



## wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 03:46 PM UTC

PDB ID : 8RDV / pdb\_00008rdv  
EMDB ID : EMD-19076  
Title : Cryo-EM structure of *P. urativorans* 70S ribosome in complex with hibernation factor Balon, mRNA and P-site tRNA (structure 2).  
Authors : Helena-Bueno, K.; Rybak, M.Y.; Gagnon, M.G.; Hill, C.H.; Melnikov, S.V.  
Deposited on : 2023-12-08  
Resolution : 2.60 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

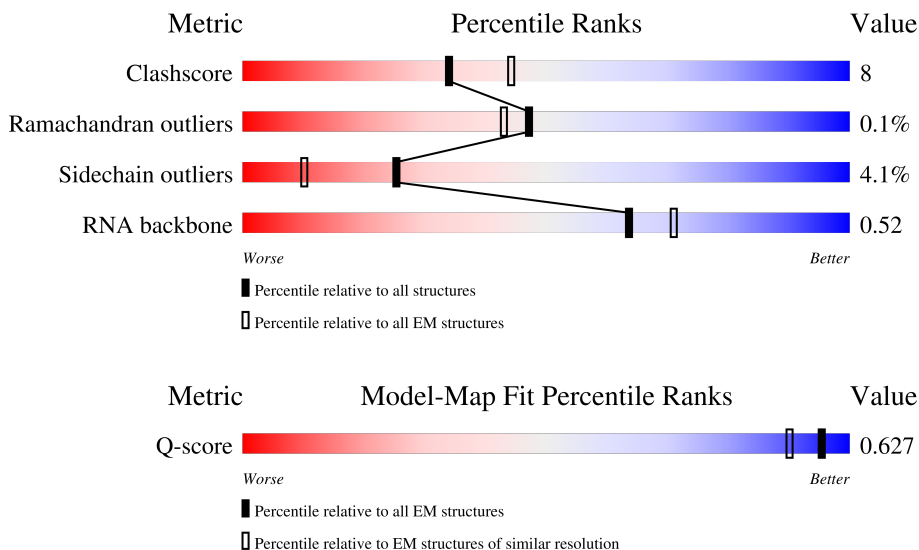
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : 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 2.60 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.








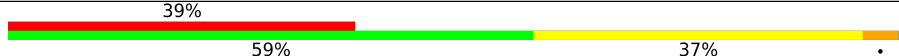
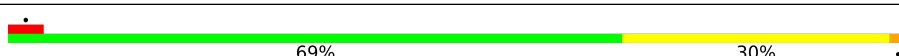
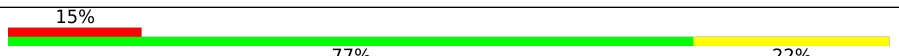
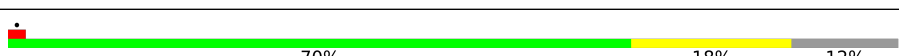
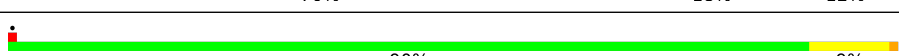
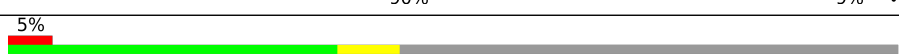

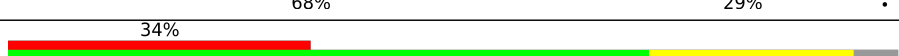
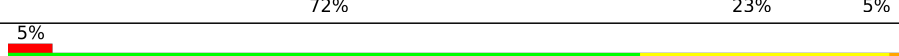
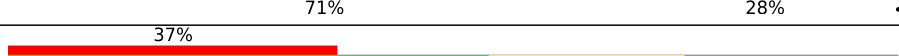
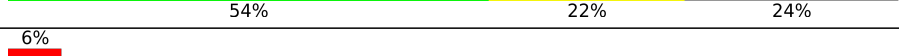


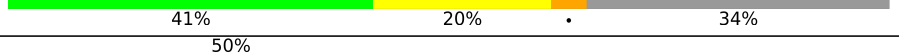





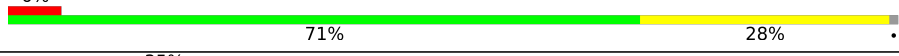
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	217187	24013	-
Ramachandran outliers	211220	23611	-
Sidechain outliers	210688	23127	-
RNA backbone	8275	3510	-
Q-score	-	25397	8728 ( 2.10 - 3.10 )

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	B	369	
2	F	128	
3	H	396	

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Mol	Chain	Length	Quality of chain
4	Z2	2882	
5	R3	76	
6	A4	269	
7	E5	171	
8	L6	124	
9	F7	178	
10	D8	115	
11	E9	200	
12	aA	60	
13	MB	119	
14	UC	219	
15	WD	78	
16	XE	65	
17	RF	109	
18	FG	134	
19	VH	85	
20	TI	105	
21	fJ	93	
22	HK	101	
23	OL	88	
24	MM	118	
25	PO	118	
26	SP	91	
27	BQ	132	
28	GR	177	




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Mol	Chain	Length	Quality of chain
29	GS	157	67% 70% 27% ..
30	CT	241	43% 57% 25% • 15%
31	KU	129	34% 69% 19% • 11%
32	NV	71	39% 61% 20% 20%
33	YW	59	• 86% 7% • 5%
34	IX	142	• 82% 18% •
35	JY	103	64% 68% 29% •
36	QZ	91	18% 69% 16% • 13%
37	Ba	44	75% 23% •
38	Qb	103	16% 71% 29%
39	Nc	116	17% 68% 29% •
40	Kd	146	5% 73% 25% •
41	Je	122	• 73% 27%
42	Af	212	• 79% 19% •
43	Lg	137	• 73% 26% •
44	dh	65	82% 15% ..
45	Oi	130	• 66% 21% • 12%
46	Pj	89	16% 71% 20% 9%
47	bk	51	• 75% 20% ..
48	Cl	274	• 80% 19% •
49	Dm	213	44% 68% 31%
50	Sn	116	• 61% 14% • 24%
51	To	88	22% 75% 24% •
52	ep	38	84% 16%
53	V	76	25% 42% 46% 12%

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Mol	Chain	Length	Quality of chain
54	Y	6	
55	C1	166	
56	iN	1590	

## 2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 142063 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Methyl-accepting chemotaxis protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	B	362	2829	1759	501	560	9	0	0

- Molecule 2 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	F	126	985	613	194	177	1	0	0

- Molecule 3 is a protein called Elongation factor Tu.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	H	185	1409	879	252	270	8	0	0

- Molecule 4 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	Z2	2710	58145	25956	10675	18804	2710	0	0

- Molecule 5 is a protein called Small ribosomal subunit protein bS18.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
5	R3	56	457	290	80	87	0	0

- Molecule 6 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	A4	233	1816	1147	327	335	7	0	0

- Molecule 7 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	E5	156	1151	716	218	211	6	0	0

- Molecule 8 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	L6	122	946	583	193	165	5	0	0

- Molecule 9 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	F7	177	1362	873	237	246	6	0	0

- Molecule 10 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
10	D8	115	2446	1093	436	802	115	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D8	85	U	-	insertion	GB 930356181
D8	88	A	C	variant	GB 930356181

- Molecule 11 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	E9	199	1537	966	282	284	5	0	0

- Molecule 12 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	aA	53	442	264	100	75	3	0	0

- Molecule 13 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	MB	119	Total	C	N	O	S	0	0
			947	587	188	164	8		

- Molecule 14 is a protein called Large ribosomal subunit protein bL25.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	UC	97	Total	C	N	O	S	0	0
			760	485	138	136	1		

- Molecule 15 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	WD	76	Total	C	N	O	S	0	0
			618	383	131	101	3		

- Molecule 16 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	XE	62	Total	C	N	O	S	0	0
			502	307	99	95	1		

- Molecule 17 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	RF	109	Total	C	N	O	S	0	0
			834	521	159	151	3		

- Molecule 18 is a protein called Small ribosomal subunit protein bS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	FG	102	Total	C	N	O	S	0	0
			849	535	154	158	2		

- Molecule 19 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	VH	84	Total	C	N	O	S	0	0
			626	389	124	110	3		

- Molecule 20 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	TI	102	Total	C	N	O	0	0
			784	487	149	148		

- Molecule 21 is a protein called Large ribosomal subunit protein bL31B.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	fJ	61	Total	C	N	O	S	0	0
			493	313	85	94	1		

- Molecule 22 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	HK	100	Total	C	N	O	S	0	0
			811	498	162	144	7		

- Molecule 23 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	OL	86	Total	C	N	O	S	0	0
			694	427	137	128	2		

- Molecule 24 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	MM	92	Total	C	N	O	S	0	0
			717	446	138	130	3		

- Molecule 25 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	PO	116	Total	C	N	O	S	0	0
			935	586	199	148	2		

- Molecule 26 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	SP	80	Total	C	N	O	S	0	0
			637	405	121	108	3		

- Molecule 27 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	BQ	131	974	602	179	187	6	0	0

- Molecule 28 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	GR	175	1357	848	248	259	2	0	0

- Molecule 29 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	GS	153	1200	744	233	216	7	0	0

- Molecule 30 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	CT	205	1613	1013	302	291	7	0	0

- Molecule 31 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	KU	115	842	521	163	157	1	0	0

- Molecule 32 is a protein called Small ribosomal subunit protein bS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	NV	57	472	299	95	77	1	0	0

- Molecule 33 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	YW	56	438	272	88	76	2	0	0

- Molecule 34 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	IX	142	Total	C	N	O	S	0	0
			1108	710	198	197	3		

- Molecule 35 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	JY	100	Total	C	N	O	S	0	0
			793	492	151	147	3		

- Molecule 36 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	QZ	79	Total	C	N	O	S	0	0
			632	395	119	116	2		

- Molecule 37 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Ba	44	Total	C	N	O	S	0	0
			369	227	89	51	2		

- Molecule 38 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Qb	103	Total	C	N	O	S	0	0
			827	524	153	148	2		

- Molecule 39 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	Nc	113	Total	C	N	O	0	0
			852	530	170	152		

- Molecule 40 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Kd	144	Total	C	N	O	S	1	0
			1062	656	206	197	3		

- Molecule 41 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Je	122	Total	C	N	O	S	0	0
			937	585	181	166	5		

- Molecule 42 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Af	211	Total	C	N	O	S	0	0
			1548	954	292	296	6		

- Molecule 43 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Lg	137	Total	C	N	O	S	0	0
			1093	697	210	179	7		

- Molecule 44 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	dh	64	Total	C	N	O	S	0	0
			519	326	107	82	4		

- Molecule 45 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	Oi	115	Total	C	N	O	0	0
			917	572	184	161		

- Molecule 46 is a protein called Small ribosomal subunit protein bS16.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Pj	81	Total	C	N	O	S	0	0
			648	409	126	111	2		

- Molecule 47 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	bk	49	Total	C	N	O	S	0	0
			394	254	68	69	3		

- Molecule 48 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Cl	272	Total	C	N	O	S	0	0
			2107	1305	432	364	6		

- Molecule 49 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Dm	212	Total	C	N	O	S	0	0
			1688	1058	318	309	3		

- Molecule 50 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Sn	88	Total	C	N	O	S	0	0
			698	446	126	124	2		

- Molecule 51 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	To	87	Total	C	N	O	S	0	0
			684	415	146	121	2		

- Molecule 52 is a protein called Large ribosomal subunit protein bL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	ep	38	Total	C	N	O	S	0	0
			298	182	66	46	4		

- Molecule 53 is a RNA chain called Heterogenous tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	V	76	Total	C	N	O	P	0	0
			1521	686	160	600	75		

- Molecule 54 is a RNA chain called Heterogenous mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	Y	6	Total	C	N	O	P	0	0
			120	54	12	48	6		

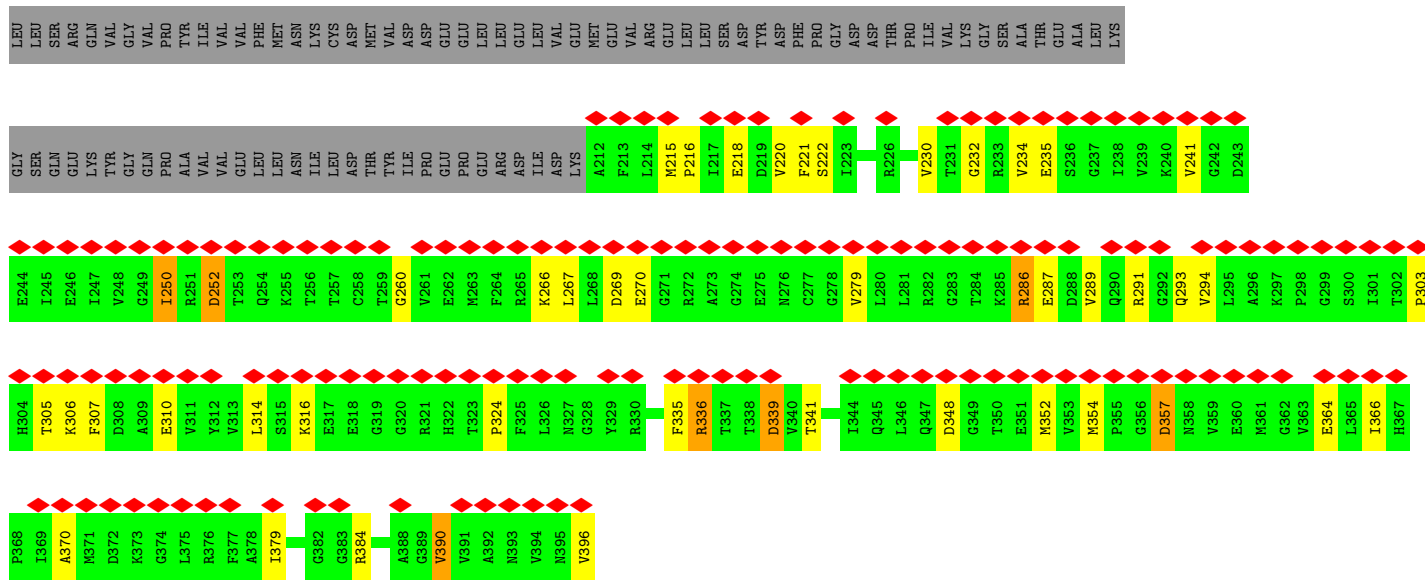
- Molecule 55 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	C1	49	374	244	64	65	1	0	0

