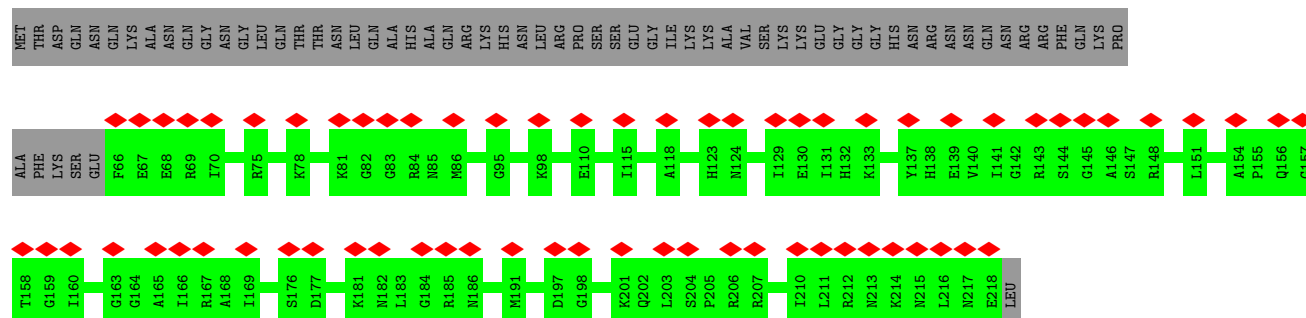
- Molecule 28: 50S ribosomal protein L22



- Molecule 29: 30S ribosomal protein S3

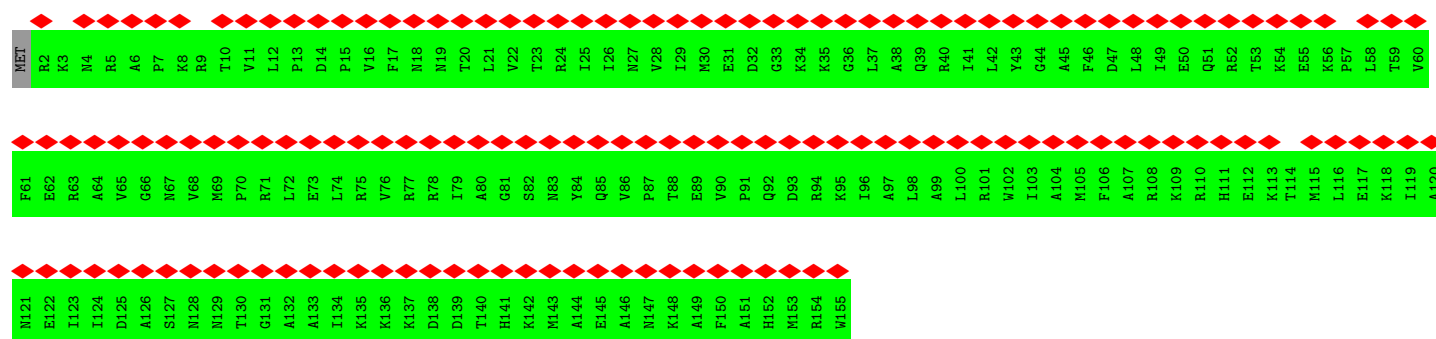


- Molecule 30: 30S ribosomal protein S5




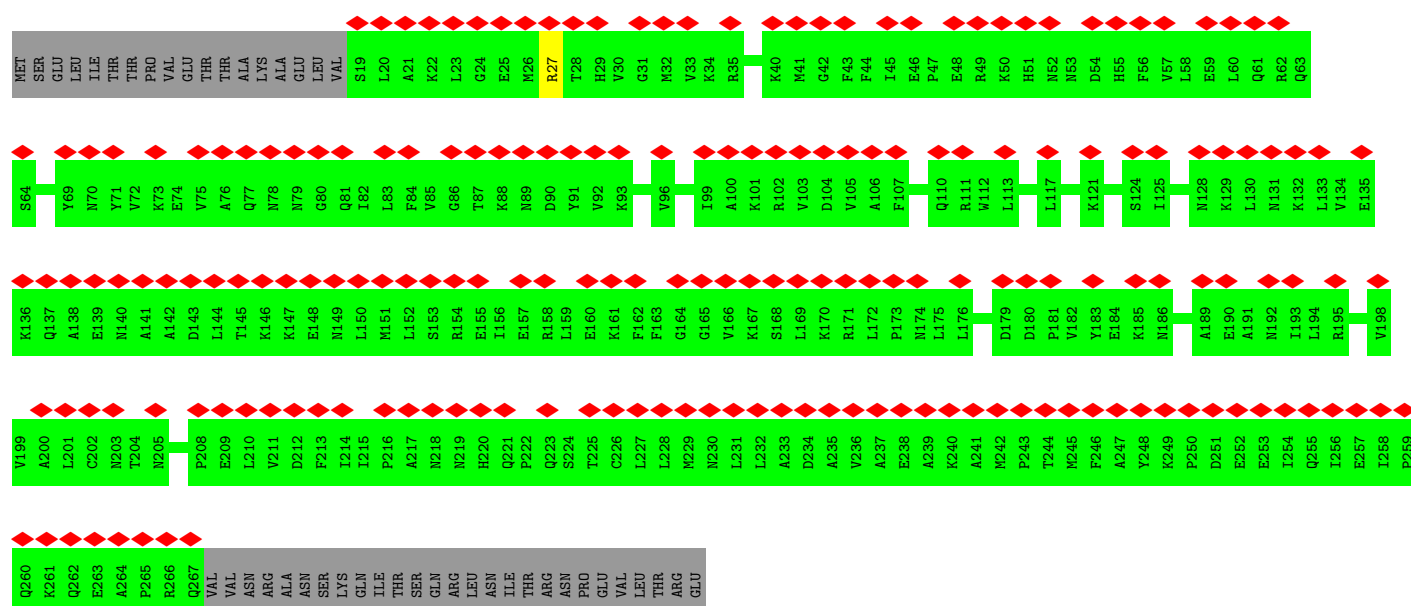
- Molecule 31: 30S ribosomal protein S7

Chain F: 

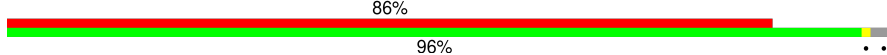


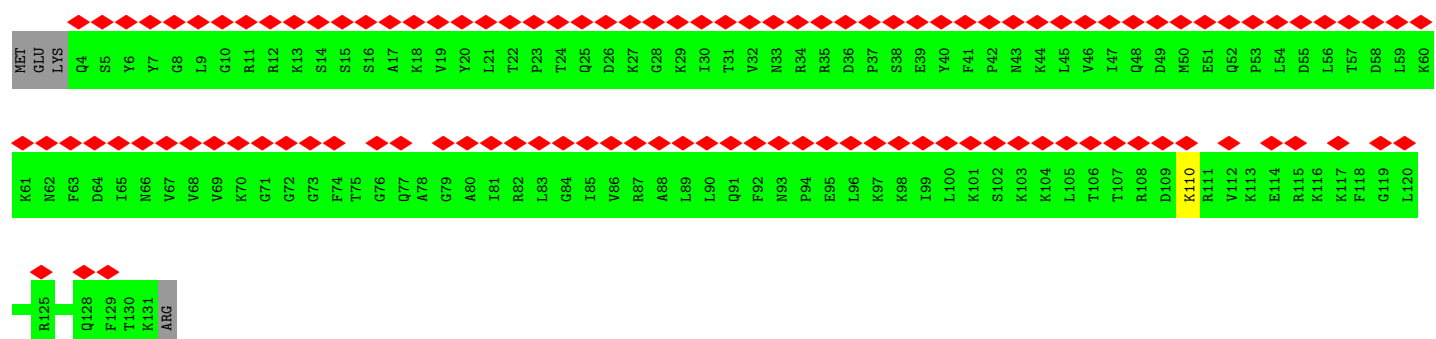
• Molecule 32: 30S ribosomal protein S2

Chain A: 

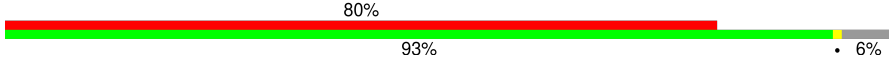


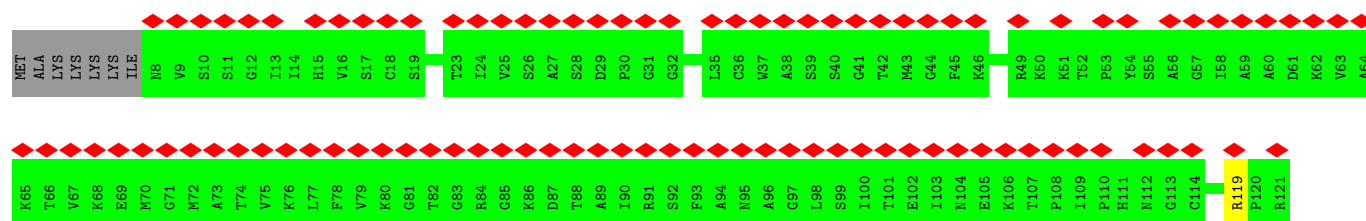
• Molecule 33: 30S ribosomal protein S9

Chain H: 

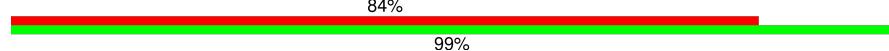


• Molecule 34: 30S ribosomal protein S11

Chain J: 




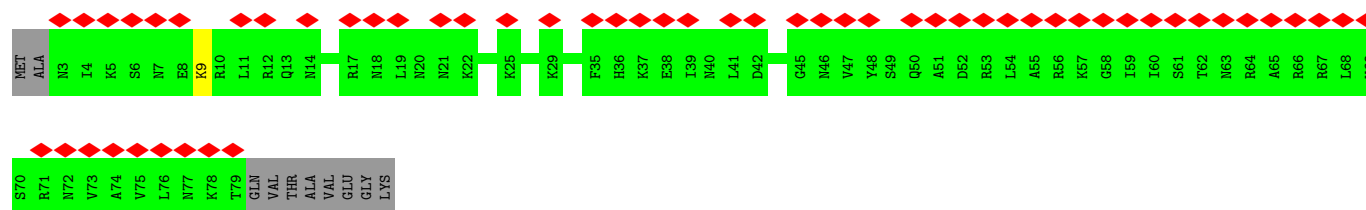
- Molecule 35: 30S ribosomal protein S4

Chain C: 

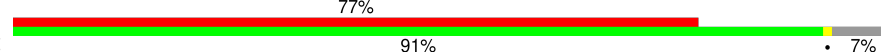


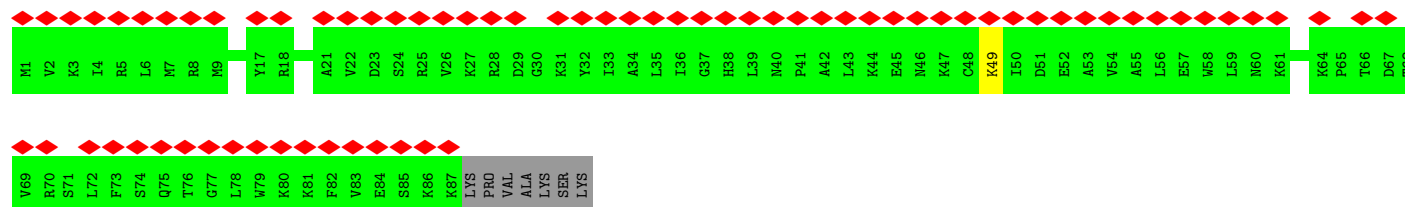
- Molecule 36: 30S ribosomal protein S20

