



## wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 08:44 PM UTC

PDB ID : 8RD8 / pdb\_00008rd8  
EMDB ID : EMD-19067  
Title : Cryo-EM structure of *P. urativorans* 70S ribosome in complex with hibernation factors Balon and RaiA (structure 1).  
Authors : Helena-Bueno, K.; Rybak, M.Y.; Gagnon, M.G.; Hill, C.H.; Melnikov, S.V.  
Deposited on : 2023-12-07  
Resolution : 2.62 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:

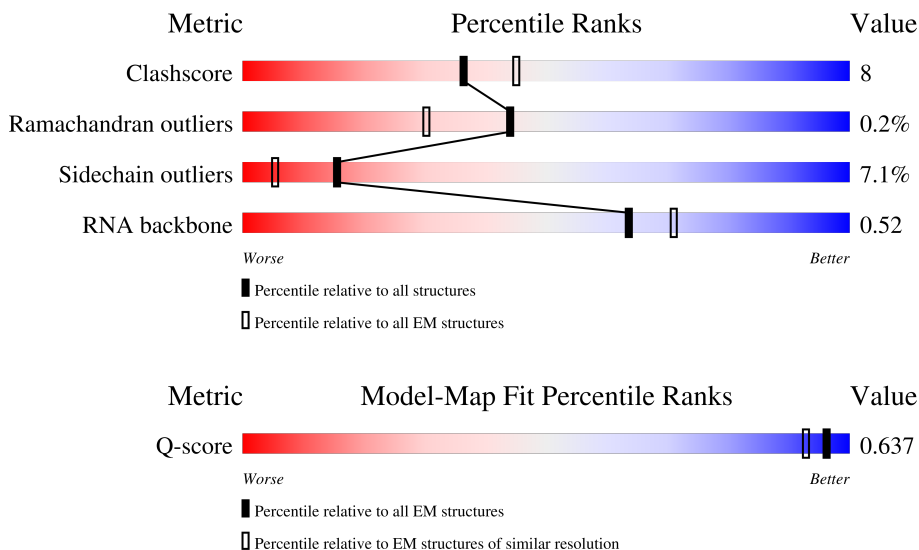
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins)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

# 1 Overall quality at a glance

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

The reported resolution of this entry is 2.62 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	8810 ( 2.12 - 3.12 )

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	C1	166	
5	Z2	2882	
6	R3	76	
7	A4	269	
8	E5	171	
9	L6	124	
10	F7	178	
11	D8	115	
12	E9	200	
13	aA	60	
14	MB	119	
15	UC	219	
16	WD	78	
17	XE	65	
18	RF	109	
19	FG	134	
20	VH	85	
21	TI	105	
22	fJ	93	
23	HK	101	
24	OL	88	
25	MM	118	
26	iN	1590	
27	PO	118	
28	SP	91	



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Mol	Chain	Length	Quality of chain
29	BQ	132	9% 75% 22% ..
30	GR	177	28% 71% 25% ..
31	GS	157	77% 70% 24% ..
32	CT	241	54% 55% 27% 15%
33	KU	129	29% 54% 29% 5% 12%
34	NV	71	41% 61% 17% 20%
35	YW	59	80% 14% 5%
36	IX	142	82% 16% .
37	JY	103	68% 52% 36% 8% .
38	QZ	91	20% 51% 34% 13%
39	Ba	44	70% 25% 5%
40	Qb	103	10% 72% 27% .
41	Nc	116	12% 83% 15% .
42	Kd	146	70% 28% ..
43	Je	122	72% 26% .
44	Af	212	76% 21% .
45	Lg	137	64% 34% .
46	dh	65	80% 18% .
47	Oi	130	63% 25% 12%
48	Pj	89	20% 72% 19% 9%
49	bk	51	75% 20% ..
50	Cl	274	74% 24% ..
51	Dm	213	47% 69% 29% .
52	Sn	116	6% 60% 15% 24%
53	To	88	25% 86% 11% .

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Mol	Chain	Length	Quality of chain
54	ep	38	 84% 16%
55	D	126	 30% 60% 21% 17%

## 2 Entry composition [i](#)

There are 56 unique types of molecules in this entry. The entry contains 141222 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	360	2812	1748	495	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	125	974	607	190	176	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	184	1404	876	251	269	8	0	0

- Molecule 4 is a protein called Large ribosomal subunit protein bL9.

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

- Molecule 5 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
5	Z2	2705	58043	25910	10660	18768	2705	0	0

- Molecule 6 is a protein called Small ribosomal subunit protein bS18.

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

- Molecule 7 is a protein called Small ribosomal subunit protein uS2.

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

- Molecule 8 is a protein called Small ribosomal subunit protein uS5.

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

- Molecule 9 is a protein called Small ribosomal subunit protein uS12.

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

- Molecule 10 is a protein called Large ribosomal subunit protein uL5.

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

- Molecule 11 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
11	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	-	variant	GB 930356181
D8	88	A	C	variant	GB 930356181

- Molecule 12 is a protein called Large ribosomal subunit protein uL4.

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

- Molecule 13 is a protein called Large ribosomal subunit protein bL32.

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

- Molecule 14 is a protein called Large ribosomal subunit protein bL17.

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

- Molecule 15 is a protein called Large ribosomal subunit protein bL25.

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

- Molecule 16 is a protein called Large ribosomal subunit protein bL28.

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

- Molecule 17 is a protein called Large ribosomal subunit protein uL29.

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

- Molecule 18 is a protein called Large ribosomal subunit protein uL22.

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

- Molecule 19 is a protein called Small ribosomal subunit protein bS6.

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

- Molecule 20 is a protein called Large ribosomal subunit protein bL27.

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

- Molecule 21 is a protein called Large ribosomal subunit protein uL24.

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

- Molecule 22 is a protein called Large ribosomal subunit protein bL31B.

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

- Molecule 23 is a protein called Small ribosomal subunit protein uS14.

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

- Molecule 24 is a protein called Small ribosomal subunit protein uS15.

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

- Molecule 25 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	MM	110	858	528	172	155	3	0	0

- Molecule 26 is a RNA chain called 16S rRNA.

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

- Molecule 27 is a protein called Large ribosomal subunit protein bL20.

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

- Molecule 28 is a protein called Small ribosomal subunit protein uS19.

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

- Molecule 29 is a protein called Small ribosomal subunit protein uS8.

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

- Molecule 30 is a protein called Large ribosomal subunit protein uL6.

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

- Molecule 31 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	GS	152	1190	738	230	215	7	0	0

- Molecule 32 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	CT	204	1609	1011	301	290	7	0	0

- Molecule 33 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	KU	114	836	518	162	155	1	0	0

- Molecule 34 is a protein called Small ribosomal subunit protein bS21.

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

- Molecule 35 is a protein called Large ribosomal subunit protein uL30.

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

- Molecule 36 is a protein called Large ribosomal subunit protein uL13.

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

- Molecule 37 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	JY	99	Total	C	N	O	S	0	0
			784	487	149	145	3		

- Molecule 38 is a protein called Small ribosomal subunit protein uS17.

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

- Molecule 39 is a protein called Large ribosomal subunit protein bL34.

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

- Molecule 40 is a protein called Large ribosomal subunit protein bL21.

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

- Molecule 41 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 42 is a protein called Large ribosomal subunit protein uL15.

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

- Molecule 43 is a protein called Large ribosomal subunit protein uL14.

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

- Molecule 44 is a protein called Large ribosomal subunit protein uL3.

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

- Molecule 45 is a protein called Large ribosomal subunit protein uL16.

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

- Molecule 46 is a protein called Large ribosomal subunit protein bL35.

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

- Molecule 47 is a protein called Large ribosomal subunit protein bL19.

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

- Molecule 48 is a protein called Small ribosomal subunit protein bS16.

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

- Molecule 49 is a protein called Large ribosomal subunit protein bL33.

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

- Molecule 50 is a protein called Large ribosomal subunit protein uL2.

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

- Molecule 51 is a protein called Small ribosomal subunit protein uS4.

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

- Molecule 52 is a protein called Large ribosomal subunit protein uL23.

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

- Molecule 53 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	To	86	Total	C	N	O	S	0	0
			675	410	144	119	2		

- Molecule 54 is a protein called Large ribosomal subunit protein bL36.

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

- Molecule 55 is a protein called 30S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	D	105	830	509	155	160	6	0	0

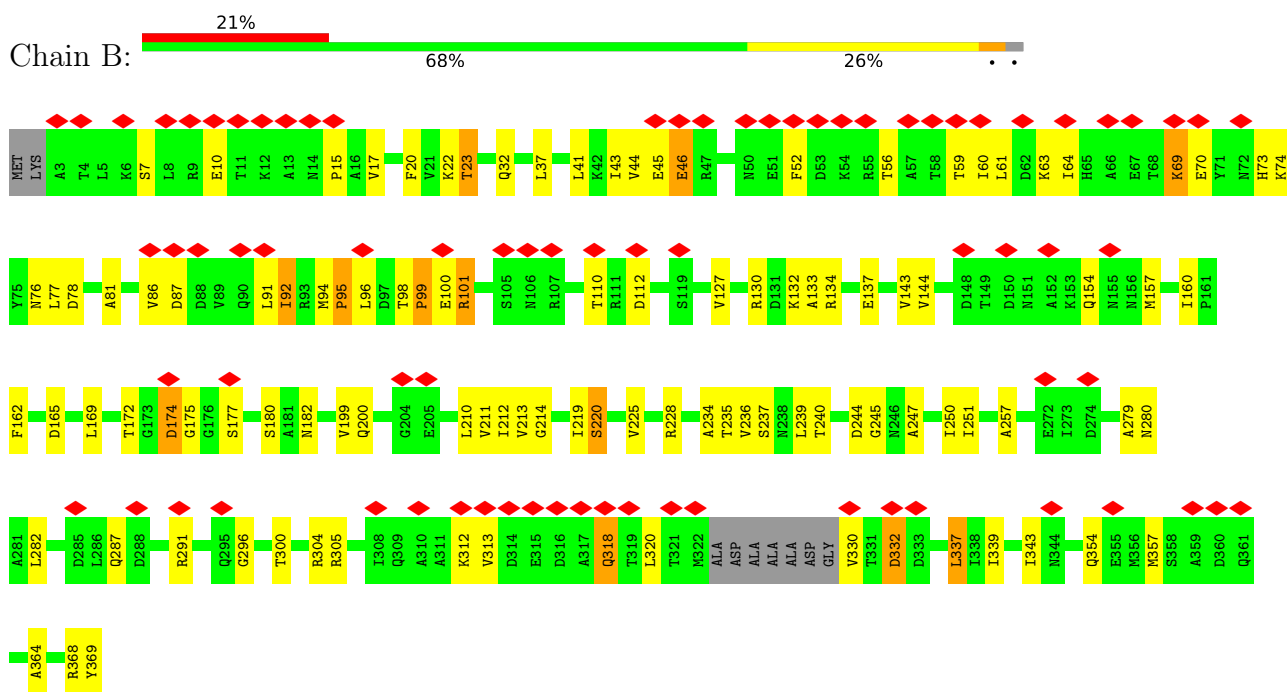
- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
56	Z2	2	2	2	0

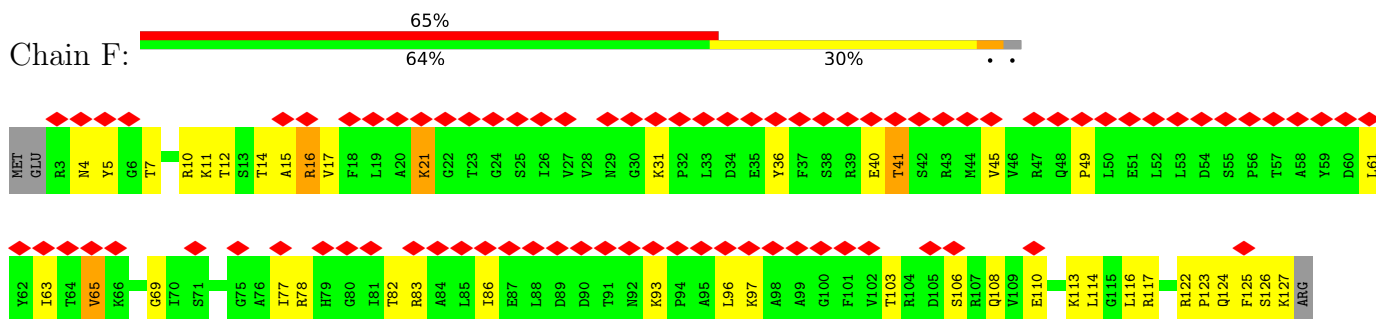
### 3 Residue-property plots [i](#)

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.

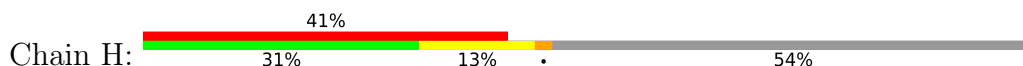
- Molecule 1: Methyl-accepting chemotaxis protein



