



## wwPDB EM Validation Summary Report ⓘ

May 18, 2024 – 11:51 am BST

PDB ID : 6RXX  
EMDB ID : EMD-10054  
Title : Cryo-EM structure of the 90S pre-ribosome (Kre33-Noc4) from *Chaetomium thermophilum*, state C, Poly-Ala  
Authors : Cheng, J.; Kellner, N.; Griesel, S.; Berninghausen, O.; Beckmann, R.; Hurt, E.  
Deposited on : 2019-06-10  
Resolution : 7.10 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:

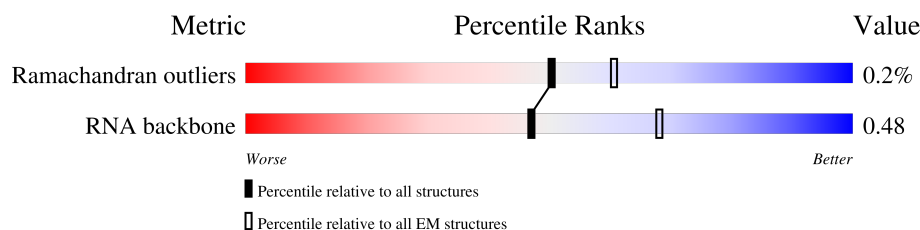
EMDB validation analysis : 0.0.1.dev92  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36.2

# 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 7.10 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
RNA backbone	4643	859

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	UA	904	<div> <div>9%</div> <div>93%</div> <div>7%</div> </div>
2	UC	648	<div> <div>11%</div> <div>89%</div> </div>
3	UF	414	<div> <div>80%</div> <div>20%</div> </div>
4	UG	558	<div> <div>17%</div> <div>85%</div> <div>14%</div> </div>
5	UK	270	<div> <div>37%</div> <div>80%</div> <div>20%</div> </div>
6	UL	962	<div> <div>6%</div> <div>81%</div> <div>18%</div> </div>
7	UM	912	<div> <div>11%</div> <div>79%</div> <div>20%</div> </div>
8	UN	938	<div> <div>19%</div> <div>81%</div> </div>
9	UR	618	<div> <div>11%</div> <div>72%</div> <div>28%</div> </div>

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Mol	Chain	Length	Quality of chain
10	UU	1049	
11	UX	193	
12	CJ	183	
13	CK	297	
14	CL	785	
15	CM	446	
16	CN	252	
16	CO	252	
17	CP	322	
18	CQ	259	
19	Ca	255	
20	Cc	212	
21	Ce	203	
22	Cg	190	
23	Ch	151	
24	Ci	150	
25	Cj	143	
26	Cm	130	
27	Cn	145	
28	Cp	68	
29	Cq	82	
30	CU	311	
31	C1	1859	
32	UV	1171	
33	CV	322	

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Mol	Chain	Length	Quality of chain
34	Cl	156	
35	CH	411	
36	CI	1163	
37	CR	1073	
37	CS	1073	
38	Cb	264	
39	Cd	239	
40	Cf	202	
41	Ck	161	
42	Co	136	
43	CW	668	
44	UT	2612	
45	CZ	609	
46	UB	907	
47	UD	884	
48	UJ	1802	
49	UO	557	
50	UQ	960	
51	CX	480	
52	UE	410	
52	UI	410	
53	UP	364	
54	UH	930	
55	US	549	
56	CA	313	

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Mol	Chain	Length	Quality of chain
56	CB	313	<div> <div>35%</div> <div>71%</div> <div>29%</div> </div>
57	CC	523	<div> <div>5%</div> <div>74%</div> <div>26%</div> </div>
58	CD	582	<div> <div>20%</div> <div>72%</div> <div>28%</div> </div>
59	CE	127	<div> <div>31%</div> <div>95%</div> <div>5%</div> </div>
59	CF	127	<div> <div>12%</div> <div>93%</div> <div>6%</div> </div>
60	CG	630	<div> <div>12%</div> <div>66%</div> <div>34%</div> </div>
61	CT	203	<div> <div>9%</div> <div>65%</div> <div>35%</div> </div>
62	C2	232	<div> <div>8%</div> <div>62%</div> <div>30%</div> <div>6%</div> </div>
63	Cr	153	<div> <div>25%</div> <div>90%</div> <div>7%</div> </div>

## 2 Entry composition

There are 64 unique types of molecules in this entry. The entry contains 146382 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 Periodic tryptophan protein 2-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	UA	839	Total	C	N	O	0	0
			4136	2458	839	839		

- Molecule 2 is a protein called Utp3.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	UC	74	Total	C	N	O	0	0
			361	213	74	74		

- Molecule 3 is a protein called Utp6.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	UF	331	Total	C	N	O	0	0
			1644	982	331	331		

- Molecule 4 is a protein called Utp7.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	UG	479	Total	C	N	O	0	0
			2361	1403	479	479		

- Molecule 5 is a protein called U3 small nucleolar RNA-associated protein 11.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	UK	217	Total	C	N	O	0	0
			1070	636	217	217		

- Molecule 6 is a protein called Utp12.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	UL	785	Total	C	N	O	0	0
			3877	2307	785	785		

- Molecule 7 is a protein called Utp13.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	UM	729	Total	C	N	O	0	0
			3602	2144	729	729		

- Molecule 8 is a protein called Utp14.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	UN	177	Total	C	N	O	0	0
			880	526	177	177		

- Molecule 9 is a protein called Utp18.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	UR	447	Total	C	N	O	0	0
			2198	1304	447	447		

- Molecule 10 is a protein called Putative U3 snoRNP protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	UU	902	Total	C	N	O	0	0
			4424	2620	902	902		

- Molecule 11 is a protein called Utp24.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	UX	190	Total	C	N	O	0	0
			942	562	190	190		

- Molecule 12 is a protein called Imp3.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	CJ	179	Total	C	N	O	0	0
			890	532	179	179		

- Molecule 13 is a protein called Putative U3 small nucleolar ribonucleoprotein.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	CK	297	Total	C	N	O	0	0
			1472	878	297	297		

- Molecule 14 is a protein called Putative U3 small nucleolar ribonucleoprotein protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	CL	231	Total	C	N	O	0	0
			1142	680	231	231		

- Molecule 15 is a protein called Sof1.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	CM	445	Total	C	N	O	0	0
			2201	1311	445	445		

- Molecule 16 is a protein called Emg1.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	CN	226	Total	C	N	O	0	0
			1122	670	226	226		
16	CO	215	Total	C	N	O	0	0
			1067	637	215	215		

- Molecule 17 is a protein called KRR1 small subunit processome component.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	CP	201	Total	C	N	O	0	0
			995	593	201	201		

- Molecule 18 is a protein called Pre-rRNA-processing protein PNO1.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	CQ	175	Total	C	N	O	0	0
			864	514	175	175		

- Molecule 19 is a protein called 40S ribosomal protein S1.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	Ca	225	Total	C	N	O	0	0
			1115	665	225	225		

- Molecule 20 is a protein called 40S ribosomal protein s5-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	Cc	192	Total	C	N	O	0	0
			953	569	192	192		

- Molecule 21 is a protein called 40S ribosomal protein S7.



Mol	Chain	Residues	Atoms				AltConf	Trace
21	Ce	159	Total	C	N	O	0	0
			786	468	159	159		

- Molecule 22 is a protein called 40S ribosomal protein s9-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	Cg	159	Total	C	N	O	0	0
			785	467	159	159		

- Molecule 23 is a protein called 40S ribosomal protein S13-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	Ch	150	Total	C	N	O	0	0
			741	441	150	150		

- Molecule 24 is a protein called 40S ribosomal protein S14-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	Ci	115	Total	C	N	O	0	0
			563	333	115	115		

- Molecule 25 is a protein called 40S ribosomal protein S16-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	Cj	126	Total	C	N	O	0	0
			622	370	126	126		

- Molecule 26 is a protein called 40S ribosomal protein S22-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	Cm	126	Total	C	N	O	0	0
			620	368	126	126		

- Molecule 27 is a protein called 40S ribosomal protein s23-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	Cn	96	Total	C	N	O	0	0
			469	277	96	96		

- Molecule 28 is a protein called 40S ribosomal protein S28-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	Cp	61	Total	C	N	O	0	0
			300	178	61	61		

- Molecule 29 is a protein called Ribosomal protein s27-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	Cq	81	Total	C	N	O	0	0
			400	238	81	81		

- Molecule 30 is a protein called Faf1.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	CU	176	Total	C	N	O	0	0
			871	519	176	176		

- Molecule 31 is a RNA chain called 35S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	C1	1221	Total	C	N	O	P	0	0
			26044	11631	4650	8542	1221		

- Molecule 32 is a protein called U3 small nucleolar RNA-associated protein 22.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	UV	1061	Total	C	N	O	0	0
			5244	3122	1061	1061		

- Molecule 33 is a protein called Rrp7.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	CV	148	Total	C	N	O	0	0
			732	436	148	148		

- Molecule 34 is a protein called Putative ribosomal protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	Cl	80	Total	C	N	O	0	0
			395	235	80	80		

- Molecule 35 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	CH	389	Total	C	N	O	0	0
			1902	1124	389	389		

- Molecule 36 is a protein called Bms1.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	CI	822	Total	C	N	O	0	0
			4061	2417	822	822		

- Molecule 37 is a protein called Kre33.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	CR	760	Total	C	N	O	0	0
			3755	2235	760	760		
37	CS	760	Total	C	N	O	0	0
			3755	2235	760	760		

- Molecule 38 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	Cb	232	Total	C	N	O	0	0
			1140	676	232	232		

- Molecule 39 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	Cd	226	Total	C	N	O	0	0
			1112	660	226	226		

- Molecule 40 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	Cf	174	Total	C	N	O	0	0
			852	504	174	174		

- Molecule 41 is a protein called 40S ribosomal protein S11-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	Ck	140	Total	C	N	O	0	0
			691	411	140	140		

- Molecule 42 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	Co	92	Total	C	N	O	0	0
			453	269	92	92		

- Molecule 43 is a protein called Ribosome biogenesis protein ENP2.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	CW	382	Total	C	N	O	0	0
			1880	1116	382	382		

- Molecule 44 is a protein called Utp20.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	UT	2018	Total	C	N	O	0	0
			10012	5976	2018	2018		

- Molecule 45 is a protein called Bfr2.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	CZ	42	Total	C	N	O	0	0
			207	123	42	42		

- Molecule 46 is a protein called Utp2.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	UB	508	Total	C	N	O	0	0
			2521	1505	508	508		

- Molecule 47 is a protein called Utp4.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	UD	772	Total	C	N	O	0	0
			3799	2255	772	772		

- Molecule 48 is a protein called UTP10.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	UJ	1090	Total	C	N	O	0	0
			5405	3225	1090	1090		

- Molecule 49 is a protein called Utp15.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	UO	504	Total	C	N	O	0	0
			2486	1478	504	504		

- Molecule 50 is a protein called Utp17.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	UQ	789	Total	C	N	O	0	0
			3899	2321	789	789		

- Molecule 51 is a protein called Enp1.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	CX	267	Total	C	N	O	0	0
			1325	791	267	267		

- Molecule 52 is a protein called Utp5.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	UI	125	Total	C	N	O	0	0
			616	366	125	125		
52	UE	125	Total	C	N	O	0	0
			616	366	125	125		

- Molecule 53 is a protein called Utp16.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	UP	54	Total	C	N	O	0	0
			265	157	54	54		

- Molecule 54 is a protein called Utp8.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	UH	359	Total	C	N	O	0	0
			1771	1053	359	359		

- Molecule 55 is a protein called Noc4.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	US	451	Total	C	N	O	0	0
			2245	1343	451	451		

- Molecule 56 is a protein called Nop1.

Mol	Chain	Residues	Atoms				AltConf	Trace
56	CA	242	Total	C	N	O	0	0
			1189	705	242	242		
56	CB	222	Total	C	N	O	0	0
			1092	648	222	222		

- Molecule 57 is a protein called Putative nucleolar protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
57	CC	387	Total	C	N	O	0	0
			1911	1137	387	387		

- Molecule 58 is a protein called Nop58.

Mol	Chain	Residues	Atoms				AltConf	Trace
58	CD	420	Total	C	N	O	0	0
			2073	1233	420	420		

- Molecule 59 is a protein called Snu13.

Mol	Chain	Residues	Atoms				AltConf	Trace
59	CE	121	Total	C	N	O	0	0
			601	359	121	121		
59	CF	120	Total	C	N	O	0	0
			596	356	120	120		

- Molecule 60 is a protein called Rrp9.

Mol	Chain	Residues	Atoms				AltConf	Trace
60	CG	416	Total	C	N	O	0	0
			2049	1217	416	416		

- Molecule 61 is a protein called Fcf2.