Chain S: 

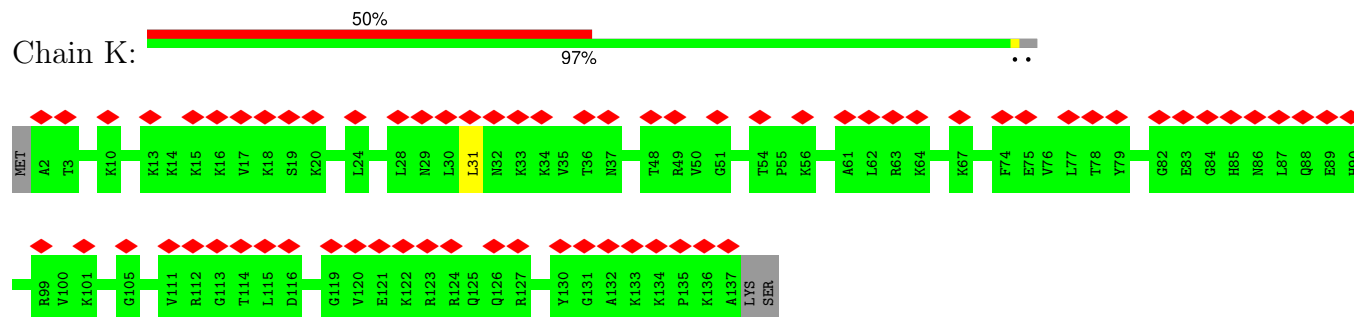


- Molecule 37: 30S ribosomal protein S16

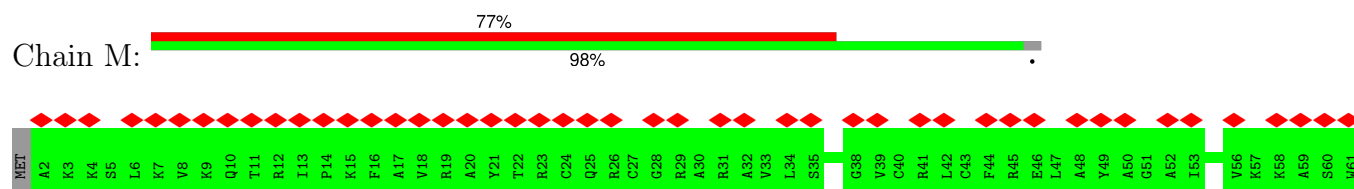
Chain O: 



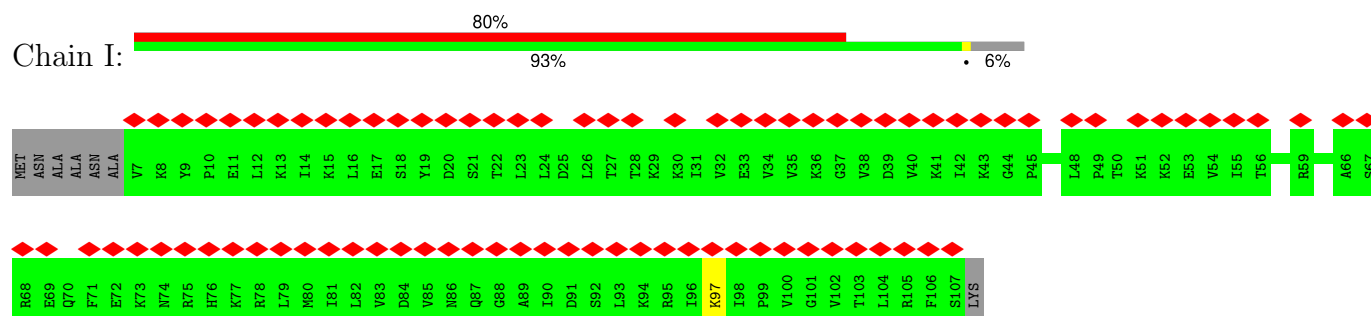
- Molecule 38: 30S ribosomal protein S12



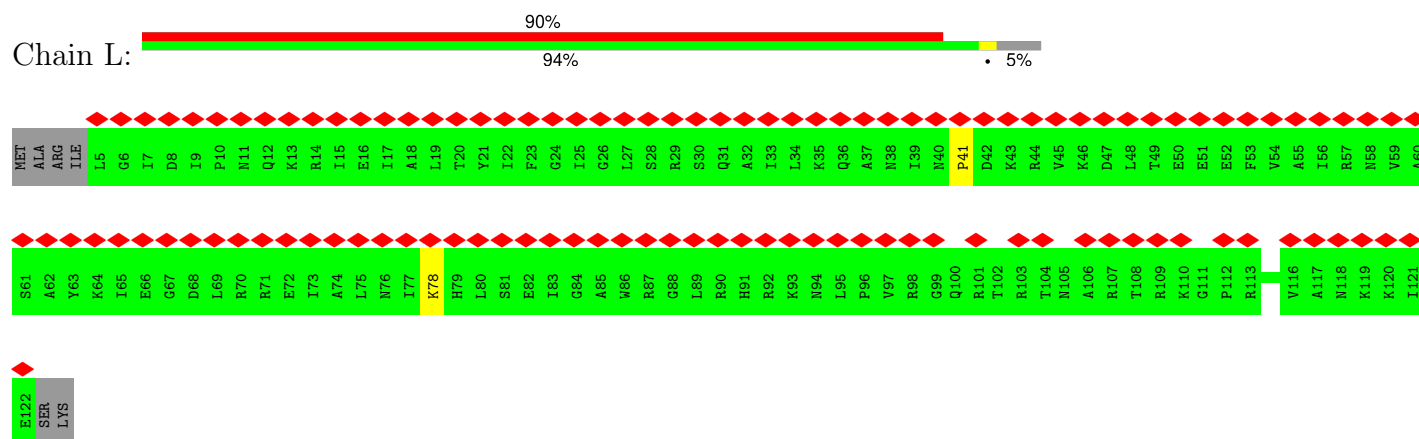
- Molecule 39: 30S ribosomal protein S14 type Z



- Molecule 40: 30S ribosomal protein S10

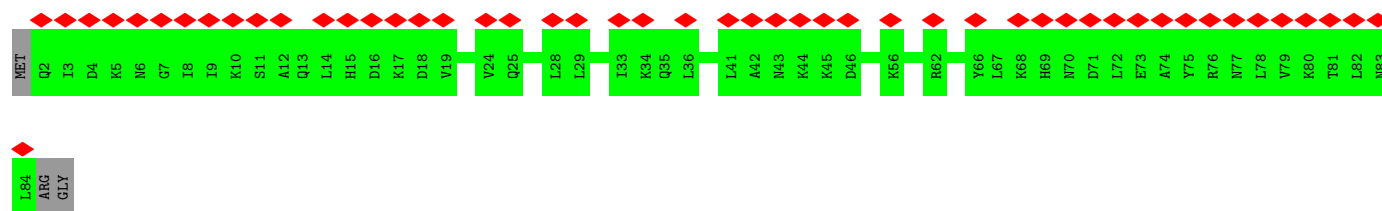


- Molecule 41: 30S ribosomal protein S13

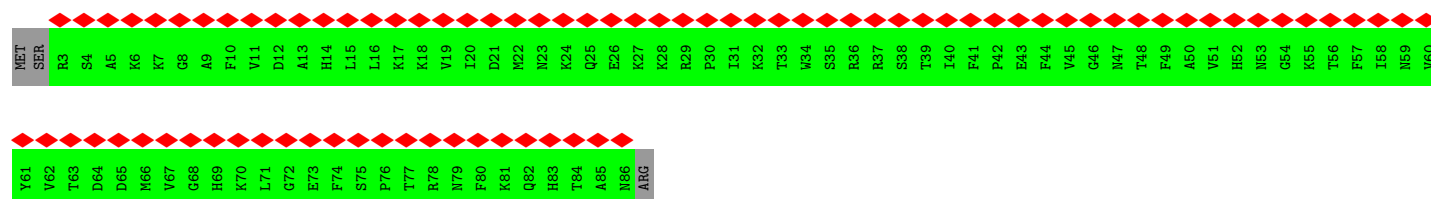


- Molecule 42: 30S ribosomal protein S15

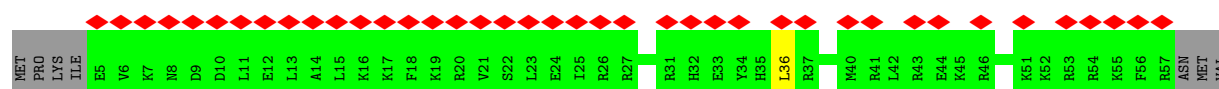
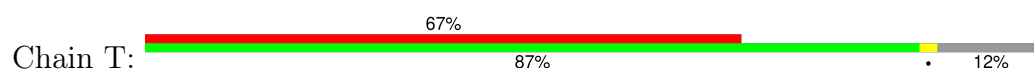




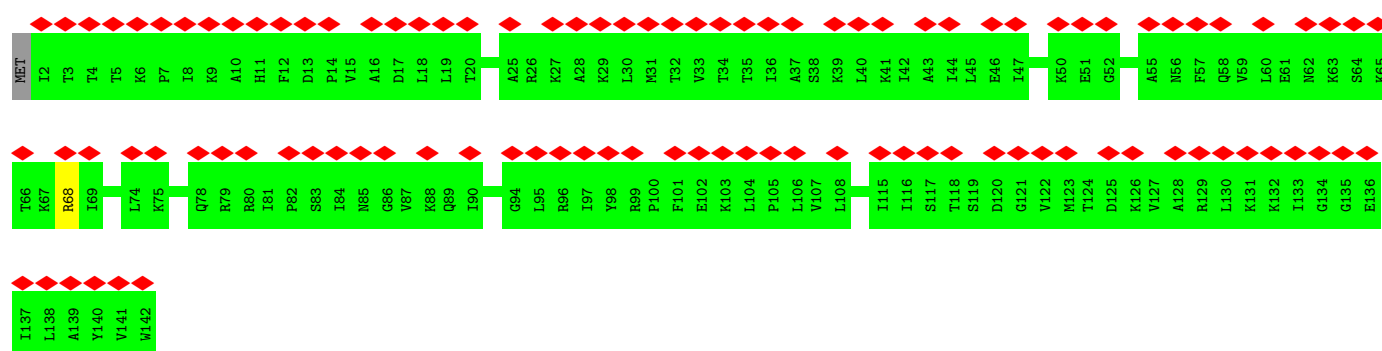
• Molecule 43: 30S ribosomal protein S19