- Molecule 2: Small ribosomal subunit protein uS9

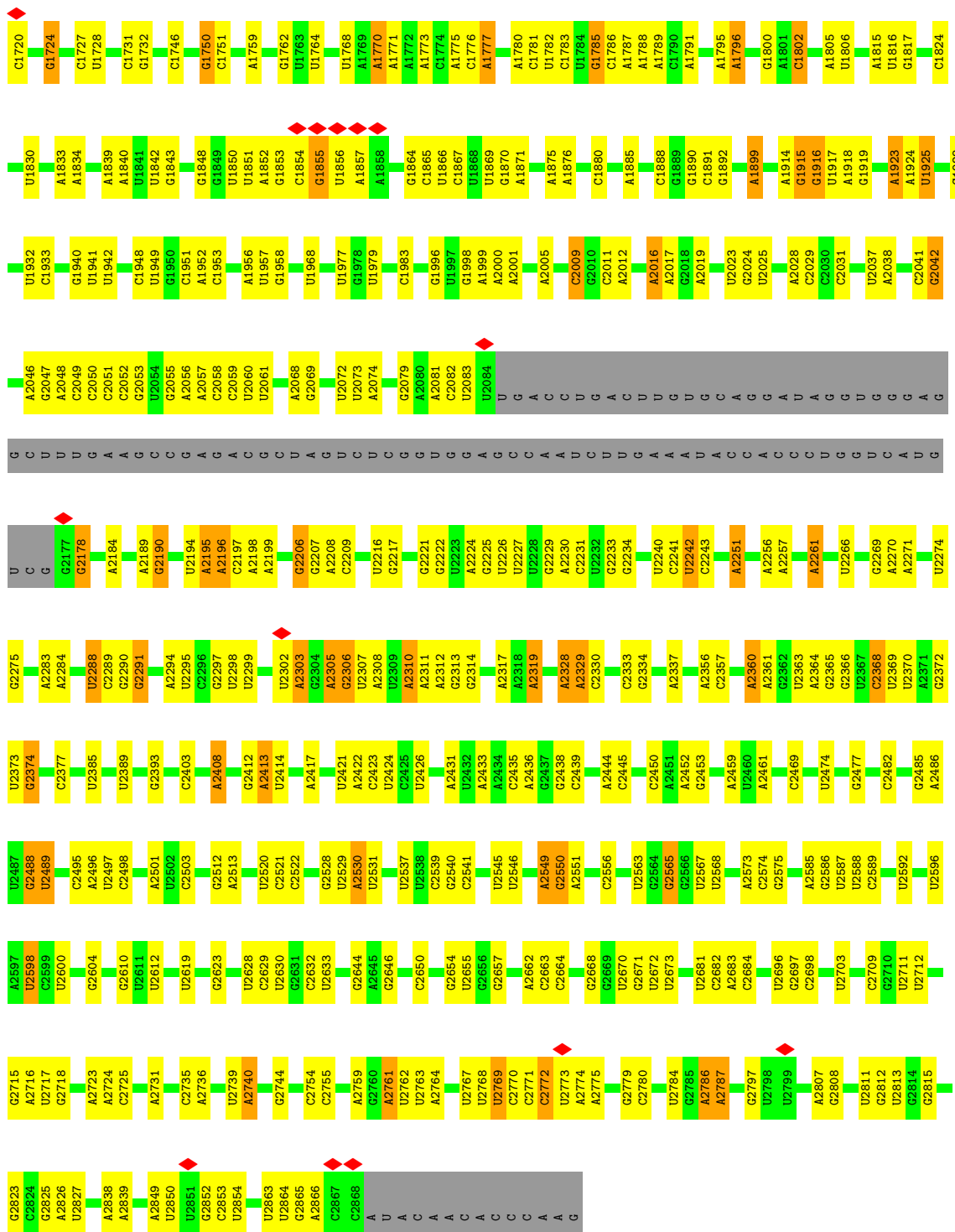


- Molecule 3: Elongation factor Tu

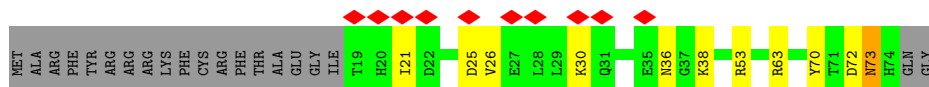




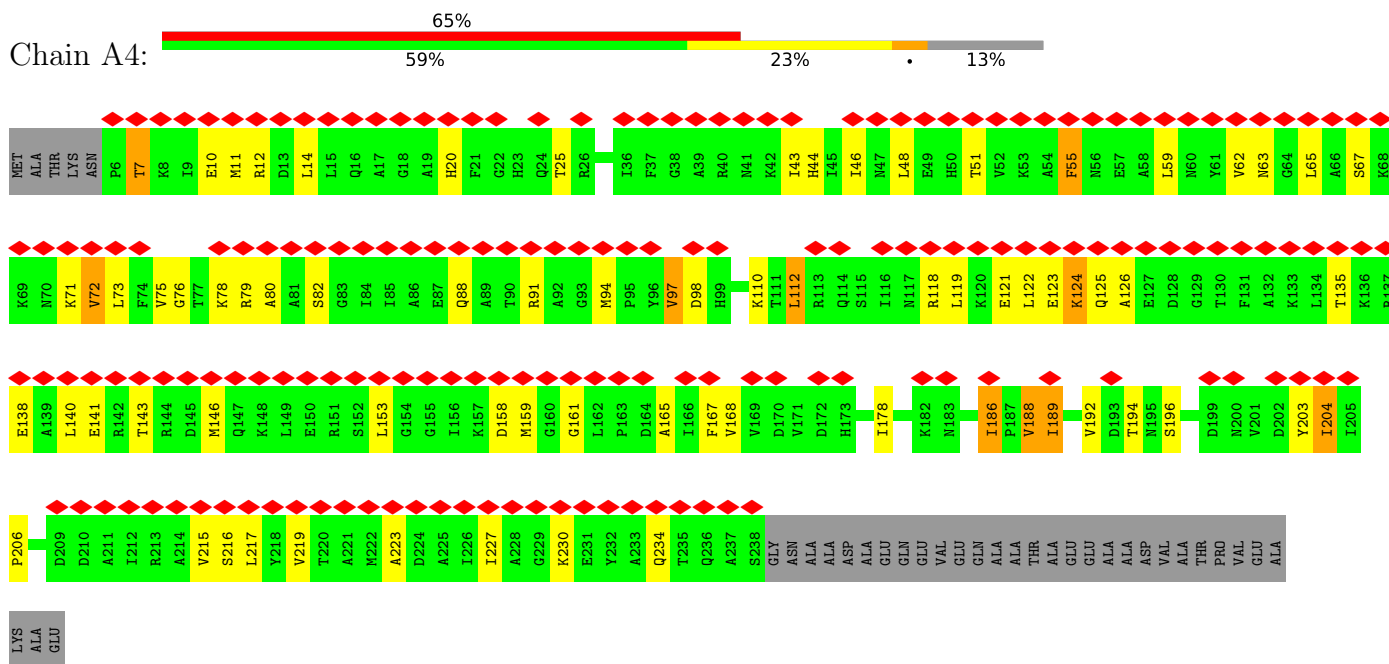




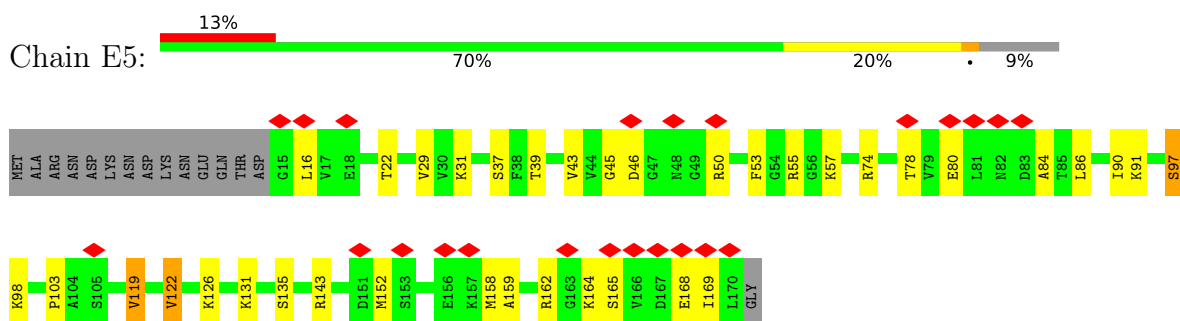
• Molecule 6: Small ribosomal subunit protein bS18



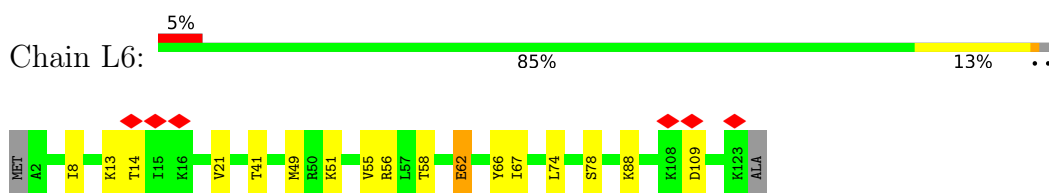
• Molecule 7: Small ribosomal subunit protein uS2



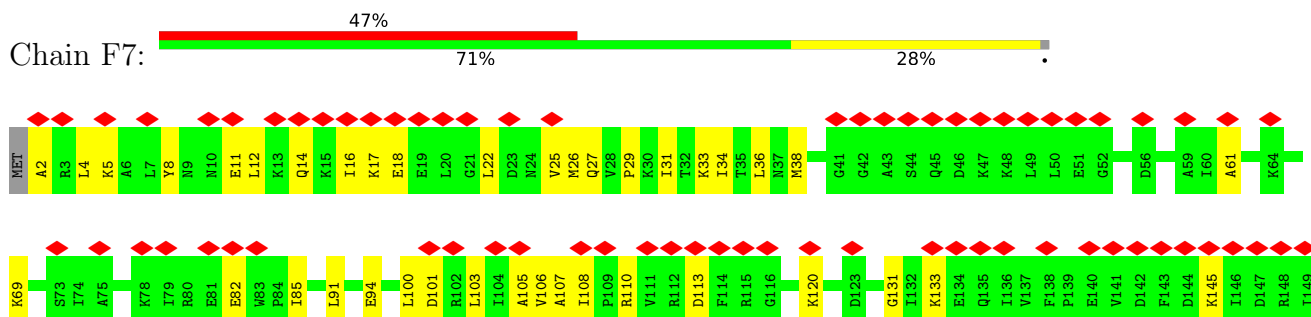
• Molecule 8: Small ribosomal subunit protein uS5



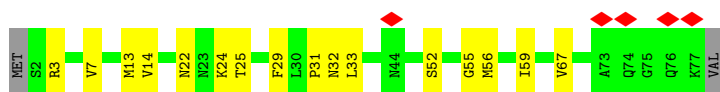
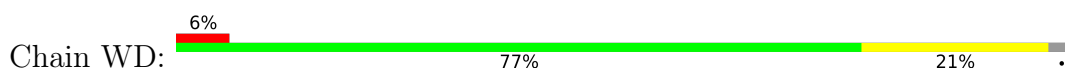
• Molecule 9: Small ribosomal subunit protein uS12



• Molecule 10: Large ribosomal subunit protein uL5



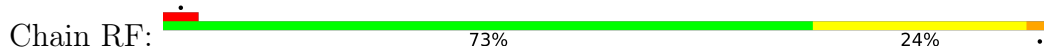




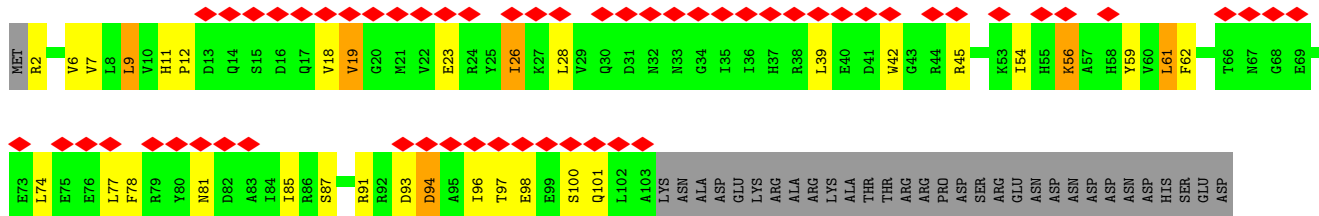
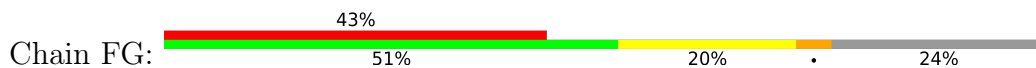
- Molecule 17: Large ribosomal subunit protein uL29



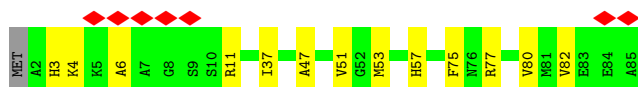
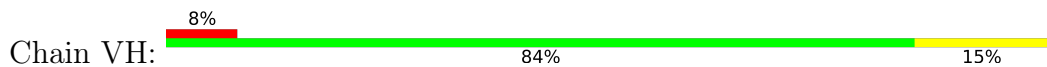
- Molecule 18: Large ribosomal subunit protein uL22



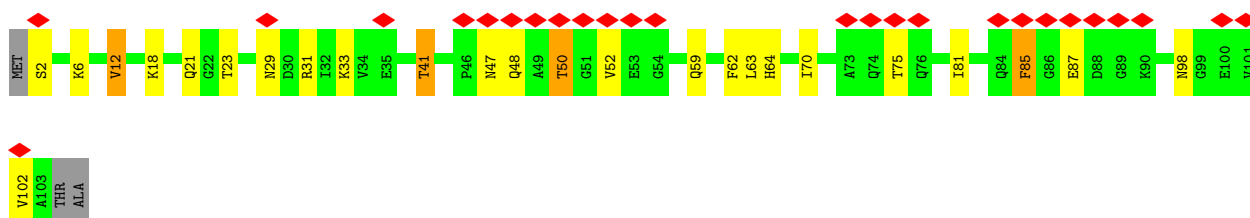
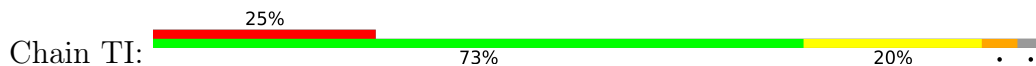
- Molecule 19: Small ribosomal subunit protein bS6



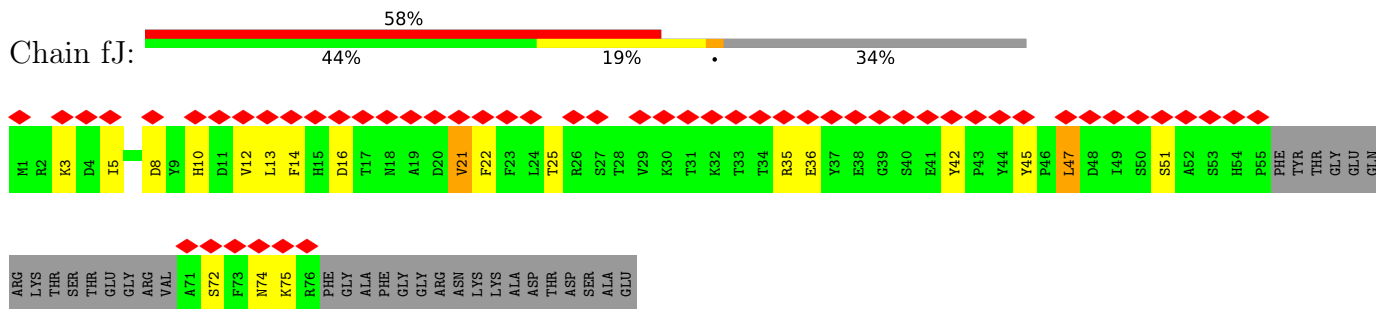
- Molecule 20: Large ribosomal subunit protein bL27



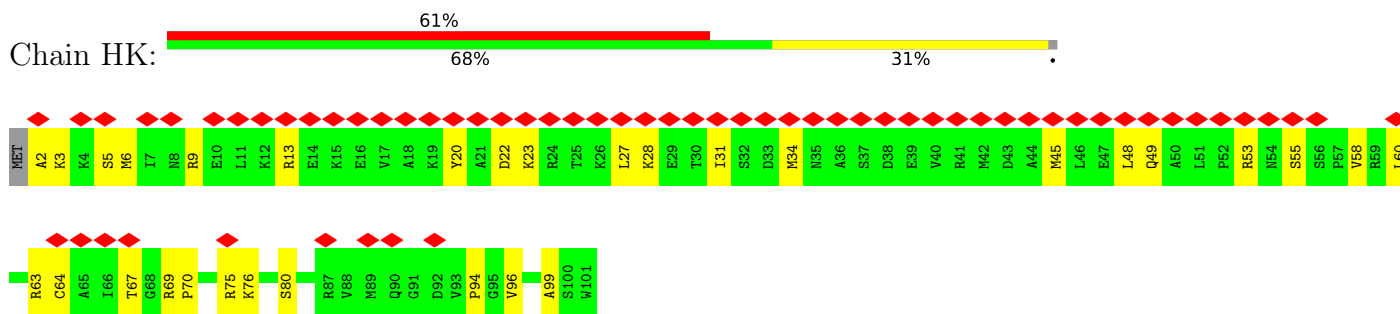
- Molecule 21: Large ribosomal subunit protein uL24



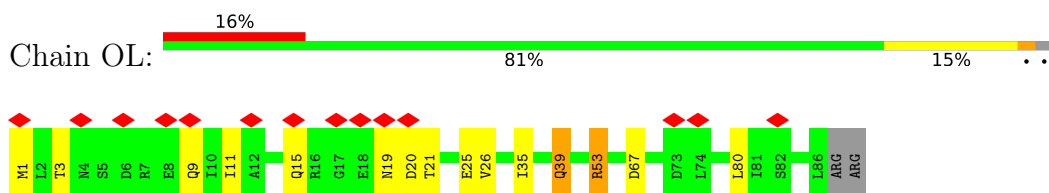
• Molecule 22: Large ribosomal subunit protein bL31B



