



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 04:15 AM UTC

PDB ID : 9B24 / pdb_00009b24
EMDB ID : EMD-44097
Title : WT strain gidB mutant mycobacterial ribosome
Authors : Young, I.D.; Chen, Y.; Javid, B.; Fraser, J.S.
Deposited on : 2024-03-14
Resolution : 2.47 Å(reported)
Based on initial models : 5o5j, 5o60

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

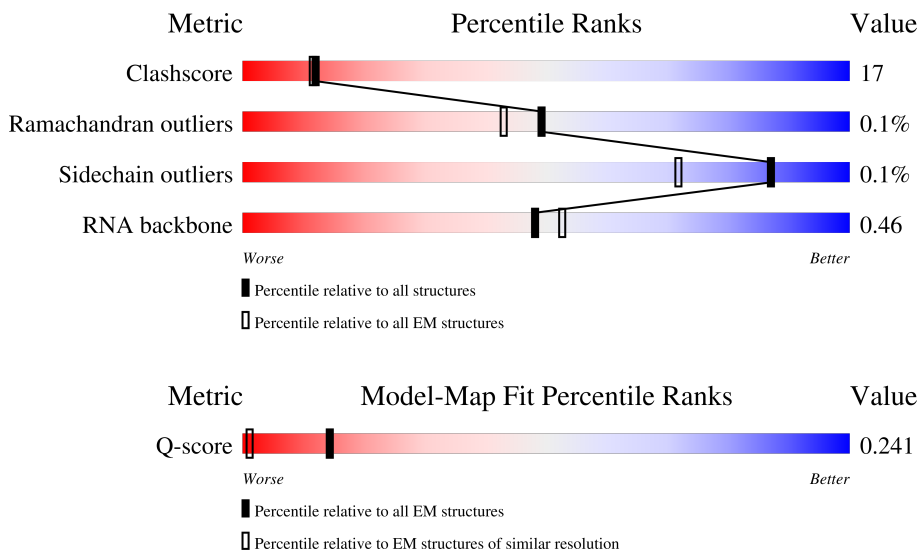
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.47 Å.

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



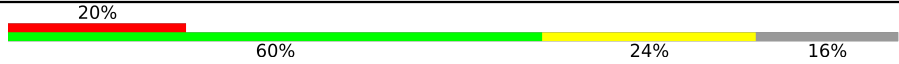
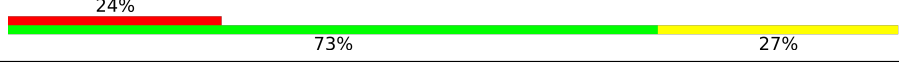
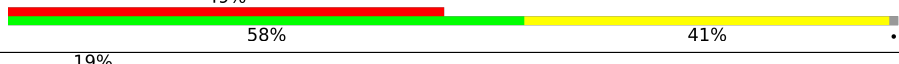



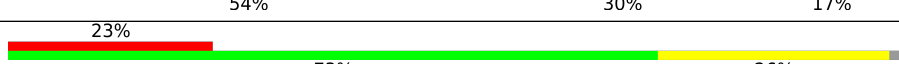

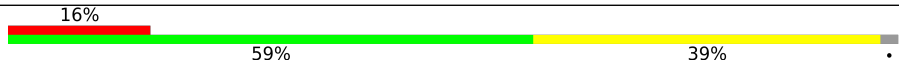

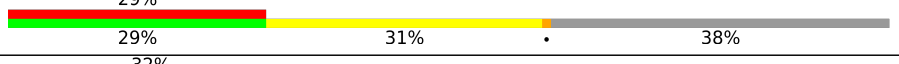
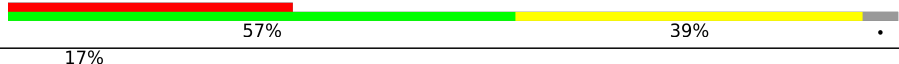
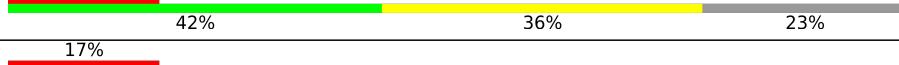

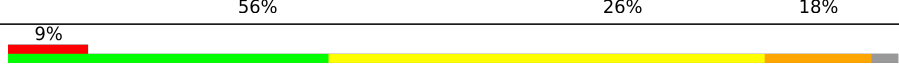
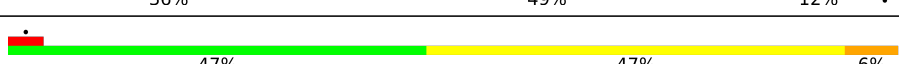



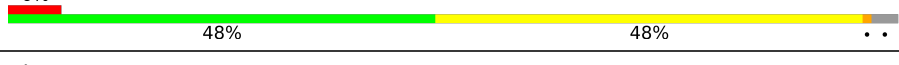





Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	6086 (1.98 - 2.97)

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	A	1528	
2	C	275	
3	D	201	

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Mol	Chain	Length	Quality of chain
4	E	214	
5	F	96	
6	G	156	
7	H	132	
8	I	150	
9	J	101	
10	K	138	
11	L	124	
12	M	124	
13	N	61	
14	O	89	
15	P	156	
16	Q	98	
17	R	84	
18	T	86	
19	V	277	
20	Y	3120	
21	U	118	
22	Z	278	
23	a	217	
24	b	215	
25	c	187	
26	d	179	
27	e	142	
28	f	147	

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Mol	Chain	Length	Quality of chain
29	g	122	9% 55% 45%
30	h	147	28% 73% 25%
31	i	138	6% 59% 39%
32	j	199	5% 35% 25% 41%
33	k	127	13% 66% 33%
34	l	113	39% 53% 46%
35	m	129	10% 64% 33%
36	n	103	78% 19%
37	o	153	52% 23% 25%
38	p	100	10% 69% 28%
39	q	105	9% 74% 18% 8%
40	r	215	47% 71% 18% 11%
41	s	88	6% 63% 27% 10%
42	t	64	5% 67% 31%
43	u	77	21% 42% 42% 17%
44	v	175	5% 49% 23% 28%
45	w	61	7% 48% 49%
46	x	57	11% 61% 33% 5%
47	y	55	9% 62% 27% 11%
48	z	47	9% 55% 43%
49	1	64	64% 34%
50	2	37	57% 43%
51	4	81	33% 51% 16%

2 Entry composition i

There are 53 unique types of molecules in this entry. The entry contains 146980 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 RNA (1528-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A	1511	32439	14448	5930	10550	1511	0	0

- Molecule 2 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	C	208	1660	1036	322	298	4	0	0

- Molecule 3 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	D	200	1641	1028	316	295	2	0	0

- Molecule 4 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	E	180	1296	812	245	235	4	0	0

- Molecule 5 is a protein called Small ribosomal subunit protein bS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	F	96	771	486	138	145	2	0	0

- Molecule 6 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	G	155	1232	768	241	221	2	0	0

- Molecule 7 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	H	131	1010	633	189	187	1	0	0

- Molecule 8 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
8	I	126	994	630	194	170	0	0

- Molecule 9 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	J	99	788	495	146	144	3	0	0

- Molecule 10 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	K	115	855	528	170	156	1	0	0

- Molecule 11 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	L	122	958	594	197	165	2	0	0

- Molecule 12 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	M	116	935	572	191	169	3	0	0

- Molecule 13 is a protein called Small ribosomal subunit protein uS14B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	N	60	477	302	97	73	5	0	0

- Molecule 14 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	O	88	Total	C	N	O	0	0
			720	449	147	124		

- Molecule 15 is a protein called Small ribosomal subunit protein bS16.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	P	96	Total	C	N	O	0	0
			764	488	142	134		

- Molecule 16 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	94	Total	C	N	O	S	0	0
			748	469	142	135	2		

- Molecule 17 is a protein called Small ribosomal subunit protein bS18B.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	65	Total	C	N	O	S	0	0
			513	318	102	90	3		

- Molecule 18 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	T	85	Total	C	N	O	0	0
			660	402	139	119		

- Molecule 19 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	V	228	Total	C	N	O	S	0	0
			1793	1132	322	330	9		

- Molecule 20 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Y	3038	Total	C	N	O	P	0	0
			65241	29079	12000	21124	3038		

- Molecule 21 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
21	U	118	2522	1126	468	810	118	0	0

- Molecule 22 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	Z	275	2110	1298	438	370	4	0	0

- Molecule 23 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	a	214	1587	982	310	290	5	0	0

- Molecule 24 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	b	209	1569	969	295	303	2	0	0

- Molecule 25 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	c	182	1445	907	271	261	6	0	0

- Molecule 26 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	d	176	1348	845	249	253	1	0	0

- Molecule 27 is a protein called Large ribosomal subunit protein uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	e	133	990	625	175	187	3	0	0

- Molecule 28 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	f	146	1130	722	207	200	1	0	0

- Molecule 29 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	g	122	938	586	179	170	3	0	0

- Molecule 30 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	h	145	1078	676	205	194	3	0	0

- Molecule 31 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	i	136	1092	690	213	187	2	0	0

- Molecule 32 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	j	118	928	583	180	163	2	0	0

- Molecule 33 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
33	k	126	956	586	199	171	0	0

- Molecule 34 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	l	113	907	570	171	165	1	0	0

- Molecule 35 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	m	124	Total	C	N	O	0	0
			988	613	203	172		

- Molecule 36 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	n	100	Total	C	N	O	0	0
			754	478	137	139		

- Molecule 37 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	o	114	Total	C	N	O	0	0
			873	543	171	159		

- Molecule 38 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	p	97	Total	C	N	O	0	0
			756	479	138	139		

- Molecule 39 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	q	97	Total	C	N	O	S	0	0
			732	456	137	137	2		

- Molecule 40 is a protein called Large ribosomal subunit protein bL25.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	r	192	Total	C	N	O	0	0
			1428	881	255	292		

- Molecule 41 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	s	79	Total	C	N	O	0	0
			586	361	123	102		

- Molecule 42 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	t	63	Total	C	N	O	S	0	0
			470	283	103	80	4		

- Molecule 43 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	u	64	Total	C	N	O	S	0	0
			531	324	103	103	1		

- Molecule 44 is a protein called Large ribosomal subunit protein uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	v	126	Total	C	N	O	S	0	0
			918	580	156	180	2		

- Molecule 45 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	w	59	Total	C	N	O	0	0
			474	292	95	87		

- Molecule 46 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	x	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 47 is a protein called Large ribosomal subunit protein bL33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	y	49	Total	C	N	O	S	0	0
			405	248	82	71	4		

- Molecule 48 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	z	46	Total	C	N	O	S	0	0
			377	225	97	54	1		

- Molecule 49 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
49	1	63	502	302	115	85	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	2	37	299	181	66	47	5	0	0

- Molecule 51 is a RNA chain called 23S rRNA part.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
51	4	81	1740	775	313	571	81	0	0

- Molecule 52 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
52	A	199	Total 199	Mg 199	0
52	D	1	Total 1	Mg 1	0
52	E	4	Total 4	Mg 4	0
52	I	1	Total 1	Mg 1	0
52	K	2	Total 2	Mg 2	0
52	N	1	Total 1	Mg 1	0
52	P	1	Total 1	Mg 1	0
52	Q	2	Total 2	Mg 2	0
52	R	1	Total 1	Mg 1	0
52	T	5	Total 5	Mg 5	0
52	Y	379	Total 379	Mg 379	0
52	U	10	Total 10	Mg 10	0

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Mol	Chain	Residues	Atoms		AltConf
52	Z	8	Total 8	Mg 8	0
52	a	1	Total 1	Mg 1	0
52	b	1	Total 1	Mg 1	0
52	h	1	Total 1	Mg 1	0
52	i	1	Total 1	Mg 1	0
52	o	1	Total 1	Mg 1	0
52	p	1	Total 1	Mg 1	0
52	t	1	Total 1	Mg 1	0
52	u	1	Total 1	Mg 1	0
52	y	1	Total 1	Mg 1	0
52	1	1	Total 1	Mg 1	0

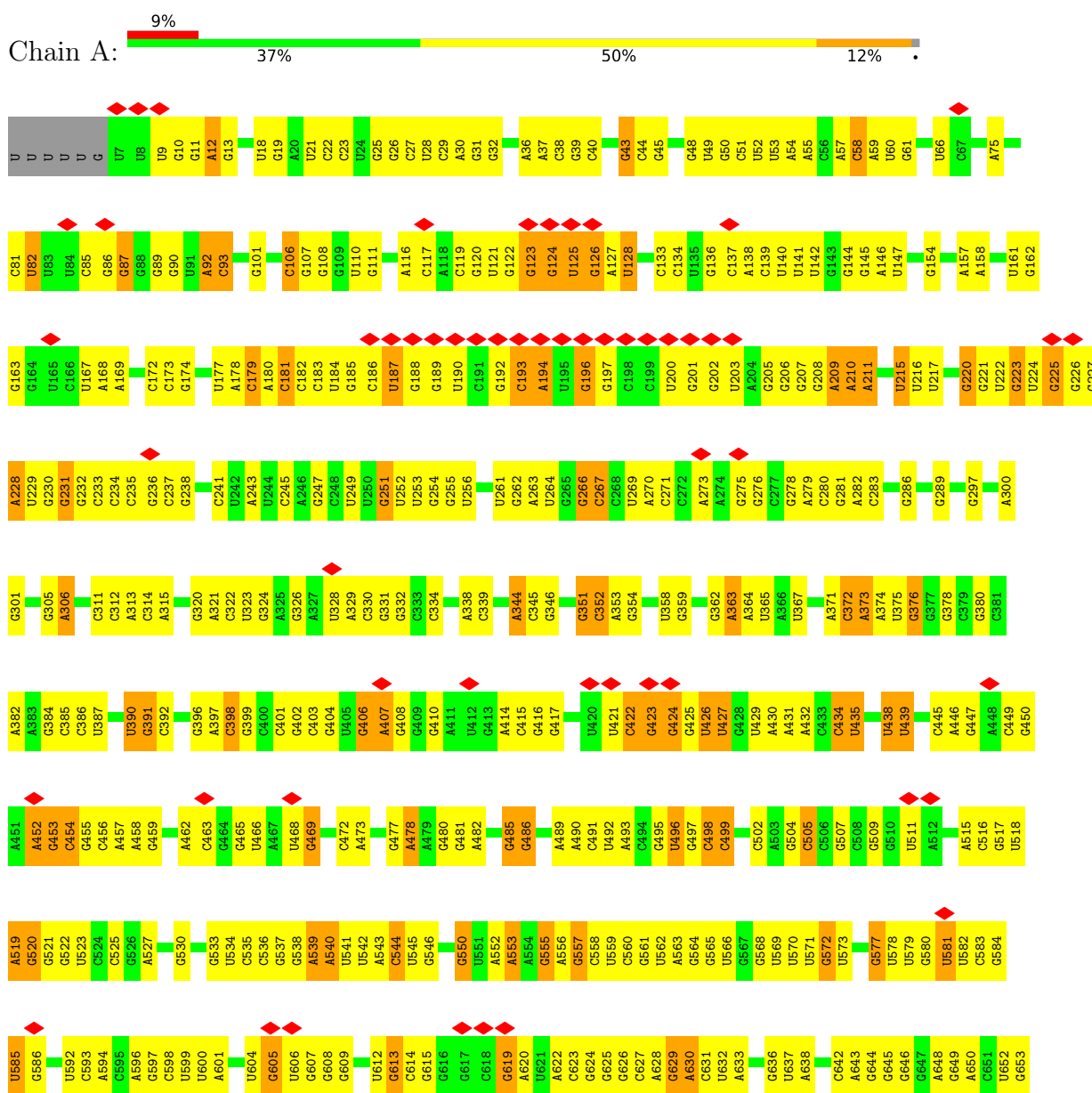
- Molecule 53 is ZINC ION (CCD ID: ZN) (formula: Zn).