Mol	Chain	Residues	Atoms				AltConf	Trace
61	CT	131	Total	C	N	O	0	0
			647	385	131	131		

- Molecule 62 is a RNA chain called U3 snoRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	C2	229	Total	C	N	O	P	0	0
			4869	2172	851	1617	229		

- Molecule 63 is a protein called 40S ribosomal protein S19-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
63	Cr	142	Total	C	N	O	0	0
			697	413	142	142		

- Molecule 64 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
64	UX	1	Total	Zn	0
			1	1	
64	Cq	1	Total	Zn	0
			1	1	

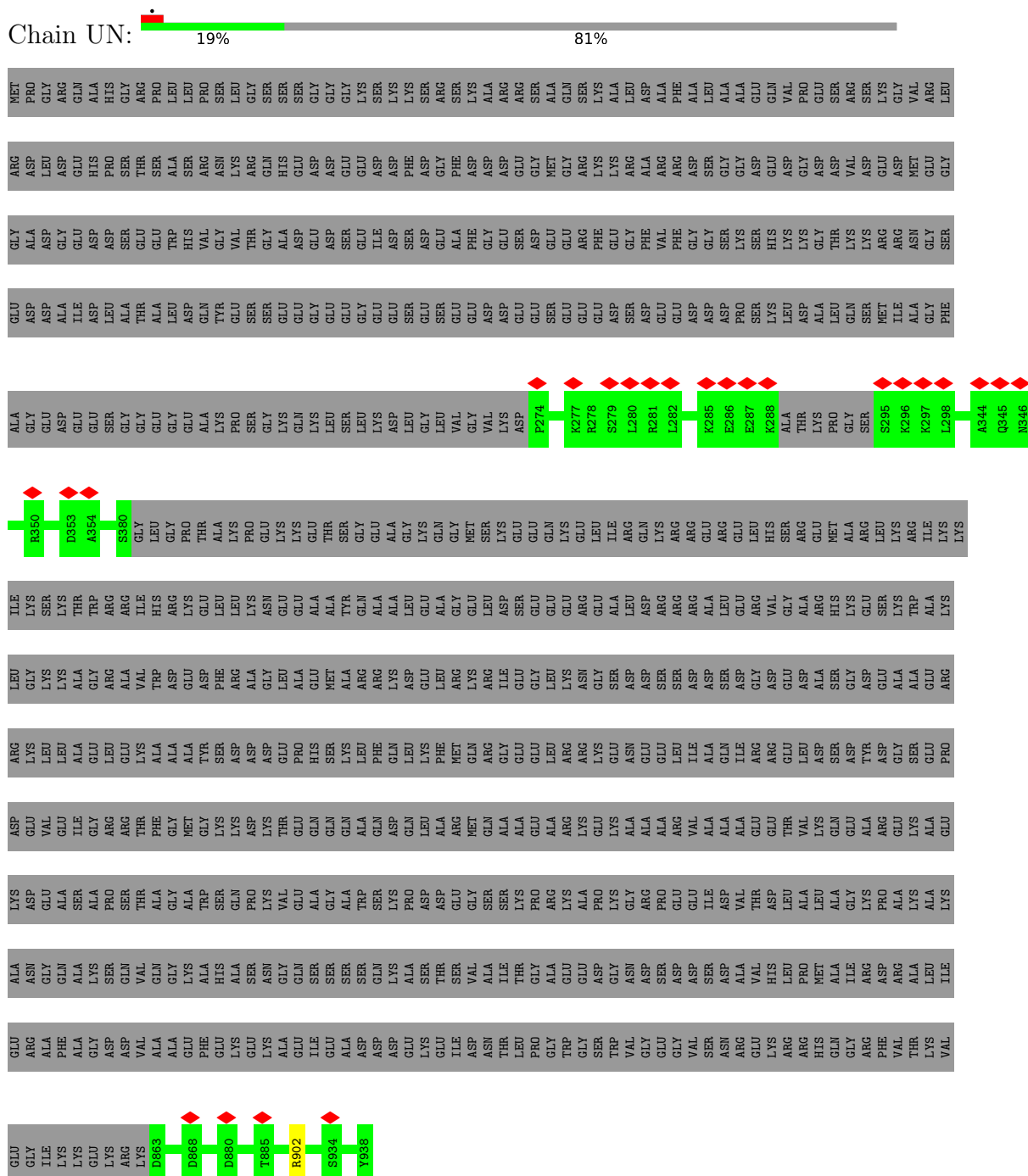




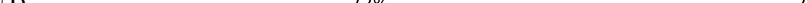


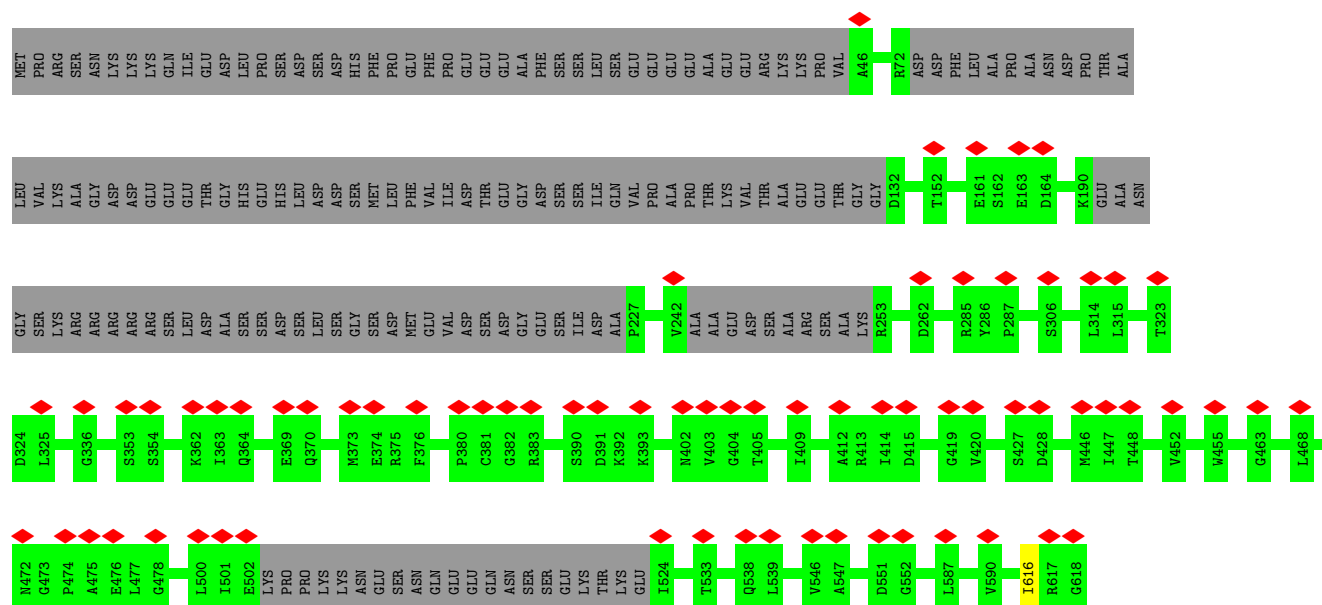


- Molecule 8: Utp14

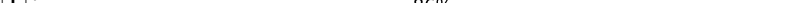


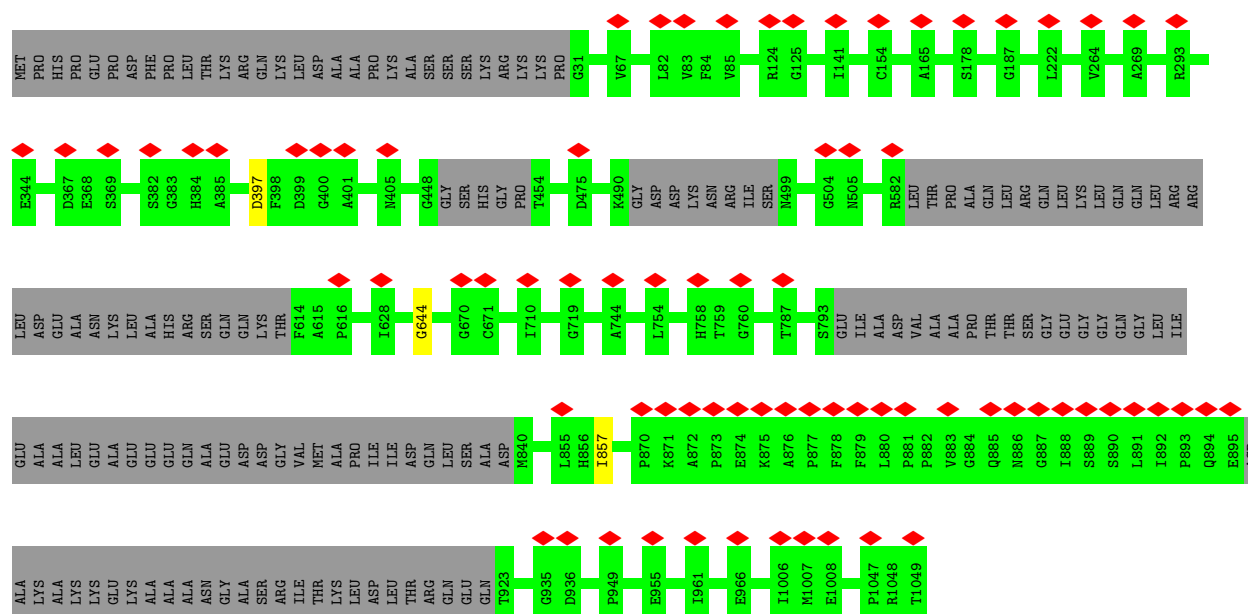
- Molecule 9: Utp18

Chain UR: 



- Molecule 10: Putative U3 snoRNP protein

Chain UU: 

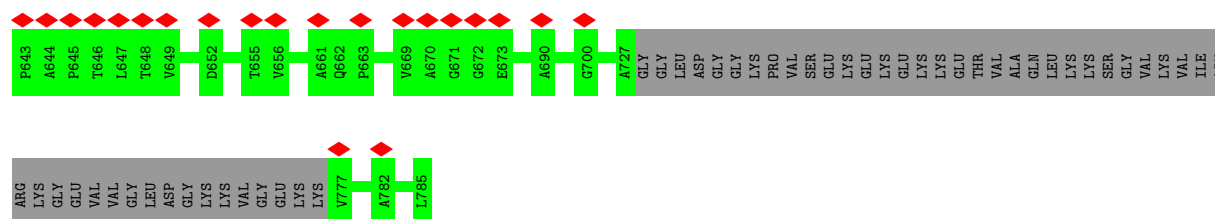


- Molecule 11: Utp24

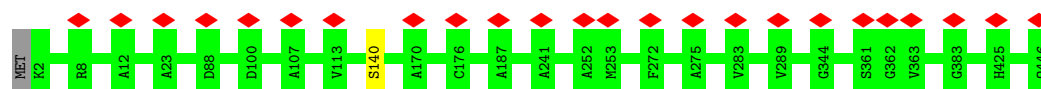
Chain UX:  26% 98%



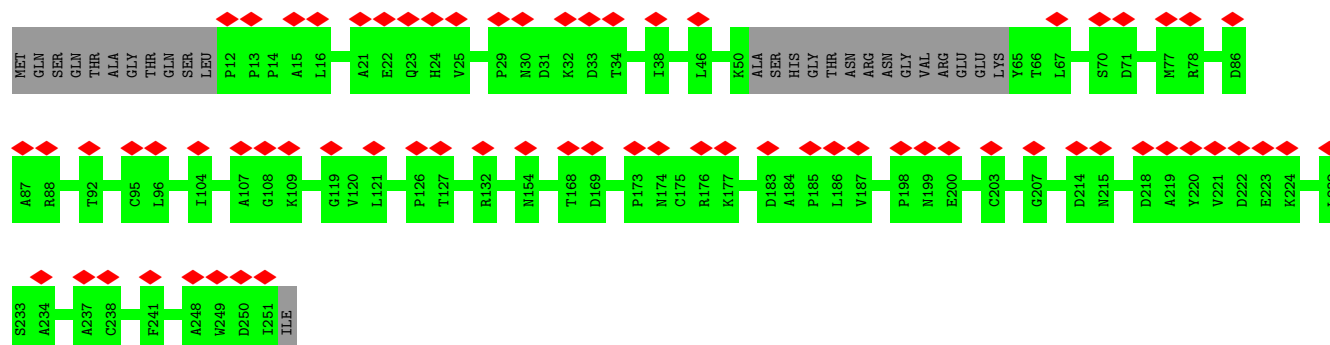




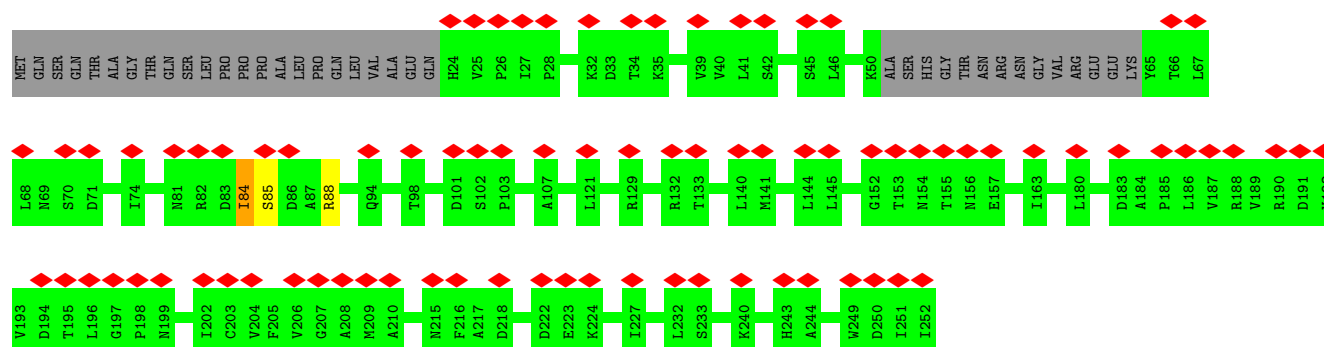
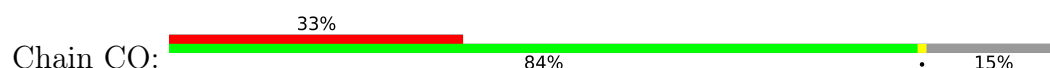
• Molecule 15: Sof1