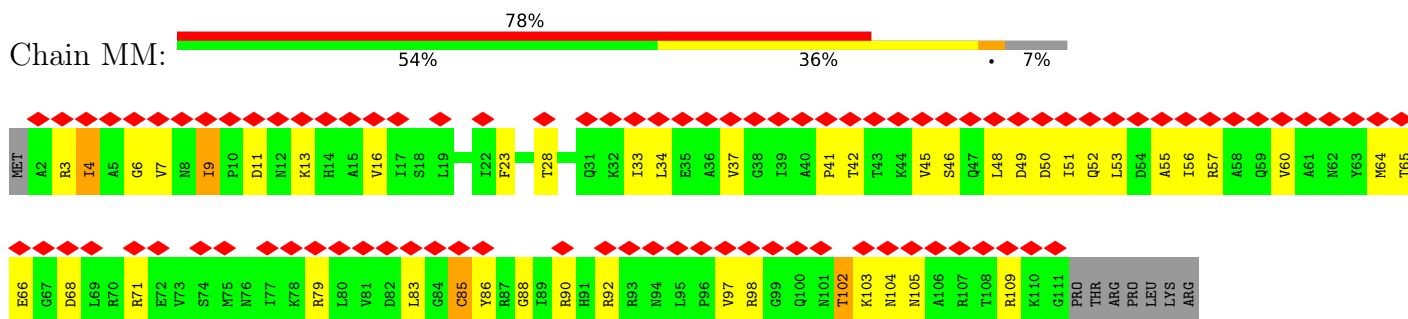
• Molecule 23: Small ribosomal subunit protein uS14



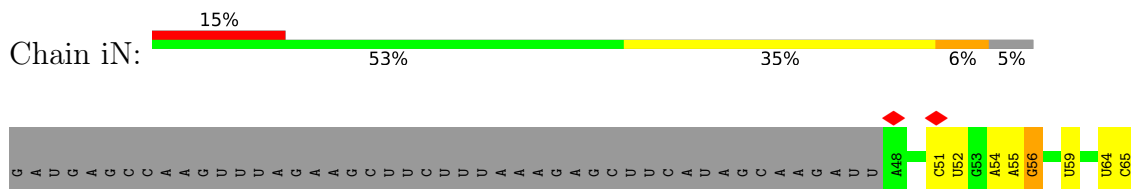
• Molecule 24: Small ribosomal subunit protein uS15

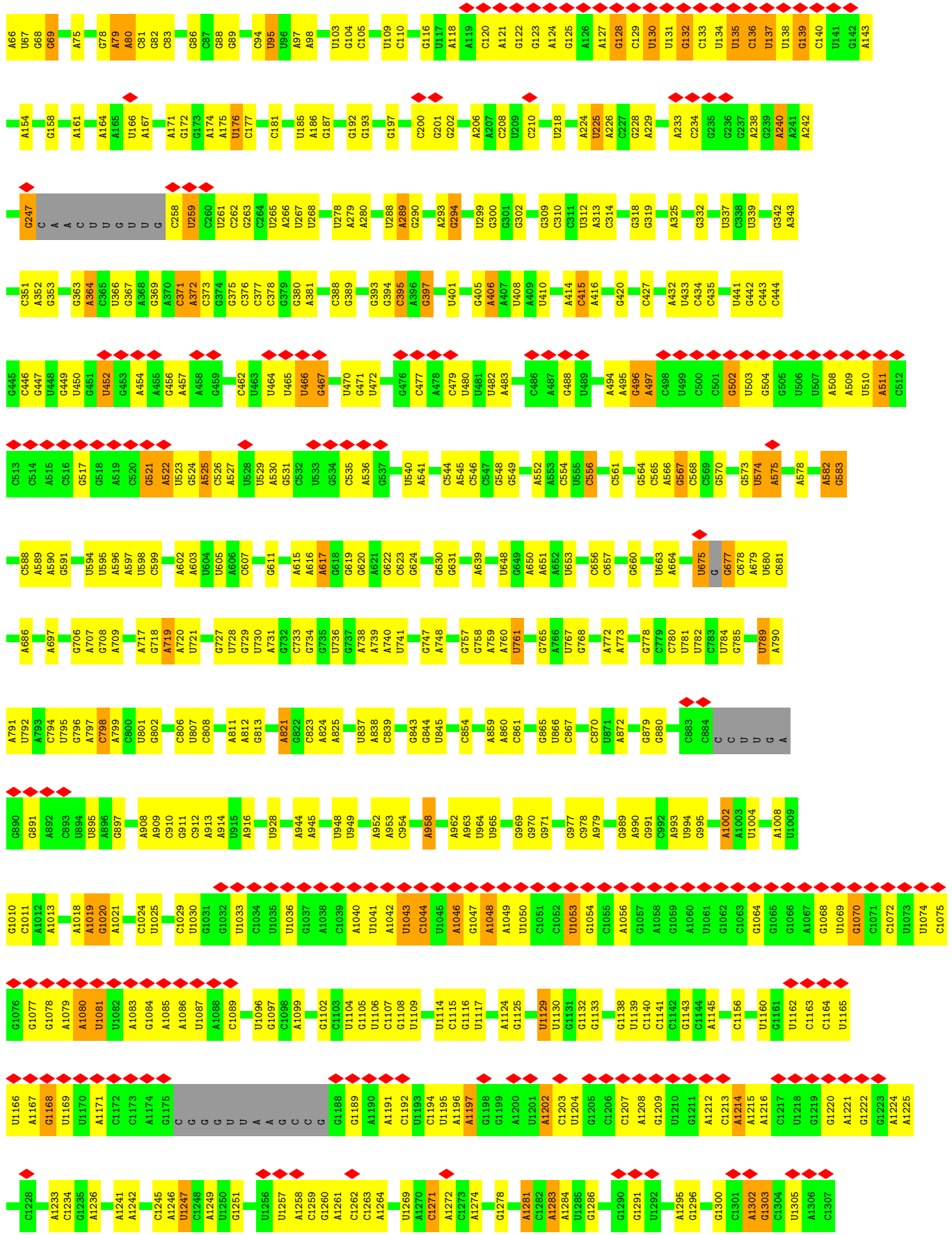


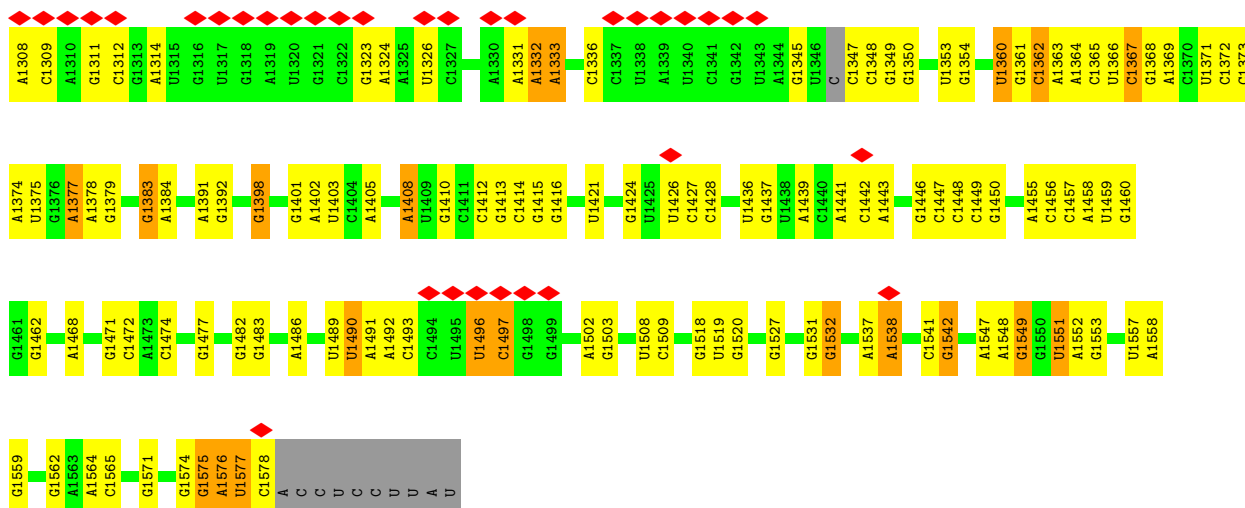
• Molecule 25: Small ribosomal subunit protein uS13



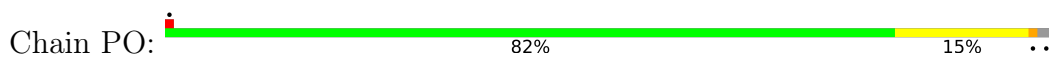
• Molecule 26: 16S rRNA



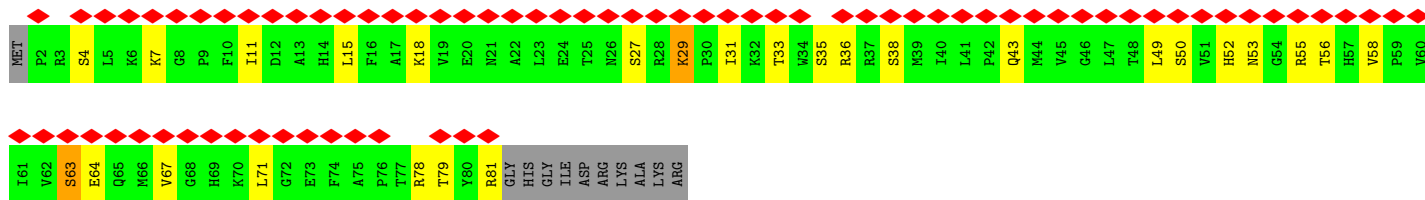
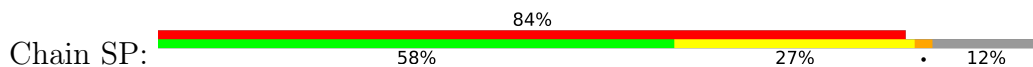




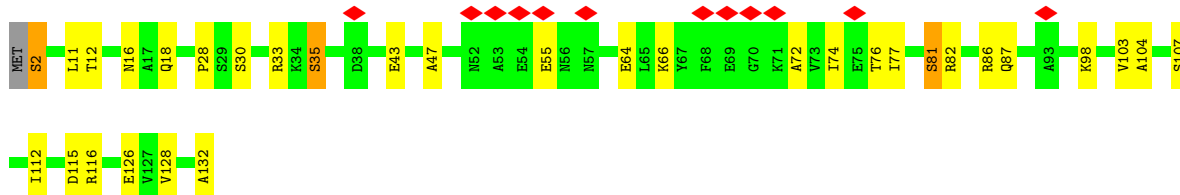
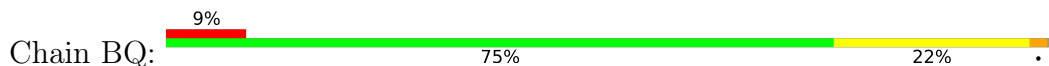
- Molecule 27: Large ribosomal subunit protein bL20



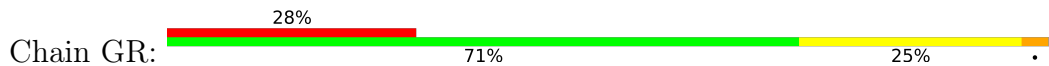
- Molecule 28: Small ribosomal subunit protein uS19

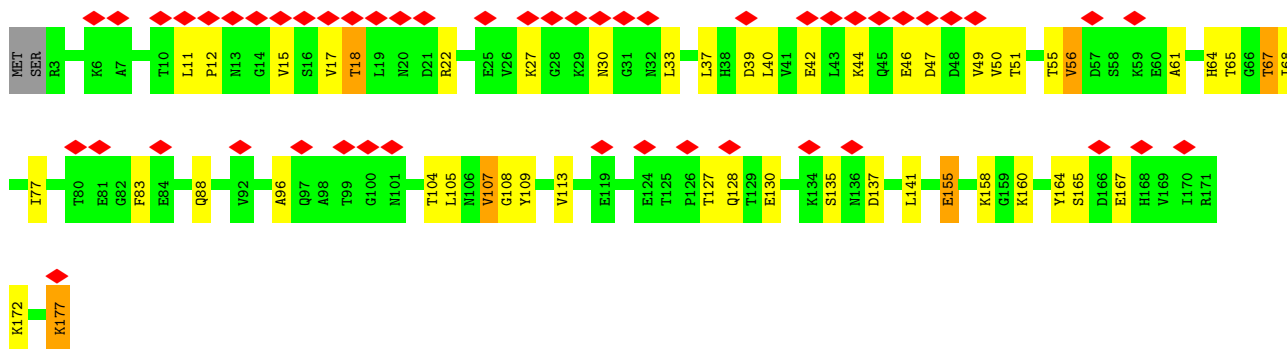


- Molecule 29: Small ribosomal subunit protein uS8

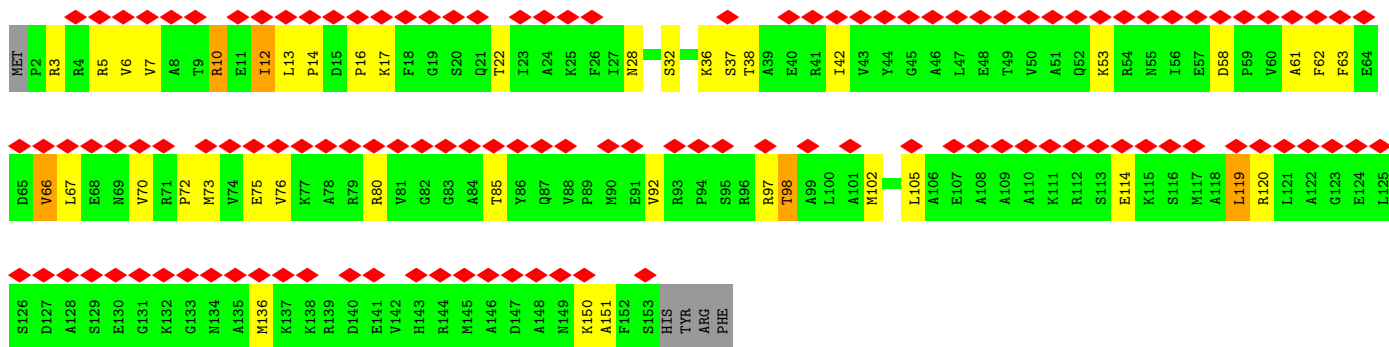
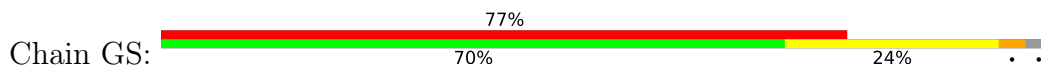