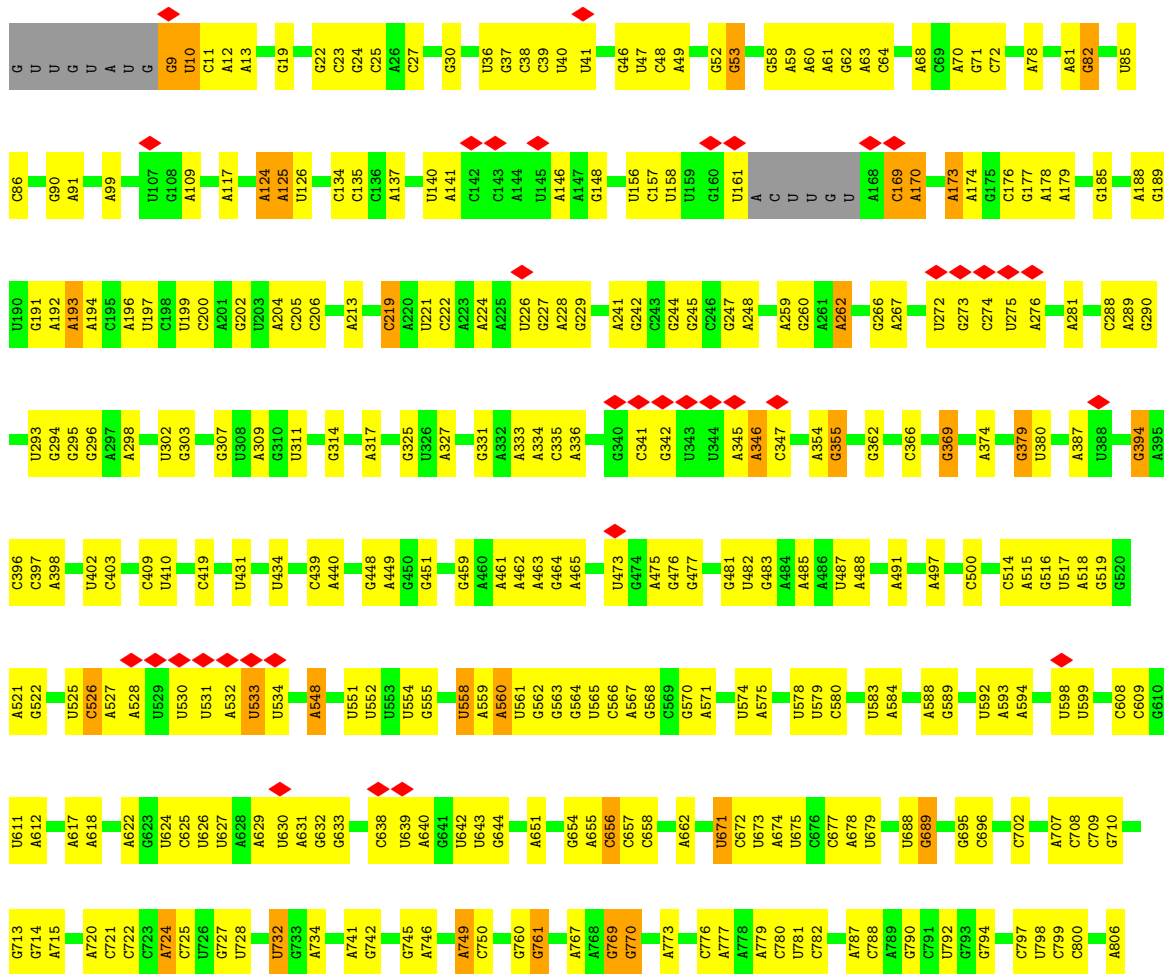
- Molecule 56 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
56	iN	1503	32246	14388	5917	10438	1503	0	0

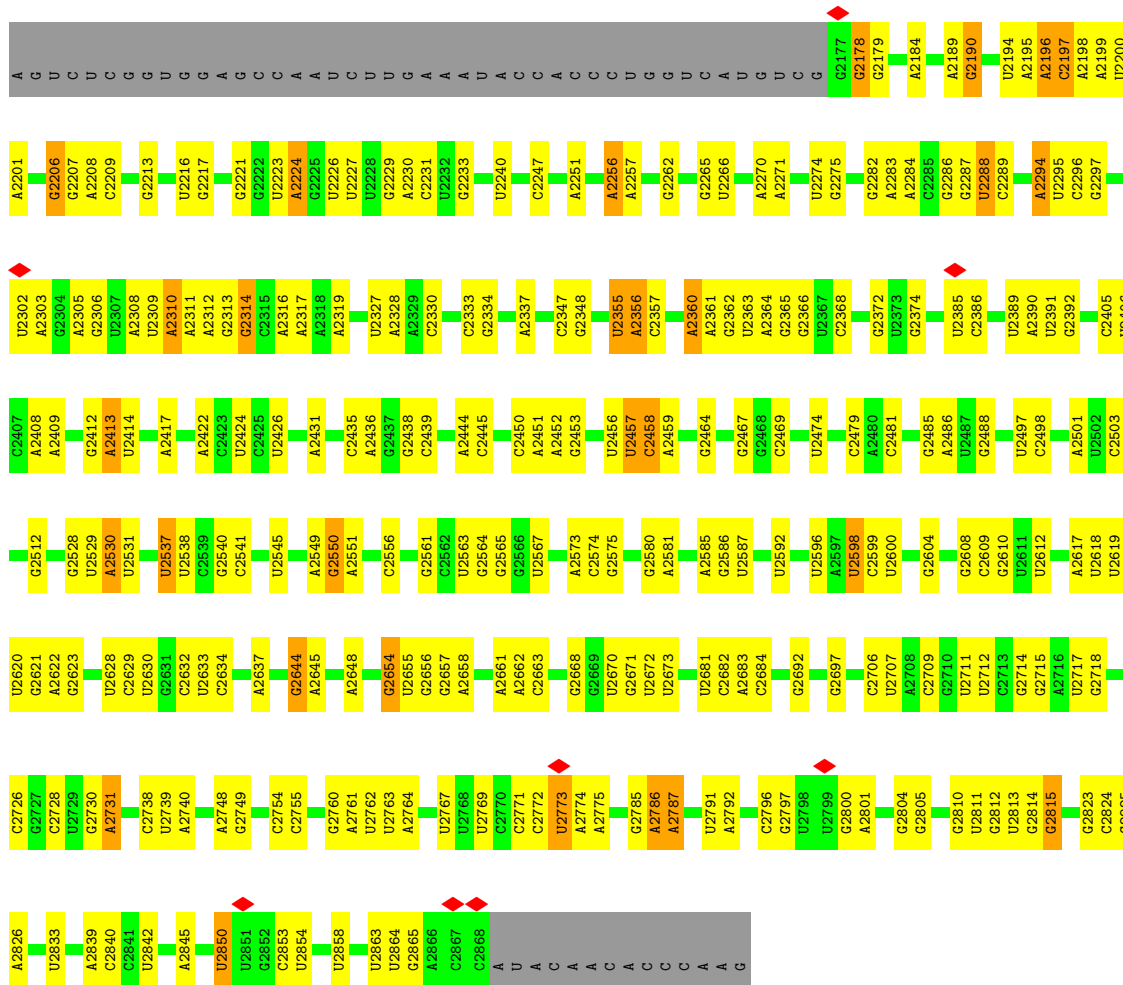


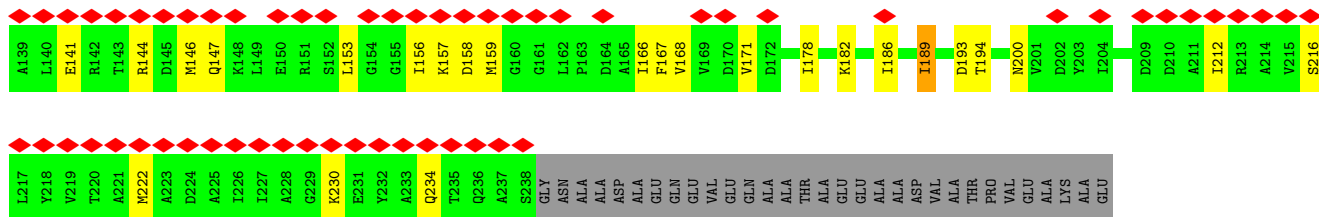


• Molecule 4: 23S rRNA

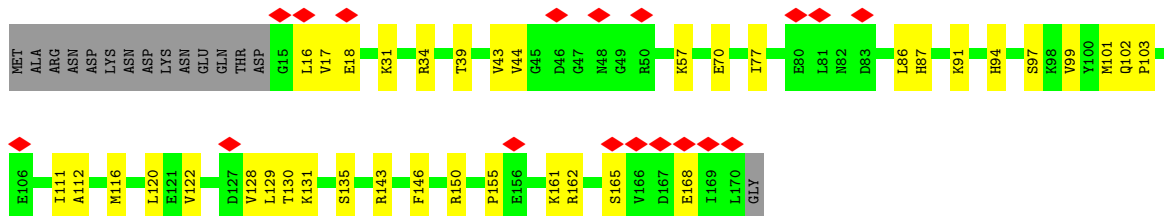




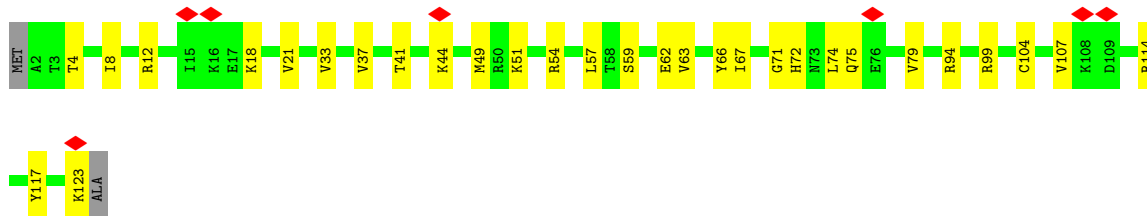
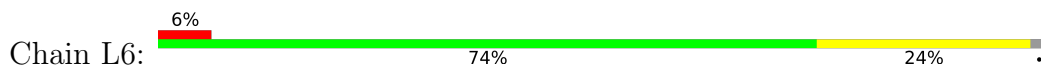




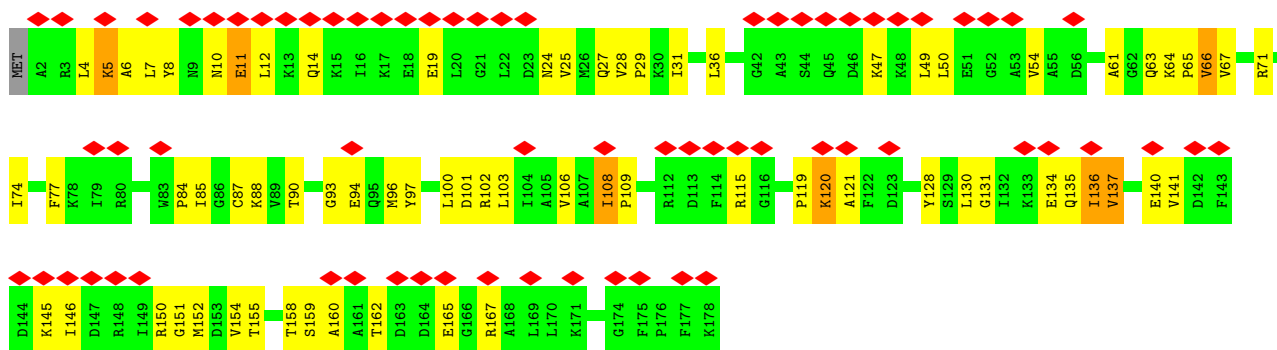
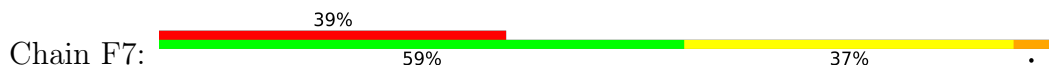
• Molecule 7: Small ribosomal subunit protein uS5



• Molecule 8: Small ribosomal subunit protein uS12



• Molecule 9: Large ribosomal subunit protein uL5

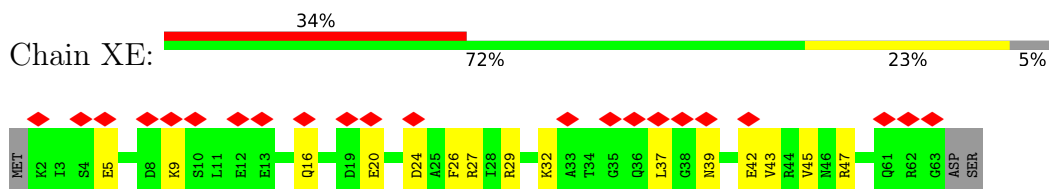


• Molecule 10: 5S rRNA

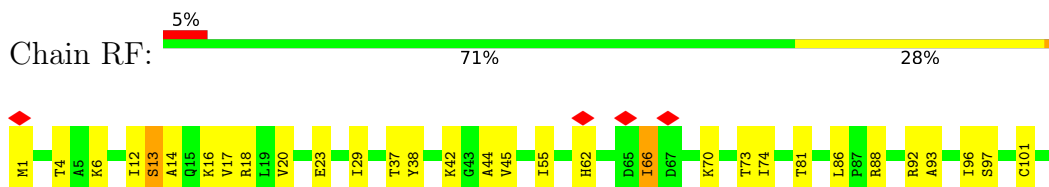




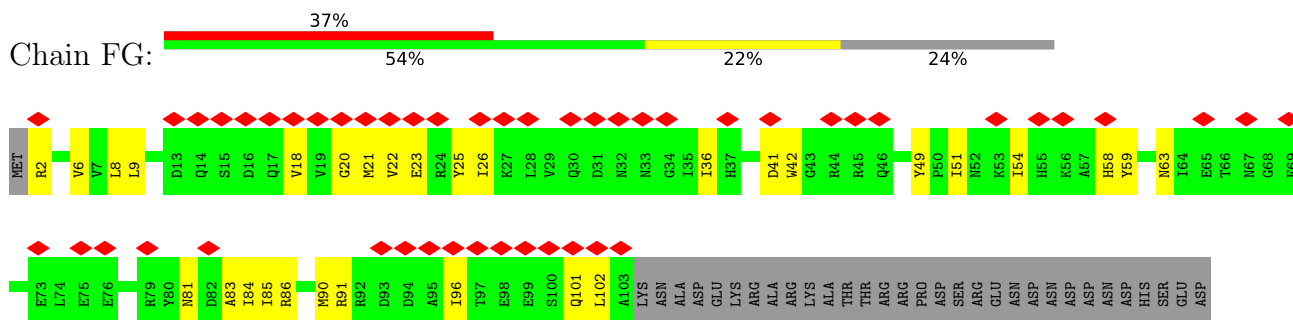
- Molecule 16: Large ribosomal subunit protein uL29



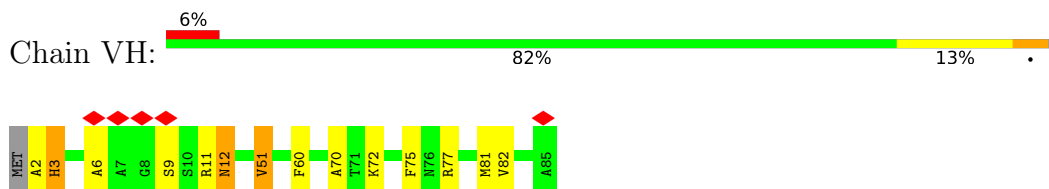
- Molecule 17: Large ribosomal subunit protein uL22



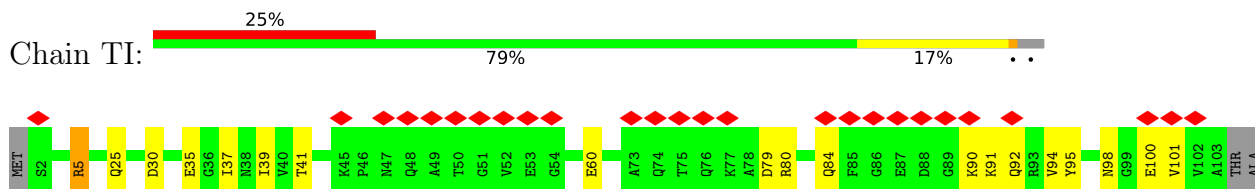
- Molecule 18: Small ribosomal subunit protein bS6



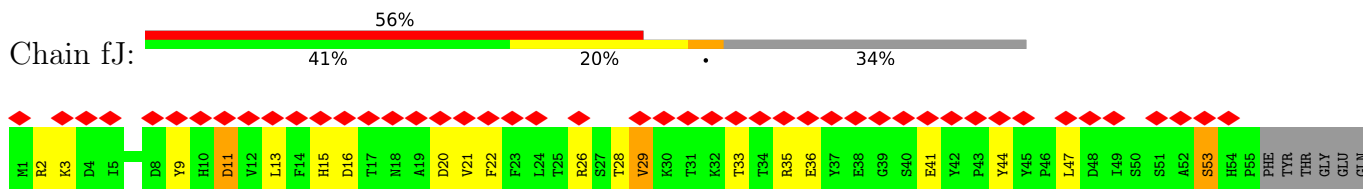
- Molecule 19: Large ribosomal subunit protein bL27

