



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 01:56 PM UTC

PDB ID : 5WYK / pdb_00005wyk
EMDB ID : EMD-6696
Title : Cryo-EM structure of the 90S small subunit pre-ribosome (Mtr4-depleted, Enp1-TAP)
Authors : Ye, K.; Zhu, X.; Sun, Q.
Deposited on : 2017-01-13
Resolution : 4.50 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:

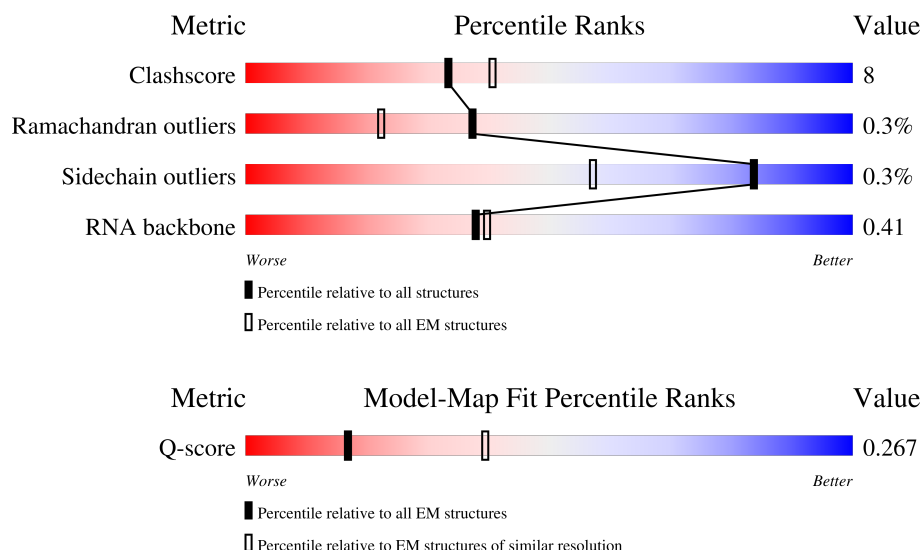
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 4.50 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	2937 (4.00 - 5.00)

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	3A	333	
2	3B	327	
2	3C	327	

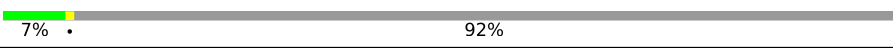
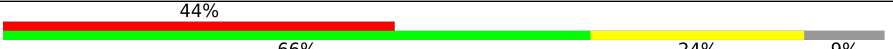
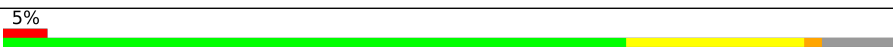
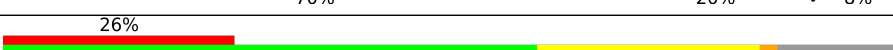
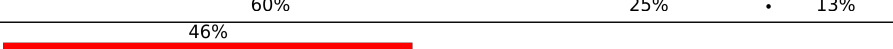
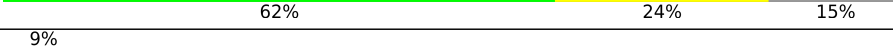
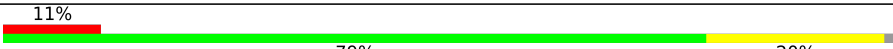
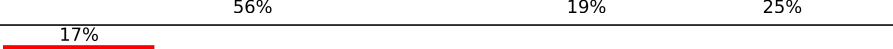
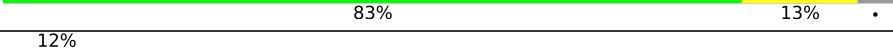
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Mol	Chain	Length	Quality of chain
3	3D	504	
4	3E	511	
5	3F	573	
6	3G	126	
6	3H	126	
7	5A	700	
8	AA	776	
9	AB	643	
10	AC	713	
11	AD	575	
12	AE	1769	
13	AF	513	
14	AG	896	
15	B1	1183	
16	BA	923	
17	BB	943	
18	BC	817	
19	BD	594	
20	BE	939	
21	CA	297	
22	CB	1237	
23	E1	252	
23	E2	252	
24	E4	707	
25	K1	316	

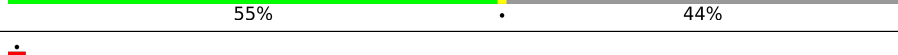
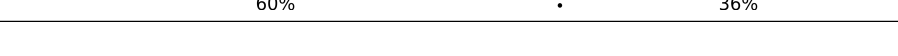
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Mol	Chain	Length	Quality of chain
26	MA	183	
27	MB	290	
28	MC	593	
29	P1	274	
30	R1	367	
31	S1	489	
32	SA	1812	
33	SC	255	
34	SF	261	
35	SG	225	
36	SI	190	
37	SJ	200	
38	SK	197	
39	SM	156	
40	SO	151	
41	SP	137	
42	SR	143	
43	SX	130	
44	SY	145	
45	SZ	135	
46	Sc	82	
47	Sd	67	
48	Sf	63	
49	U1	554	
50	U2	250	

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Mol	Chain	Length	Quality of chain
51	U4	189	
52	U5	274	
53	UA	1615	
54	UB	987	
55	UC	1033	

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 150760 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called U3 RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	3A	157	Total	C	N	O	P	0	0
			3327	1488	575	1107	157		

- Molecule 2 is a protein called rRNA 2'-O-methyltransferase fibrillarin.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	3B	239	Total	C	N	O	S	0	0
			1866	1183	332	341	10		
2	3C	239	Total	C	N	O	S	0	0
			1866	1183	332	341	10		

- Molecule 3 is a protein called Nucleolar protein 56.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3D	370	Total	C	N	O	S	0	0
			2915	1843	503	560	9		

- Molecule 4 is a protein called Nucleolar protein 58.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3E	382	Total	C	N	O	S	0	0
			2935	1859	498	570	8		

- Molecule 5 is a protein called Ribosomal RNA-processing protein 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	3F	365	Total	C	N	O	S	0	0
			2916	1871	506	529	10		

- Molecule 6 is a protein called 13 kDa ribonucleoprotein-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	3G	122	Total	C	N	O	S	0	0
			924	589	159	172	4		
6	3H	122	Total	C	N	O	S	0	0
			924	589	159	172	4		

- Molecule 7 is a RNA chain called 5ETS RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	5A	462	Total	C	N	O	P	0	0
			9867	4406	1749	3250	462		

- Molecule 8 is a protein called Utp4.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	AA	569	Total	C	N	O	0	0
			2845	1707	569	569		

- Molecule 9 is a protein called Utp5.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	AB	403	Total	C	N	O	0	0
			2015	1209	403	403		

- Molecule 10 is a protein called Utp8.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	AC	472	Total	C	N	O	0	0
			2360	1416	472	472		

- Molecule 11 is a protein called Utp9.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	AD	101	Total	C	N	O	0	0
			505	303	101	101		

- Molecule 12 is a protein called U3 small nucleolar RNA-associated protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AE	413	Total	C	N	O	S	0	0
			3331	2156	547	616	12		

- Molecule 13 is a protein called Utp15.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	AF	376	Total	C	N	O	0	0
			1880	1128	376	376		

- Molecule 14 is a protein called Utp17.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	AG	612	Total	C	N	O	0	0
			3060	1836	612	612		

- Molecule 15 is a protein called Ribosome biogenesis protein BMS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	B1	536	Total	C	N	O	S	0	0
			4325	2801	758	746	20		

- Molecule 16 is a protein called Periodic tryptophan protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	BA	755	Total	C	N	O	S	0	0
			6026	3862	1025	1123	16		

- Molecule 17 is a protein called U3 small nucleolar RNA-associated protein 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	BB	778	Total	C	N	O	S	0	0
			6138	3931	1019	1161	27		

- Molecule 18 is a protein called U3 small nucleolar RNA-associated protein 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	BC	783	Total	C	N	O	S	0	0
			6117	3870	1033	1187	27		

- Molecule 19 is a protein called U3 small nucleolar RNA-associated protein 18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	BD	325	Total	C	N	O	S	0	0
			2539	1606	458	466	9		

- Molecule 20 is a protein called U3 small nucleolar RNA-associated protein 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	BE	753	Total	C	N	O	S	0	0
			5936	3769	1020	1126	21		

- Molecule 21 is a protein called Ribosomal RNA-processing protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	CA	196	Total	C	N	O	S	0	0
			1582	1016	259	300	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
22	CB	1098	Total	C	N	O	S	0	0
			8870	5763	1462	1621	24		

- Molecule 23 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	E1	217	Total	C	N	O	S	0	0
			1689	1073	293	312	11		
23	E2	216	Total	C	N	O	S	0	0
			1695	1078	295	313	9		

- Molecule 24 is a protein called Enp2.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	E4	285	Total	C	N	O	0	0
			1425	855	285	285		

- Molecule 25 is a protein called KRR1 small subunit processome component.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	K1	175	Total	C	N	O	S	0	0
			1410	903	252	245	10		

- Molecule 26 is a protein called U3 small nucleolar ribonucleoprotein protein IMP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	MA	133	Total	C	N	O	S	0	0
			1097	692	204	194	7		

- Molecule 27 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	MB	184	Total	C	N	O	S	0	0
			1465	926	273	260	6		

- Molecule 28 is a protein called Mpp10,U3 small nucleolar RNA-associated protein MPP10.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	MC	46	Total	C	N	O	0	0
			307	193	52	62		

- Molecule 29 is a protein called Pre-rRNA-processing protein PNO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	P1	173	Total	C	N	O	S	0	0
			1368	876	245	243	4		

- Molecule 30 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	R1	355	Total	C	N	O	S	0	0
			2742	1756	466	509	11		

- Molecule 31 is a protein called Sof1.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	S1	285	Total	C	N	O	0	0
			1425	855	285	285		

- Molecule 32 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	SA	1000	Total	C	N	O	P	0	0
			21307	9529	3794	6984	1000		

- Molecule 33 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	SC	214	Total	C	N	O	S	0	0
			1709	1084	310	311	4		

- Molecule 34 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	SF	237	Total	C	N	O	S	0	0
			1881	1205	345	328	3		

- Molecule 35 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	SG	206	Total	C	N	O	S	0	0
			1609	1007	300	299	3		

- Molecule 36 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	SI	165	Total	C	N	O	S	0	0
			1322	856	227	239			

- Molecule 37 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	SJ	170	Total	C	N	O	S	0	0
			1350	839	268	241	2		

- Molecule 38 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	SK	175	Total	C	N	O	S	0	0
			1412	892	272	247	1		

- Molecule 39 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	SM	141	Total	C	N	O	S	0	0
			1143	733	216	191	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	SO	134	Total	C	N	O	S	0	0
			1087	698	202	186	1		

- Molecule 41 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	SP	112	Total	C	N	O	S	0	0
			771	477	150	143	1		

- Molecule 42 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	SR	125	Total	C	N	O		0	0
			973	625	174	174			

- Molecule 43 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	SX	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 44 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	SY	103	Total	C	N	O	S	0	0
			785	501	144	138	2		

- Molecule 45 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	SZ	101	Total	C	N	O		0	0
			801	512	144	145			

- Molecule 46 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Sc	79	Total	C	N	O	S	0	0
			595	371	108	111	5		

- Molecule 47 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Sd	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 48 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	Sf	30	Total	C	N	O	0	0
			251	162	50	39		

- Molecule 49 is a protein called Utp7.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	U1	285	Total	C	N	O	0	0
			1425	855	285	285		

- Molecule 50 is a protein called Utp11.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	U2	73	Total	C	N	O	0	0
			365	219	73	73		

- Molecule 51 is a protein called rRNA-processing protein FCF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	U4	126	Total	C	N	O	S	0	0
			990	633	179	168	10		

- Molecule 52 is a protein called Ribosome biogenesis protein UTP30.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	U5	248	Total	C	N	O	S	0	0
			2009	1285	357	359	8		

- Molecule 53 is a protein called Helical domain protein.

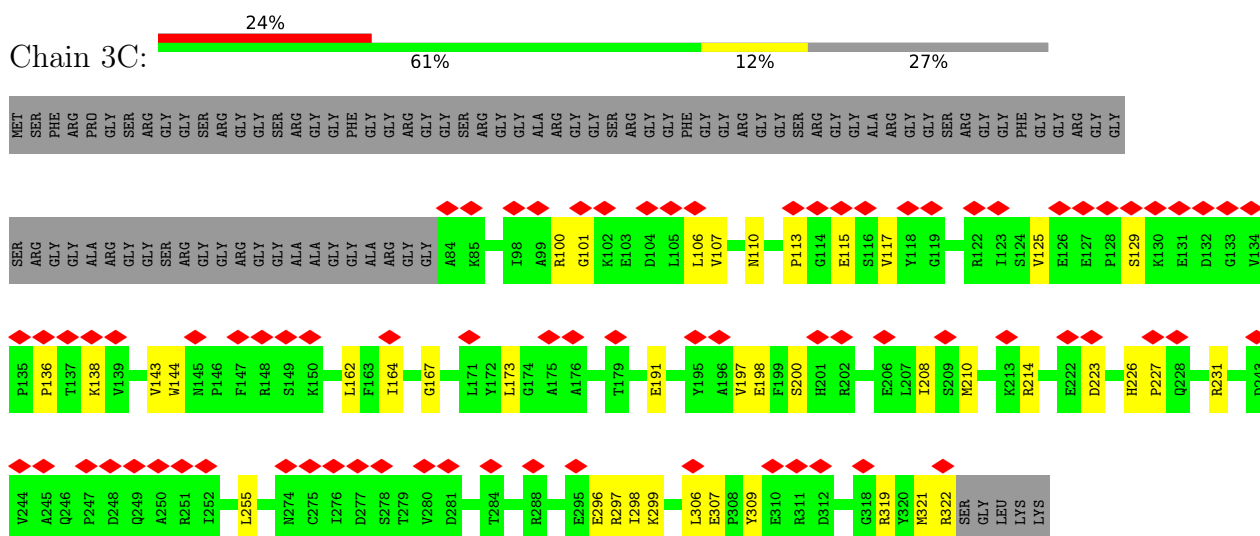
Mol	Chain	Residues	Atoms				AltConf	Trace
53	UA	338	Total	C	N	O	0	0
			1690	1014	338	338		

- Molecule 54 is a protein called Helical domain protein.

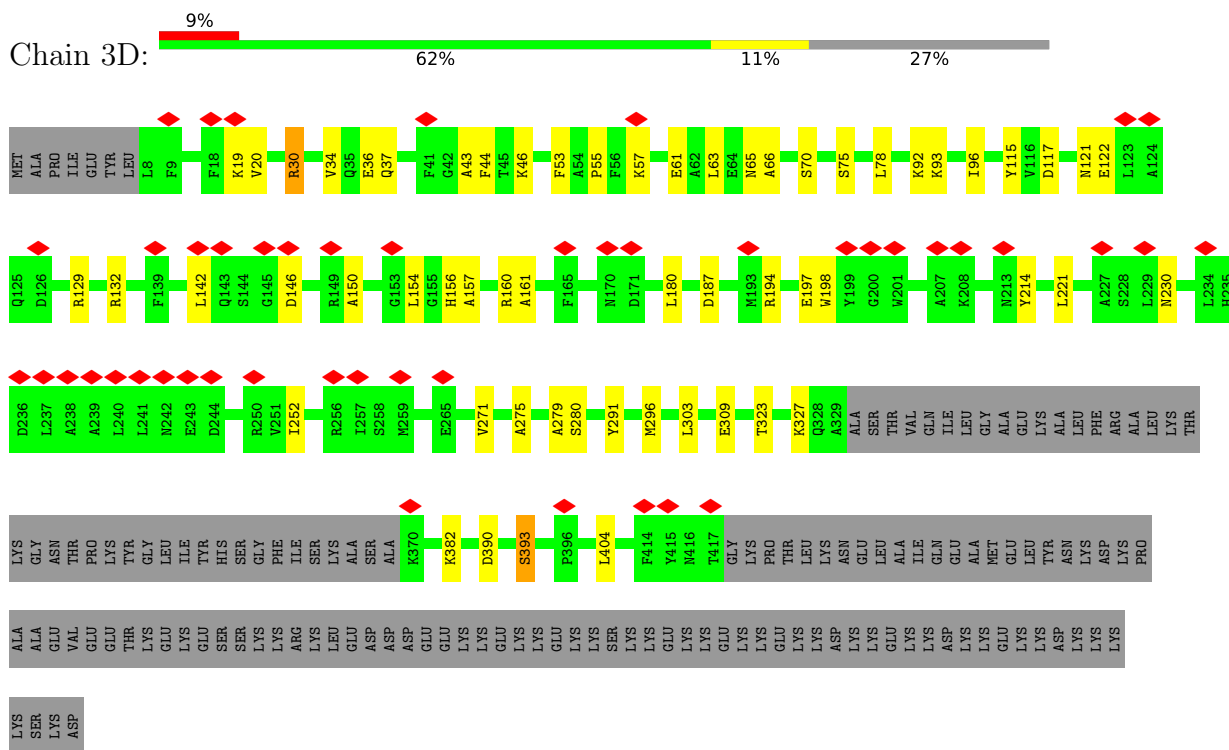
Mol	Chain	Residues	Atoms				AltConf	Trace
54	UB	555	Total	C	N	O	0	0
			2775	1665	555	555		

- Molecule 55 is a protein called Unassigned helices.

