



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 10:44 PM UTC

PDB ID : 8RDW / pdb_00008rdw
EMDB ID : EMD-19077
Title : Cryo-EM structure of P. urativorans 70S ribosome in complex with hibernation factor Balon and EF-Tu(GDP) (structure 3).
Authors : Helena-Bueno, K.; Rybak, M.Y.; Gagnon, M.G.; Hill, C.H.; Melnikov, S.V.
Deposited on : 2023-12-08
Resolution : 2.74 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

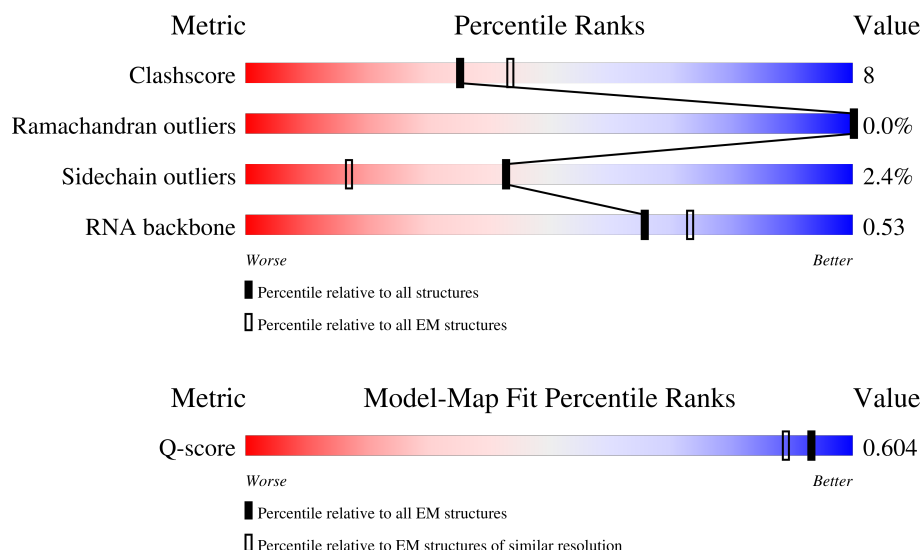
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 2.74 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	10492 (2.24 - 3.24)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	B	369	11% 72% 24% .
2	D	123	20% 19% 80% .
3	F	128	60% 69% 27% ..

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Mol	Chain	Length	Quality of chain
4	H	396	
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	
30	GR	177	
31	GS	157	
32	CT	241	
33	KU	129	
34	NV	71	
35	YW	59	
36	IX	142	
37	JY	103	
38	QZ	91	
39	Ba	44	
40	Qb	103	
41	Nc	116	
42	Kd	146	
43	Je	122	
44	Af	212	
45	Lg	137	
46	dh	65	
47	Oi	130	
48	Pj	89	
49	bk	51	
50	Cl	274	
51	Dm	213	
52	Sn	116	
53	To	88	

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Mol	Chain	Length	Quality of chain
54	ep	38	 79% 21%
55	C1	166	 17% 22% 7% 70%

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 142686 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
1	B	368	Total	C	N	O	S	0	0
			2871	1784	507	571	9		

- Molecule 2 is a protein called Large ribosomal subunit protein bL12.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	D	25	Total	C	N	O	0	0
			127	76	25	26		

- Molecule 3 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	F	124	Total	C	N	O	S	0	0
			965	601	188	175	1		

- Molecule 4 is a protein called Elongation factor Tu.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	H	386	Total	C	N	O	S	0	0
			2918	1820	505	578	15		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	Z2	2729	Total	C	N	O	P	0	0
			58553	26138	10749	18937	2729		

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

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

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

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

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

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

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

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

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

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

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

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

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D8	83	U	-	insertion	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
12	E9	199	Total	C	N	O	S	0	0
			1537	966	282	284	5		

- 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
20	VH	84	Total	C	N	O	S	0	0
			626	389	124	110	3		

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	MM	116	Total	C	N	O	S	0	0
			907	560	182	162	3		

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
28	SP	78	Total	C	N	O	S	0	0
			614	390	116	105	3		

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

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

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

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

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

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

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

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

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

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

- 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	100	Total	C	N	O	S	0	0
			793	492	151	147	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
			1062	656	206	197	3	0

- 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
			937	585	181	166	5	0

- 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
			1548	954	292	296	6	0

- 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
			1093	697	210	179	7	0

- 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
			519	326	107	82	4	0

- 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
			1689	1058	318	310	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	87	Total	C	N	O	S	0	0
			684	415	146	121	2		

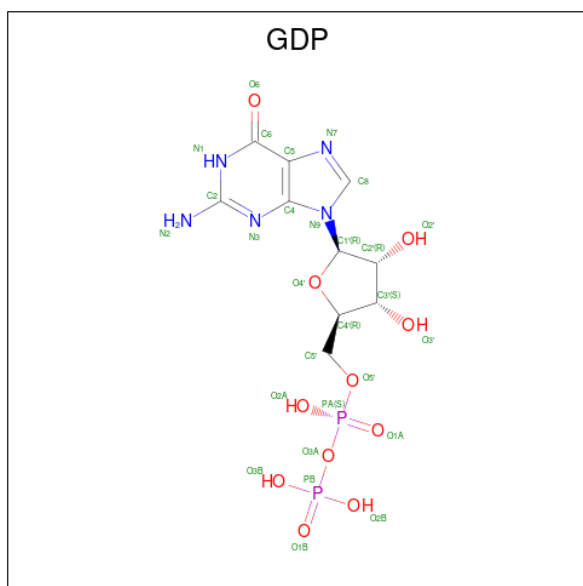
- Molecule 54 is a protein called Large ribosomal subunit protein bL36.

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 Large ribosomal subunit protein bL9.

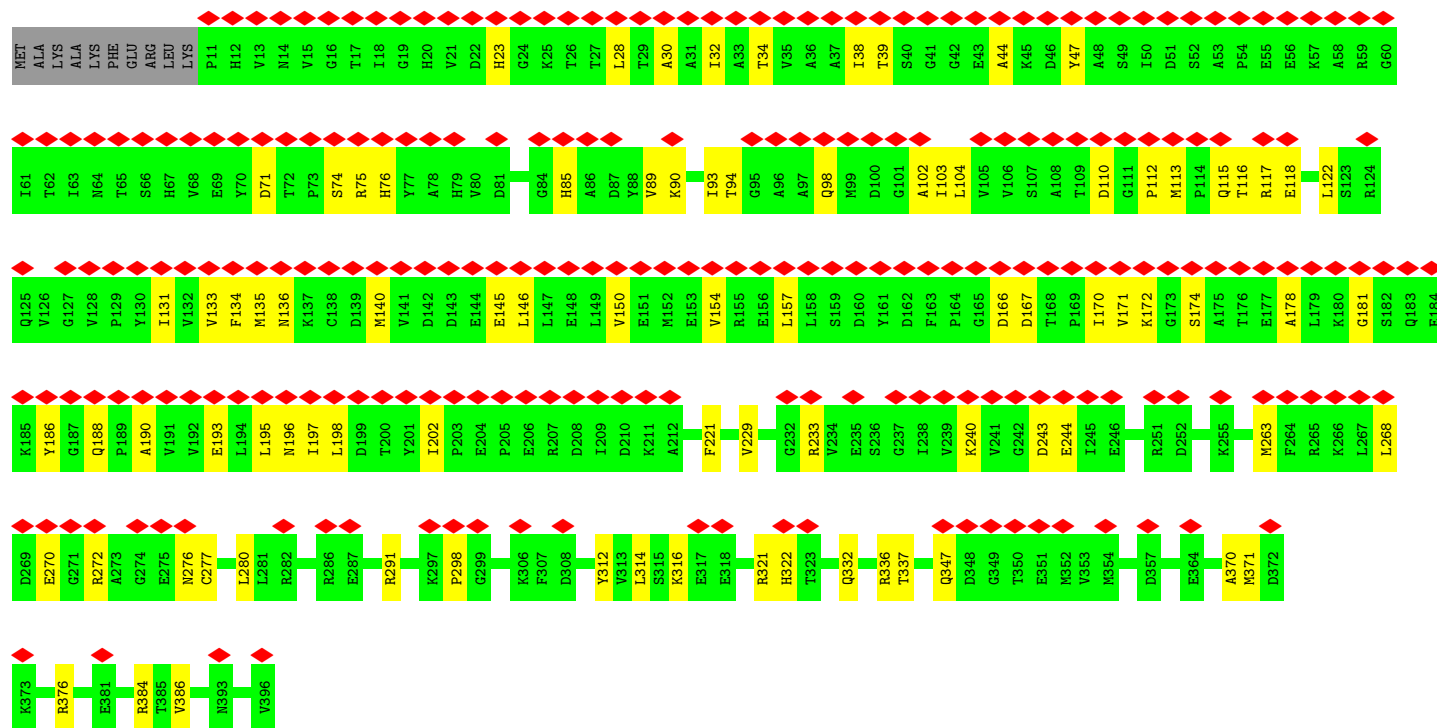
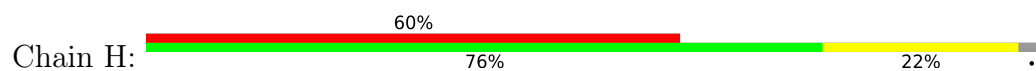
Mol	Chain	Residues	Atoms					AltConf	Trace
55	C1	49	Total	C	N	O	S	0	0
			374	244	64	65	1		

- Molecule 56 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$) (labeled as "Ligand of Interest" by depositor).