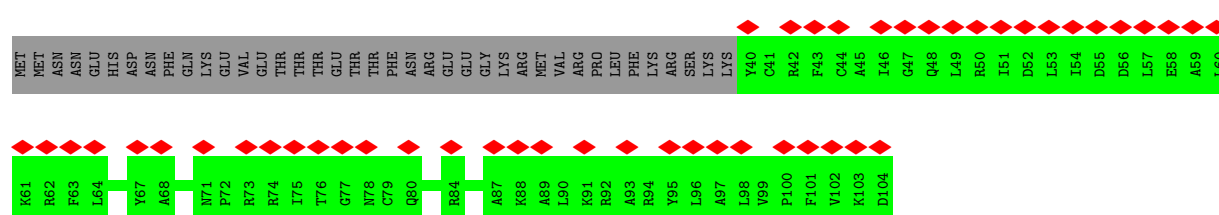
• Molecule 44: 30S ribosomal protein S21



• Molecule 45: 30S ribosomal protein S8

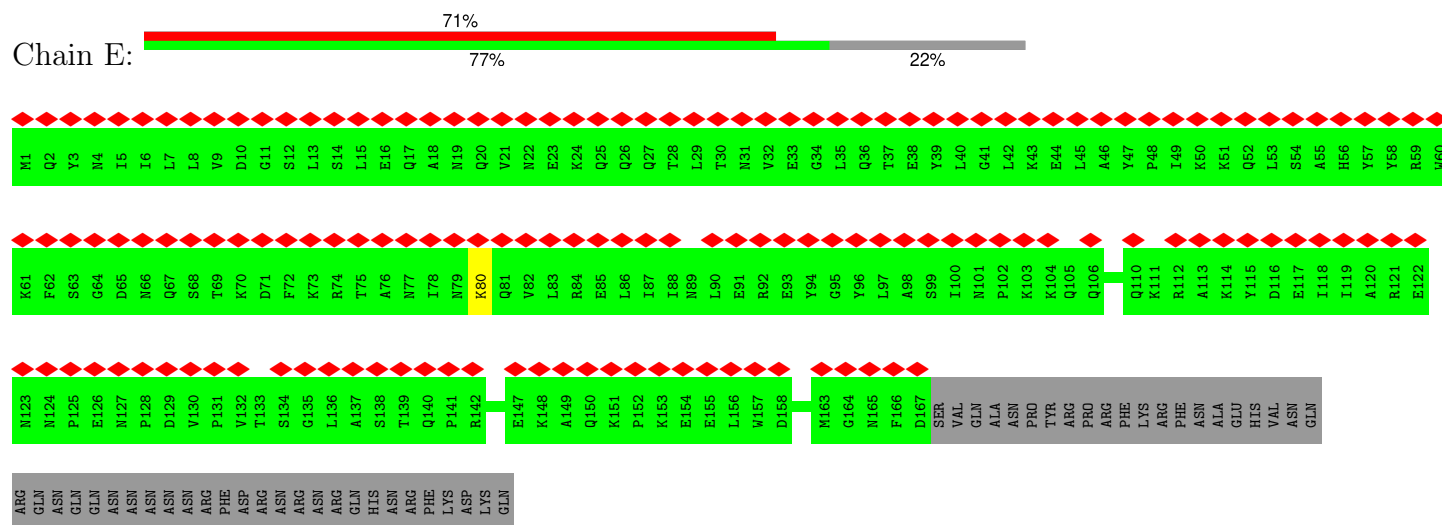


• Molecule 46: 30S ribosomal protein S18



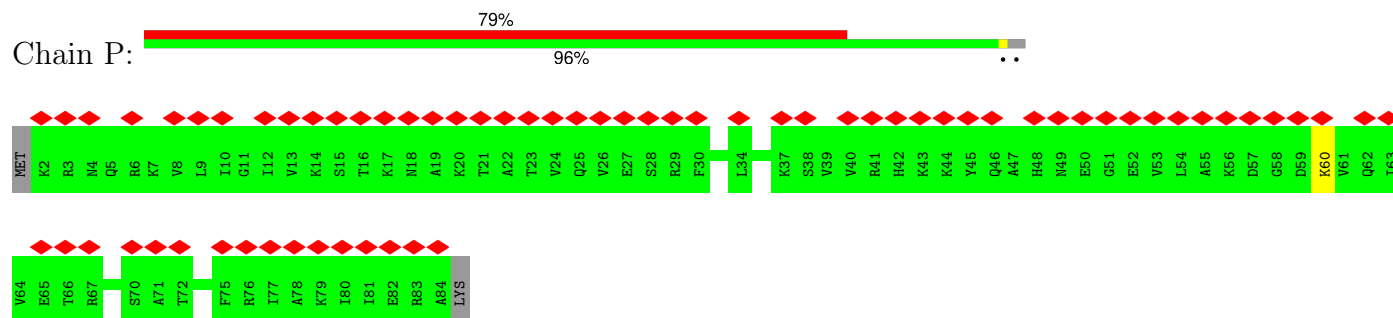
- Molecule 47: 30S ribosomal protein S6

Chain E:



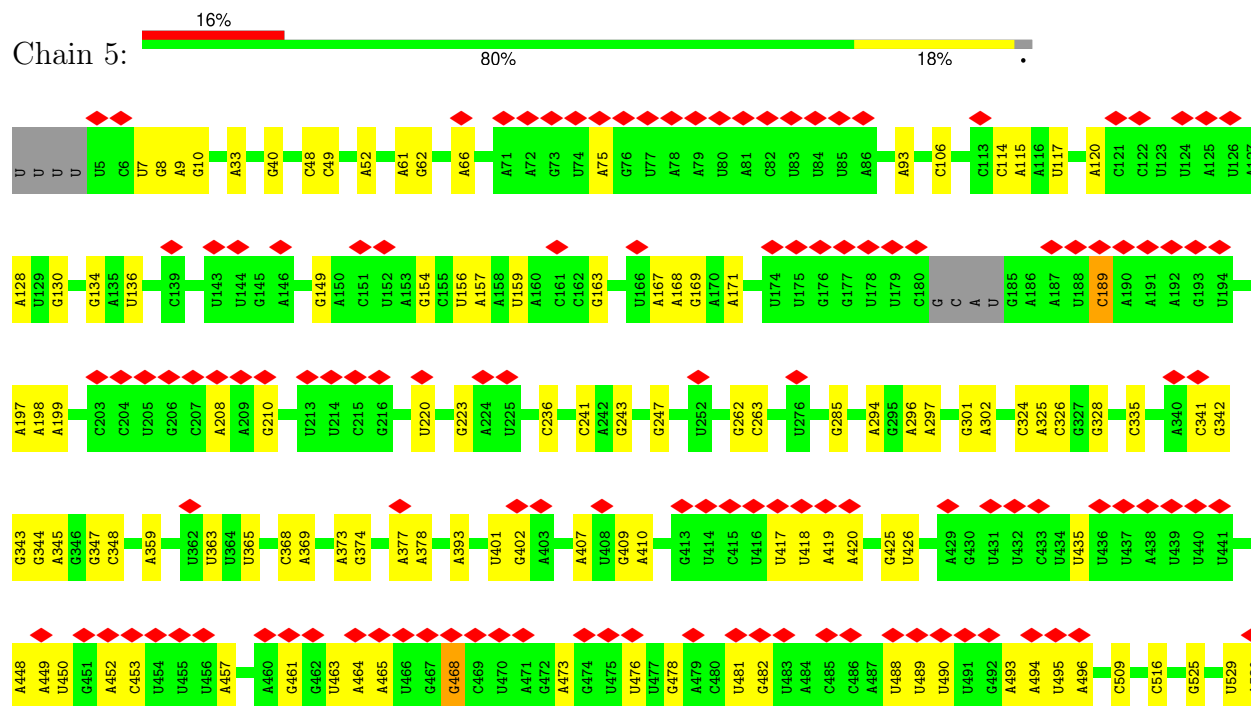
- Molecule 48: 30S ribosomal protein S17

Chain P:

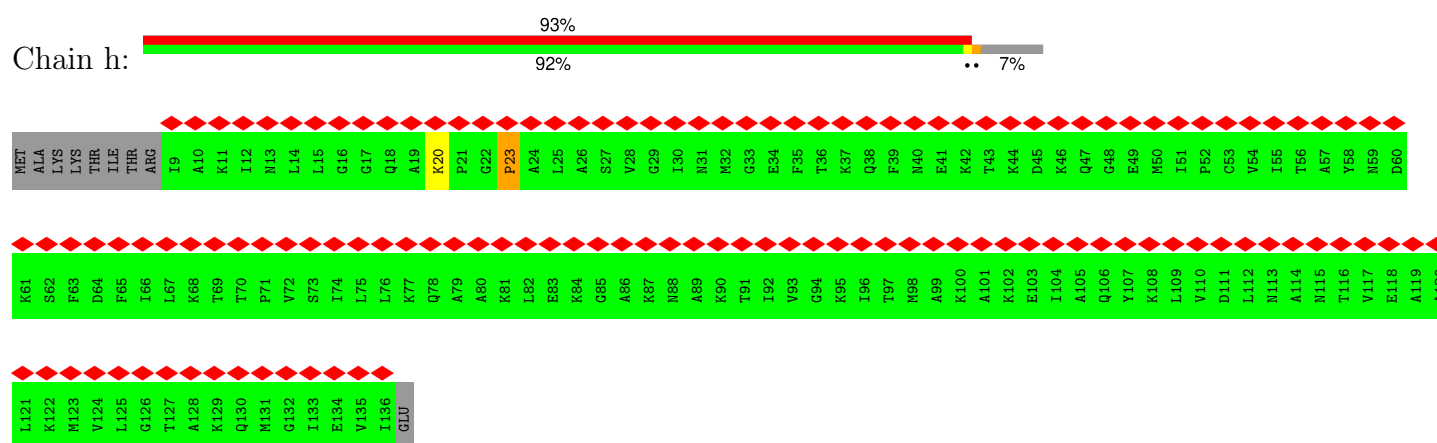


- Molecule 49: 16S ribosomal RNA

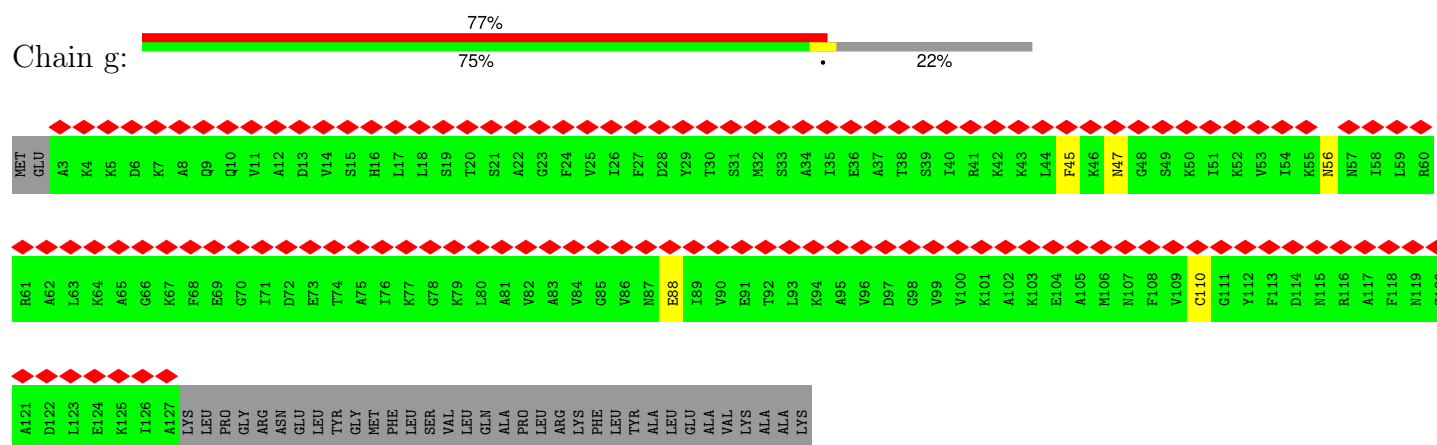
Chain 5:



- Molecule 54: 50S ribosomal protein L11



- Molecule 55: 50S ribosomal protein L10



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	77539	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 ($e^-/\text{\AA}^2$)	3.2	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3750	Depositor
Magnification	81000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.009	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.000	Depositor
Recommended contour level	0.0024	Depositor
Map size (Å)	571.368, 571.368, 571.368	wwPDB
Map dimensions	336, 336, 336	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.7004999, 1.7004999, 1.7004999	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	3	0.26	1/69100 (0.0%)	0.80	21/107749 (0.0%)
2	4	0.22	0/2511	0.79	0/3910
3	w	0.27	0/806	0.52	0/1080
4	a	0.25	0/2241	0.47	0/3013
5	c	0.26	0/1639	0.51	0/2209
6	e	0.26	0/1373	0.45	0/1854
7	k	0.35	0/1155	0.55	0/1541
8	i	0.25	0/1180	0.47	0/1585
9	m	0.25	0/972	0.48	0/1308
10	q	0.27	0/826	0.53	0/1109
11	u	0.25	0/649	0.52	0/867
12	y	0.24	0/440	0.52	0/582
13	0	0.24	0/380	0.43	0/501
14	2	0.24	0/305	0.50	0/401
15	1	0.24	0/484	0.47	0/637
16	o	0.28	0/905	0.51	0/1211
17	s	0.27	0/726	0.49	0/981
18	v	0.23	0/510	0.46	0/684
19	x	0.25	0/217	0.48	0/301
20	z	0.24	0/412	0.47	0/547
21	d	0.26	0/1264	0.54	0/1719
22	b	0.26	0/1791	0.50	0/2408
23	l	0.27	0/1082	0.49	0/1456
24	p	0.25	0/955	0.43	0/1271
25	j	0.26	0/953	0.52	0/1275
26	n	0.25	0/861	0.50	0/1156
27	t	0.24	0/712	0.49	0/954
28	r	0.27	0/1077	0.46	0/1441
29	B	0.27	0/1705	0.52	0/2304
30	D	0.26	0/1168	0.49	0/1568
31	F	0.27	0/1250	0.51	0/1682
32	A	0.26	0/1951	0.50	0/2652

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	H	0.26	0/1009	0.50	0/1354
34	J	0.30	0/843	0.57	2/1136 (0.2%)
35	C	0.26	0/1635	0.50	0/2202
36	S	0.30	0/631	0.62	0/838
37	O	0.25	0/703	0.49	0/945
38	K	0.25	0/1073	0.55	1/1445 (0.1%)
39	M	0.27	0/482	0.48	0/643
40	I	0.26	0/814	0.57	0/1096
41	L	0.30	0/933	0.62	2/1254 (0.2%)
42	N	0.25	0/679	0.43	0/907
43	R	0.27	0/670	0.52	0/904
44	T	0.39	0/442	0.61	1/582 (0.2%)
45	G	0.26	0/1119	0.53	0/1508
46	Q	0.26	0/545	0.52	0/730
47	E	0.28	0/1229	0.51	0/1670
48	P	0.24	0/684	0.51	0/913
49	5	0.23	0/35777	0.80	8/55776 (0.0%)
51	7	0.25	0/1808	0.89	3/2817 (0.1%)
52	Y	0.89	3/194 (1.5%)	1.11	0/298
53	f	0.44	0/711	0.75	0/988
54	h	0.62	0/629	1.00	1/873 (0.1%)
55	g	0.76	0/616	1.03	1/856 (0.1%)
All	All	0.26	4/154826 (0.0%)	0.74	40/231691 (0.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
52	Y	2	U	C1'-N1	6.47	1.58	1.48
52	Y	9	U	C1'-N1	6.20	1.58	1.48
52	Y	1	U	C1'-N1	6.00	1.57	1.48
1	3	1201	A	O3'-P	-5.30	1.54	1.61

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	L	41	PRO	CA-N-CD	-8.81	99.16	111.50
1	3	1486	U	C2-N1-C1'	8.30	127.66	117.70
1	3	1659	C	N3-C2-O2	-7.93	116.35	121.90
1	3	1659	C	N1-C2-O2	7.80	123.58	118.90
1	3	14	U	C2-N1-C1'	7.73	126.98	117.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	w	95/111 (86%)	91 (96%)	4 (4%)	0	100	100
4	a	283/287 (99%)	265 (94%)	18 (6%)	0	100	100
5	c	208/212 (98%)	190 (91%)	18 (9%)	0	100	100
6	e	174/184 (95%)	168 (97%)	6 (3%)	0	100	100
7	k	146/151 (97%)	126 (86%)	20 (14%)	0	100	100
8	i	142/146 (97%)	133 (94%)	9 (6%)	0	100	100
9	m	117/124 (94%)	113 (97%)	4 (3%)	0	100	100
10	q	97/100 (97%)	88 (91%)	9 (9%)	0	100	100
11	u	84/104 (81%)	79 (94%)	5 (6%)	0	100	100
12	y	54/57 (95%)	49 (91%)	5 (9%)	0	100	100
13	0	45/48 (94%)	44 (98%)	1 (2%)	0	100	100
14	2	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
15	1	57/59 (97%)	55 (96%)	2 (4%)	0	100	100
16	o	113/119 (95%)	101 (89%)	12 (11%)	0	100	100
17	s	90/237 (38%)	84 (93%)	6 (7%)	0	100	100
18	v	61/65 (94%)	58 (95%)	3 (5%)	0	100	100
19	x	42/97 (43%)	38 (90%)	4 (10%)	0	100	100
20	z	48/53 (91%)	46 (96%)	2 (4%)	0	100	100
21	d	173/180 (96%)	156 (90%)	17 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	b	227/287 (79%)	217 (96%)	10 (4%)	0	100	100
23	l	134/139 (96%)	127 (95%)	7 (5%)	0	100	100
24	p	112/127 (88%)	109 (97%)	3 (3%)	0	100	100
25	j	120/122 (98%)	106 (88%)	14 (12%)	0	100	100
26	n	108/116 (93%)	102 (94%)	6 (6%)	0	100	100
27	t	92/111 (83%)	83 (90%)	9 (10%)	0	100	100
28	r	137/159 (86%)	127 (93%)	10 (7%)	0	100	100
29	B	213/273 (78%)	200 (94%)	13 (6%)	0	100	100
30	D	151/219 (69%)	142 (94%)	9 (6%)	0	100	100
31	F	152/155 (98%)	135 (89%)	17 (11%)	0	100	100
32	A	247/294 (84%)	228 (92%)	19 (8%)	0	100	100
33	H	126/132 (96%)	104 (82%)	22 (18%)	0	100	100
34	J	112/121 (93%)	105 (94%)	7 (6%)	0	100	100
35	C	201/205 (98%)	191 (95%)	10 (5%)	0	100	100
36	S	75/87 (86%)	72 (96%)	3 (4%)	0	100	100
37	O	85/94 (90%)	79 (93%)	6 (7%)	0	100	100
38	K	134/139 (96%)	117 (87%)	17 (13%)	0	100	100
39	M	58/61 (95%)	55 (95%)	3 (5%)	0	100	100
40	I	99/108 (92%)	87 (88%)	12 (12%)	0	100	100
41	L	116/124 (94%)	103 (89%)	13 (11%)	0	100	100
42	N	81/86 (94%)	80 (99%)	1 (1%)	0	100	100
43	R	82/87 (94%)	77 (94%)	5 (6%)	0	100	100
44	T	51/60 (85%)	44 (86%)	7 (14%)	0	100	100
45	G	139/142 (98%)	122 (88%)	17 (12%)	0	100	100
46	Q	63/104 (61%)	57 (90%)	6 (10%)	0	100	100
47	E	165/215 (77%)	148 (90%)	17 (10%)	0	100	100
48	P	81/85 (95%)	75 (93%)	6 (7%)	0	100	100
53	f	140/149 (94%)	124 (89%)	15 (11%)	1 (1%)	19	53
54	h	126/137 (92%)	116 (92%)	8 (6%)	2 (2%)	8	38
55	g	123/161 (76%)	115 (94%)	4 (3%)	4 (3%)	3	25
All	All	5814/6670 (87%)	5364 (92%)	443 (8%)	7 (0%)	50	79

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
53	f	115	ASP
54	h	20	LYS
55	g	45	PHE
55	g	110	CYS
54	h	23	PRO

5.3.2 Protein sidechains ⓘ

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	
3	w	83/98 (85%)	83 (100%)	0	100	100
4	a	233/243 (96%)	233 (100%)	0	100	100
5	c	174/184 (95%)	174 (100%)	0	100	100
6	e	138/159 (87%)	138 (100%)	0	100	100
7	k	118/126 (94%)	118 (100%)	0	100	100
8	i	124/128 (97%)	124 (100%)	0	100	100
9	m	104/109 (95%)	104 (100%)	0	100	100
10	q	88/91 (97%)	88 (100%)	0	100	100
11	u	64/85 (75%)	64 (100%)	0	100	100
12	y	45/49 (92%)	45 (100%)	0	100	100
13	0	39/41 (95%)	39 (100%)	0	100	100
14	2	35/35 (100%)	35 (100%)	0	100	100
15	1	51/51 (100%)	51 (100%)	0	100	100
16	o	91/105 (87%)	91 (100%)	0	100	100
17	s	80/208 (38%)	80 (100%)	0	100	100
18	v	55/60 (92%)	55 (100%)	0	100	100
20	z	47/50 (94%)	46 (98%)	1 (2%)	48	71
21	d	111/154 (72%)	110 (99%)	1 (1%)	75	86
22	b	185/233 (79%)	185 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	l	107/115 (93%)	107 (100%)	0	100	100
24	p	99/108 (92%)	97 (98%)	2 (2%)	50	72
25	j	103/103 (100%)	103 (100%)	0	100	100
26	n	85/99 (86%)	85 (100%)	0	100	100
27	t	69/96 (72%)	69 (100%)	0	100	100
28	r	116/132 (88%)	116 (100%)	0	100	100
29	B	176/232 (76%)	175 (99%)	1 (1%)	84	91
30	D	117/178 (66%)	117 (100%)	0	100	100
31	F	128/132 (97%)	128 (100%)	0	100	100
32	A	200/262 (76%)	199 (100%)	1 (0%)	86	93
33	H	101/115 (88%)	100 (99%)	1 (1%)	73	84
34	J	91/97 (94%)	91 (100%)	0	100	100
35	C	164/183 (90%)	164 (100%)	0	100	100
36	S	70/77 (91%)	69 (99%)	1 (1%)	62	79
37	O	71/82 (87%)	70 (99%)	1 (1%)	62	79
38	K	111/120 (92%)	111 (100%)	0	100	100
39	M	47/48 (98%)	47 (100%)	0	100	100
40	I	93/99 (94%)	92 (99%)	1 (1%)	70	83
41	L	92/105 (88%)	91 (99%)	1 (1%)	70	83
42	N	76/78 (97%)	76 (100%)	0	100	100
43	R	66/77 (86%)	66 (100%)	0	100	100
44	T	43/56 (77%)	43 (100%)	0	100	100
45	G	121/124 (98%)	120 (99%)	1 (1%)	79	88
46	Q	56/94 (60%)	56 (100%)	0	100	100
47	E	107/196 (55%)	106 (99%)	1 (1%)	75	86
48	P	73/75 (97%)	72 (99%)	1 (1%)	62	79
All	All	4447/5292 (84%)	4433 (100%)	14 (0%)	90	96