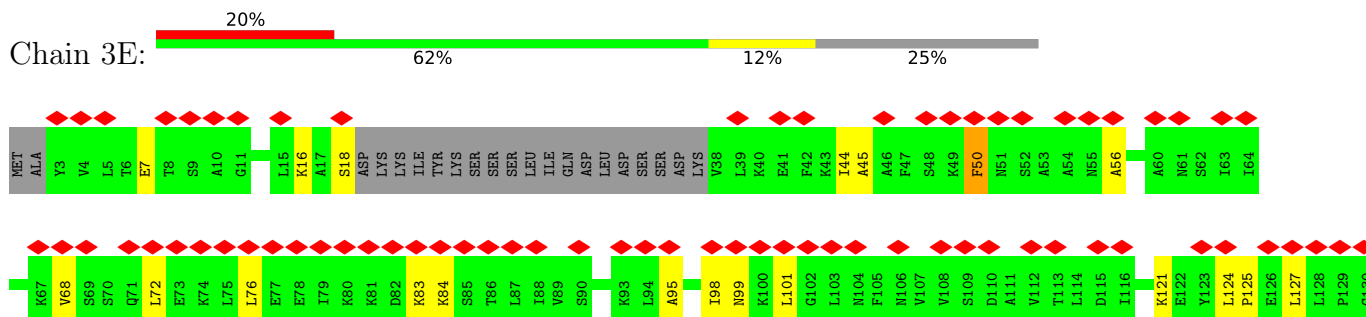
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
55	UC	660	3300	1980	660	660	0	0



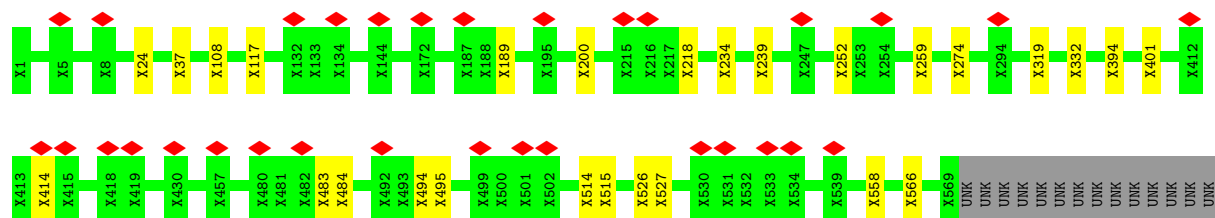
- Molecule 3: Nucleolar protein 56



- Molecule 4: Nucleolar protein 58

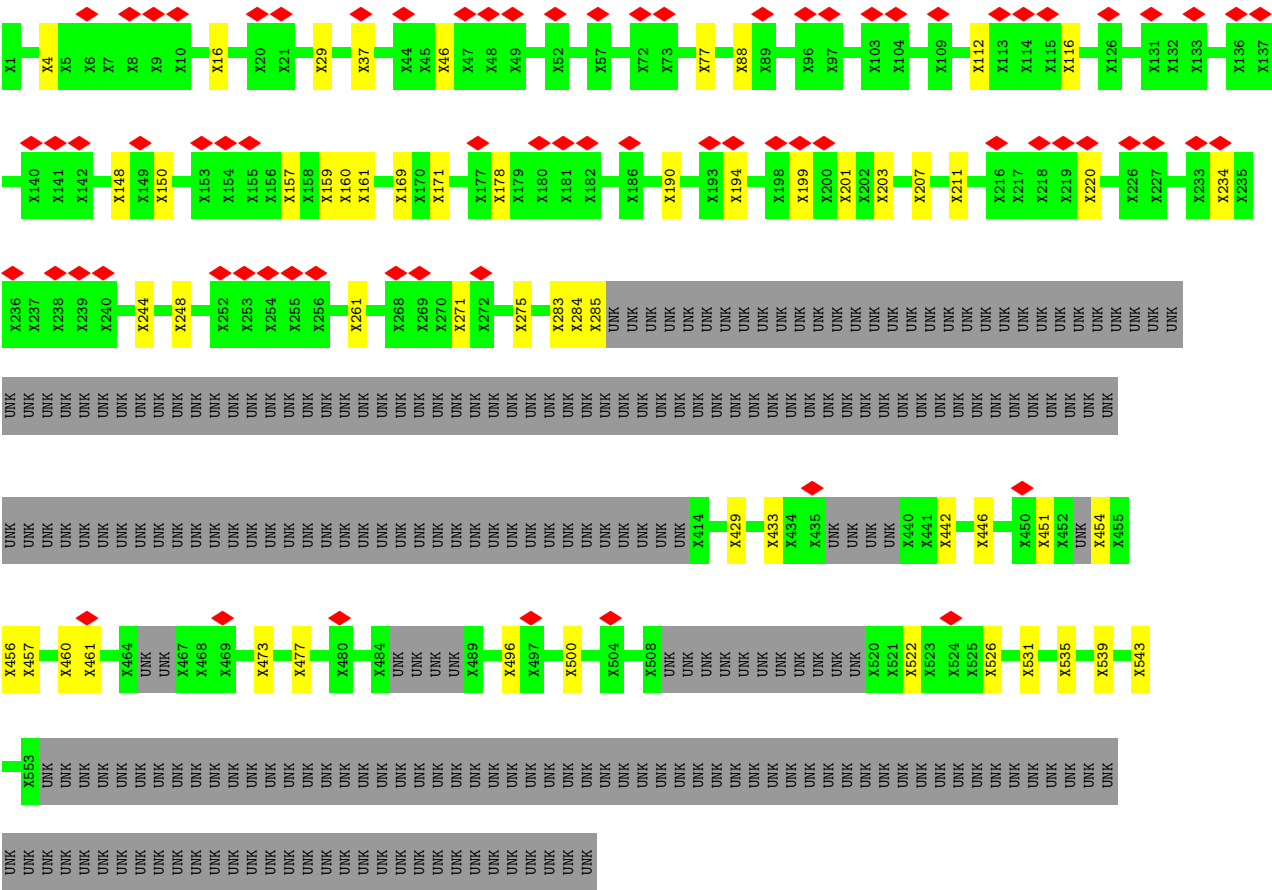


Chain 5A:

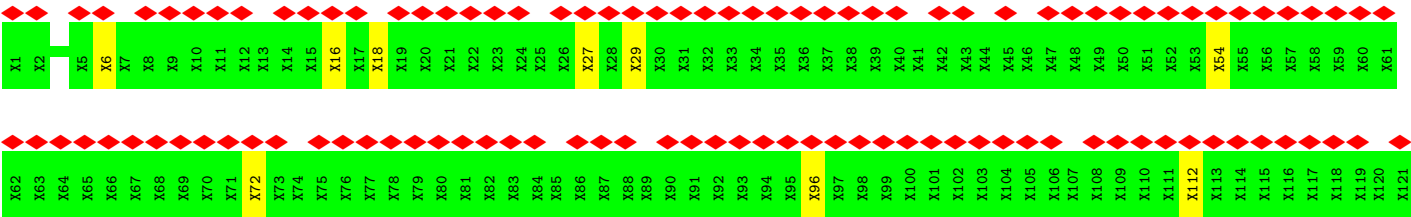


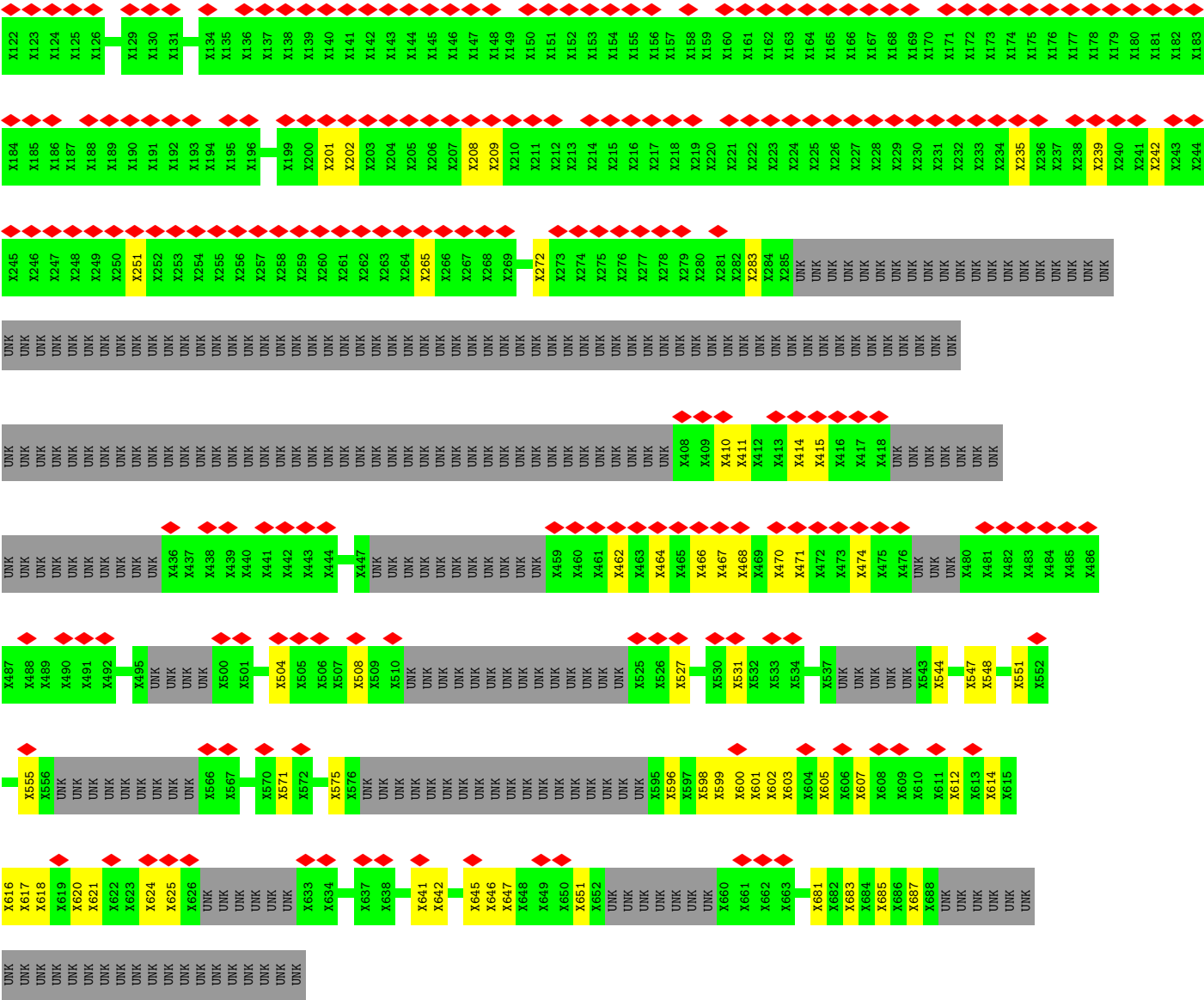


• Molecule 9: Utp5

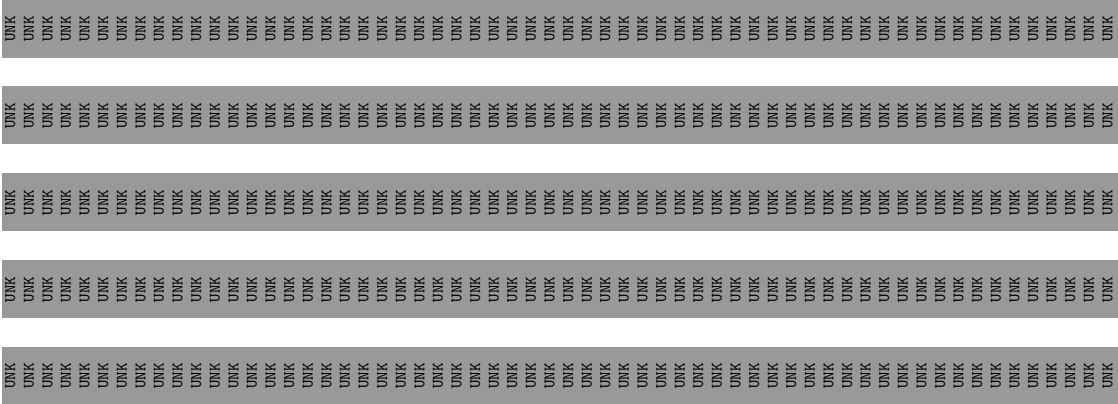


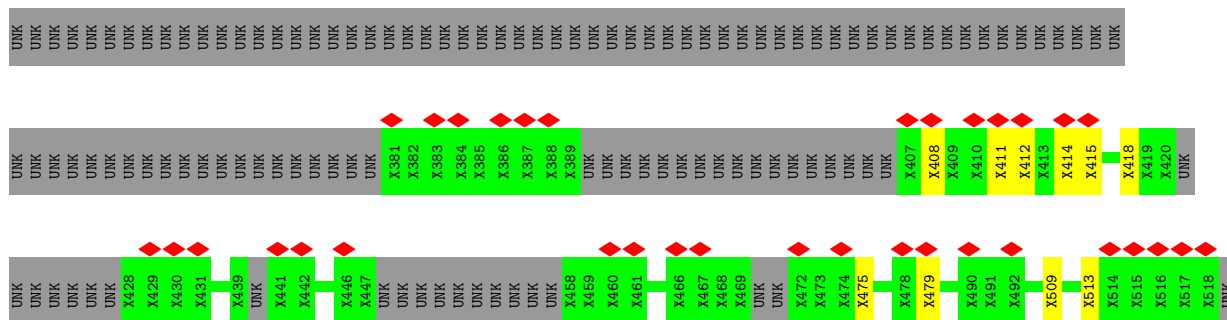
• Molecule 10: Utp8





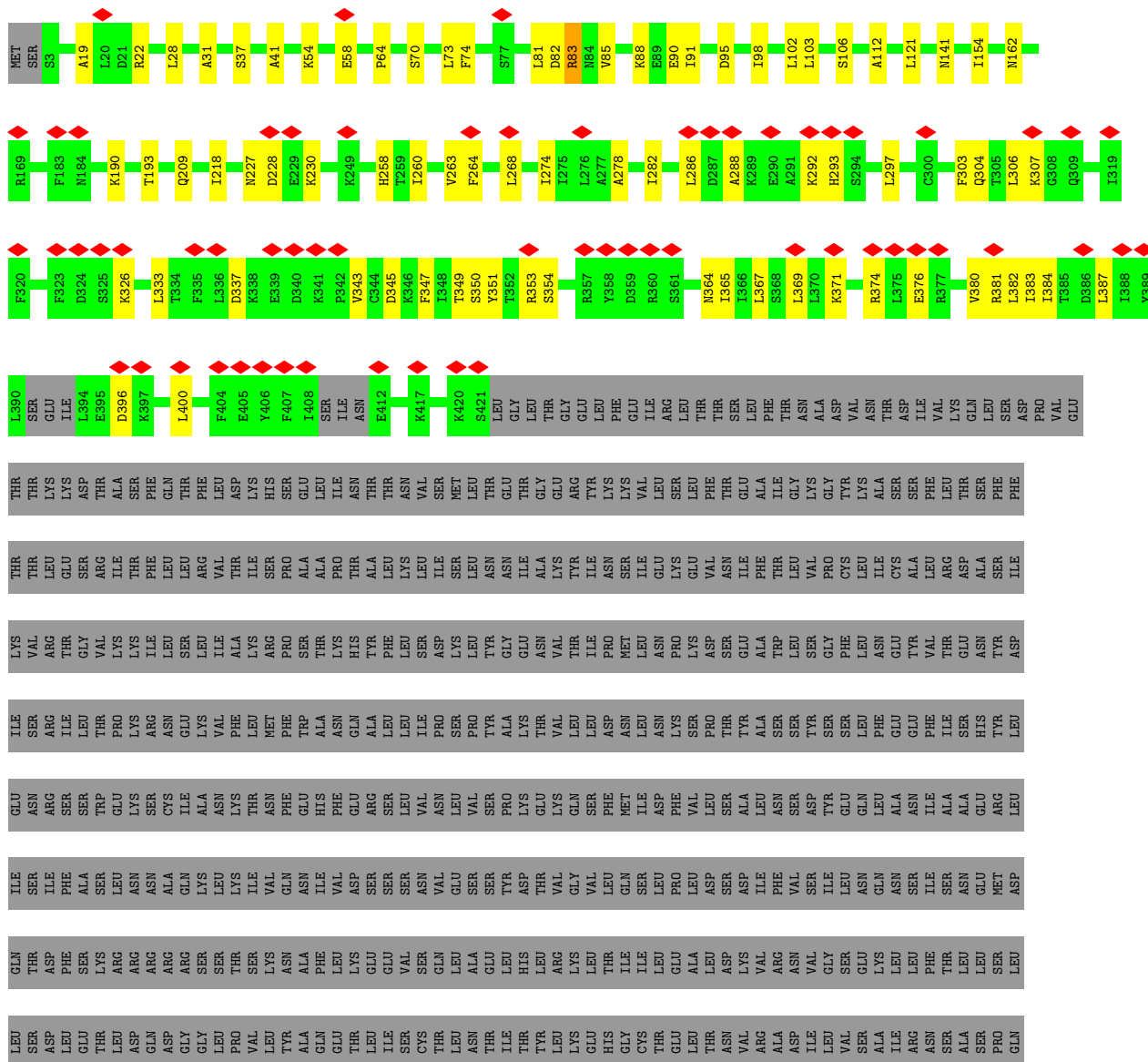
• Molecule 11: Utp9



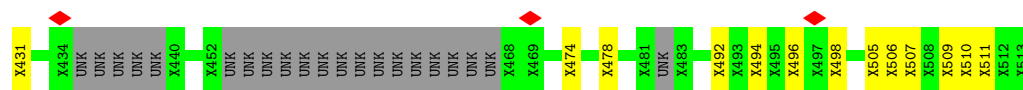


• Molecule 12: U3 small nucleolar RNA-associated protein 10

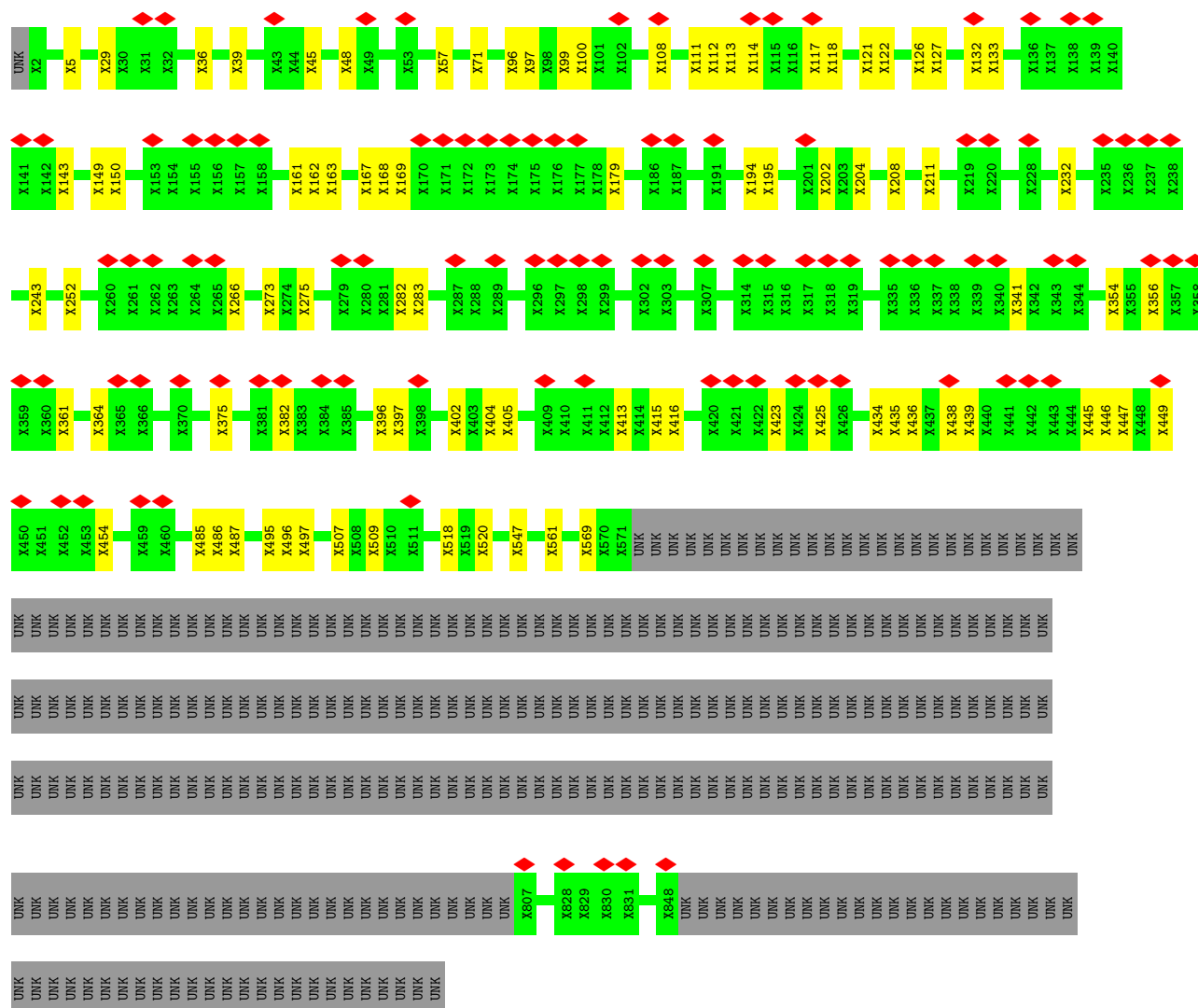
Chain AE: 19% 77%



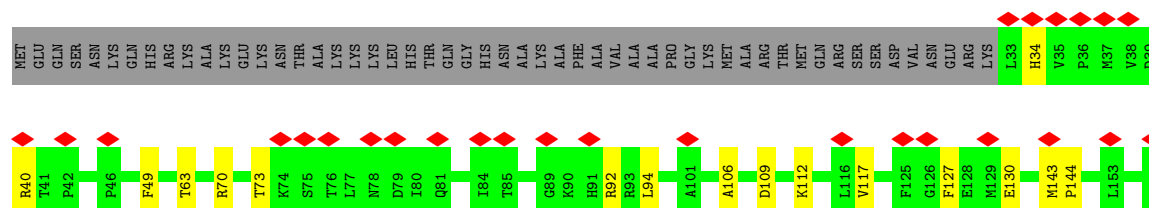
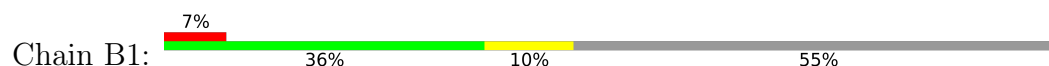


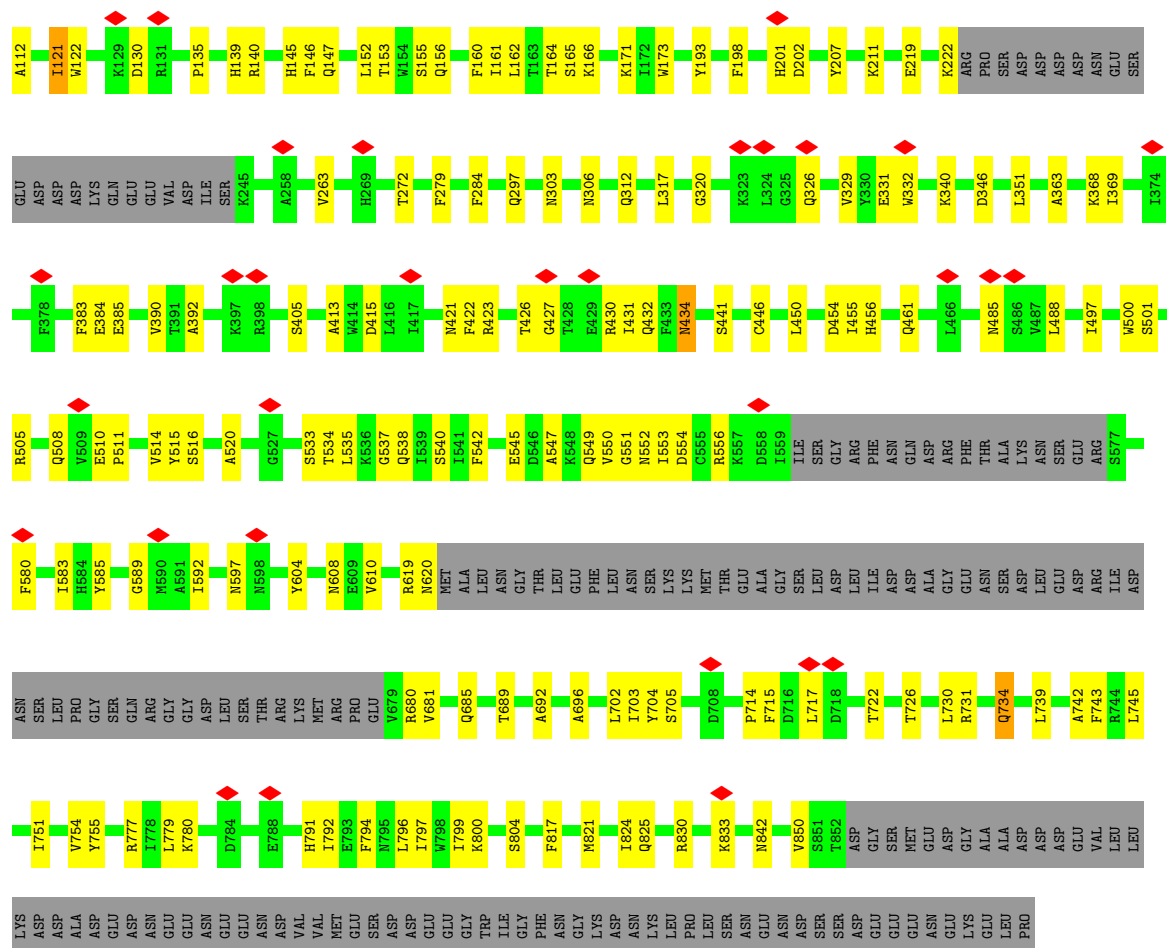


• Molecule 14: Utp17

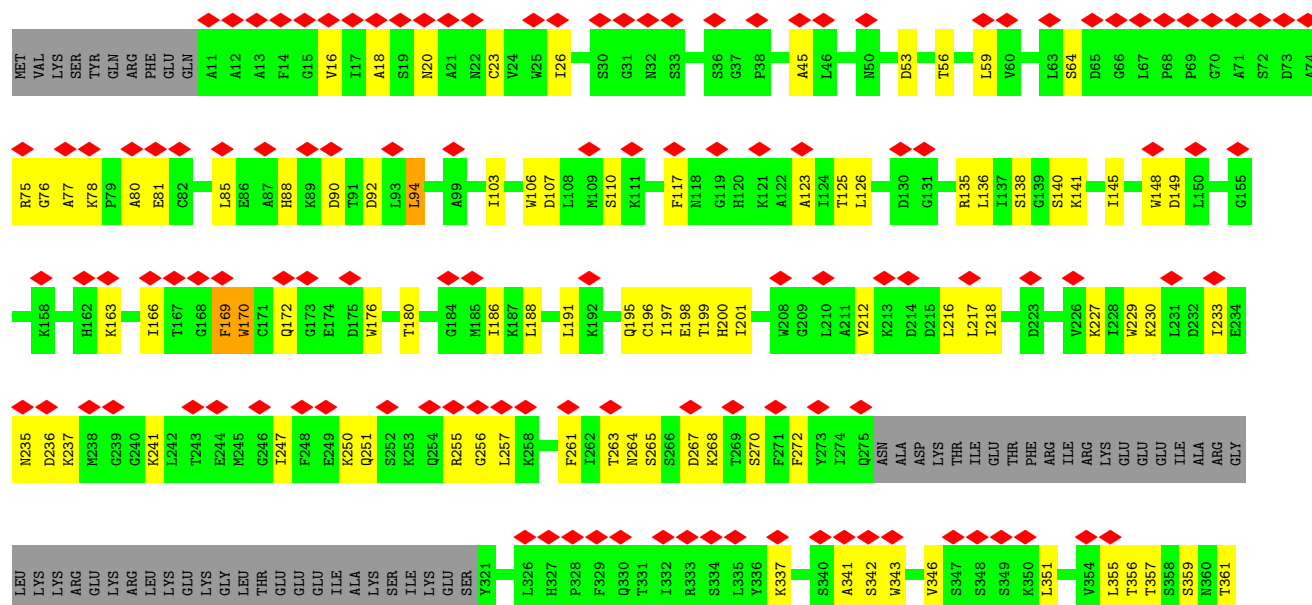


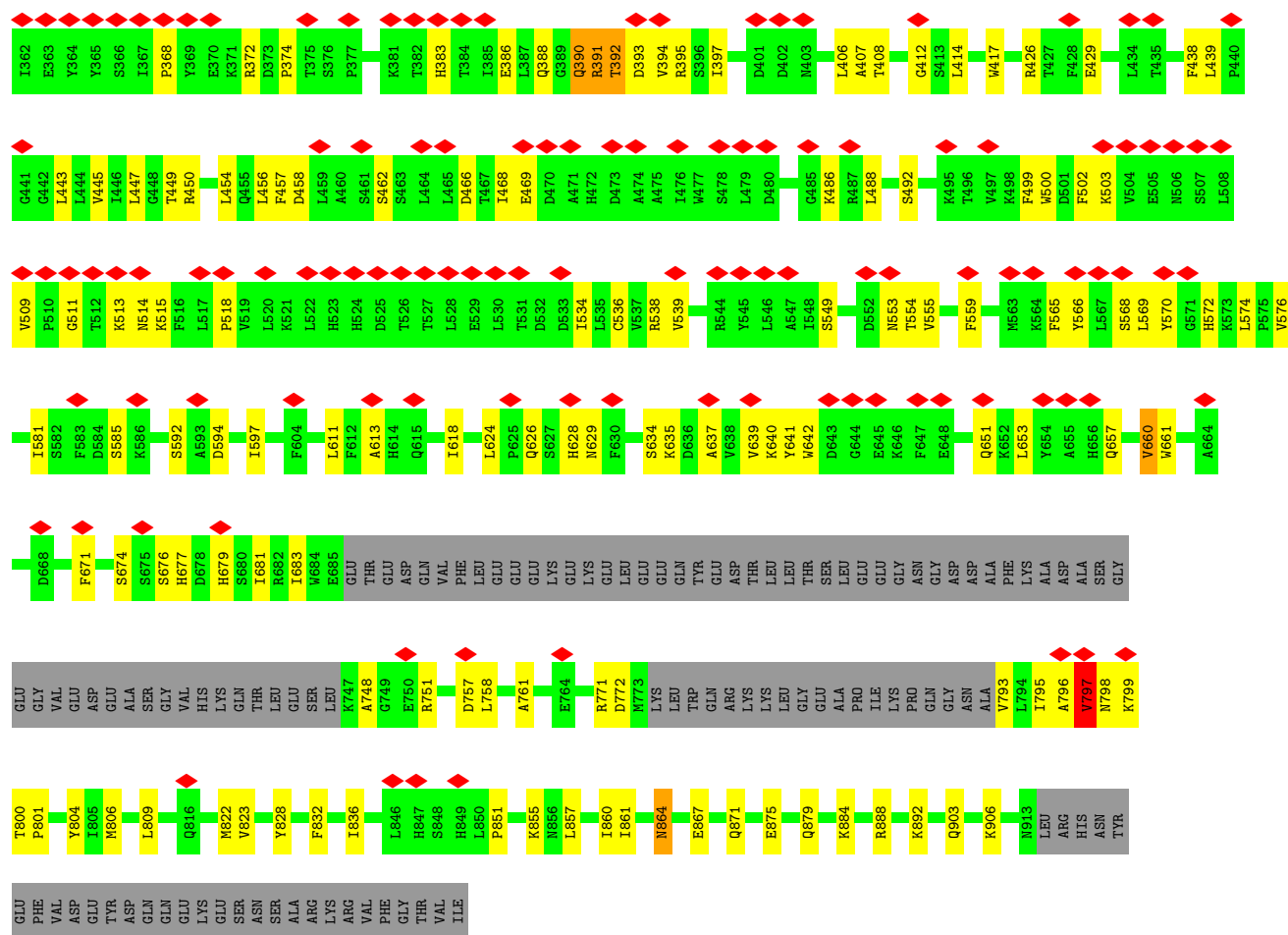
• Molecule 15: Ribosome biogenesis protein BMS1



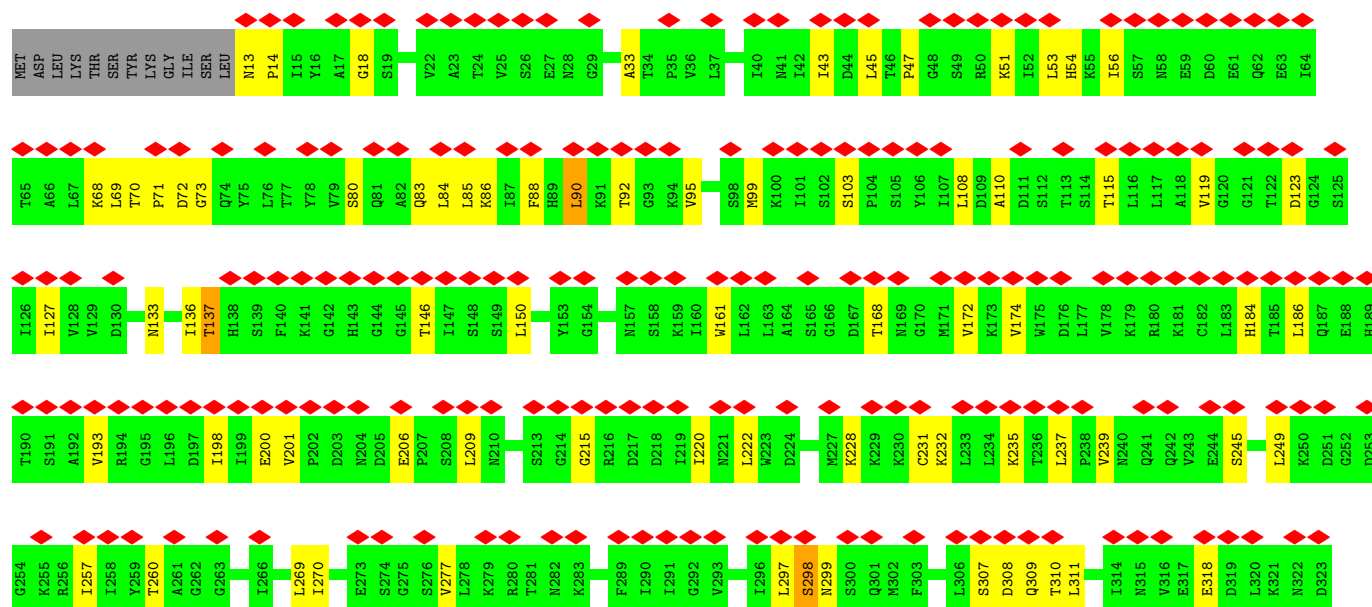
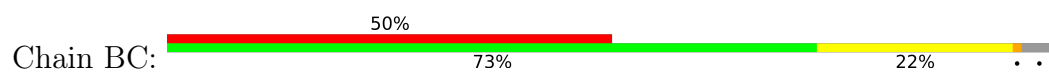