• Molecule 16: Emg1



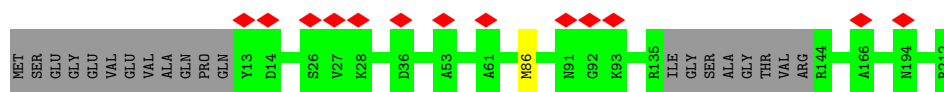
• Molecule 16: Emg1



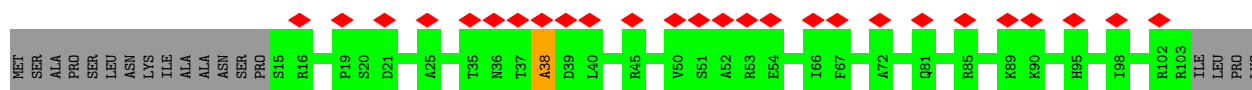
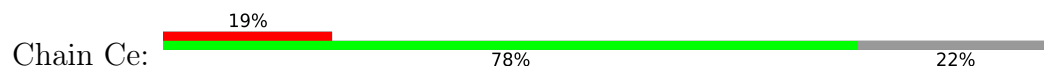
• Molecule 17: KRR1 small subunit processome component



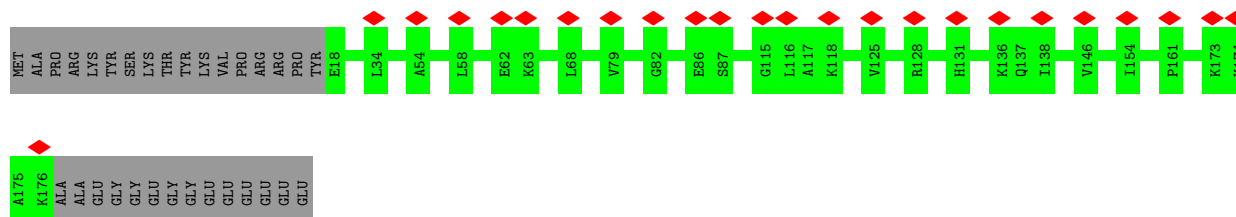
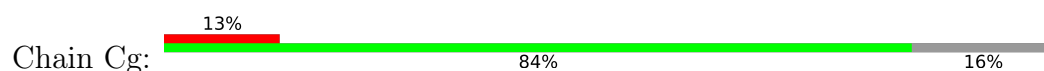




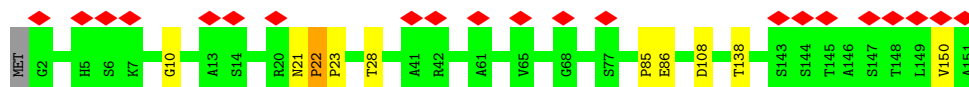
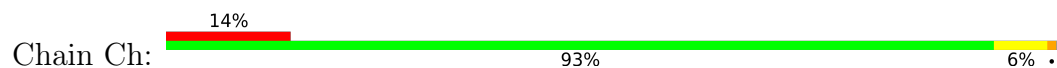
- Molecule 21: 40S ribosomal protein S7



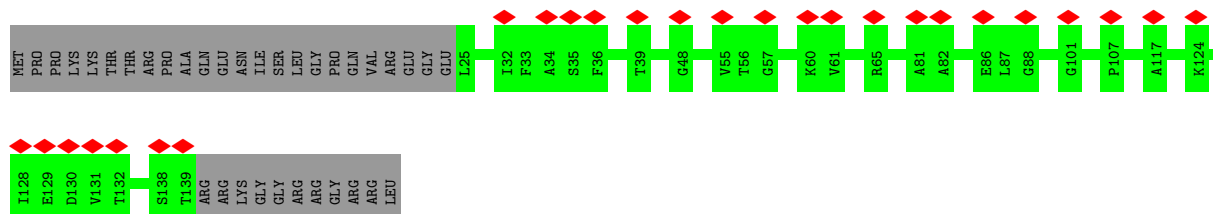
- Molecule 22: 40S ribosomal protein s9-like protein



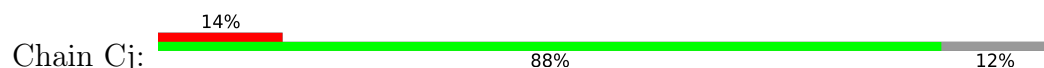
- Molecule 23: 40S ribosomal protein S13-like protein



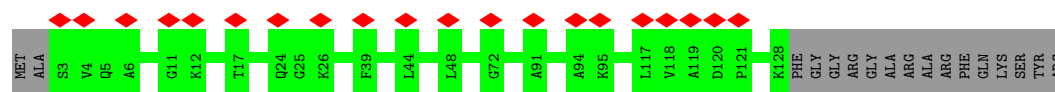
- Molecule 24: 40S ribosomal protein S14-like protein



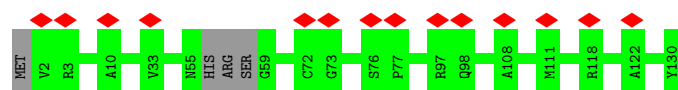
- Molecule 25: 40S ribosomal protein S16-like protein



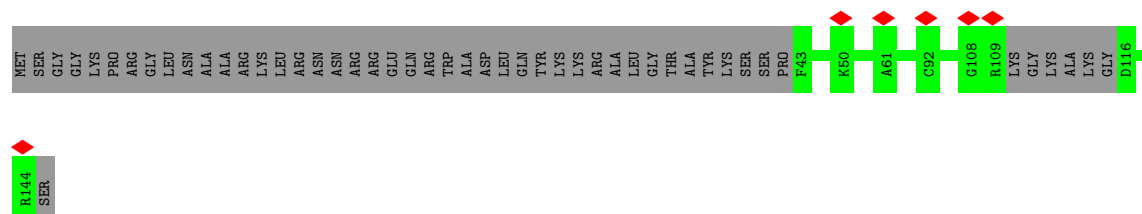




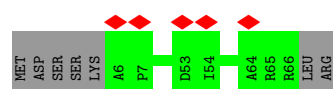
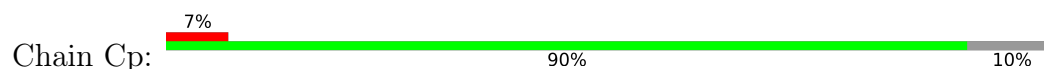
- Molecule 26: 40S ribosomal protein S22-like protein



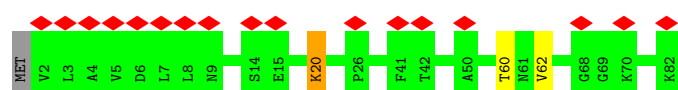
- Molecule 27: 40S ribosomal protein s23-like protein



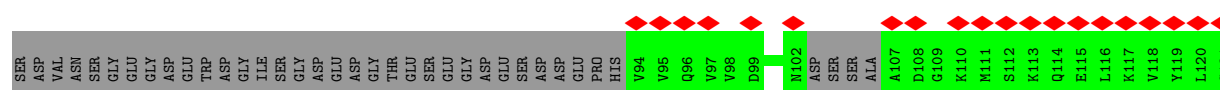
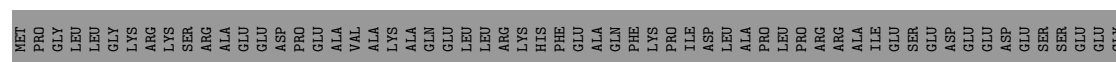
- Molecule 28: 40S ribosomal protein S28-like protein



- Molecule 29: Ribosomal protein s27-like protein



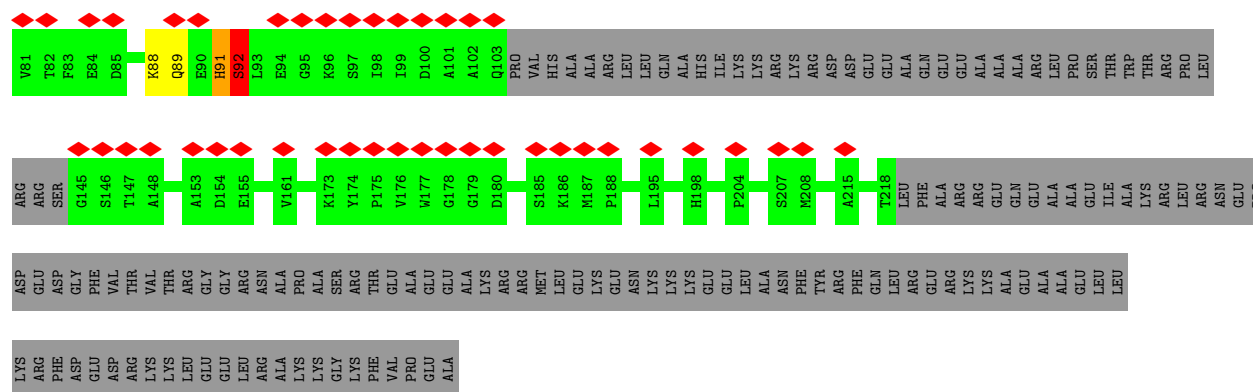
- Molecule 30: Faf1



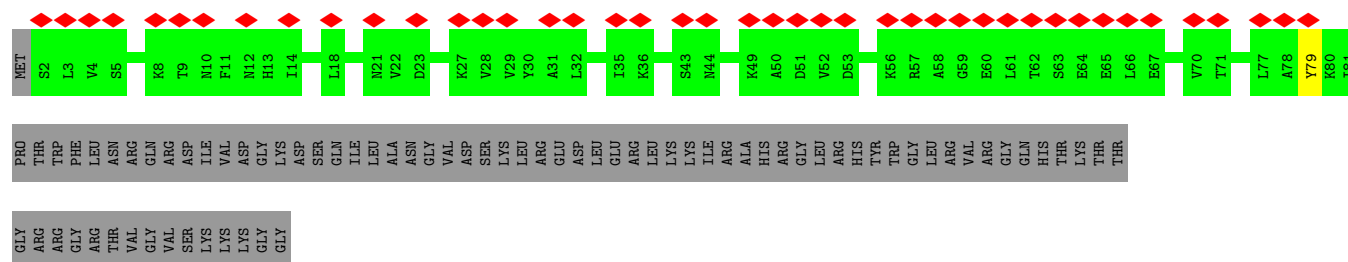




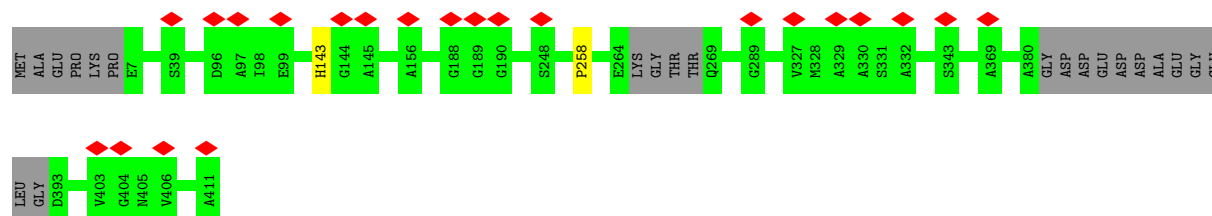




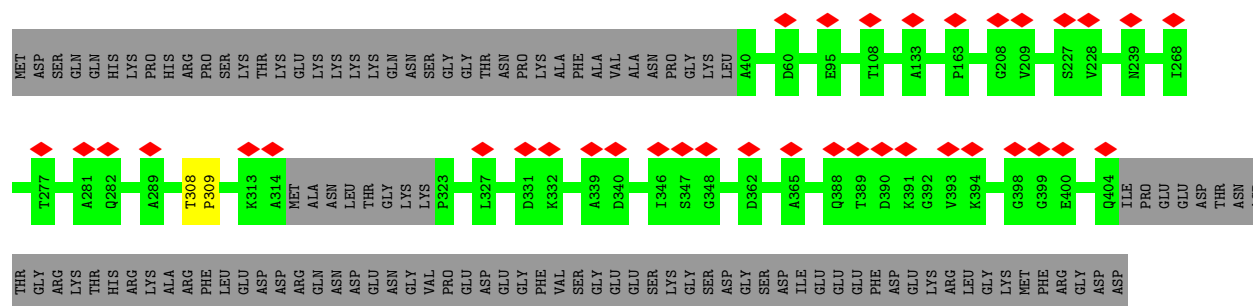
• Molecule 34: Putative ribosomal protein