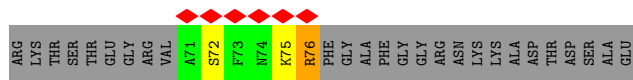


- Molecule 20: Large ribosomal subunit protein uL24

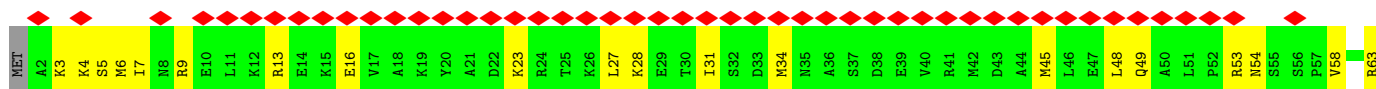


- Molecule 21: Large ribosomal subunit protein bL31B

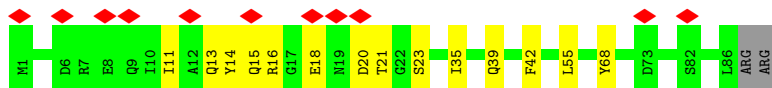
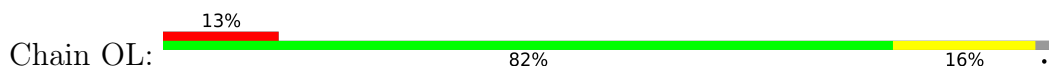




• Molecule 22: Small ribosomal subunit protein uS14



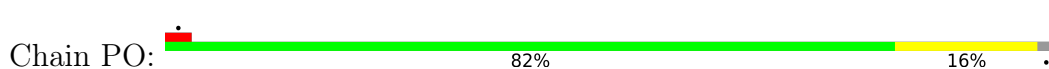
• Molecule 23: Small ribosomal subunit protein uS15



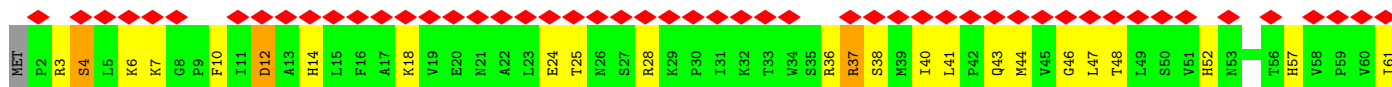
• Molecule 24: Small ribosomal subunit protein uS13

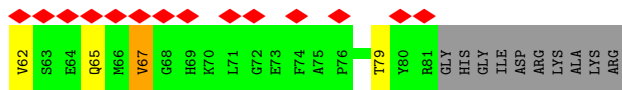


• Molecule 25: Large ribosomal subunit protein bL20

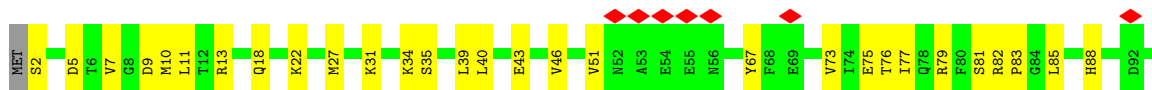
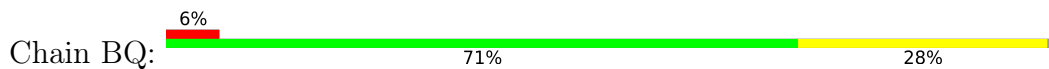


• Molecule 26: Small ribosomal subunit protein uS19

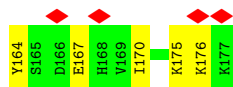
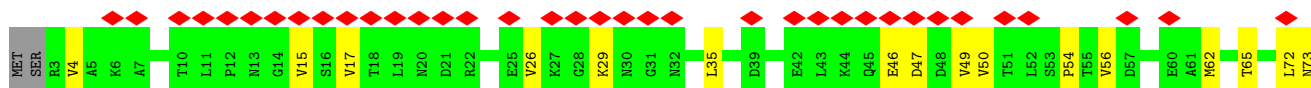
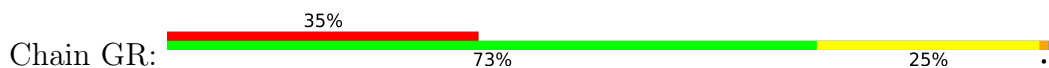




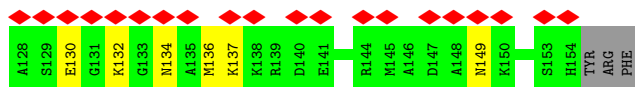
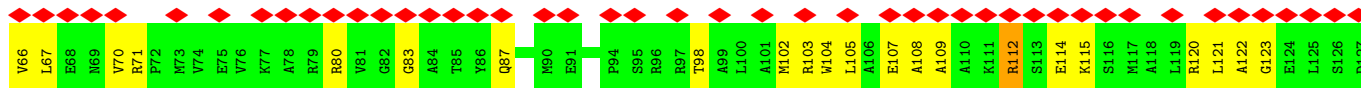
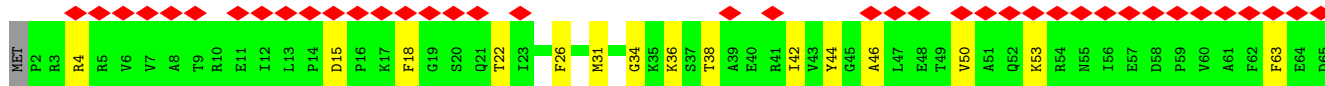
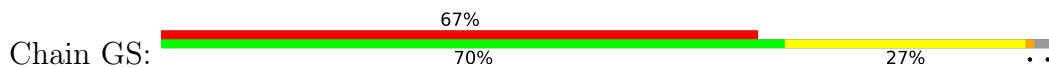
- Molecule 27: Small ribosomal subunit protein uS8



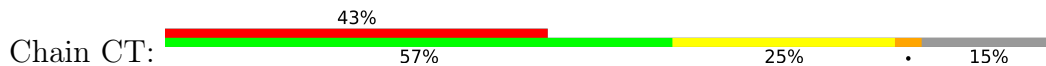
- Molecule 28: Large ribosomal subunit protein uL6

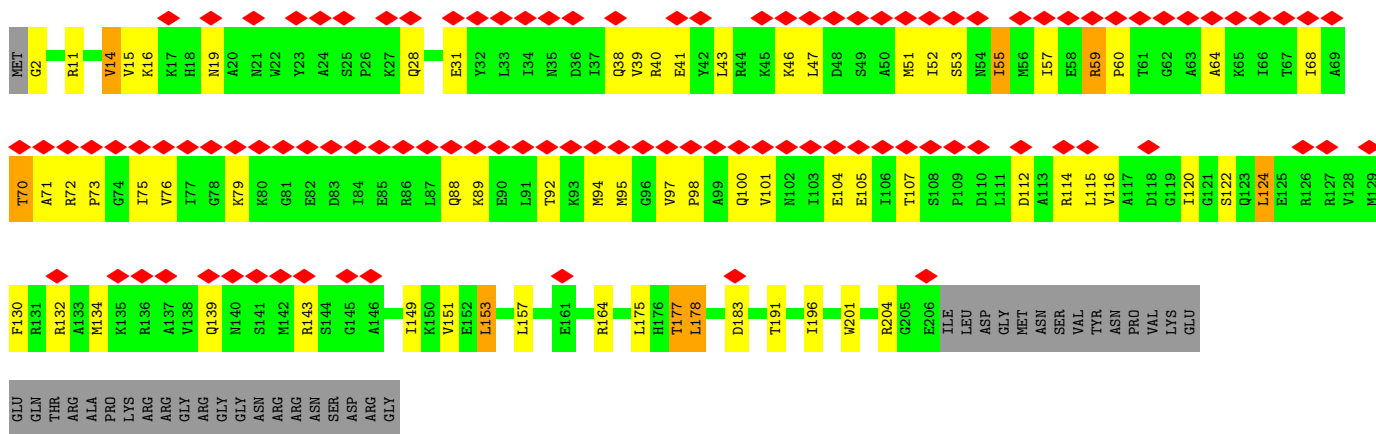


- Molecule 29: Small ribosomal subunit protein uS7

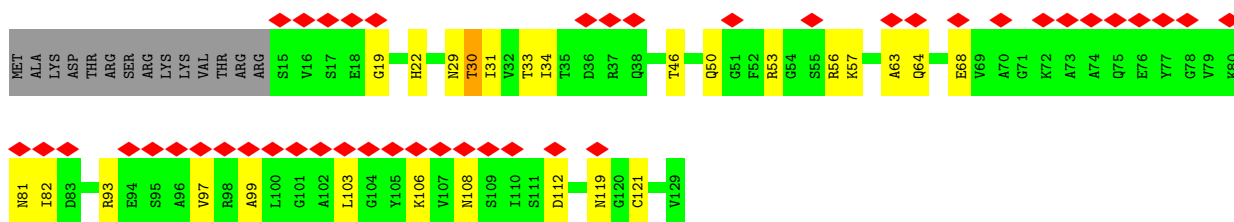


- Molecule 30: Small ribosomal subunit protein uS3

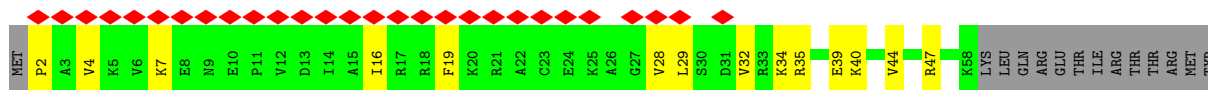
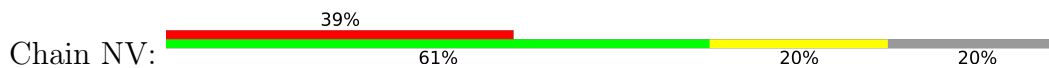




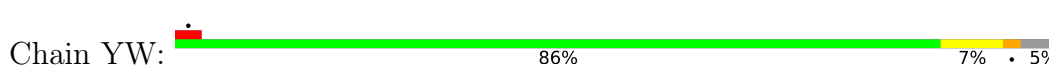
• Molecule 31: Small ribosomal subunit protein uS11



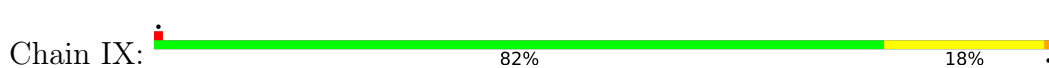
• Molecule 32: Small ribosomal subunit protein bS21



• Molecule 33: Large ribosomal subunit protein uL30

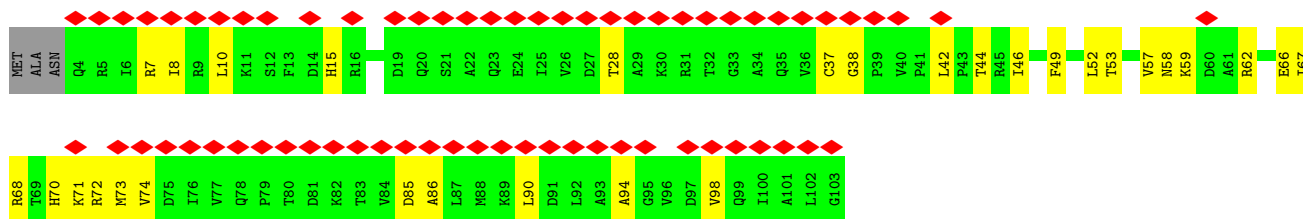


• Molecule 34: Large ribosomal subunit protein uL13

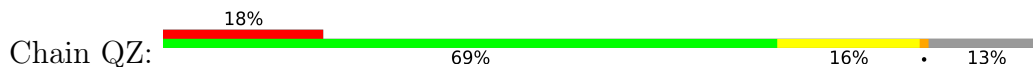


• Molecule 35: Small ribosomal subunit protein uS10

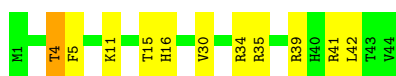
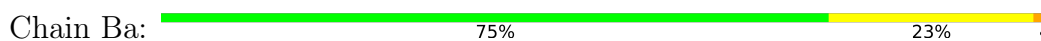




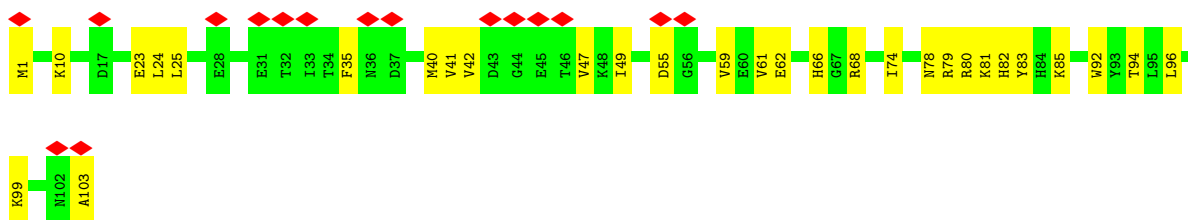
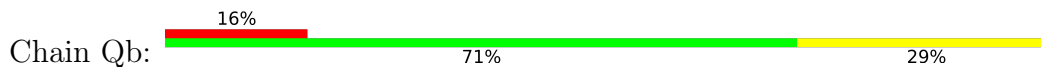
- Molecule 36: Small ribosomal subunit protein uS17



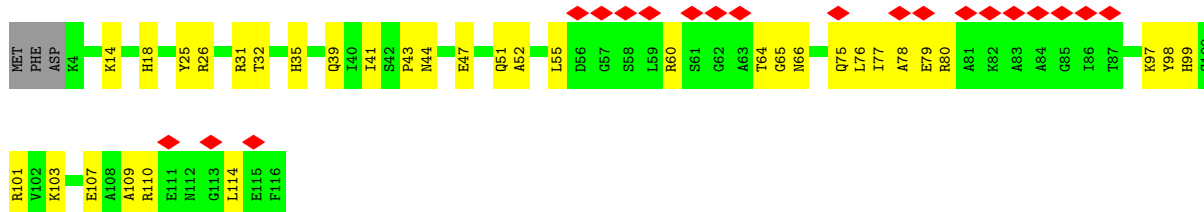
- Molecule 37: Large ribosomal subunit protein bL34



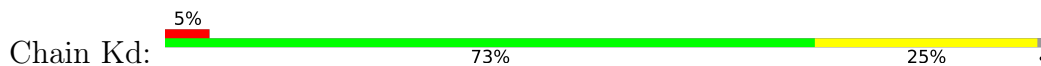
- Molecule 38: Large ribosomal subunit protein bL21

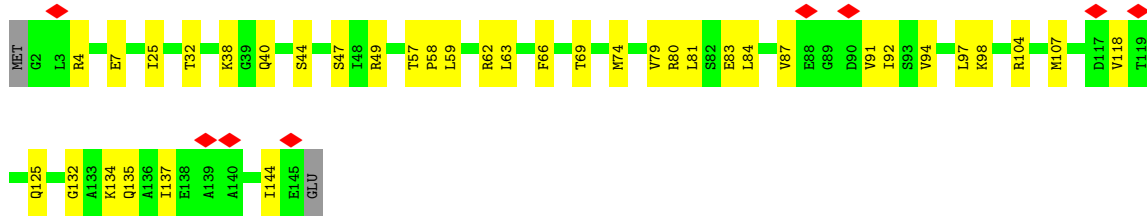


- Molecule 39: Large ribosomal subunit protein uL18



- Molecule 40: Large ribosomal subunit protein uL15

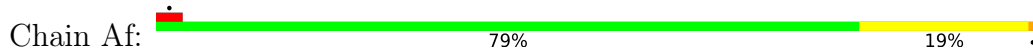




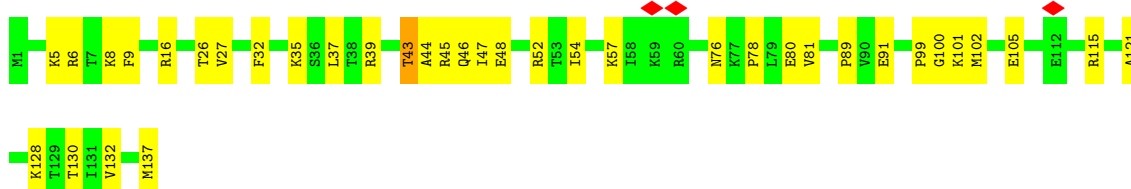
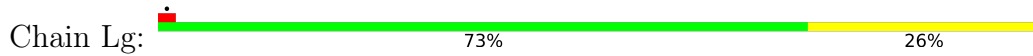
• Molecule 41: Large ribosomal subunit protein uL14