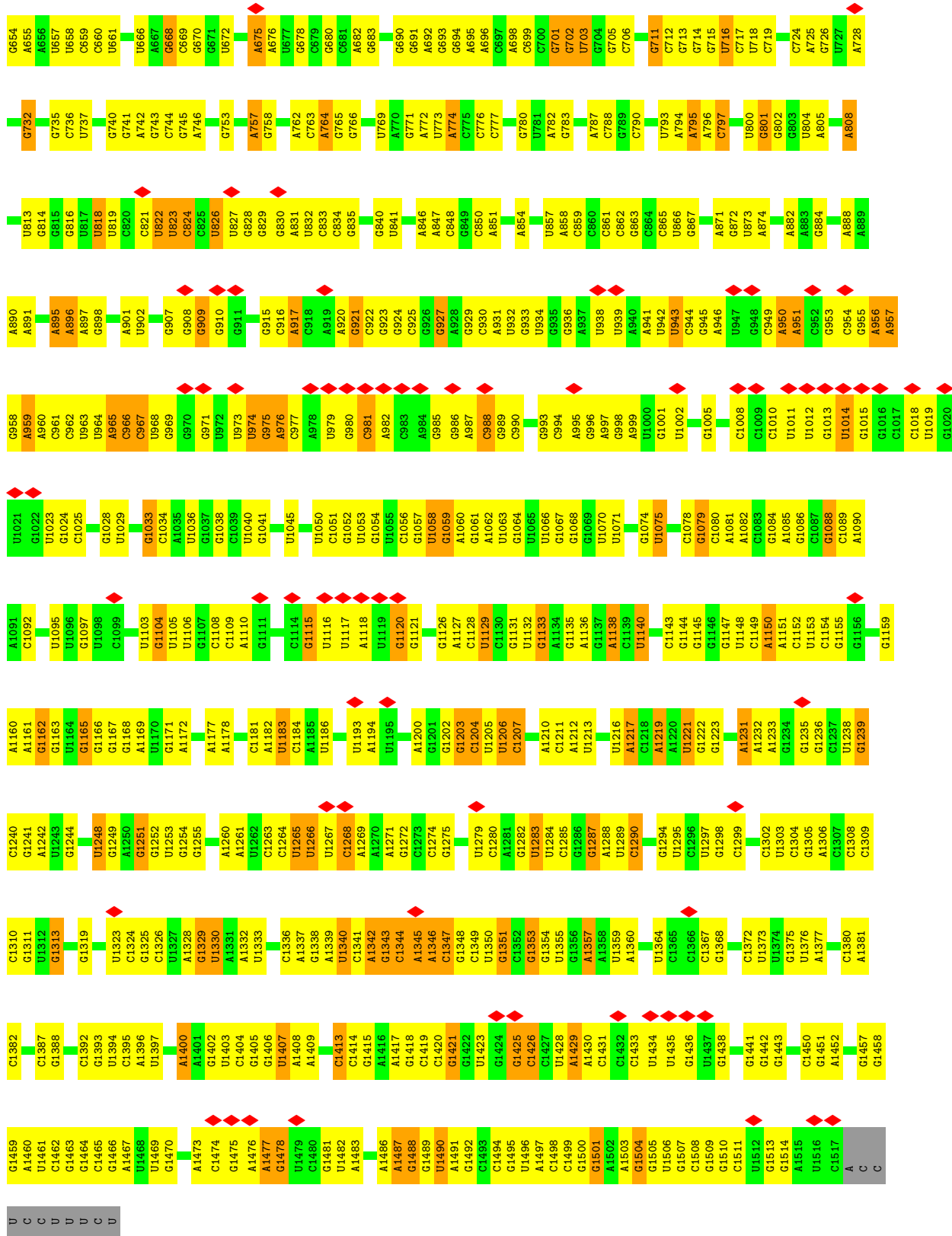
Mol	Chain	Residues	Atoms		AltConf
53	N	1	Total 1	Zn 1	0
53	R	1	Total 1	Zn 1	0
53	t	1	Total 1	Zn 1	0
53	y	1	Total 1	Zn 1	0
53	2	1	Total 1	Zn 1	0

3 Residue-property plots [i](#)

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

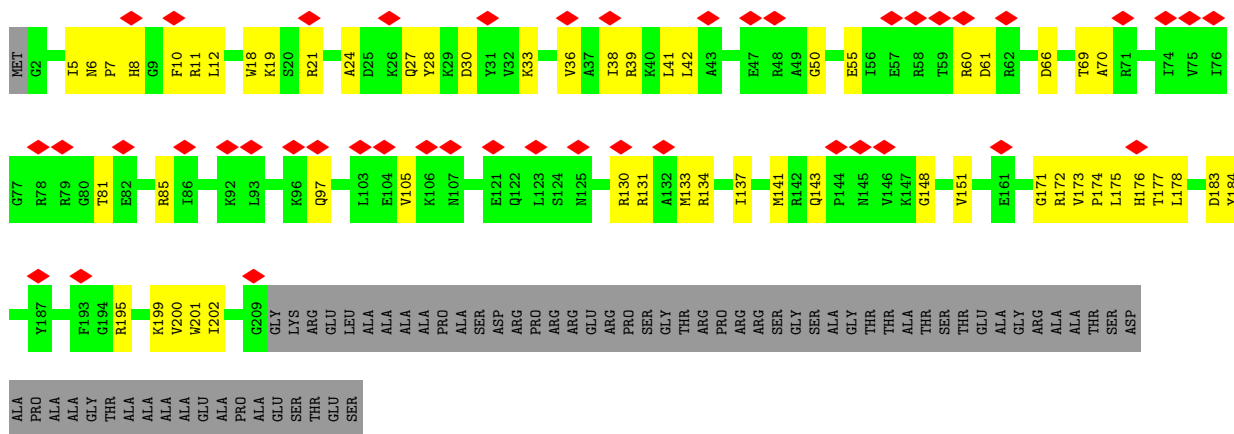
- Molecule 1: RNA (1528-MER)



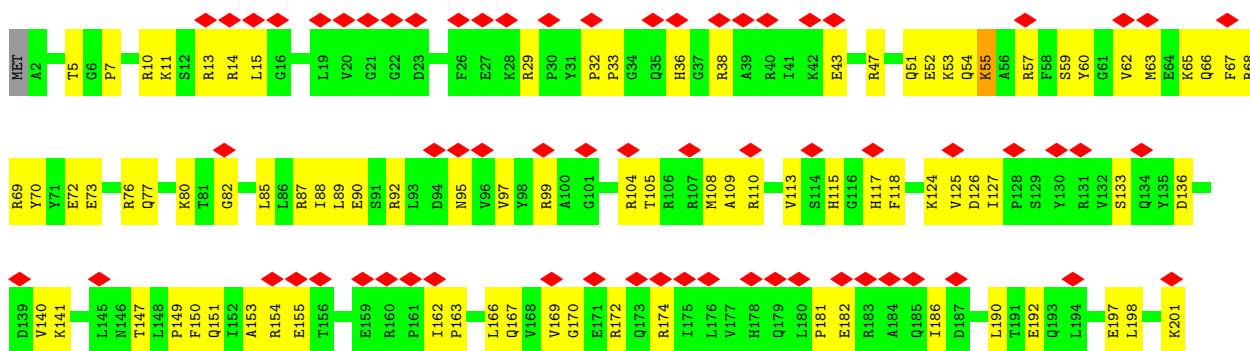


• Molecule 2: Small ribosomal subunit protein uS3

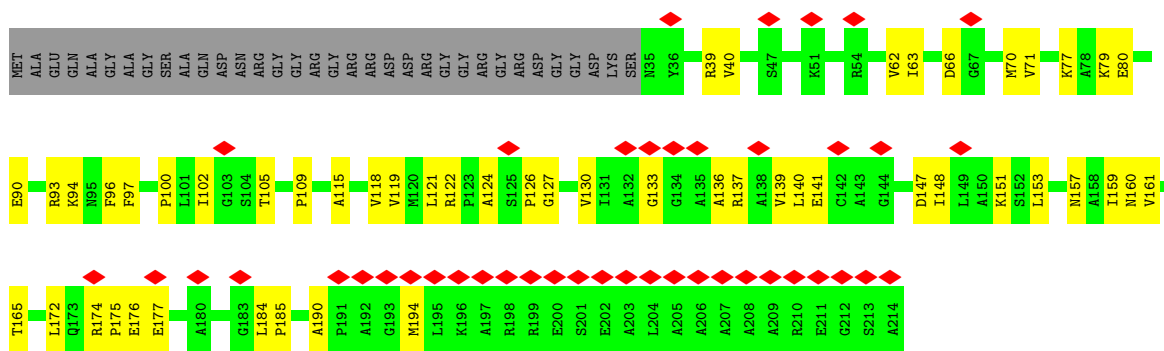




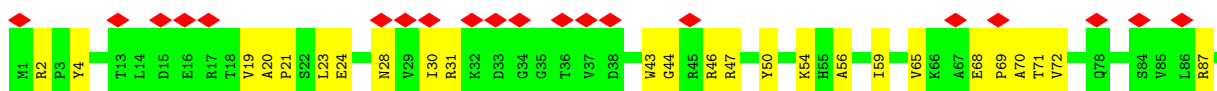
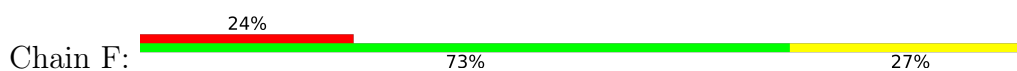
• Molecule 3: Small ribosomal subunit protein uS4

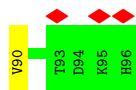


• Molecule 4: Small ribosomal subunit protein uS5

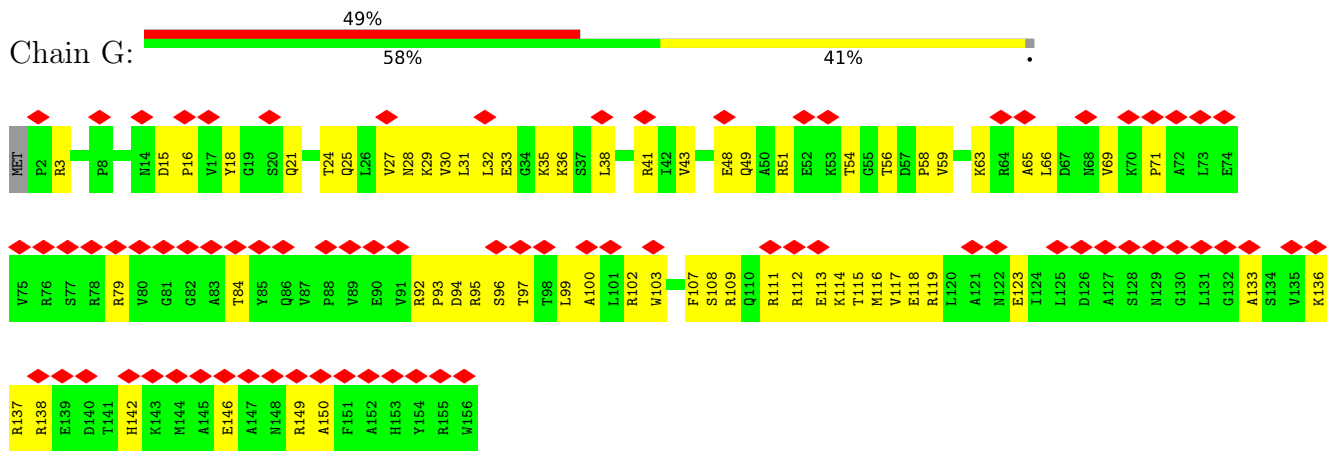


• Molecule 5: Small ribosomal subunit protein bS6

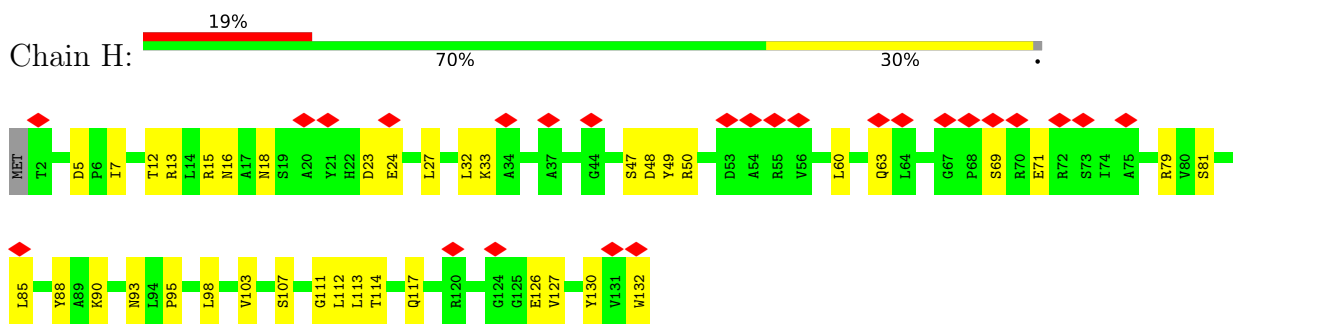




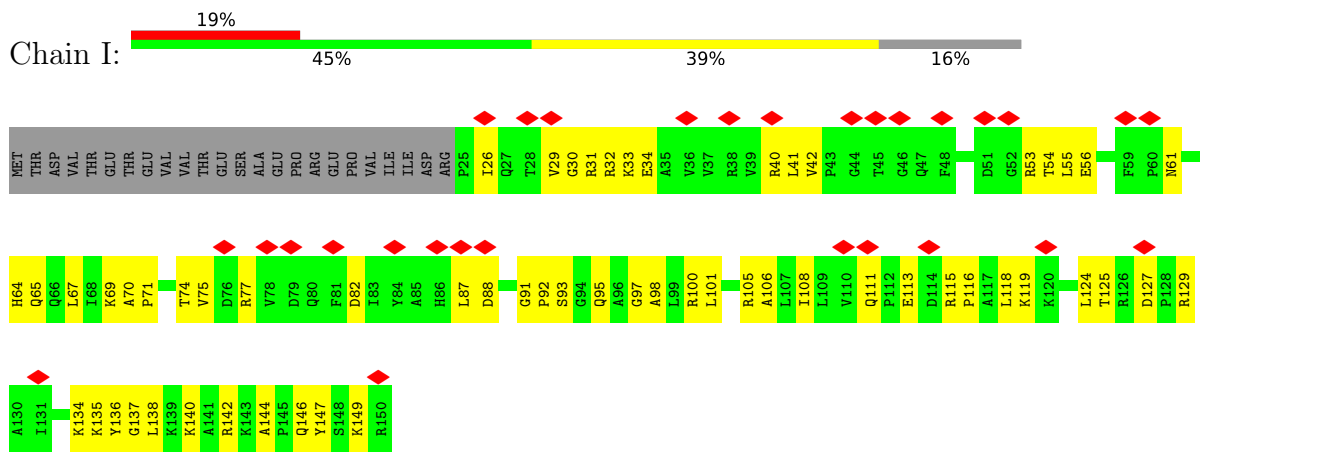
• Molecule 6: Small ribosomal subunit protein uS7