• Molecule 35: RNA 3'-terminal phosphate cyclase-like protein



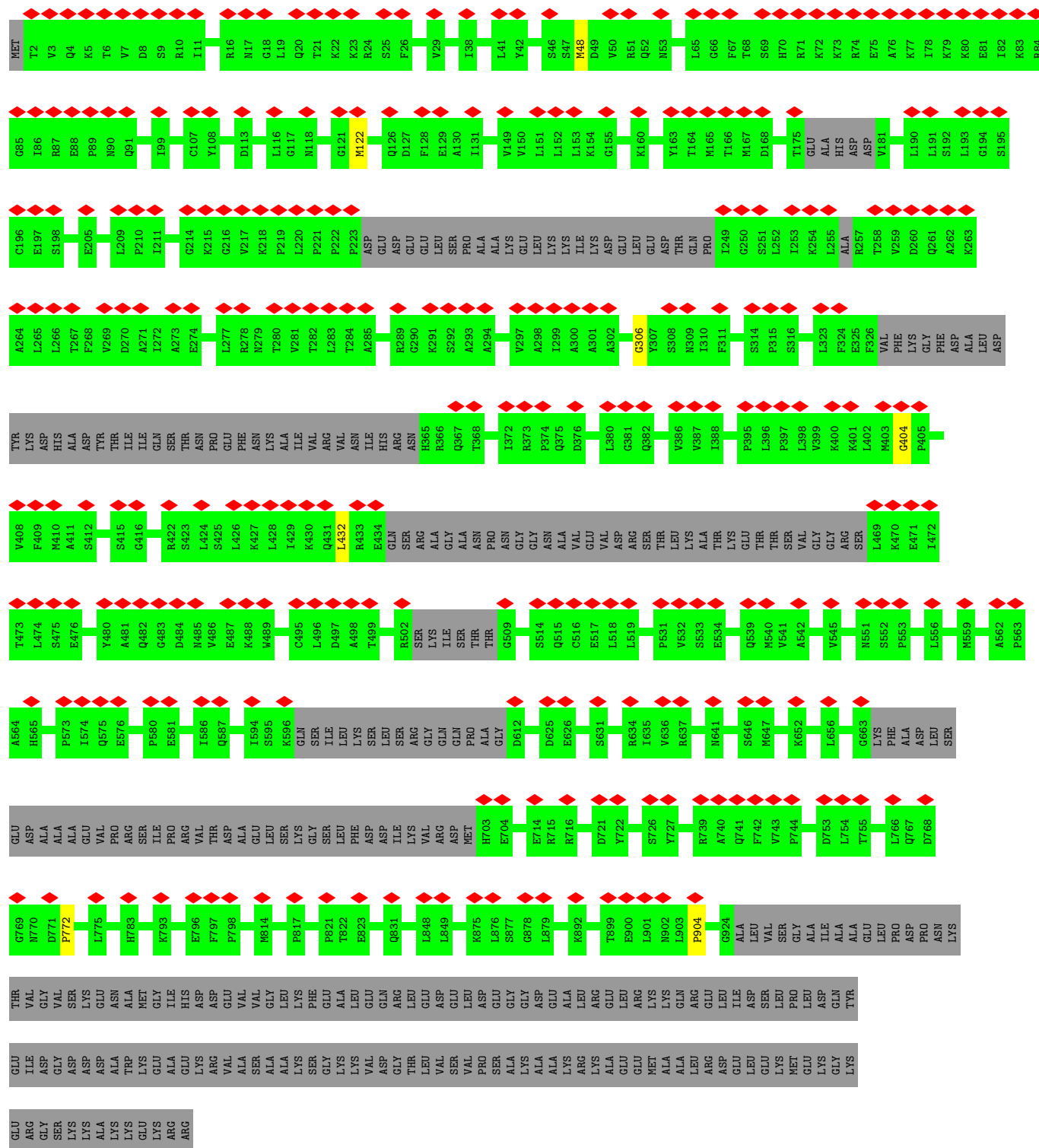
• Molecule 36: Bms1



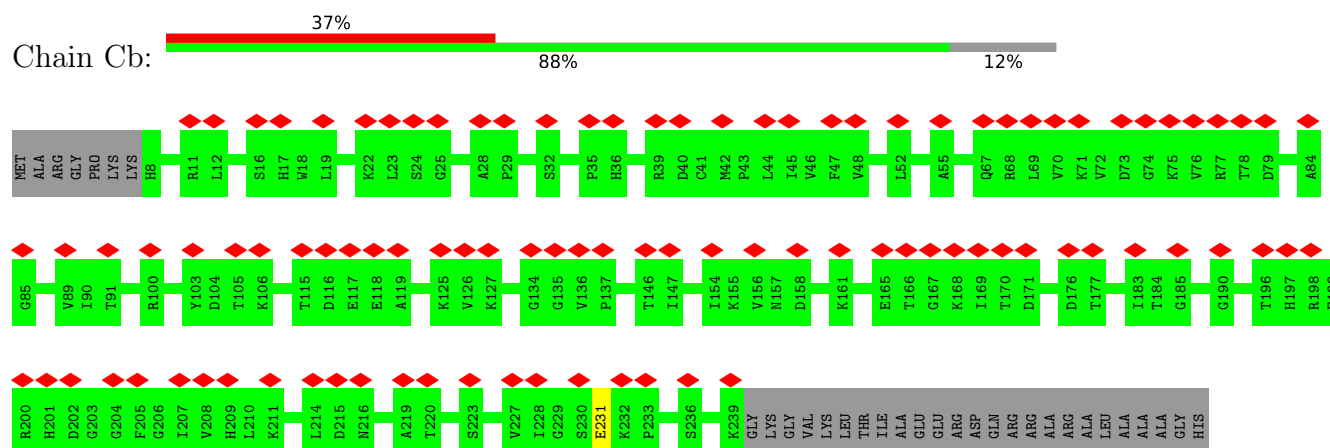


LYS  
GLY  
LYS  
GLU  
GLY  
ARG  
GLY  
SER  
LYS  
LYS  
ALA  
LYS  
GLU  
LYS  
ARG  
ARG

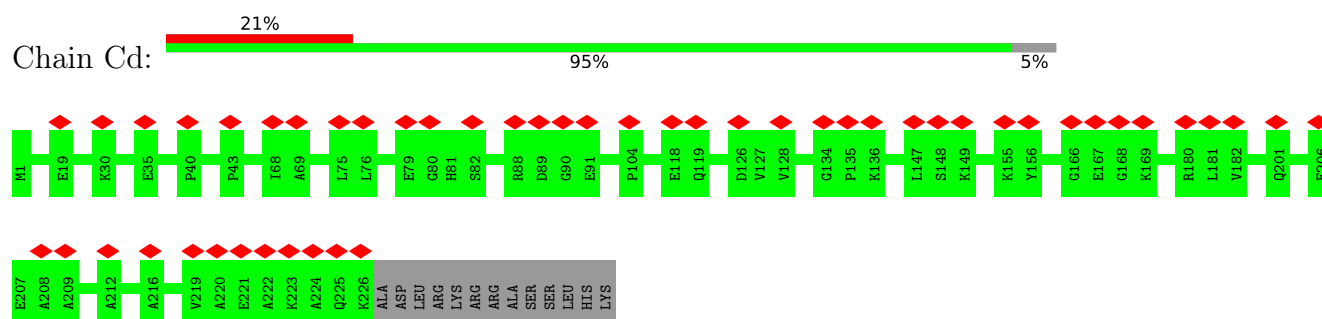
• Molecule 37: Kre33



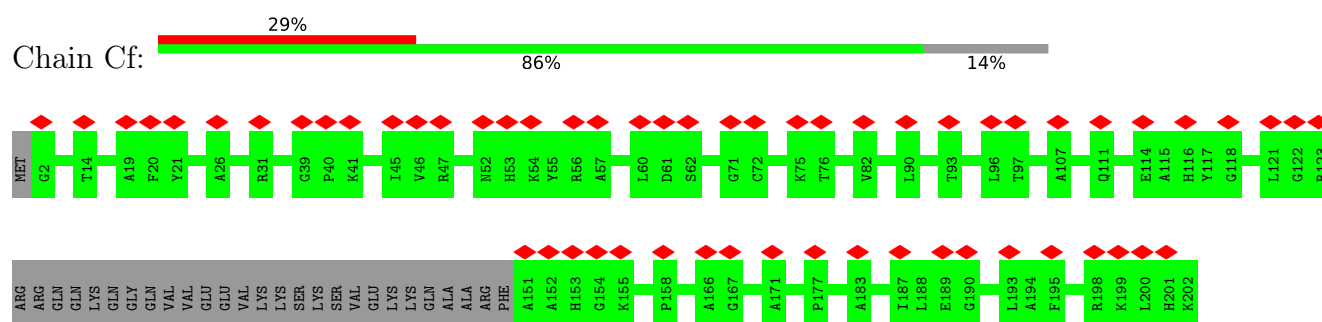
- Molecule 38: 40S ribosomal protein S4



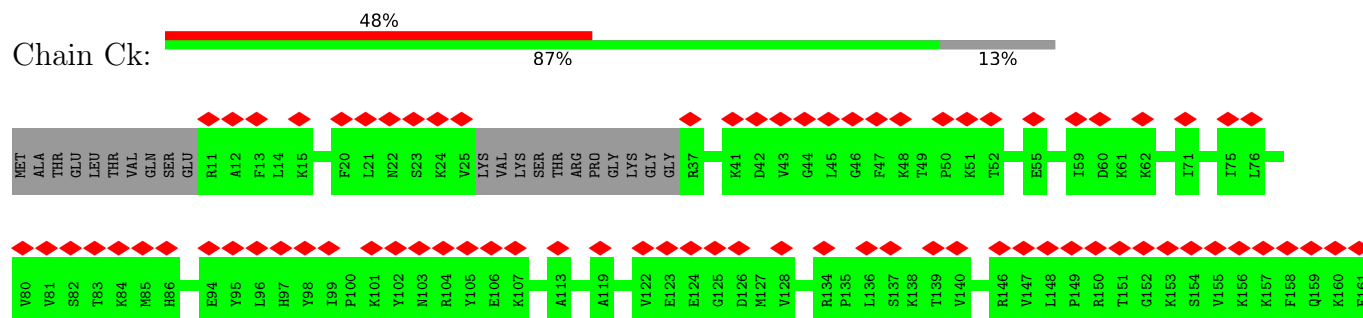
- Molecule 39: 40S ribosomal protein S6



- Molecule 40: 40S ribosomal protein S8



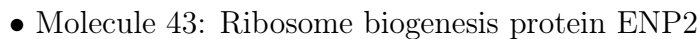
- Molecule 41: 40S ribosomal protein S11-like protein