- Molecule 17: U3 small nucleolar RNA-associated protein 12

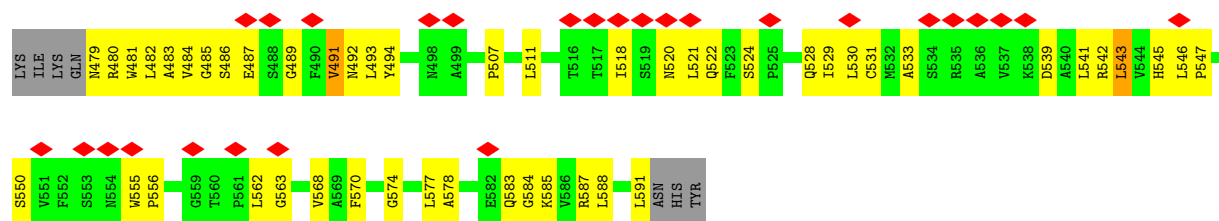




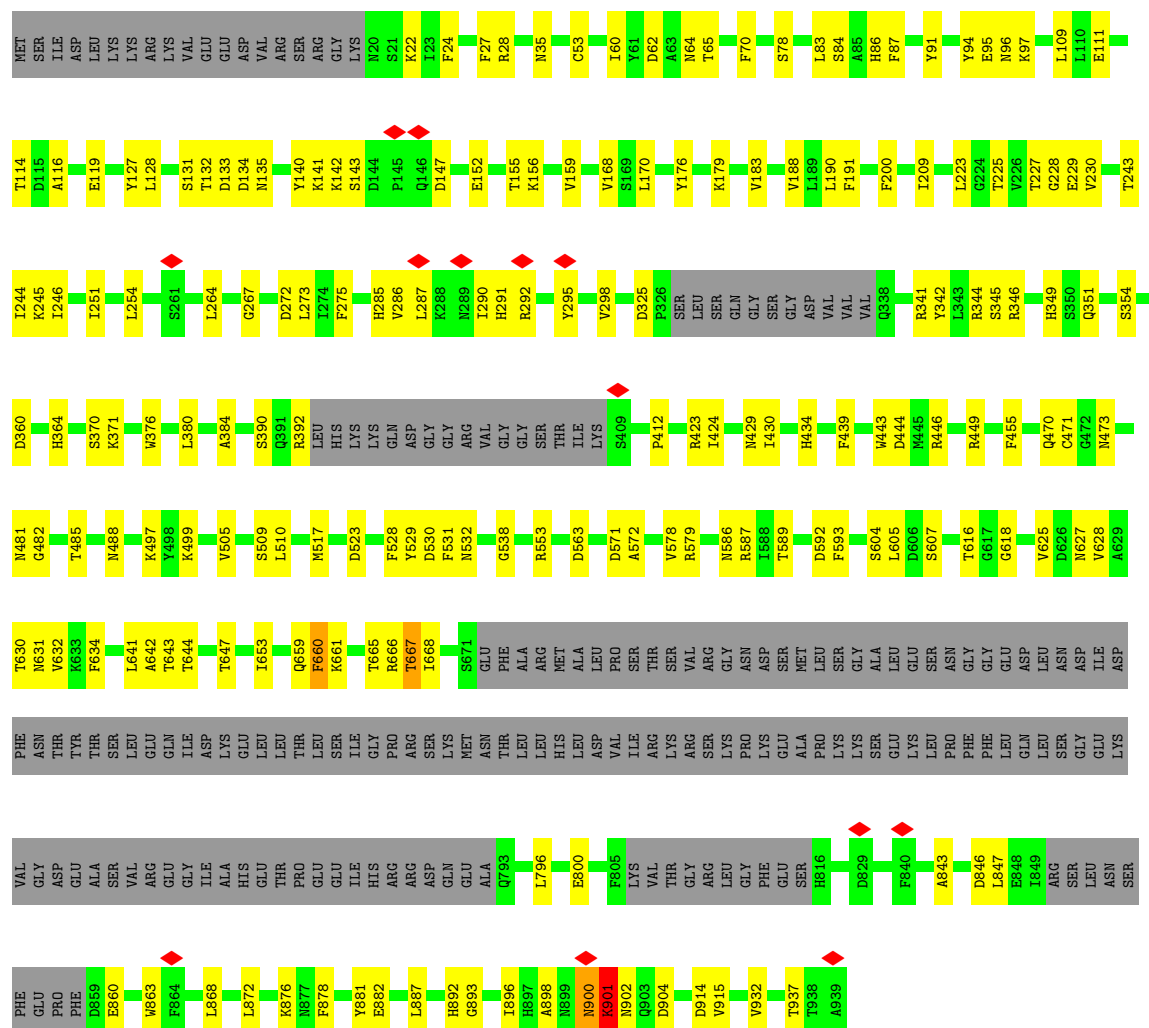
• Molecule 18: U3 small nucleolar RNA-associated protein 13



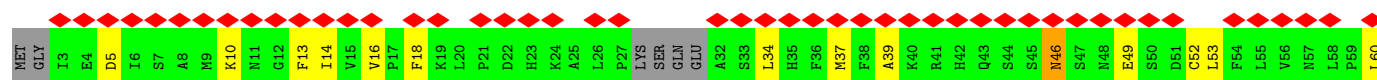




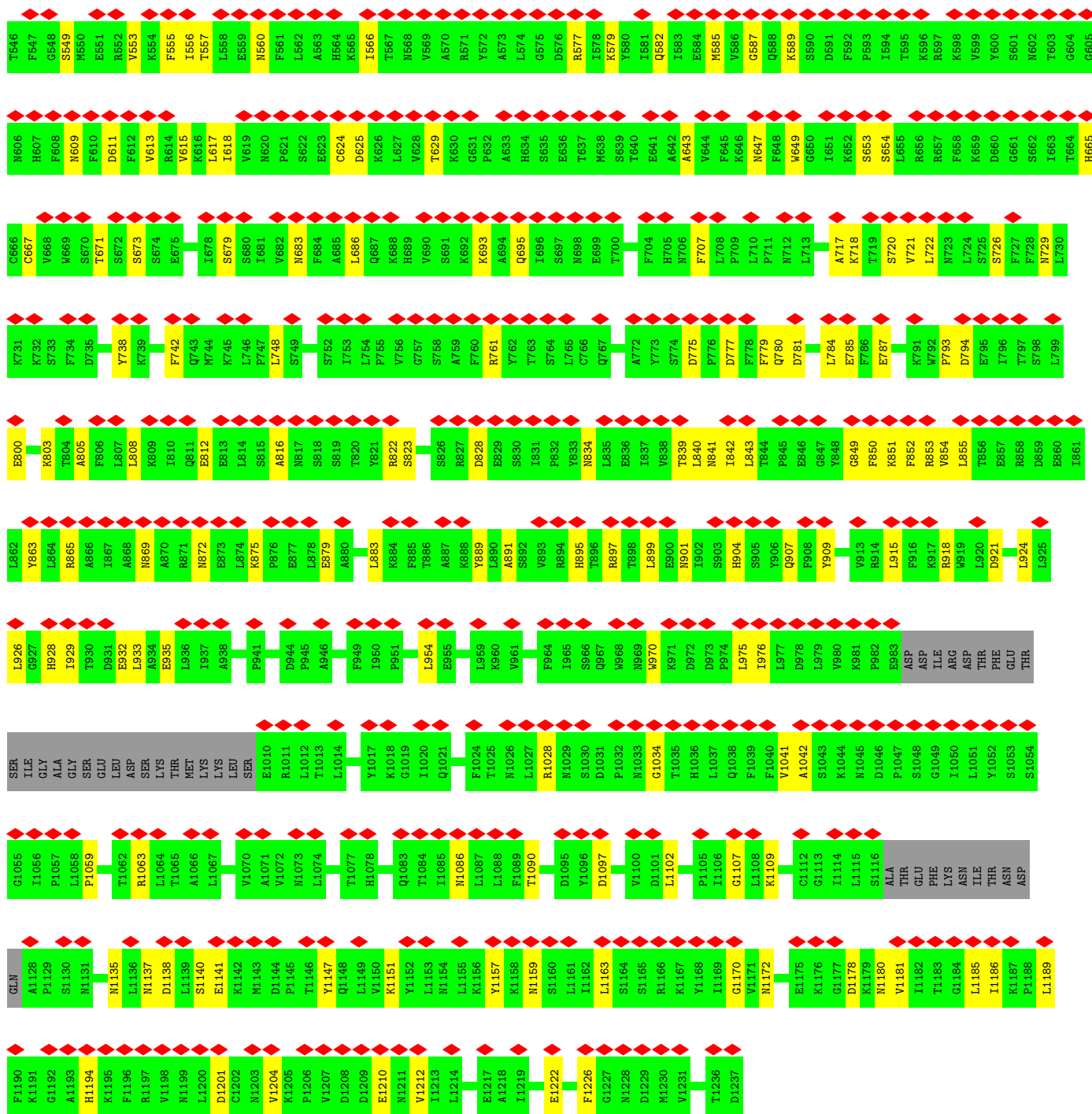
• Molecule 20: U3 small nucleolar RNA-associated protein 21



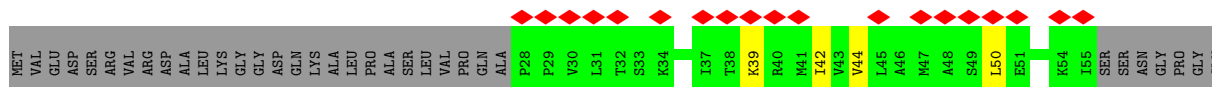
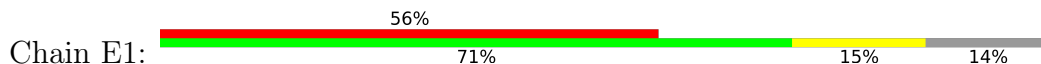
• Molecule 21: Ribosomal RNA-processing protein 7