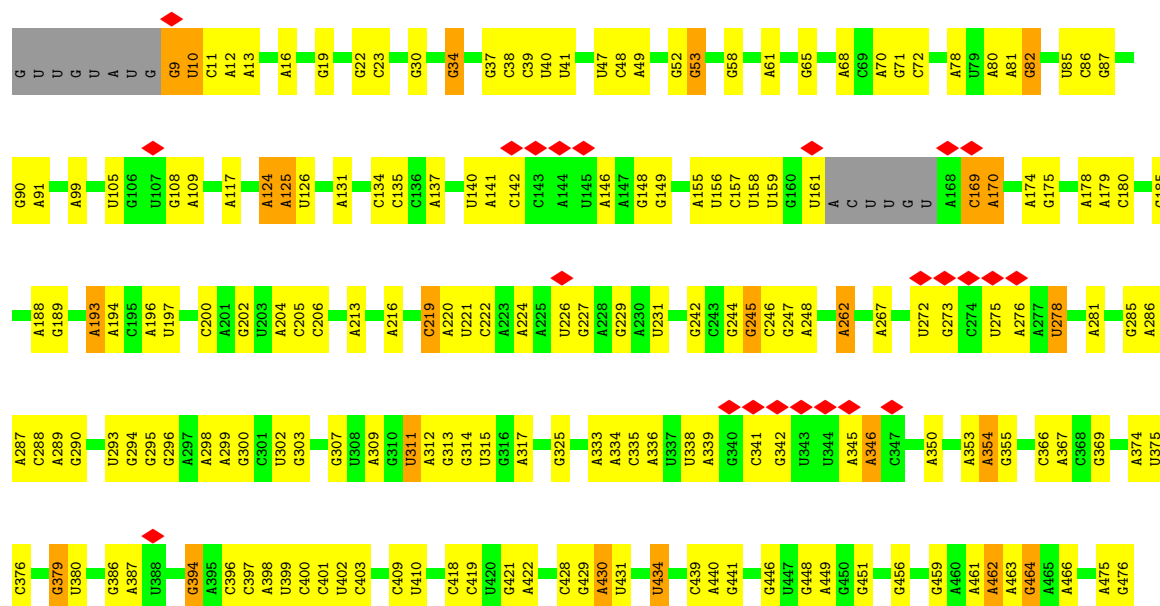


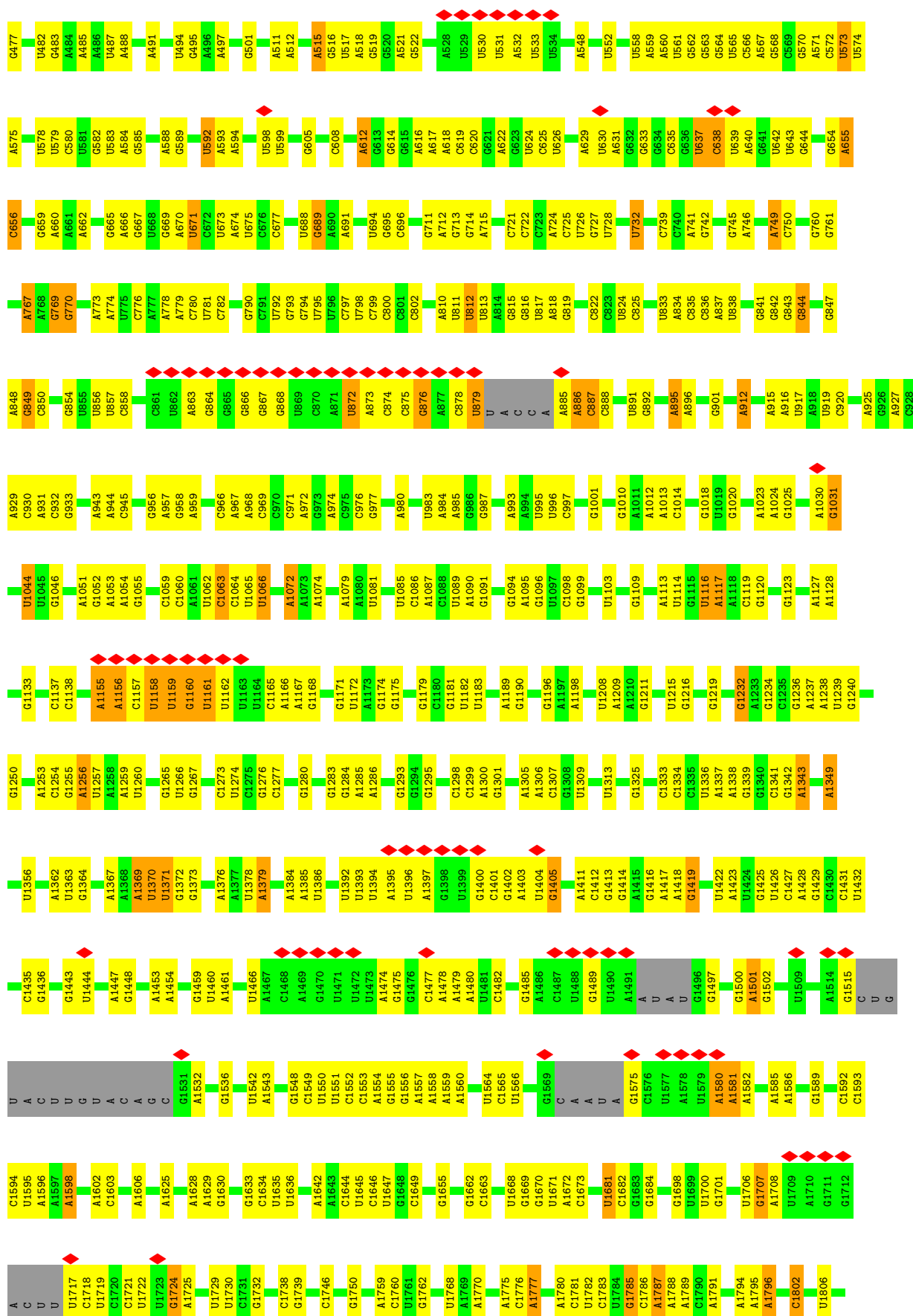


• Molecule 4: Elongation factor Tu



• Molecule 5: 23S rRNA

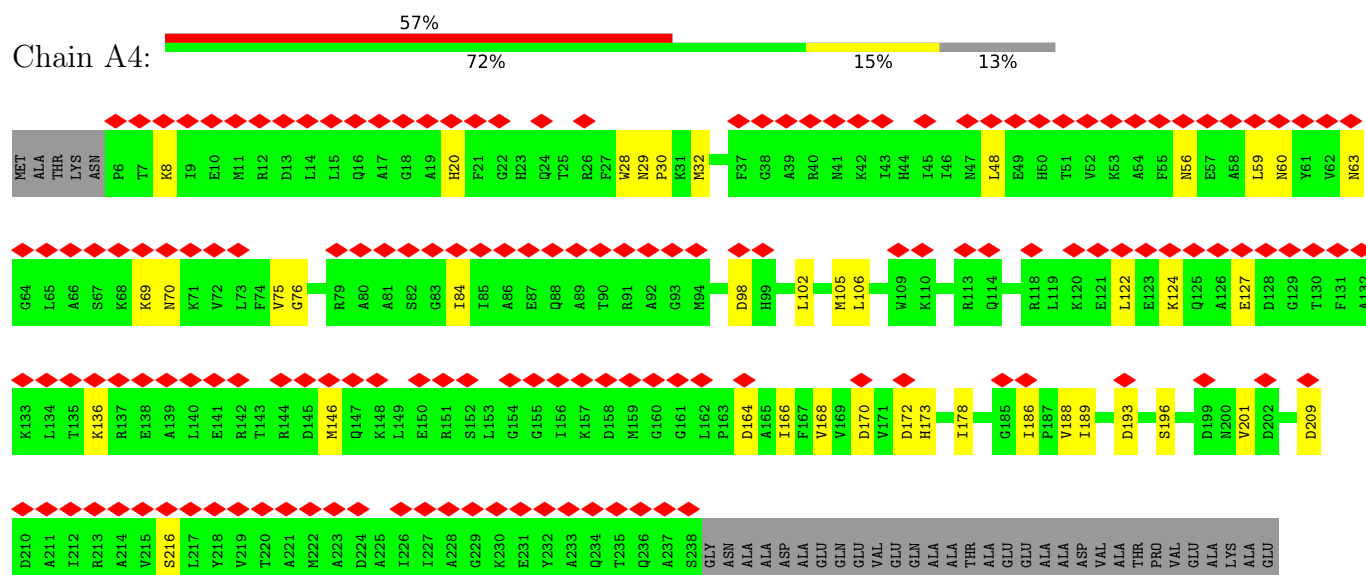






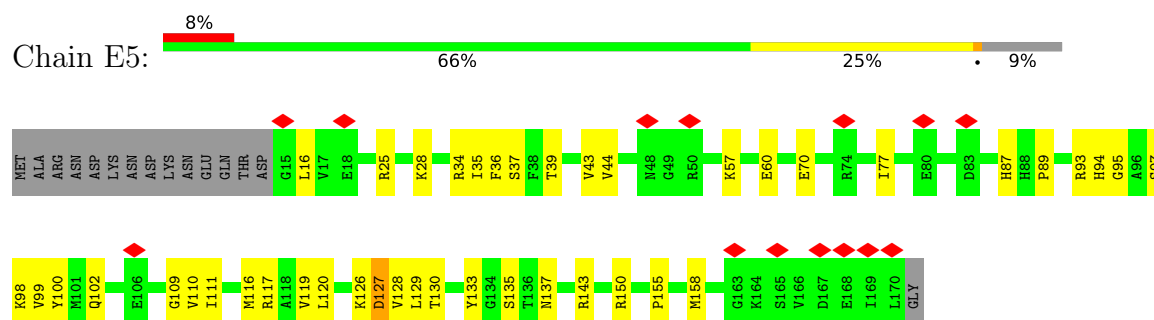
- Molecule 7: Small ribosomal subunit protein uS2

Chain A4:



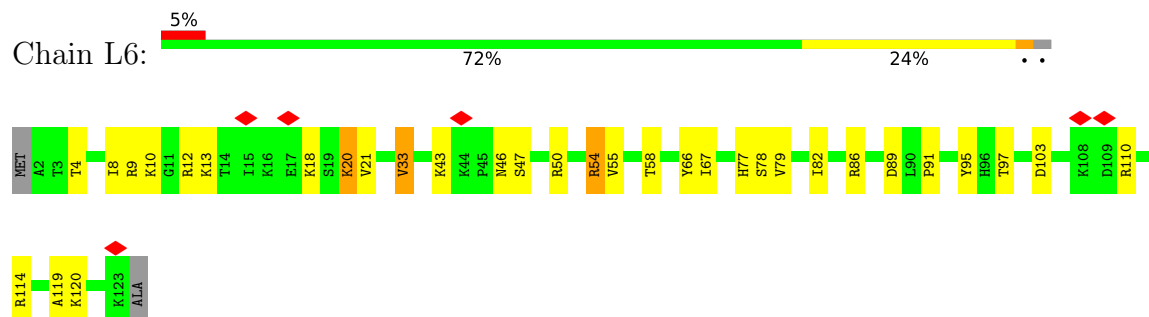
- Molecule 8: Small ribosomal subunit protein uS5

Chain E5:



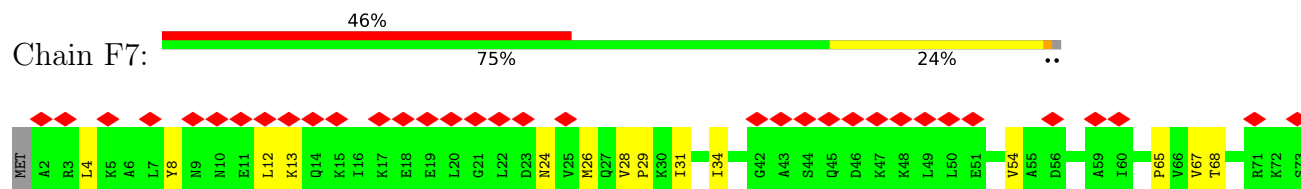
- Molecule 9: Small ribosomal subunit protein uS12

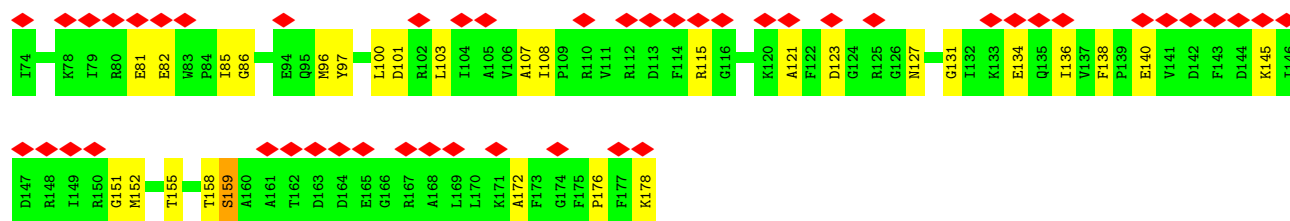
Chain L6:



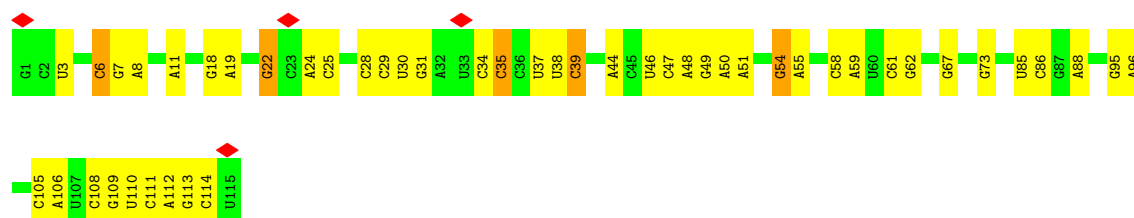
- Molecule 10: Large ribosomal subunit protein uL5

Chain F7:

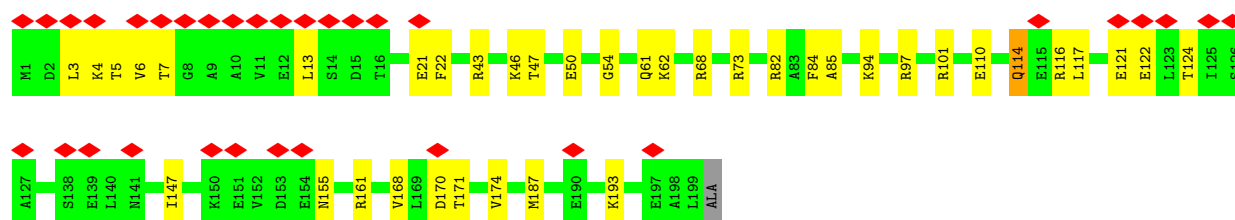
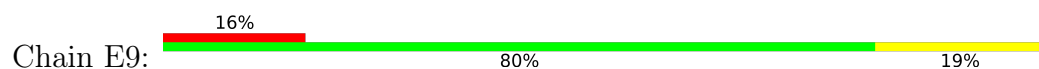




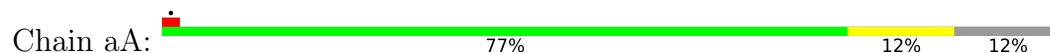
• Molecule 11: 5S rRNA



• Molecule 12: Large ribosomal subunit protein uL4



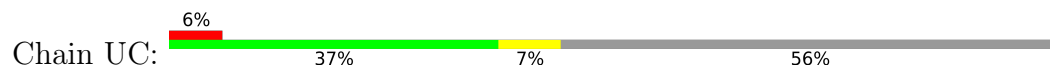
• Molecule 13: Large ribosomal subunit protein bL32

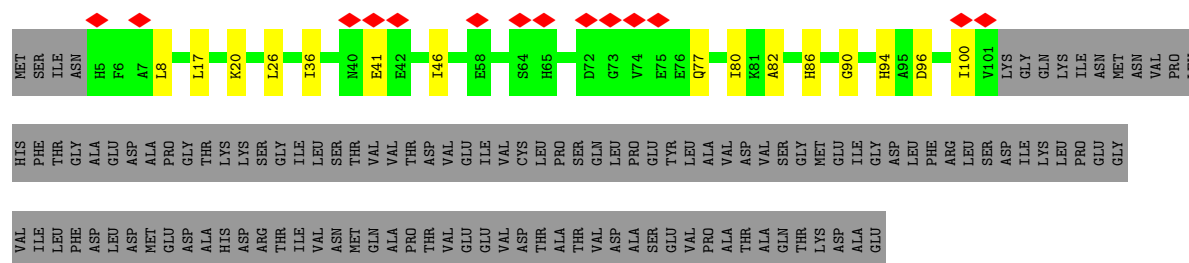


• Molecule 14: Large ribosomal subunit protein bL17

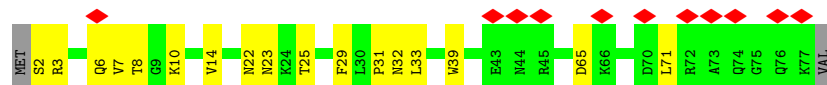
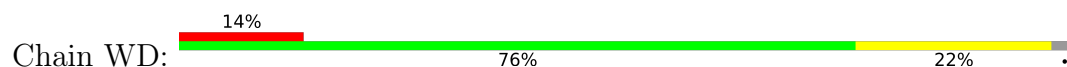


• Molecule 15: Large ribosomal subunit protein bL25

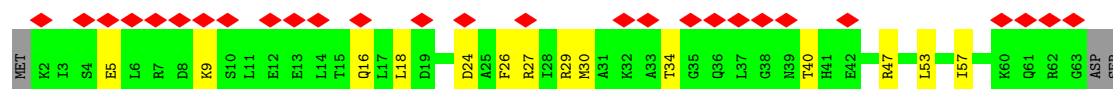
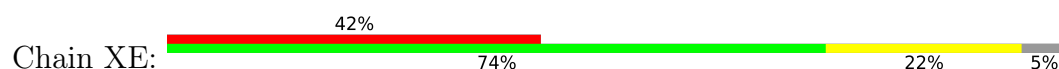




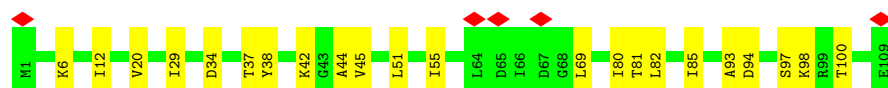
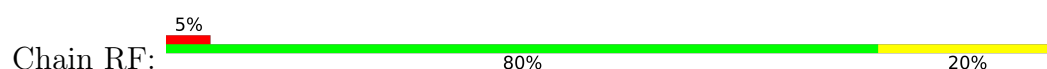
- Molecule 16: Large ribosomal subunit protein bL28



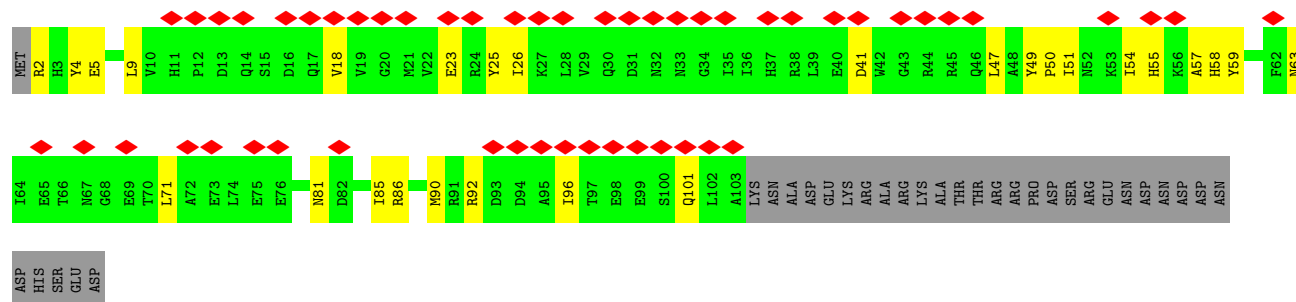
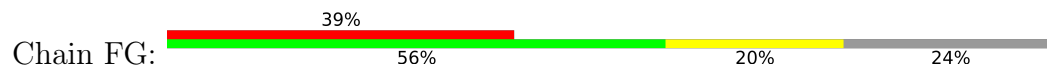
- Molecule 17: Large ribosomal subunit protein uL29



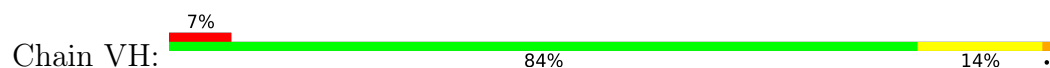
- Molecule 18: Large ribosomal subunit protein uL22



- Molecule 19: Small ribosomal subunit protein bS6

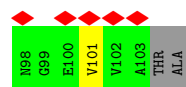
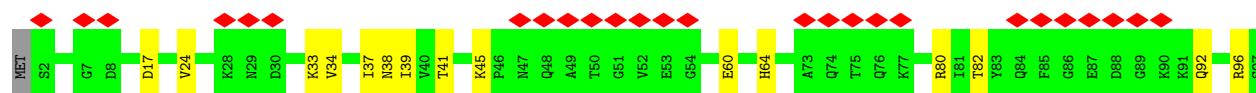
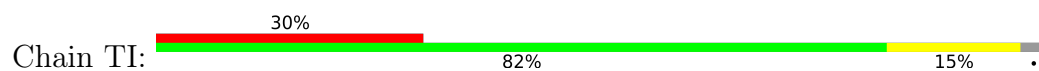


- Molecule 20: Large ribosomal subunit protein bL27





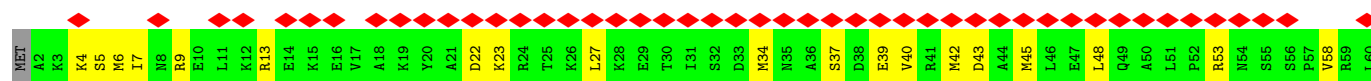
- Molecule 21: Large ribosomal subunit protein uL24



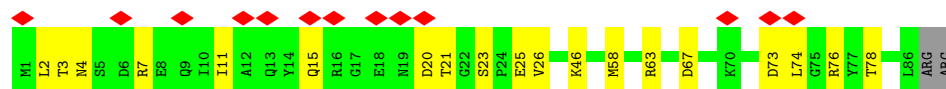
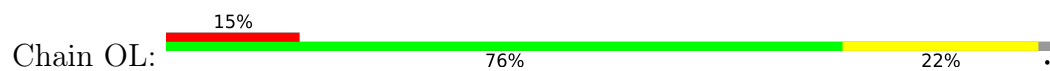
- Molecule 22: Large ribosomal subunit protein bL31B



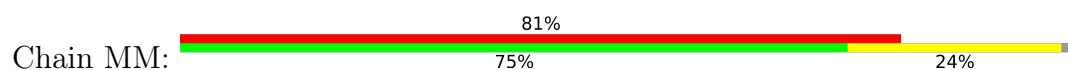
- Molecule 23: Small ribosomal subunit protein uS14