- Molecule 42: 40S ribosomal protein S24



Frequency	Percentage
Often	68%
Not often	32%



Category	Percentage
Very bad	19%
Bad	57%
Good	43%

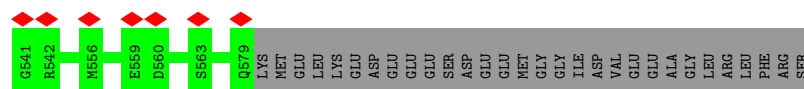


Response	Percentage
Doing a good job	30%
Not doing a good job	77%

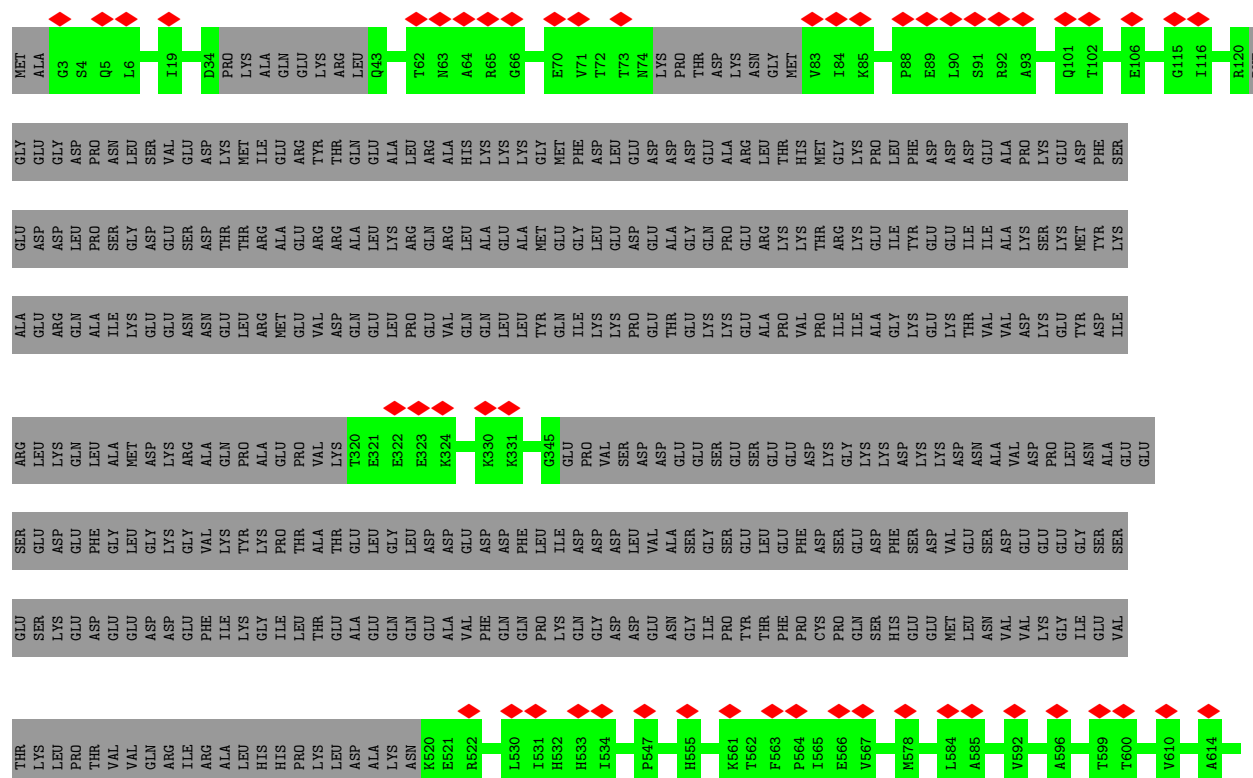






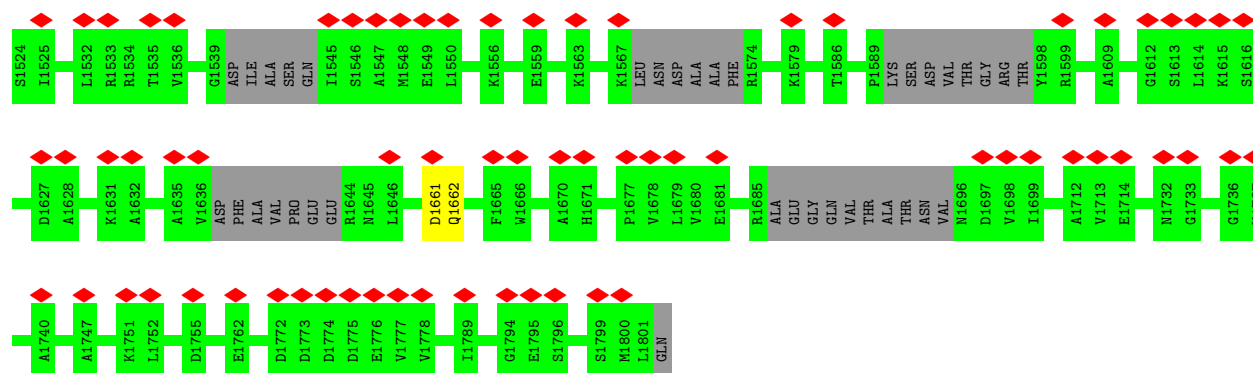


- Molecule 46: Utp2

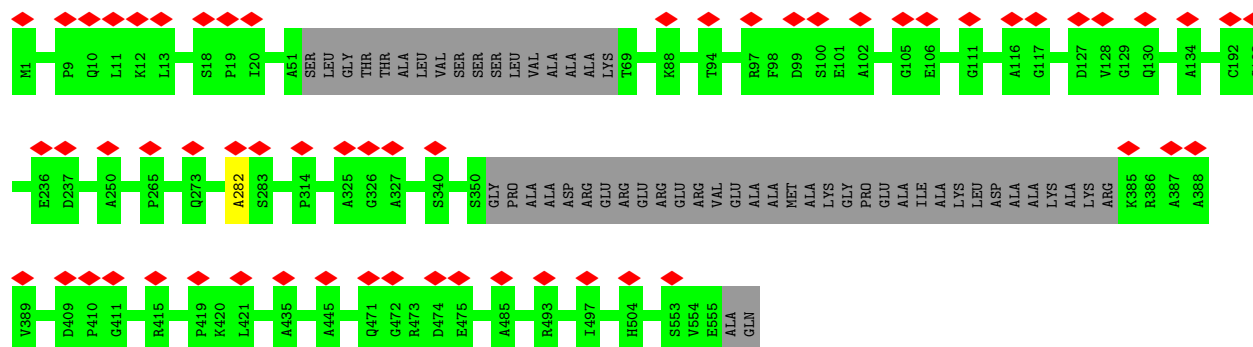




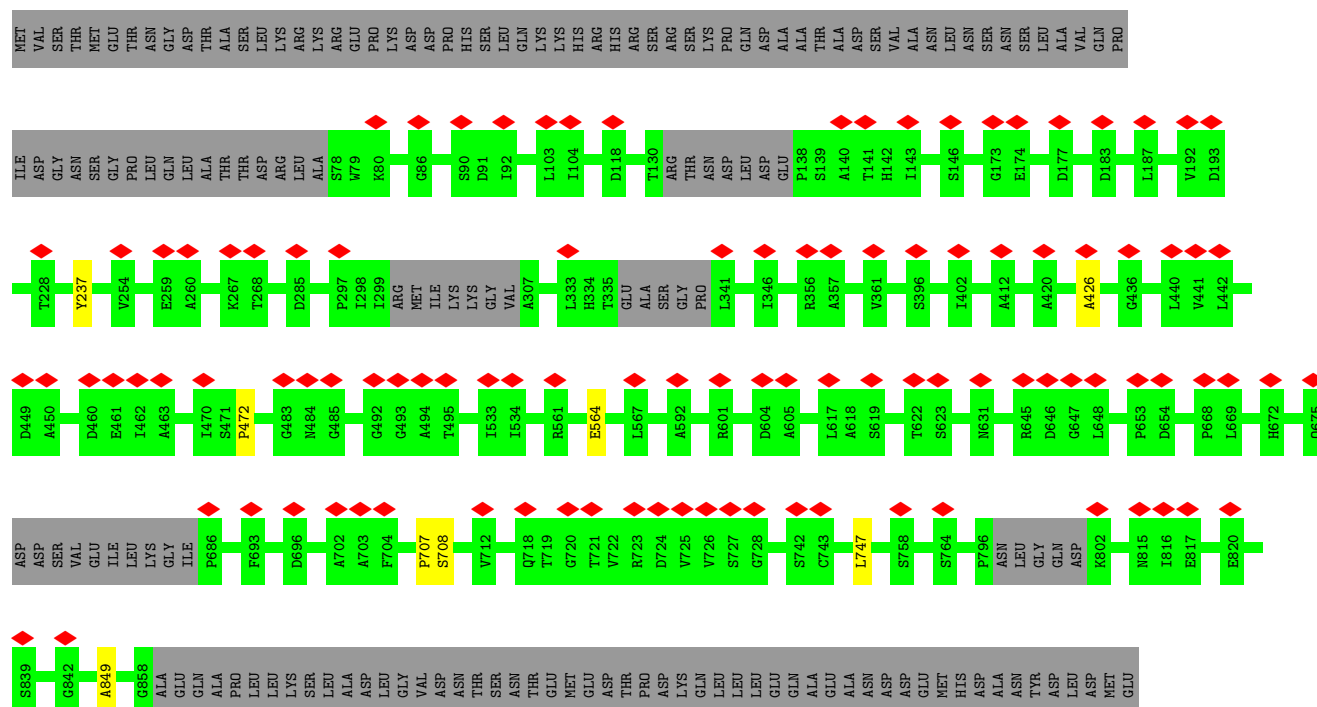
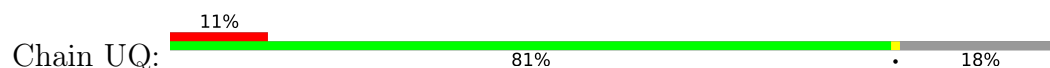




• Molecule 49: Utp15



• Molecule 50: Utp17

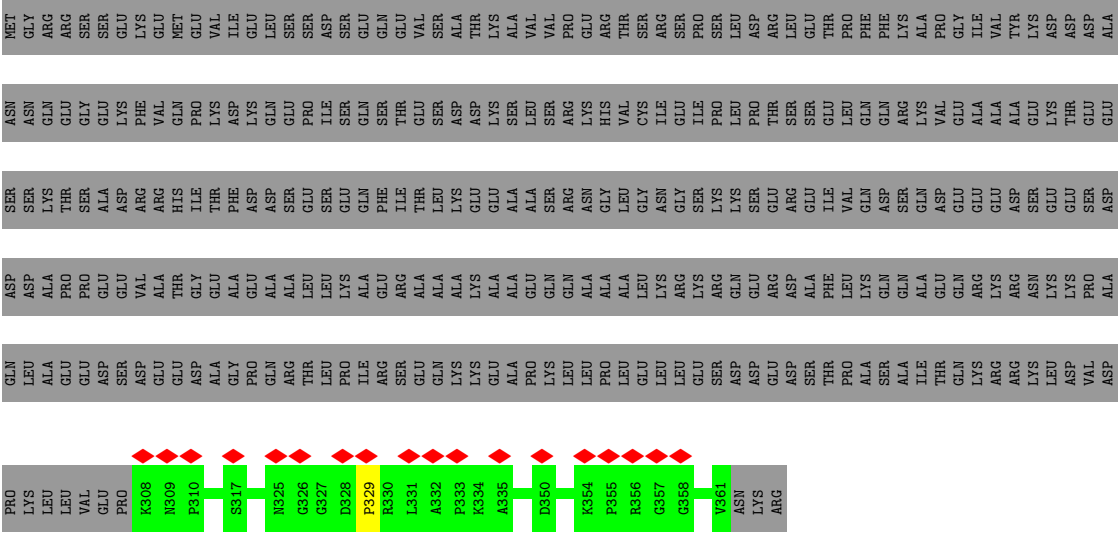




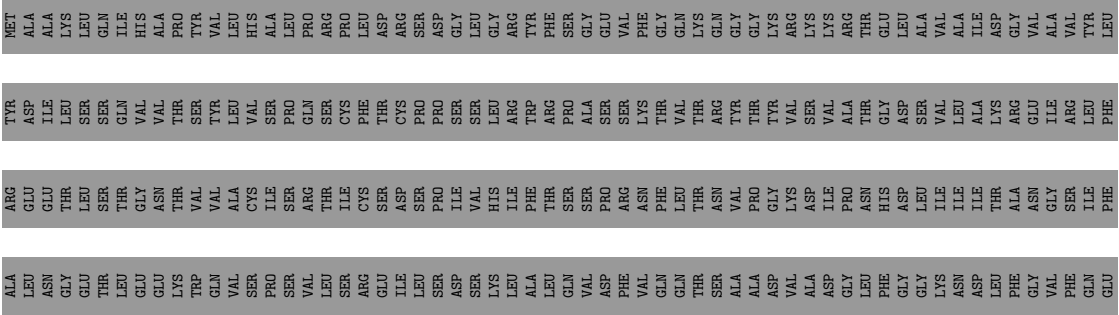




• Molecule 53: Utp16



• Molecule 54: Utp8











## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	9041	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	28	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.171	Depositor
Minimum map value	-0.104	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	520.32, 520.32, 520.32	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.084, 1.084, 1.084	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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

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	UA	0.35	0/4134	0.61	1/5749 (0.0%)
2	UC	0.33	0/360	0.50	0/497
3	UF	0.29	0/1641	0.48	0/2286
4	UG	0.34	0/2359	0.58	0/3279
5	UK	0.32	0/1067	0.44	0/1480
6	UL	0.31	0/3868	0.59	0/5372
7	UM	0.28	0/3590	0.57	0/4981
8	UN	0.32	0/877	0.52	0/1220
9	UR	0.33	0/2193	0.55	0/3040
10	UU	0.34	0/4418	0.57	0/6124
11	UX	0.32	0/941	0.56	0/1311
12	CJ	0.33	0/889	0.51	0/1240
13	CK	0.35	0/1471	0.57	0/2050
14	CL	0.31	0/1139	0.49	0/1582
15	CM	0.34	0/2200	0.59	0/3064
16	CN	0.29	0/1120	0.51	0/1560
16	CO	0.29	0/1065	0.56	0/1483
17	CP	0.30	0/993	0.54	0/1381
18	CQ	0.26	0/862	0.50	0/1197
19	Ca	0.30	0/1114	0.58	0/1552
20	Cc	0.29	0/951	0.49	0/1324
21	Ce	0.32	0/784	0.62	1/1089 (0.1%)
22	Cg	0.32	0/784	0.50	0/1090
23	Ch	0.57	0/740	0.76	0/1029
24	Ci	0.31	0/562	0.50	0/778
25	Cj	0.32	0/621	0.56	0/863
26	Cm	0.30	0/618	0.54	0/856
27	Cn	0.30	0/467	0.54	0/644
28	Cp	0.31	0/299	0.52	0/414
29	Cq	0.70	0/399	1.23	1/554 (0.2%)
30	CU	0.27	0/867	0.52	0/1202
31	C1	0.61	5/29104 (0.0%)	1.24	309/45308 (0.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
32	UV	0.32	0/5242	0.59	1/7299 (0.0%)
33	CV	0.47	1/730 (0.1%)	0.76	3/1014 (0.3%)
34	Cl	0.27	0/394	0.56	0/547
35	CH	0.32	0/1899	0.55	0/2628
36	CI	0.33	0/4056	0.55	0/5641
37	CR	0.30	0/3748	0.63	0/5209
37	CS	0.30	0/3748	0.63	0/5209
38	Cb	0.29	0/1139	0.58	0/1581
39	Cd	0.31	0/1111	0.54	0/1543
40	Cf	0.31	0/850	0.55	0/1176
41	Ck	0.27	0/689	0.55	0/956
42	Co	0.31	0/452	0.57	0/627
43	CW	0.30	0/1879	0.62	0/2611
44	UT	0.30	0/9990	0.54	0/13904
45	CZ	0.29	0/206	0.64	0/285
46	UB	0.29	0/2515	0.48	0/3500
47	UD	0.31	0/3790	0.56	0/5255
48	UJ	0.29	0/5391	0.52	0/7498
49	UO	0.32	0/2483	0.56	0/3451
50	UQ	0.32	0/3892	0.61	2/5410 (0.0%)
51	CX	0.26	0/1324	0.48	0/1846
52	UE	0.29	0/614	0.50	0/851
52	UI	0.24	0/614	0.40	0/851
53	UP	0.29	0/264	0.54	0/365
54	UH	0.29	0/1766	0.50	0/2450
55	US	0.29	0/2241	0.52	0/3125
56	CA	0.33	0/1187	0.56	0/1646
56	CB	0.28	0/1090	0.52	0/1512
57	CC	0.31	0/1909	0.52	0/2655
58	CD	0.31	0/2071	0.52	0/2880
59	CE	0.34	0/600	0.54	0/836
59	CF	0.34	0/595	0.56	0/829
60	CG	0.30	0/2042	0.57	0/2829
61	CT	0.31	0/645	0.54	0/895
62	C2	0.65	0/5434	1.40	69/8459 (0.8%)
63	Cr	0.70	0/696	1.21	2/965 (0.2%)
All	All	0.41	6/149793 (0.0%)	0.80	389/213937 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.



Mol	Chain	#Chirality outliers	#Planarity outliers
1	UA	0	1
6	UL	0	2
7	UM	0	4
9	UR	0	1
10	UU	0	3
13	CK	0	1
15	CM	0	1
16	CO	0	2
18	CQ	0	1
20	Cc	0	1
21	Ce	0	1
23	Ch	0	1
32	UV	0	3
33	CV	0	2
34	CI	0	1
35	CH	0	1
36	CI	0	2
37	CR	0	3
37	CS	0	3
38	Cb	0	1
43	CW	0	2
44	UT	0	10
47	UD	0	1
48	UJ	0	2
49	UO	0	1
50	UQ	0	4
52	UE	0	1
55	US	0	1
56	CB	0	1
59	CF	0	1
60	CG	0	1
63	Cr	0	1
All	All	0	61

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
31	C1	2076	C	C1'-N1	5.83	1.57	1.48
31	C1	2094	G	C1'-N9	-5.69	1.38	1.46
31	C1	2075	U	C1'-N1	5.68	1.57	1.48
31	C1	1081	G	C2-N3	-5.57	1.28	1.32
33	CV	91	HIS	N-CA	5.49	1.57	1.46

The worst 5 of 389 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	C2	2	G	O5'-P-OP1	-30.50	74.10	110.70
62	C2	2	G	OP1-P-OP2	-27.22	78.76	119.60
62	C2	2	G	O5'-P-OP2	18.20	132.55	110.70
62	C2	1	A	OP1-P-O3'	13.82	135.61	105.20
62	C2	1	A	OP2-P-O3'	-13.12	76.34	105.20

There are no chirality outliers.