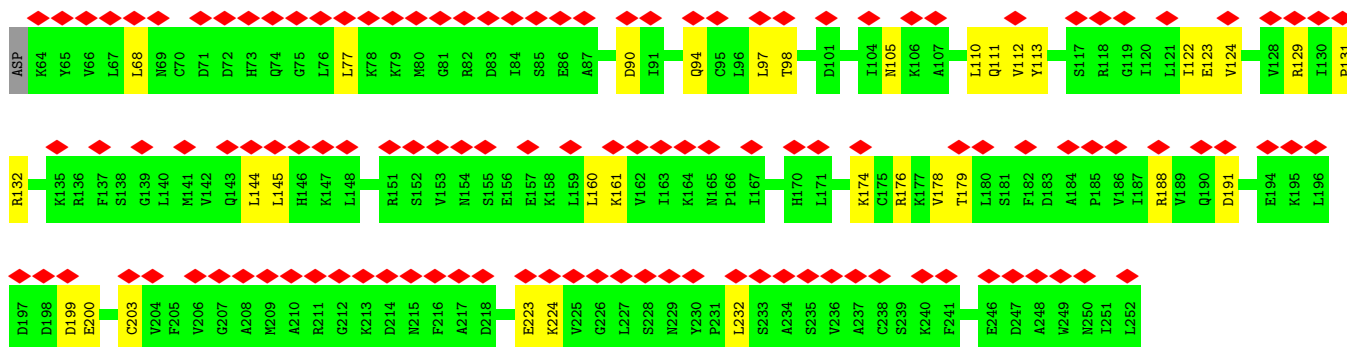




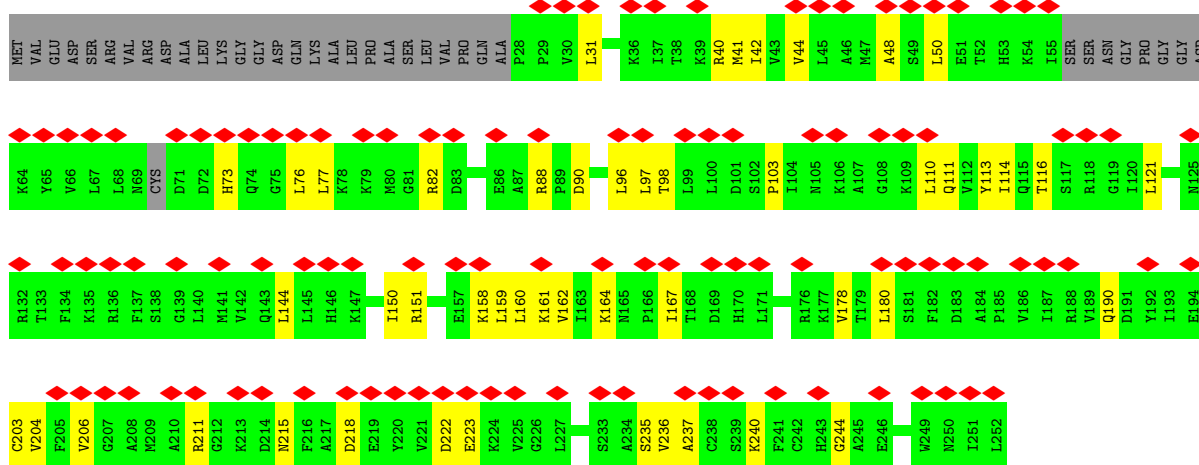


• Molecule 23: Ribosomal RNA small subunit methyltransferase NEP1

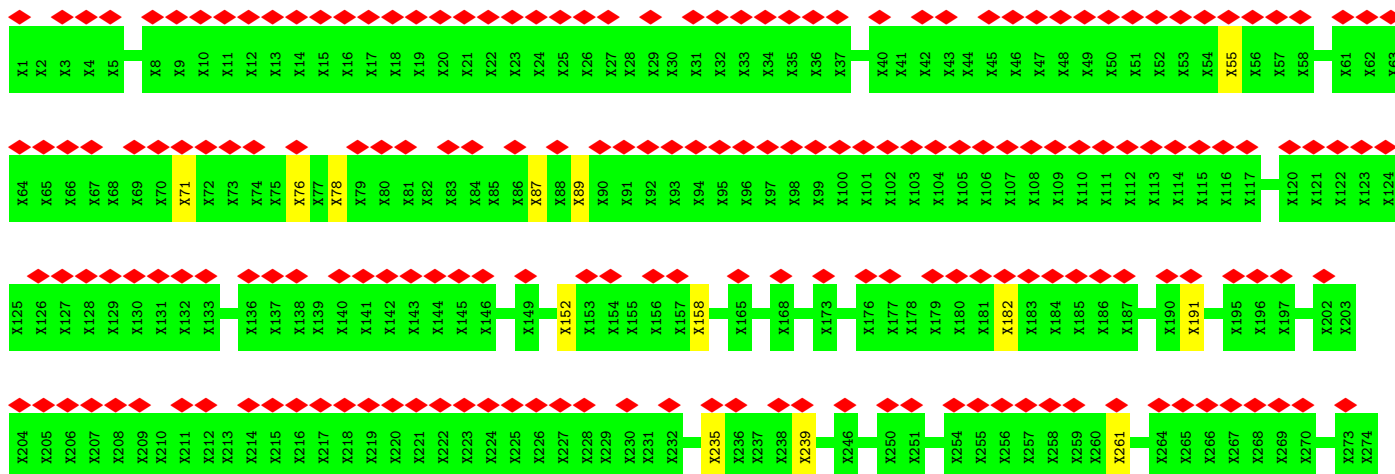


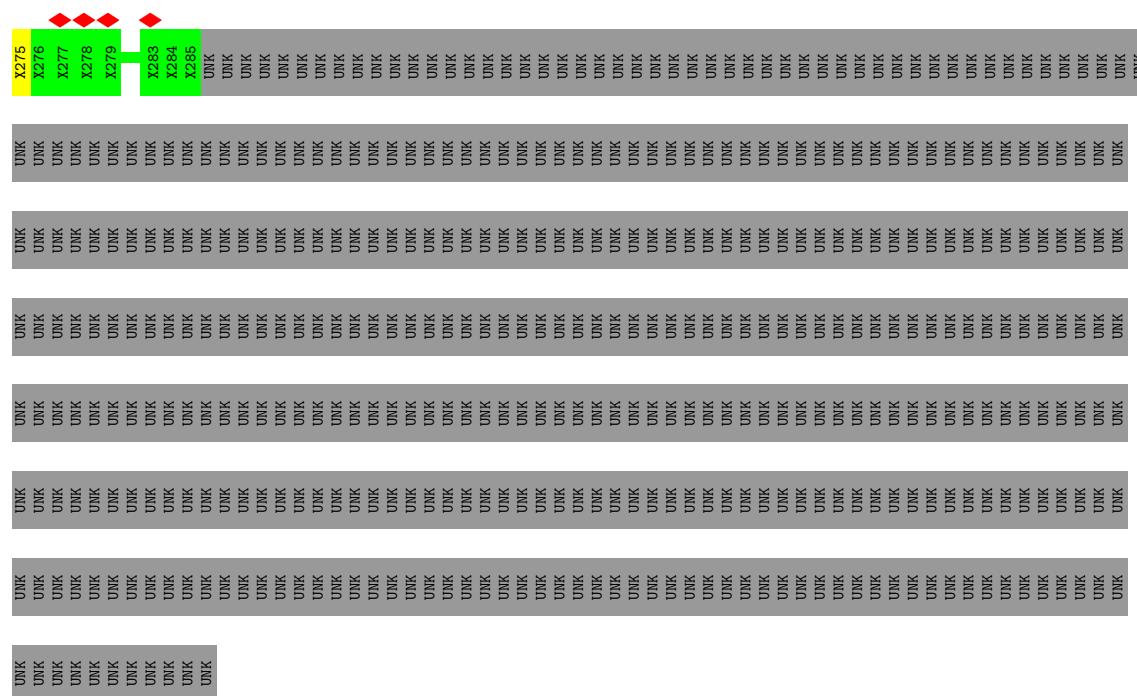


• Molecule 23: Ribosomal RNA small subunit methyltransferase NEP1

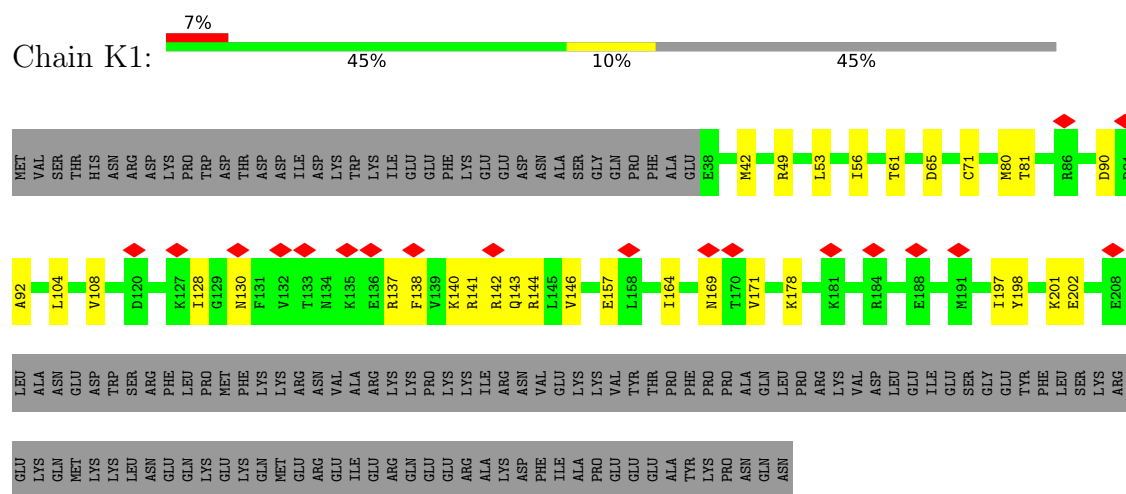


• Molecule 24: Enp2

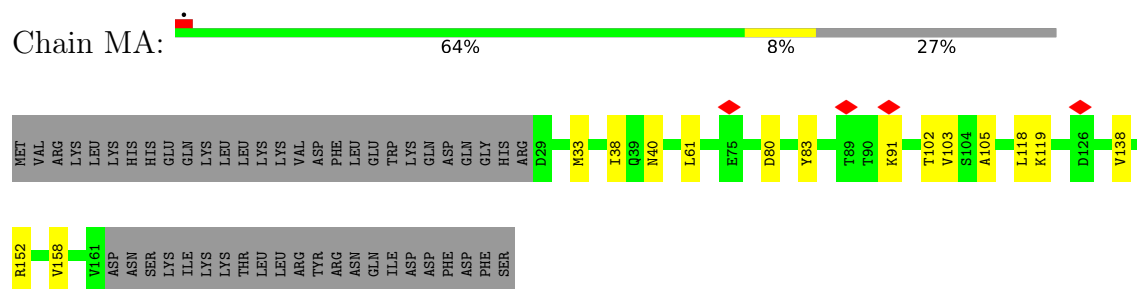




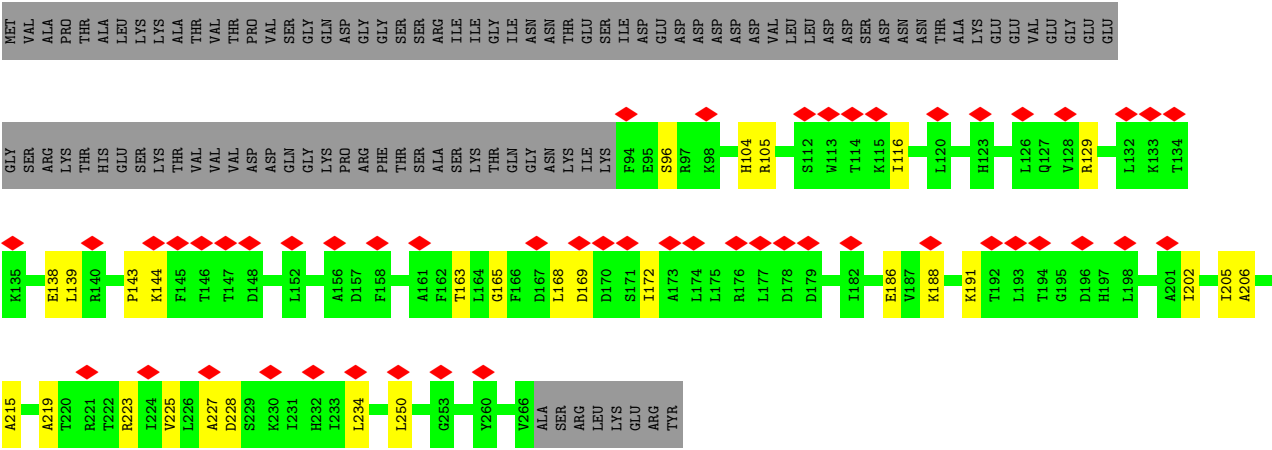
- Molecule 25: KRR1 small subunit processome component



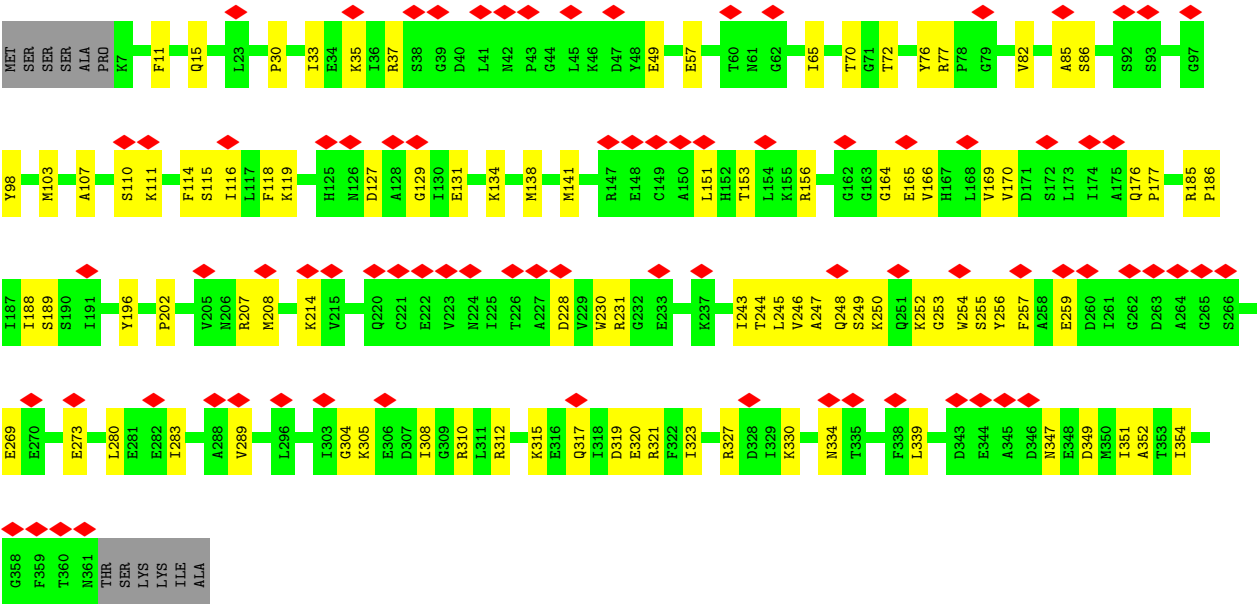
- Molecule 26: U3 small nucleolar ribonucleoprotein protein IMP3



- Molecule 27: U3 small nucleolar ribonucleoprotein protein IMP4



• Molecule 30: RNA 3'-terminal phosphate cyclase-like protein

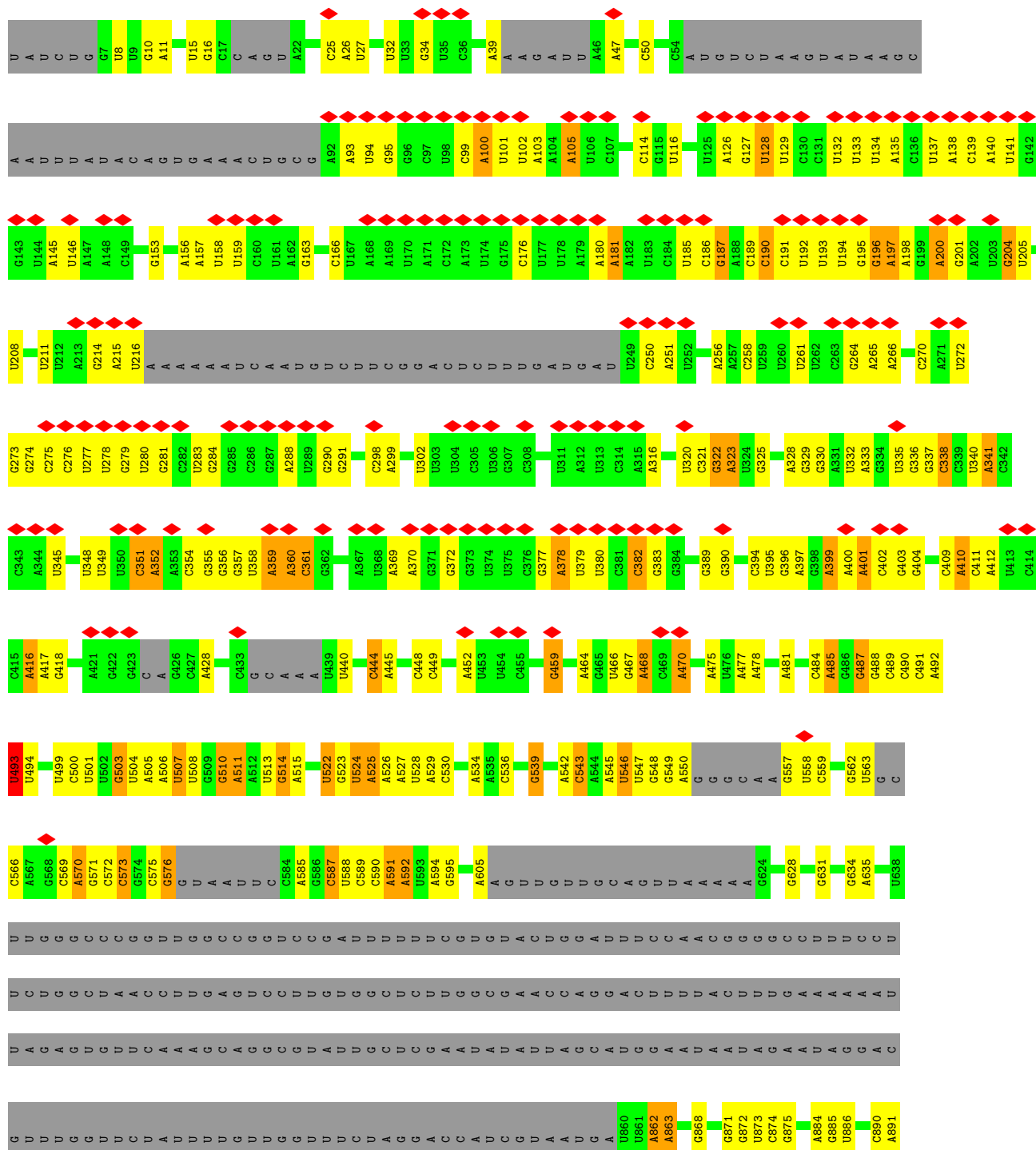
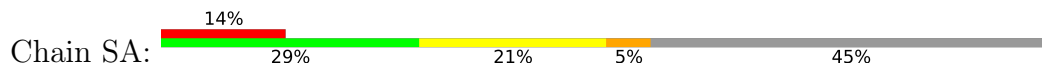