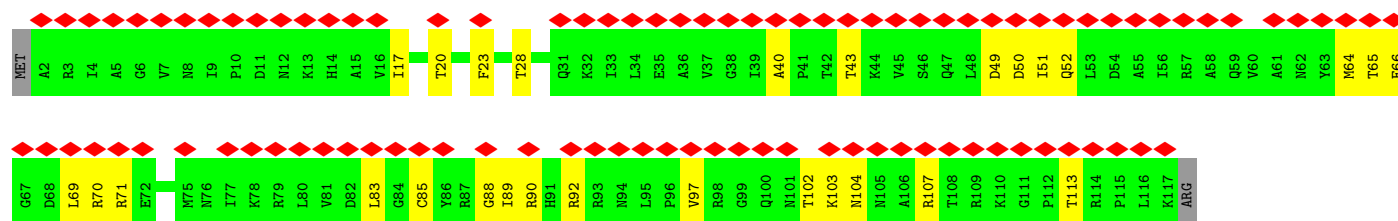


- Molecule 24: Small ribosomal subunit protein uS15

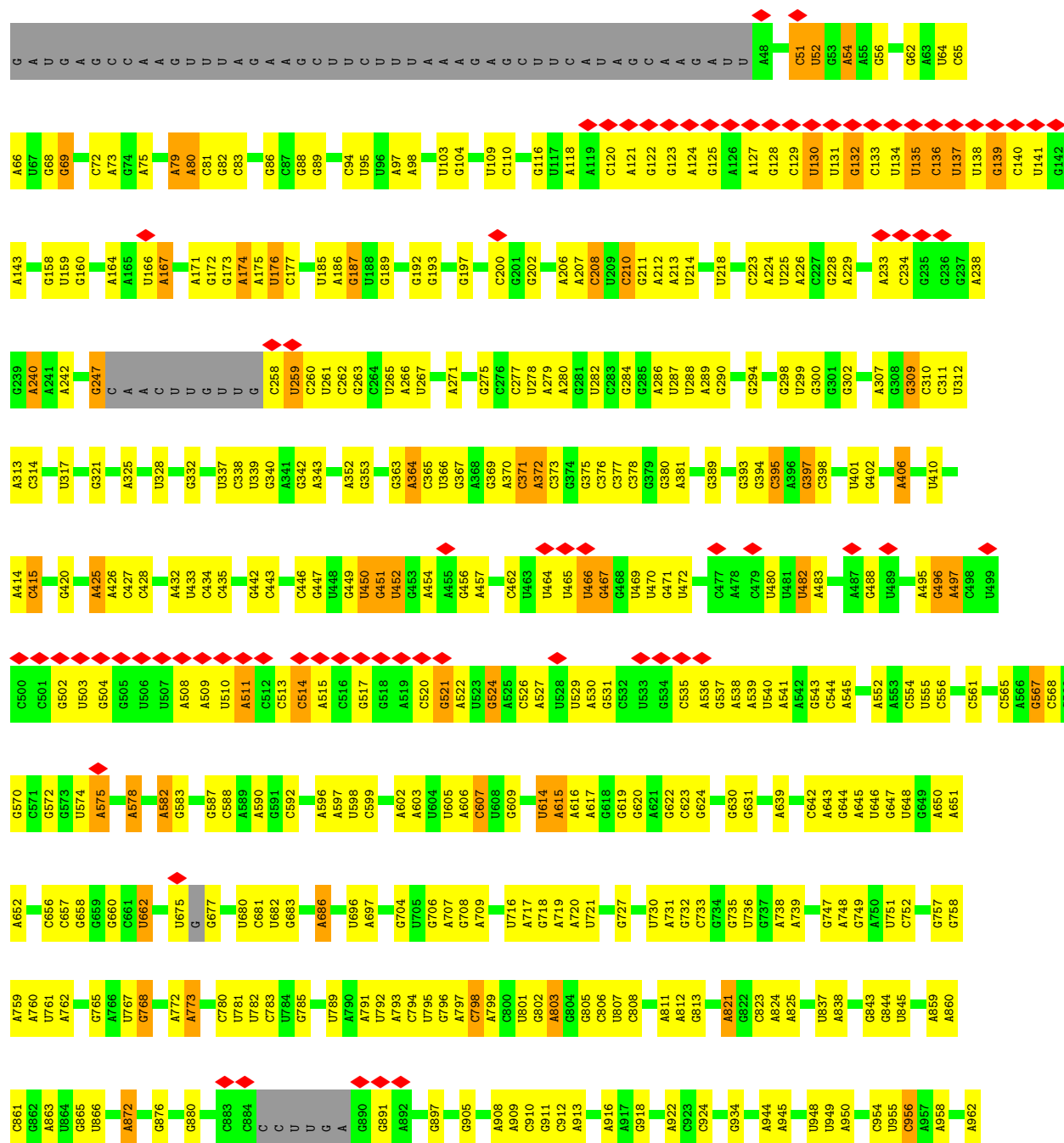


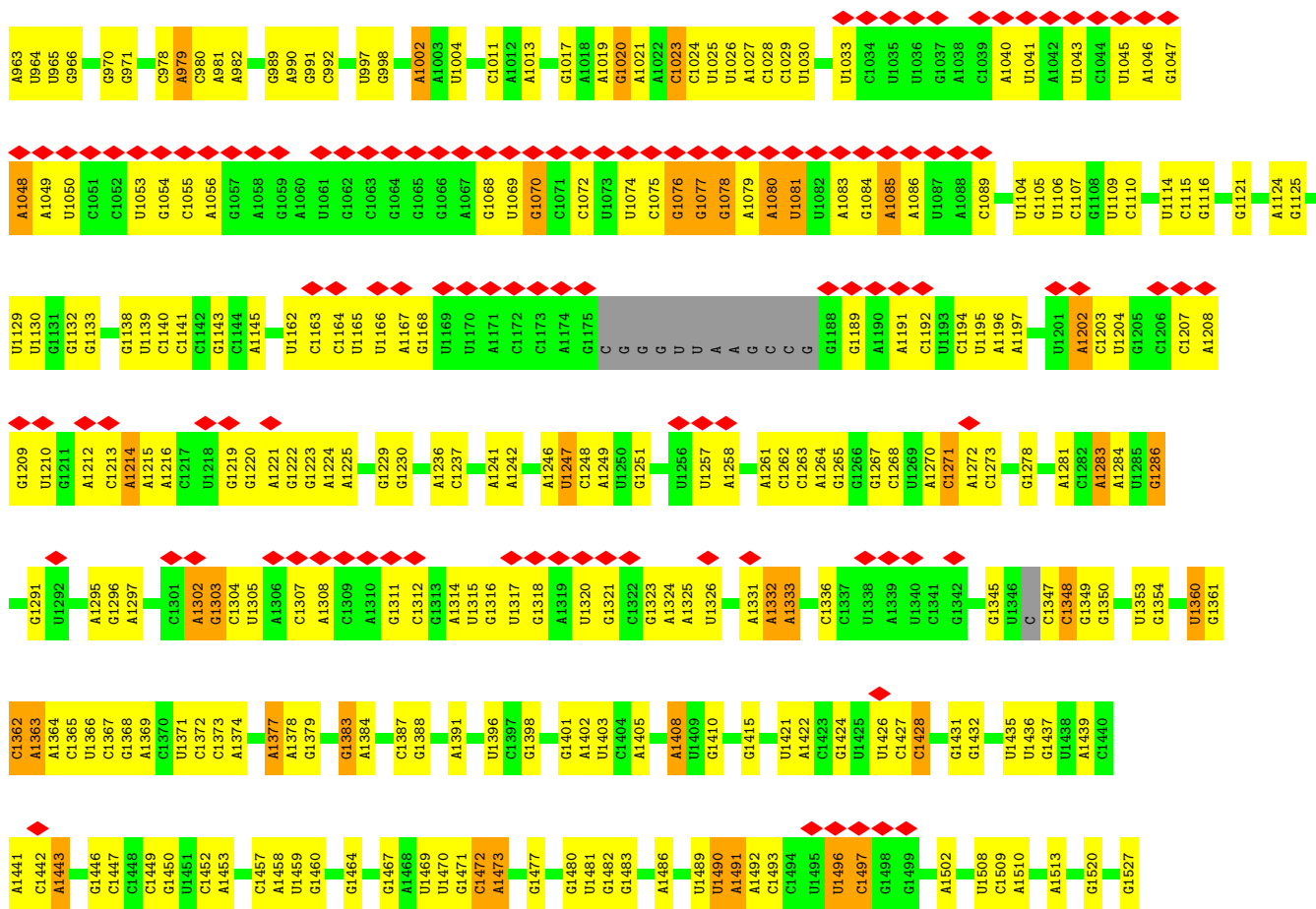
- Molecule 25: Small ribosomal subunit protein uS13



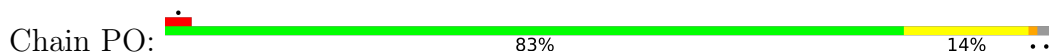


• Molecule 26: 16S rRNA

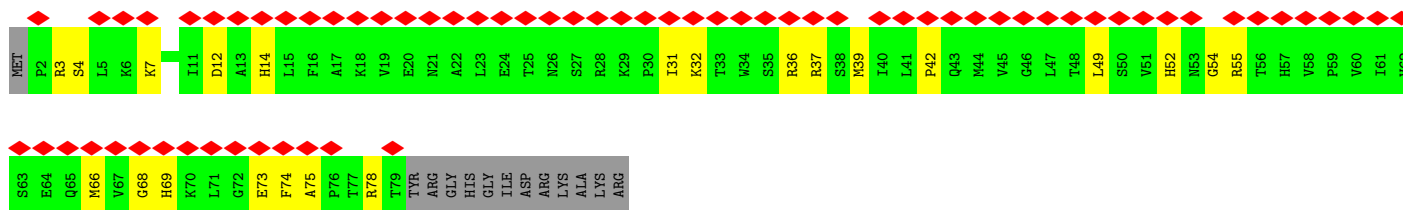
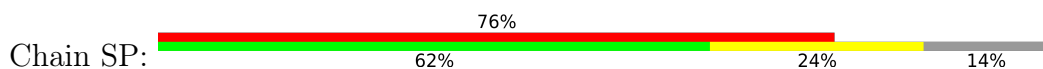




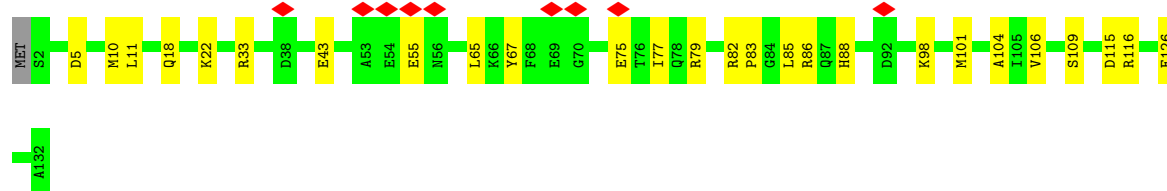
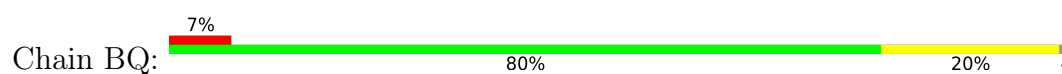
- Molecule 27: Large ribosomal subunit protein bL20



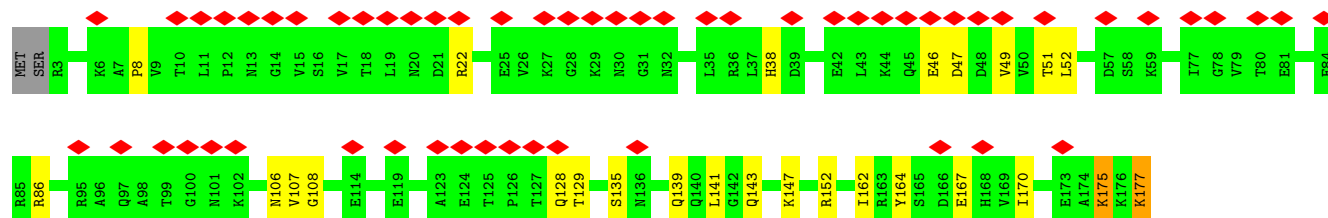
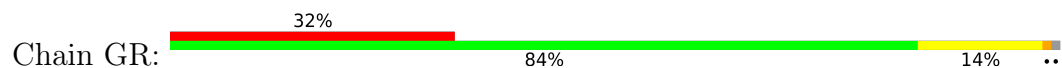
- Molecule 28: Small ribosomal subunit protein uS19



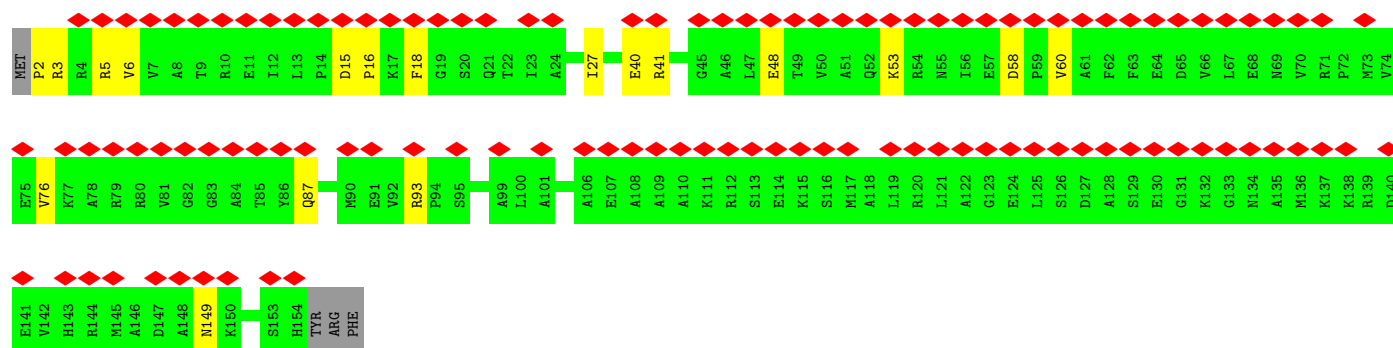
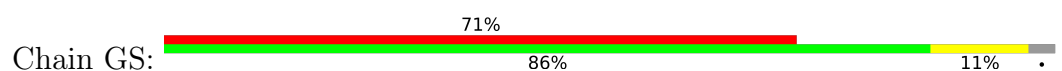
- Molecule 29: Small ribosomal subunit protein uS8



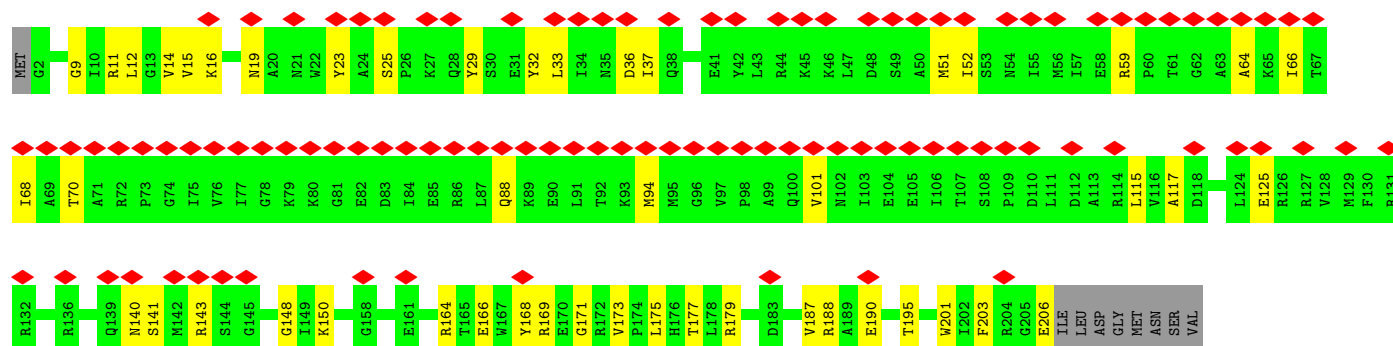
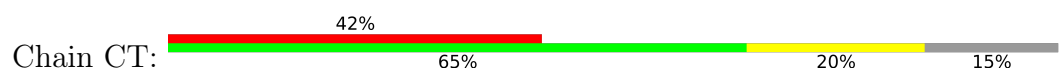
- Molecule 30: Large ribosomal subunit protein uL6