• Molecule 7: Small ribosomal subunit protein uS8

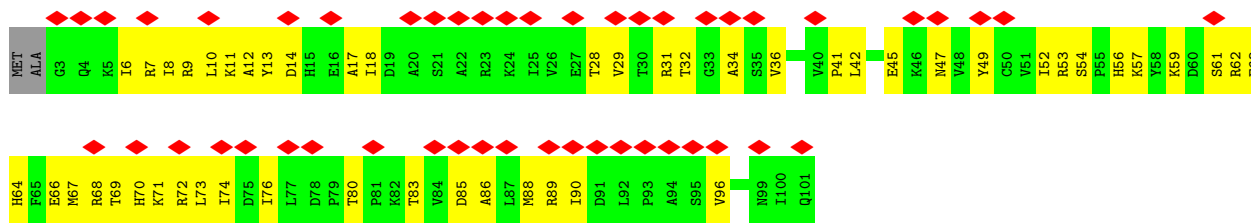


• Molecule 8: Small ribosomal subunit protein uS9

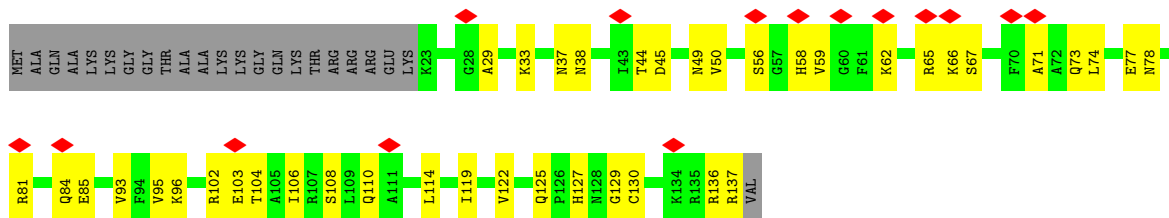


• Molecule 9: Small ribosomal subunit protein uS10

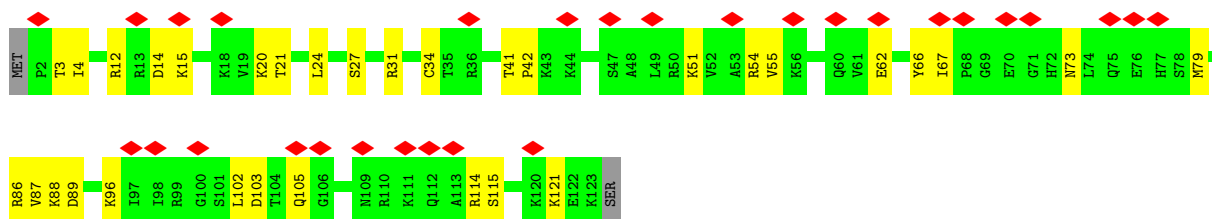




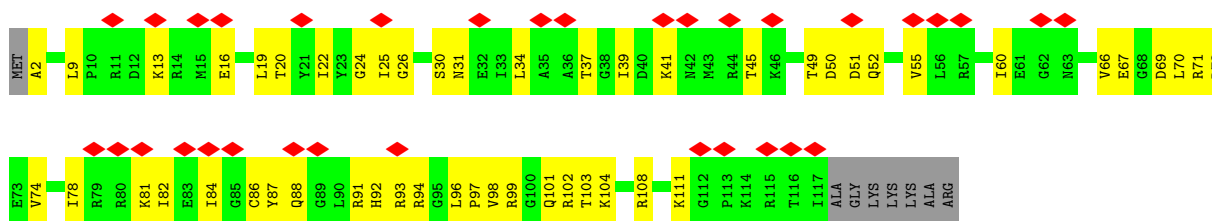
• Molecule 10: Small ribosomal subunit protein uS11



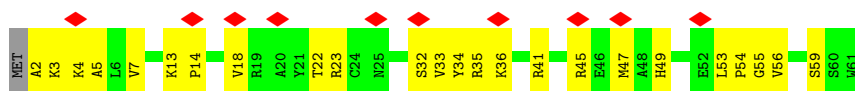
• Molecule 11: Small ribosomal subunit protein uS12



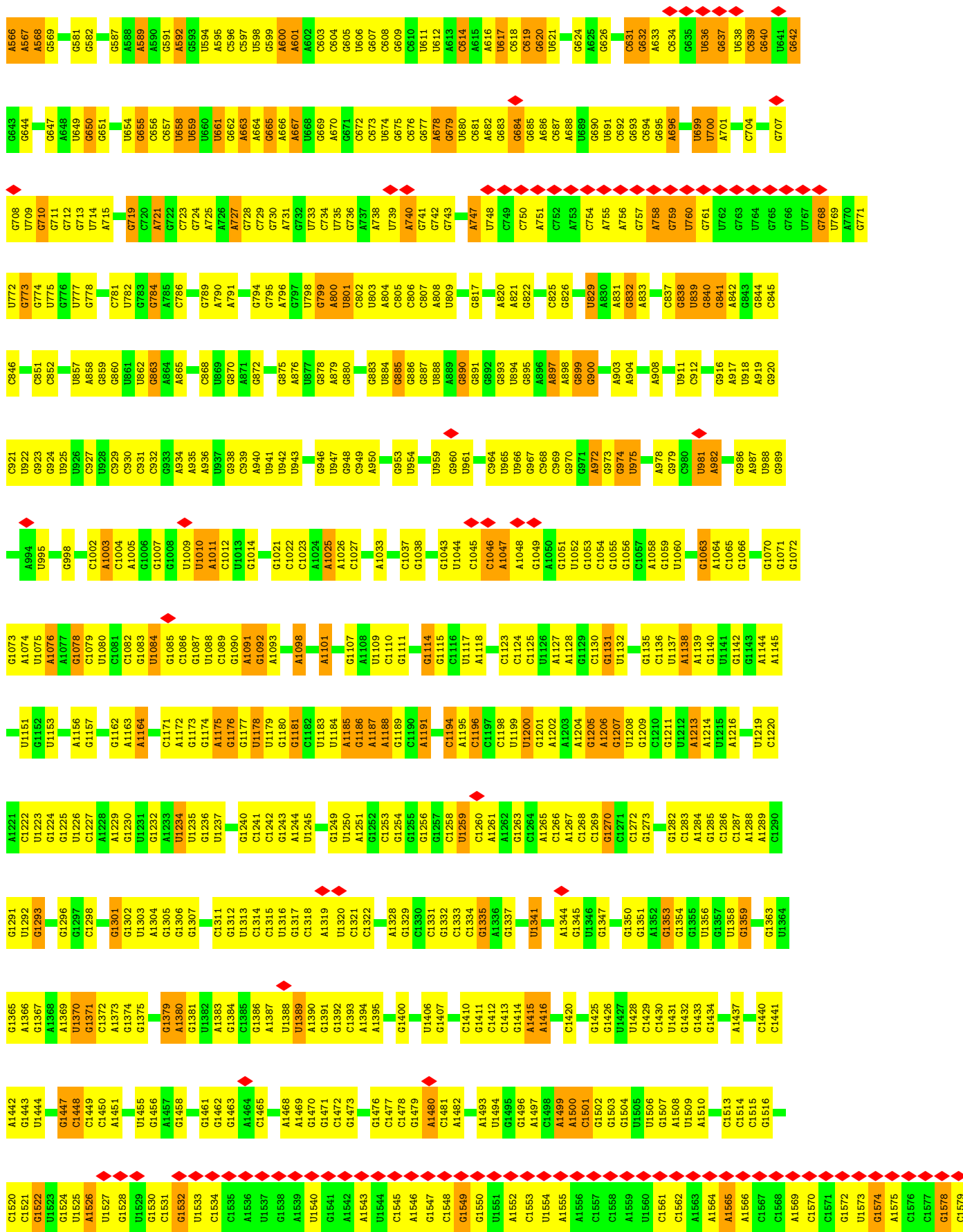
• Molecule 12: Small ribosomal subunit protein uS13

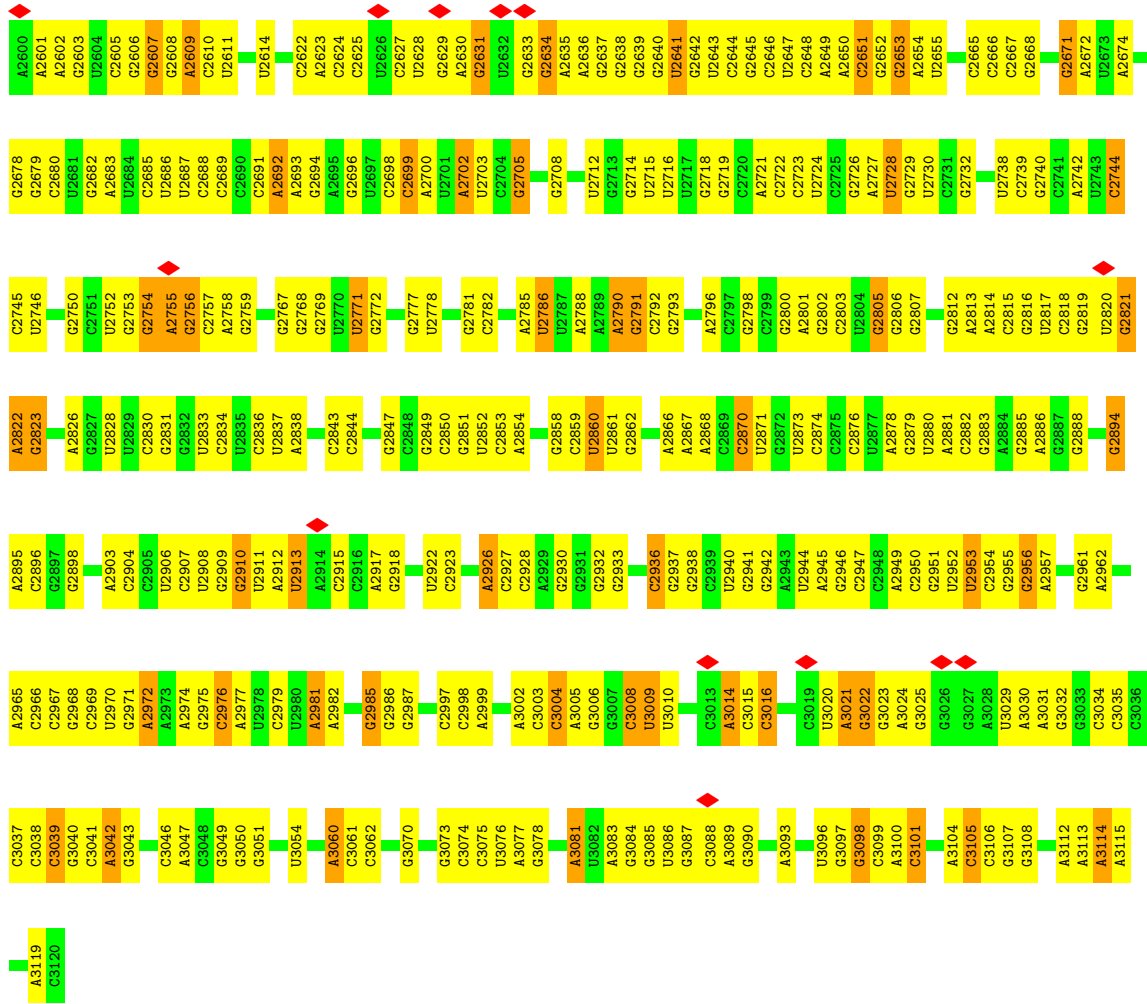


• Molecule 13: Small ribosomal subunit protein uS14B

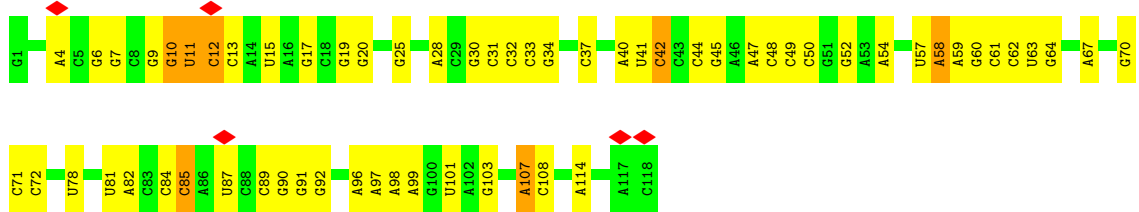


• Molecule 14: Small ribosomal subunit protein uS15

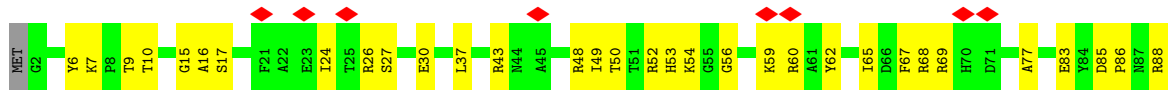


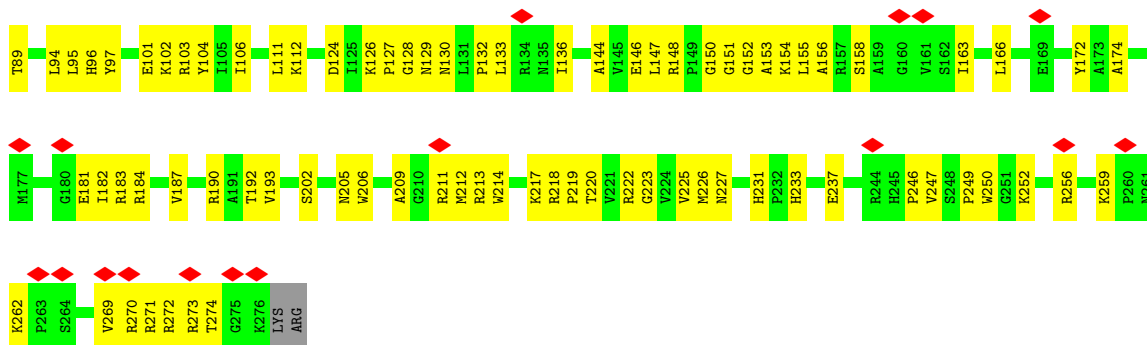


- Molecule 21: 5S rRNA

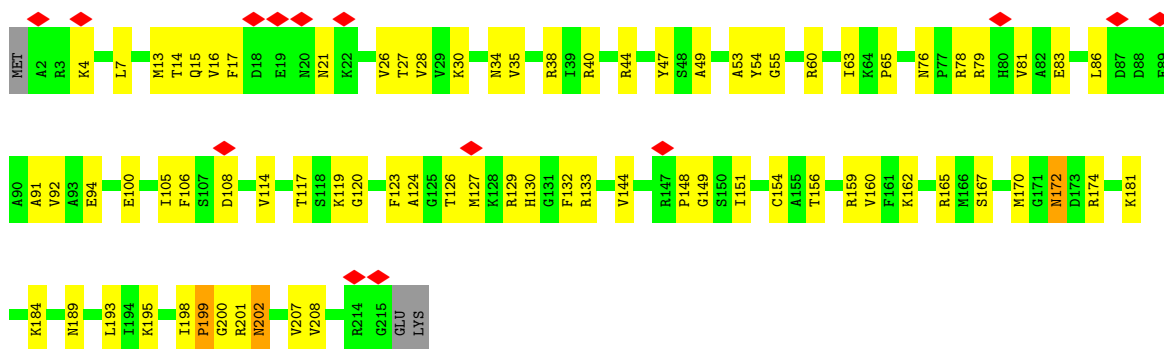


- Molecule 22: Large ribosomal subunit protein uL2

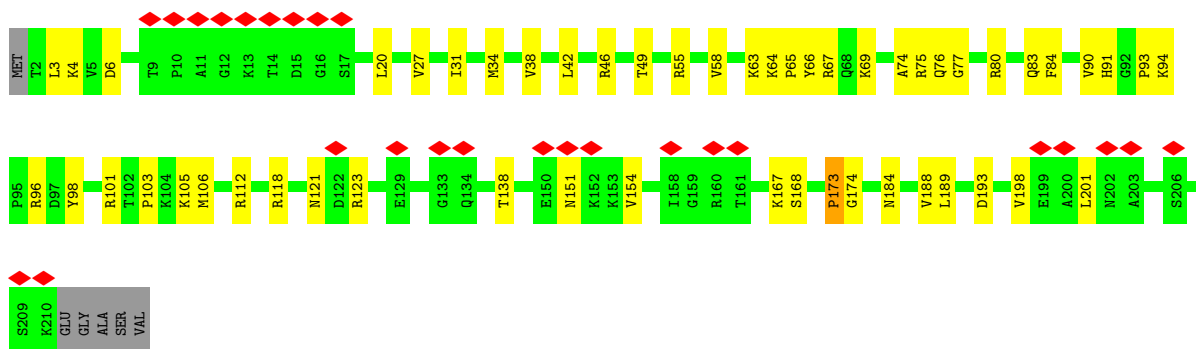




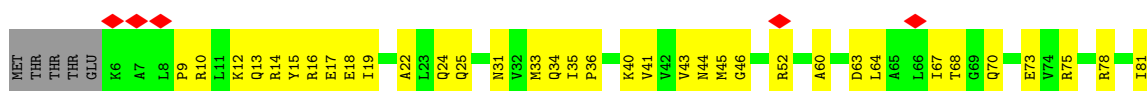
• Molecule 23: Large ribosomal subunit protein uL3