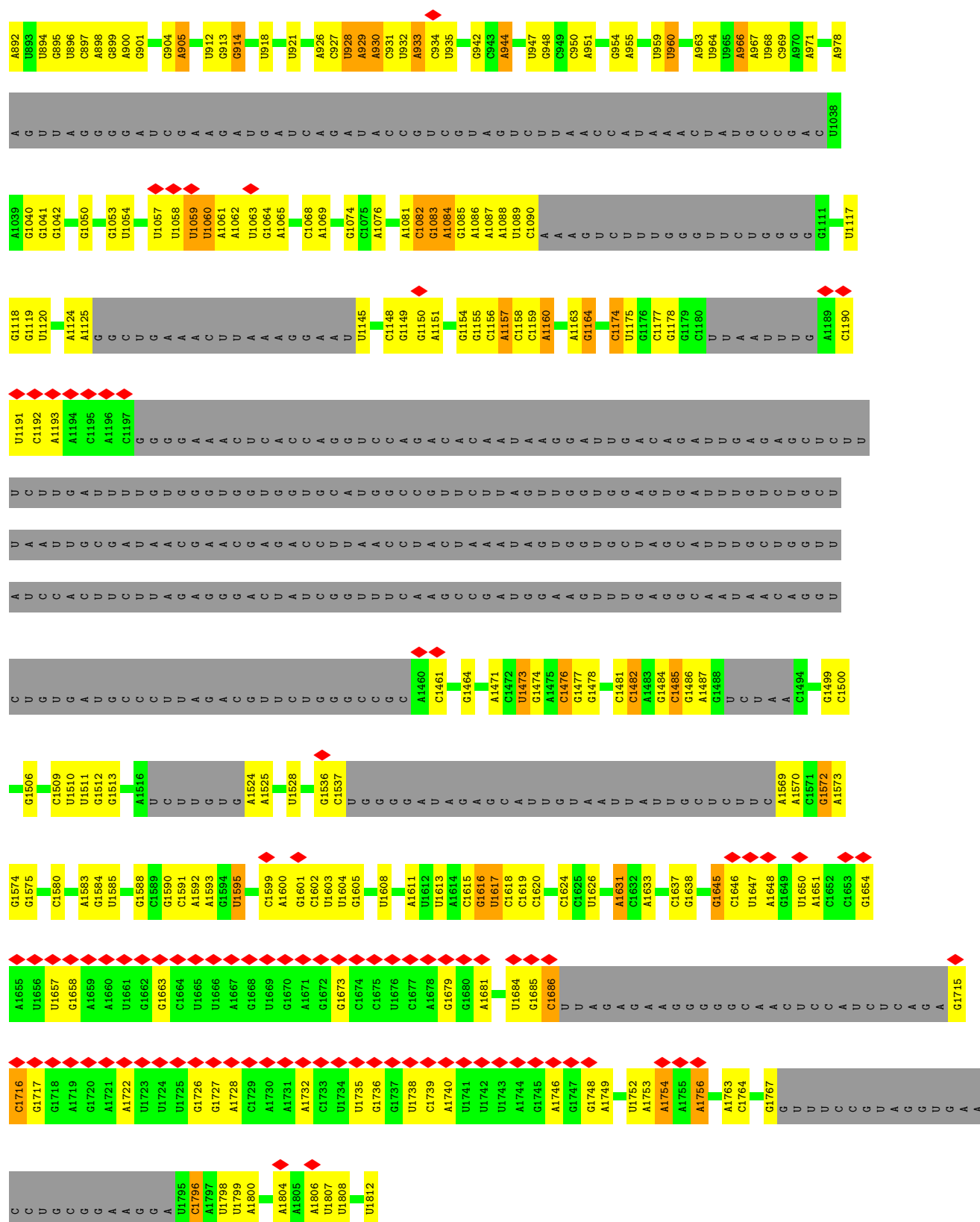
• Molecule 31: Sof1





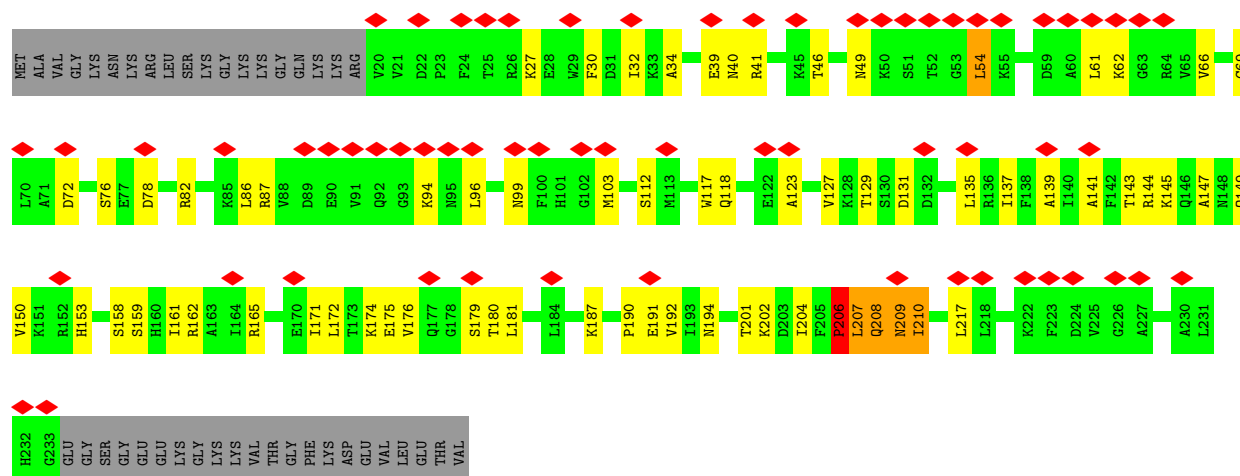
• Molecule 32: 18S ribosomal RNA



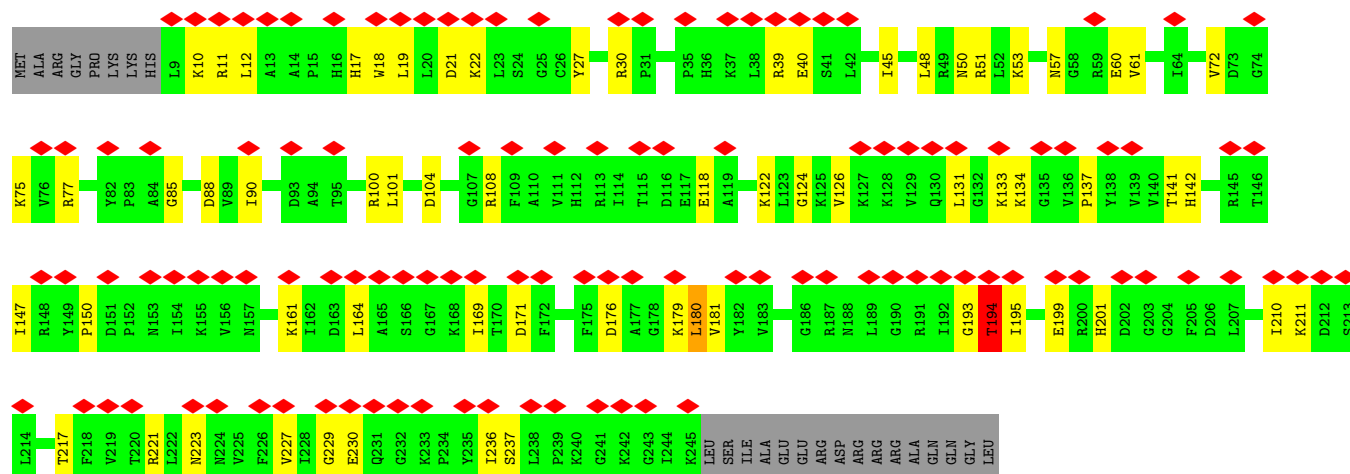


• Molecule 33: 40S ribosomal protein S1-A

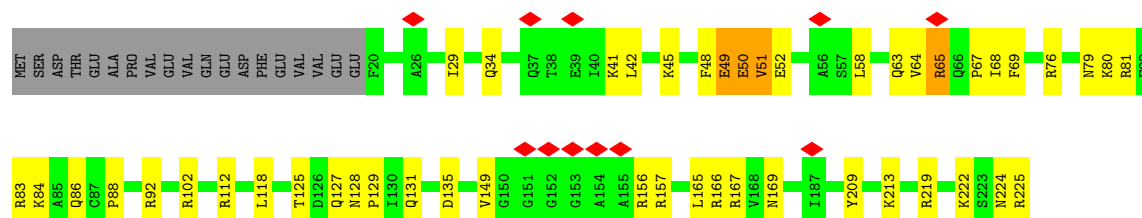




• Molecule 34: 40S ribosomal protein S4-A

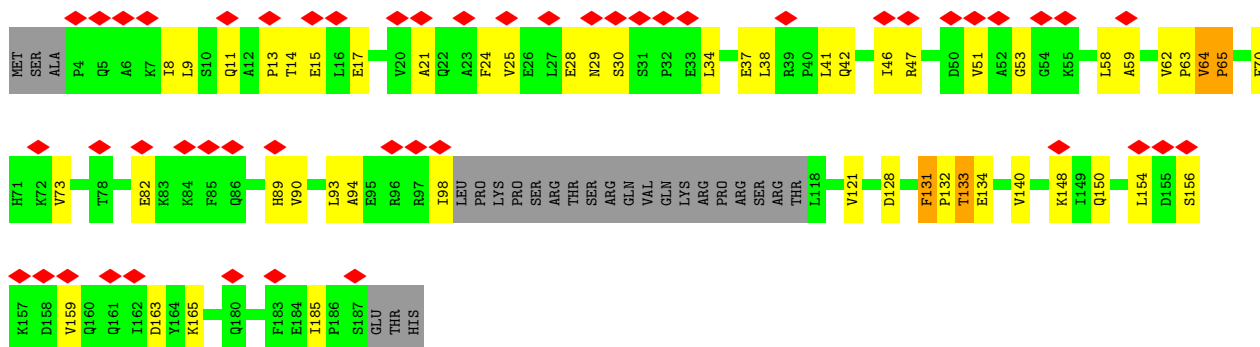


• Molecule 35: 40S ribosomal protein S5

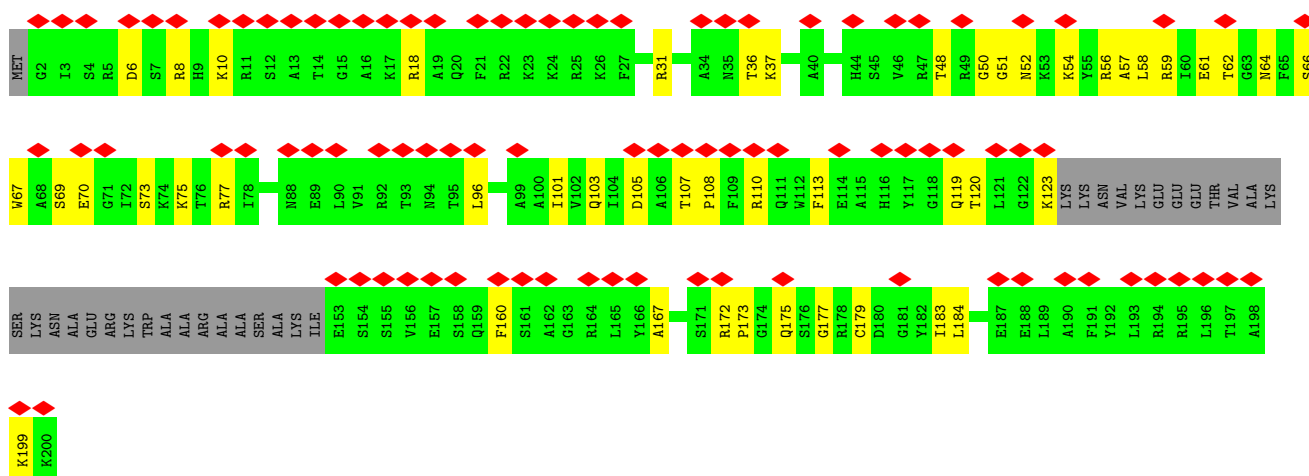


• Molecule 36: 40S ribosomal protein S7-A

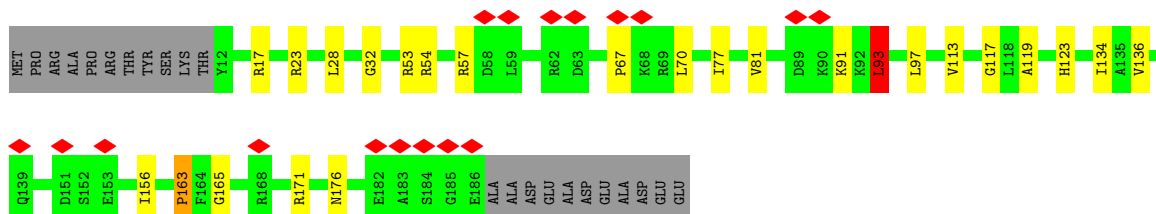
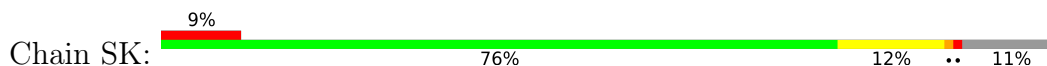




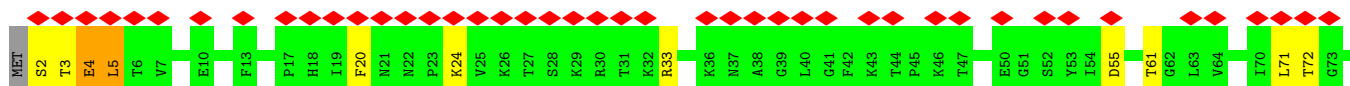
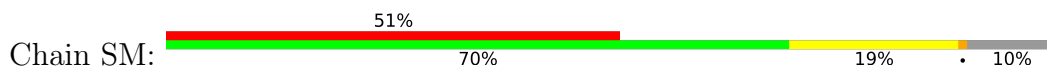
• Molecule 37: 40S ribosomal protein S8-A

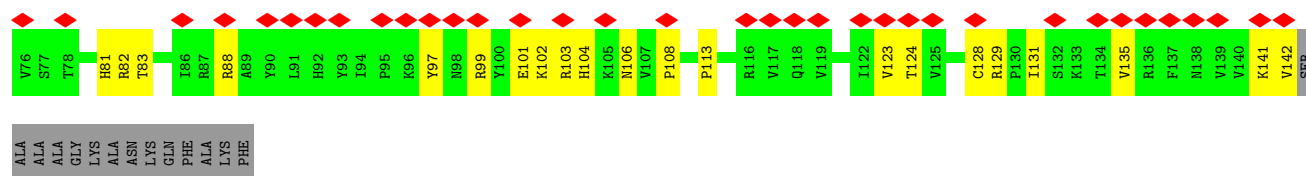


• Molecule 38: 40S ribosomal protein S9-A

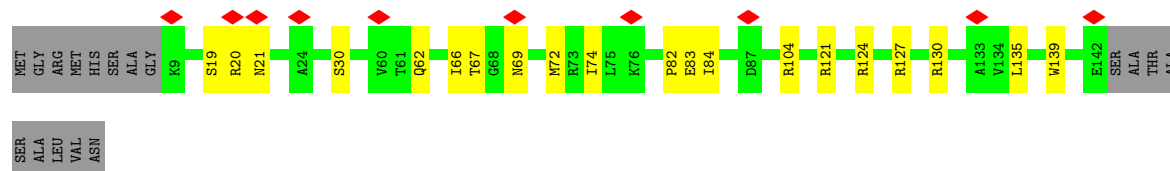
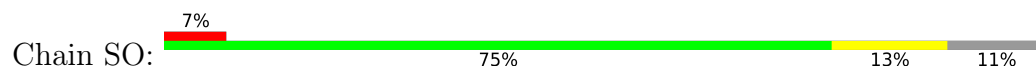


• Molecule 39: 40S ribosomal protein S11-A

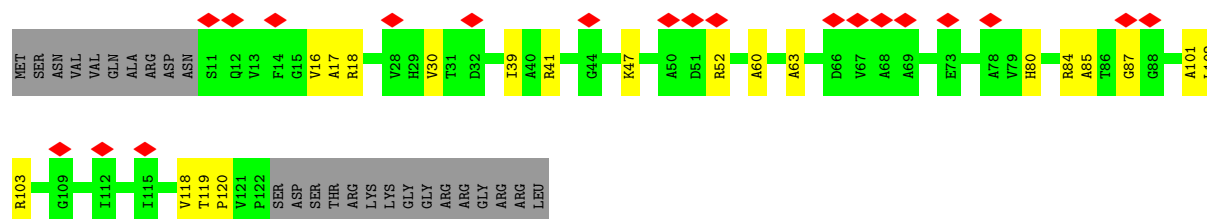




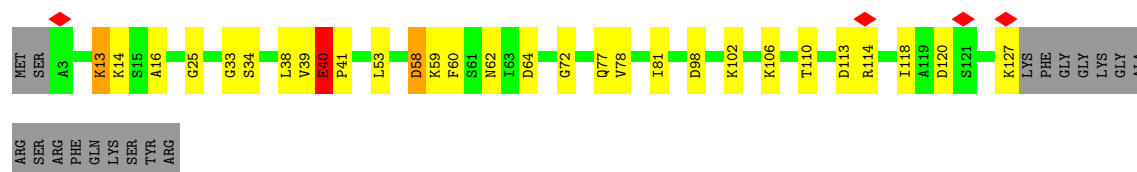
- Molecule 40: 40S ribosomal protein S13



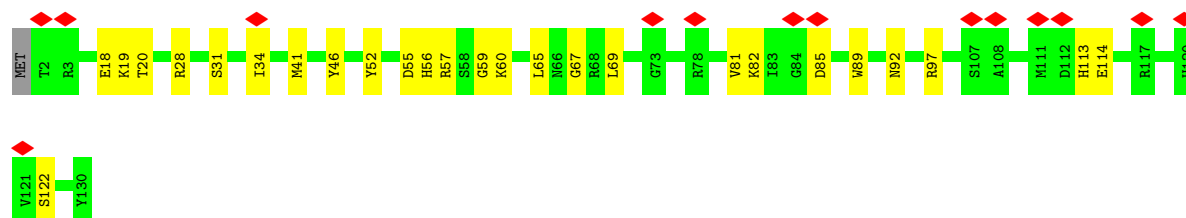
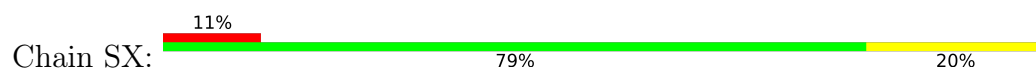
- Molecule 41: 40S ribosomal protein S14-A



- Molecule 42: 40S ribosomal protein S16-A



- Molecule 43: 40S ribosomal protein S22-A



- Molecule 44: 40S ribosomal protein S23-A

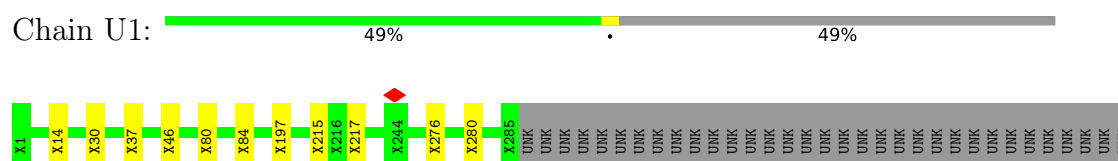
- Molecule 45: 40S ribosomal protein S24-A

- Molecule 46: 40S ribosomal protein S27-A

- Molecule 47: 40S ribosomal protein S28-A

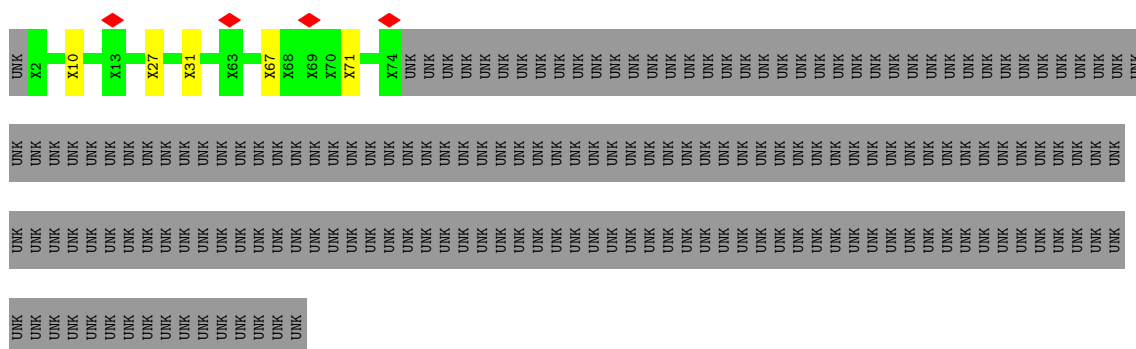
- Molecule 48: 40S ribosomal protein S30-A