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
36	S	9	LYS
37	O	49	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
48	P	60	LYS
45	G	68	ARG
47	E	80	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
35	C	171	ASN
48	P	62	GLN
48	P	25	GLN
32	A	70	ASN
35	C	70	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3	2877/2907 (98%)	532 (18%)	37 (1%)
2	4	103/108 (95%)	28 (27%)	2 (1%)
49	5	1490/1520 (98%)	274 (18%)	6 (0%)
51	7	75/76 (98%)	20 (26%)	1 (1%)
52	Y	8/9 (88%)	0	0
All	All	4553/4620 (98%)	854 (18%)	46 (1%)

5 of 854 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	3	17	G
1	3	37	G
1	3	48	G
1	3	53	G
1	3	64	U

5 of 46 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	3	1588	A
1	3	2764	U
1	3	1618	U
1	3	2506	C
2	4	54	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 30 ligands modelled in this entry, 30 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

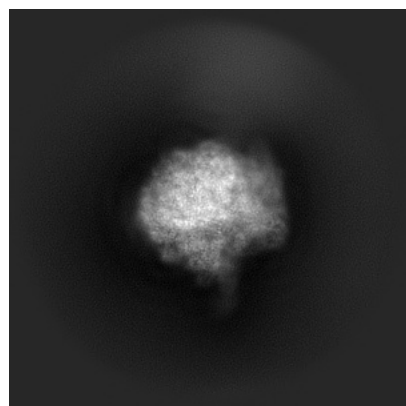
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13234. These allow visual inspection of the internal detail of the map and identification of artifacts.

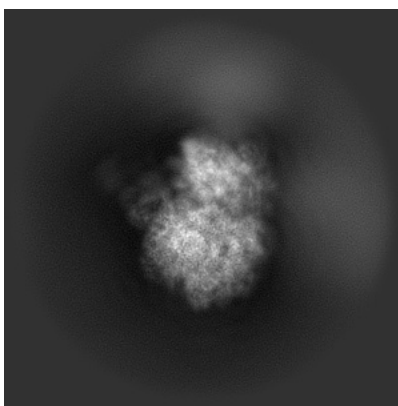
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

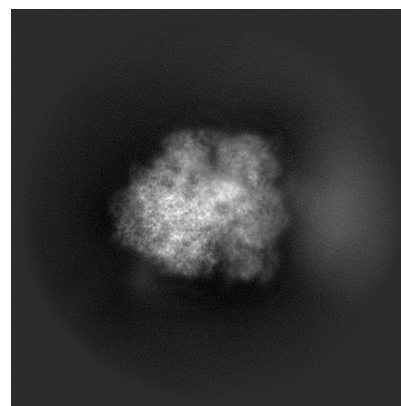
6.1.1 Primary map



X

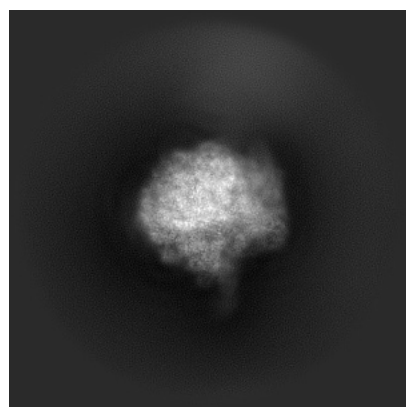


Y

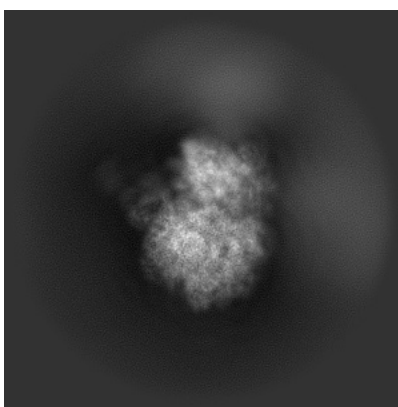


Z

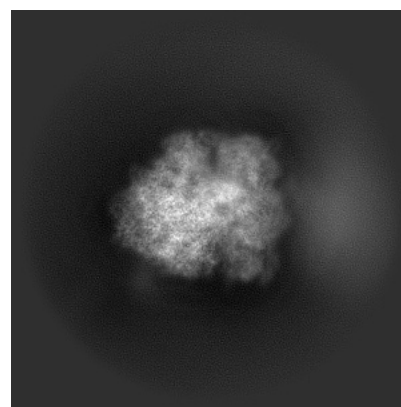
6.1.2 Raw map



X



Y

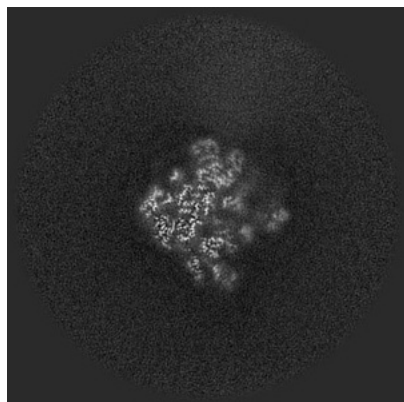


Z

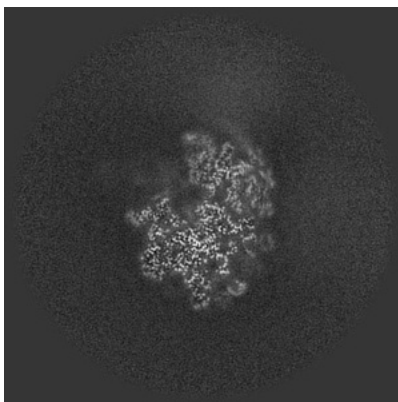
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

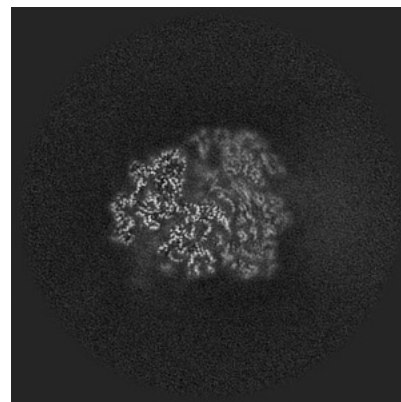
6.2.1 Primary map



X Index: 168

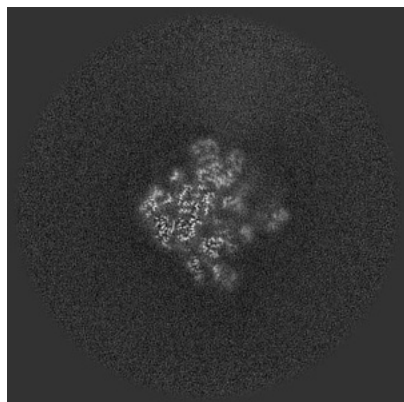


Y Index: 168

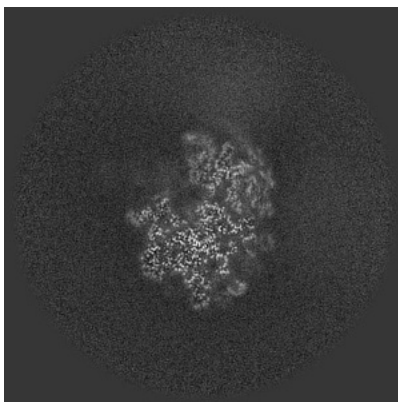


Z Index: 168

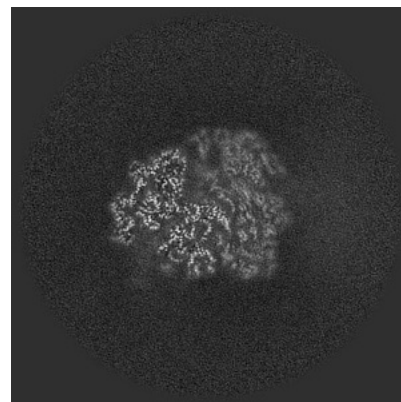
6.2.2 Raw map



X Index: 168



Y Index: 168

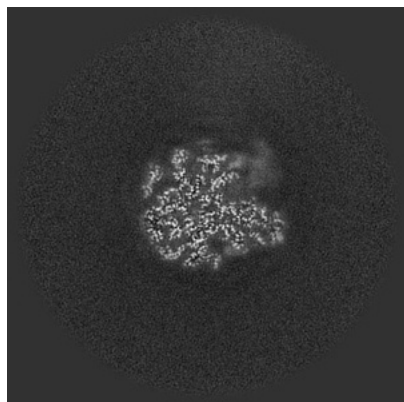


Z Index: 168

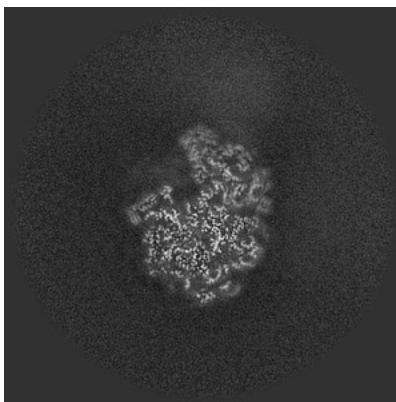
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