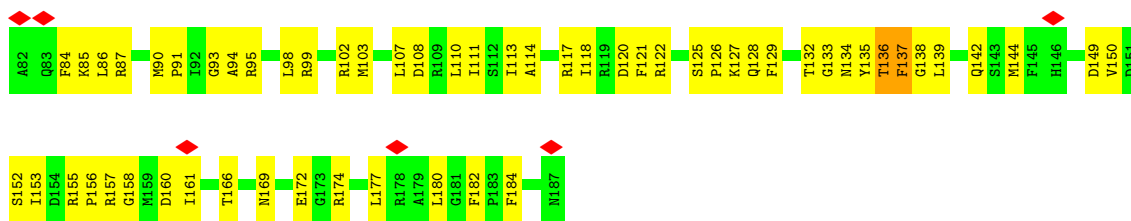


• Molecule 24: Large ribosomal subunit protein uL4

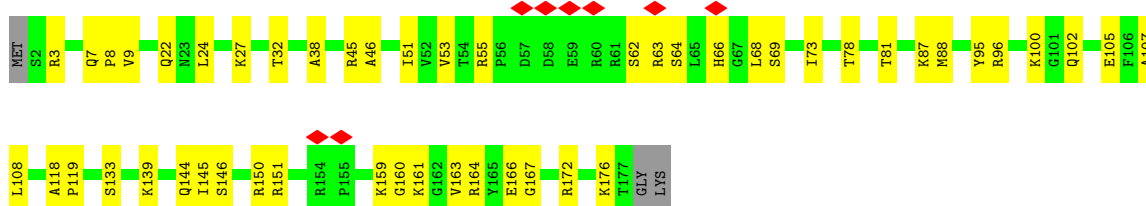


• Molecule 25: Large ribosomal subunit protein uL5

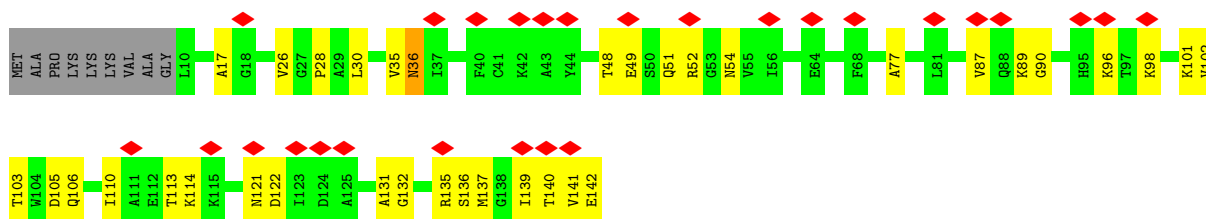




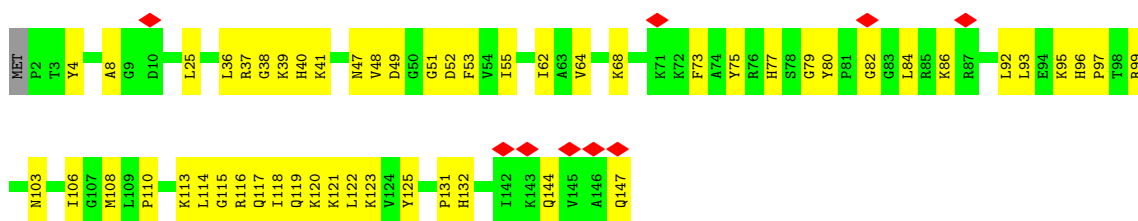
- Molecule 26: Large ribosomal subunit protein uL6



- Molecule 27: Large ribosomal subunit protein uL11



- Molecule 28: Large ribosomal subunit protein uL13

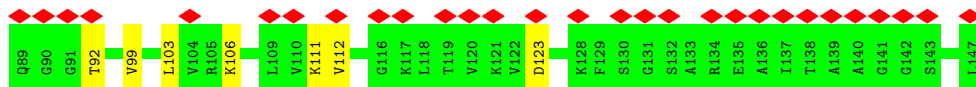
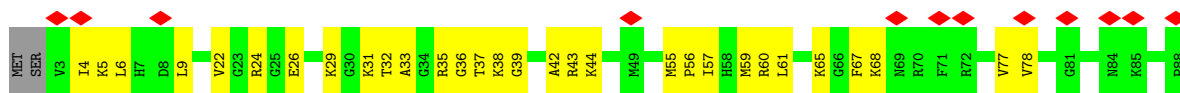
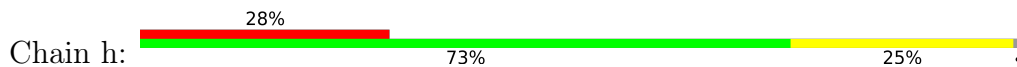


- Molecule 29: Large ribosomal subunit protein uL14

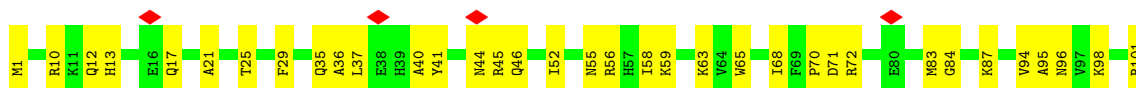




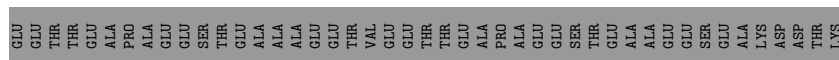
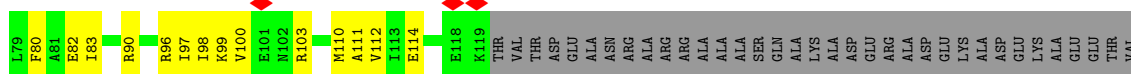
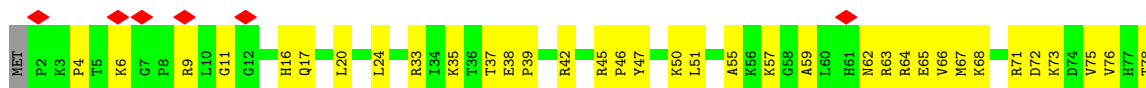
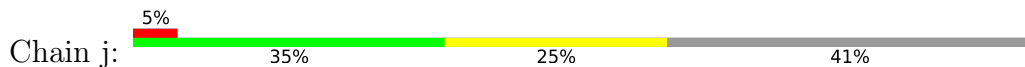
• Molecule 30: Large ribosomal subunit protein uL15



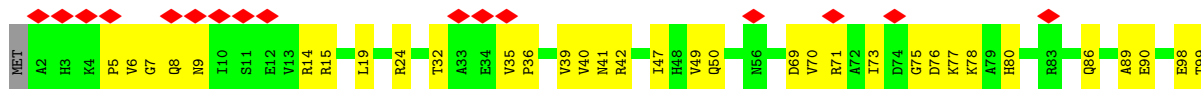
• Molecule 31: Large ribosomal subunit protein uL16



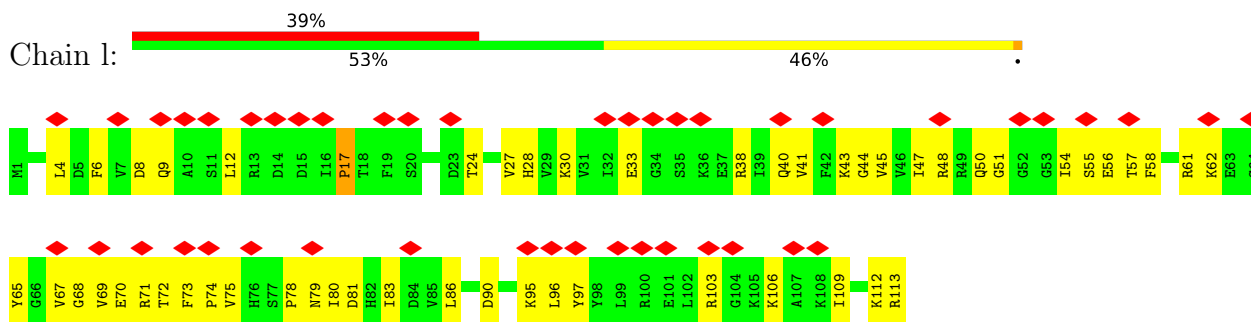
• Molecule 32: Large ribosomal subunit protein bL17



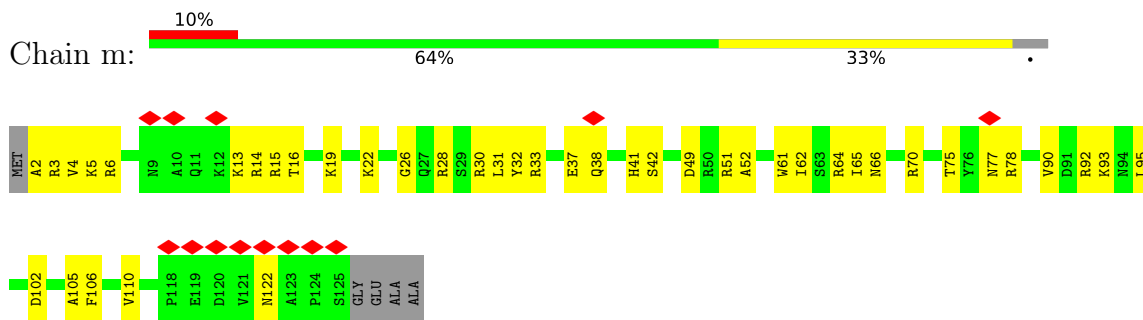
• Molecule 33: Large ribosomal subunit protein uL18



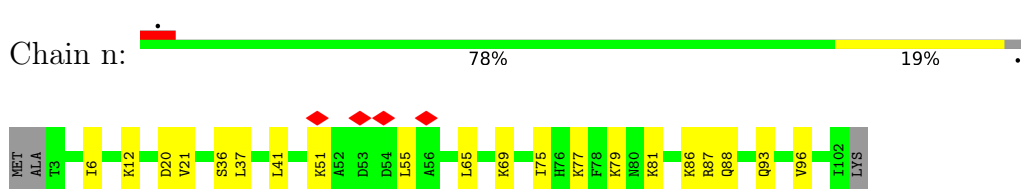
• Molecule 34: Large ribosomal subunit protein bL19



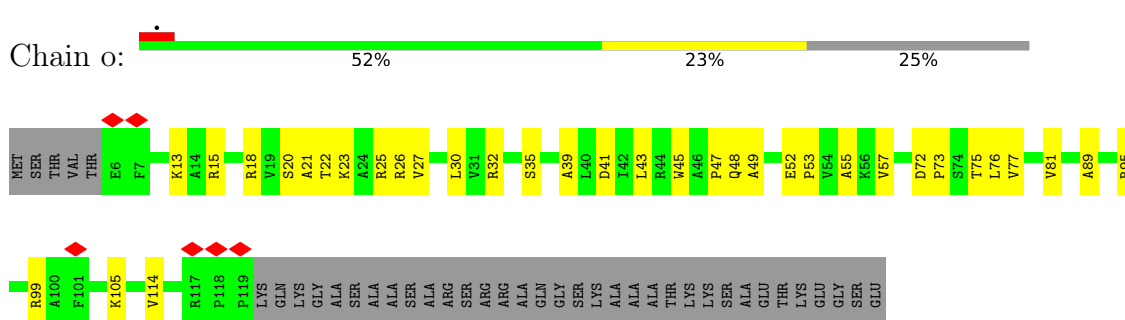
• Molecule 35: Large ribosomal subunit protein bL20



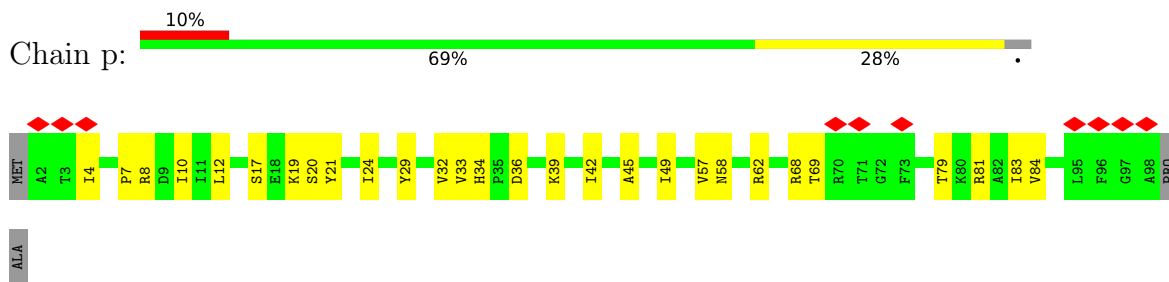
• Molecule 36: Large ribosomal subunit protein bL21



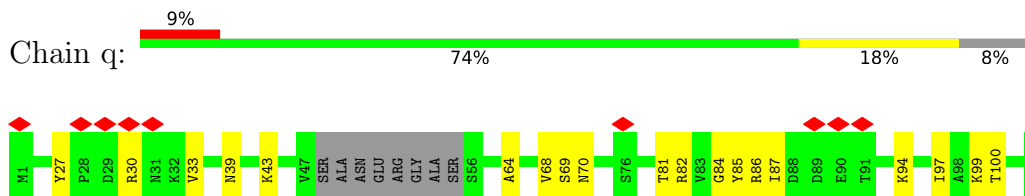
• Molecule 37: Large ribosomal subunit protein uL22



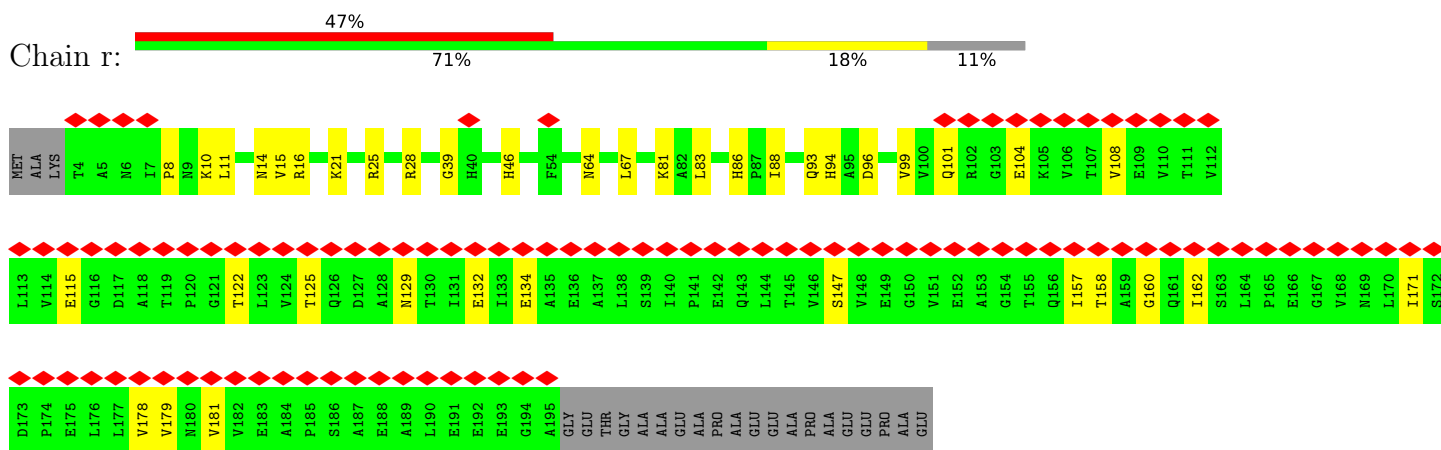
• Molecule 38: Large ribosomal subunit protein uL23



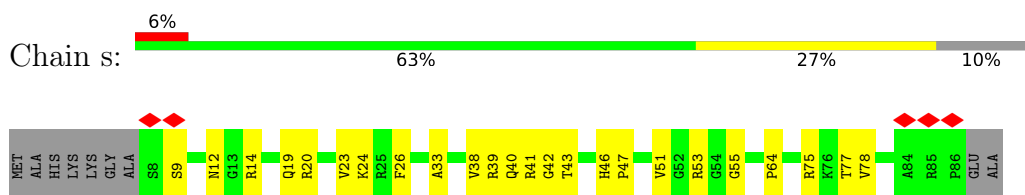
• Molecule 39: Large ribosomal subunit protein uL24



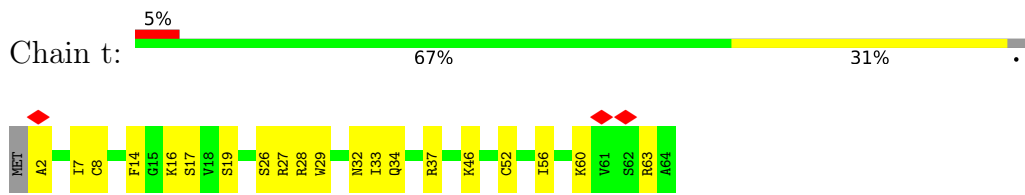
• Molecule 40: Large ribosomal subunit protein bL25