- Molecule 30: Large ribosomal subunit protein uL6

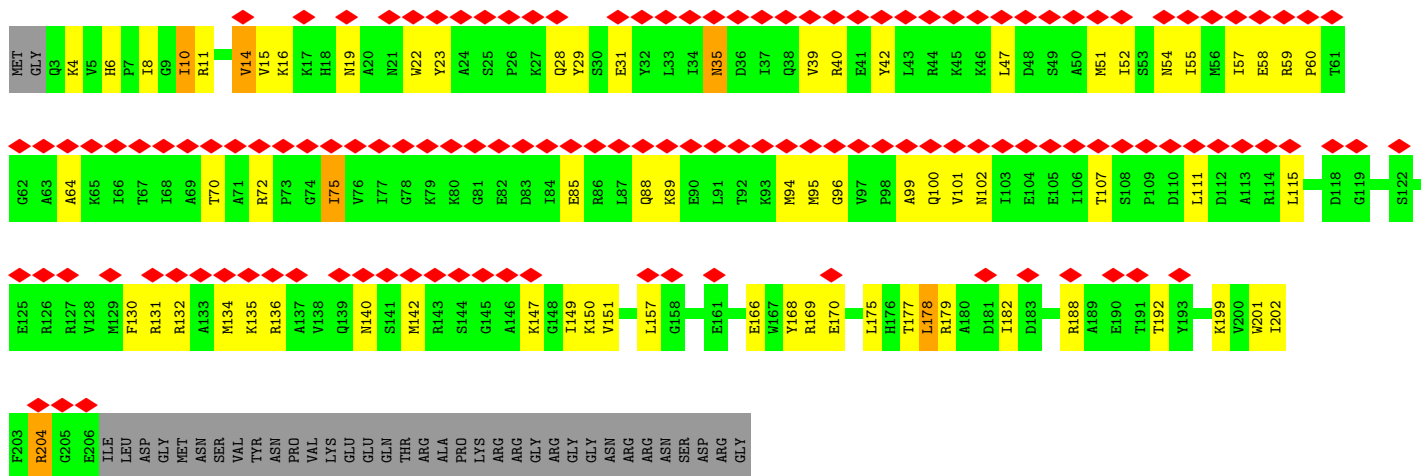




• Molecule 31: Small ribosomal subunit protein uS7

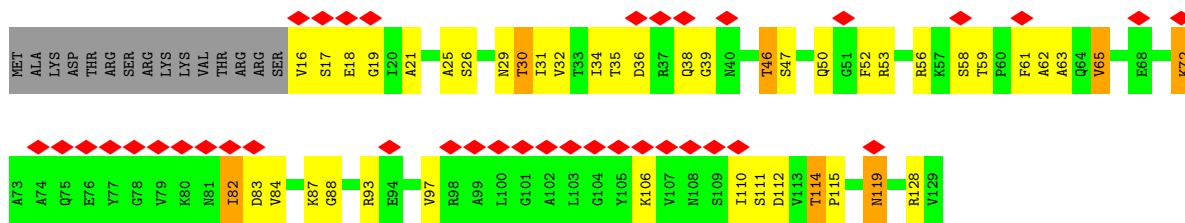


• Molecule 32: Small ribosomal subunit protein uS3

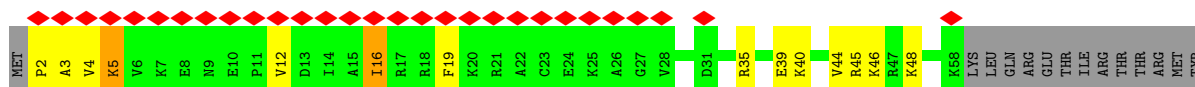
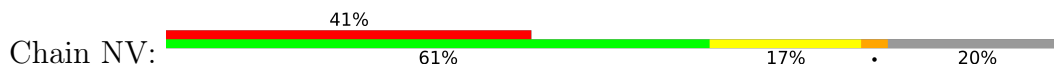


• Molecule 33: Small ribosomal subunit protein uS11

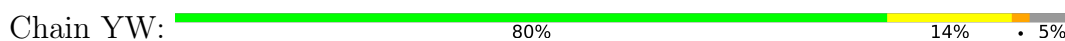




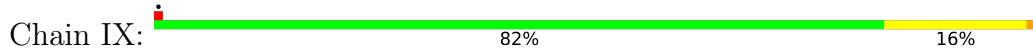
• Molecule 34: Small ribosomal subunit protein bS21



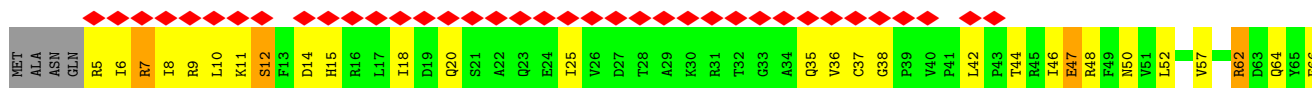
• Molecule 35: Large ribosomal subunit protein uL30



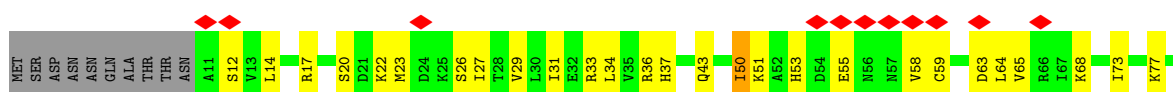
• Molecule 36: Large ribosomal subunit protein uL13



• Molecule 37: Small ribosomal subunit protein uS10



• Molecule 38: Small ribosomal subunit protein uS17

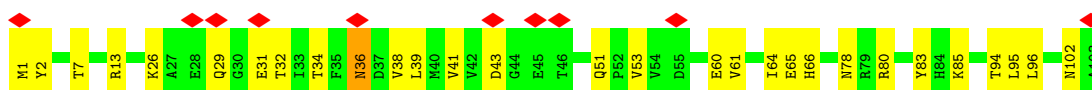
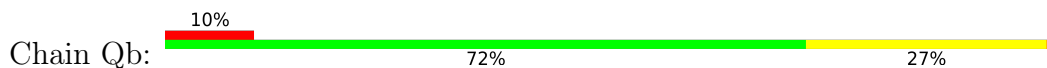




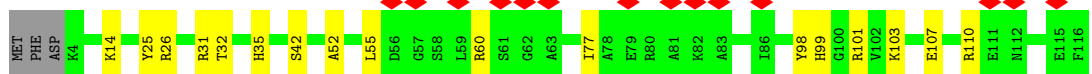
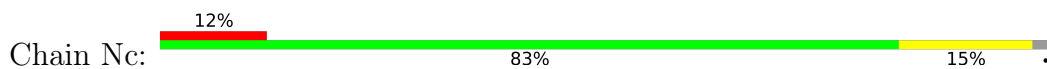
• Molecule 39: Large ribosomal subunit protein bL34



• Molecule 40: Large ribosomal subunit protein bL21



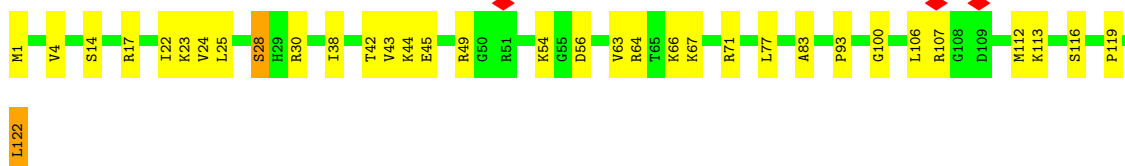
• Molecule 41: Large ribosomal subunit protein uL18



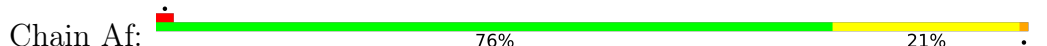
• Molecule 42: Large ribosomal subunit protein uL15

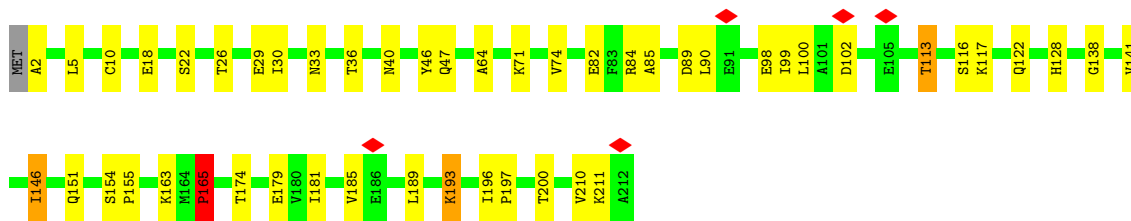


• Molecule 43: Large ribosomal subunit protein uL14

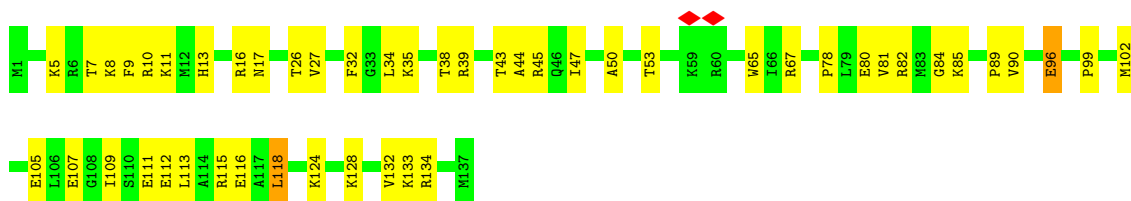


• Molecule 44: Large ribosomal subunit protein uL3

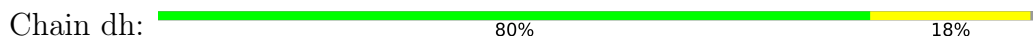




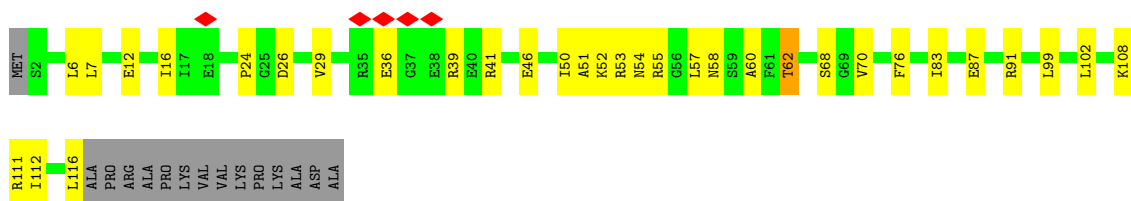
• Molecule 45: Large ribosomal subunit protein uL16



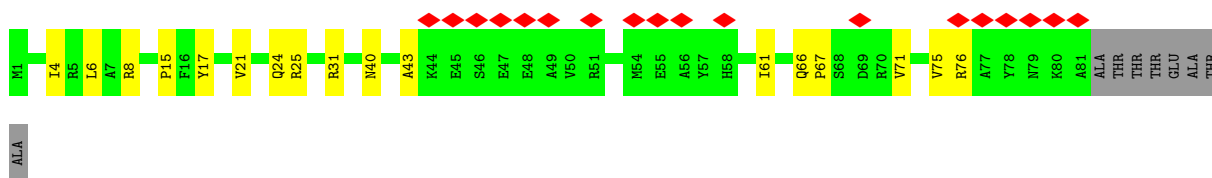
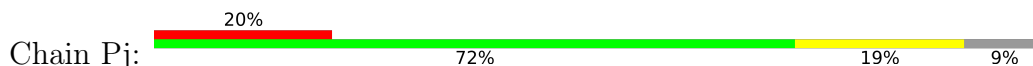
• Molecule 46: Large ribosomal subunit protein bL35



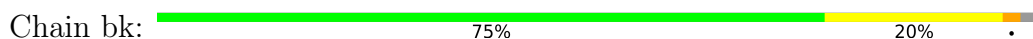
• Molecule 47: Large ribosomal subunit protein bL19

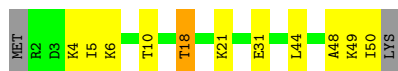


• Molecule 48: Small ribosomal subunit protein bS16

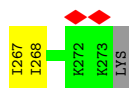
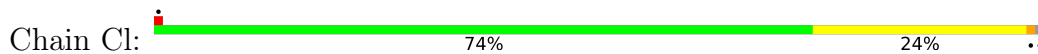


• Molecule 49: Large ribosomal subunit protein bL33

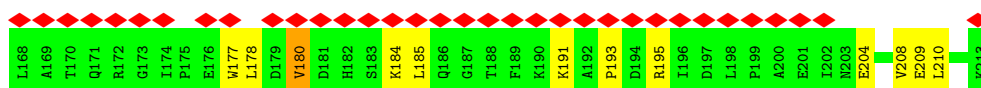
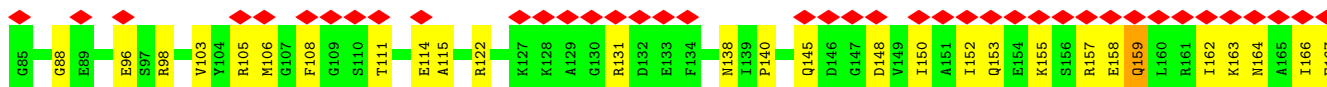
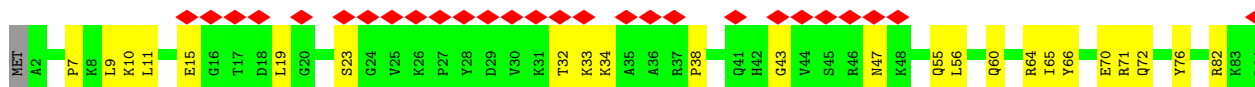
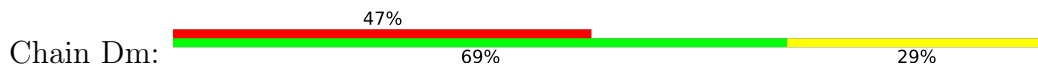




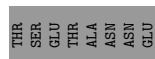
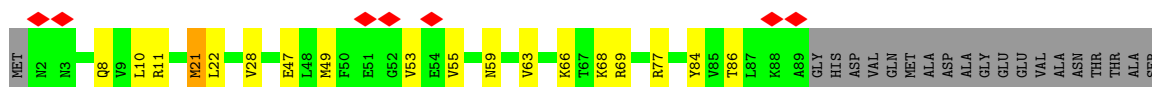
• Molecule 50: Large ribosomal subunit protein uL2



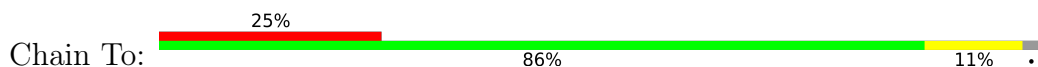
• Molecule 51: Small ribosomal subunit protein uS4



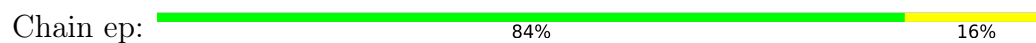
• Molecule 52: Large ribosomal subunit protein uL23



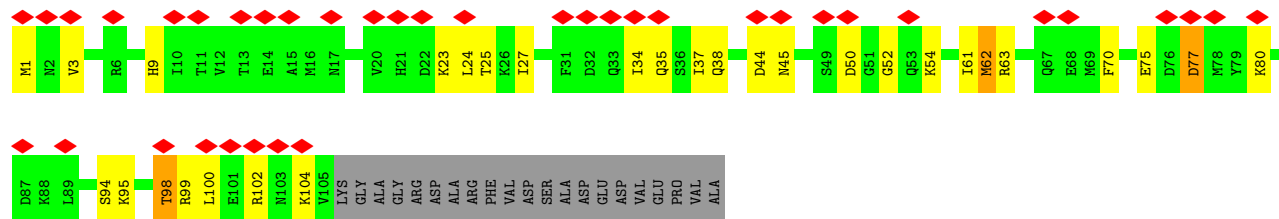
• Molecule 53: Small ribosomal subunit protein bS20