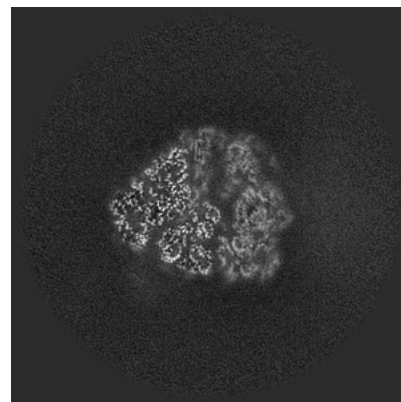
6.3.1 Primary map



X Index: 142

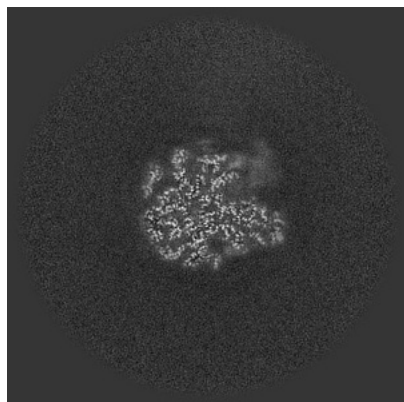


Y Index: 160

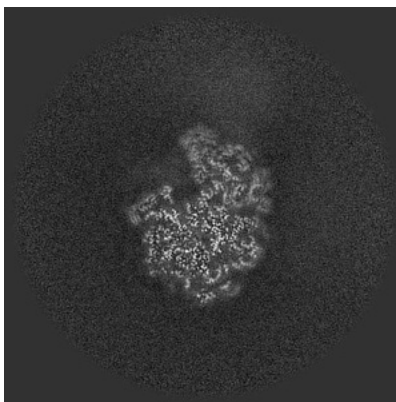


Z Index: 163

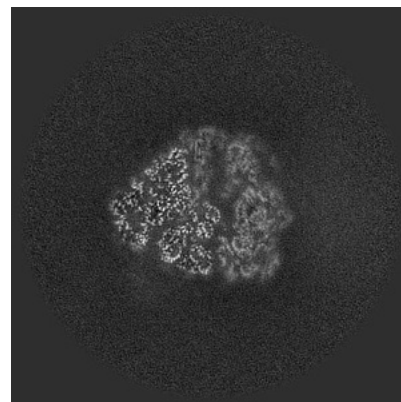
6.3.2 Raw map



X Index: 142



Y Index: 160

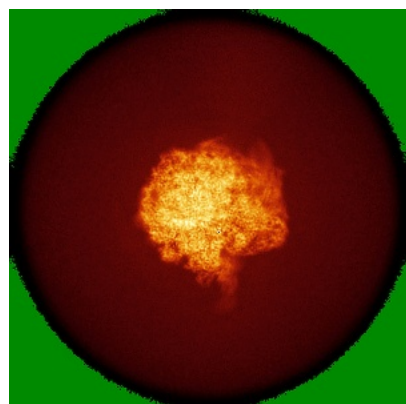


Z Index: 163

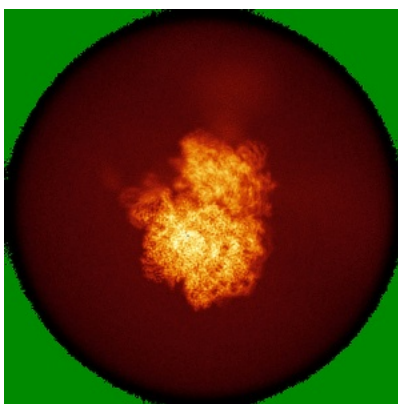
The images above show the largest variance slices of the map in three orthogonal directions.

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

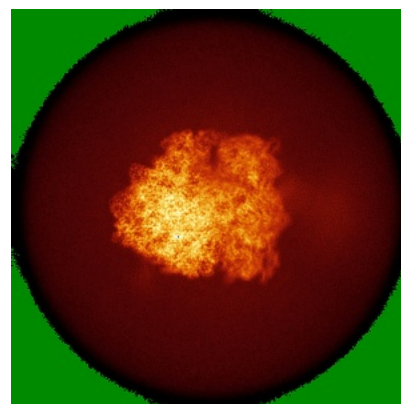
6.4.1 Primary map



X

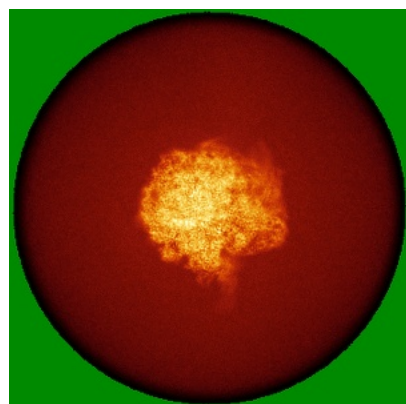


Y

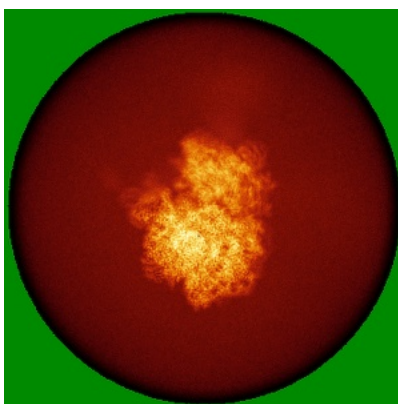


Z

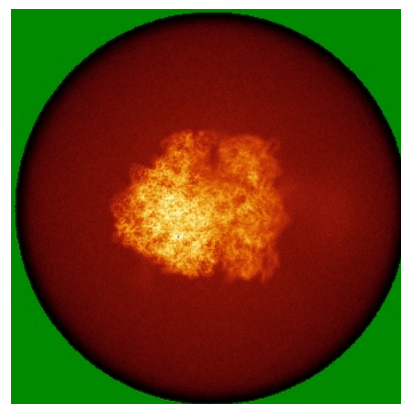
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



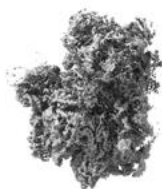
Z

The images above show the 3D surface view of the map at the recommended contour level 0.0024. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X



Y



Z

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

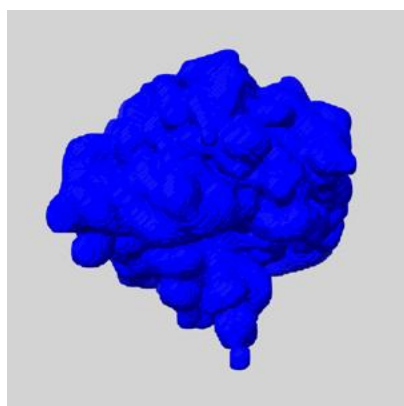
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

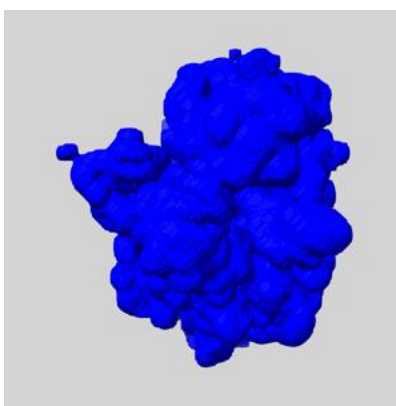
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

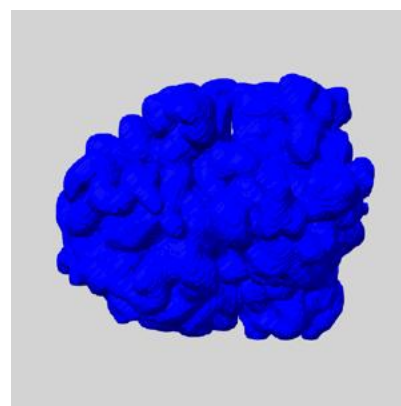
6.6.1 emd_13234_msk_1.map [i](#)