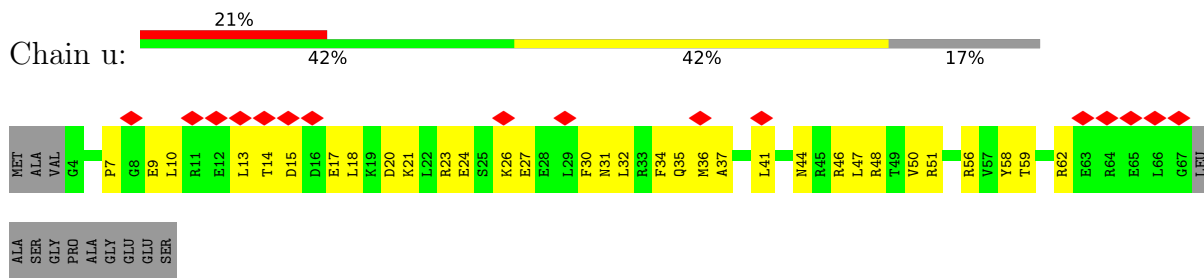
• Molecule 41: Large ribosomal subunit protein bL27



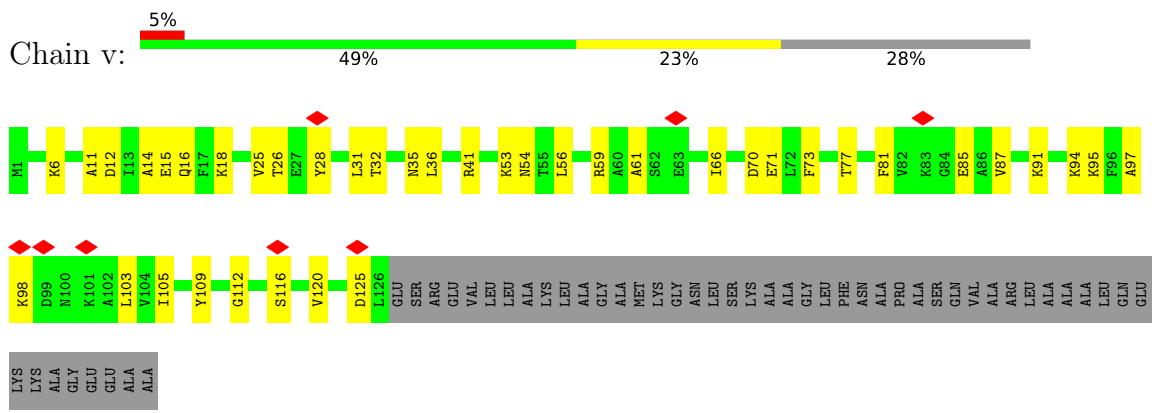
• Molecule 42: Large ribosomal subunit protein bL28



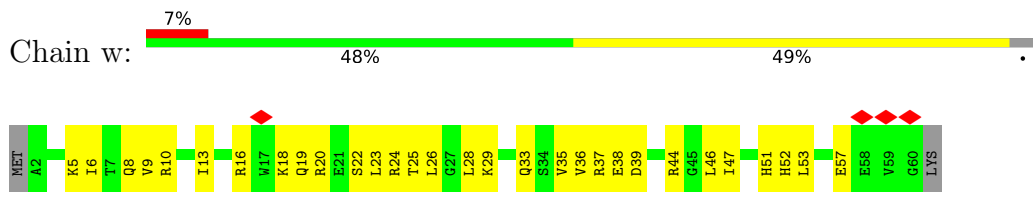
• Molecule 43: Large ribosomal subunit protein uL29



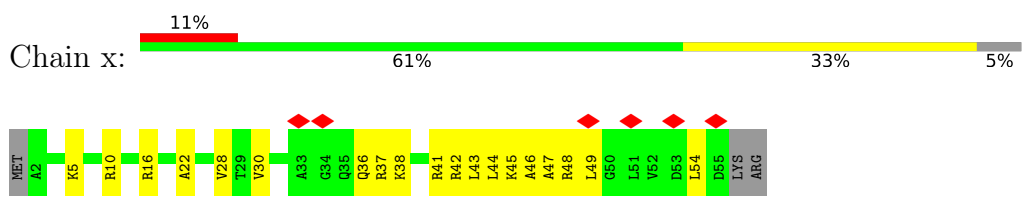
• Molecule 44: Large ribosomal subunit protein uL10



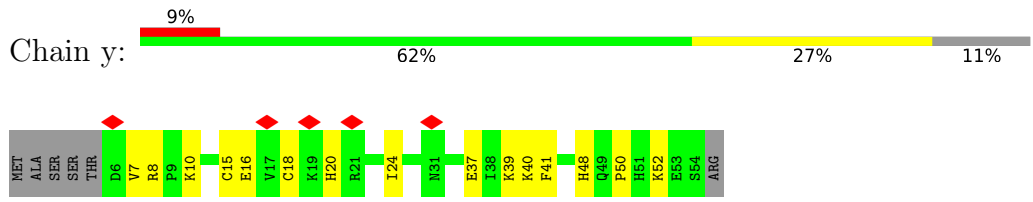
• Molecule 45: Large ribosomal subunit protein uL30



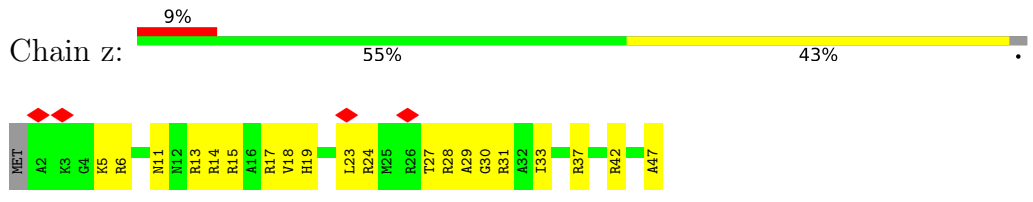
• Molecule 46: Large ribosomal subunit protein bL32



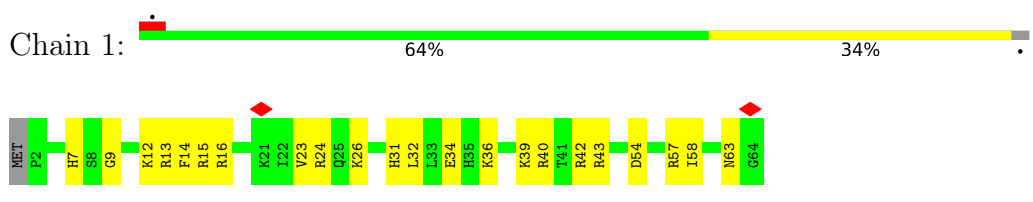
• Molecule 47: Large ribosomal subunit protein bL33A



• Molecule 48: Large ribosomal subunit protein bL34



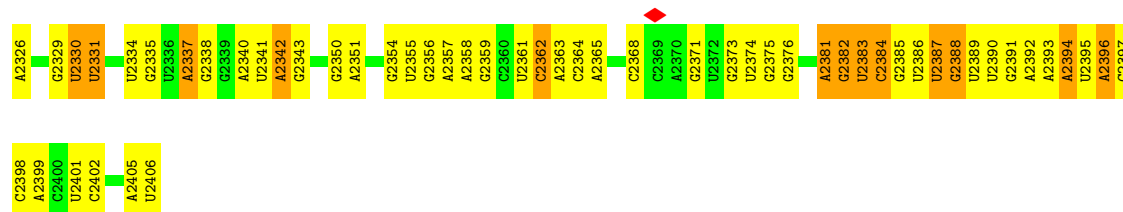
• Molecule 49: Large ribosomal subunit protein bL35



- Molecule 50: 50S ribosomal protein L36



- Molecule 51: 23S rRNA part



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1466881	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	901.165	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	21.903	Depositor
Minimum map value	-12.598	Depositor
Average map value	-0.005	Depositor
Map value standard deviation	0.580	Depositor
Recommended contour level	1.04	Depositor
Map size (Å)	539.784, 539.784, 539.784	wwPDB
Map dimensions	648, 648, 648	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.833, 0.833, 0.833	Depositor

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: 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	A	0.10	0/36304	0.25	0/56637
2	C	0.16	0/1684	0.43	0/2261
3	D	0.24	0/1672	0.50	1/2251 (0.0%)
4	E	0.15	0/1312	0.42	0/1772
5	F	0.12	0/782	0.37	0/1059
6	G	0.16	0/1252	0.48	0/1690
7	H	0.14	0/1025	0.39	0/1385
8	I	0.20	0/1012	0.49	0/1362
9	J	0.18	0/802	0.53	0/1086
10	K	0.15	0/873	0.43	0/1180
11	L	0.14	0/969	0.40	0/1294
12	M	0.18	0/942	0.51	0/1260
13	N	0.15	0/488	0.45	0/650
14	O	0.17	0/729	0.42	0/977
15	P	0.17	0/778	0.42	0/1049
16	Q	0.17	0/759	0.49	0/1016
17	R	0.25	0/518	0.55	0/693
18	T	0.16	0/663	0.43	0/882
19	V	0.15	0/1822	0.42	0/2457
20	Y	0.28	9/73003 (0.0%)	0.30	14/113787 (0.0%)
21	U	0.12	0/2821	0.25	0/4396
22	Z	0.20	0/2153	0.50	0/2895
23	a	0.20	0/1609	0.52	1/2165 (0.0%)
24	b	0.20	0/1592	0.51	2/2153 (0.1%)
25	c	0.29	0/1467	0.64	1/1973 (0.1%)
26	d	0.16	0/1369	0.38	0/1848
27	e	0.16	0/986	0.45	2/1303 (0.2%)
28	f	0.21	0/1157	0.42	0/1567
29	g	0.23	0/946	0.53	0/1268
30	h	0.20	0/1091	0.50	0/1457
31	i	0.18	0/1118	0.51	1/1506 (0.1%)
32	j	0.24	0/945	0.53	0/1267

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	k	0.16	0/966	0.40	0/1298
34	l	0.26	0/921	0.61	2/1236 (0.2%)
35	m	0.23	0/1000	0.50	0/1341
36	n	0.16	0/764	0.35	0/1030
37	o	0.20	0/887	0.42	0/1204
38	p	0.21	0/766	0.45	0/1030
39	q	0.13	0/738	0.29	0/987
40	r	0.12	0/1443	0.31	0/1970
41	s	0.17	0/595	0.38	0/798
42	t	0.25	0/478	0.59	0/641
43	u	0.25	0/534	0.73	0/713
44	v	0.19	0/925	0.40	0/1246
45	w	0.23	0/477	0.46	0/640
46	x	0.26	0/427	0.53	0/572
47	y	0.15	0/413	0.40	0/553
48	z	0.26	0/380	0.64	2/500 (0.4%)
49	1	0.20	0/507	0.46	0/672
50	2	0.28	0/303	0.57	0/401
51	4	0.12	0/1943	0.38	2/3020 (0.1%)
All	All	0.22	9/159110 (0.0%)	0.34	28/238398 (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
25	c	0	1

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
20	Y	268	G	C1'-N9	37.54	2.04	1.48
20	Y	360	G	N1-C2	24.85	1.87	1.37
20	Y	360	G	C6-N1	23.08	1.85	1.39
20	Y	360	G	C2-N3	20.54	1.73	1.32
20	Y	360	G	N3-C4	20.10	1.75	1.35

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	Y	268	G	C8-N9-C4	-12.45	69.06	106.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	Y	268	G	N9-C1'-C2'	11.56	129.34	112.00
24	b	173	PRO	CA-N-CD	-11.07	96.51	112.00
34	l	17	PRO	CA-N-CD	-10.84	96.82	112.00
20	Y	268	G	N7-C8-N9	10.82	145.57	113.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
25	c	136	THR	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32439	0	16320	909	0
2	C	1660	0	1707	46	0
3	D	1641	0	1668	82	0
4	E	1296	0	1360	45	0
5	F	771	0	797	18	0
6	G	1232	0	1282	71	0
7	H	1010	0	1046	33	0
8	I	994	0	1050	50	0
9	J	788	0	819	56	0
10	K	855	0	863	38	0
11	L	958	0	1045	31	0
12	M	935	0	986	53	0
13	N	477	0	499	22	0
14	O	720	0	760	23	0
15	P	764	0	806	54	0
16	Q	748	0	795	49	0
17	R	513	0	537	39	0
18	T	660	0	711	27	0
19	V	1793	0	1839	57	0
20	Y	65241	0	32857	1806	0
21	U	2522	0	1285	51	0
22	Z	2110	0	2164	115	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
23	a	1587	0	1630	77	0
24	b	1569	0	1607	48	0
25	c	1445	0	1476	102	0
26	d	1348	0	1399	39	0
27	e	990	0	1002	26	0
28	f	1130	0	1167	45	0
29	g	938	0	1000	61	0
30	h	1078	0	1151	36	0
31	i	1092	0	1128	49	0
32	j	928	0	972	48	0
33	k	956	0	991	49	0
34	l	907	0	938	52	0
35	m	988	0	1038	47	0
36	n	754	0	802	16	0
37	o	873	0	909	29	0
38	p	756	0	802	31	0
39	q	732	0	782	16	0
40	r	1428	0	1443	29	0
41	s	586	0	601	25	0
42	t	470	0	480	25	0
43	u	531	0	541	34	0
44	v	918	0	959	28	0
45	w	474	0	500	33	0
46	x	423	0	463	28	0
47	y	405	0	407	10	0
48	z	377	0	411	20	0
49	1	502	0	541	22	0
50	2	299	0	321	16	0
51	4	1740	0	874	45	0
52	1	1	0	0	0	0
52	A	199	0	0	0	0
52	D	1	0	0	0	0
52	E	4	0	0	0	0
52	I	1	0	0	0	0
52	K	2	0	0	0	0
52	N	1	0	0	0	0
52	P	1	0	0	0	0
52	Q	2	0	0	0	0
52	R	1	0	0	0	0
52	T	5	0	0	0	0
52	U	10	0	0	0	0
52	Y	379	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	Z	8	0	0	0	0
52	a	1	0	0	0	0
52	b	1	0	0	0	0
52	h	1	0	0	0	0
52	i	1	0	0	0	0
52	o	1	0	0	0	0
52	p	1	0	0	0	0
52	t	1	0	0	0	0
52	u	1	0	0	0	0
52	y	1	0	0	0	0
53	2	1	0	0	0	0
53	N	1	0	0	0	0
53	R	1	0	0	0	0
53	t	1	0	0	0	0
53	y	1	0	0	0	0
All	All	146980	0	97531	4070	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 17.