5 of 61 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	UA	115	LEU	Peptide
6	UL	153	ASP	Peptide
6	UL	636	LEU	Peptide
7	UM	328	LEU	Peptide
7	UM	382	ILE	Peptide

## 5.2 Too-close contacts [i](#)

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

## 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	UA	835/904 (92%)	768 (92%)	67 (8%)	0	100	100
2	UC	72/648 (11%)	64 (89%)	8 (11%)	0	100	100
3	UF	325/414 (78%)	310 (95%)	14 (4%)	1 (0%)	41	77
4	UG	475/558 (85%)	441 (93%)	32 (7%)	2 (0%)	34	72
5	UK	211/270 (78%)	210 (100%)	1 (0%)	0	100	100
6	UL	767/962 (80%)	711 (93%)	56 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	UM	705/912 (77%)	656 (93%)	48 (7%)	1 (0%)	51	86
8	UN	171/938 (18%)	167 (98%)	3 (2%)	1 (1%)	25	66
9	UR	437/618 (71%)	416 (95%)	21 (5%)	0	100	100
10	UU	890/1049 (85%)	833 (94%)	57 (6%)	0	100	100
11	UX	188/193 (97%)	176 (94%)	12 (6%)	0	100	100
12	CJ	177/183 (97%)	166 (94%)	11 (6%)	0	100	100
13	CK	295/297 (99%)	284 (96%)	11 (4%)	0	100	100
14	CL	225/785 (29%)	212 (94%)	12 (5%)	1 (0%)	34	72
15	CM	443/446 (99%)	416 (94%)	27 (6%)	0	100	100
16	CN	222/252 (88%)	210 (95%)	12 (5%)	0	100	100
16	CO	211/252 (84%)	198 (94%)	11 (5%)	2 (1%)	17	57
17	CP	197/322 (61%)	191 (97%)	6 (3%)	0	100	100
18	CQ	171/259 (66%)	164 (96%)	7 (4%)	0	100	100
19	Ca	223/255 (88%)	212 (95%)	11 (5%)	0	100	100
20	Cc	188/212 (89%)	179 (95%)	9 (5%)	0	100	100
21	Ce	155/203 (76%)	139 (90%)	16 (10%)	0	100	100
22	Cg	157/190 (83%)	152 (97%)	5 (3%)	0	100	100
23	Ch	148/151 (98%)	127 (86%)	11 (7%)	10 (7%)	1	15
24	Ci	113/150 (75%)	107 (95%)	6 (5%)	0	100	100
25	Cj	124/143 (87%)	116 (94%)	8 (6%)	0	100	100
26	Cm	122/130 (94%)	117 (96%)	5 (4%)	0	100	100
27	Cn	92/145 (63%)	89 (97%)	3 (3%)	0	100	100
28	Cp	59/68 (87%)	55 (93%)	4 (7%)	0	100	100
29	Cq	79/82 (96%)	64 (81%)	12 (15%)	3 (4%)	3	24
30	CU	168/311 (54%)	156 (93%)	12 (7%)	0	100	100
32	UV	1057/1171 (90%)	975 (92%)	80 (8%)	2 (0%)	47	81
33	CV	144/322 (45%)	131 (91%)	10 (7%)	3 (2%)	7	36
34	Cl	78/156 (50%)	73 (94%)	5 (6%)	0	100	100
35	CH	383/411 (93%)	346 (90%)	36 (9%)	1 (0%)	41	77
36	CI	812/1163 (70%)	761 (94%)	49 (6%)	2 (0%)	47	81
37	CR	746/1073 (70%)	682 (91%)	60 (8%)	4 (0%)	29	69

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	CS	746/1073 (70%)	682 (91%)	60 (8%)	4 (0%)	29	69
38	Cb	230/264 (87%)	204 (89%)	26 (11%)	0	100	100
39	Cd	224/239 (94%)	211 (94%)	13 (6%)	0	100	100
40	Cf	170/202 (84%)	164 (96%)	6 (4%)	0	100	100
41	Ck	136/161 (84%)	129 (95%)	7 (5%)	0	100	100
42	Co	90/136 (66%)	82 (91%)	8 (9%)	0	100	100
43	CW	380/668 (57%)	349 (92%)	31 (8%)	0	100	100
44	UT	1974/2612 (76%)	1859 (94%)	109 (6%)	6 (0%)	41	77
45	CZ	40/609 (7%)	32 (80%)	8 (20%)	0	100	100
46	UB	496/907 (55%)	464 (94%)	32 (6%)	0	100	100
47	UD	754/884 (85%)	721 (96%)	33 (4%)	0	100	100
48	UJ	1062/1802 (59%)	1010 (95%)	52 (5%)	0	100	100
49	UO	498/557 (89%)	475 (95%)	23 (5%)	0	100	100
50	UQ	775/960 (81%)	712 (92%)	61 (8%)	2 (0%)	41	77
51	CX	265/480 (55%)	255 (96%)	10 (4%)	0	100	100
52	UE	121/410 (30%)	117 (97%)	4 (3%)	0	100	100
52	UI	121/410 (30%)	121 (100%)	0	0	100	100
53	UP	52/364 (14%)	46 (88%)	5 (10%)	1 (2%)	8	38
54	UH	349/930 (38%)	340 (97%)	9 (3%)	0	100	100
55	US	443/549 (81%)	415 (94%)	28 (6%)	0	100	100
56	CA	238/313 (76%)	225 (94%)	13 (6%)	0	100	100
56	CB	218/313 (70%)	204 (94%)	14 (6%)	0	100	100
57	CC	383/523 (73%)	367 (96%)	16 (4%)	0	100	100
58	CD	416/582 (72%)	393 (94%)	23 (6%)	0	100	100
59	CE	119/127 (94%)	111 (93%)	8 (7%)	0	100	100
59	CF	118/127 (93%)	110 (93%)	7 (6%)	1 (1%)	19	60
60	CG	402/630 (64%)	375 (93%)	27 (7%)	0	100	100
61	CT	127/203 (63%)	119 (94%)	8 (6%)	0	100	100
63	Cr	140/153 (92%)	122 (87%)	13 (9%)	5 (4%)	3	25
All	All	22952/33786 (68%)	21488 (94%)	1412 (6%)	52 (0%)	50	81

5 of 52 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	CO	85	SER
23	Ch	23	PRO
23	Ch	86	GLU
23	Ch	150	VAL
29	Cq	20	LYS

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

There are no protein residues with a non-rotameric sidechain to report in this entry.

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
31	C1	1197/1859 (64%)	376 (31%)	25 (2%)
62	C2	225/232 (96%)	67 (29%)	4 (1%)
All	All	1422/2091 (68%)	443 (31%)	29 (2%)

5 of 443 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
31	C1	4	G
31	C1	5	G
31	C1	7	A
31	C1	13	G
31	C1	14	G

5 of 29 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
31	C1	1264	U
62	C2	91	G
31	C1	1712	C
31	C1	2219	C
31	C1	1638	G

## 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 monosaccharides 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
31	C1	4
62	C2	2

The worst 5 of 6 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C1	74:C	O3'	244:G	P	56.87
1	C1	257:G	O3'	417:G	P	43.92
1	C2	206:G	O3'	240:C	P	18.77
1	C2	105:C	O3'	110:A	P	16.05
1	C1	34:C	O3'	36:C	P	5.49

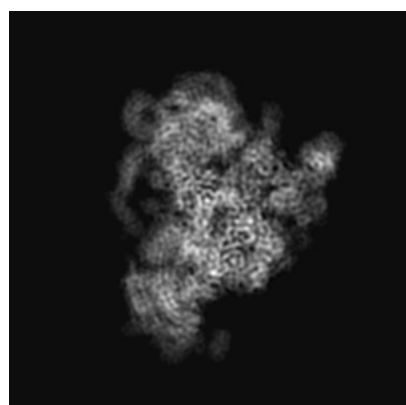
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10054. These allow visual inspection of the internal detail of the map and identification of artifacts.

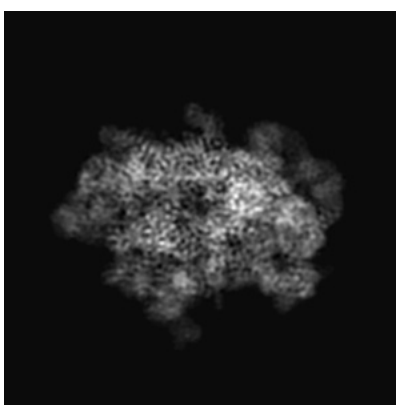
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

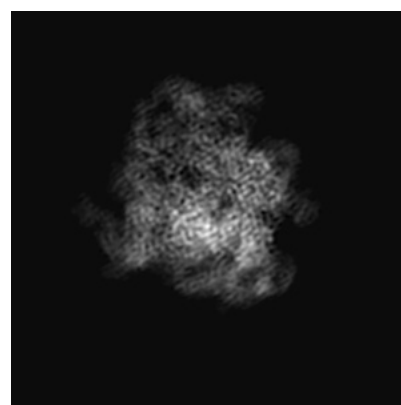
#### 6.1.1 Primary map



X



Y

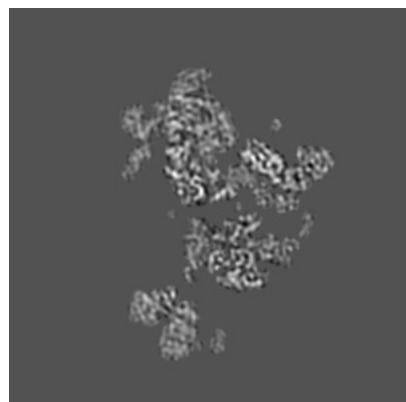


Z

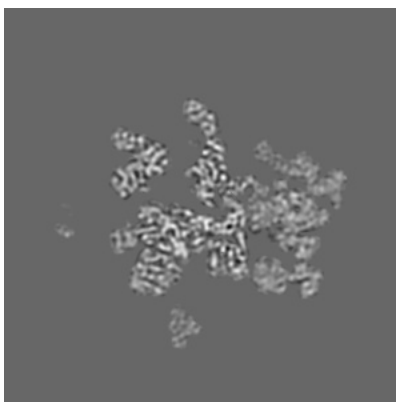
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

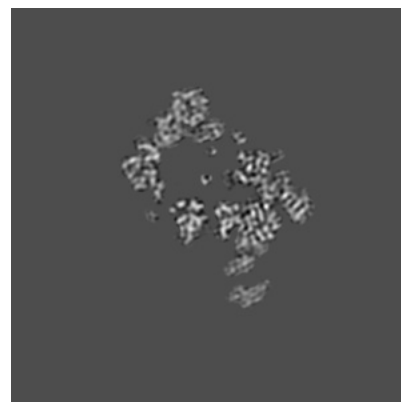
#### 6.2.1 Primary map



X Index: 240



Y Index: 240

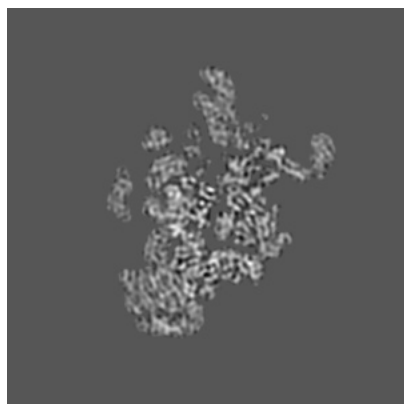


Z Index: 240

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: 279



Y Index: 213

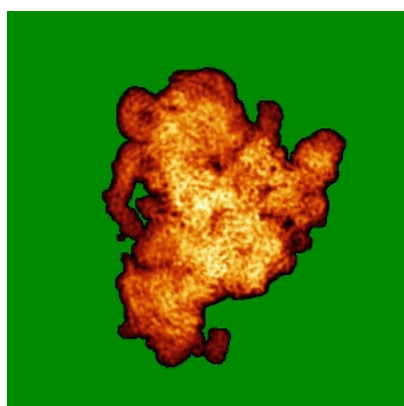


Z Index: 247

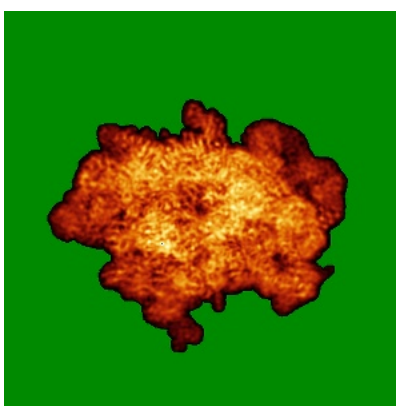
The images above show the largest variance slices of the map in three orthogonal directions.