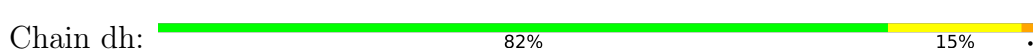
• Molecule 42: Large ribosomal subunit protein uL3



• Molecule 43: Large ribosomal subunit protein uL16

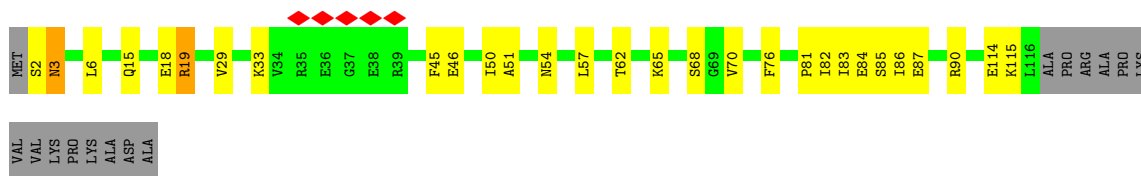


• Molecule 44: Large ribosomal subunit protein bL35



• Molecule 45: Large ribosomal subunit protein bL19

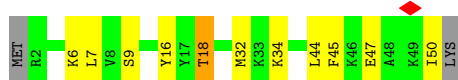
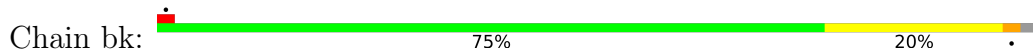




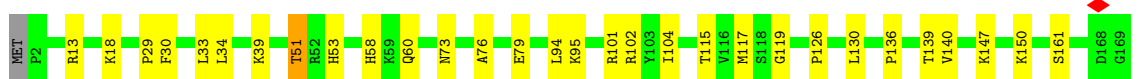
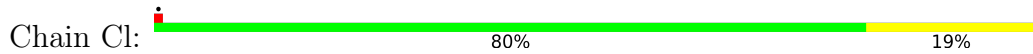
• Molecule 46: Small ribosomal subunit protein bS16



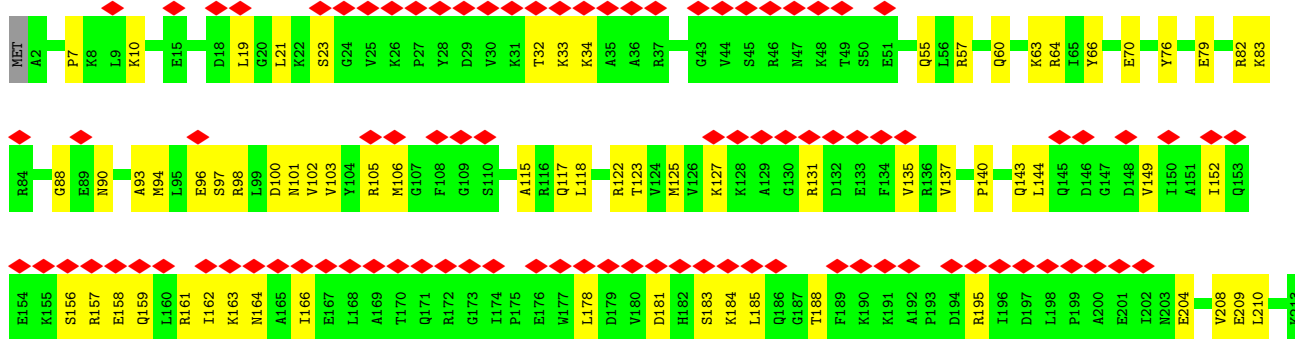
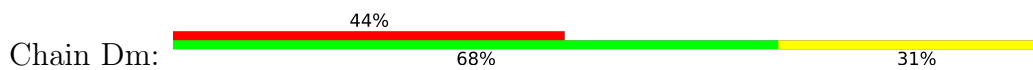
• Molecule 47: Large ribosomal subunit protein bL33



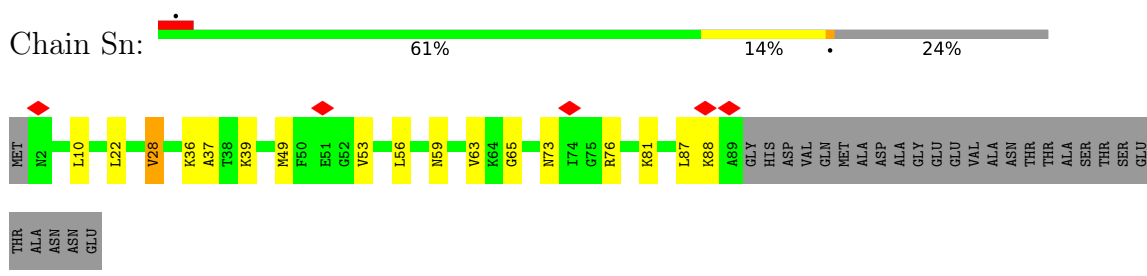
• Molecule 48: Large ribosomal subunit protein uL2



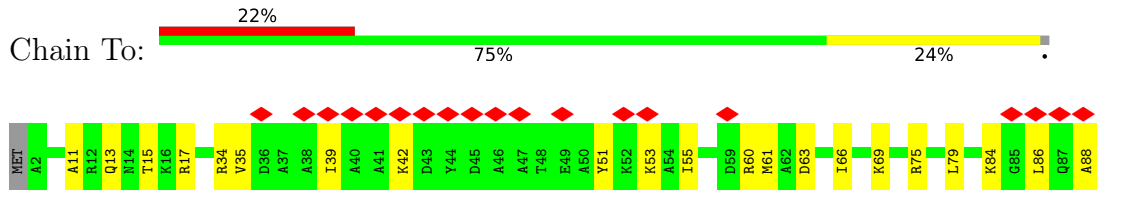
• Molecule 49: Small ribosomal subunit protein uS4



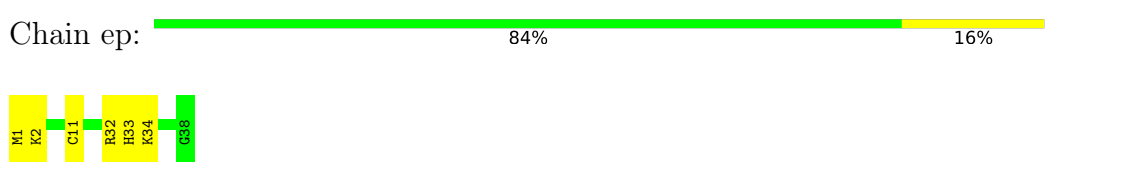
• Molecule 50: Large ribosomal subunit protein uL23



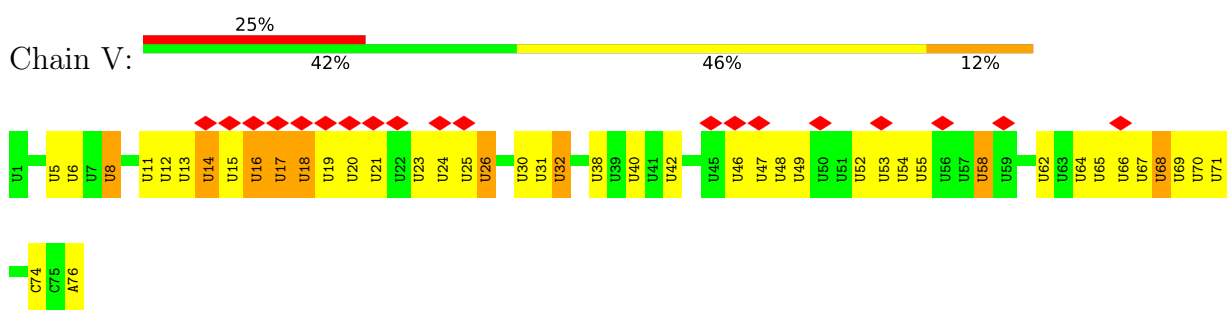
• Molecule 51: Small ribosomal subunit protein bS20



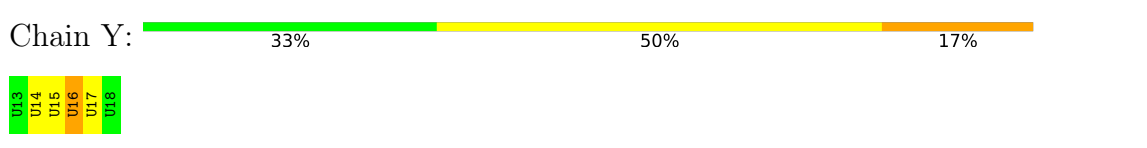
• Molecule 52: Large ribosomal subunit protein bL36



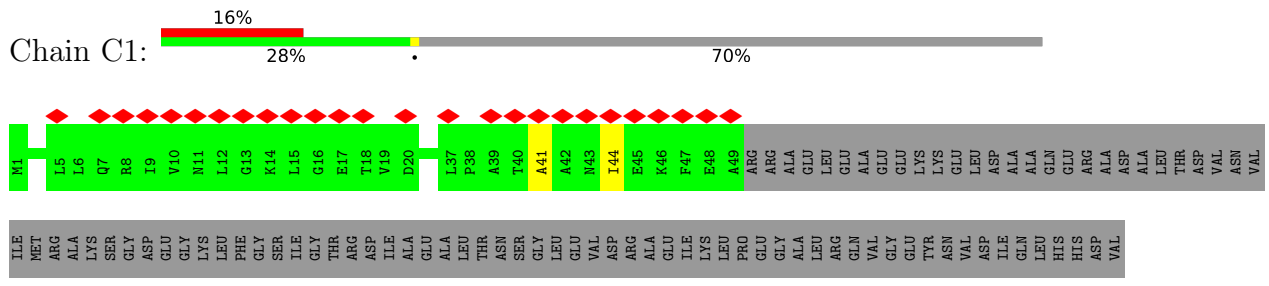
• Molecule 53: Heterogenous tRNA



• Molecule 54: Heterogenous mRNA

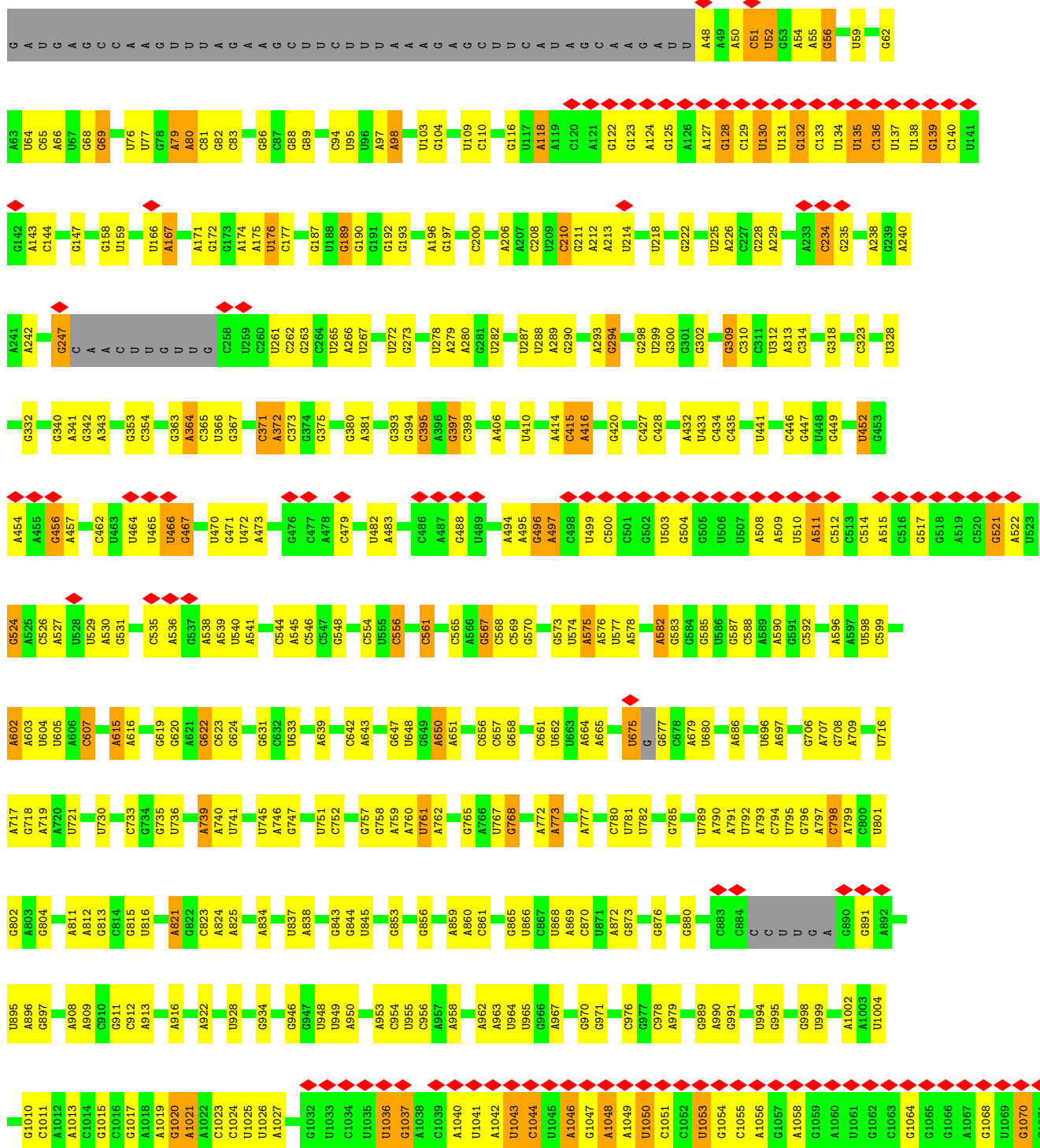


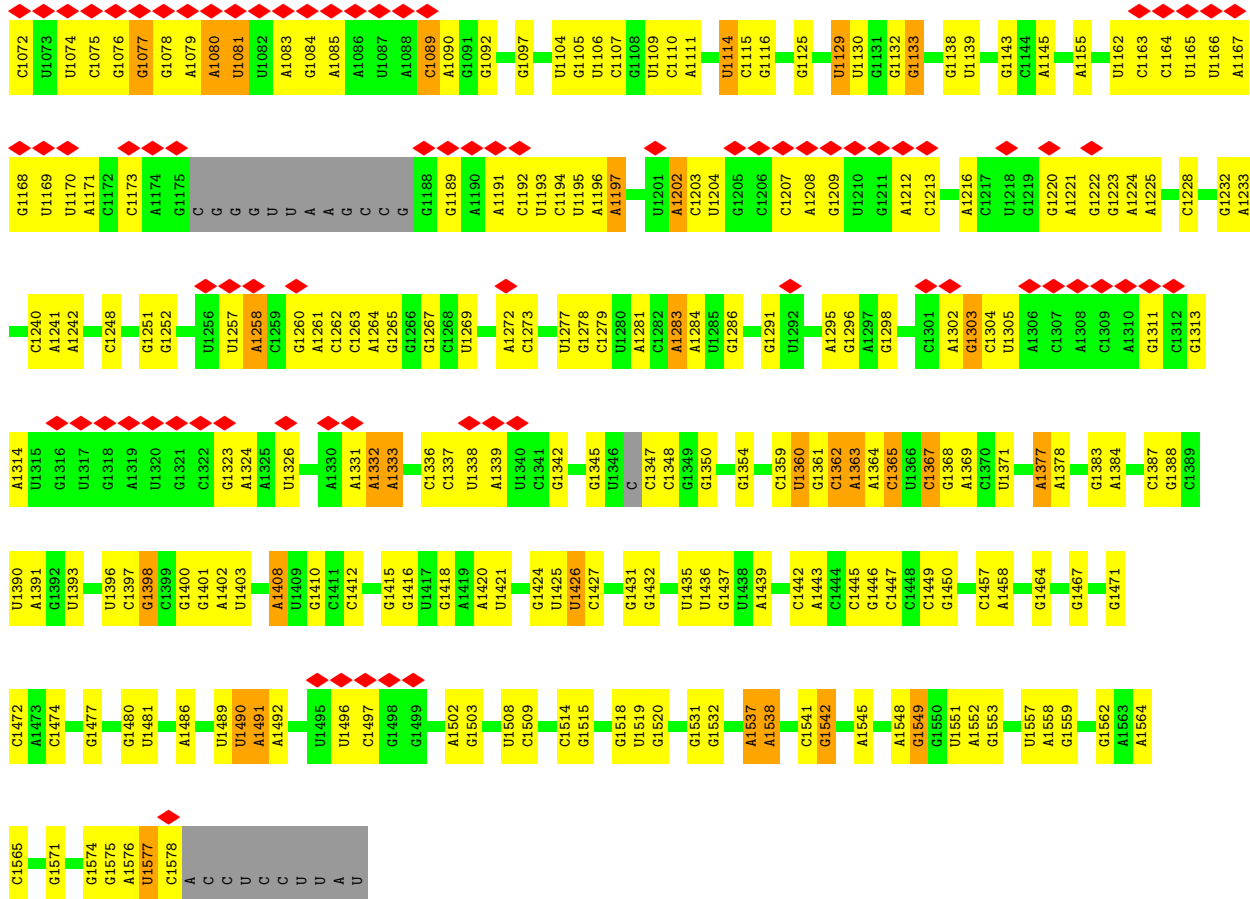
• Molecule 55: Large ribosomal subunit protein bL9