- Molecule 31: Small ribosomal subunit protein uS7



- Molecule 32: Small ribosomal subunit protein uS3



TYR ASN ASP VAL LYS GLU GLU GLN THR ARG ALA VAL LYS ARG ARG ARG GLY ARG GLY GLY ASN ARG ARG ASN SER ASP ARG GLY

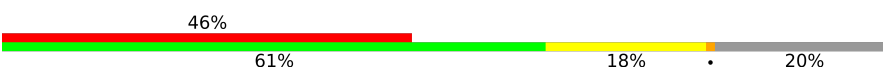
- Molecule 33: Small ribosomal subunit protein uS11

Chain KU: 

MET ALA LYS ASP THR ARG SER ARG LYS VAL THR ARG ARG S15 V16 E18 G19 I20 H24 A25 N29 T30 I31 T34 T35 D36 R37 Q38 G39 N40 A41 T46 R56 K57 F61 A62 A63 Q64 V65 E68 K72 A73 A74 Q75 E76 Y77 G78 V79 K80 N81

I82 D83 V84 L85 V86 K87 G88 P89 R93 E94 R98 A99 L100 G101 A102 L103 G104 Y105 K106 V107 N108 S109 I110 D112 P115 H118 N119 G120 V129

- Molecule 34: Small ribosomal subunit protein bS21

Chain NV: 

MET P2 A3 V4 K5 V6 K7 E8 N9 E10 P11 V12 D13 I14 A15 I16 R17 R18 F19 K20 R21 A22 C23 S24 K25 A26 G27 V28 D31 V32 R33 K34 R35 E39 K40 P41 R45 K54 R55 Y56 K57 K58 LYS LEU GLN ARG GLU THR ILE THR ARG MET TYR

- Molecule 35: Large ribosomal subunit protein uL30

Chain YW: 

MET K2 K5 L9 K24 E38 D39 T40 T43 M46 M47 M48 M51 K55 V56 E57 GLU ALA

- Molecule 36: Large ribosomal subunit protein uL13

Chain IX: 

H1 P8 V11 V15 F16 V17 V18 D19 L25 L28 Q31 R35 T42 T45 V48 T54 V55 N58 T62 K73 Y80 T84 N88 F89 V100 V105 L109 P113 K120 K123 E133 A134 Q135 Q136 P137 K138

E139 L140 D141 I142

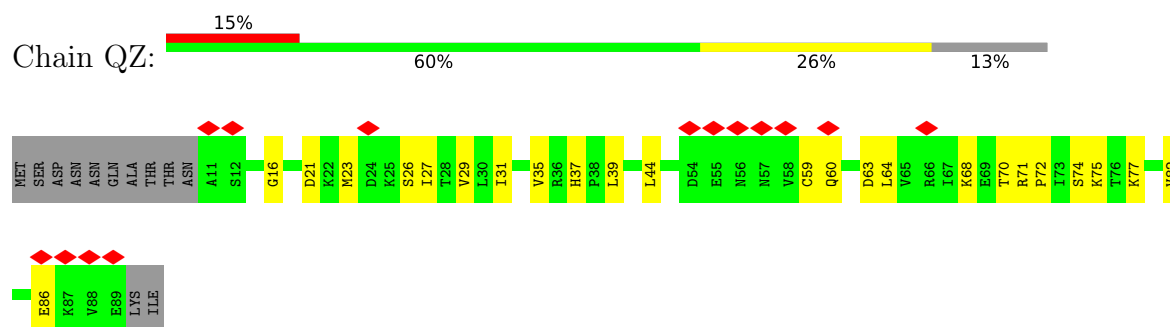
- Molecule 37: Small ribosomal subunit protein uS10

Chain JY: 

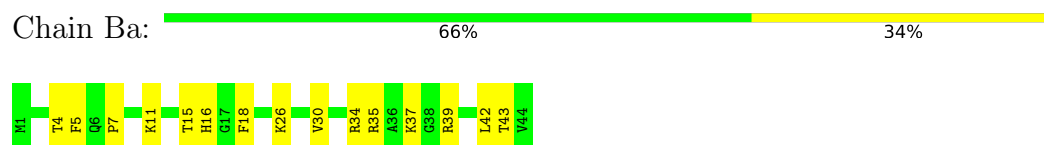
MET ALA ASN Q4 R5 I6 I7 R8 R9 L10 K11 S12 F13 D14 H15 R16 L17 I18 D19 Q20 S21 A22 Q23 E24 T25 V26 D27 T28 A29 K30 R31 T32 G33 A34 Q35 V36 C37 G38 P39 V40 P43 T44 R45 T46 E47 N50 V51 L52 V57 N58 K59 R62 E66 T67 R68

T69 H70 K71 R72 M73 V74 D75 I76 V77 Q78 T79 D81 K82 T83 V84 D85 A86 L87 K88 K89 L90 D91 L92 L93 A94 G95 V96 D97 V98 Q99 I100 A101 L102 G103

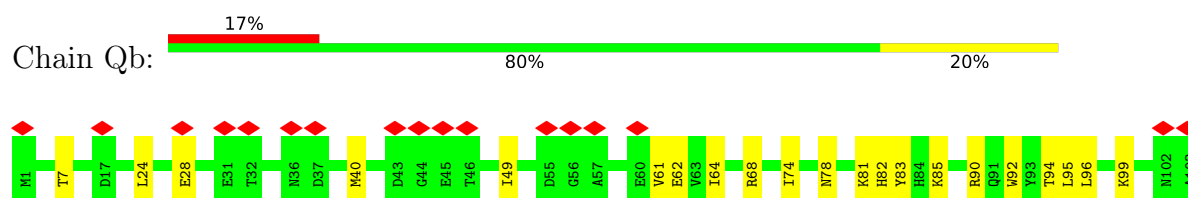
- Molecule 38: Small ribosomal subunit protein uS17



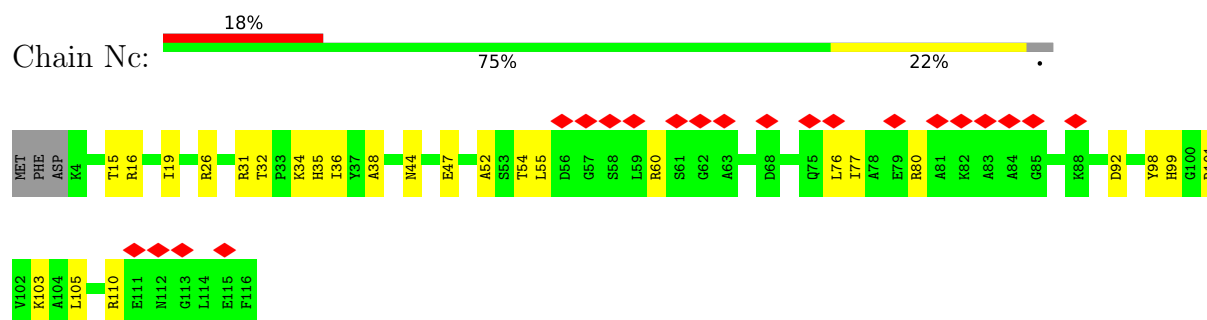
- Molecule 39: Large ribosomal subunit protein bL34



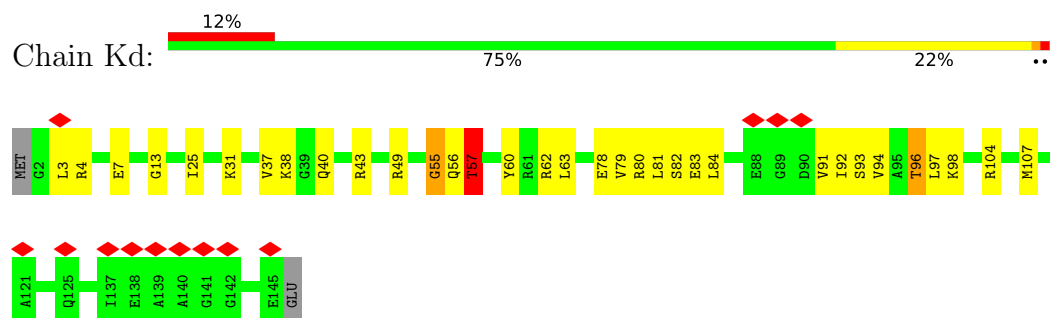
- Molecule 40: Large ribosomal subunit protein bL21



- Molecule 41: Large ribosomal subunit protein uL18



- Molecule 42: Large ribosomal subunit protein uL15



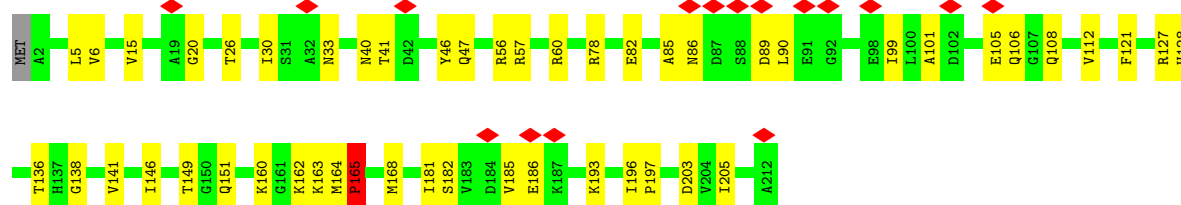
- Molecule 43: Large ribosomal subunit protein uL14

Chain Je: 



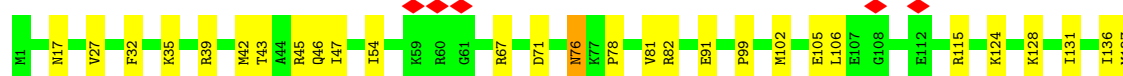
- Molecule 44: Large ribosomal subunit protein uL3

Chain Af: 



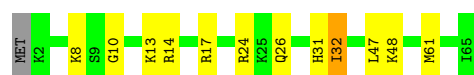
- Molecule 45: Large ribosomal subunit protein uL16

Chain Lg: 



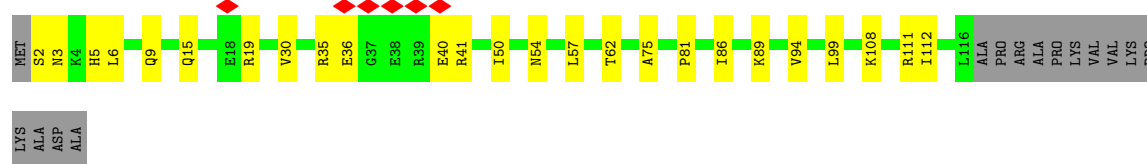
- Molecule 46: Large ribosomal subunit protein bL35

Chain dh: 



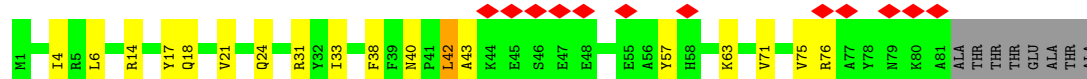
- Molecule 47: Large ribosomal subunit protein bL19

Chain Oi: 

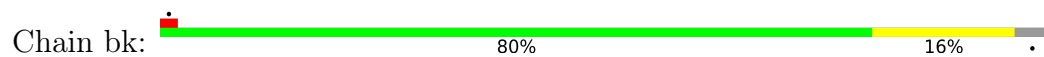


- Molecule 48: Small ribosomal subunit protein bS16

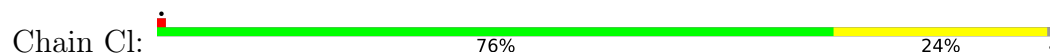
Chain Pj: 



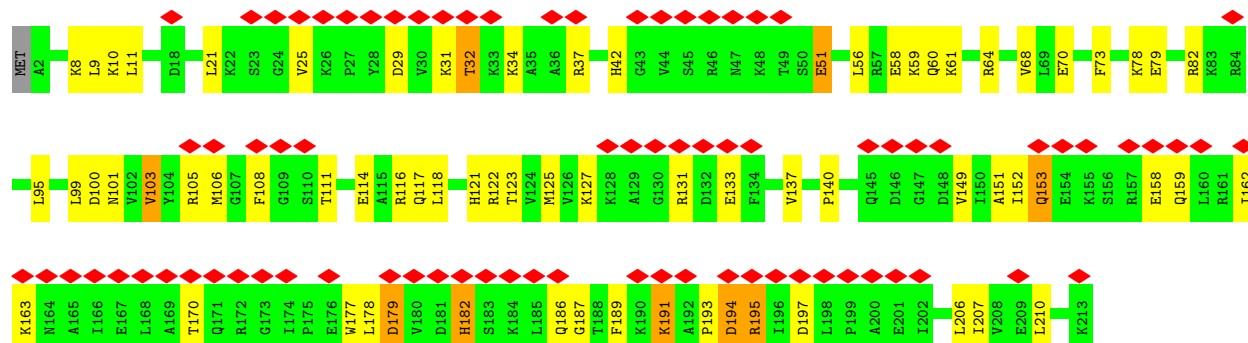
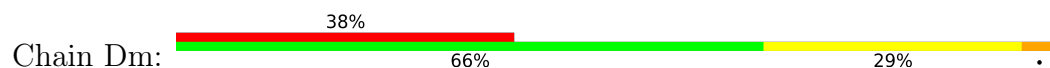
- Molecule 49: Large ribosomal subunit protein bL33



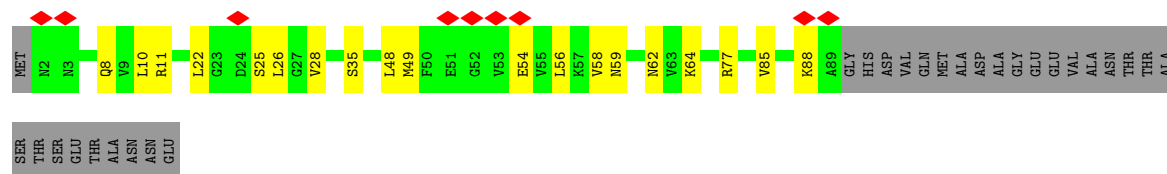
- Molecule 50: Large ribosomal subunit protein uL2



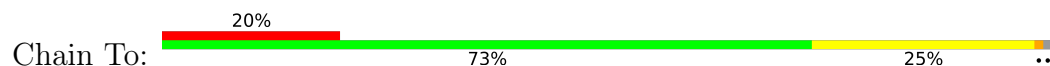
- Molecule 51: Small ribosomal subunit protein uS4



- Molecule 52: Large ribosomal subunit protein uL23

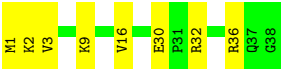
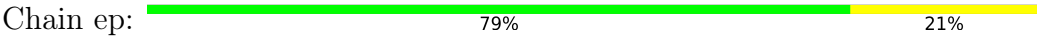


- Molecule 53: Small ribosomal subunit protein bS20

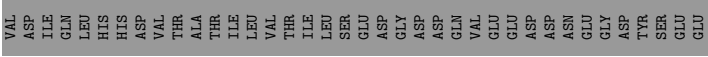
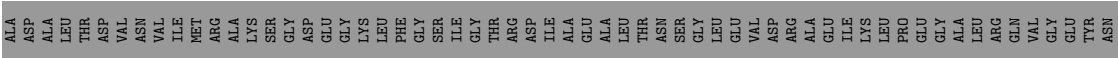
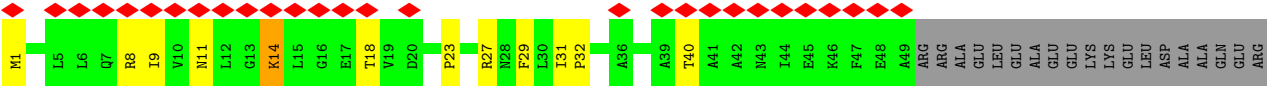




• Molecule 54: Large ribosomal subunit protein bL36



• Molecule 55: Large ribosomal subunit protein bL9



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	12151	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	0.156	Depositor
Minimum map value	-0.070	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.0189	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, GDP