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

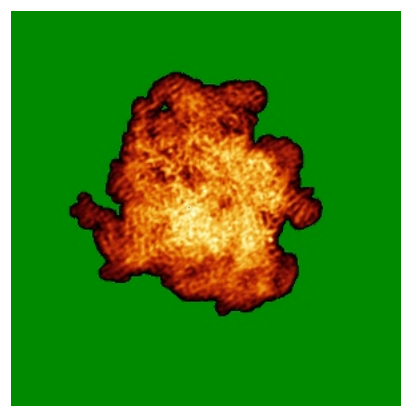
### 6.4.1 Primary map



X



Y



Z

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

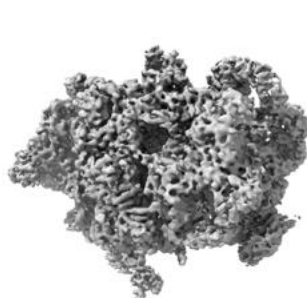


## 6.5 Orthogonal surface views [i](#)

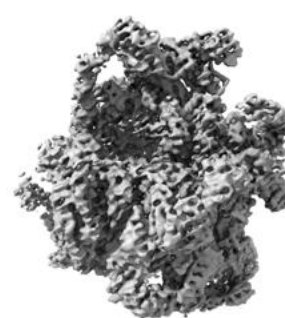
### 6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

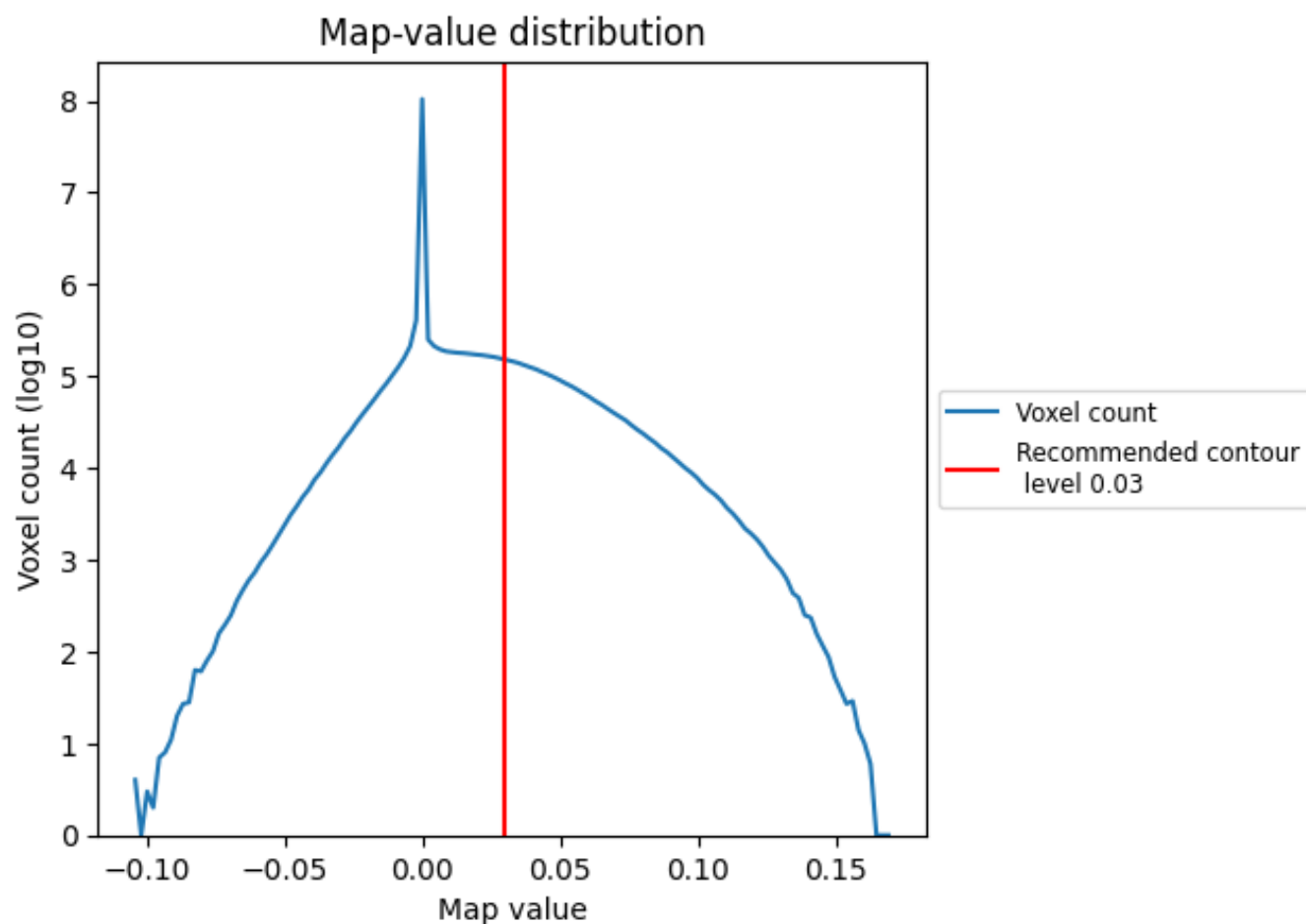
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

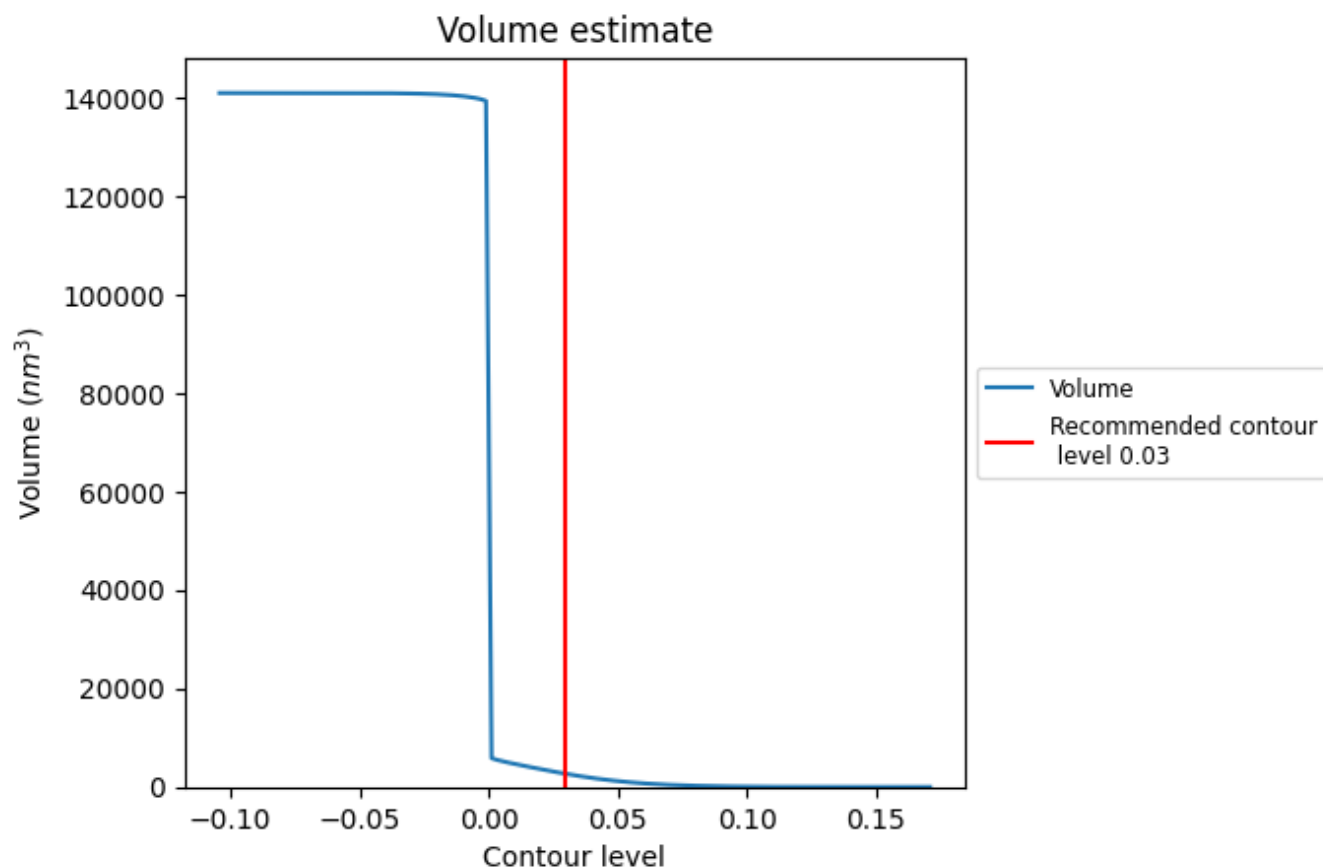
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



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

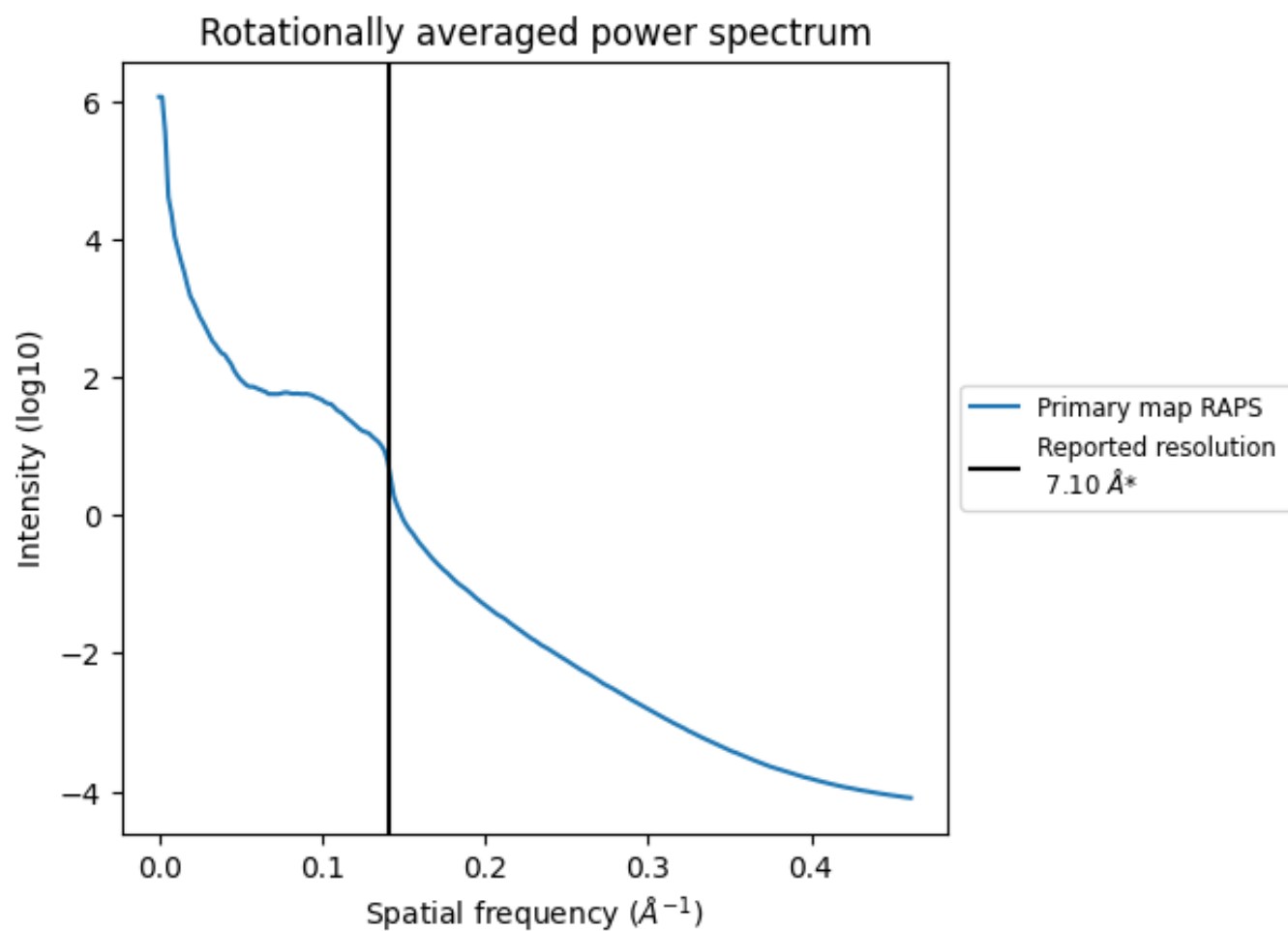
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2664 nm<sup>3</sup>; this corresponds to an approximate mass of 2407 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 ⓘ