The worst 5 of 4070 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:Y:360:G:C5	20:Y:360:G:C6	1.80	1.60
20:Y:360:G:N3	20:Y:360:G:C2	1.73	1.52
20:Y:360:G:N3	20:Y:360:G:C4	1.75	1.51
20:Y:360:G:C6	20:Y:360:G:N1	1.85	1.43
20:Y:268:G:N9	20:Y:360:G:C2	1.86	1.42

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	C	206/275 (75%)	198 (96%)	8 (4%)	0	100	100
3	D	198/201 (98%)	194 (98%)	4 (2%)	0	100	100
4	E	178/214 (83%)	171 (96%)	7 (4%)	0	100	100
5	F	94/96 (98%)	93 (99%)	1 (1%)	0	100	100
6	G	153/156 (98%)	147 (96%)	6 (4%)	0	100	100
7	H	129/132 (98%)	123 (95%)	6 (5%)	0	100	100
8	I	124/150 (83%)	114 (92%)	10 (8%)	0	100	100
9	J	97/101 (96%)	89 (92%)	8 (8%)	0	100	100
10	K	113/138 (82%)	106 (94%)	7 (6%)	0	100	100
11	L	120/124 (97%)	115 (96%)	5 (4%)	0	100	100
12	M	114/124 (92%)	109 (96%)	5 (4%)	0	100	100
13	N	58/61 (95%)	54 (93%)	4 (7%)	0	100	100
14	O	86/89 (97%)	84 (98%)	2 (2%)	0	100	100
15	P	94/156 (60%)	87 (93%)	7 (7%)	0	100	100
16	Q	92/98 (94%)	86 (94%)	6 (6%)	0	100	100
17	R	63/84 (75%)	61 (97%)	2 (3%)	0	100	100
18	T	83/86 (96%)	83 (100%)	0	0	100	100
19	V	226/277 (82%)	216 (96%)	9 (4%)	1 (0%)	30	46
22	Z	273/278 (98%)	260 (95%)	13 (5%)	0	100	100
23	a	212/217 (98%)	191 (90%)	21 (10%)	0	100	100
24	b	207/215 (96%)	203 (98%)	4 (2%)	0	100	100
25	c	180/187 (96%)	176 (98%)	4 (2%)	0	100	100
26	d	174/179 (97%)	173 (99%)	1 (1%)	0	100	100
27	e	96/142 (68%)	91 (95%)	5 (5%)	0	100	100
28	f	144/147 (98%)	139 (96%)	5 (4%)	0	100	100
29	g	120/122 (98%)	114 (95%)	6 (5%)	0	100	100
30	h	143/147 (97%)	131 (92%)	12 (8%)	0	100	100
31	i	134/138 (97%)	126 (94%)	8 (6%)	0	100	100
32	j	116/199 (58%)	110 (95%)	6 (5%)	0	100	100
33	k	124/127 (98%)	120 (97%)	4 (3%)	0	100	100
34	l	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
35	m	122/129 (95%)	118 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	n	98/103 (95%)	95 (97%)	3 (3%)	0	100	100
37	o	112/153 (73%)	107 (96%)	5 (4%)	0	100	100
38	p	95/100 (95%)	89 (94%)	6 (6%)	0	100	100
39	q	93/105 (89%)	92 (99%)	1 (1%)	0	100	100
40	r	190/215 (88%)	186 (98%)	4 (2%)	0	100	100
41	s	77/88 (88%)	75 (97%)	2 (3%)	0	100	100
42	t	61/64 (95%)	57 (93%)	4 (7%)	0	100	100
43	u	62/77 (80%)	61 (98%)	1 (2%)	0	100	100
44	v	124/175 (71%)	120 (97%)	3 (2%)	1 (1%)	16	28
45	w	57/61 (93%)	55 (96%)	2 (4%)	0	100	100
46	x	52/57 (91%)	52 (100%)	0	0	100	100
47	y	47/55 (86%)	45 (96%)	1 (2%)	1 (2%)	5	8
48	z	44/47 (94%)	44 (100%)	0	0	100	100
49	1	61/64 (95%)	59 (97%)	2 (3%)	0	100	100
50	2	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
All	All	5592/6303 (89%)	5356 (96%)	233 (4%)	3 (0%)	49	66

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
19	V	155	GLN
44	v	85	GLU
47	y	7	VAL

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	C	170/212 (80%)	170 (100%)	0	100	100
3	D	175/176 (99%)	175 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	E	127/147 (86%)	127 (100%)	0	100	100
5	F	85/85 (100%)	85 (100%)	0	100	100
6	G	131/132 (99%)	131 (100%)	0	100	100
7	H	107/108 (99%)	106 (99%)	1 (1%)	70	86
8	I	102/125 (82%)	102 (100%)	0	100	100
9	J	89/90 (99%)	89 (100%)	0	100	100
10	K	89/105 (85%)	89 (100%)	0	100	100
11	L	103/105 (98%)	103 (100%)	0	100	100
12	M	99/104 (95%)	99 (100%)	0	100	100
13	N	49/50 (98%)	49 (100%)	0	100	100
14	O	76/77 (99%)	76 (100%)	0	100	100
15	P	79/118 (67%)	78 (99%)	1 (1%)	61	80
16	Q	80/83 (96%)	80 (100%)	0	100	100
17	R	55/72 (76%)	55 (100%)	0	100	100
18	T	69/70 (99%)	69 (100%)	0	100	100
19	V	191/218 (88%)	191 (100%)	0	100	100
22	Z	215/218 (99%)	215 (100%)	0	100	100
23	a	160/163 (98%)	158 (99%)	2 (1%)	61	80
24	b	169/173 (98%)	169 (100%)	0	100	100
25	c	151/156 (97%)	151 (100%)	0	100	100
26	d	148/150 (99%)	148 (100%)	0	100	100
27	e	102/108 (94%)	101 (99%)	1 (1%)	68	84
28	f	119/120 (99%)	119 (100%)	0	100	100
29	g	100/100 (100%)	100 (100%)	0	100	100
30	h	112/114 (98%)	112 (100%)	0	100	100
31	i	114/116 (98%)	114 (100%)	0	100	100
32	j	97/158 (61%)	97 (100%)	0	100	100
33	k	93/94 (99%)	92 (99%)	1 (1%)	65	83
34	l	100/100 (100%)	100 (100%)	0	100	100
35	m	97/99 (98%)	97 (100%)	0	100	100
36	n	81/83 (98%)	81 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	o	90/117 (77%)	90 (100%)	0	100	100
38	p	83/85 (98%)	83 (100%)	0	100	100
39	q	81/86 (94%)	81 (100%)	0	100	100
40	r	155/168 (92%)	155 (100%)	0	100	100
41	s	58/63 (92%)	58 (100%)	0	100	100
42	t	50/51 (98%)	50 (100%)	0	100	100
43	u	58/66 (88%)	58 (100%)	0	100	100
44	v	89/120 (74%)	89 (100%)	0	100	100
45	w	52/54 (96%)	52 (100%)	0	100	100
46	x	43/46 (94%)	43 (100%)	0	100	100
47	y	47/52 (90%)	47 (100%)	0	100	100
48	z	35/36 (97%)	35 (100%)	0	100	100
49	1	53/54 (98%)	53 (100%)	0	100	100
50	2	35/35 (100%)	35 (100%)	0	100	100
All	All	4663/5062 (92%)	4657 (100%)	6 (0%)	87	95

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
23	a	202	ASN
27	e	36	ASN
33	k	50	GLN
15	P	15	ASN
7	H	18	ASN

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

Mol	Chain	Res	Type
22	Z	91	ASN
43	u	35	GLN
23	a	139	HIS
40	r	126	GLN
48	z	19	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1506/1528 (98%)	324 (21%)	14 (0%)
20	Y	3009/3120 (96%)	684 (22%)	25 (0%)
21	U	117/118 (99%)	20 (17%)	1 (0%)
51	4	76/81 (93%)	27 (35%)	1 (1%)
All	All	4708/4847 (97%)	1055 (22%)	41 (0%)

5 of 1055 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	9	U
1	A	12	A
1	A	13	G
1	A	36	A
1	A	43	G

5 of 41 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
20	Y	1205	G
20	Y	2094	G
20	Y	1500	A
20	Y	1999	U
20	Y	2820	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 629 ligands modelled in this entry, 629 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
20	Y	49
27	e	20
1	A	5
51	4	4

The worst 5 of 78 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Y	2406:U	O3'	2407:C	P	20.52
1	Y	1549:G	O3'	1550:G	P	13.74
1	4	2385:G	O3'	2386:U	P	13.50
1	Y	1600:G	O3'	1601:G	P	12.53
1	Y	1008:G	O3'	1009:U	P	11.19

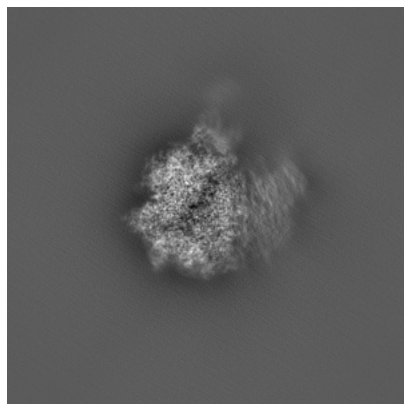
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-44097. These allow visual inspection of the internal detail of the map and identification of artifacts.

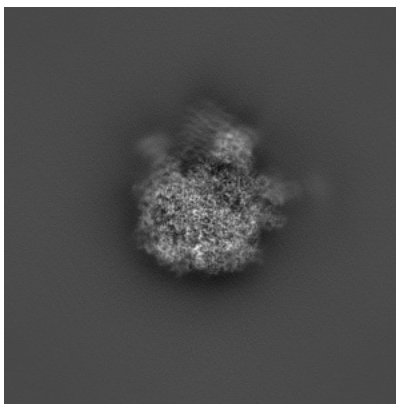
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

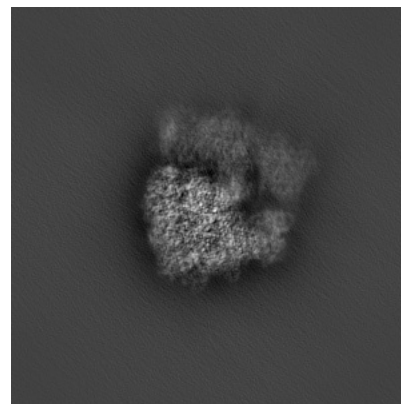
6.1.1 Primary map



X

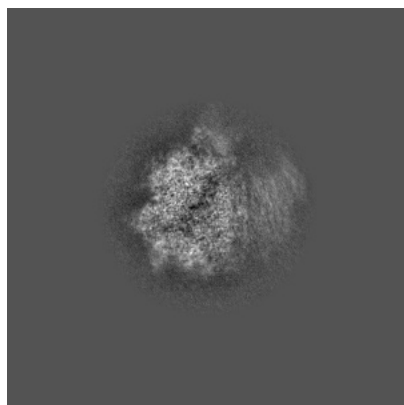


Y

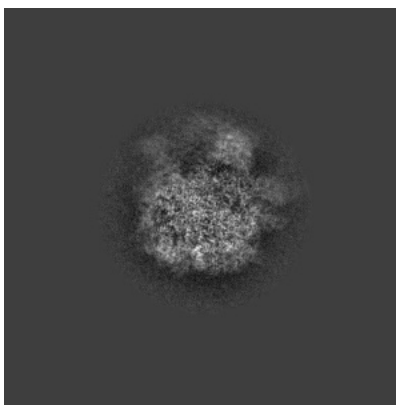


Z

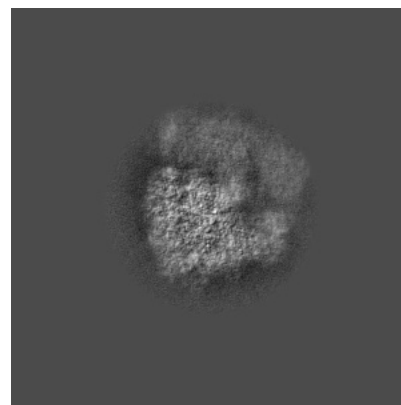
6.1.2 Raw map



X



Y

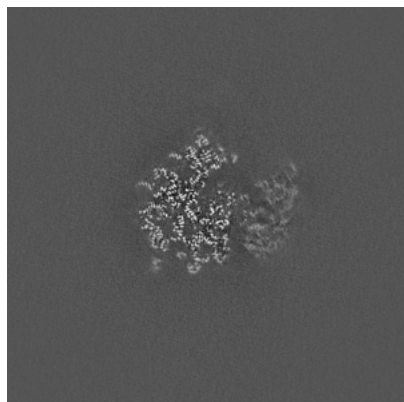


Z

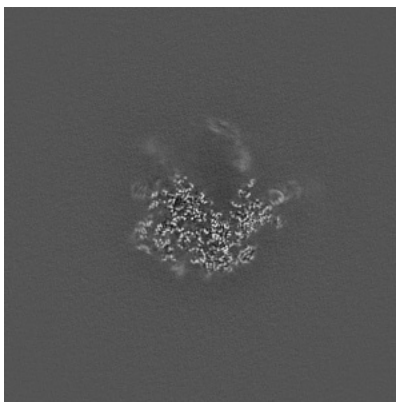
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

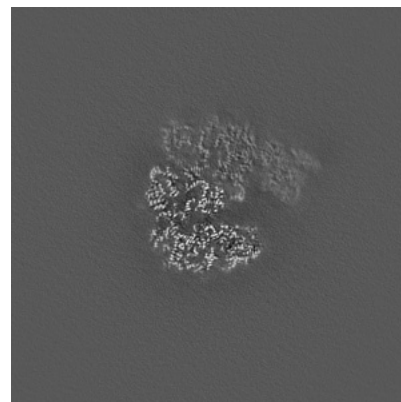
6.2.1 Primary map



X Index: 324

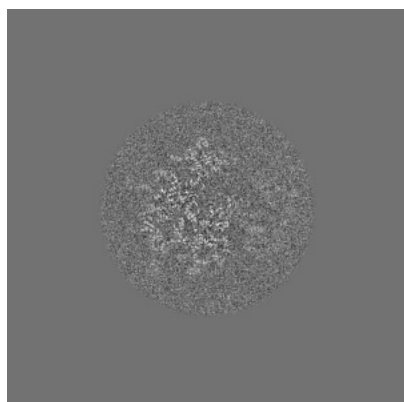


Y Index: 324

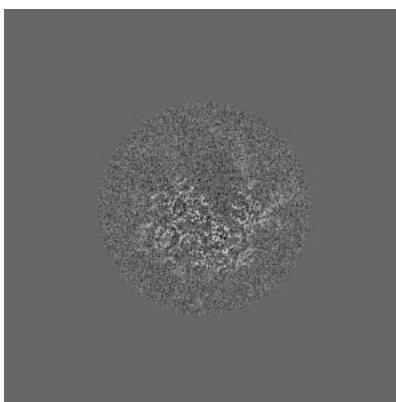


Z Index: 324

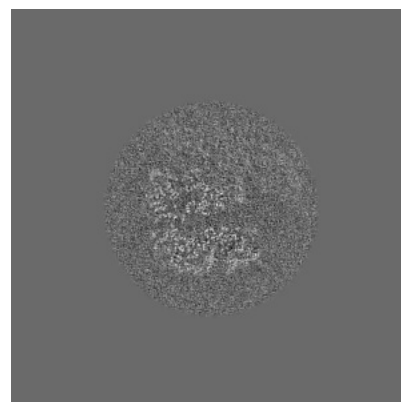
6.2.2 Raw map



X Index: 324



Y Index: 324

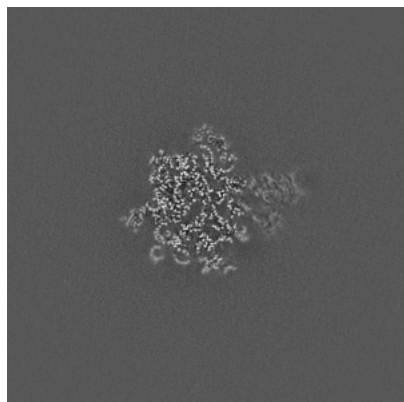


Z Index: 324

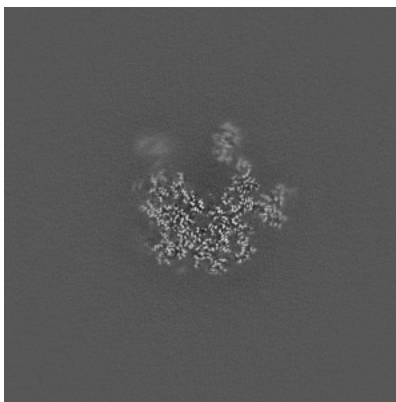
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

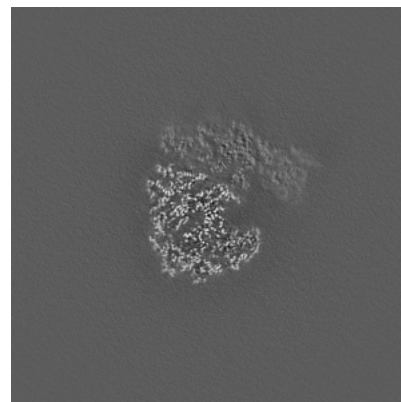
6.3.1 Primary map



X Index: 297

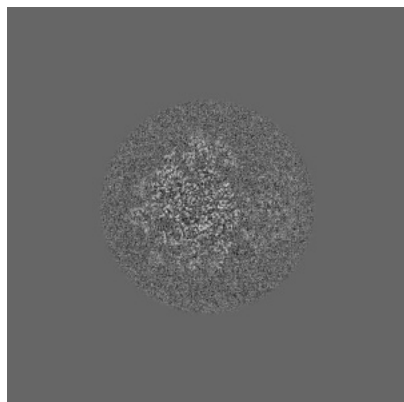


Y Index: 310

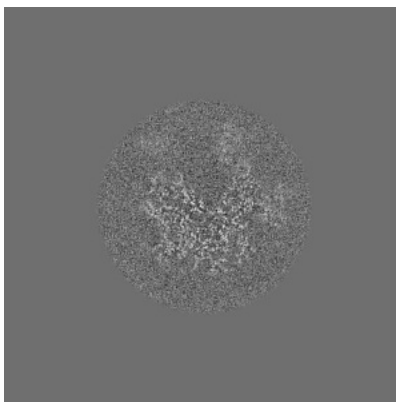


Z Index: 317

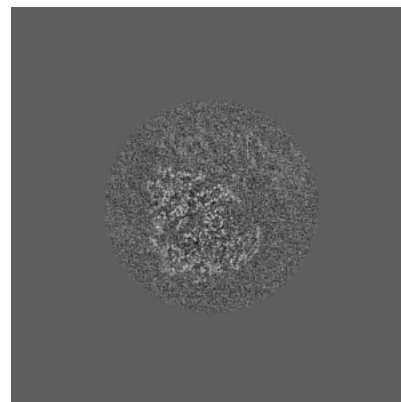
6.3.2 Raw map



X Index: 312



Y Index: 310

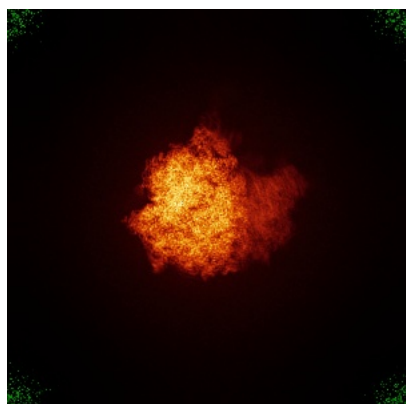


Z Index: 317

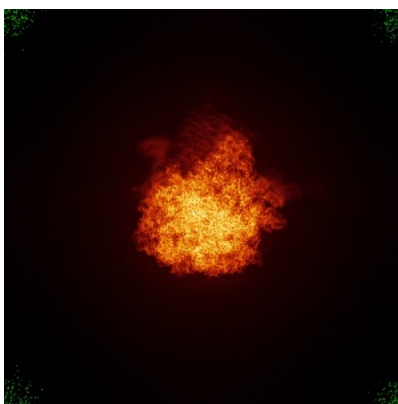
The images above show the largest variance slices of the map in three orthogonal directions.