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	0.25	0/2914	0.48	1/3952 (0.0%)
2	D	0.08	0/126	0.19	0/173
3	F	0.16	0/978	0.37	0/1311
4	H	0.18	0/2968	0.41	0/4026
5	Z2	0.24	0/65580	0.32	0/102277
6	R3	0.16	0/465	0.31	0/629
7	A4	0.16	0/1848	0.35	0/2494
8	E5	0.18	0/1163	0.37	0/1564
9	L6	0.19	0/959	0.44	0/1282
10	F7	0.16	0/1383	0.33	0/1858
11	D8	0.18	0/2733	0.26	0/4256
12	E9	0.20	0/1559	0.36	0/2103
13	aA	0.20	0/450	0.33	0/596
14	MB	0.22	0/961	0.32	0/1282
15	UC	0.17	0/774	0.33	0/1043
16	WD	0.20	0/628	0.33	0/841
17	XE	0.14	0/503	0.34	0/670
18	RF	0.20	0/840	0.32	0/1125
19	FG	0.13	0/864	0.28	0/1169
20	VH	0.22	0/635	0.38	0/847
21	TI	0.16	0/790	0.36	0/1057
22	fJ	0.12	0/508	0.31	0/690
23	HK	0.14	0/821	0.28	0/1091
24	OL	0.17	0/702	0.28	0/941
25	MM	0.11	0/917	0.27	0/1236
26	iN	0.19	0/36109	0.28	0/56319
27	PO	0.21	0/947	0.34	0/1261
28	SP	0.11	0/628	0.26	0/847
29	BQ	0.17	0/982	0.28	0/1318
30	GR	0.15	0/1377	0.33	0/1861
31	GS	0.12	0/1219	0.26	0/1634
32	CT	0.15	0/1637	0.38	0/2200

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	KU	0.13	0/857	0.28	0/1158
34	NV	0.13	0/478	0.31	0/632
35	YW	0.19	0/442	0.32	0/590
36	IX	0.21	0/1134	0.34	0/1529
37	JY	0.16	0/803	0.40	0/1084
38	QZ	0.17	0/638	0.32	0/858
39	Ba	0.26	0/373	0.37	0/489
40	Qb	0.20	0/839	0.34	0/1127
41	Nc	0.18	0/863	0.31	0/1158
42	Kd	0.40	1/1073 (0.1%)	0.54	3/1429 (0.2%)
43	Je	0.20	0/946	0.34	0/1271
44	Af	0.33	1/1566 (0.1%)	0.52	3/2103 (0.1%)
45	Lg	0.26	0/1112	0.45	0/1483
46	dh	0.26	0/524	0.48	0/686
47	Oi	0.23	0/927	0.41	0/1239
48	Pj	0.22	0/660	0.41	0/887
49	bk	0.22	0/401	0.37	0/534
50	Cl	0.24	0/2147	0.40	0/2883
51	Dm	0.19	0/1713	0.50	0/2296
52	Sn	0.21	0/705	0.42	0/939
53	To	0.19	0/688	0.50	0/916
54	ep	0.26	0/300	0.38	0/395
55	C1	0.21	0/379	0.51	0/511
All	All	0.22	2/154536 (0.0%)	0.33	7/230150 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	Af	165	PRO	CG-CD	-8.05	1.23	1.50
42	Kd	55	GLY	C-O	-5.02	1.17	1.23

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	Af	165	PRO	N-CD-CG	-11.81	85.49	103.20
44	Af	165	PRO	CA-CB-CG	-10.19	85.14	104.50
44	Af	165	PRO	N-CA-CB	-6.16	96.91	103.38
1	B	7	SER	N-CA-C	-6.12	107.64	114.62
42	Kd	56	GLN	N-CA-CB	5.79	118.48	109.97

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	2871	0	2815	56	0
2	D	127	0	75	1	0
3	F	965	0	1009	29	0
4	H	2918	0	2868	57	0
5	Z2	58553	0	29435	655	0
6	R3	457	0	466	12	0
7	A4	1816	0	1843	25	0
8	E5	1151	0	1205	32	0
9	L6	946	0	1008	26	0
10	F7	1362	0	1402	31	0
11	D8	2446	0	1241	34	0
12	E9	1537	0	1590	31	0
13	aA	442	0	432	5	0
14	MB	947	0	988	9	0
15	UC	760	0	774	9	0
16	WD	618	0	637	13	0
17	XE	502	0	527	9	0
18	RF	834	0	898	17	0
19	FG	849	0	838	19	0
20	VH	626	0	629	11	0
21	TI	784	0	820	13	0
22	fJ	493	0	441	9	0
23	HK	811	0	845	29	0
24	OL	694	0	710	15	0
25	MM	907	0	955	21	0
26	iN	32246	0	16223	430	0
27	PO	935	0	999	15	0
28	SP	614	0	643	15	0
29	BQ	974	0	1009	19	0
30	GR	1357	0	1397	17	0
31	GS	1200	0	1231	12	0
32	CT	1613	0	1677	31	0
33	KU	842	0	850	20	0
34	NV	472	0	520	9	0
35	YW	438	0	476	7	0
36	IX	1108	0	1145	21	0
37	JY	793	0	821	25	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	QZ	632	0	676	17	0
39	Ba	369	0	418	14	0
40	Qb	827	0	862	15	0
41	Nc	852	0	880	18	0
42	Kd	1062	0	1123	32	0
43	Je	937	0	1003	18	0
44	Af	1548	0	1574	35	0
45	Lg	1093	0	1188	21	0
46	dh	519	0	581	9	0
47	Oi	917	0	969	21	0
48	Pj	648	0	661	13	0
49	bk	394	0	412	4	0
50	Cl	2107	0	2195	53	0
51	Dm	1689	0	1745	45	0
52	Sn	698	0	750	14	0
53	To	684	0	727	16	0
54	ep	298	0	334	6	0
55	C1	374	0	406	5	0
56	H	28	0	12	1	0
57	H	1	0	0	0	0
58	Z2	1	0	0	1	0
All	All	142686	0	97958	1862	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 1862 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)
44:Af:127:ARG:HA	44:Af:168:MET:HE3	1.56	0.86
14:MB:37:THR:HG22	14:MB:39:PRO:HD2	1.59	0.84
45:Lg:102:MET:H	45:Lg:102:MET:HE2	1.43	0.83
5:Z2:142:C:O2	5:Z2:149:G:N2	2.11	0.82
23:HK:58:VAL:HG21	26:iN:1361:G:H4'	1.62	0.82

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	366/369 (99%)	345 (94%)	21 (6%)	0	100	100
2	D	23/123 (19%)	23 (100%)	0	0	100	100
3	F	122/128 (95%)	111 (91%)	11 (9%)	0	100	100
4	H	384/396 (97%)	371 (97%)	13 (3%)	0	100	100
6	R3	54/76 (71%)	54 (100%)	0	0	100	100
7	A4	231/269 (86%)	217 (94%)	14 (6%)	0	100	100
8	E5	154/171 (90%)	148 (96%)	6 (4%)	0	100	100
9	L6	120/124 (97%)	113 (94%)	7 (6%)	0	100	100
10	F7	175/178 (98%)	167 (95%)	8 (5%)	0	100	100
12	E9	197/200 (98%)	191 (97%)	6 (3%)	0	100	100
13	aA	51/60 (85%)	50 (98%)	1 (2%)	0	100	100
14	MB	117/119 (98%)	112 (96%)	5 (4%)	0	100	100
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%)	59 (98%)	1 (2%)	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%)	77 (94%)	5 (6%)	0	100	100
21	TI	100/105 (95%)	95 (95%)	5 (5%)	0	100	100
22	fJ	57/93 (61%)	54 (95%)	3 (5%)	0	100	100
23	HK	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
24	OL	84/88 (96%)	80 (95%)	4 (5%)	0	100	100
25	MM	114/118 (97%)	113 (99%)	1 (1%)	0	100	100
27	PO	114/118 (97%)	114 (100%)	0	0	100	100
28	SP	76/91 (84%)	76 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	BQ	129/132 (98%)	129 (100%)	0	0	100	100
30	GR	173/177 (98%)	164 (95%)	9 (5%)	0	100	100
31	GS	151/157 (96%)	148 (98%)	3 (2%)	0	100	100
32	CT	203/241 (84%)	190 (94%)	13 (6%)	0	100	100
33	KU	113/129 (88%)	108 (96%)	5 (4%)	0	100	100
34	NV	55/71 (78%)	55 (100%)	0	0	100	100
35	YW	54/59 (92%)	53 (98%)	1 (2%)	0	100	100
36	IX	140/142 (99%)	137 (98%)	3 (2%)	0	100	100
37	JY	98/103 (95%)	93 (95%)	5 (5%)	0	100	100
38	QZ	77/91 (85%)	75 (97%)	2 (3%)	0	100	100
39	Ba	42/44 (96%)	39 (93%)	3 (7%)	0	100	100
40	Qb	101/103 (98%)	98 (97%)	3 (3%)	0	100	100
41	Nc	111/116 (96%)	106 (96%)	5 (4%)	0	100	100
42	Kd	143/146 (98%)	133 (93%)	10 (7%)	0	100	100
43	Je	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
44	Af	209/212 (99%)	198 (95%)	10 (5%)	1 (0%)	24	40
45	Lg	135/137 (98%)	132 (98%)	3 (2%)	0	100	100
46	dh	62/65 (95%)	61 (98%)	0	1 (2%)	7	13
47	Oi	113/130 (87%)	105 (93%)	8 (7%)	0	100	100
48	Pj	79/89 (89%)	79 (100%)	0	0	100	100
49	bk	47/51 (92%)	46 (98%)	1 (2%)	0	100	100
50	Cl	270/274 (98%)	260 (96%)	10 (4%)	0	100	100
51	Dm	210/213 (99%)	201 (96%)	9 (4%)	0	100	100
52	Sn	86/116 (74%)	85 (99%)	1 (1%)	0	100	100
53	To	85/88 (97%)	84 (99%)	1 (1%)	0	100	100
54	ep	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
55	C1	47/166 (28%)	45 (96%)	2 (4%)	0	100	100
All	All	6244/7029 (89%)	6007 (96%)	235 (4%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
46	dh	32	ILE

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Mol	Chain	Res	Type
44	Af	141	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	306/310 (99%)	270 (88%)	36 (12%)	5	9
2	D	2/87 (2%)	2 (100%)	0	100	100
3	F	101/105 (96%)	99 (98%)	2 (2%)	48	67
4	H	314/327 (96%)	312 (99%)	2 (1%)	78	87
6	R3	51/67 (76%)	50 (98%)	1 (2%)	48	67
7	A4	188/211 (89%)	187 (100%)	1 (0%)	81	88
8	E5	118/131 (90%)	116 (98%)	2 (2%)	53	71
9	L6	102/103 (99%)	93 (91%)	9 (9%)	9	17
10	F7	139/146 (95%)	138 (99%)	1 (1%)	76	85
12	E9	159/159 (100%)	158 (99%)	1 (1%)	78	87
13	aA	46/53 (87%)	45 (98%)	1 (2%)	45	65
14	MB	101/102 (99%)	99 (98%)	2 (2%)	48	67
15	UC	79/184 (43%)	78 (99%)	1 (1%)	61	75
16	WD	67/71 (94%)	65 (97%)	2 (3%)	36	58
17	XE	54/57 (95%)	53 (98%)	1 (2%)	50	68
18	RF	88/88 (100%)	87 (99%)	1 (1%)	65	79
19	FG	92/121 (76%)	92 (100%)	0	100	100
20	VH	60/62 (97%)	59 (98%)	1 (2%)	53	71
21	TI	83/85 (98%)	83 (100%)	0	100	100
22	fJ	52/81 (64%)	52 (100%)	0	100	100
23	HK	87/88 (99%)	86 (99%)	1 (1%)	65	79
24	OL	75/77 (97%)	73 (97%)	2 (3%)	39	61
25	MM	97/99 (98%)	97 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	PO	88/90 (98%)	87 (99%)	1 (1%)	65	79
28	SP	69/79 (87%)	69 (100%)	0	100	100
29	BQ	103/104 (99%)	103 (100%)	0	100	100
30	GR	149/151 (99%)	147 (99%)	2 (1%)	61	75
31	GS	124/128 (97%)	123 (99%)	1 (1%)	73	83
32	CT	168/198 (85%)	165 (98%)	3 (2%)	51	69
33	KU	85/98 (87%)	83 (98%)	2 (2%)	43	63
34	NV	49/63 (78%)	47 (96%)	2 (4%)	27	48
35	YW	50/52 (96%)	50 (100%)	0	100	100
36	IX	116/117 (99%)	116 (100%)	0	100	100
37	JY	88/90 (98%)	88 (100%)	0	100	100
38	QZ	73/84 (87%)	71 (97%)	2 (3%)	39	61
39	Ba	37/37 (100%)	37 (100%)	0	100	100
40	Qb	89/89 (100%)	88 (99%)	1 (1%)	65	79
41	Nc	81/85 (95%)	81 (100%)	0	100	100
42	Kd	108/110 (98%)	106 (98%)	2 (2%)	50	68
43	Je	102/102 (100%)	100 (98%)	2 (2%)	48	67
44	Af	161/162 (99%)	159 (99%)	2 (1%)	63	77
45	Lg	114/114 (100%)	112 (98%)	2 (2%)	51	69
46	dh	55/56 (98%)	54 (98%)	1 (2%)	51	69
47	Oi	97/108 (90%)	94 (97%)	3 (3%)	35	57
48	Pj	63/68 (93%)	62 (98%)	1 (2%)	55	72
49	bk	42/46 (91%)	42 (100%)	0	100	100
50	Cl	219/221 (99%)	218 (100%)	1 (0%)	81	88
51	Dm	177/181 (98%)	158 (89%)	19 (11%)	6	12
52	Sn	76/97 (78%)	75 (99%)	1 (1%)	61	75
53	To	67/69 (97%)	65 (97%)	2 (3%)	36	58
54	ep	33/33 (100%)	33 (100%)	0	100	100
55	C1	39/135 (29%)	33 (85%)	6 (15%)	2	3
All	All	5183/5781 (90%)	5060 (98%)	123 (2%)	43	63

5 of 123 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
14	MB	95	LEU
51	Dm	191	LYS
32	CT	16	LYS
51	Dm	182	HIS
55	C1	11	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 47 such sidechains are listed below:

Mol	Chain	Res	Type
36	IX	136	GLN
43	Je	110	GLN
38	QZ	43	GLN
43	Je	13	ASN
44	Af	65	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	D8	114/115 (99%)	16 (14%)	0
26	iN	1499/1590 (94%)	272 (18%)	0
5	Z2	2723/2882 (94%)	425 (15%)	19 (0%)
All	All	4336/4587 (94%)	713 (16%)	19 (0%)

5 of 713 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	Z2	10	U
5	Z2	16	A
5	Z2	19	G
5	Z2	22	G
5	Z2	30	G

5 of 19 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	Z2	2223	U
5	Z2	2457	U
5	Z2	2739	U
5	Z2	2355	U
5	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](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
56	GDP	H	401	57	29,30,30	1.18	3 (10%)	45,47,47	1.75	7 (15%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
56	GDP	H	401	57	-	3/16/32/32	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	H	401	GDP	C5-C4	3.27	1.47	1.38
56	H	401	GDP	C6-N1	-2.52	1.34	1.38
56	H	401	GDP	C5-N7	-2.11	1.34	1.39

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	H	401	GDP	C5-C4-N3	-6.24	118.46	128.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	H	401	GDP	N9-C4-N3	4.78	135.51	125.95
56	H	401	GDP	C2-N3-C4	4.77	120.52	112.30
56	H	401	GDP	C6-C5-N7	2.81	135.41	130.29
56	H	401	GDP	C4-C5-N7	-2.46	106.78	110.67

There are no chirality outliers.