- Molecule 49: Utp7

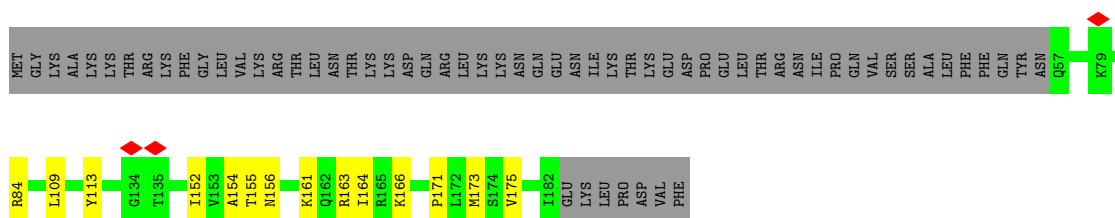




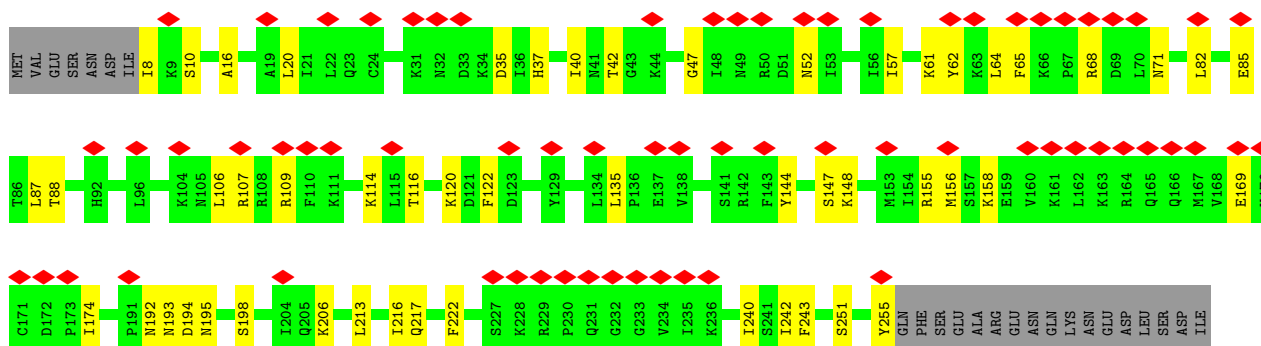
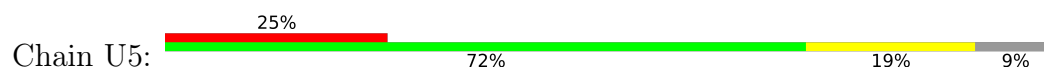
• Molecule 50: Utp11



• Molecule 51: rRNA-processing protein FCF1

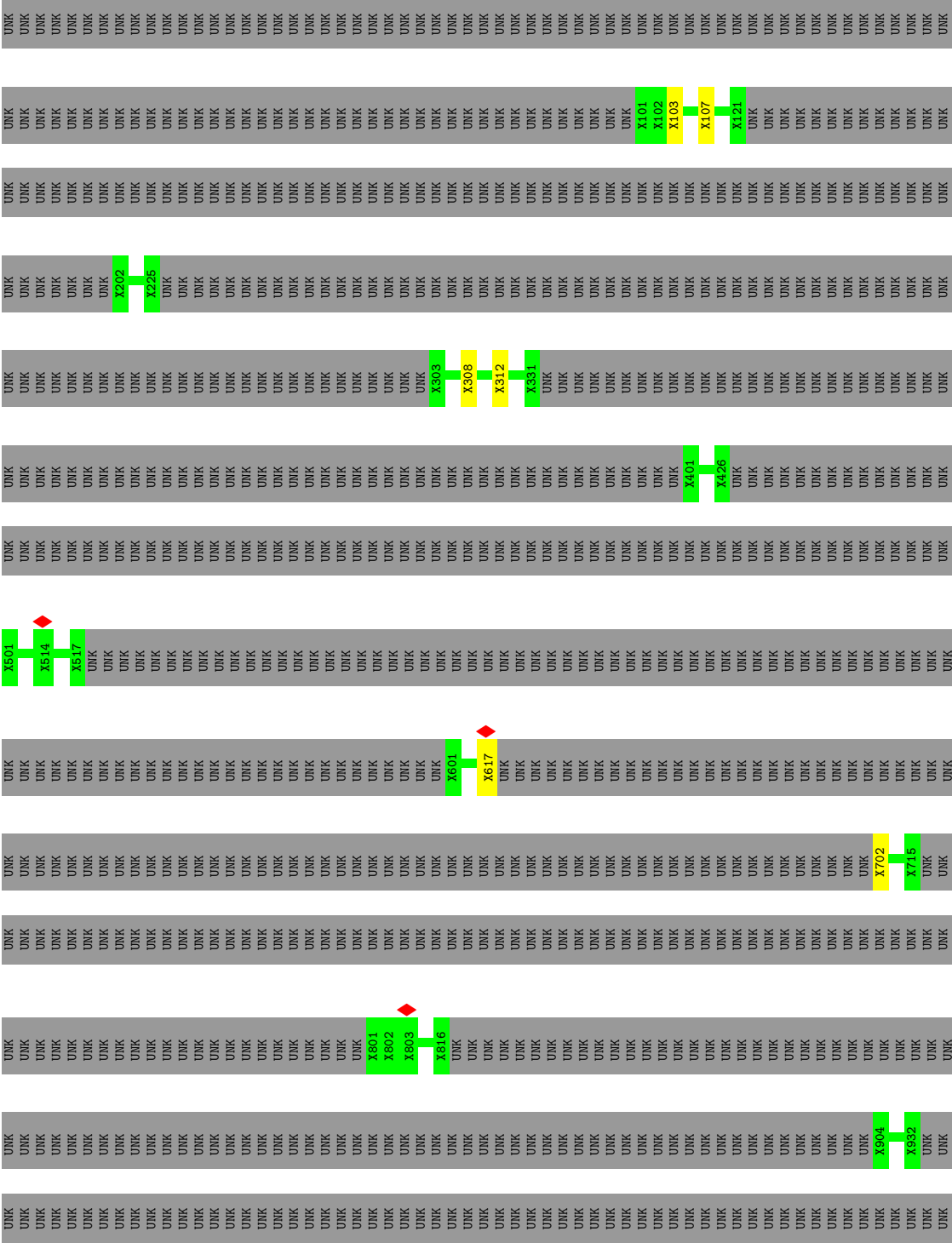


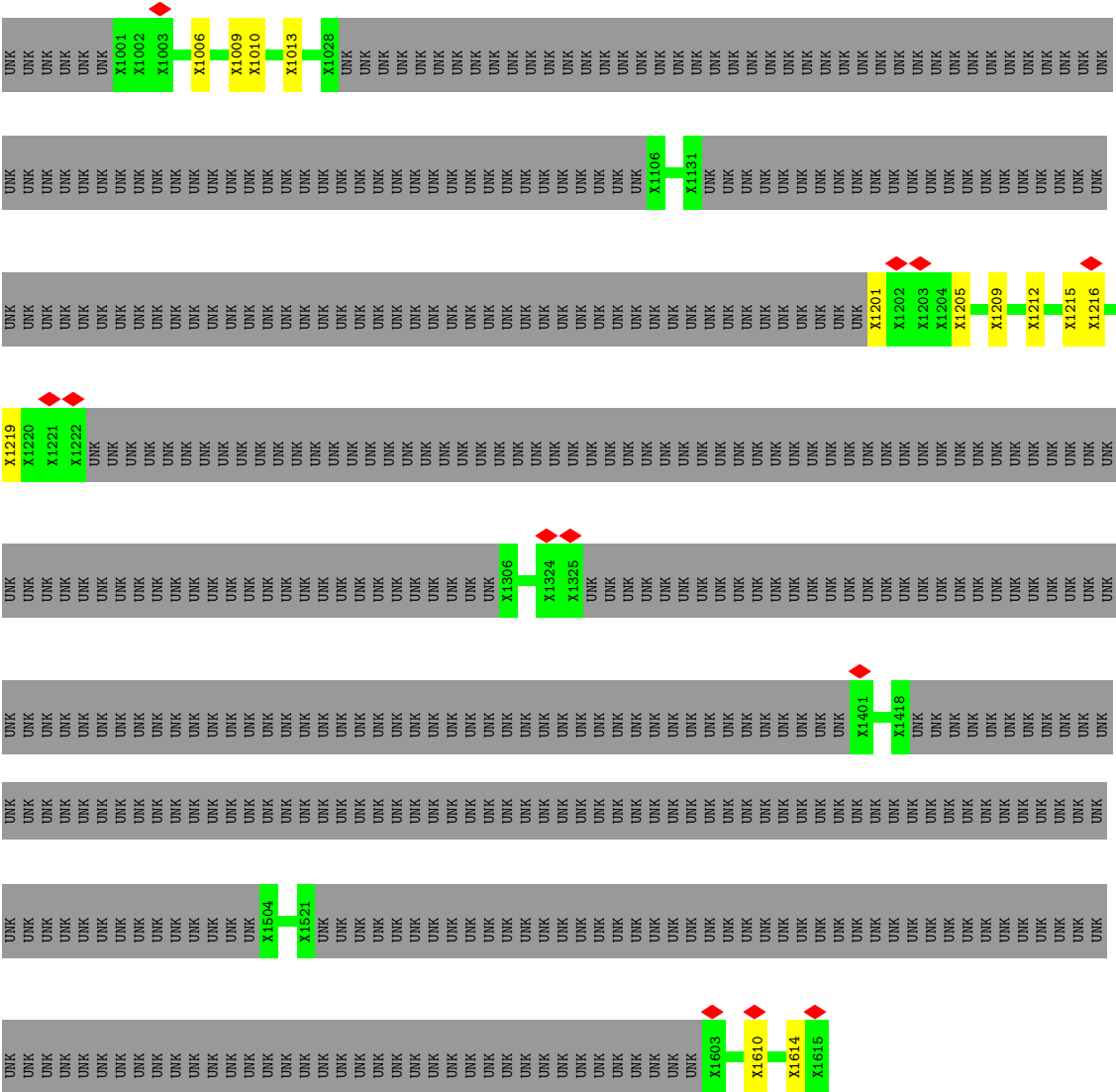
• Molecule 52: Ribosome biogenesis protein UTP30



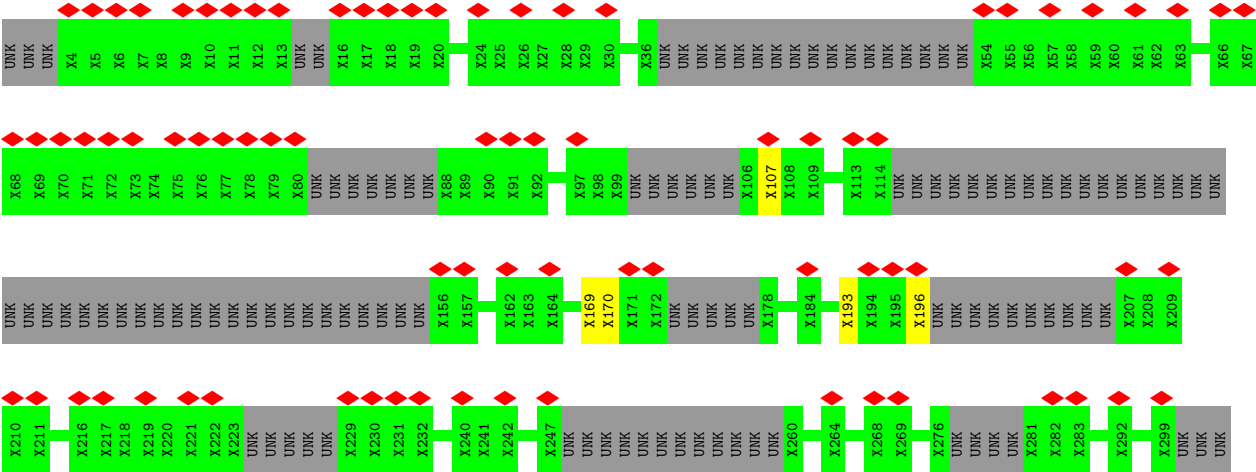
LYS
LED

● Molecule 53: Helical domain protein

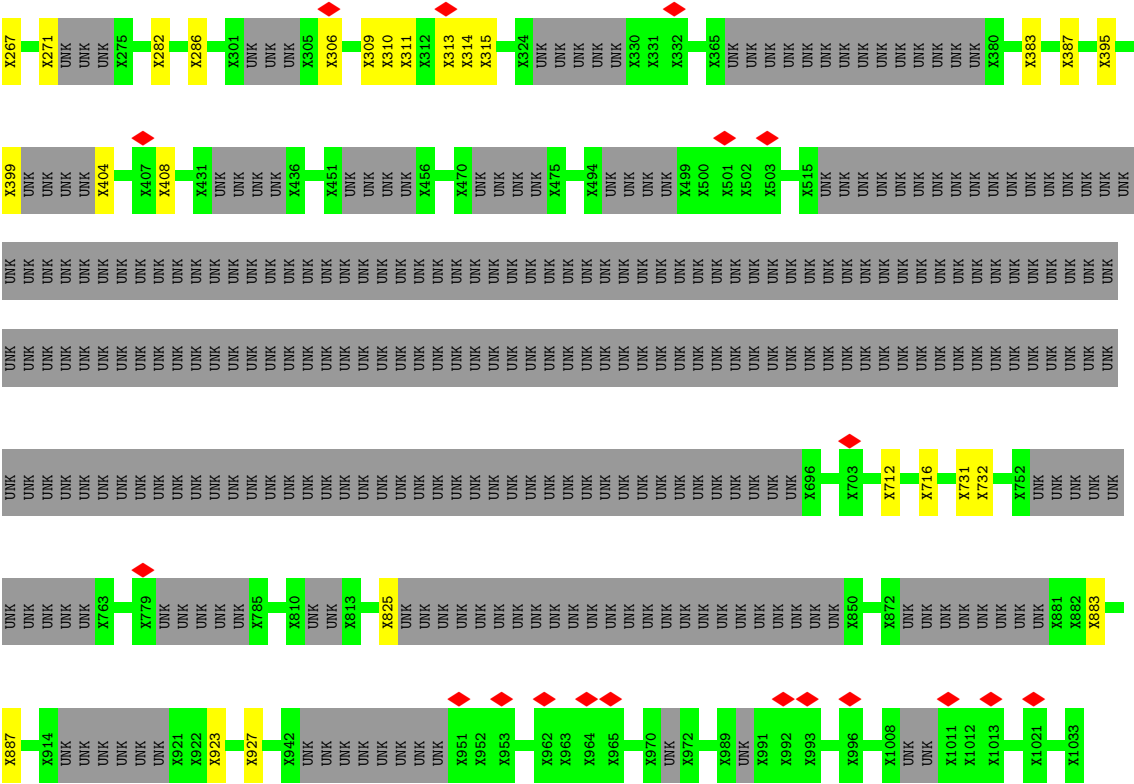




● Molecule 54: Helical domain protein







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	73543	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	79545	Depositor
Image detector	OTHER	Depositor
Maximum map value	0.552	Depositor
Minimum map value	-0.267	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.020	Depositor
Recommended contour level	0.09	Depositor
Map size ($\text{\AA}$)	704.0, 704.0, 704.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.76, 1.76, 1.76	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	3A	0.26	0/3710	0.45	0/5763
2	3B	0.34	0/1903	0.72	2/2572 (0.1%)
2	3C	0.25	0/1903	0.64	2/2572 (0.1%)
3	3D	0.31	0/2960	0.75	6/3987 (0.2%)
4	3E	0.26	0/2970	0.62	1/4004 (0.0%)
5	3F	0.26	0/2975	0.65	2/4008 (0.0%)
6	3G	0.28	0/936	0.61	0/1273
6	3H	0.30	0/936	0.61	0/1273
7	5A	0.25	0/11029	0.44	0/17170
12	AE	0.30	1/3386 (0.0%)	0.68	0/4577
15	B1	0.32	0/4431	0.76	8/5988 (0.1%)
16	BA	0.37	0/6164	0.80	4/8349 (0.0%)
17	BB	0.27	0/6264	0.74	12/8473 (0.1%)
18	BC	0.28	0/6226	0.75	11/8442 (0.1%)
19	BD	0.34	0/2597	0.76	2/3520 (0.1%)
20	BE	0.34	0/6056	0.70	9/8189 (0.1%)
21	CA	0.28	0/1621	0.63	1/2196 (0.0%)
22	CB	0.21	0/9081	0.52	2/12283 (0.0%)
23	E1	0.20	0/1716	0.54	0/2319
23	E2	0.23	0/1721	0.54	0/2323
25	K1	0.30	0/1432	0.68	0/1926
26	MA	0.38	0/1117	0.73	0/1509
27	MB	0.35	0/1496	0.76	5/2025 (0.2%)
28	MC	0.30	0/209	0.60	0/282
29	P1	0.27	0/1394	0.68	0/1881
30	R1	0.24	0/2793	0.54	0/3774
32	SA	0.23	0/23814	0.44	2/37055 (0.0%)
33	SC	0.34	0/1735	0.96	8/2335 (0.3%)
34	SF	0.28	0/1920	0.76	5/2589 (0.2%)
35	SG	0.42	0/1629	0.87	2/2202 (0.1%)
36	SI	0.30	0/1343	0.75	2/1808 (0.1%)
37	SJ	0.25	0/1373	0.76	1/1834 (0.1%)
38	SK	0.31	0/1434	0.80	1/1920 (0.1%)
39	SM	0.27	0/1169	0.65	0/1576

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
40	SO	0.25	0/1109	0.64	0/1495
41	SP	0.28	0/781	0.74	0/1062
42	SR	0.36	0/990	1.11	6/1335 (0.4%)
43	SX	0.29	0/1038	0.69	0/1395
44	SY	0.30	0/796	0.89	2/1062 (0.2%)
45	SZ	0.25	0/814	0.78	3/1093 (0.3%)
46	Sc	0.28	0/605	0.76	0/817
47	Sd	0.34	0/499	0.75	0/670
48	Sf	0.39	0/255	1.01	1/339 (0.3%)
51	U4	0.33	0/1007	0.69	0/1357
52	U5	0.28	0/2043	0.69	1/2747 (0.0%)
All	All	0.28	1/131380 (0.0%)	0.63	101/185369 (0.1%)

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
2	3B	0	1
3	3D	0	2
5	3F	0	1
12	AE	0	1
15	B1	0	3
16	BA	0	5
17	BB	0	7
18	BC	0	6
19	BD	0	1
20	BE	0	5
21	CA	0	1
29	P1	0	1
32	SA	0	1
33	SC	0	4
34	SF	0	1
35	SG	0	8
36	SI	0	4
37	SJ	0	1
38	SK	0	2
39	SM	0	1
42	SR	0	1
44	SY	0	2
45	SZ	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
46	Sc	0	2
52	U5	0	1
55	UC	0	2
All	All	0	65

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	AE	112	ALA	C-N	5.08	1.40	1.34

The worst 5 of 101 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	SR	40	GLU	CA-C-N	15.02	134.54	119.82
42	SR	40	GLU	C-N-CA	15.02	134.54	119.82
42	SR	41	PRO	N-CA-C	9.09	125.71	113.98
15	B1	808	PHE	CA-C-N	8.63	129.17	119.93
15	B1	808	PHE	C-N-CA	8.63	129.17	119.93

There are no chirality outliers.