- Molecule 54: Large ribosomal subunit protein bL36



- Molecule 55: 30S ribosomal protein S30



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	53372	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	0.211	Depositor
Minimum map value	-0.099	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.0198	Depositor
Map size (Å)	390.41998, 390.41998, 390.41998	wwPDB
Map dimensions	540, 540, 540	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.723, 0.723, 0.723	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: 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	B	0.27	0/2853	0.50	2/3869 (0.1%)
2	F	0.19	0/987	0.37	0/1322
3	H	0.17	0/1424	0.39	0/1918
4	C1	0.24	0/379	0.38	0/511
5	Z2	0.47	0/65009	0.42	0/101385
6	R3	0.24	0/465	0.34	0/629
7	A4	0.17	0/1848	0.34	0/2494
8	E5	0.25	0/1163	0.37	0/1564
9	L6	0.27	0/959	0.40	0/1282
10	F7	0.21	0/1383	0.39	0/1858
11	D8	0.33	0/2733	0.31	0/4256
12	E9	0.32	0/1559	0.43	0/2103
13	aA	0.36	0/450	0.40	0/596
14	MB	0.36	0/961	0.48	0/1282
15	UC	0.29	0/774	0.40	0/1043
16	WD	0.34	0/628	0.44	0/841
17	XE	0.22	0/503	0.34	0/670
18	RF	0.34	0/840	0.44	0/1125
19	FG	0.18	0/864	0.34	0/1169
20	VH	0.38	0/635	0.46	0/847
21	TI	0.25	0/790	0.37	0/1057
22	fJ	0.15	0/508	0.32	0/690
23	HK	0.18	0/821	0.31	0/1091
24	OL	0.24	0/702	0.37	0/941
25	MM	0.16	0/866	0.35	0/1166
26	iN	0.29	0/36108	0.32	0/56315
27	PO	0.38	0/947	0.45	0/1261
28	SP	0.17	0/652	0.34	0/879
29	BQ	0.24	0/982	0.33	0/1318
30	GR	0.25	0/1377	0.39	0/1861
31	GS	0.19	0/1208	0.38	0/1619
32	CT	0.19	0/1633	0.39	0/2195

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	KU	0.21	0/851	0.37	0/1150
34	NV	0.19	0/478	0.34	0/632
35	YW	0.33	0/442	0.44	0/590
36	IX	0.37	0/1134	0.42	0/1529
37	JY	0.22	0/794	0.47	0/1072
38	QZ	0.24	0/638	0.41	0/858
39	Ba	0.42	0/373	0.52	0/489
40	Qb	0.32	0/839	0.43	0/1127
41	Nc	0.30	0/863	0.41	0/1158
42	Kd	0.36	0/1073	0.45	0/1429
43	Je	0.35	0/946	0.45	0/1271
44	Af	0.42	0/1566	0.58	2/2103 (0.1%)
45	Lg	0.37	0/1112	0.45	0/1483
46	dh	0.42	0/524	0.50	0/686
47	Oi	0.34	0/927	0.43	0/1239
48	Pj	0.26	0/660	0.41	0/887
49	bk	0.36	0/401	0.49	0/534
50	Cl	0.37	0/2147	0.47	0/2883
51	Dm	0.21	0/1712	0.44	0/2296
52	Sn	0.34	0/705	0.47	0/939
53	To	0.25	0/679	0.43	0/904
54	ep	0.39	0/300	0.52	0/395
55	D	0.21	0/838	0.42	0/1121
All	All	0.38	0/153013	0.39	4/227932 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	99	PRO	CA-N-CD	-10.93	96.69	112.00
44	Af	165	PRO	N-CD-CG	-8.00	91.21	103.20
44	Af	165	PRO	CA-CB-CG	-6.74	91.70	104.50
1	B	99	PRO	N-CD-CG	-5.14	95.49	103.20

There are no chirality outliers.

There are no planarity outliers.

## 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	2812	0	2754	68	0
2	F	974	0	1022	31	0
3	H	1404	0	1411	34	0
4	C1	374	0	406	10	0
5	Z2	58043	0	29179	550	0
6	R3	457	0	466	7	0
7	A4	1816	0	1843	47	0
8	E5	1151	0	1205	23	0
9	L6	946	0	1008	12	0
10	F7	1362	0	1402	38	0
11	D8	2446	0	1241	20	0
12	E9	1537	0	1590	29	0
13	aA	442	0	432	7	0
14	MB	947	0	988	9	0
15	UC	760	0	774	13	0
16	WD	618	0	637	11	0
17	XE	502	0	527	14	0
18	RF	834	0	898	22	0
19	FG	849	0	838	15	0
20	VH	626	0	629	12	0
21	TI	784	0	820	9	0
22	fJ	493	0	441	10	0
23	HK	811	0	845	28	0
24	OL	694	0	710	8	0
25	MM	858	0	897	34	0
26	iN	32246	0	16224	368	0
27	PO	935	0	999	14	0
28	SP	637	0	665	16	0
29	BQ	974	0	1009	22	0
30	GR	1357	0	1397	29	0
31	GS	1190	0	1224	26	0
32	CT	1609	0	1674	46	0
33	KU	836	0	845	33	0
34	NV	472	0	520	11	0
35	YW	438	0	476	7	0
36	IX	1108	0	1145	19	0
37	JY	784	0	813	38	0
38	QZ	632	0	676	23	0
39	Ba	369	0	418	10	0
40	Qb	827	0	862	15	0
41	Nc	852	0	880	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	Kd	1062	0	1123	30	0
43	Je	937	0	1003	24	0
44	Af	1548	0	1574	31	0
45	Lg	1093	0	1188	34	0
46	dh	519	0	581	8	0
47	Oi	917	0	969	20	0
48	Pj	648	0	661	11	0
49	bk	394	0	412	6	0
50	Cl	2107	0	2195	53	0
51	Dm	1688	0	1745	45	0
52	Sn	698	0	750	14	0
53	To	675	0	716	8	0
54	ep	298	0	334	4	0
55	D	830	0	838	16	0
56	Z2	2	0	0	0	0
All	All	141222	0	96879	1796	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 1796 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)
26:iN:675:U:H3'	26:iN:677:G:P	1.37	1.63
26:iN:675:U:C3'	26:iN:677:G:P	2.34	1.16
50:Cl:40:THR:HG23	50:Cl:42:GLY:H	1.30	0.96
26:iN:867:C:HO2'	29:BQ:2:SER:N	1.73	0.87
26:iN:1490:U:H3	26:iN:1502:A:H61	1.22	0.87

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	
1	B	356/369 (96%)	330 (93%)	24 (7%)	2 (1%)	21	39
2	F	123/128 (96%)	117 (95%)	5 (4%)	1 (1%)	16	31
3	H	182/396 (46%)	173 (95%)	7 (4%)	2 (1%)	11	23
4	C1	47/166 (28%)	46 (98%)	1 (2%)	0	100	100
6	R3	54/76 (71%)	54 (100%)	0	0	100	100
7	A4	231/269 (86%)	221 (96%)	10 (4%)	0	100	100
8	E5	154/171 (90%)	145 (94%)	9 (6%)	0	100	100
9	L6	120/124 (97%)	113 (94%)	7 (6%)	0	100	100
10	F7	175/178 (98%)	165 (94%)	10 (6%)	0	100	100
12	E9	197/200 (98%)	192 (98%)	5 (2%)	0	100	100
13	aA	51/60 (85%)	50 (98%)	1 (2%)	0	100	100
14	MB	117/119 (98%)	112 (96%)	4 (3%)	1 (1%)	14	28
15	UC	95/219 (43%)	91 (96%)	4 (4%)	0	100	100
16	WD	74/78 (95%)	72 (97%)	2 (3%)	0	100	100
17	XE	60/65 (92%)	60 (100%)	0	0	100	100
18	RF	107/109 (98%)	104 (97%)	3 (3%)	0	100	100
19	FG	100/134 (75%)	98 (98%)	2 (2%)	0	100	100
20	VH	82/85 (96%)	75 (92%)	7 (8%)	0	100	100
21	TI	100/105 (95%)	97 (97%)	3 (3%)	0	100	100
22	fJ	57/93 (61%)	55 (96%)	2 (4%)	0	100	100
23	HK	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
24	OL	84/88 (96%)	81 (96%)	3 (4%)	0	100	100
25	MM	108/118 (92%)	98 (91%)	9 (8%)	1 (1%)	14	28
27	PO	114/118 (97%)	113 (99%)	1 (1%)	0	100	100
28	SP	78/91 (86%)	76 (97%)	2 (3%)	0	100	100
29	BQ	129/132 (98%)	128 (99%)	1 (1%)	0	100	100
30	GR	173/177 (98%)	162 (94%)	11 (6%)	0	100	100
31	GS	150/157 (96%)	140 (93%)	8 (5%)	2 (1%)	9	19
32	CT	202/241 (84%)	187 (93%)	15 (7%)	0	100	100
33	KU	112/129 (87%)	108 (96%)	4 (4%)	0	100	100
34	NV	55/71 (78%)	54 (98%)	1 (2%)	0	100	100
35	YW	54/59 (92%)	54 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	IX	140/142 (99%)	134 (96%)	6 (4%)	0	100	100
37	JY	97/103 (94%)	88 (91%)	9 (9%)	0	100	100
38	QZ	77/91 (85%)	72 (94%)	5 (6%)	0	100	100
39	Ba	42/44 (96%)	41 (98%)	1 (2%)	0	100	100
40	Qb	101/103 (98%)	100 (99%)	1 (1%)	0	100	100
41	Nc	111/116 (96%)	110 (99%)	1 (1%)	0	100	100
42	Kd	143/146 (98%)	135 (94%)	8 (6%)	0	100	100
43	Je	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
44	Af	209/212 (99%)	196 (94%)	12 (6%)	1 (0%)	24	44
45	Lg	135/137 (98%)	130 (96%)	5 (4%)	0	100	100
46	dh	62/65 (95%)	60 (97%)	2 (3%)	0	100	100
47	Oi	113/130 (87%)	107 (95%)	6 (5%)	0	100	100
48	Pj	79/89 (89%)	78 (99%)	1 (1%)	0	100	100
49	bk	47/51 (92%)	47 (100%)	0	0	100	100
50	Cl	270/274 (98%)	260 (96%)	10 (4%)	0	100	100
51	Dm	210/213 (99%)	200 (95%)	10 (5%)	0	100	100
52	Sn	86/116 (74%)	86 (100%)	0	0	100	100
53	To	84/88 (96%)	83 (99%)	1 (1%)	0	100	100
54	ep	36/38 (95%)	36 (100%)	0	0	100	100
55	D	103/126 (82%)	100 (97%)	3 (3%)	0	100	100
All	All	6104/7032 (87%)	5848 (96%)	246 (4%)	10 (0%)	44	64

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	96	LEU
3	H	250	ILE
31	GS	17	LYS
2	F	11	LYS
3	H	301	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	302/310 (97%)	275 (91%)	27 (9%)	9	19
2	F	102/105 (97%)	92 (90%)	10 (10%)	7	15
3	H	151/327 (46%)	132 (87%)	19 (13%)	4	8
4	C1	39/135 (29%)	39 (100%)	0	100	100
6	R3	51/67 (76%)	49 (96%)	2 (4%)	28	53
7	A4	188/211 (89%)	165 (88%)	23 (12%)	5	9
8	E5	118/131 (90%)	108 (92%)	10 (8%)	10	21
9	L6	102/103 (99%)	98 (96%)	4 (4%)	28	53
10	F7	139/146 (95%)	137 (99%)	2 (1%)	59	80
12	E9	159/159 (100%)	148 (93%)	11 (7%)	14	30
13	aA	46/53 (87%)	44 (96%)	2 (4%)	26	49
14	MB	101/102 (99%)	97 (96%)	4 (4%)	28	53
15	UC	79/184 (43%)	78 (99%)	1 (1%)	61	81
16	WD	67/71 (94%)	64 (96%)	3 (4%)	24	48
17	XE	54/57 (95%)	48 (89%)	6 (11%)	6	11
18	RF	88/88 (100%)	83 (94%)	5 (6%)	18	38
19	FG	92/121 (76%)	76 (83%)	16 (17%)	2	3
20	VH	60/62 (97%)	60 (100%)	0	100	100
21	TI	83/85 (98%)	67 (81%)	16 (19%)	1	2
22	fJ	52/81 (64%)	42 (81%)	10 (19%)	1	2
23	HK	87/88 (99%)	87 (100%)	0	100	100
24	OL	75/77 (97%)	69 (92%)	6 (8%)	11	23
25	MM	91/99 (92%)	82 (90%)	9 (10%)	7	15
27	PO	88/90 (98%)	86 (98%)	2 (2%)	44	69
28	SP	71/79 (90%)	65 (92%)	6 (8%)	10	21
29	BQ	103/104 (99%)	96 (93%)	7 (7%)	14	30
30	GR	149/151 (99%)	136 (91%)	13 (9%)	9	20
31	GS	123/128 (96%)	111 (90%)	12 (10%)	7	15
32	CT	168/198 (85%)	151 (90%)	17 (10%)	7	14

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	KU	84/98 (86%)	71 (84%)	13 (16%)	2	4
34	NV	49/63 (78%)	47 (96%)	2 (4%)	27	52
35	YW	50/52 (96%)	49 (98%)	1 (2%)	48	73
36	IX	116/117 (99%)	111 (96%)	5 (4%)	26	49
37	JY	87/90 (97%)	75 (86%)	12 (14%)	3	6
38	QZ	73/84 (87%)	65 (89%)	8 (11%)	6	12
39	Ba	37/37 (100%)	33 (89%)	4 (11%)	6	12
40	Qb	89/89 (100%)	77 (86%)	12 (14%)	4	7
41	Nc	81/85 (95%)	81 (100%)	0	100	100
42	Kd	108/110 (98%)	102 (94%)	6 (6%)	19	39
43	Je	102/102 (100%)	97 (95%)	5 (5%)	22	44
44	Af	161/162 (99%)	148 (92%)	13 (8%)	11	23
45	Lg	114/114 (100%)	106 (93%)	8 (7%)	14	29
46	dh	55/56 (98%)	52 (94%)	3 (6%)	19	39
47	Oi	97/108 (90%)	93 (96%)	4 (4%)	27	52
48	Pj	63/68 (93%)	63 (100%)	0	100	100
49	bk	42/46 (91%)	40 (95%)	2 (5%)	23	45
50	Cl	219/221 (99%)	214 (98%)	5 (2%)	44	69
51	Dm	177/181 (98%)	174 (98%)	3 (2%)	53	76
52	Sn	76/97 (78%)	72 (95%)	4 (5%)	20	41
53	To	66/69 (96%)	65 (98%)	1 (2%)	57	79
54	ep	33/33 (100%)	33 (100%)	0	100	100
55	D	91/106 (86%)	83 (91%)	8 (9%)	9	19
All	All	5098/5800 (88%)	4736 (93%)	362 (7%)	15	29

5 of 362 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	CT	54	ASN
39	Ba	24	THR
32	CT	151	VAL
36	IX	45	THR
42	Kd	12	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 54 such sidechains are listed below:

Mol	Chain	Res	Type
30	GR	13	ASN
35	YW	51	ASN
52	Sn	20	GLN
30	GR	20	ASN
32	CT	6	HIS

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	D8	114/115 (99%)	12 (10%)	1 (0%)
26	iN	1499/1590 (94%)	266 (17%)	0
5	Z2	2698/2882 (93%)	390 (14%)	14 (0%)
All	All	4311/4587 (93%)	668 (15%)	15 (0%)

5 of 668 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	Z2	10	U
5	Z2	16	A
5	Z2	19	G
5	Z2	21	A
5	Z2	22	G

5 of 15 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	Z2	968	A
5	Z2	2739	U
5	Z2	1053	A
11	D8	13	A
5	Z2	2195	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](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

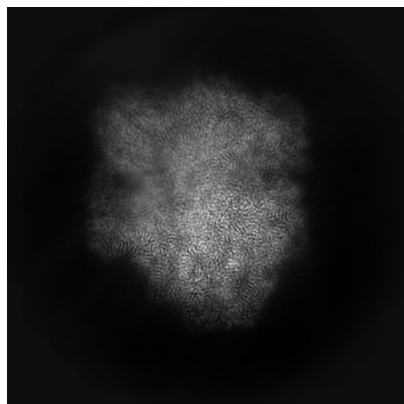
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-19067. These allow visual inspection of the internal detail of the map and identification of artifacts.