All (3) torsion outliers are listed below:

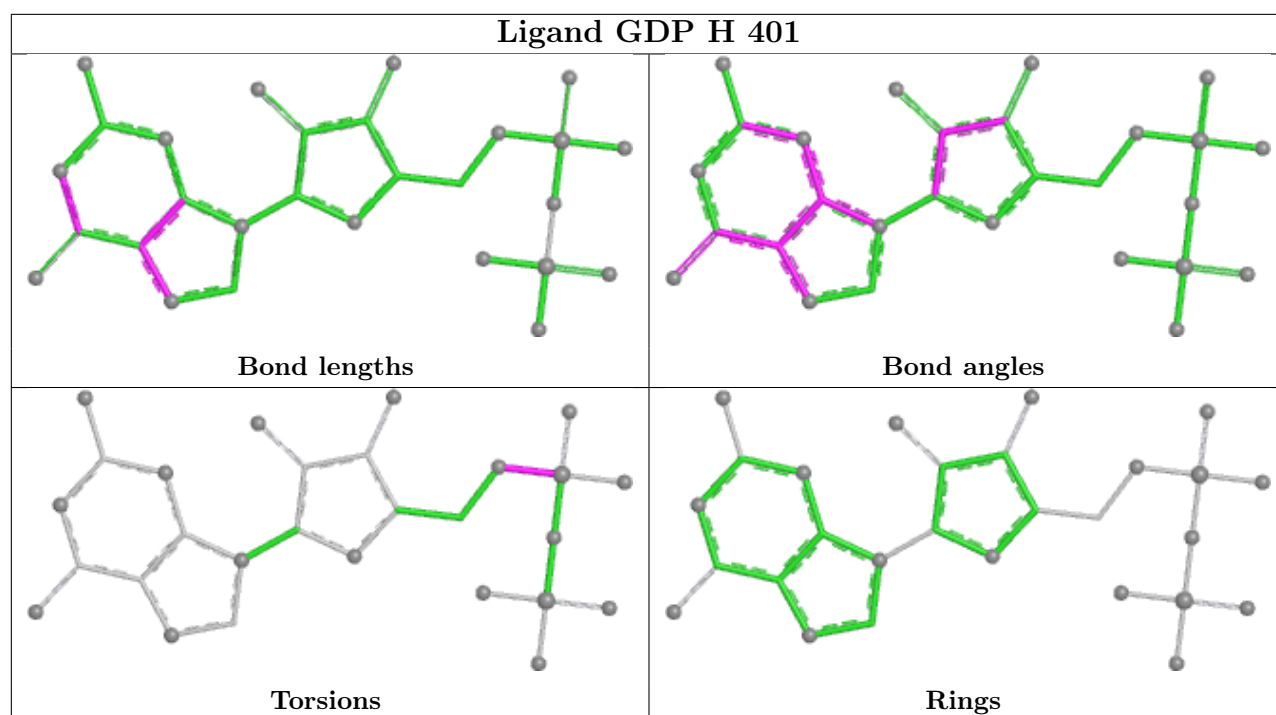
Mol	Chain	Res	Type	Atoms
56	H	401	GDP	C5'-O5'-PA-O1A
56	H	401	GDP	C5'-O5'-PA-O3A
56	H	401	GDP	C5'-O5'-PA-O2A

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
56	H	401	GDP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

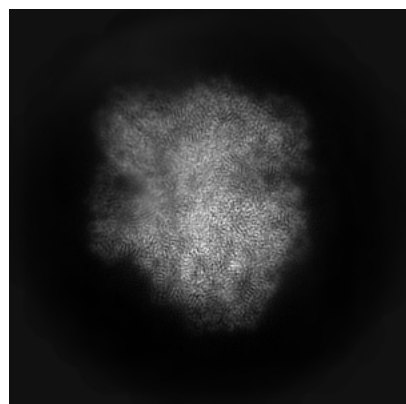
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-19077. These allow visual inspection of the internal detail of the map and identification of artifacts.

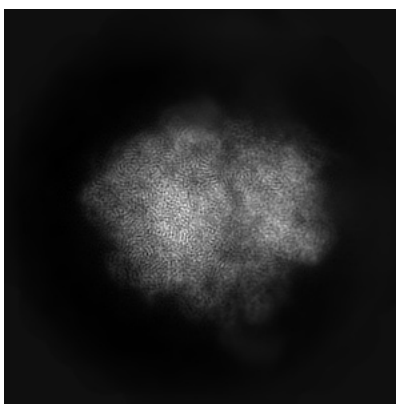
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

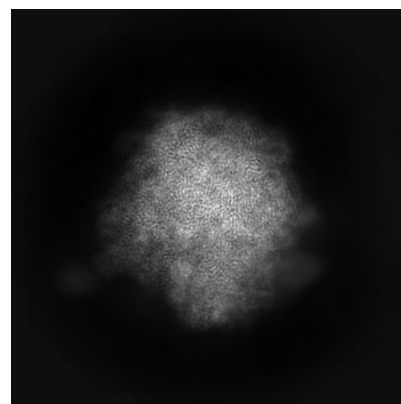
6.1.1 Primary map



X

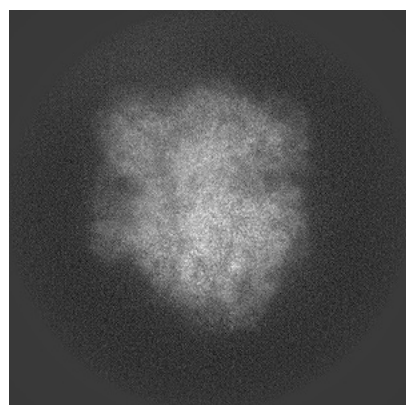


Y

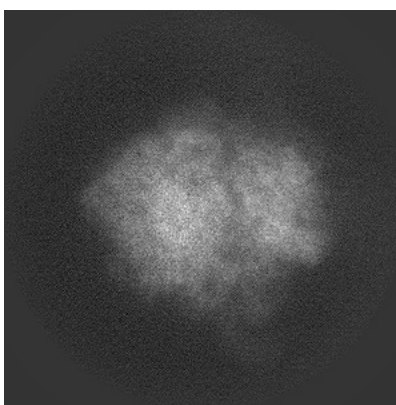


Z

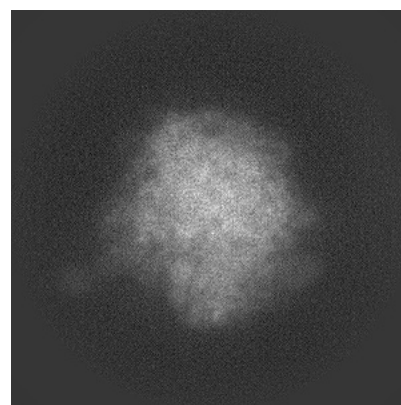
6.1.2 Raw map



X



Y

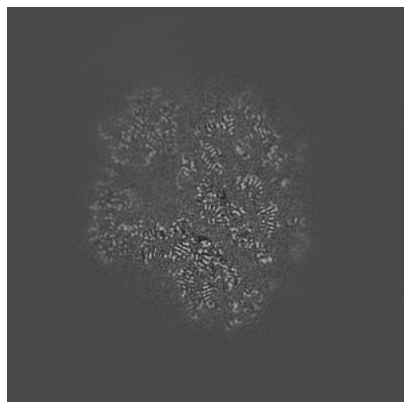


Z

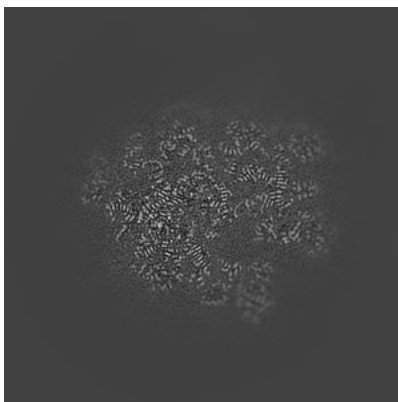
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

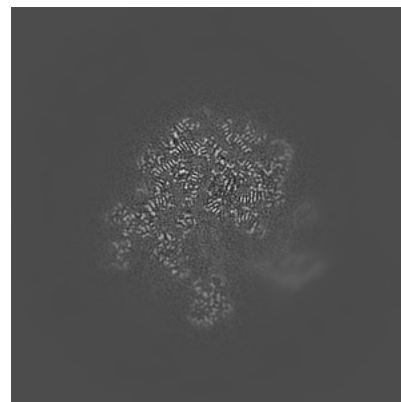
6.2.1 Primary map



X Index: 270

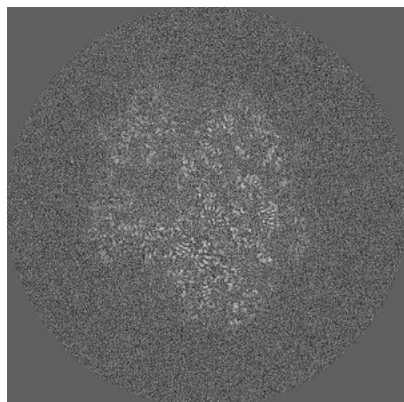


Y Index: 270

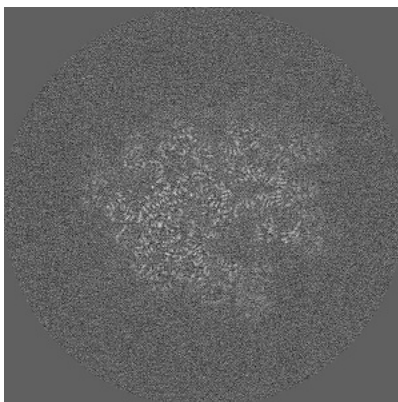


Z Index: 270

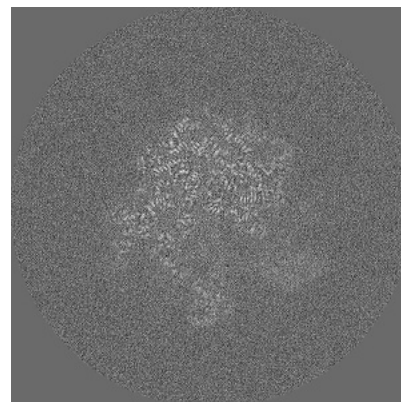
6.2.2 Raw map



X Index: 270



Y Index: 270

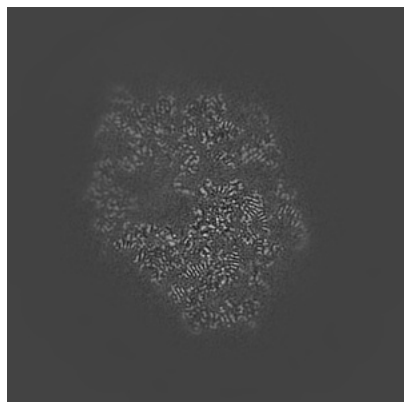


Z Index: 270

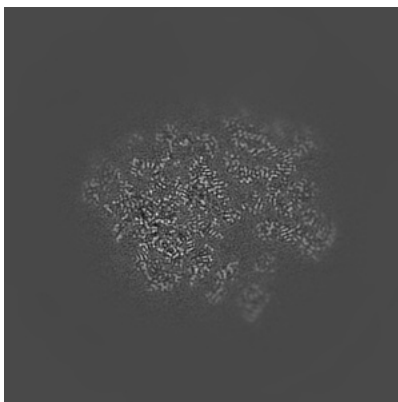
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

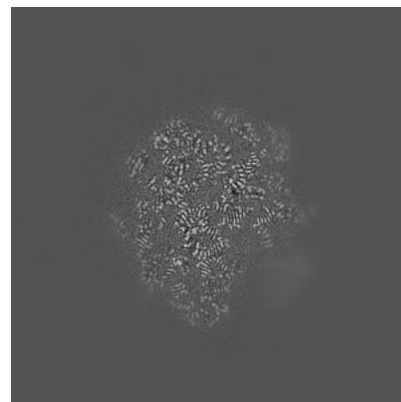
6.3.1 Primary map



X Index: 286

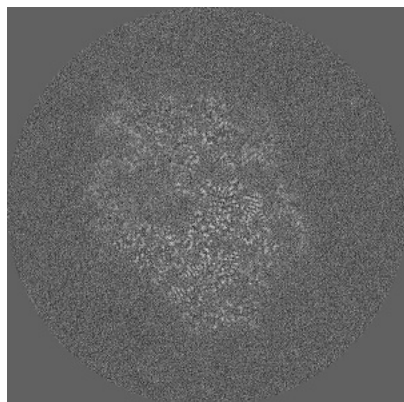


Y Index: 277

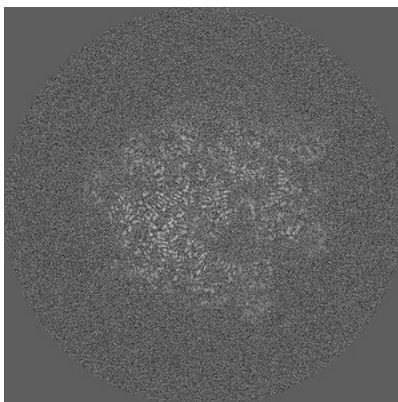


Z Index: 237

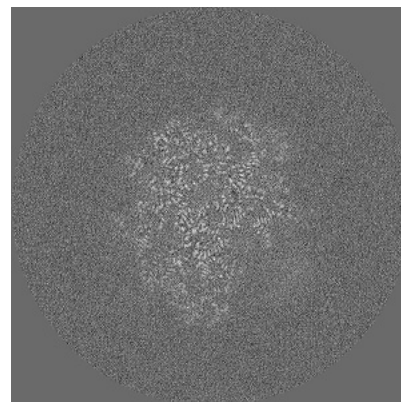
6.3.2 Raw map



X Index: 286



Y Index: 268

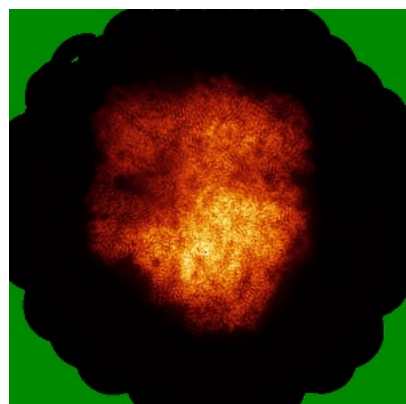


Z Index: 237

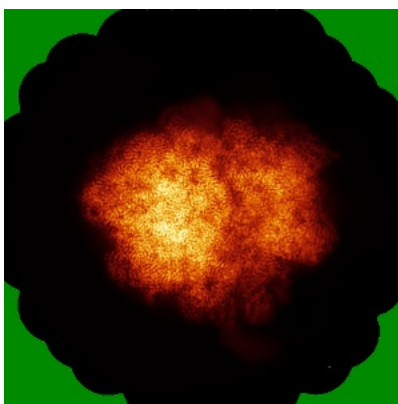
The images above show the largest variance slices of the map in three orthogonal directions.