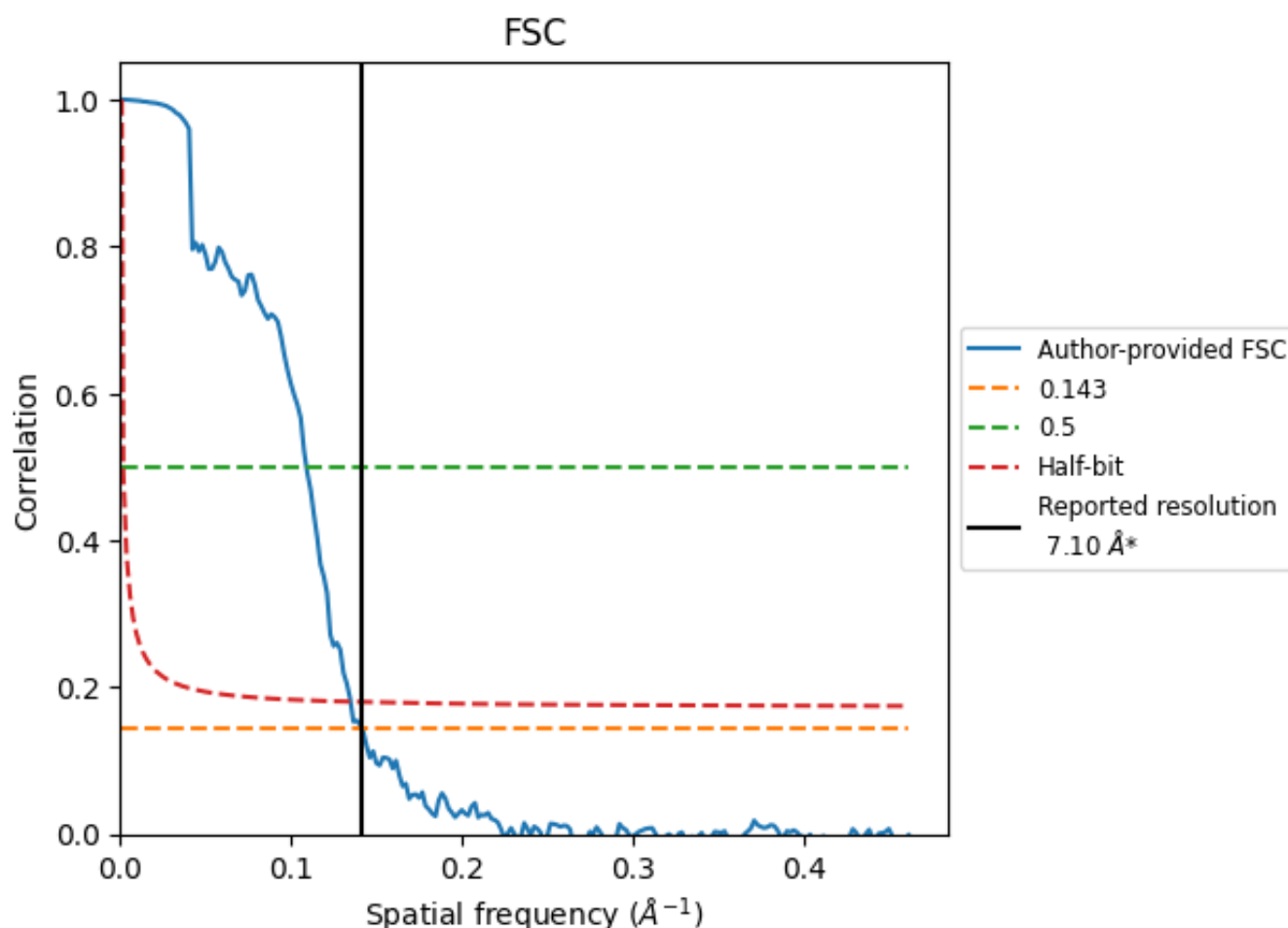


\*Reported resolution corresponds to spatial frequency of 0.141 Å<sup>-1</sup>

## 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 0.141 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

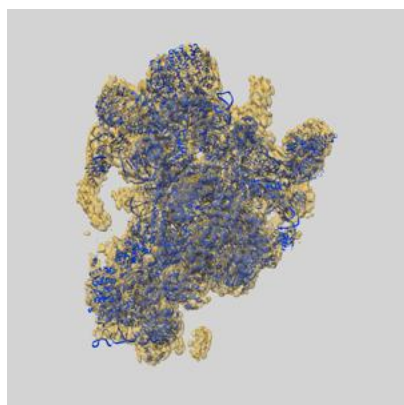
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.10	-	-
Author-provided FSC curve	7.07	9.17	7.42
Unmasked-calculated*	-	-	-

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

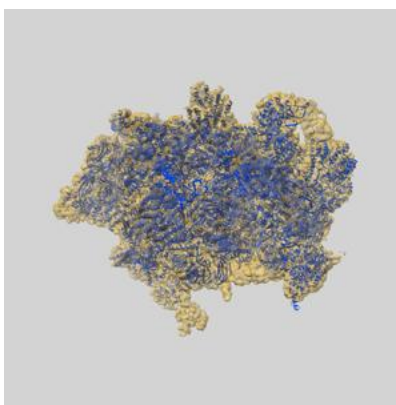
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10054 and PDB model 6RXX. Per-residue inclusion information can be found in section [3](#) on page [16](#).

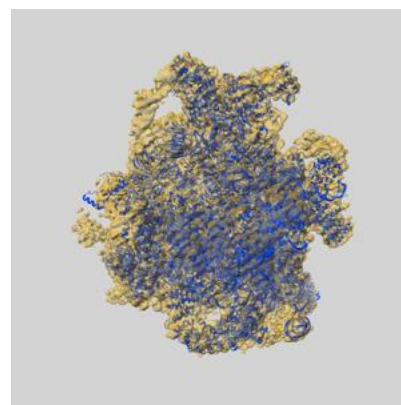
### 9.1 Map-model overlay [i](#)



X



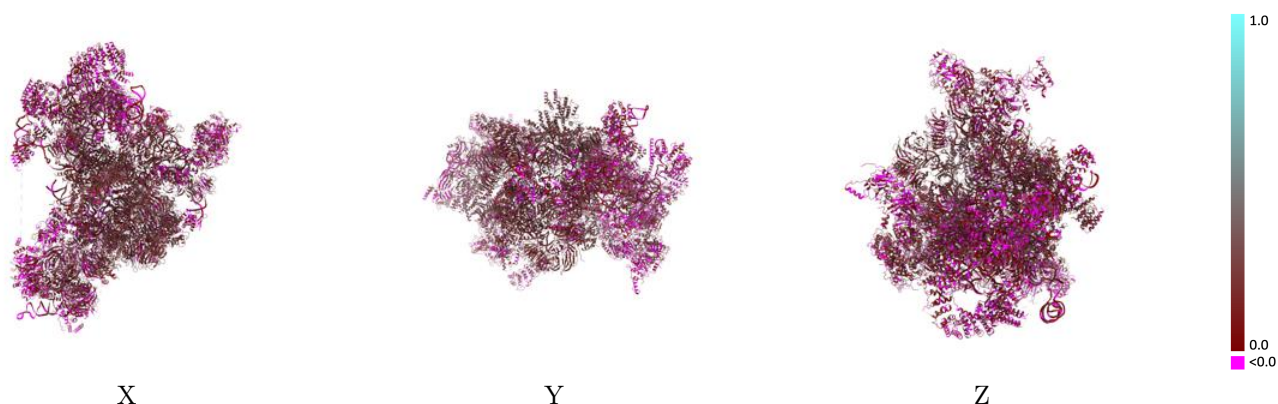
Y



Z

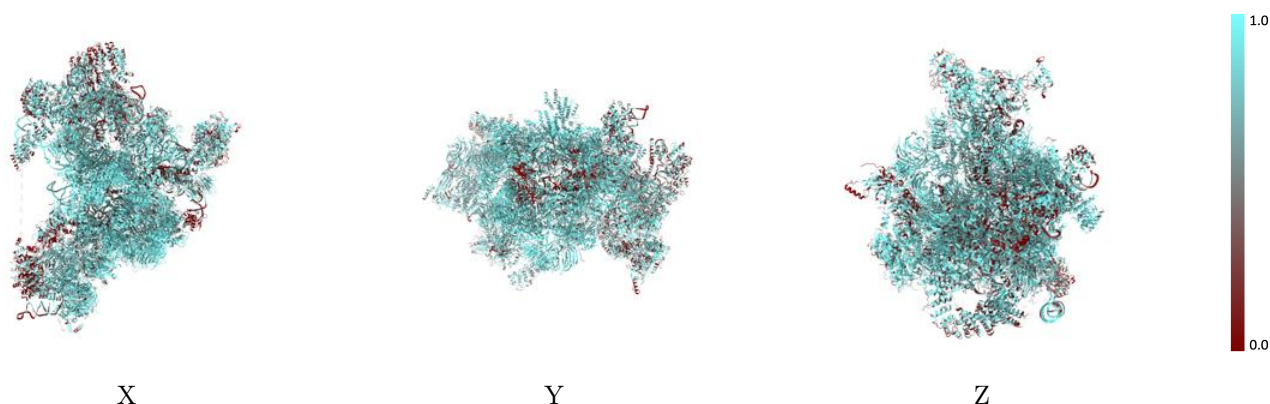
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 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.

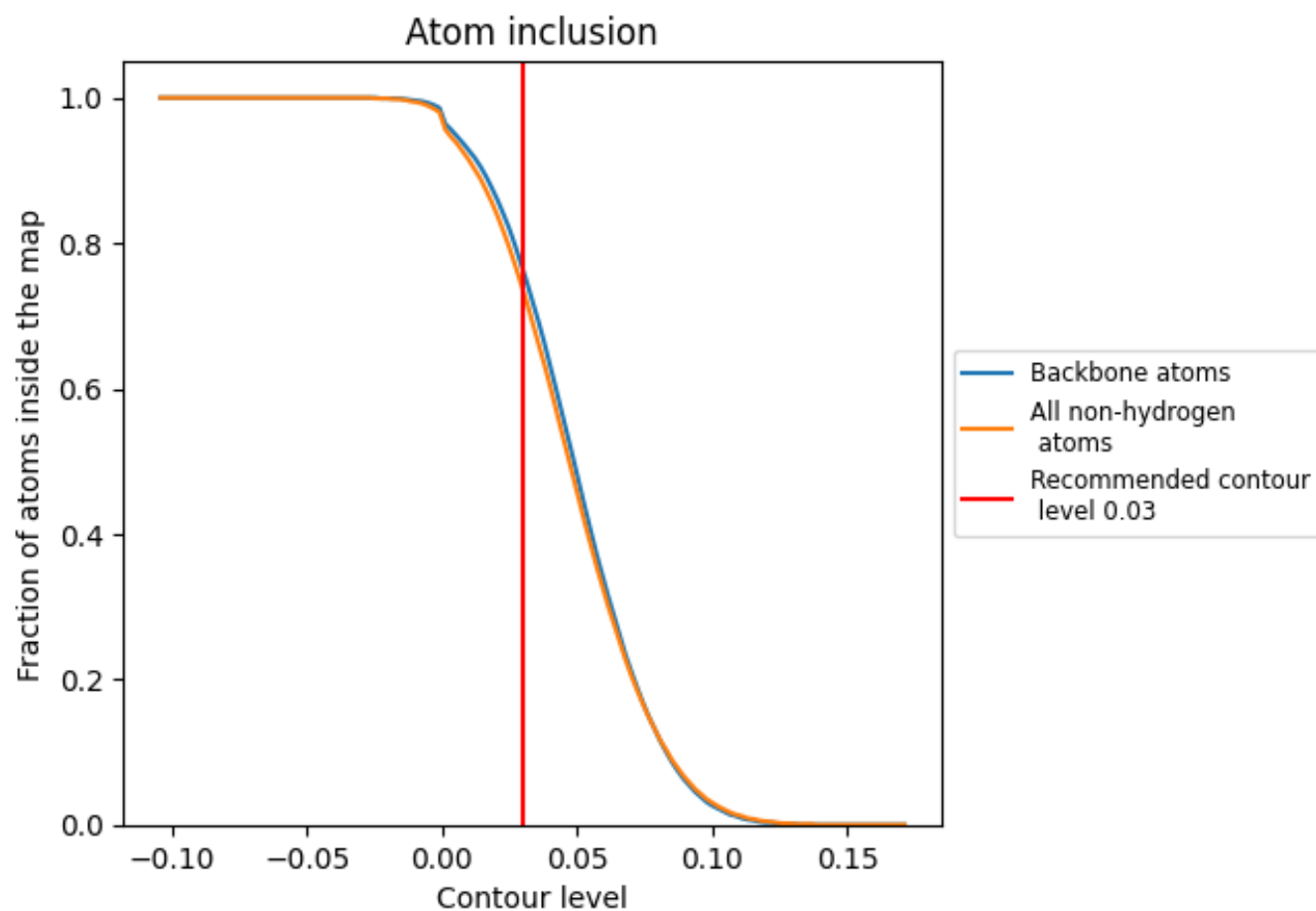
## 9.3 Atom inclusion mapped to coordinate model [i](#)



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 (0.03).









































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 73% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7340	 0.1560
C1	 0.7620	 0.1390
C2	 0.7890	 0.1470
CA	 0.8520	 0.2410
CB	 0.4950	 0.0480
CC	 0.8760	 0.2410
CD	 0.6950	 0.1650
CE	 0.6750	 0.1340
CF	 0.8020	 0.1880
CG	 0.7790	 0.1600
CH	 0.8760	 0.2290
CI	 0.8590	 0.2360
CJ	 0.7890	 0.2200
CK	 0.7640	 0.2260
CL	 0.7440	 0.2110
CM	 0.8640	 0.2390
CN	 0.6790	 0.1520
CO	 0.5950	 0.0800
CP	 0.5040	 0.1520
CQ	 0.2070	 0.0590
CR	 0.7820	 0.1690
CS	 0.5920	 0.0780
CT	 0.8070	 0.2310
CU	 0.1680	 0.0390
CV	 0.5900	 0.0810
CW	 0.6390	 0.1150
CX	 0.6180	 0.0520
CZ	 0.7340	 0.1480
Ca	 0.7750	 0.1940
Cb	 0.5740	 0.0950
Cc	 0.8580	 0.2280
Cd	 0.7430	 0.1650
Ce	 0.7350	 0.1770
Cf	 0.6350	 0.0500
Cg	 0.8200	 0.2110



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Chain	Atom inclusion	Q-score
Ch	 0.8120	 0.2250
Ci	 0.7270	 0.1540
Cj	 0.7830	 0.2250
Ck	 0.4700	 0.0310
Cl	 0.4710	 0.0900
Cm	 0.8130	 0.2230
Cn	 0.8380	 0.2450
Co	 0.9030	 0.2100
Cp	 0.8470	 0.2140
Cq	 0.7800	 0.1910
Cr	 0.6660	 0.1870
UA	 0.8430	 0.2220
UB	 0.7490	 0.1500
UC	 0.8860	 0.2630
UD	 0.7280	 0.1210
UE	 0.8470	 0.2050
UF	 0.9040	 0.2370
UG	 0.7480	 0.1850
UH	 0.7470	 0.1370
UI	 0.6880	 0.1450
UJ	 0.6260	 0.1430
UK	 0.5090	 0.1030
UL	 0.8870	 0.2260
UM	 0.8170	 0.1760
UN	 0.8010	 0.2300
UO	 0.8260	 0.2060
UP	 0.6080	 0.1550
UQ	 0.8180	 0.1600
UR	 0.7850	 0.1700
US	 0.6640	 0.1290
UT	 0.6010	 0.0860
UU	 0.8600	 0.2110
UV	 0.5870	 0.0900
UX	 0.6630	 0.1970