THR	ALA	THR	ILE	LEU	VAL	THR	ILE	LEU	SER	GLY	ASP	ASP	GLN	ASN	GLY	GLY	TYR	SER	GLY
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● Molecule 56: 16S rRNA





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	30469	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 ( $e^-/\text{\AA}^2$ )	40	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.183	Depositor
Minimum map value	-0.089	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.02	Depositor
Map size ( $\text{\AA}$ )	390.41998, 390.41998, 390.41998	wwPDB
Map dimensions	540, 540, 540	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	0.723, 0.723, 0.723	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	B	0.24	0/2870	0.41	1/3890 (0.0%)
2	F	0.22	0/998	0.42	0/1336
3	H	0.16	0/1429	0.42	0/1925
4	Z2	0.40	0/65123	0.38	0/101564
5	R3	0.25	0/465	0.39	0/629
6	A4	0.20	0/1848	0.39	0/2494
7	E5	0.27	0/1163	0.41	0/1564
8	L6	0.29	0/959	0.45	0/1282
9	F7	0.21	0/1383	0.38	0/1858
10	D8	0.28	0/2733	0.28	0/4256
11	E9	0.31	0/1559	0.44	0/2103
12	aA	0.29	0/450	0.37	0/596
13	MB	0.34	0/961	0.44	0/1282
14	UC	0.27	0/774	0.40	0/1043
15	WD	0.31	0/628	0.41	0/841
16	XE	0.20	0/503	0.34	0/670
17	RF	0.31	0/840	0.45	0/1125
18	FG	0.20	0/864	0.37	0/1169
19	VH	0.31	0/635	0.43	0/847
20	TI	0.24	0/790	0.36	0/1057
21	fJ	0.14	0/508	0.36	0/690
22	HK	0.16	0/821	0.29	0/1091
23	OL	0.26	0/702	0.41	0/941
24	MM	0.15	0/724	0.31	0/976
25	PO	0.35	0/947	0.46	0/1261
26	SP	0.16	0/652	0.41	0/879
27	BQ	0.23	0/982	0.34	0/1318
28	GR	0.22	0/1377	0.40	0/1861
29	GS	0.20	0/1219	0.40	0/1634
30	CT	0.20	0/1637	0.42	0/2200
31	KU	0.20	0/857	0.36	0/1158
32	NV	0.20	0/478	0.36	0/632
33	YW	0.30	0/442	0.43	0/590
34	IX	0.32	0/1134	0.41	0/1529

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
35	JY	0.20	0/803	0.41	0/1084
36	QZ	0.23	0/638	0.41	0/858
37	Ba	0.37	0/373	0.50	0/489
38	Qb	0.31	0/839	0.45	0/1127
39	Nc	0.25	0/863	0.41	0/1158
40	Kd	0.31	0/1073	0.48	0/1429
41	Je	0.32	0/946	0.45	0/1271
42	Af	0.34	0/1566	0.45	0/2103
43	Lg	0.35	0/1112	0.52	0/1483
44	dh	0.35	0/524	0.48	0/686
45	Oi	0.32	0/927	0.49	0/1239
46	Pj	0.28	0/660	0.43	0/887
47	bk	0.31	0/401	0.46	0/534
48	Cl	0.33	0/2147	0.44	0/2883
49	Dm	0.22	0/1712	0.45	0/2296
50	Sn	0.29	0/705	0.45	0/939
51	To	0.25	0/688	0.50	0/916
52	ep	0.32	0/300	0.47	0/395
53	V	0.21	0/1674	0.38	0/2586
54	Y	0.21	0/131	0.38	0/200
55	C1	0.21	0/379	0.39	0/511
56	iN	0.28	0/36108	0.31	0/56315
All	All	0.33	0/154024	0.37	1/229680 (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
19	VH	0	1
29	GS	0	1
All	All	0	2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	99	PRO	CA-N-CD	-7.73	101.18	112.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
29	GS	112	ARG	Sidechain
19	VH	2	ALA	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	B	2829	0	2781	59	0
2	F	985	0	1035	38	0
3	H	1409	0	1416	27	0
4	Z2	58145	0	29231	584	0
5	R3	457	0	466	10	0
6	A4	1816	0	1843	42	0
7	E5	1151	0	1205	26	0
8	L6	946	0	1008	21	0
9	F7	1362	0	1402	50	0
10	D8	2446	0	1241	27	0
11	E9	1537	0	1590	29	0
12	aA	442	0	432	9	0
13	MB	947	0	988	10	0
14	UC	760	0	774	8	0
15	WD	618	0	637	19	0
16	XE	502	0	527	11	0
17	RF	834	0	898	19	0
18	FG	849	0	838	21	0
19	VH	626	0	629	12	0
20	TI	784	0	820	13	0
21	fJ	493	0	441	16	0
22	HK	811	0	845	28	0
23	OL	694	0	710	10	0
24	MM	717	0	748	24	0
25	PO	935	0	999	19	0
26	SP	637	0	665	19	0
27	BQ	974	0	1009	26	0
28	GR	1357	0	1397	27	0
29	GS	1200	0	1231	37	0
30	CT	1613	0	1677	37	0

*Continued on next page...*

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	KU	842	0	850	21	0
32	NV	472	0	520	10	0
33	YW	438	0	476	4	0
34	IX	1108	0	1145	18	0
35	JY	793	0	821	25	0
36	QZ	632	0	676	15	0
37	Ba	369	0	418	9	0
38	Qb	827	0	862	25	0
39	Nc	852	0	880	24	0
40	Kd	1062	0	1123	32	0
41	Je	937	0	1003	23	0
42	Af	1548	0	1574	34	0
43	Lg	1093	0	1188	29	0
44	dh	519	0	581	9	0
45	Oi	917	0	969	22	0
46	Pj	648	0	661	11	0
47	bk	394	0	412	6	0
48	Cl	2107	0	2195	43	0
49	Dm	1688	0	1745	48	0
50	Sn	698	0	750	12	0
51	To	684	0	727	15	0
52	ep	298	0	334	4	0
53	V	1521	0	766	20	0
54	Y	120	0	61	1	0
55	C1	374	0	406	1	0
56	iN	32246	0	16224	382	0
All	All	142063	0	96850	1829	0

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

The worst 5 of 1829 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)
56:iN:675:U:H3'	56:iN:677:G:P	1.90	1.11
4:Z2:281:A:N7	4:Z2:331:G:N2	2.12	0.96
4:Z2:2083:U:H3	4:Z2:2178:G:H1	0.94	0.93
4:Z2:655:A:H4'	4:Z2:656:C:H5'	1.58	0.84
42:Af:26:THR:HG21	42:Af:196:ILE:HG12	1.58	0.84

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	358/369 (97%)	344 (96%)	13 (4%)	1 (0%)	36	58
2	F	124/128 (97%)	117 (94%)	7 (6%)	0	100	100
3	H	183/396 (46%)	175 (96%)	8 (4%)	0	100	100
5	R3	54/76 (71%)	53 (98%)	1 (2%)	0	100	100
6	A4	231/269 (86%)	220 (95%)	11 (5%)	0	100	100
7	E5	154/171 (90%)	147 (96%)	7 (4%)	0	100	100
8	L6	120/124 (97%)	111 (92%)	9 (8%)	0	100	100
9	F7	175/178 (98%)	166 (95%)	9 (5%)	0	100	100
11	E9	197/200 (98%)	191 (97%)	6 (3%)	0	100	100
12	aA	51/60 (85%)	51 (100%)	0	0	100	100
13	MB	117/119 (98%)	112 (96%)	5 (4%)	0	100	100
14	UC	95/219 (43%)	92 (97%)	3 (3%)	0	100	100
15	WD	74/78 (95%)	72 (97%)	2 (3%)	0	100	100
16	XE	60/65 (92%)	58 (97%)	2 (3%)	0	100	100
17	RF	107/109 (98%)	104 (97%)	3 (3%)	0	100	100
18	FG	100/134 (75%)	98 (98%)	2 (2%)	0	100	100
19	VH	82/85 (96%)	78 (95%)	4 (5%)	0	100	100
20	TI	100/105 (95%)	96 (96%)	4 (4%)	0	100	100
21	fJ	57/93 (61%)	56 (98%)	1 (2%)	0	100	100
22	HK	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
23	OL	84/88 (96%)	81 (96%)	3 (4%)	0	100	100
24	MM	90/118 (76%)	87 (97%)	3 (3%)	0	100	100
25	PO	114/118 (97%)	111 (97%)	3 (3%)	0	100	100
26	SP	78/91 (86%)	75 (96%)	3 (4%)	0	100	100
27	BQ	129/132 (98%)	127 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	GR	173/177 (98%)	163 (94%)	10 (6%)	0	100	100
29	GS	151/157 (96%)	148 (98%)	3 (2%)	0	100	100
30	CT	203/241 (84%)	185 (91%)	18 (9%)	0	100	100
31	KU	113/129 (88%)	106 (94%)	7 (6%)	0	100	100
32	NV	55/71 (78%)	55 (100%)	0	0	100	100
33	YW	54/59 (92%)	54 (100%)	0	0	100	100
34	IX	140/142 (99%)	136 (97%)	4 (3%)	0	100	100
35	JY	98/103 (95%)	87 (89%)	11 (11%)	0	100	100
36	QZ	77/91 (85%)	75 (97%)	2 (3%)	0	100	100
37	Ba	42/44 (96%)	40 (95%)	2 (5%)	0	100	100
38	Qb	101/103 (98%)	99 (98%)	2 (2%)	0	100	100
39	Nc	111/116 (96%)	109 (98%)	2 (2%)	0	100	100
40	Kd	143/146 (98%)	133 (93%)	10 (7%)	0	100	100
41	Je	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
42	Af	209/212 (99%)	199 (95%)	9 (4%)	1 (0%)	24	46
43	Lg	135/137 (98%)	128 (95%)	7 (5%)	0	100	100
44	dh	62/65 (95%)	61 (98%)	0	1 (2%)	7	16
45	Oi	113/130 (87%)	105 (93%)	8 (7%)	0	100	100
46	Pj	79/89 (89%)	78 (99%)	1 (1%)	0	100	100
47	bk	47/51 (92%)	45 (96%)	2 (4%)	0	100	100
48	Cl	270/274 (98%)	258 (96%)	12 (4%)	0	100	100
49	Dm	210/213 (99%)	195 (93%)	15 (7%)	0	100	100
50	Sn	86/116 (74%)	85 (99%)	1 (1%)	0	100	100
51	To	85/88 (97%)	82 (96%)	3 (4%)	0	100	100
52	ep	36/38 (95%)	36 (100%)	0	0	100	100
55	C1	47/166 (28%)	44 (94%)	3 (6%)	0	100	100
All	All	5992/6906 (87%)	5742 (96%)	247 (4%)	3 (0%)	47	70

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	140	ASN
42	Af	141	VAL

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Mol	Chain	Res	Type
44	dh	32	ILE

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	B	303/310 (98%)	286 (94%)	17 (6%)	19 40
2	F	103/105 (98%)	98 (95%)	5 (5%)	22 47
3	H	151/327 (46%)	131 (87%)	20 (13%)	4 8
5	R3	51/67 (76%)	50 (98%)	1 (2%)	48 74
6	A4	188/211 (89%)	187 (100%)	1 (0%)	81 92
7	E5	118/131 (90%)	116 (98%)	2 (2%)	53 78
8	L6	102/103 (99%)	97 (95%)	5 (5%)	22 47
9	F7	139/146 (95%)	117 (84%)	22 (16%)	2 4
11	E9	159/159 (100%)	156 (98%)	3 (2%)	50 75
12	aA	46/53 (87%)	46 (100%)	0	100 100
13	MB	101/102 (99%)	98 (97%)	3 (3%)	36 64
14	UC	79/184 (43%)	77 (98%)	2 (2%)	42 69
15	WD	67/71 (94%)	66 (98%)	1 (2%)	57 80
16	XE	54/57 (95%)	53 (98%)	1 (2%)	50 75
17	RF	88/88 (100%)	81 (92%)	7 (8%)	11 25
18	FG	92/121 (76%)	91 (99%)	1 (1%)	65 84
19	VH	60/62 (97%)	55 (92%)	5 (8%)	10 23
20	TI	83/85 (98%)	79 (95%)	4 (5%)	23 47
21	fJ	52/81 (64%)	45 (86%)	7 (14%)	4 7
22	HK	87/88 (99%)	86 (99%)	1 (1%)	65 84
23	OL	75/77 (97%)	74 (99%)	1 (1%)	61 82
24	MM	76/99 (77%)	64 (84%)	12 (16%)	2 4
25	PO	88/90 (98%)	86 (98%)	2 (2%)	44 71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
26	SP	71/79 (90%)	60 (84%)	11 (16%)	2	5
27	BQ	103/104 (99%)	101 (98%)	2 (2%)	50	75
28	GR	149/151 (99%)	142 (95%)	7 (5%)	23	48
29	GS	124/128 (97%)	124 (100%)	0	100	100
30	CT	168/198 (85%)	147 (88%)	21 (12%)	4	9
31	KU	85/98 (87%)	83 (98%)	2 (2%)	43	70
32	NV	49/63 (78%)	48 (98%)	1 (2%)	48	74
33	YW	50/52 (96%)	49 (98%)	1 (2%)	48	74
34	IX	116/117 (99%)	115 (99%)	1 (1%)	70	87
35	JY	88/90 (98%)	88 (100%)	0	100	100
36	QZ	73/84 (87%)	71 (97%)	2 (3%)	39	67
37	Ba	37/37 (100%)	36 (97%)	1 (3%)	39	67
38	Qb	89/89 (100%)	89 (100%)	0	100	100
39	Nc	81/85 (95%)	80 (99%)	1 (1%)	63	83
40	Kd	108/110 (98%)	108 (100%)	0	100	100
41	Je	102/102 (100%)	98 (96%)	4 (4%)	28	55
42	Af	161/162 (99%)	157 (98%)	4 (2%)	42	69
43	Lg	114/114 (100%)	112 (98%)	2 (2%)	51	76
44	dh	55/56 (98%)	54 (98%)	1 (2%)	51	76
45	Oi	97/108 (90%)	93 (96%)	4 (4%)	27	54
46	Pj	63/68 (93%)	60 (95%)	3 (5%)	23	47
47	bk	42/46 (91%)	39 (93%)	3 (7%)	13	31
48	Cl	219/221 (99%)	215 (98%)	4 (2%)	51	76
49	Dm	177/181 (98%)	173 (98%)	4 (2%)	44	71
50	Sn	76/97 (78%)	73 (96%)	3 (4%)	28	55
51	To	67/69 (97%)	66 (98%)	1 (2%)	57	80
52	ep	33/33 (100%)	33 (100%)	0	100	100
55	C1	39/135 (29%)	39 (100%)	0	100	100
All	All	4998/5694 (88%)	4792 (96%)	206 (4%)	25	54

5 of 206 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
24	MM	48	LEU
30	CT	14	VAL
49	Dm	135	VAL
24	MM	87	ARG
26	SP	41	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 46 such sidechains are listed below:

Mol	Chain	Res	Type
34	IX	95	HIS
42	Af	133	GLN
34	IX	102	HIS
42	Af	40	ASN
43	Lg	22	HIS

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	D8	114/115 (99%)	14 (12%)	0
4	Z2	2705/2882 (93%)	388 (14%)	20 (0%)
53	V	75/76 (98%)	26 (34%)	0
54	Y	5/6 (83%)	3 (60%)	0
56	iN	1498/1590 (94%)	266 (17%)	0
All	All	4397/4669 (94%)	697 (15%)	20 (0%)

5 of 697 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	Z2	10	U
4	Z2	19	G
4	Z2	22	G
4	Z2	30	G
4	Z2	41	U

5 of 20 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	Z2	2405	C
4	Z2	2457	U
4	Z2	2739	U
4	Z2	2464	G

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Mol	Chain	Res	Type
4	Z2	916	A

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

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

#### 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

#### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

#### 5.7 Other polymers [i](#)

There are no such residues in this entry.