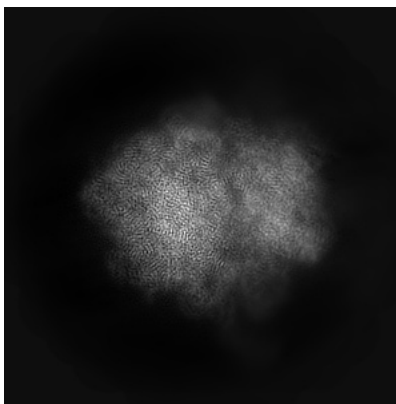
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

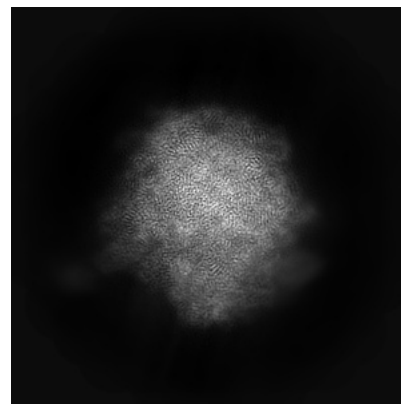
#### 6.1.1 Primary map



X

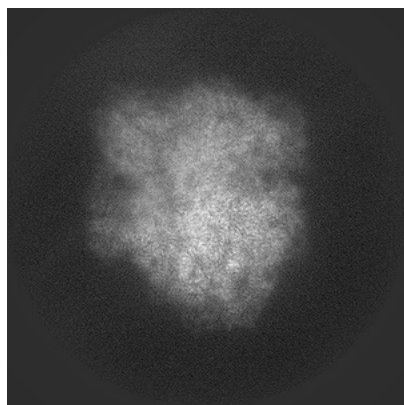


Y

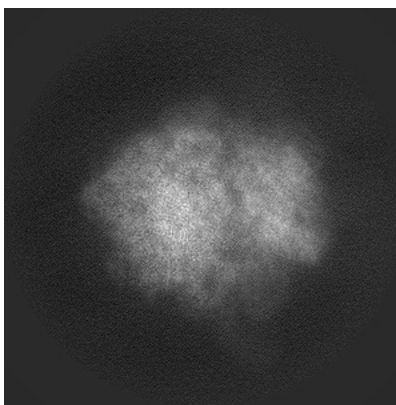


Z

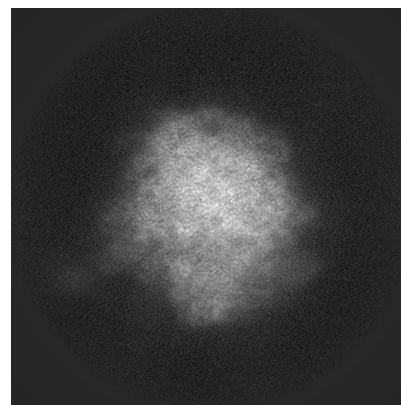
#### 6.1.2 Raw map



X



Y

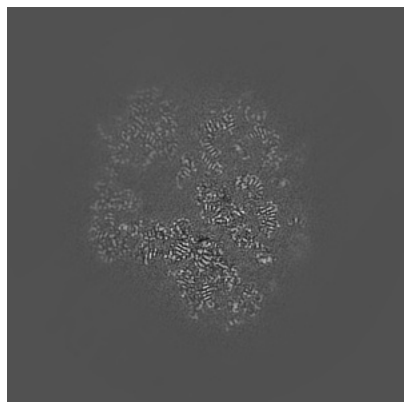


Z

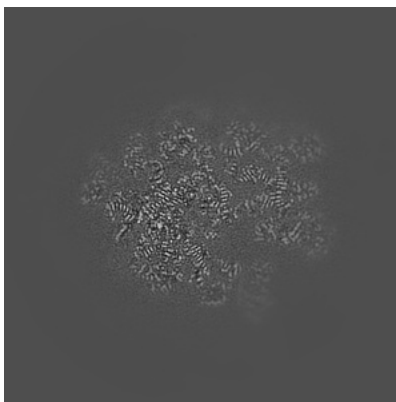
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

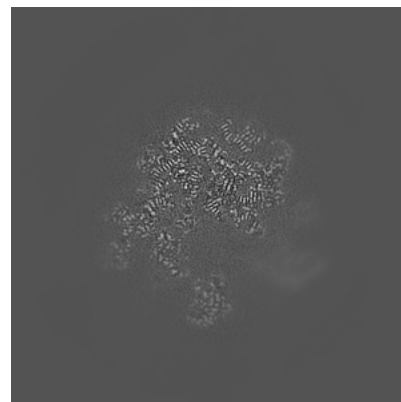
### 6.2.1 Primary map



X Index: 270

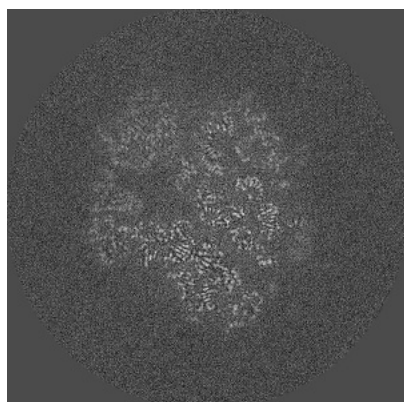


Y Index: 270

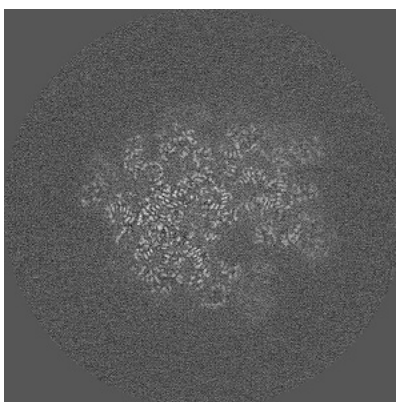


Z Index: 270

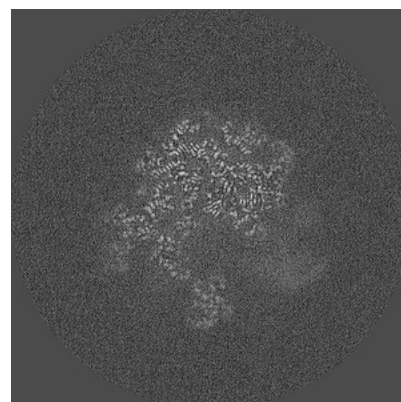
### 6.2.2 Raw map



X Index: 270



Y Index: 270

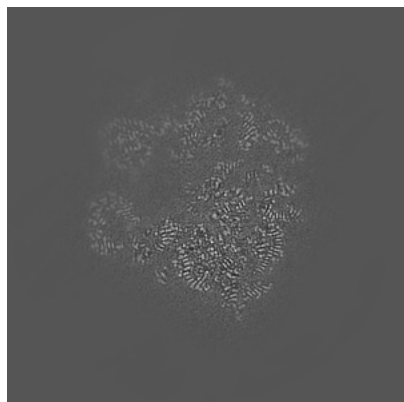


Z Index: 270

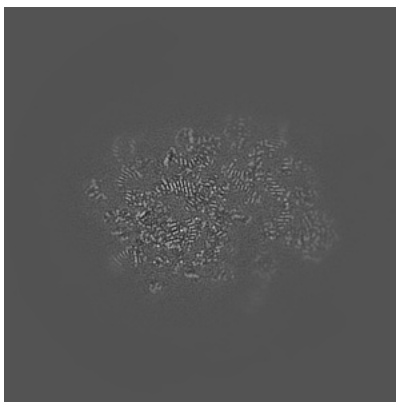
The images above show central slices of the map in three orthogonal directions.

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

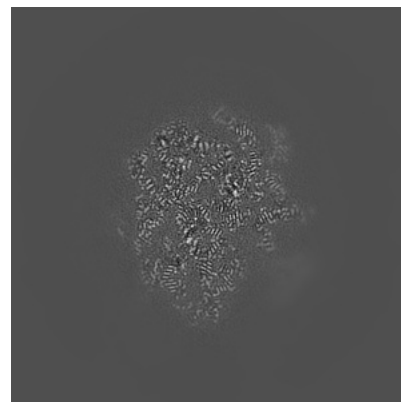
### 6.3.1 Primary map



X Index: 250

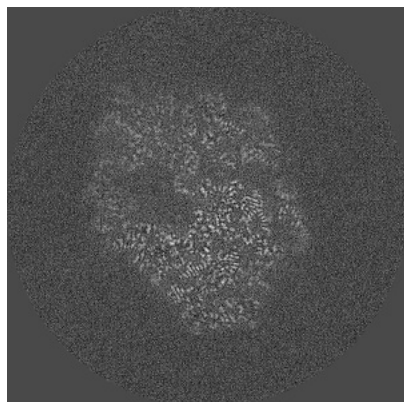


Y Index: 290

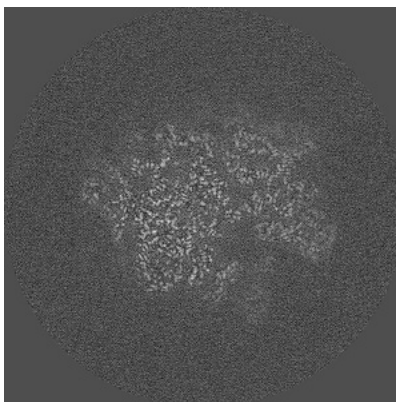


Z Index: 234

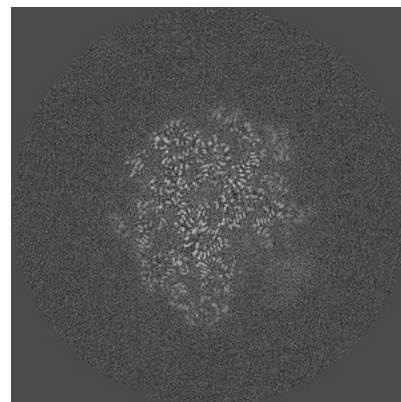
### 6.3.2 Raw map



X Index: 286



Y Index: 276

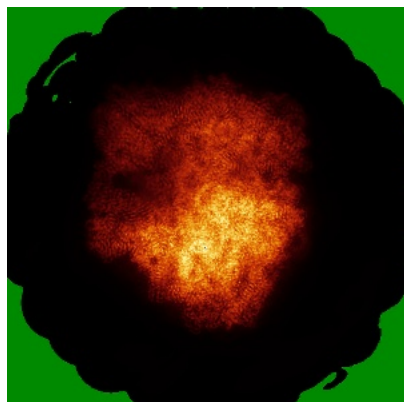


Z Index: 237

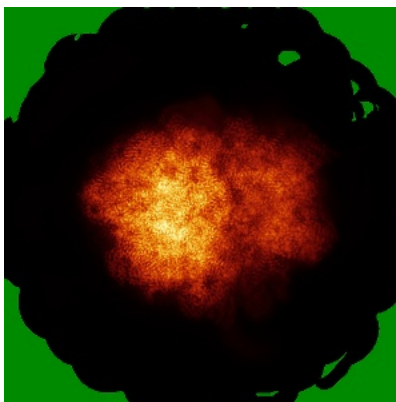
The images above show the largest variance slices of the map in three orthogonal directions.

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

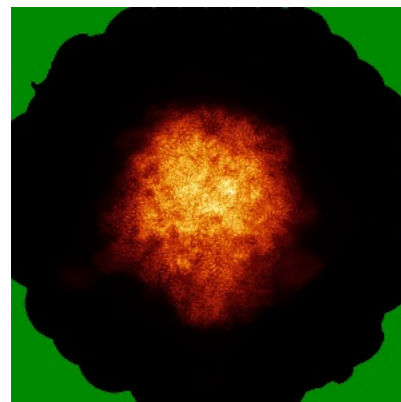
### 6.4.1 Primary map



X

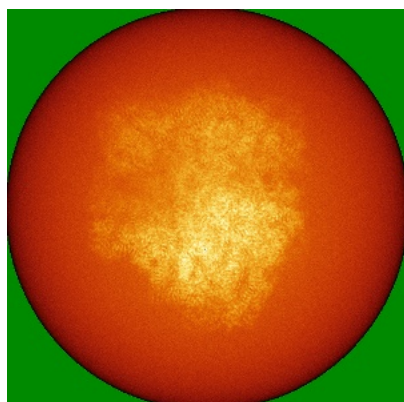


Y

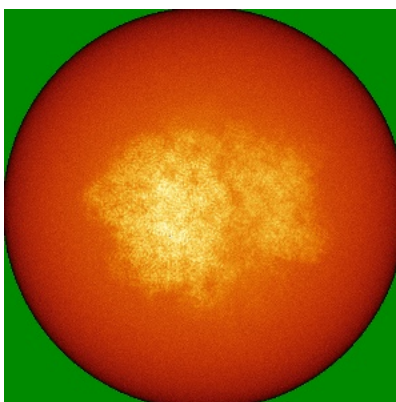


Z

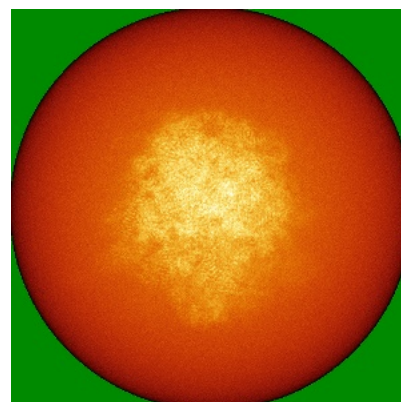
### 6.4.2 Raw map



X



Y

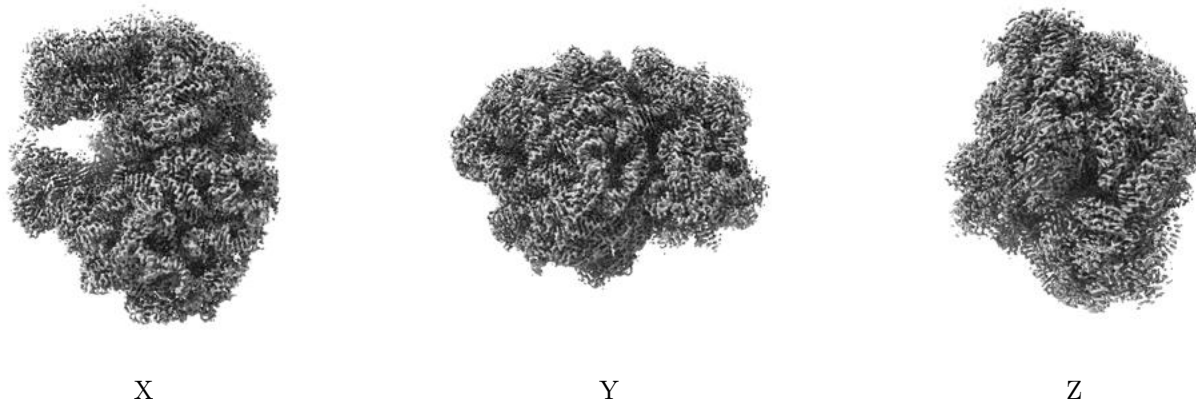


Z

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.