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

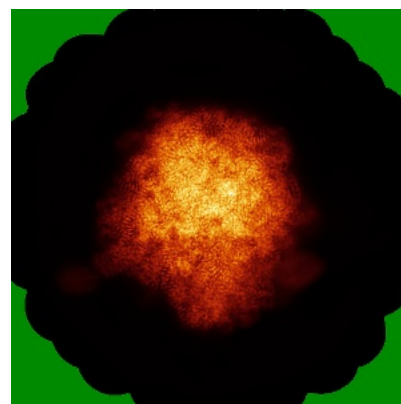
6.4.1 Primary map



X

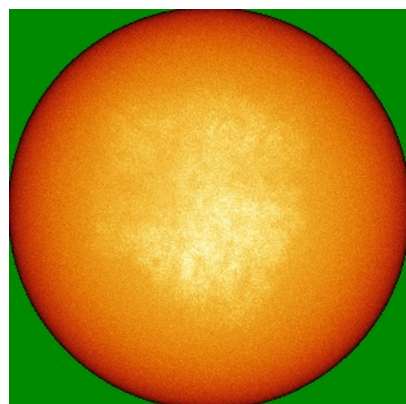


Y

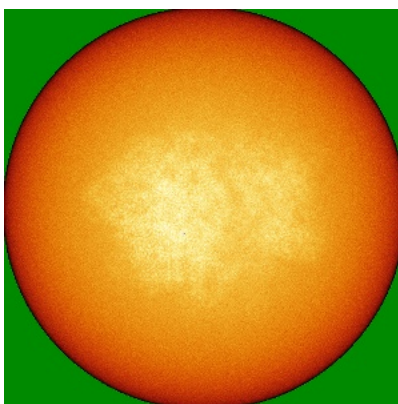


Z

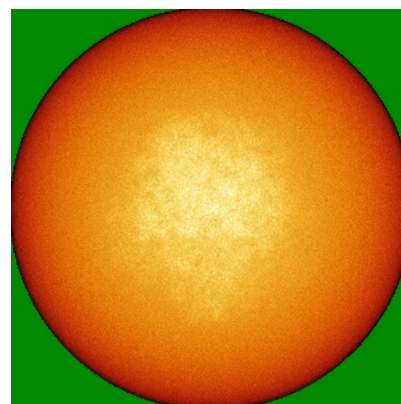
6.4.2 Raw map



X



Y

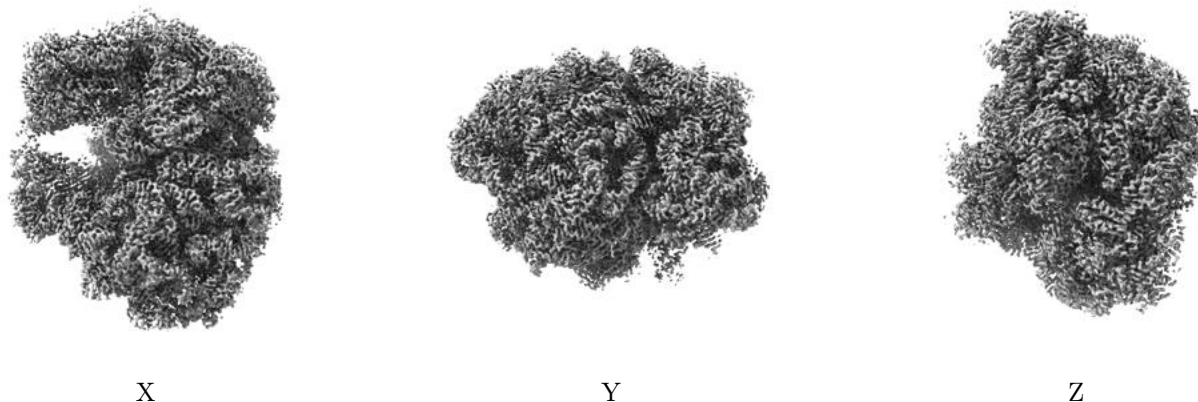


Z

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.

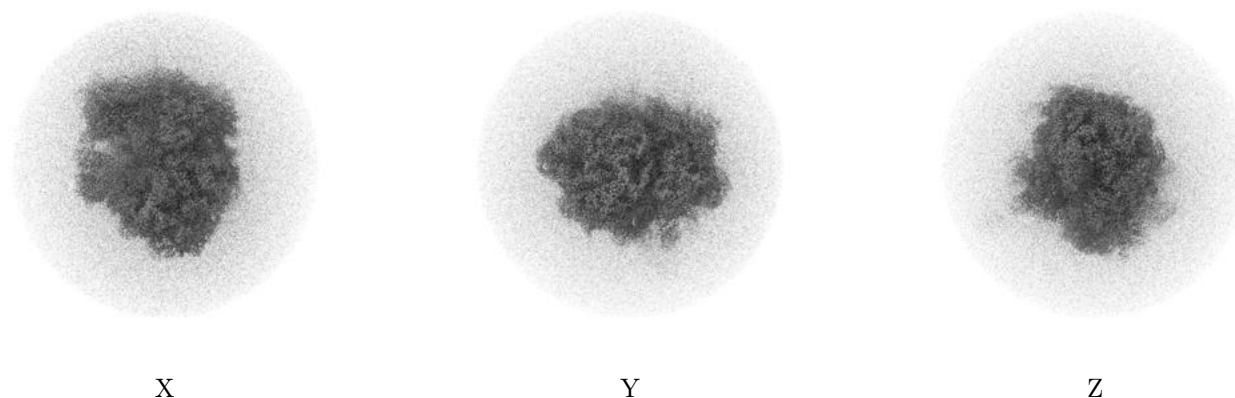
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0189. 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.

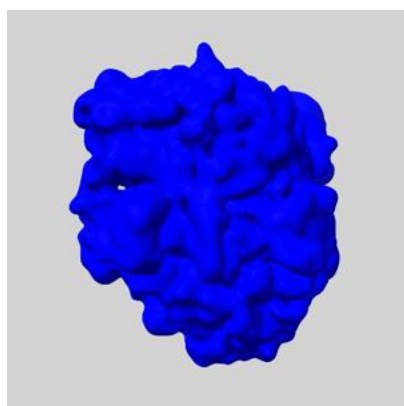
6.6 Mask visualisation [i](#)

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

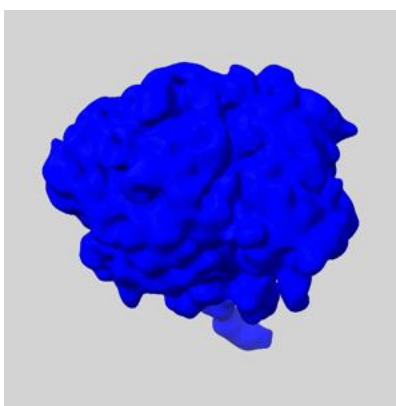
A mask typically either:

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

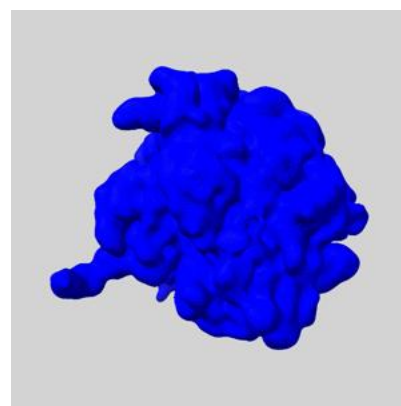
6.6.1 emd_19077_msk_1.map [i](#)



X



Y

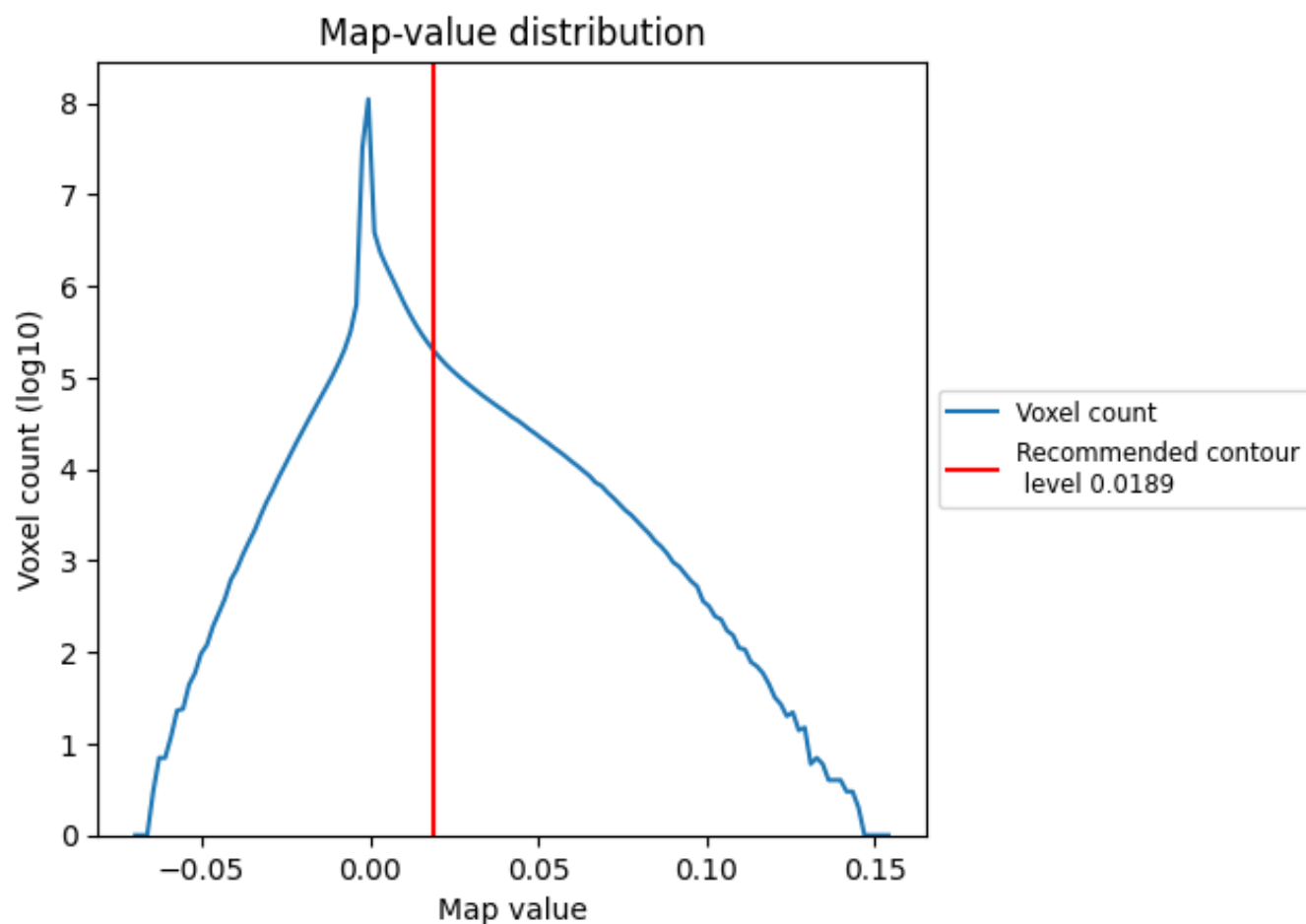


Z

7 Map analysis [i](#)

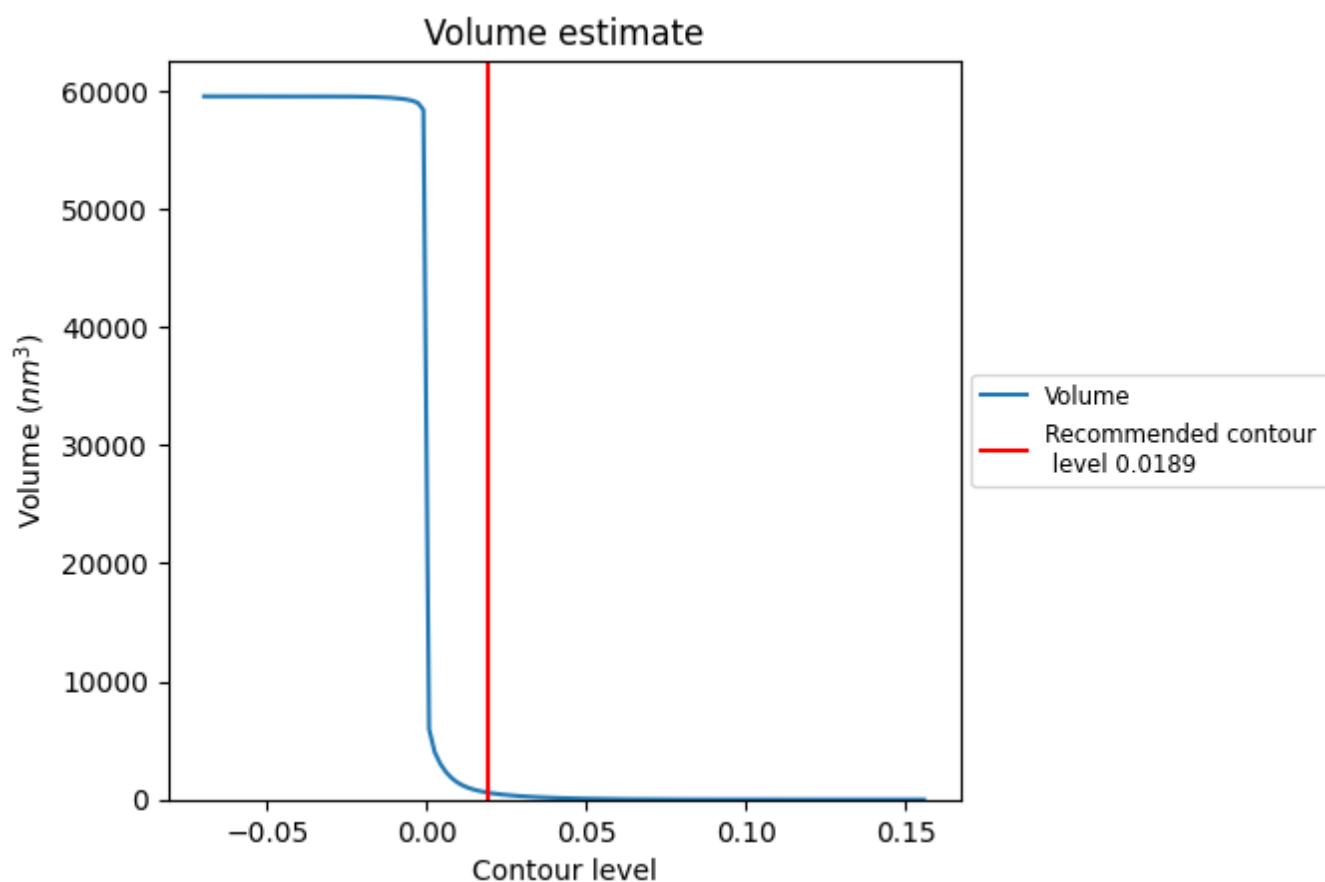
This section contains the results of statistical analysis of the map.

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.

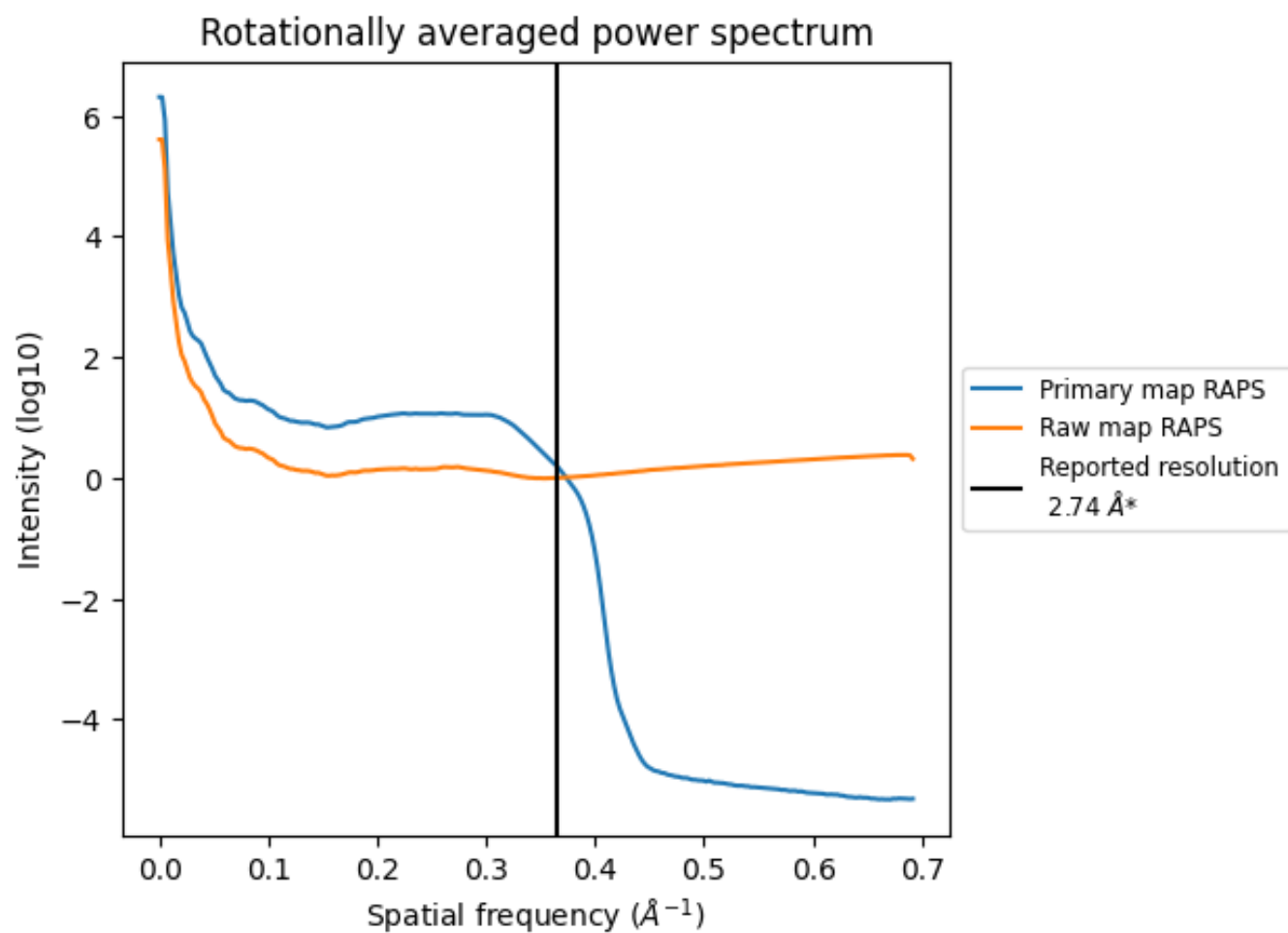
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 597 nm³; this corresponds to an approximate mass of 539 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