#### 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

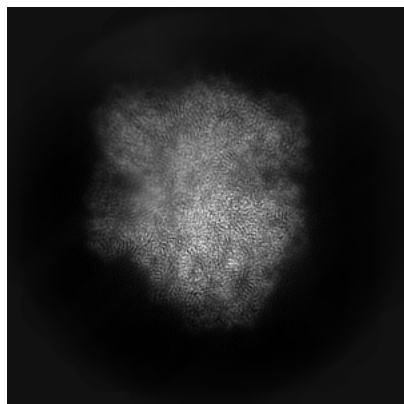
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-19076. These allow visual inspection of the internal detail of the map and identification of artifacts.

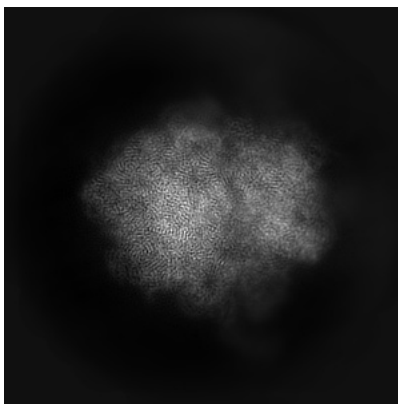
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

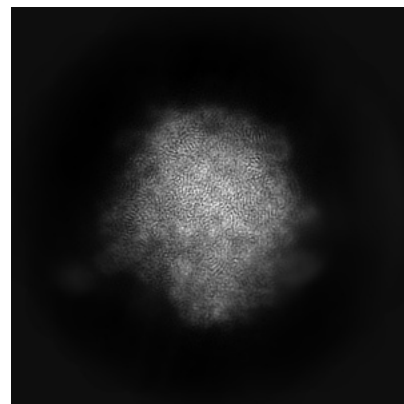
#### 6.1.1 Primary map



X

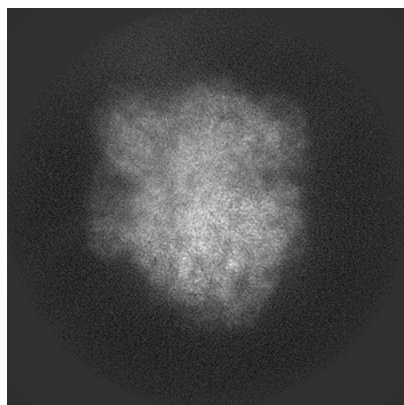


Y

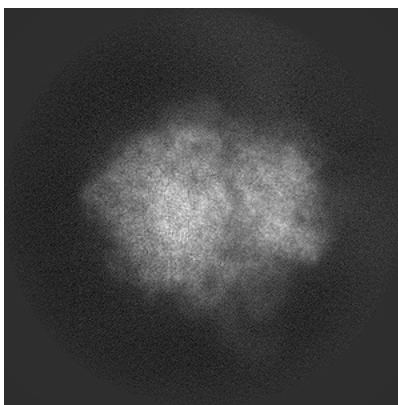


Z

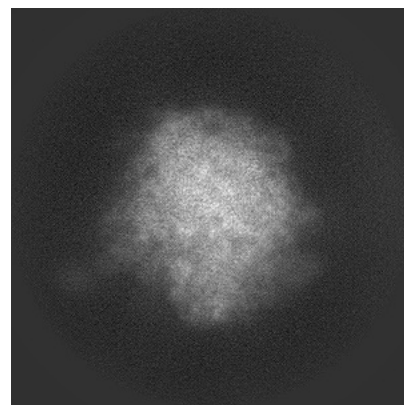
#### 6.1.2 Raw map



X



Y

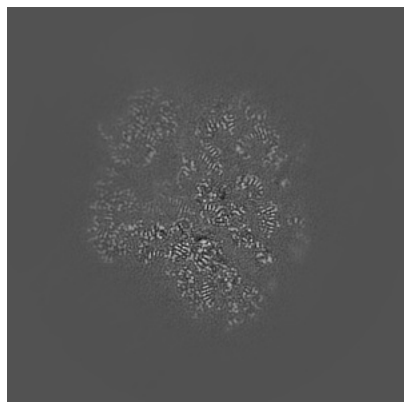


Z

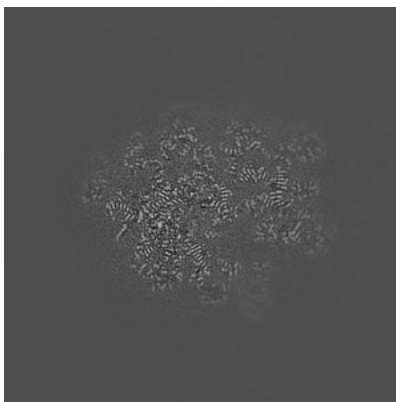
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

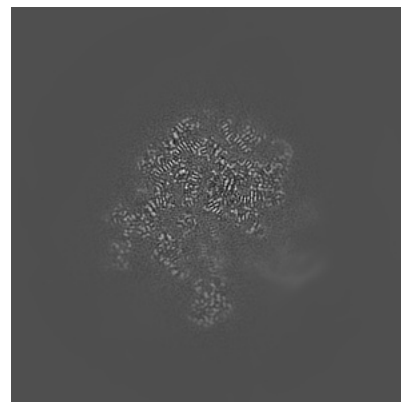
### 6.2.1 Primary map



X Index: 270

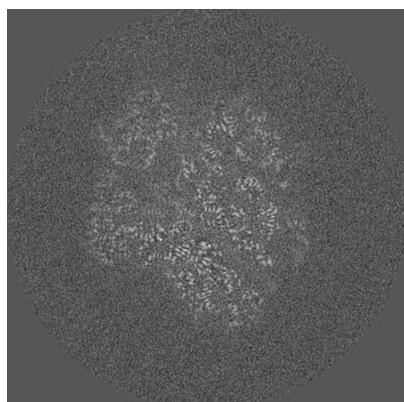


Y Index: 270

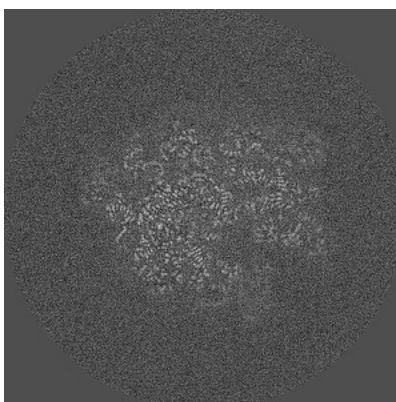


Z Index: 270

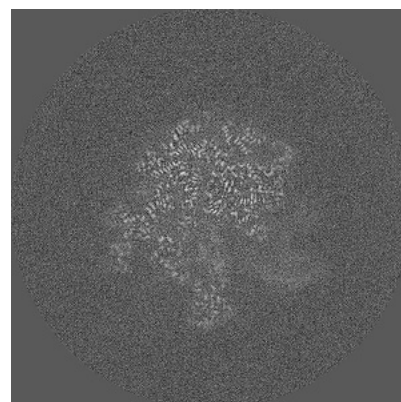
### 6.2.2 Raw map



X Index: 270



Y Index: 270

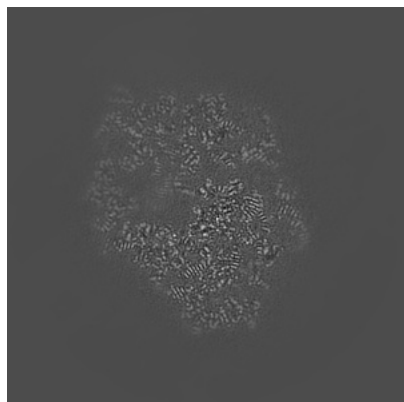


Z Index: 270

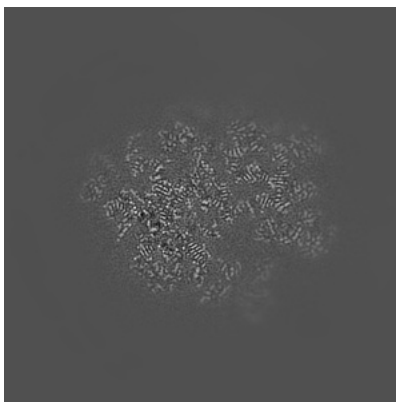
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

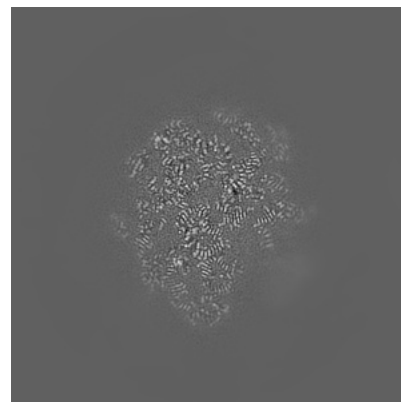
### 6.3.1 Primary map



X Index: 286

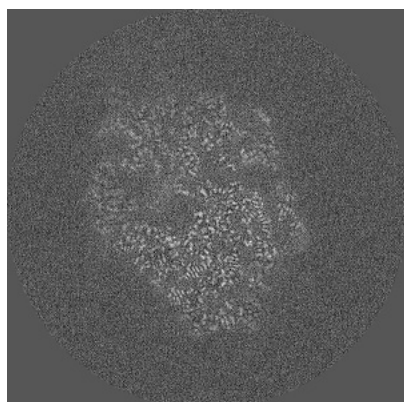


Y Index: 272

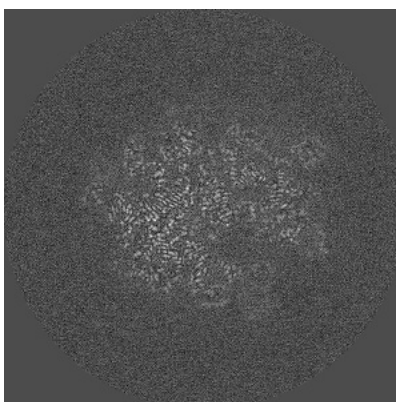


Z Index: 237

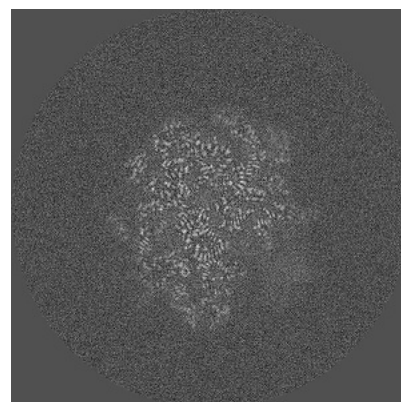
### 6.3.2 Raw map



X Index: 287



Y Index: 268

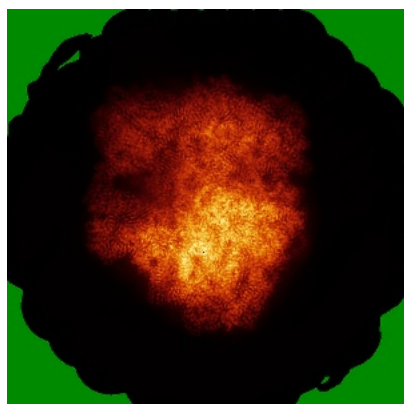


Z Index: 238

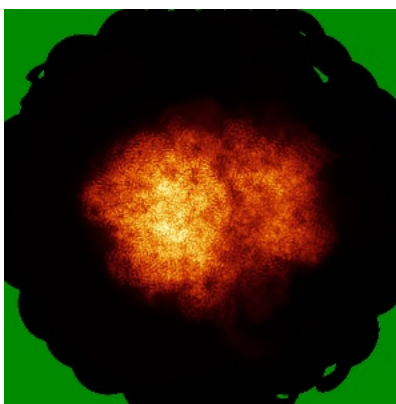
The images above show the largest variance slices of the map in three orthogonal directions.

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

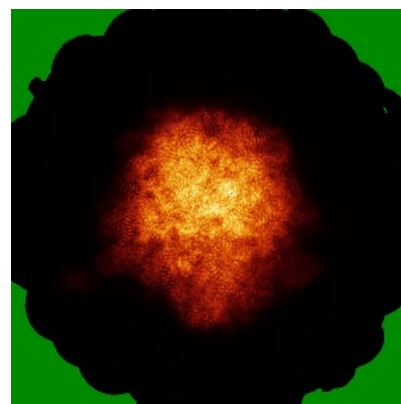
### 6.4.1 Primary map



X

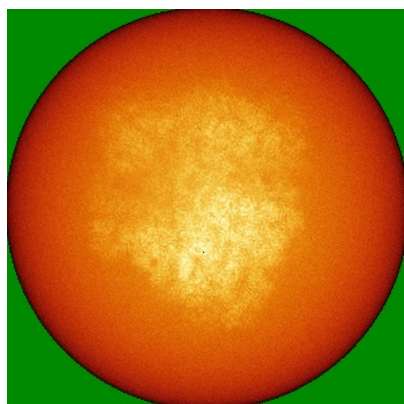


Y

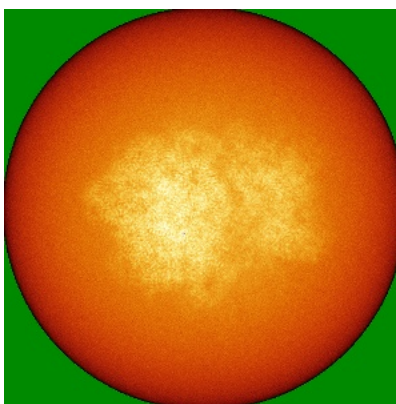


Z

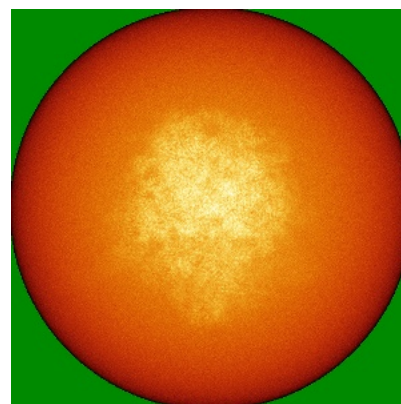
### 6.4.2 Raw map



X



Y

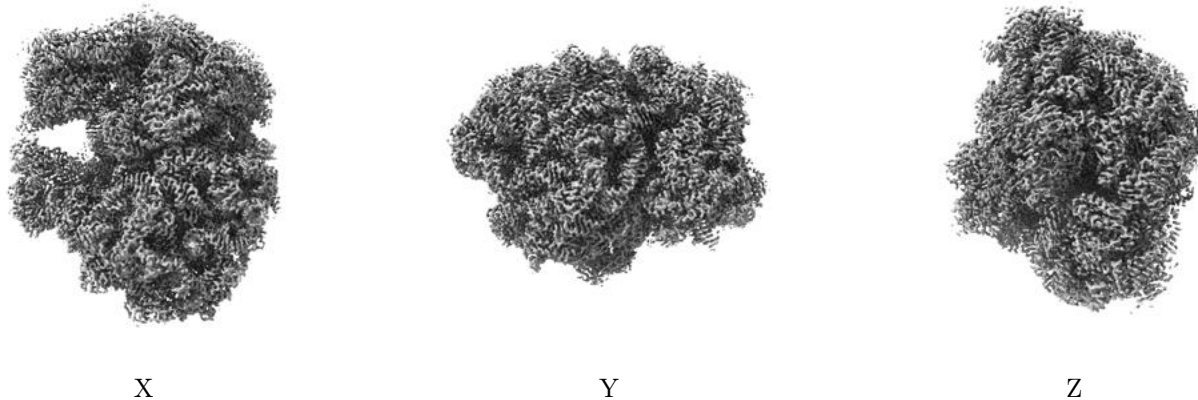


Z

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.