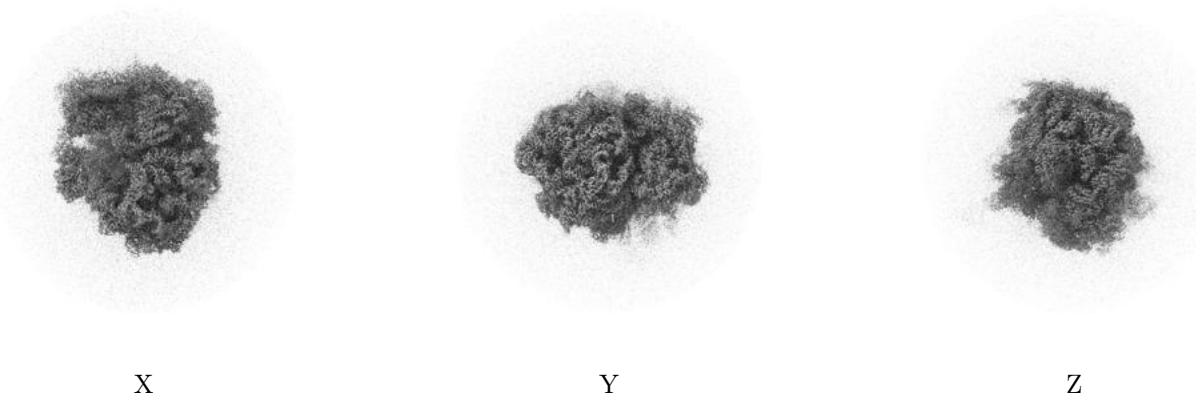
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0198. 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.

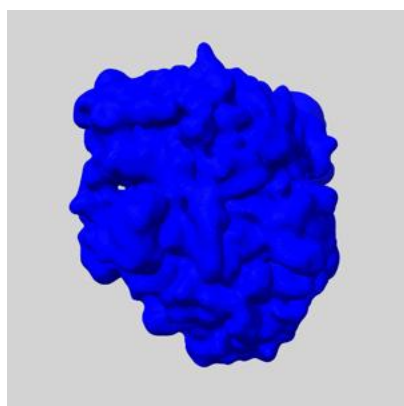
## 6.6 Mask visualisation [i](#)

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

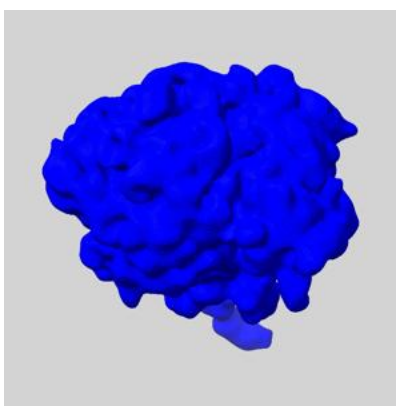
A mask typically either:

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

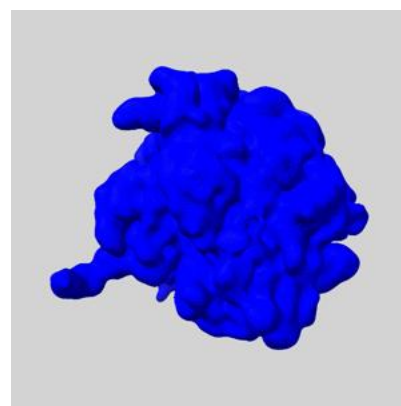
### 6.6.1 emd\_19067\_msk\_1.map [i](#)



X



Y

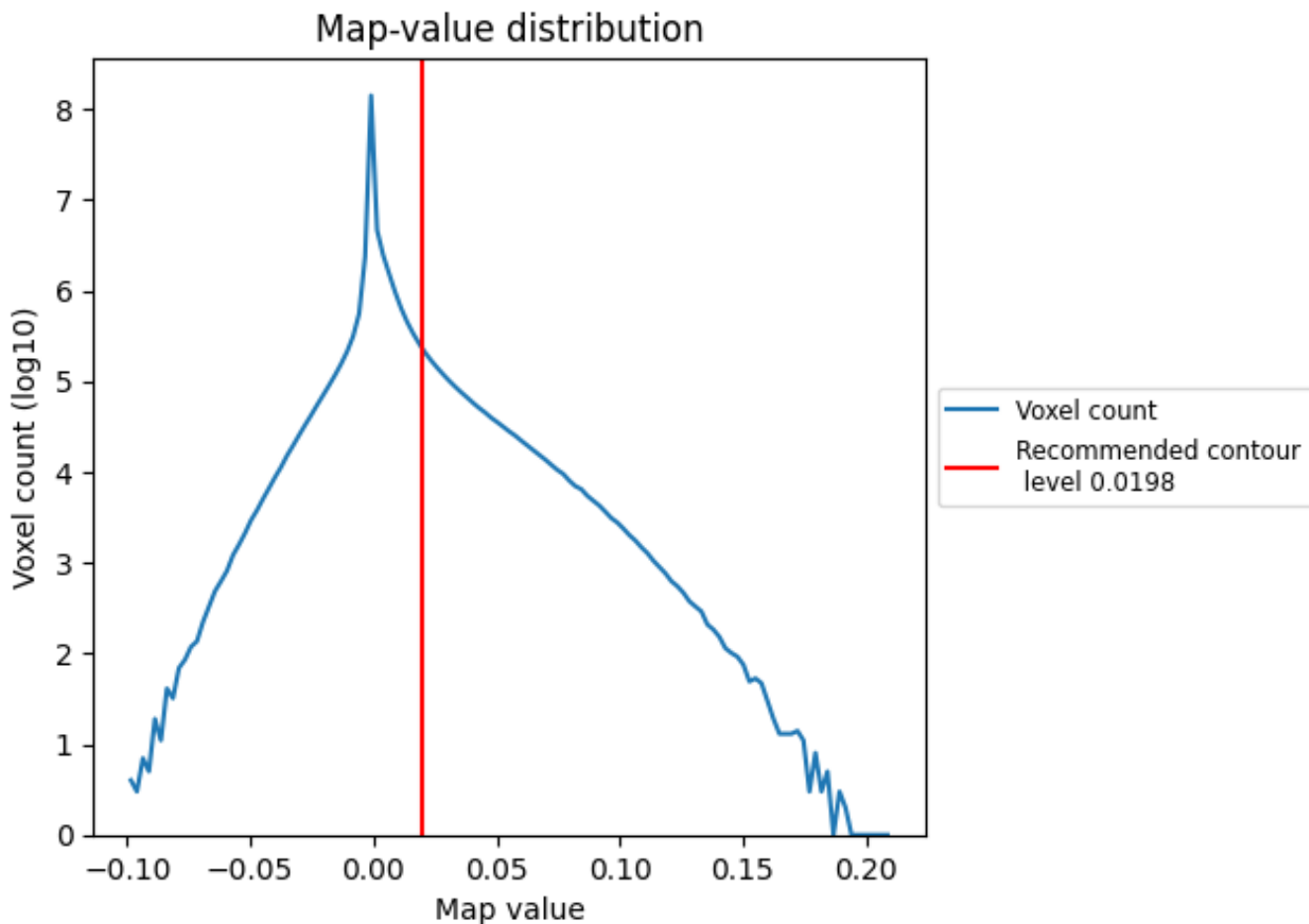


Z

## 7 Map analysis [i](#)

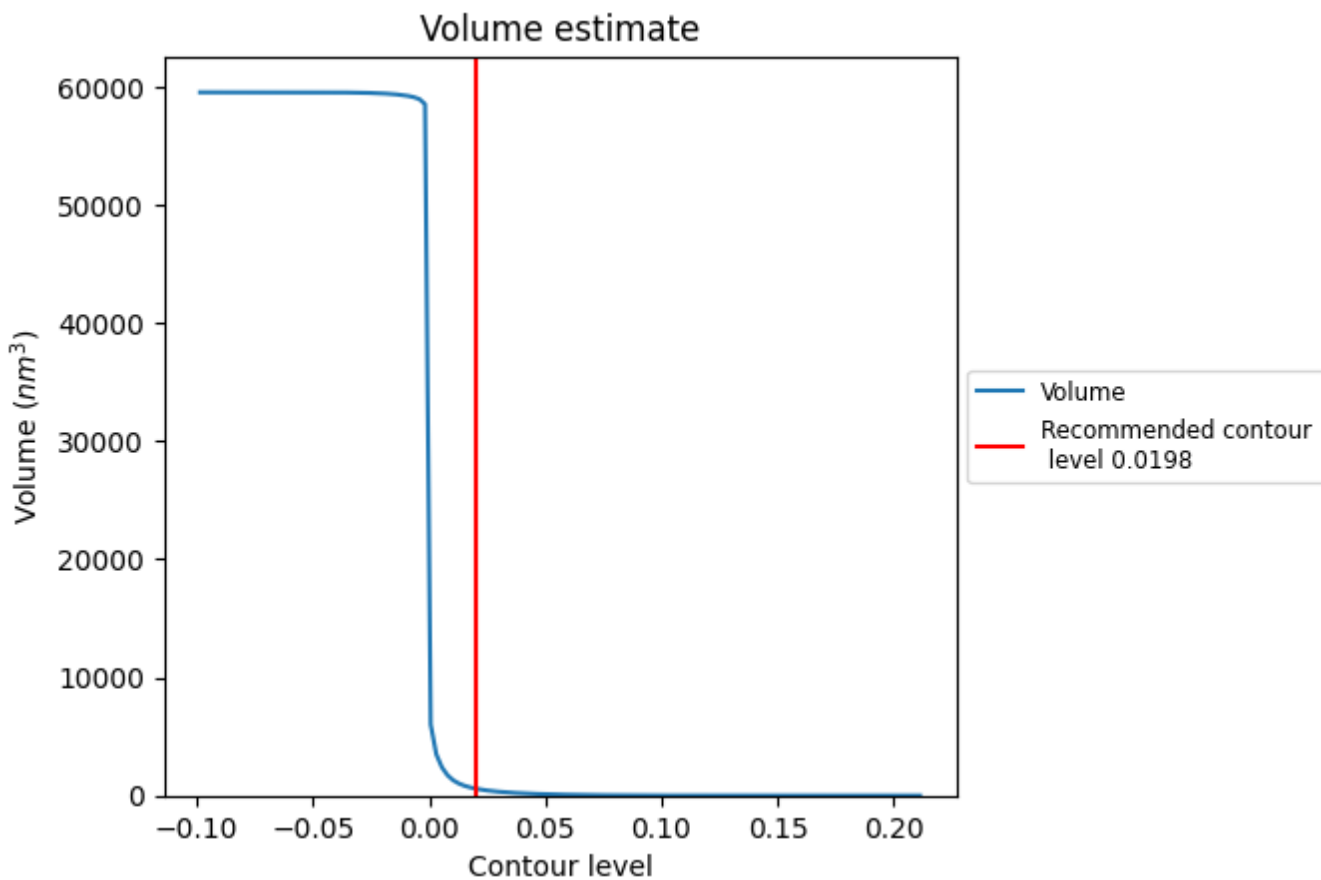
This section contains the results of statistical analysis of the map.

### 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.

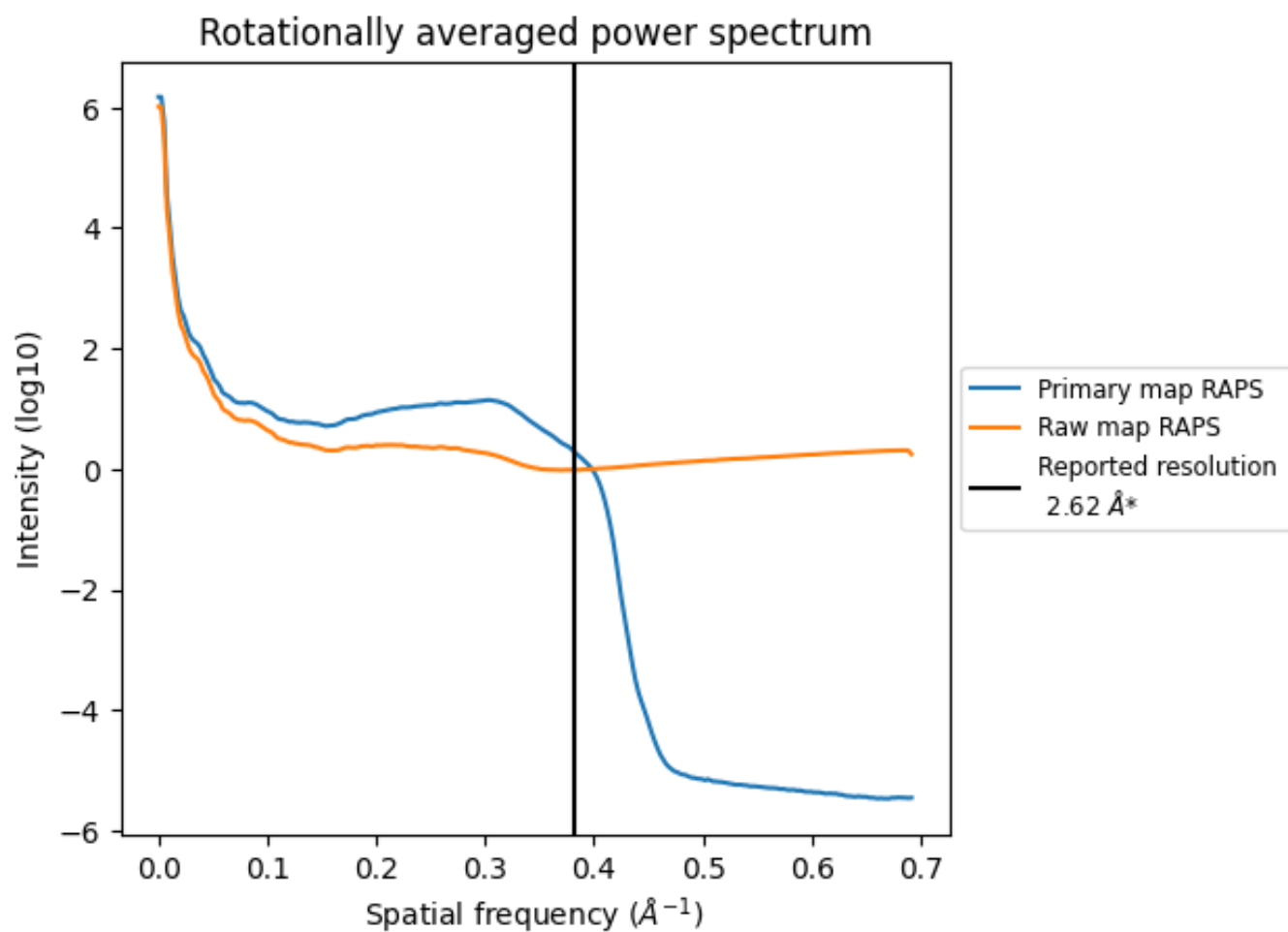
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 598 nm<sup>3</sup>; this corresponds to an approximate mass of 540 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