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

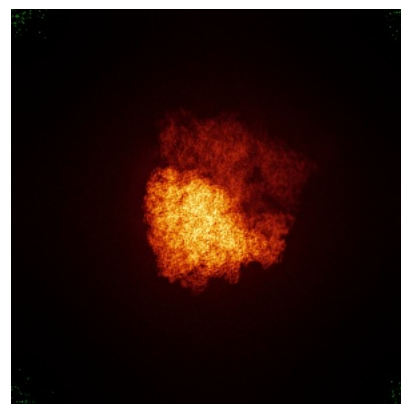
6.4.1 Primary map



X

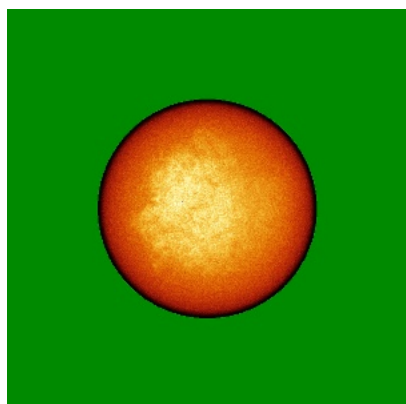


Y

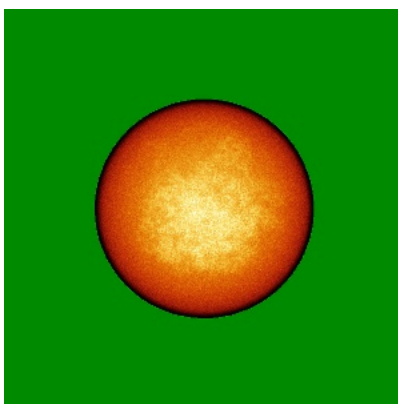


Z

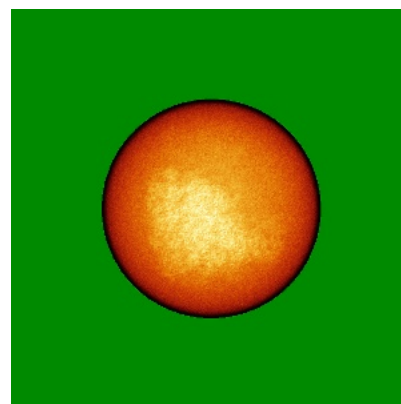
6.4.2 Raw map



X



Y

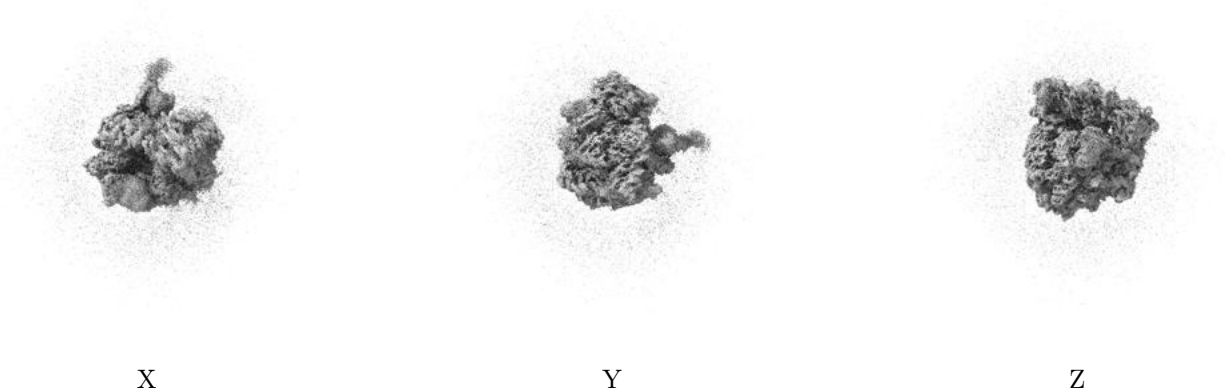


Z

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

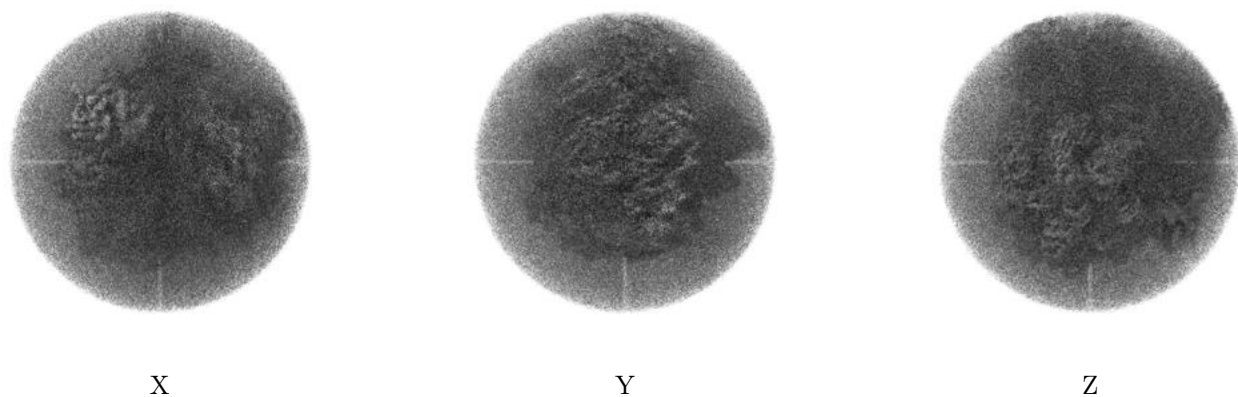
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

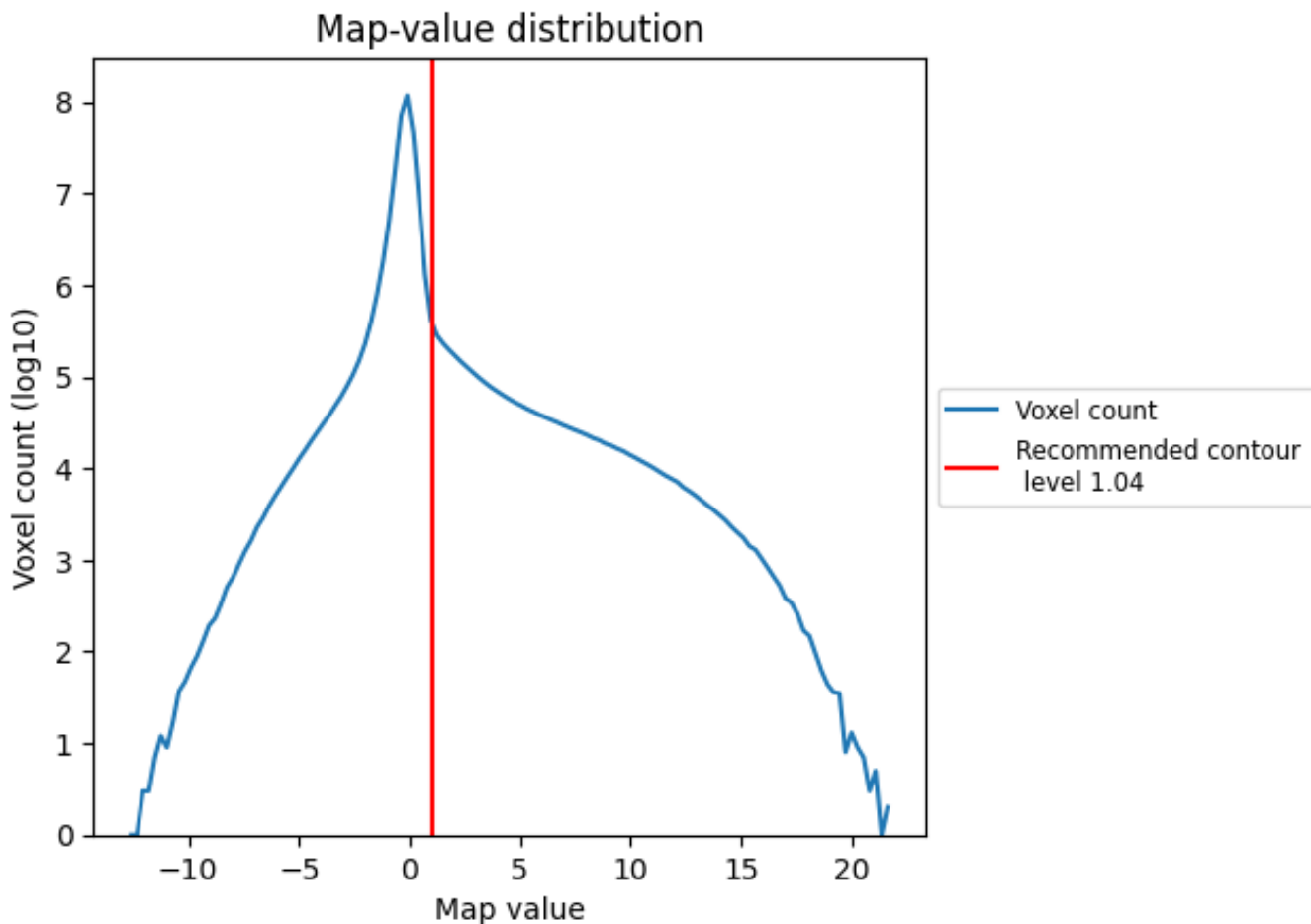
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

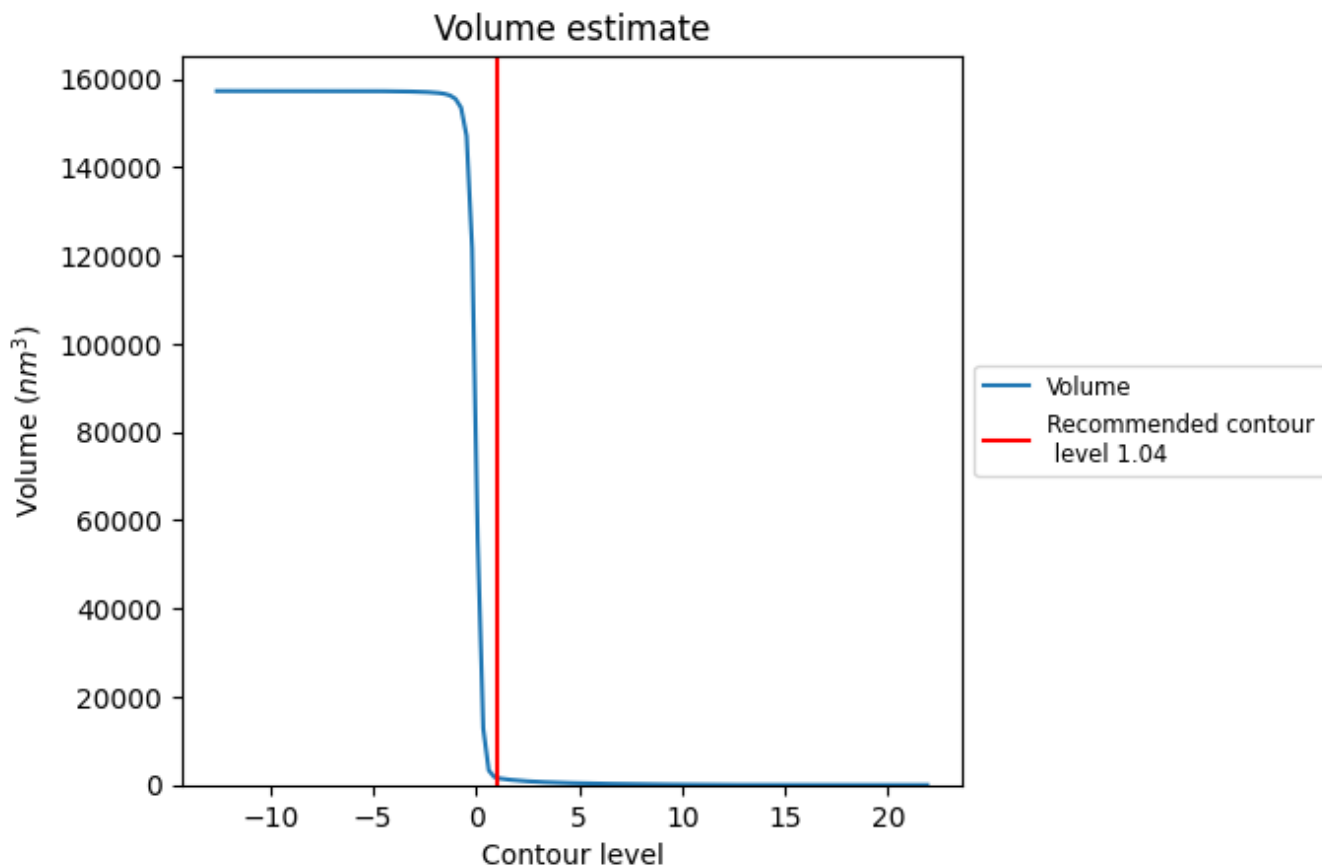
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