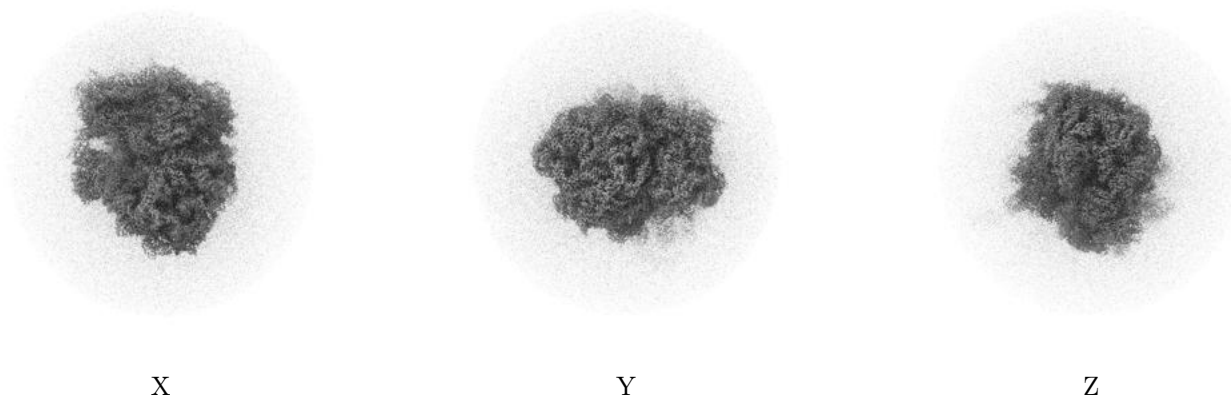
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. 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.

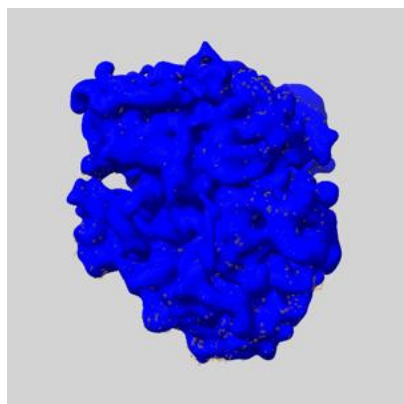
## 6.6 Mask visualisation [i](#)

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

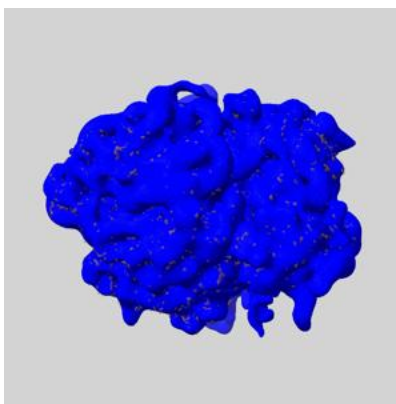
A mask typically either:

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

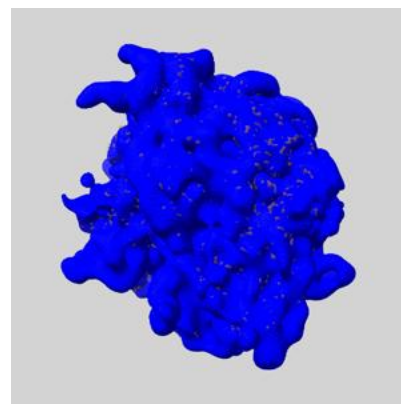
### 6.6.1 emd\_19076\_msk\_1.map [i](#)



X



Y

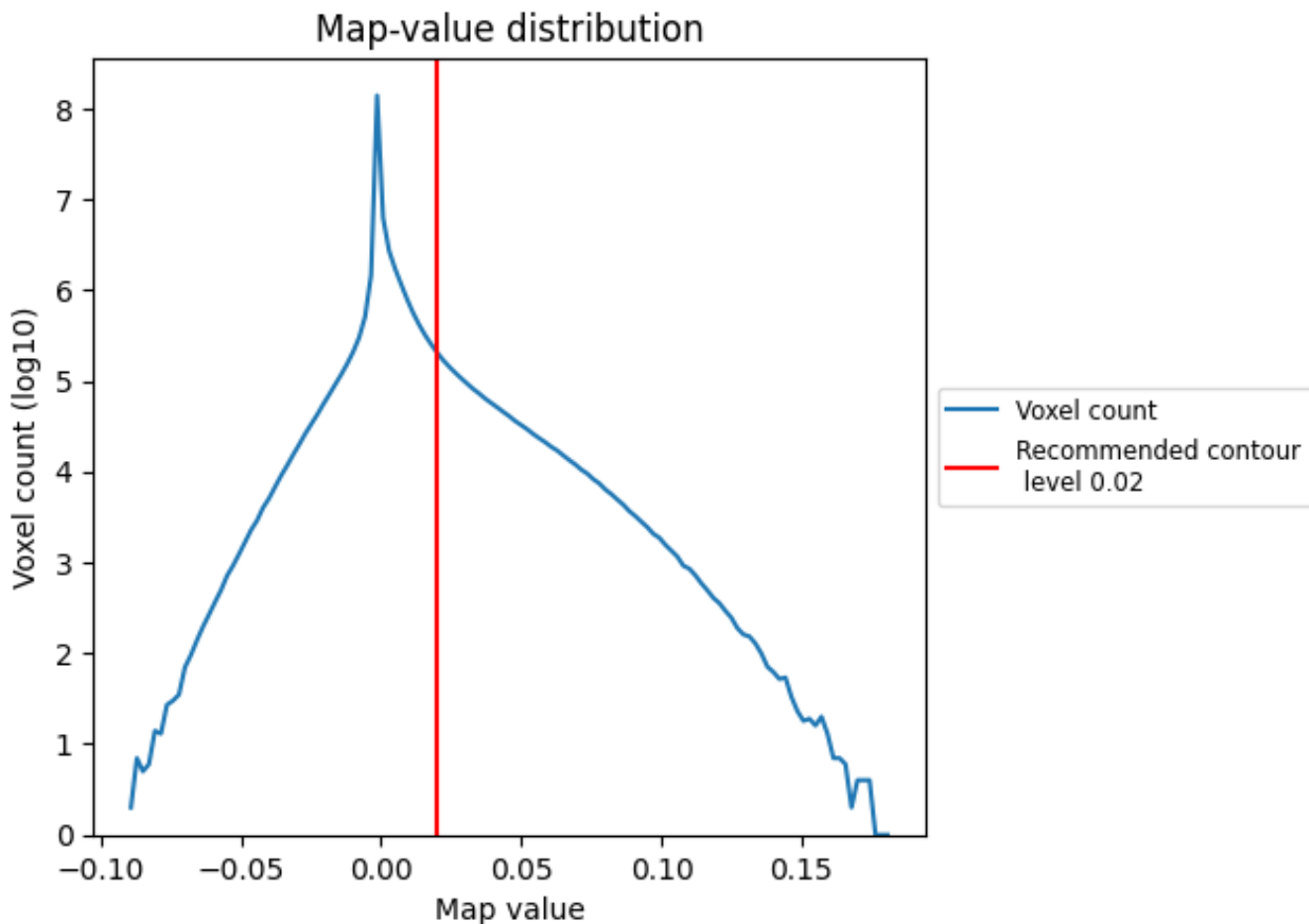


Z

## 7 Map analysis [i](#)

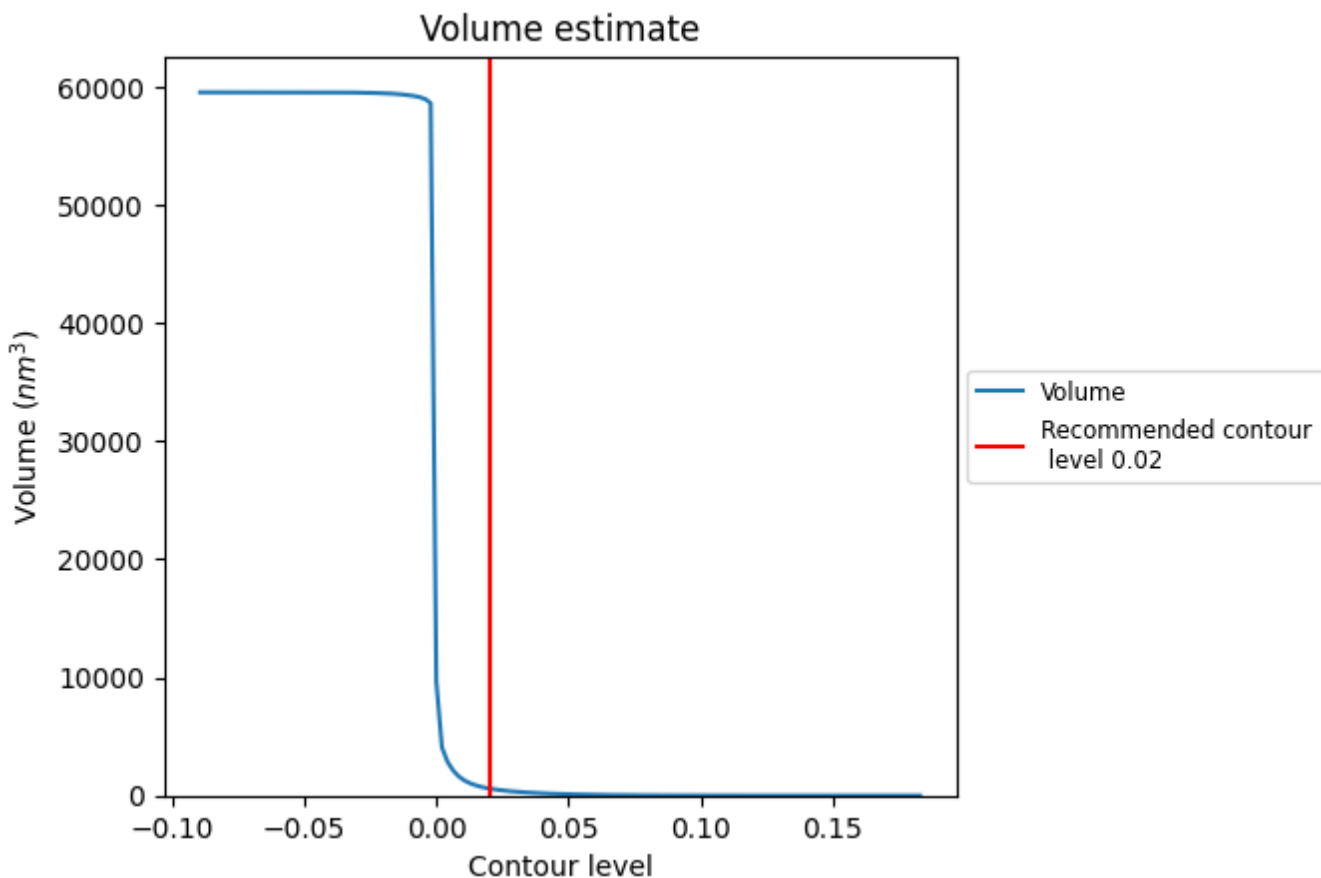
This section contains the results of statistical analysis of the map.

### 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.

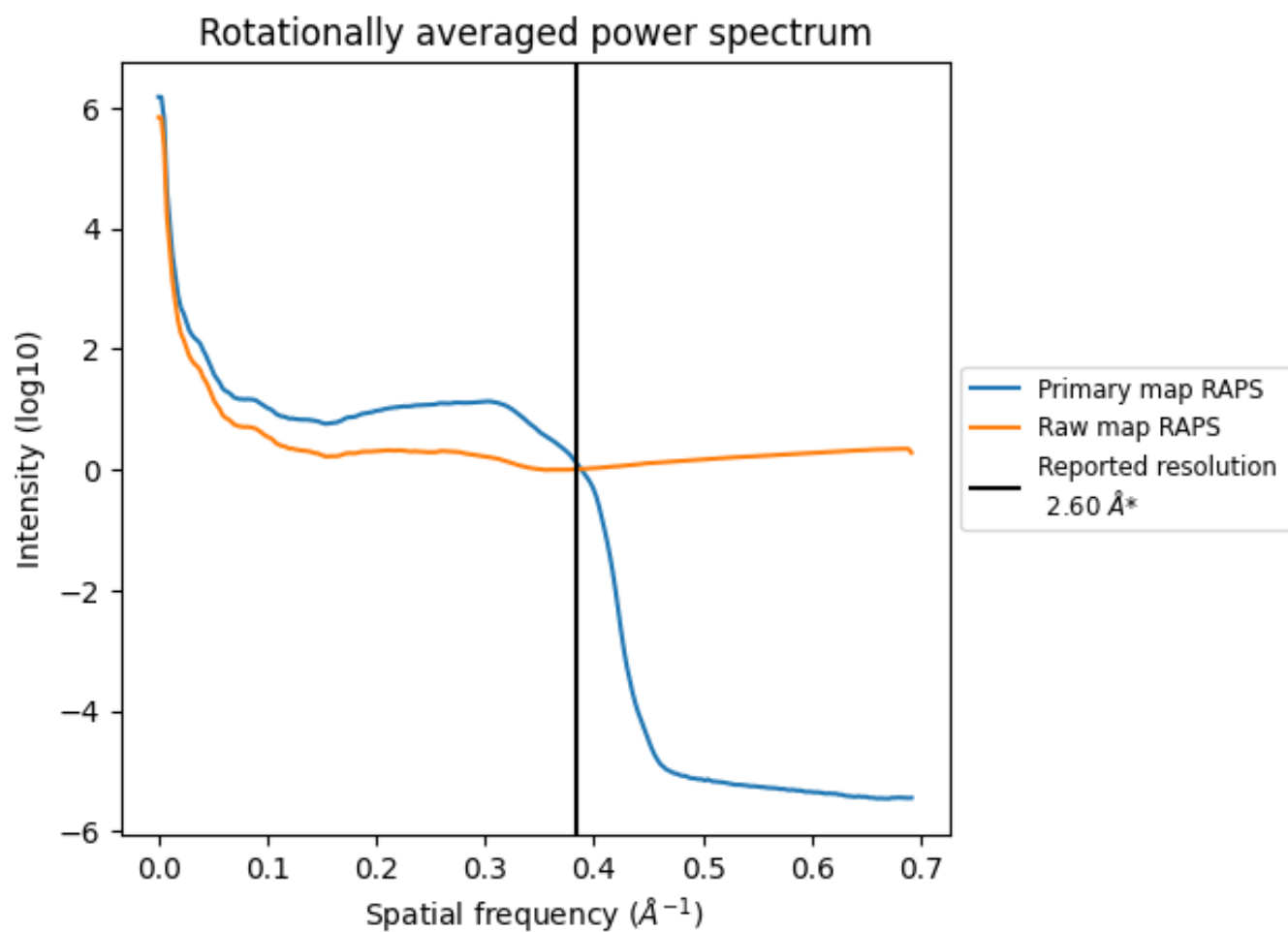
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 599  $\text{nm}^3$ ; this corresponds to an approximate mass of 541 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