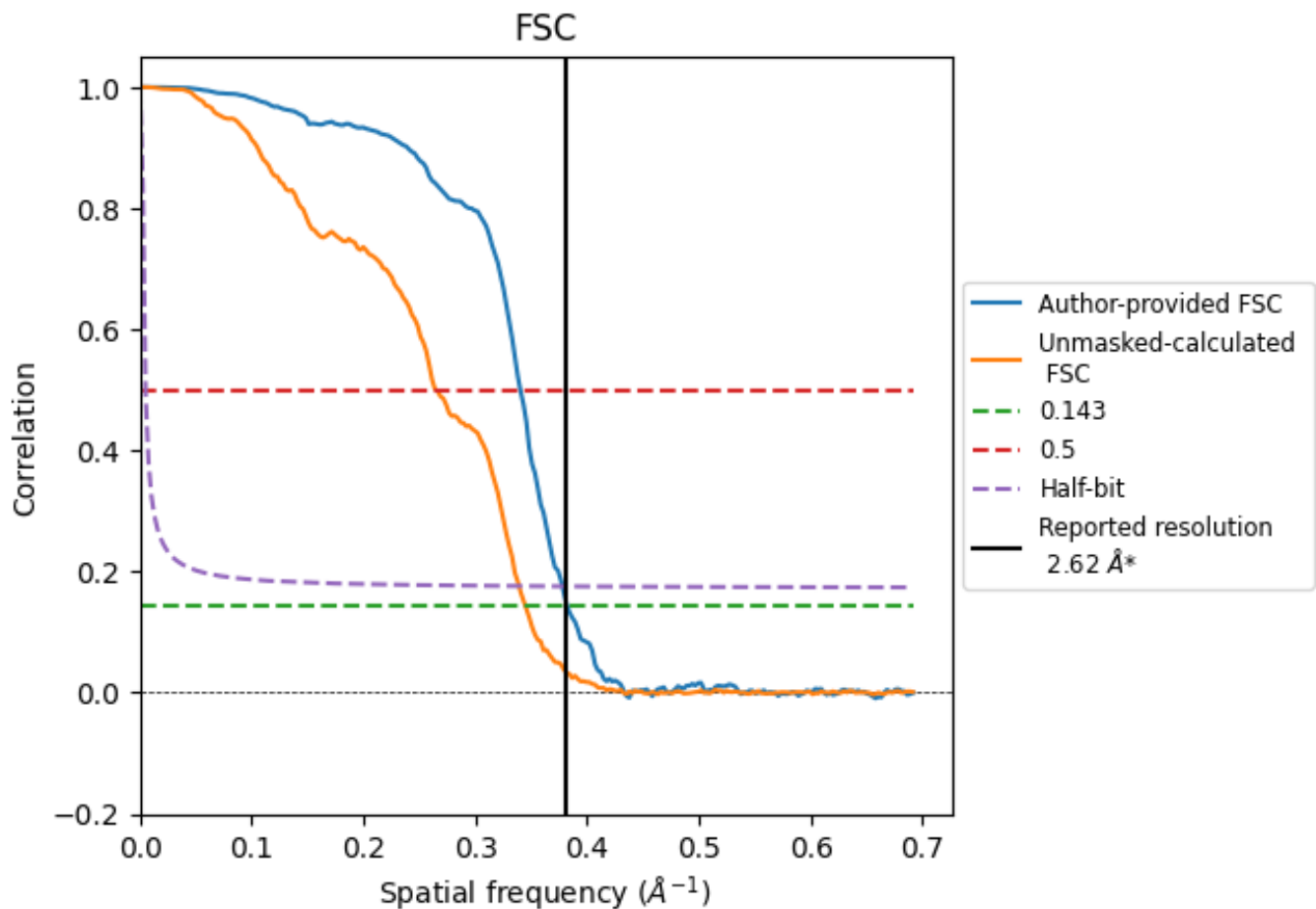


\*Reported resolution corresponds to spatial frequency of 0.382 Å<sup>-1</sup>

## 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 0.382 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

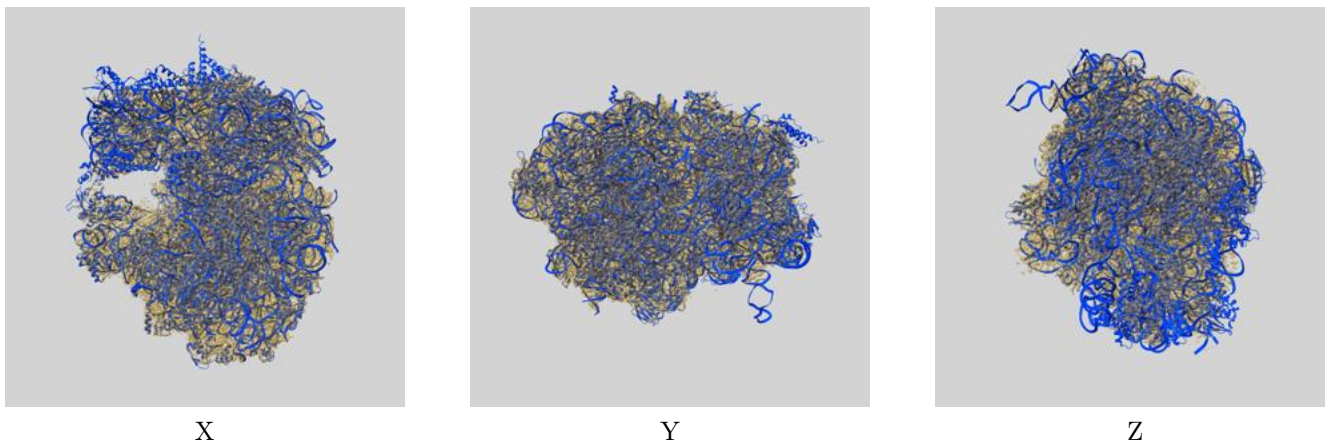
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.62	-	-
Author-provided FSC curve	2.62	2.94	2.65
Unmasked-calculated*	2.90	3.77	2.95

\*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 2.90 differs from the reported value 2.62 by more than 10 %

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

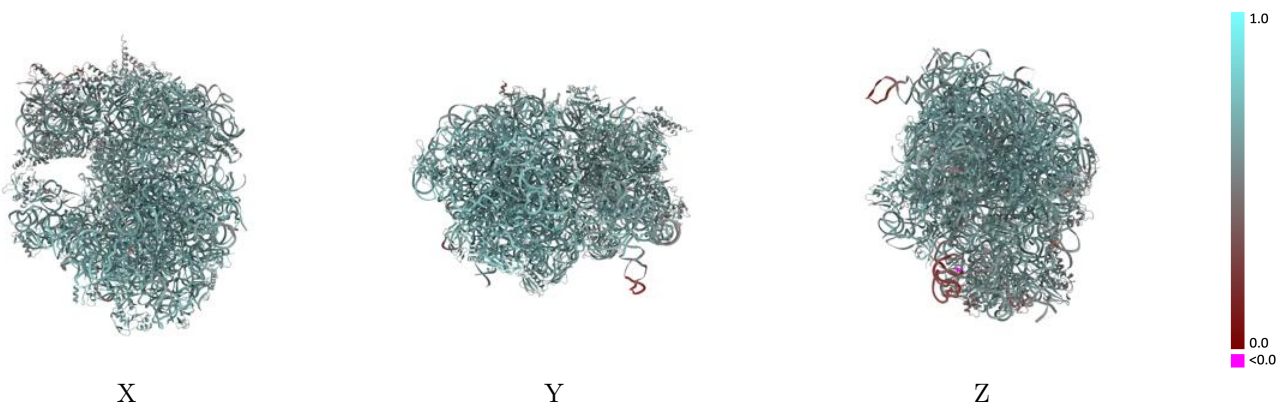
This section contains information regarding the fit between EMDB map EMD-19067 and PDB model 8RD8. Per-residue inclusion information can be found in section 3 on page 15.

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



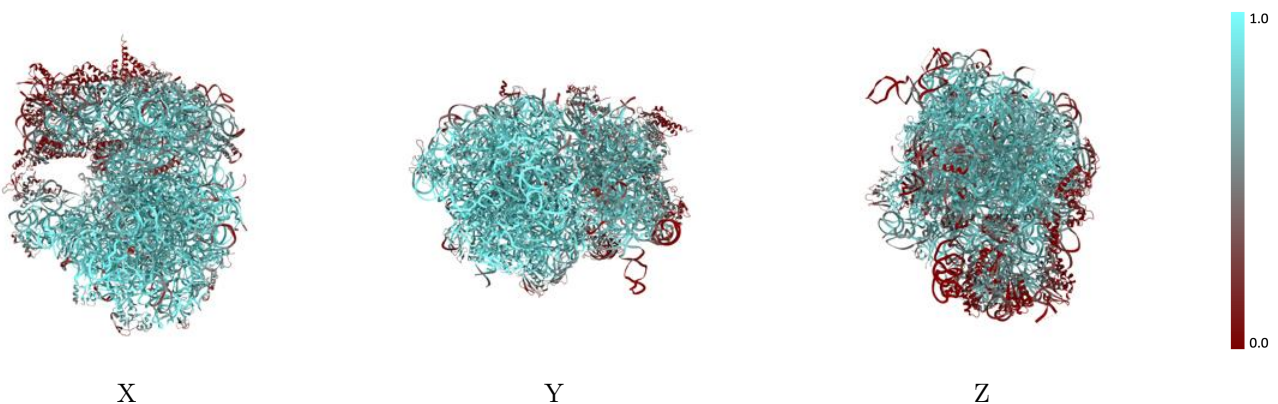
The images above show the 3D surface view of the map at the recommended contour level 0.0198 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



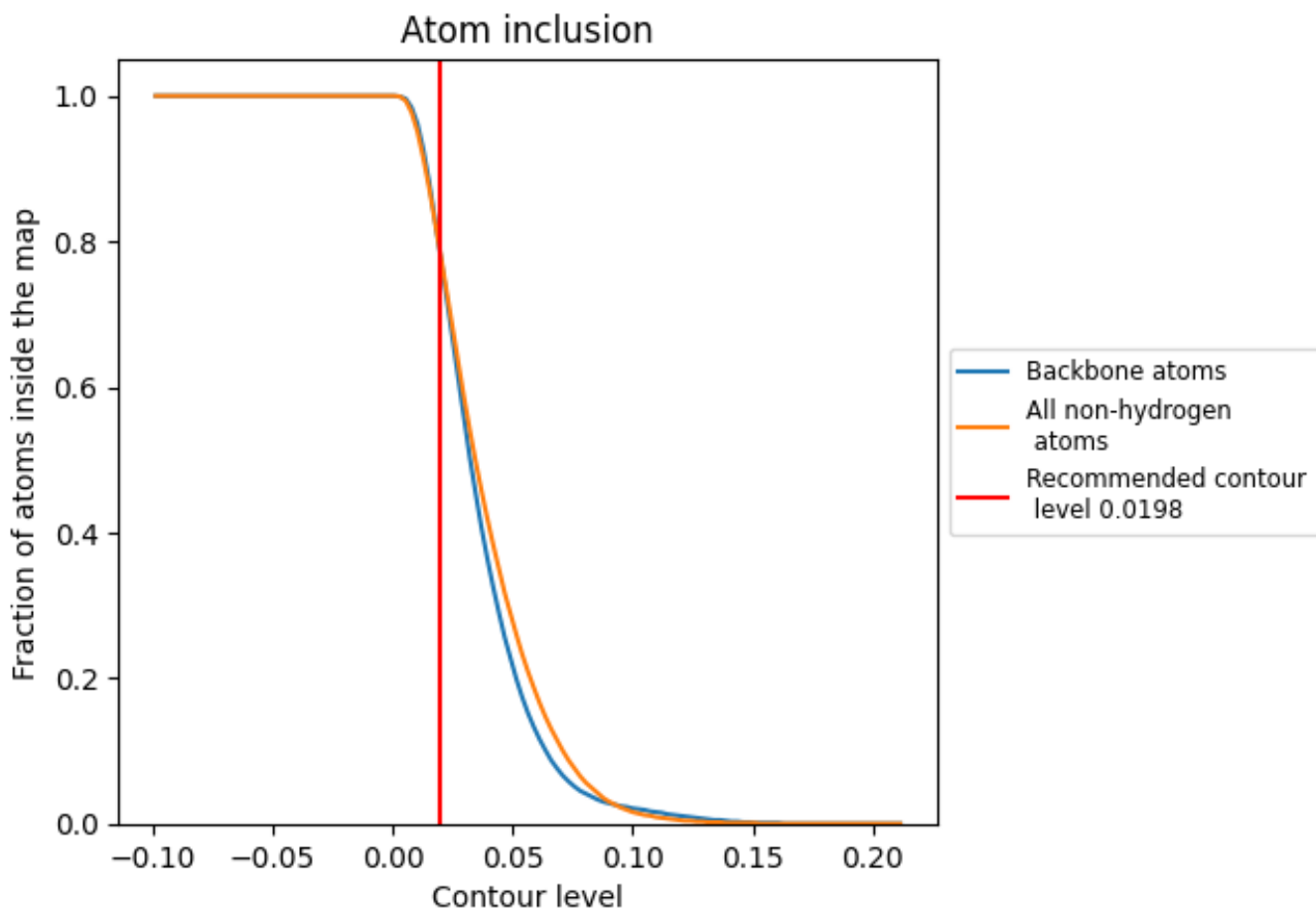
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0198).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 79% 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 (0.0198) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7860	 0.6370
A4	 0.2270	 0.5450
Af	 0.9160	 0.6860
B	 0.6660	 0.6290
BQ	 0.6980	 0.6390
Ba	 0.9910	 0.7030
C1	 0.5090	 0.5390
CT	 0.3250	 0.5580
Cl	 0.9370	 0.6830
D	 0.5200	 0.5840
D8	 0.8440	 0.6350
Dm	 0.4010	 0.5550
E5	 0.6950	 0.6290
E9	 0.8040	 0.6660
F	 0.2910	 0.5540
F7	 0.4130	 0.5640
FG	 0.3870	 0.5870
GR	 0.5680	 0.6090
GS	 0.2190	 0.5320
H	 0.1270	 0.5690
HK	 0.3230	 0.5310
IX	 0.9310	 0.6870
JY	 0.2520	 0.5170
Je	 0.8910	 0.6630
KU	 0.5210	 0.5990
Kd	 0.8800	 0.6700
L6	 0.8260	 0.6340
Lg	 0.9070	 0.6700
MB	 0.9640	 0.6930
MM	 0.1820	 0.5460
NV	 0.4050	 0.5820
Nc	 0.7480	 0.6260
OL	 0.7000	 0.6270
Oi	 0.9000	 0.6740
PO	 0.9430	 0.6980



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Chain	Atom inclusion	Q-score
Pj	0.6470	0.6000
QZ	0.6490	0.6250
Qb	0.8000	0.6630
R3	0.6050	0.5890
RF	0.9110	0.6780
SP	0.1300	0.5300
Sn	0.8010	0.6430
TI	0.6480	0.6160
To	0.6770	0.6230
UC	0.7700	0.6480
VH	0.8950	0.6690
WD	0.8610	0.6540
XE	0.5760	0.6160
YW	0.9300	0.6810
Z2	0.9320	0.6670
aA	0.9030	0.6820
bk	0.8910	0.6650
dh	0.9720	0.7020
ep	0.9510	0.6730
fJ	0.1600	0.5480
iN	0.7450	0.6060