X



Y

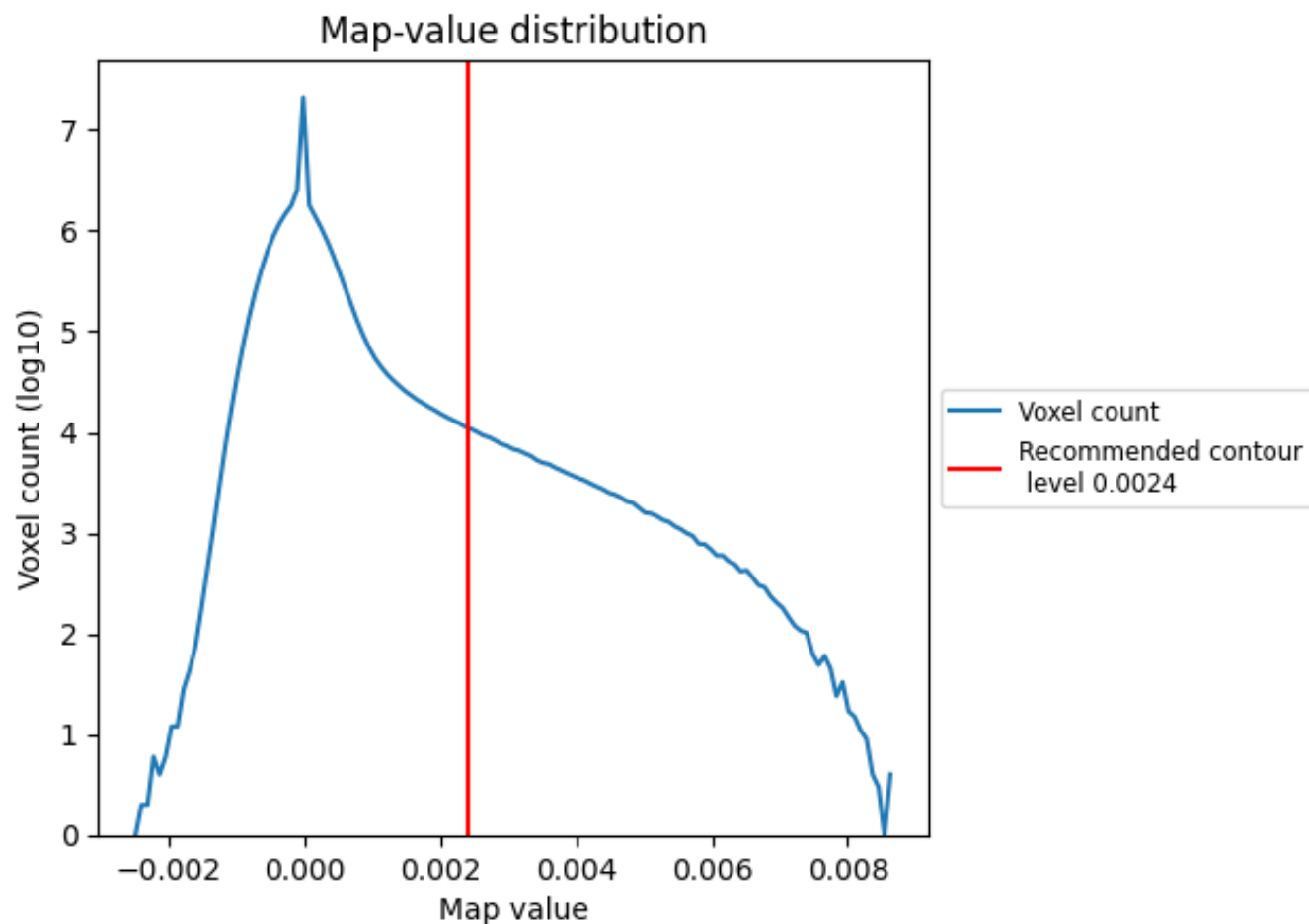


Z

7 Map analysis [i](#)

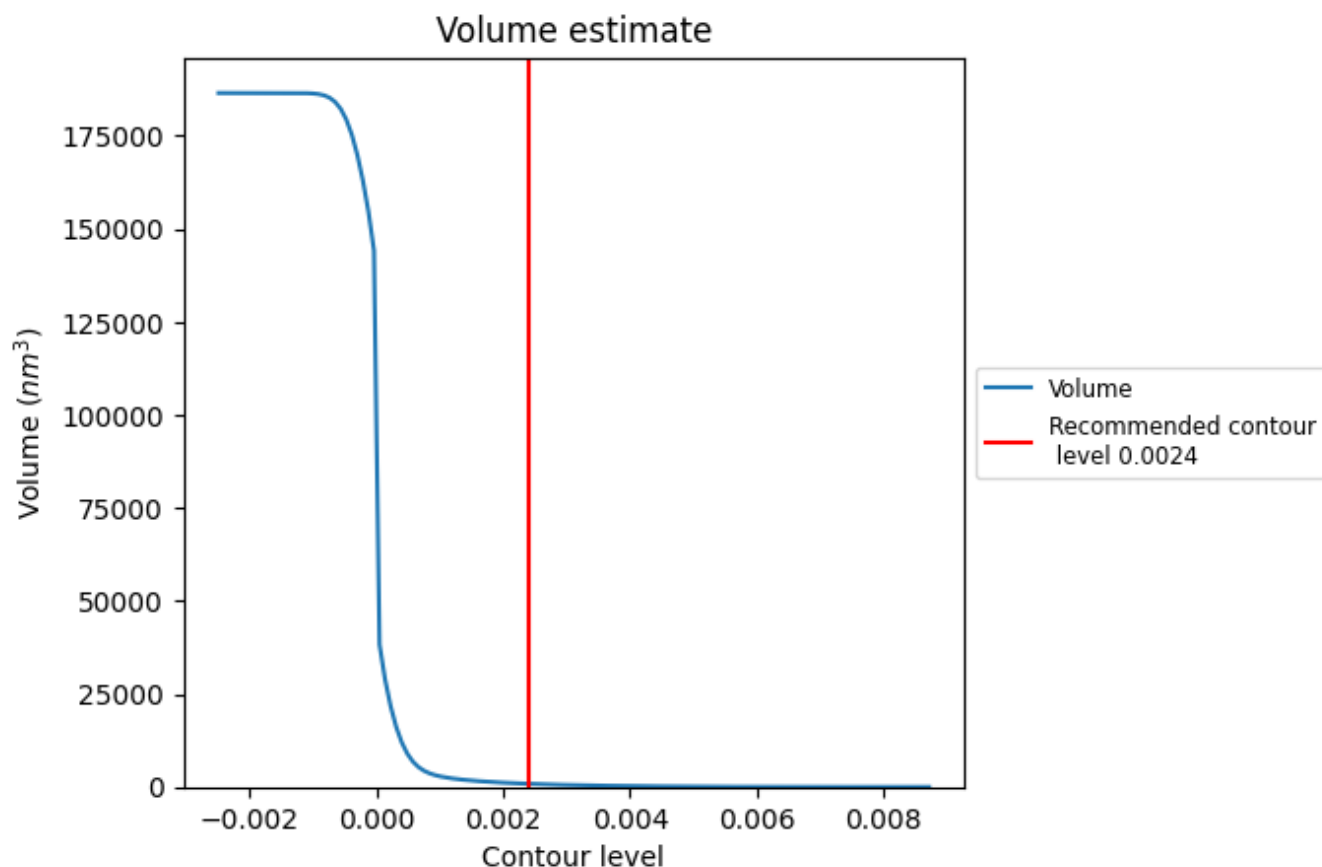
This section contains the results of statistical analysis of the map.

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.

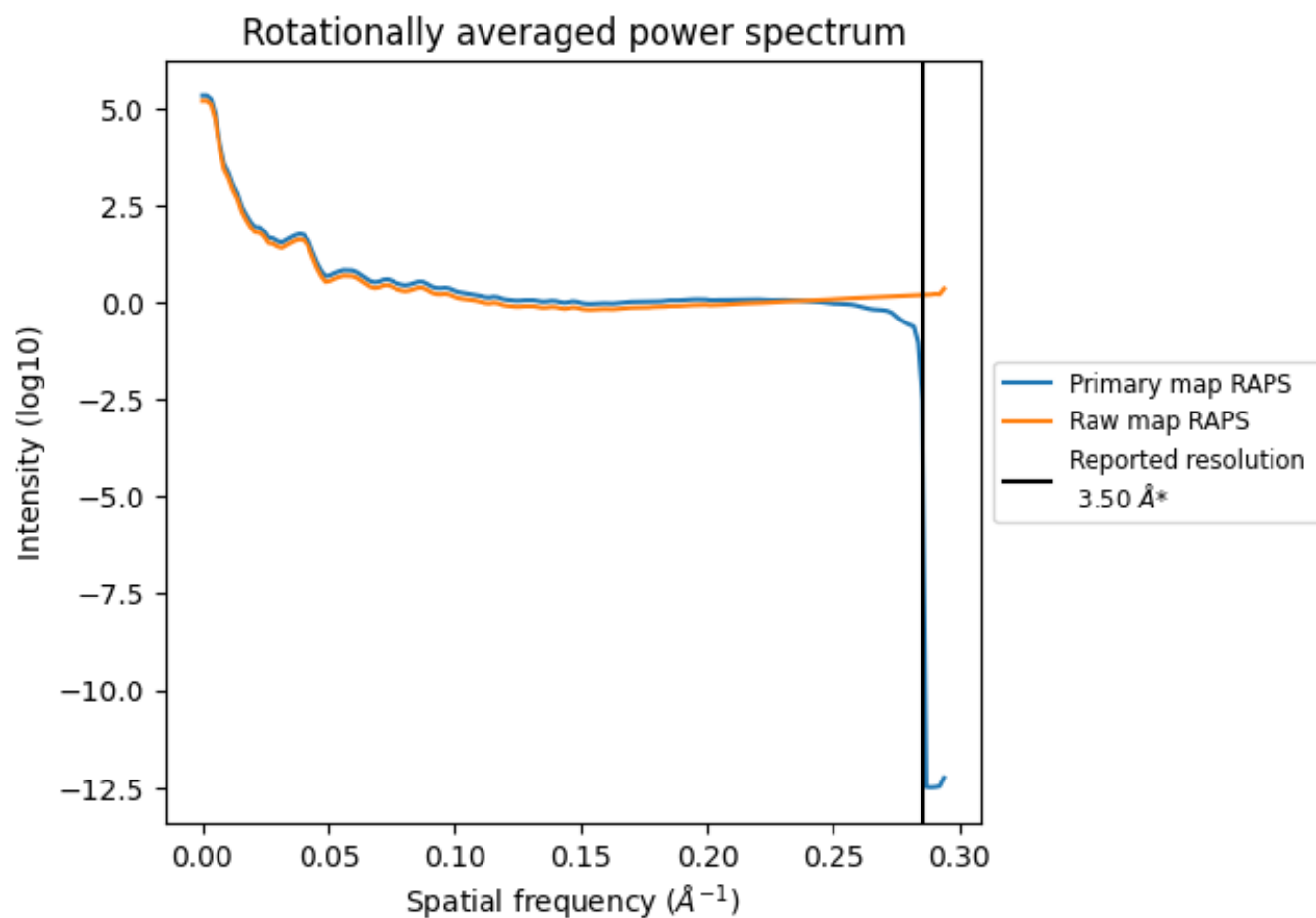
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 852 nm^3 ; this corresponds to an approximate mass of 770 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

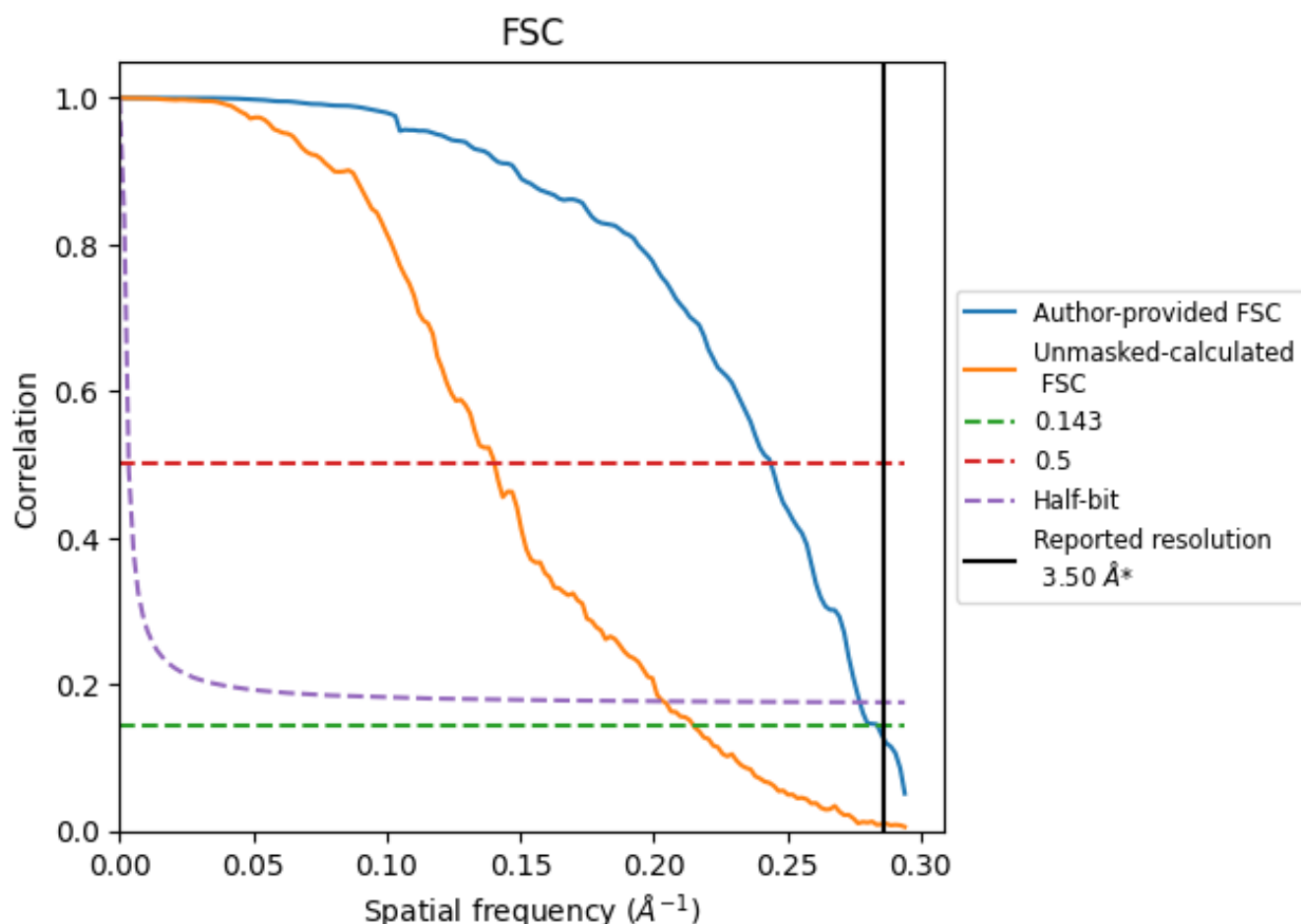


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.286 \AA^{-1}

8.2 Resolution estimates [i](#)

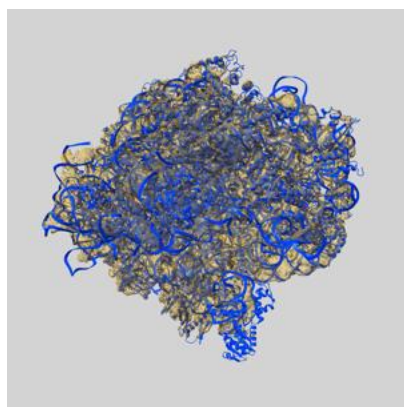
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.52	4.10	3.61
Unmasked-calculated*	4.65	7.12	4.91