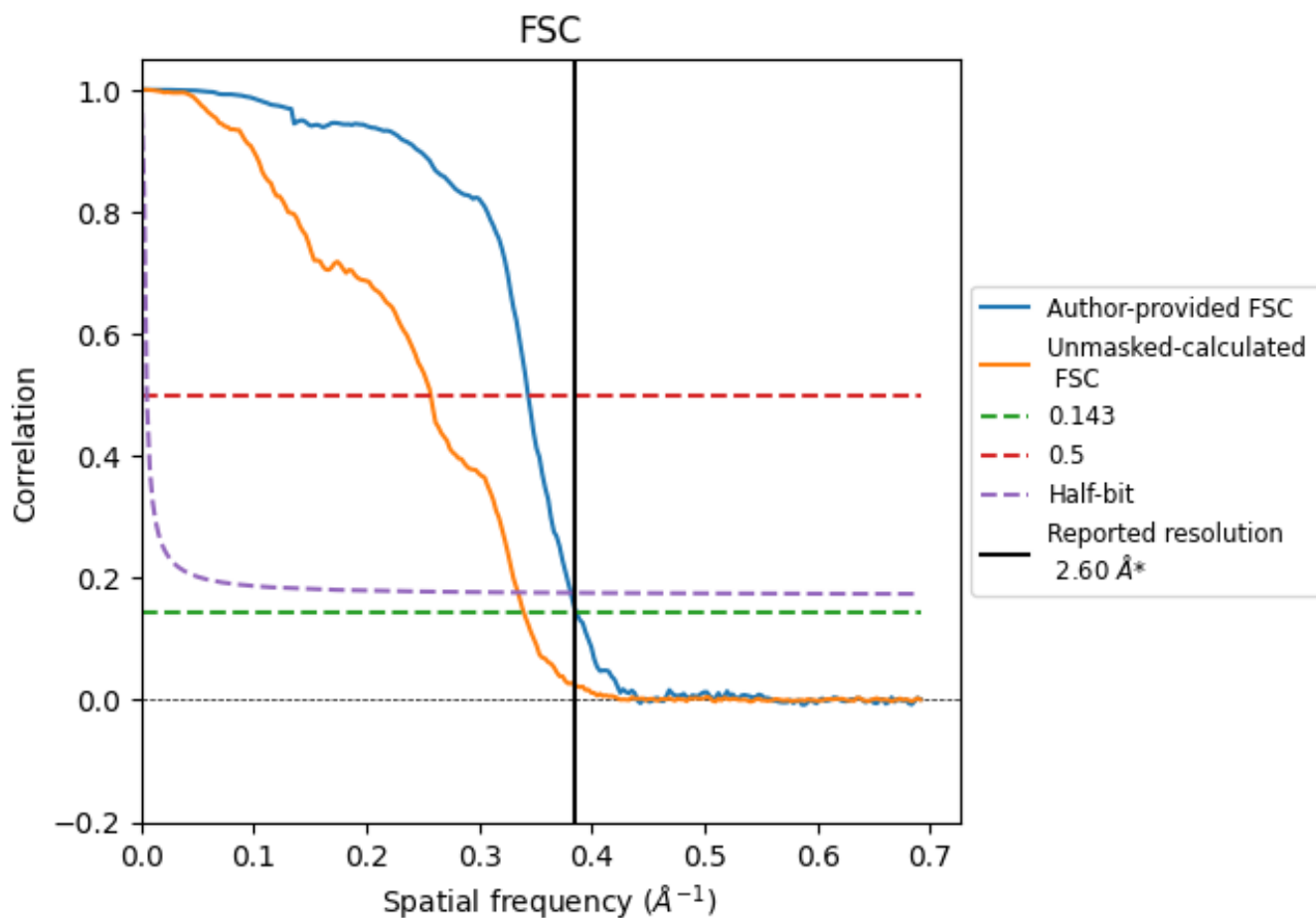


\*Reported resolution corresponds to spatial frequency of 0.385 Å<sup>-1</sup>

## 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 0.385 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

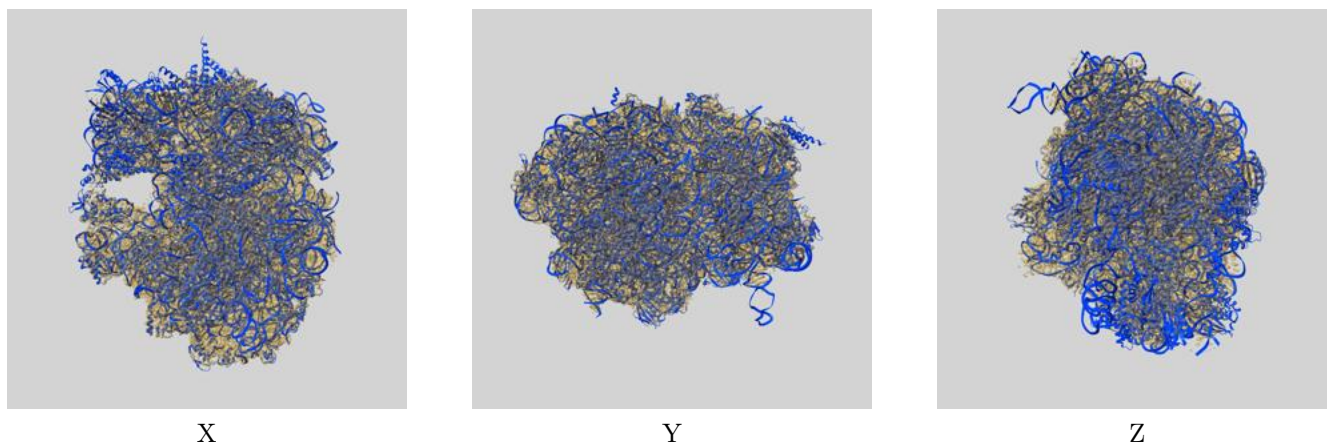
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.60	-	-
Author-provided FSC curve	2.59	2.91	2.62
Unmasked-calculated*	2.94	3.89	2.99

\*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 2.94 differs from the reported value 2.6 by more than 10 %

## 9 Map-model fit [i](#)

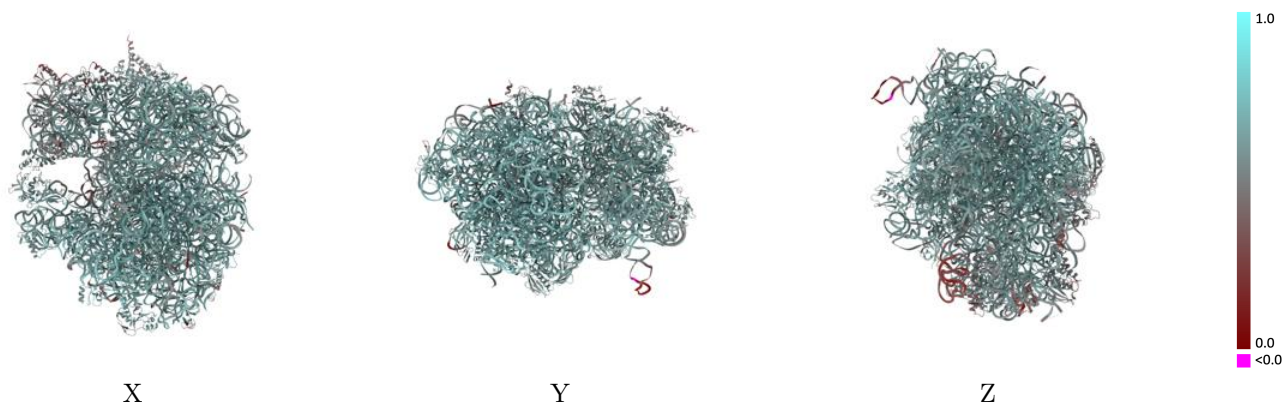
This section contains information regarding the fit between EMDB map EMD-19076 and PDB model 8RDV. Per-residue inclusion information can be found in section 3 on page 15.

### 9.1 Map-model overlay [i](#)



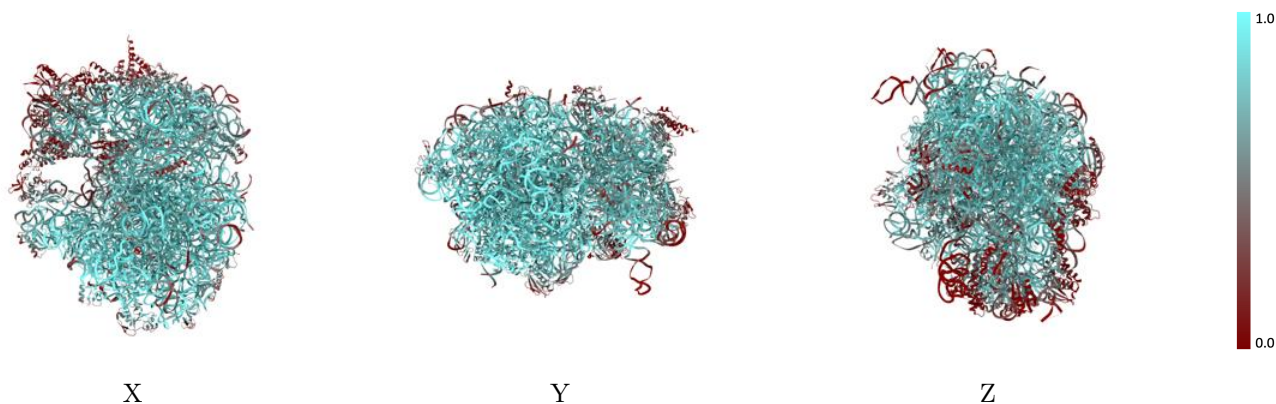
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



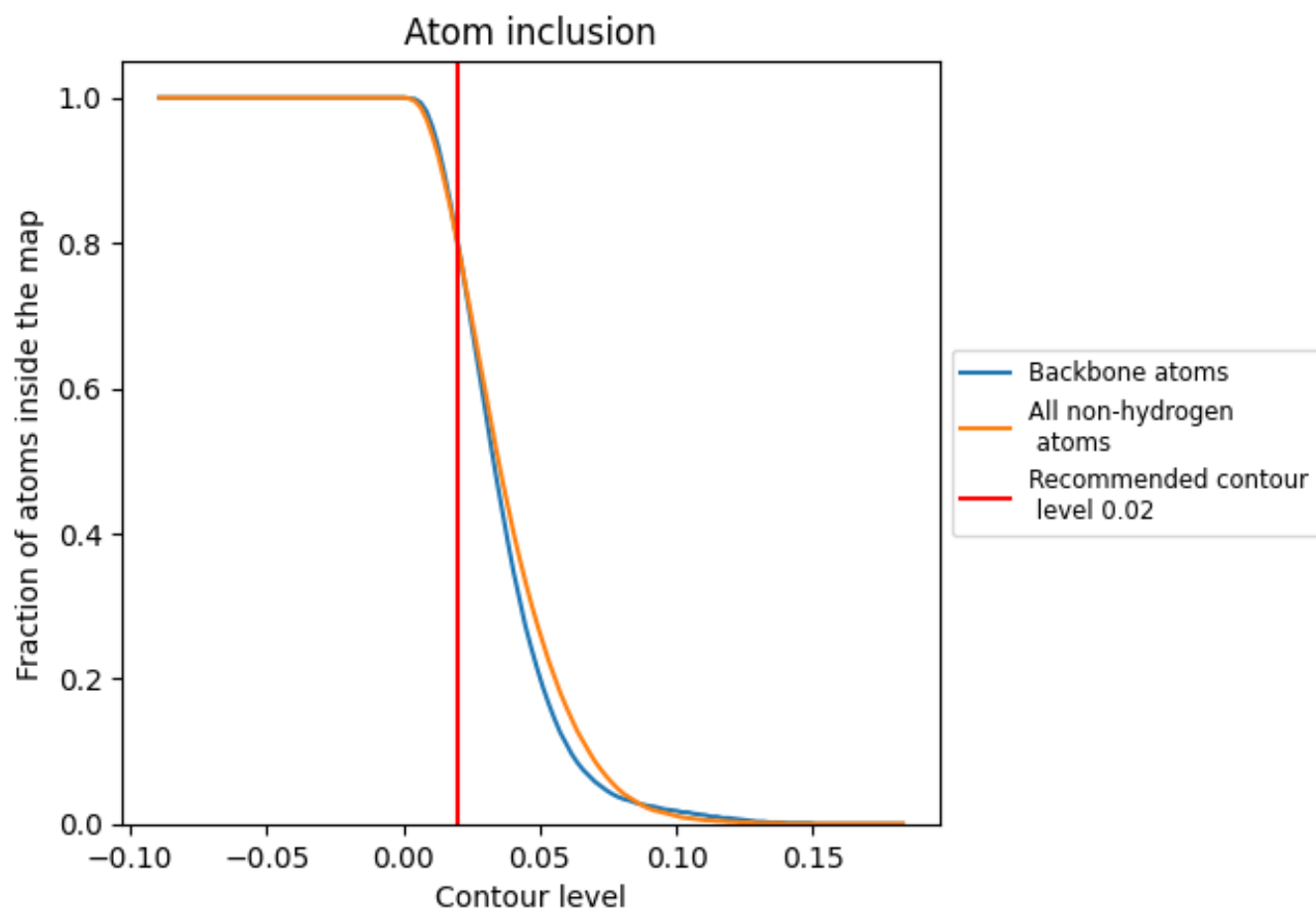
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.02).







































































## 9.4 Atom inclusion [i](#)



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

## 9.5 Map-model fit summary













































The table lists the average atom inclusion at the recommended contour level (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7960	 0.6270
A4	 0.3010	 0.5170
Af	 0.8940	 0.6670
B	 0.7040	 0.6230
BQ	 0.7260	 0.6320
Ba	 0.9860	 0.6950
C1	 0.4340	 0.5300
CT	 0.4160	 0.5710
Cl	 0.9330	 0.6720
D8	 0.8340	 0.6280
Dm	 0.4440	 0.5650
E5	 0.7520	 0.6260
E9	 0.7720	 0.6430
F	 0.3750	 0.5310
F7	 0.4600	 0.5900
FG	 0.4350	 0.5390
GR	 0.5420	 0.5910
GS	 0.3030	 0.4890
H	 0.1710	 0.5690
HK	 0.3830	 0.5170
IX	 0.9070	 0.6640
JY	 0.2900	 0.4670
Je	 0.8960	 0.6650
KU	 0.5390	 0.5710
Kd	 0.8550	 0.6530
L6	 0.8240	 0.6340
Lg	 0.8750	 0.6510
MB	 0.9450	 0.6780
MM	 0.2540	 0.5480
NV	 0.4180	 0.5520
Nc	 0.7180	 0.6250
OL	 0.7440	 0.6140
Oi	 0.8800	 0.6490
PO	 0.9180	 0.6760
Pj	 0.7080	 0.6100



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Chain	Atom inclusion	Q-score
QZ	 0.6720	 0.6010
Qb	 0.7370	 0.6280
R3	 0.6570	 0.5770
RF	 0.8940	 0.6670
SP	 0.1690	 0.5220
Sn	 0.7940	 0.6350
TI	 0.6060	 0.5740
To	 0.6900	 0.6150
UC	 0.7440	 0.6300
V	 0.5730	 0.5220
VH	 0.9020	 0.6670
WD	 0.8370	 0.6410
XE	 0.5350	 0.5690
Y	 0.7750	 0.5720
YW	 0.8920	 0.6730
Z2	 0.9260	 0.6590
aA	 0.8840	 0.6670
bk	 0.8840	 0.6610
dh	 0.9800	 0.6950
ep	 0.9240	 0.6580
fJ	 0.2000	 0.5460
iN	 0.7790	 0.6060