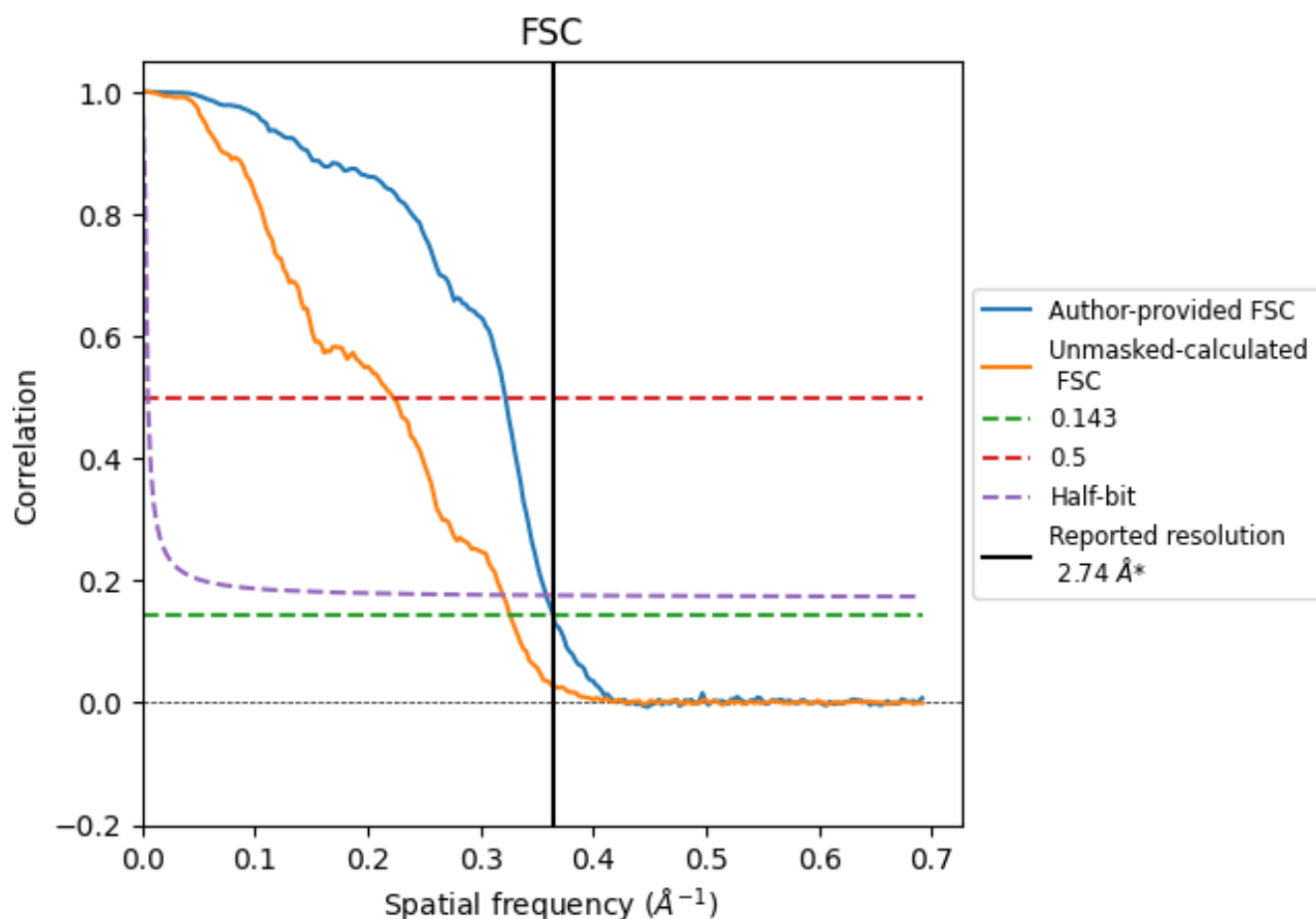


*Reported resolution corresponds to spatial frequency of 0.365 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.365 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

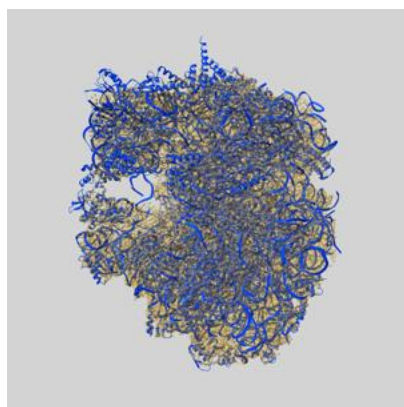
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.74	-	-
Author-provided FSC curve	2.74	3.11	2.79
Unmasked-calculated*	3.07	4.50	3.12

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.07 differs from the reported value 2.74 by more than 10 %

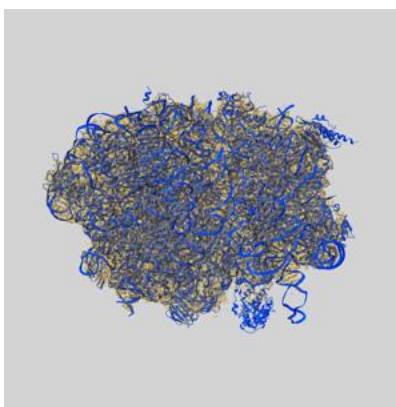
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-19077 and PDB model 8RDW. Per-residue inclusion information can be found in section [3](#) on page [15](#).

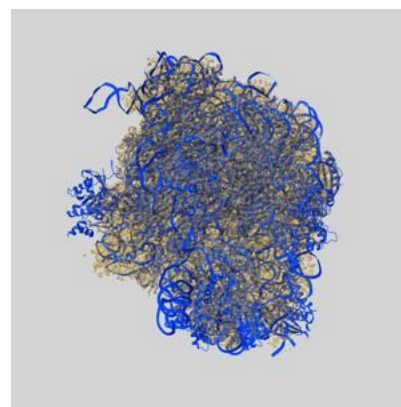
9.1 Map-model overlay [i](#)



X



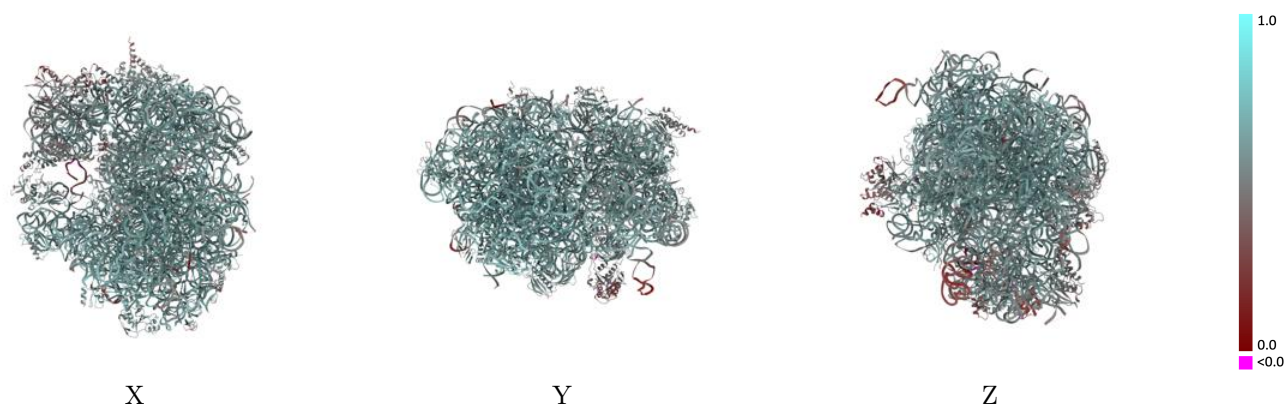
Y



Z

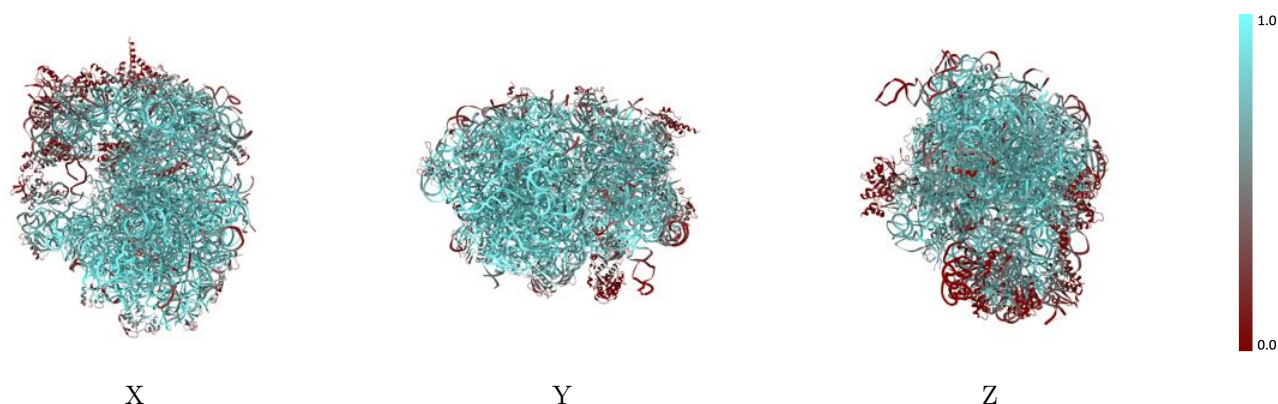
The images above show the 3D surface view of the map at the recommended contour level 0.0189 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



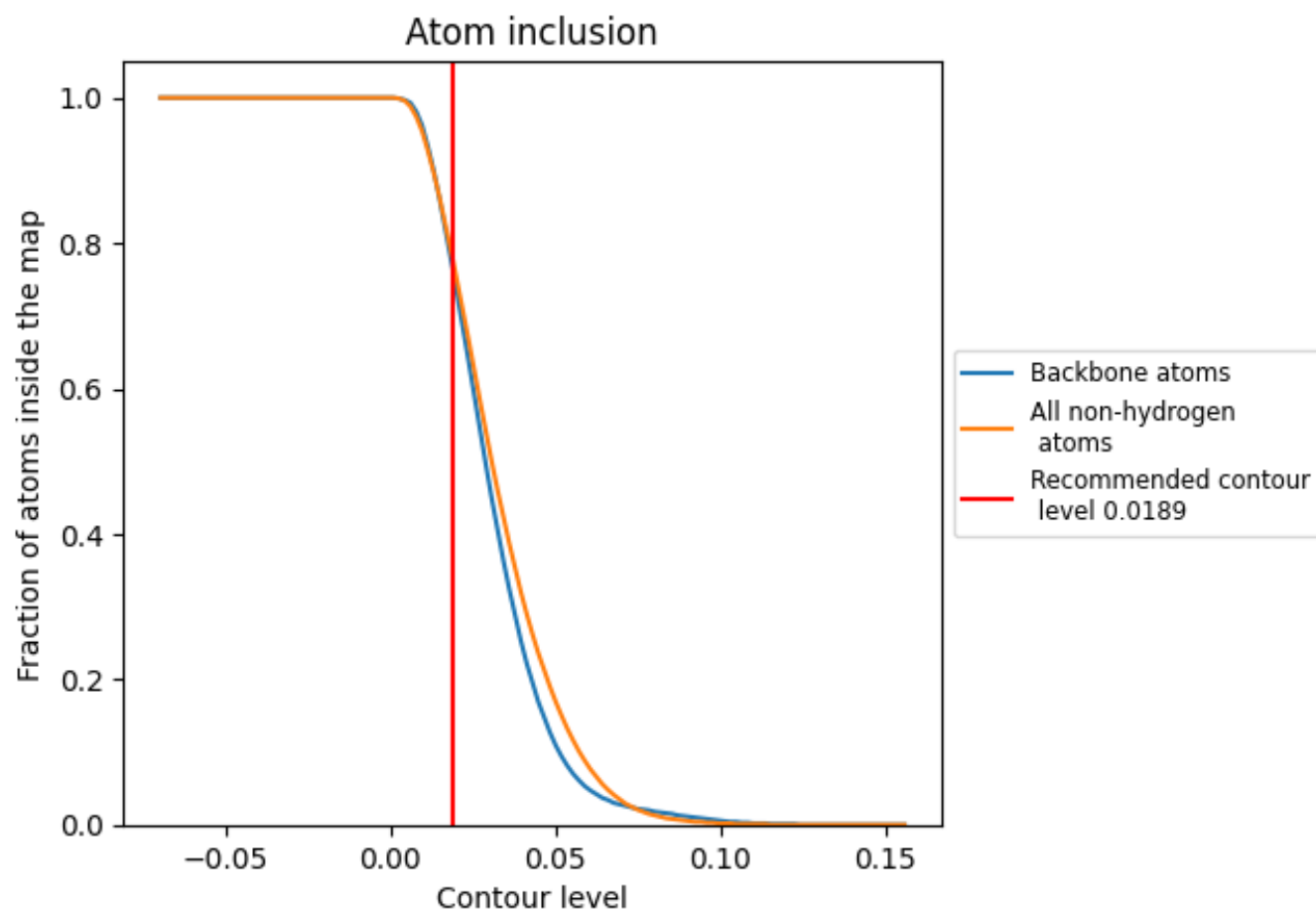
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0189).

9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 78% 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 (0.0189) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7760	 0.6040
A4	 0.2830	 0.4890
Af	 0.8530	 0.6440
B	 0.7490	 0.6110
BQ	 0.7080	 0.6110
Ba	 0.9710	 0.6650
C1	 0.3960	 0.5530
CT	 0.3990	 0.5150
Cl	 0.8880	 0.6460
D	 0.0000	 0.2270
D8	 0.8080	 0.6110
Dm	 0.4900	 0.5720
E5	 0.7180	 0.6030
E9	 0.7330	 0.6190
F	 0.3380	 0.5080
F7	 0.4150	 0.5300
FG	 0.4120	 0.5320
GR	 0.5370	 0.5720
GS	 0.2850	 0.4850
H	 0.2960	 0.4770
HK	 0.4000	 0.5100
IX	 0.8760	 0.6450
JY	 0.2760	 0.4470
Je	 0.8530	 0.6380
KU	 0.5010	 0.5470
Kd	 0.7870	 0.6230
L6	 0.8680	 0.6290
Lg	 0.8420	 0.6270
MB	 0.9170	 0.6520
MM	 0.2040	 0.4770
NV	 0.3550	 0.5370
Nc	 0.6620	 0.5960
OL	 0.6830	 0.5870
Oi	 0.8200	 0.6290
PO	 0.8940	 0.6550



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Chain	Atom inclusion	Q-score
Pj	 0.6810	 0.5980
QZ	 0.6480	 0.5710
Qb	 0.6910	 0.6110
R3	 0.6300	 0.5580
RF	 0.8600	 0.6440
SP	 0.1560	 0.4680
Sn	 0.7180	 0.6030
TI	 0.5490	 0.5430
To	 0.6740	 0.5890
UC	 0.6960	 0.6080
VH	 0.8710	 0.6360
WD	 0.7850	 0.6210
XE	 0.4510	 0.5510
YW	 0.8570	 0.6500
Z2	 0.9100	 0.6350
aA	 0.8740	 0.6530
bk	 0.8010	 0.6280
dh	 0.9620	 0.6560
ep	 0.9170	 0.6340
fJ	 0.1690	 0.4860
iN	 0.7760	 0.5870