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.65 differs from the reported value 3.5 by more than 10 %

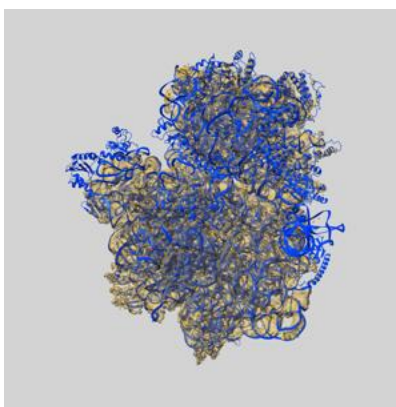
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13234 and PDB model 7P6Z. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

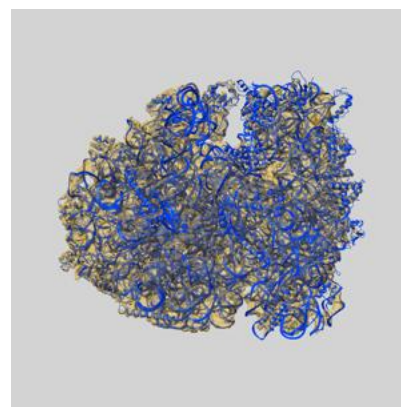
9.1 Map-model overlay [i](#)



X



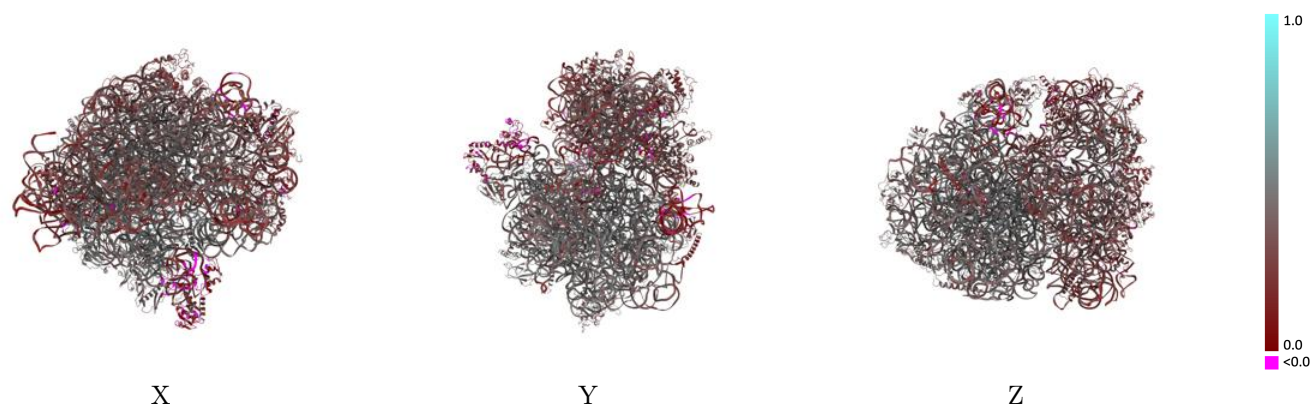
Y



Z

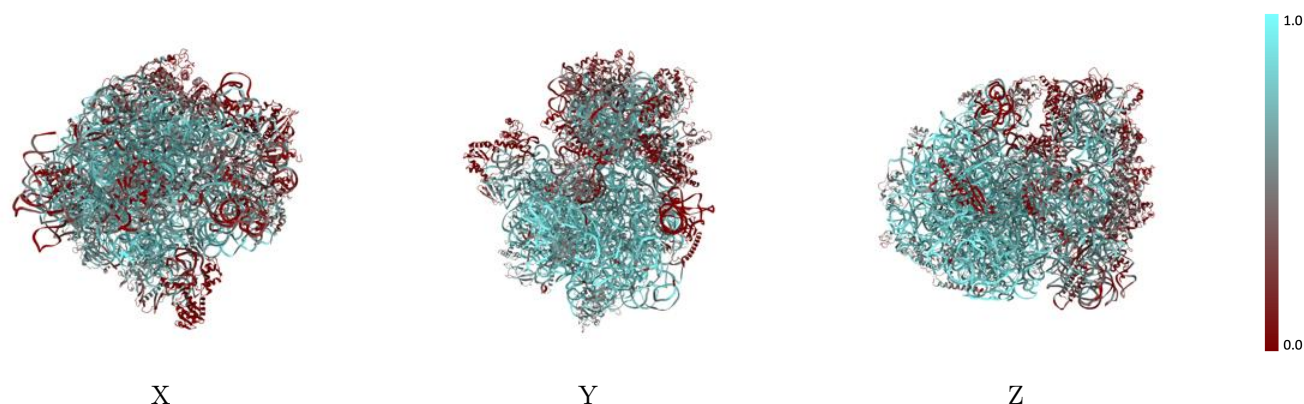
The images above show the 3D surface view of the map at the recommended contour level 0.0024 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



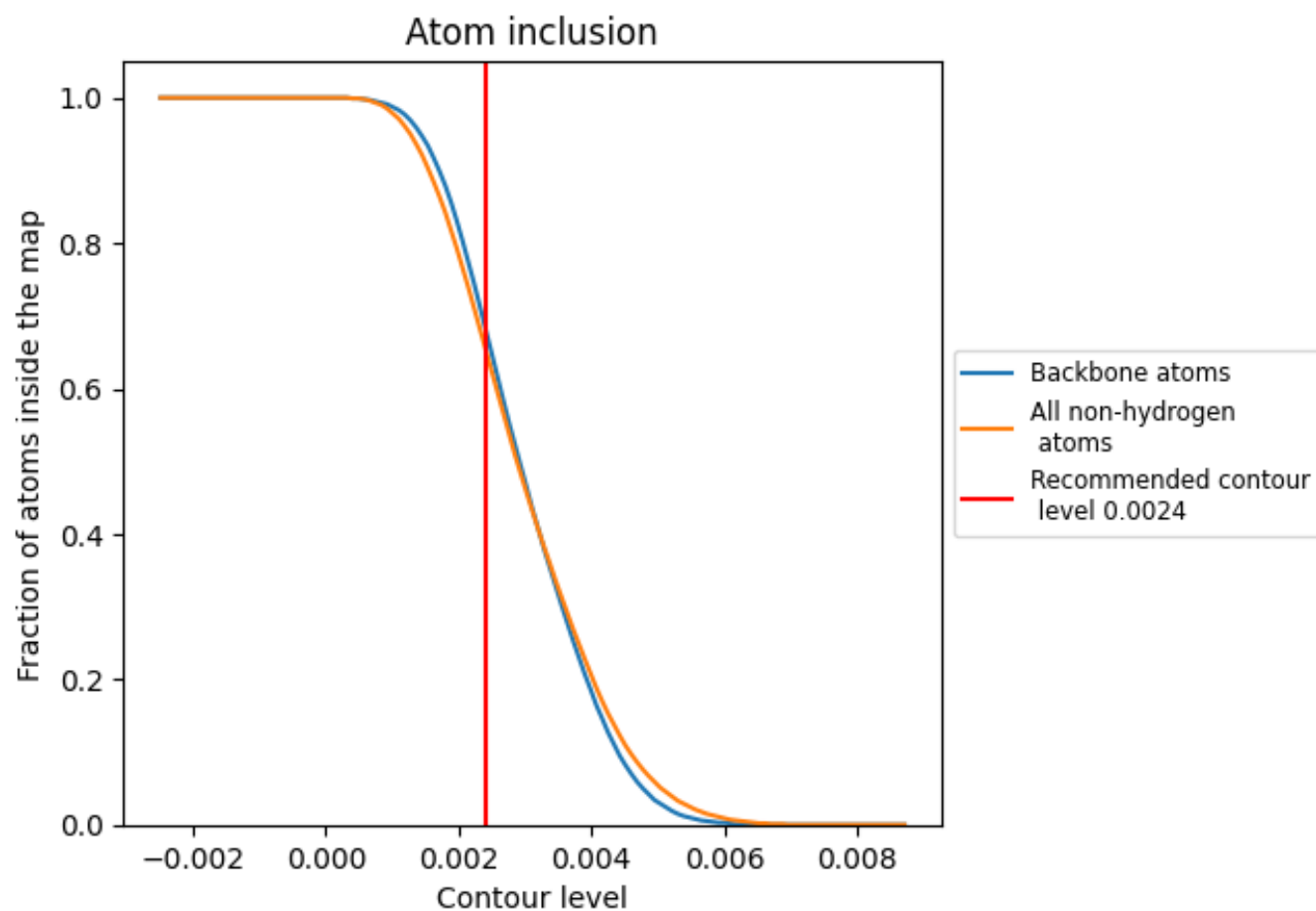
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0024).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 68% of all backbone atoms, 66% 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 (0.0024) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6560	 0.3850
0	 0.7400	 0.4890
1	 0.6250	 0.4890
2	 0.6550	 0.4960
3	 0.8260	 0.4190
4	 0.7900	 0.3920
5	 0.6650	 0.3330
7	 0.4130	 0.2870
A	 0.2560	 0.3130
B	 0.3260	 0.3640
C	 0.1810	 0.2840
D	 0.4440	 0.3790
E	 0.1370	 0.2990
F	 0.0730	 0.2520
G	 0.2910	 0.3320
H	 0.1410	 0.2910
I	 0.1610	 0.3110
J	 0.1810	 0.3320
K	 0.3930	 0.3910
L	 0.0730	 0.2260
M	 0.2420	 0.3610
N	 0.3160	 0.2880
O	 0.1970	 0.3180
P	 0.1890	 0.2940
Q	 0.2520	 0.3370
R	 0.0330	 0.2340
S	 0.2770	 0.2470
T	 0.3010	 0.3340
Y	 0.7680	 0.4050
Z	 0.4620	 0.4520
a	 0.6720	 0.4760
b	 0.6260	 0.4640
c	 0.6010	 0.4470
d	 0.3720	 0.3530
e	 0.4140	 0.4210



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Chain	Atom inclusion	Q-score
f	 0.1360	 0.2600
g	 0.0150	 0.1680
h	 0.0000	 0.0500
i	 0.6360	 0.4600
j	 0.5840	 0.4740
k	 0.6070	 0.4570
l	 0.6540	 0.4710
m	 0.6380	 0.4660
n	 0.5490	 0.4160
o	 0.6020	 0.4660
p	 0.6540	 0.4630
q	 0.6110	 0.4780
r	 0.6660	 0.4580
s	 0.5760	 0.4550
t	 0.4690	 0.4420
u	 0.6070	 0.4830
v	 0.6210	 0.4680
w	 0.5150	 0.3970
x	 0.2290	 0.3570
y	 0.7030	 0.4800
z	 0.6010	 0.4670