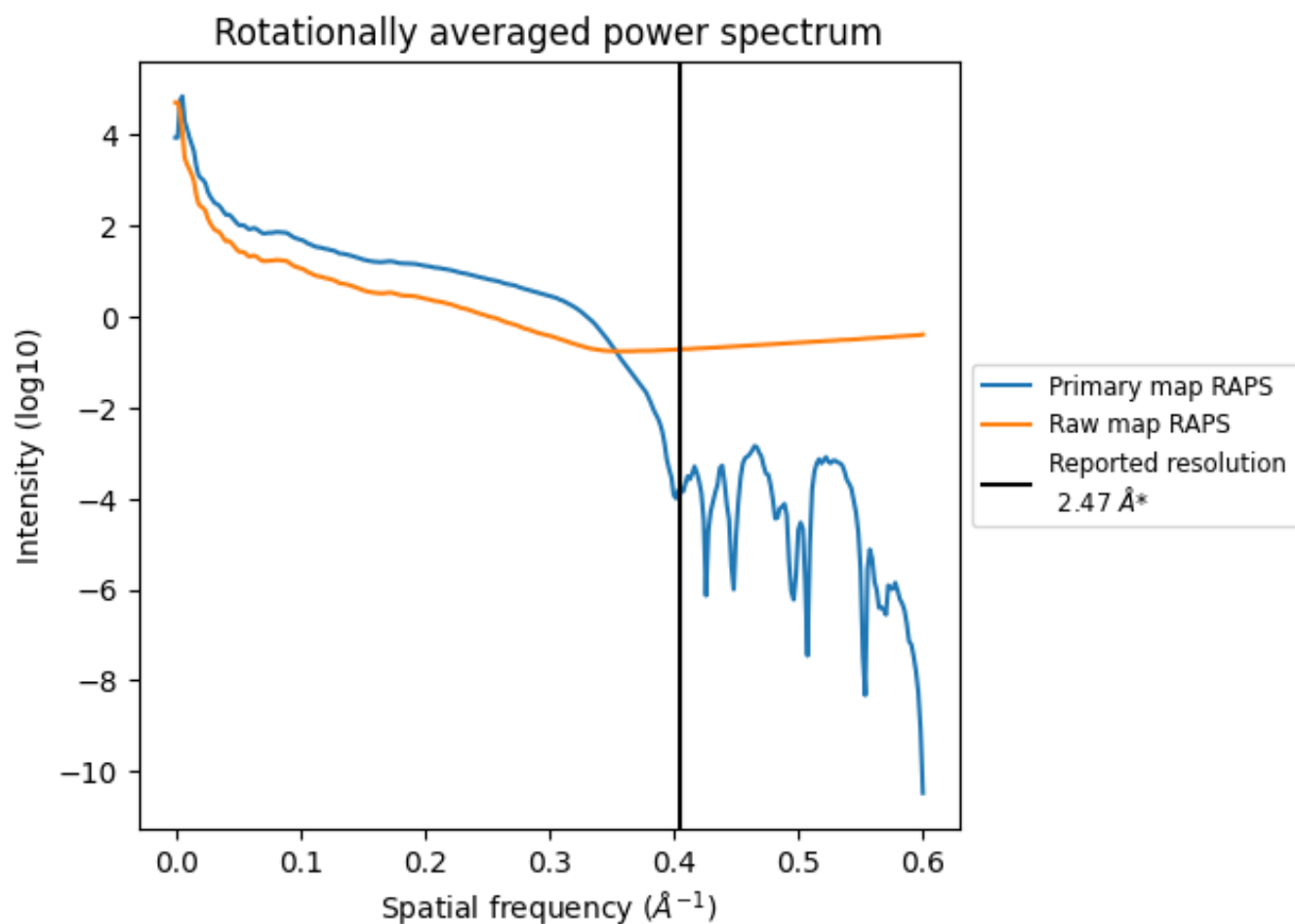
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1605 nm^3 ; this corresponds to an approximate mass of 1450 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](#)

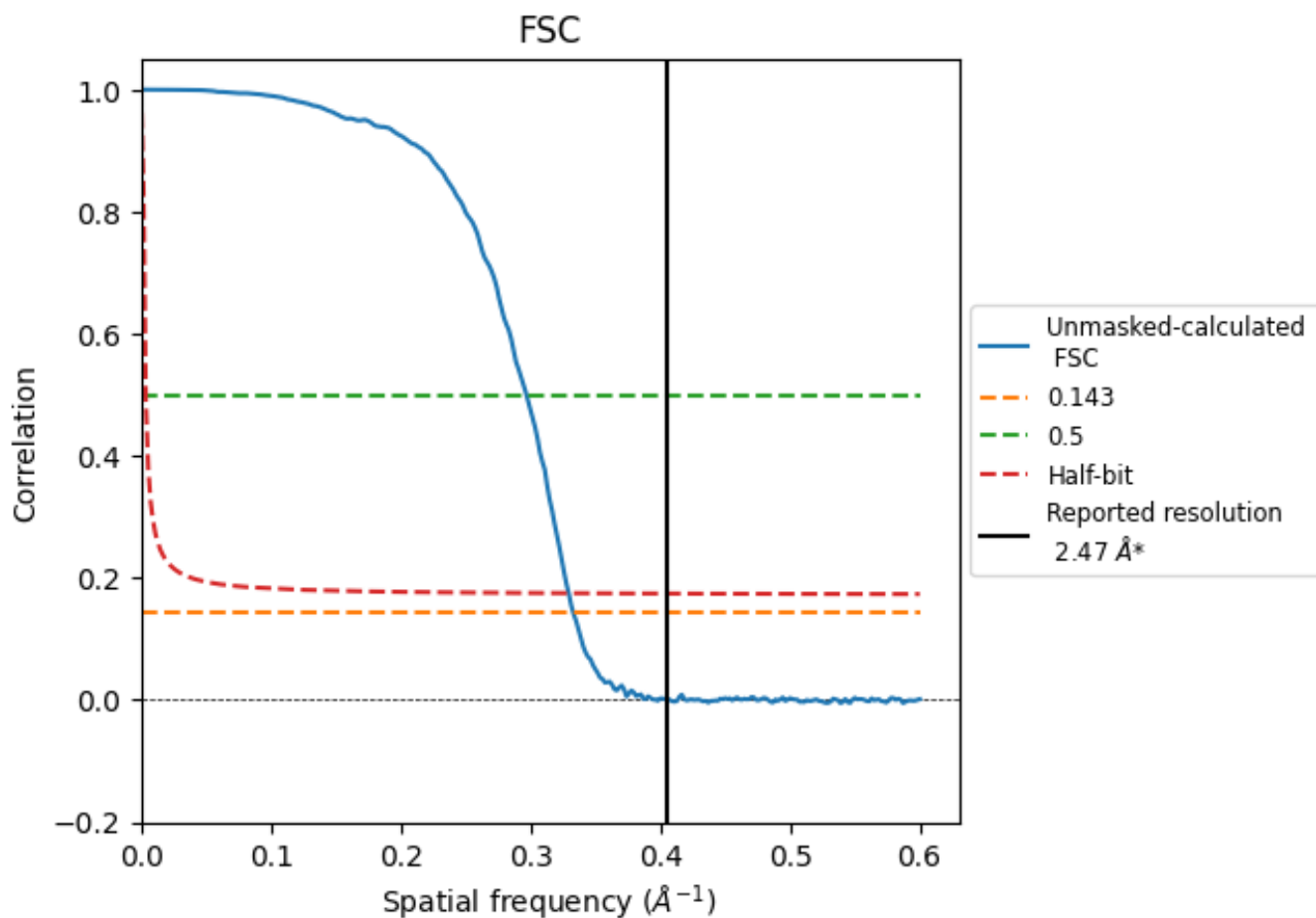


*Reported resolution corresponds to spatial frequency of 0.405 Å⁻¹

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 0.405 Å⁻¹

8.2 Resolution estimates [i](#)

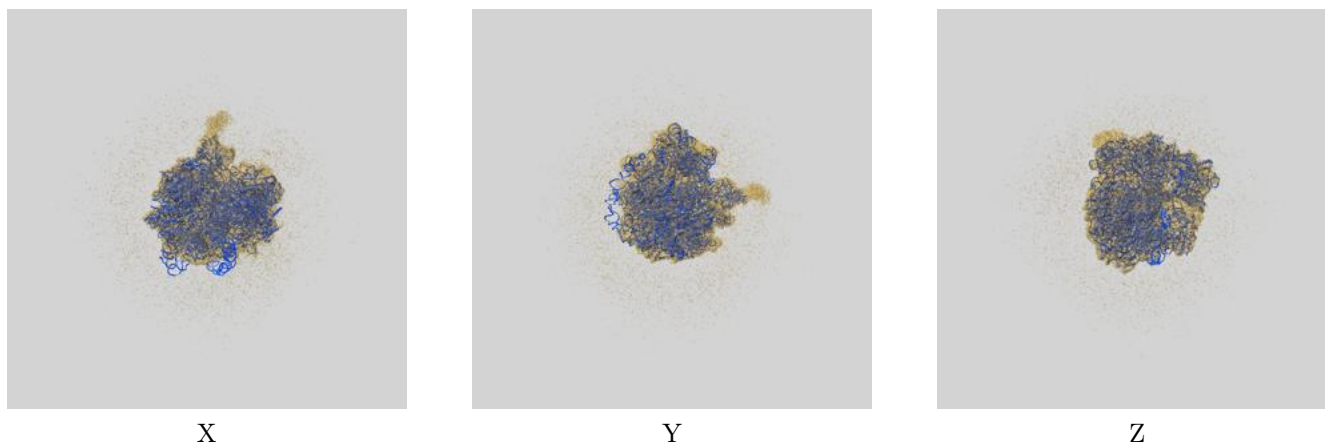
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.47	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.00	3.37	3.03

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.00 differs from the reported value 2.47 by more than 10 %

9 Map-model fit [i](#)

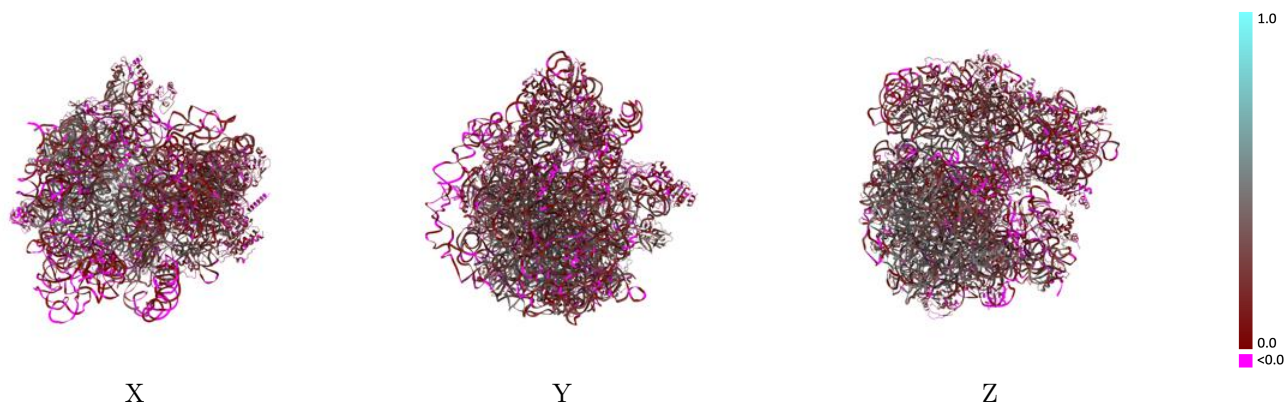
This section contains information regarding the fit between EMDB map EMD-44097 and PDB model 9B24. Per-residue inclusion information can be found in section [3](#) on page [14](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 1.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

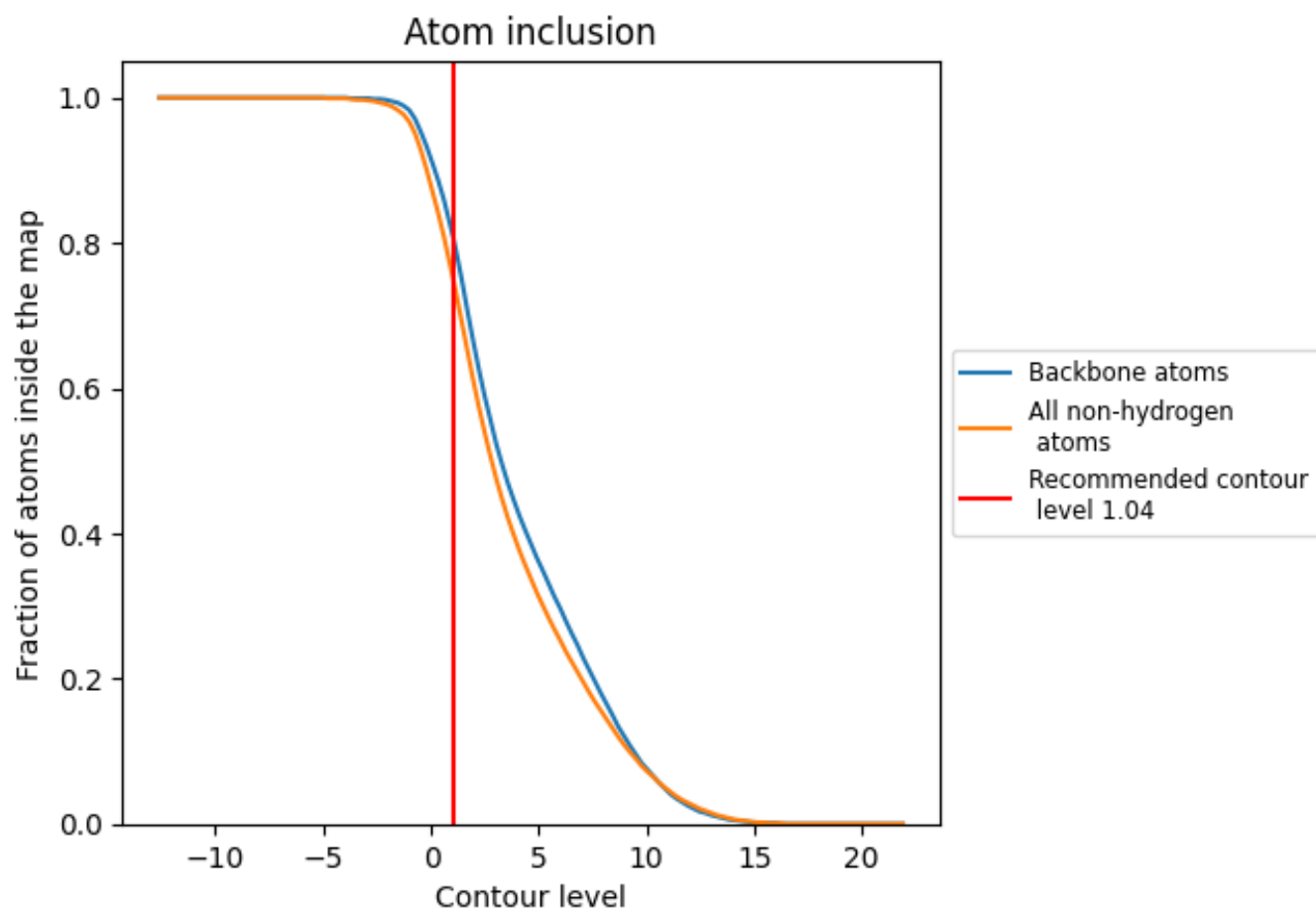


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 75% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary



































The table lists the average atom inclusion at the recommended contour level (1.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7490	 0.2410
1	 0.8130	 0.3200
2	 0.8510	 0.3230
4	 0.9120	 0.0500
A	 0.7240	 0.2050
C	 0.6050	 0.2110
D	 0.5390	 0.1860
E	 0.5760	 0.2020
F	 0.6200	 0.2140
G	 0.4150	 0.1640
H	 0.6190	 0.2510
I	 0.6350	 0.1550
J	 0.4300	 0.1870
K	 0.6980	 0.2580
L	 0.6120	 0.2430
M	 0.5920	 0.1490
N	 0.6250	 0.1600
O	 0.6780	 0.2800
P	 0.4420	 0.1110
Q	 0.5340	 0.1690
R	 0.6800	 0.1970
T	 0.6500	 0.2450
U	 0.8970	 0.2630
V	 0.4320	 0.1740
Y	 0.8060	 0.2690
Z	 0.7440	 0.2730
a	 0.7890	 0.3230
b	 0.7350	 0.2680
c	 0.8180	 0.1970
d	 0.8110	 0.2720
e	 0.6820	 0.0600
f	 0.8150	 0.3360
g	 0.7700	 0.2880
h	 0.6100	 0.1850
i	 0.7730	 0.2940



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Chain	Atom inclusion	Q-score
j	 0.7540	 0.3120
k	 0.7690	 0.2510
l	 0.4990	 0.0740
m	 0.7930	 0.3320
n	 0.8350	 0.3510
o	 0.7820	 0.3750
p	 0.7600	 0.2800
q	 0.8250	 0.3170
r	 0.4090	 0.1550
s	 0.7510	 0.2950
t	 0.7980	 0.2940
u	 0.6500	 0.1410
v	 0.7960	 0.1630
w	 0.7860	 0.3280
x	 0.6820	 0.2300
y	 0.7750	 0.2350
z	 0.7650	 0.3400