5 of 65 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	3B	102	LYS	Peptide
3	3D	393	SER	Peptide
3	3D	46	LYS	Peptide
5	3F	437	ARG	Peptide
12	AE	64	PRO	Peptide

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	3A	3327	0	1687	53	0
2	3B	1866	0	1904	25	0
2	3C	1866	0	1904	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	3D	2915	0	2930	36	0
4	3E	2935	0	3033	44	0
5	3F	2916	0	2947	61	0
6	3G	924	0	975	14	0
6	3H	924	0	975	11	0
7	5A	9867	0	4954	86	0
8	AA	2845	0	688	14	0
9	AB	2015	0	470	28	0
10	AC	2360	0	542	38	0
11	AD	505	0	116	5	0
12	AE	3331	0	3466	52	0
13	AF	1880	0	442	18	0
14	AG	3060	0	735	50	0
15	B1	4325	0	4434	80	0
16	BA	6026	0	5940	118	0
17	BB	6138	0	6163	129	0
18	BC	6117	0	6141	106	0
19	BD	2539	0	2520	83	0
20	BE	5936	0	5882	121	0
21	CA	1582	0	1528	40	0
22	CB	8870	0	8975	170	0
23	E1	1689	0	1738	23	0
23	E2	1695	0	1757	38	0
24	E4	1425	0	329	8	0
25	K1	1410	0	1503	24	0
26	MA	1097	0	1130	10	0
27	MB	1465	0	1486	35	0
28	MC	307	0	231	4	0
29	P1	1368	0	1436	17	0
30	R1	2742	0	2829	62	0
31	S1	1425	0	335	7	0
32	SA	21307	0	10756	270	0
33	SC	1709	0	1784	39	0
34	SF	1881	0	1958	44	0
35	SG	1609	0	1675	44	0
36	SI	1322	0	1394	30	0
37	SJ	1350	0	1374	31	0
38	SK	1412	0	1486	26	0
39	SM	1143	0	1210	26	0
40	SO	1087	0	1152	14	0
41	SP	771	0	751	14	0
42	SR	973	0	1029	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	SX	1021	0	1060	17	0
44	SY	785	0	840	24	0
45	SZ	801	0	828	17	0
46	Sc	595	0	613	6	0
47	Sd	497	0	535	12	0
48	Sf	251	0	277	34	0
49	U1	1425	0	351	6	0
50	U2	365	0	75	3	0
51	U4	990	0	1054	8	0
52	U5	2009	0	2130	32	0
53	UA	1690	0	373	10	0
54	UB	2775	0	625	6	0
55	UC	3300	0	731	21	0
All	All	150760	0	116186	2165	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 2165 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)
38:SK:32:GLY:HA3	48:Sf:40:TYR:CD2	1.51	1.42
38:SK:28:LEU:CD1	48:Sf:43:ARG:HD3	1.44	1.38
38:SK:28:LEU:HD13	48:Sf:43:ARG:CD	1.22	1.37
38:SK:32:GLY:CA	48:Sf:40:TYR:CD2	2.35	1.09
38:SK:123:HIS:ND1	48:Sf:37:ARG:HD2	1.69	1.07

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	3B	237/327 (72%)	222 (94%)	15 (6%)	0	100	100
2	3C	237/327 (72%)	218 (92%)	19 (8%)	0	100	100
3	3D	366/504 (73%)	339 (93%)	27 (7%)	0	100	100
4	3E	378/511 (74%)	352 (93%)	26 (7%)	0	100	100
5	3F	353/573 (62%)	332 (94%)	21 (6%)	0	100	100
6	3G	120/126 (95%)	114 (95%)	6 (5%)	0	100	100
6	3H	120/126 (95%)	115 (96%)	5 (4%)	0	100	100
12	AE	407/1769 (23%)	380 (93%)	27 (7%)	0	100	100
15	B1	528/1183 (45%)	477 (90%)	50 (10%)	1 (0%)	43	77
16	BA	747/923 (81%)	657 (88%)	89 (12%)	1 (0%)	48	83
17	BB	770/943 (82%)	681 (88%)	86 (11%)	3 (0%)	30	67
18	BC	779/817 (95%)	682 (88%)	93 (12%)	4 (0%)	24	63
19	BD	317/594 (53%)	265 (84%)	52 (16%)	0	100	100
20	BE	741/939 (79%)	683 (92%)	57 (8%)	1 (0%)	48	83
21	CA	190/297 (64%)	182 (96%)	8 (4%)	0	100	100
22	CB	1086/1237 (88%)	1050 (97%)	36 (3%)	0	100	100
23	E1	213/252 (84%)	209 (98%)	4 (2%)	0	100	100
23	E2	210/252 (83%)	200 (95%)	10 (5%)	0	100	100
25	K1	173/316 (55%)	163 (94%)	10 (6%)	0	100	100
26	MA	131/183 (72%)	126 (96%)	5 (4%)	0	100	100
27	MB	182/290 (63%)	164 (90%)	18 (10%)	0	100	100
28	MC	24/593 (4%)	24 (100%)	0	0	100	100
29	P1	171/274 (62%)	163 (95%)	8 (5%)	0	100	100
30	R1	353/367 (96%)	339 (96%)	14 (4%)	0	100	100
33	SC	212/255 (83%)	169 (80%)	37 (18%)	6 (3%)	4	24
34	SF	235/261 (90%)	212 (90%)	22 (9%)	1 (0%)	30	67
35	SG	204/225 (91%)	178 (87%)	24 (12%)	2 (1%)	12	47
36	SI	161/190 (85%)	141 (88%)	19 (12%)	1 (1%)	21	58
37	SJ	166/200 (83%)	144 (87%)	22 (13%)	0	100	100
38	SK	173/197 (88%)	150 (87%)	22 (13%)	1 (1%)	21	58
39	SM	139/156 (89%)	129 (93%)	8 (6%)	2 (1%)	9	39
40	SO	132/151 (87%)	128 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	SP	110/137 (80%)	97 (88%)	13 (12%)	0	100	100
42	SR	123/143 (86%)	107 (87%)	12 (10%)	4 (3%)	3	21
43	SX	127/130 (98%)	112 (88%)	14 (11%)	1 (1%)	16	53
44	SY	101/145 (70%)	78 (77%)	21 (21%)	2 (2%)	6	31
45	SZ	99/135 (73%)	91 (92%)	8 (8%)	0	100	100
46	Sc	77/82 (94%)	70 (91%)	7 (9%)	0	100	100
47	Sd	61/67 (91%)	51 (84%)	10 (16%)	0	100	100
48	Sf	28/63 (44%)	27 (96%)	1 (4%)	0	100	100
51	U4	124/189 (66%)	111 (90%)	12 (10%)	1 (1%)	16	53
52	U5	246/274 (90%)	222 (90%)	24 (10%)	0	100	100
All	All	11351/16723 (68%)	10354 (91%)	966 (8%)	31 (0%)	37	71

5 of 31 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
20	BE	901	LYS
33	SC	206	PRO
33	SC	207	LEU
33	SC	209	ASN
34	SF	195	ILE

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	
2	3B	202/240 (84%)	201 (100%)	1 (0%)	81	81
2	3C	202/240 (84%)	202 (100%)	0	100	100
3	3D	317/435 (73%)	317 (100%)	0	100	100
4	3E	314/433 (72%)	313 (100%)	1 (0%)	86	84
5	3F	317/503 (63%)	317 (100%)	0	100	100
6	3G	101/104 (97%)	100 (99%)	1 (1%)	68	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	3H	101/104 (97%)	101 (100%)	0	100	100
12	AE	381/1633 (23%)	380 (100%)	1 (0%)	86	84
15	B1	471/1039 (45%)	471 (100%)	0	100	100
16	BA	663/812 (82%)	659 (99%)	4 (1%)	78	80
17	BB	687/832 (83%)	683 (99%)	4 (1%)	78	80
18	BC	687/719 (96%)	684 (100%)	3 (0%)	84	82
19	BD	281/529 (53%)	278 (99%)	3 (1%)	65	74
20	BE	657/819 (80%)	656 (100%)	1 (0%)	87	85
21	CA	178/274 (65%)	176 (99%)	2 (1%)	65	74
22	CB	1000/1125 (89%)	1000 (100%)	0	100	100
23	E1	191/222 (86%)	191 (100%)	0	100	100
23	E2	193/222 (87%)	193 (100%)	0	100	100
25	K1	158/289 (55%)	158 (100%)	0	100	100
26	MA	123/172 (72%)	122 (99%)	1 (1%)	73	77
27	MB	164/258 (64%)	164 (100%)	0	100	100
28	MC	24/148 (16%)	24 (100%)	0	100	100
29	P1	151/238 (63%)	151 (100%)	0	100	100
30	R1	302/312 (97%)	302 (100%)	0	100	100
33	SC	191/224 (85%)	189 (99%)	2 (1%)	68	76
34	SF	203/222 (91%)	202 (100%)	1 (0%)	81	81
35	SG	173/191 (91%)	173 (100%)	0	100	100
36	SI	146/170 (86%)	146 (100%)	0	100	100
37	SJ	138/161 (86%)	138 (100%)	0	100	100
38	SK	149/166 (90%)	148 (99%)	1 (1%)	76	79
39	SM	128/137 (93%)	128 (100%)	0	100	100
40	SO	117/128 (91%)	117 (100%)	0	100	100
41	SP	69/105 (66%)	69 (100%)	0	100	100
42	SR	105/119 (88%)	105 (100%)	0	100	100
43	SX	110/111 (99%)	110 (100%)	0	100	100
44	SY	85/120 (71%)	85 (100%)	0	100	100
45	SZ	85/113 (75%)	84 (99%)	1 (1%)	63	73

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	Sc	68/71 (96%)	68 (100%)	0	100	100
47	Sd	56/60 (93%)	56 (100%)	0	100	100
48	Sf	27/54 (50%)	26 (96%)	1 (4%)	30	51
51	U4	110/169 (65%)	110 (100%)	0	100	100
52	U5	231/256 (90%)	231 (100%)	0	100	100
All	All	10056/14279 (70%)	10028 (100%)	28 (0%)	84	84

5 of 28 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
18	BC	764	LEU
48	Sf	39	LEU
19	BD	543	LEU
34	SF	180	LEU
19	BD	491	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 201 such sidechains are listed below:

Mol	Chain	Res	Type
21	CA	151	HIS
23	E1	111	GLN
52	U5	215	ASN
22	CB	197	GLN
22	CB	665	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3A	151/333 (45%)	40 (26%)	1 (0%)
32	SA	978/1812 (53%)	257 (26%)	18 (1%)
7	5A	452/700 (64%)	114 (25%)	5 (1%)
All	All	1581/2845 (55%)	411 (25%)	24 (1%)

5 of 411 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	3A	14	A
1	3A	15	U

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Mol	Chain	Res	Type
1	3A	19	A
1	3A	22	A
1	3A	24	U

5 of 24 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
32	SA	467	G
32	SA	591	A
32	SA	503	G
32	SA	913	G
32	SA	25	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

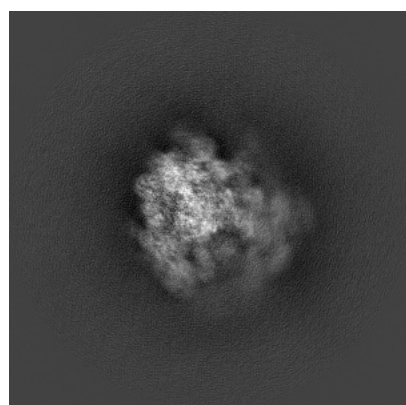
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6696. These allow visual inspection of the internal detail of the map and identification of artifacts.

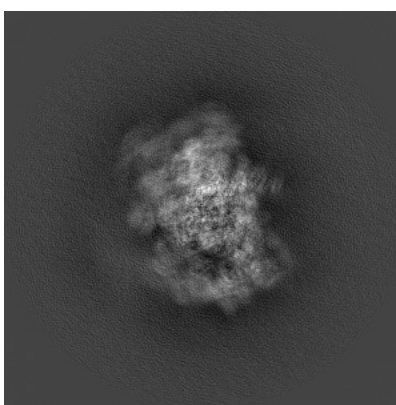
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

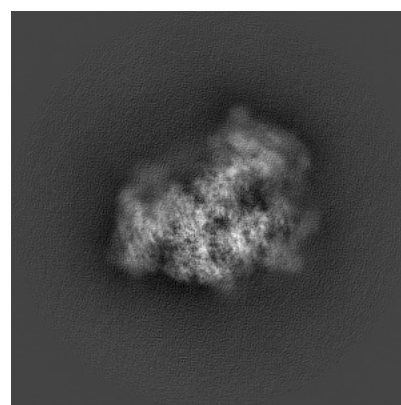
6.1.1 Primary map



X



Y

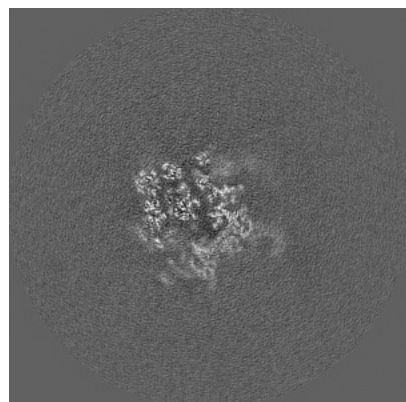


Z

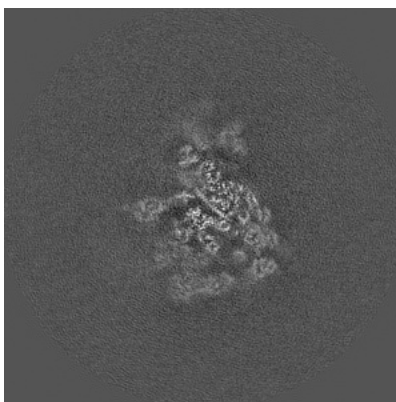
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

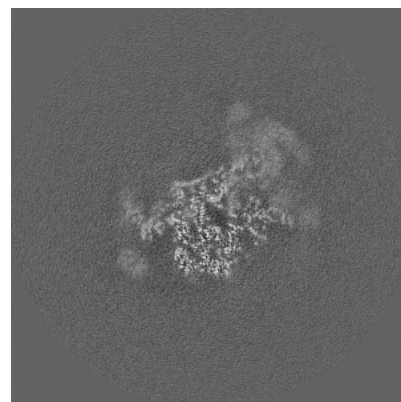
6.2.1 Primary map



X Index: 200



Y Index: 200

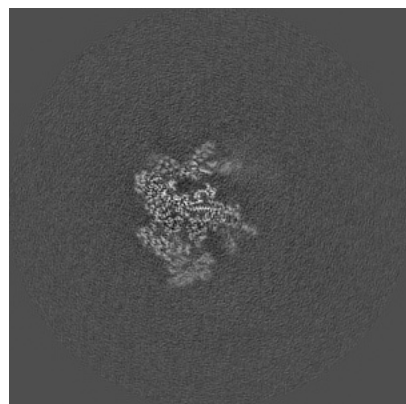


Z Index: 200

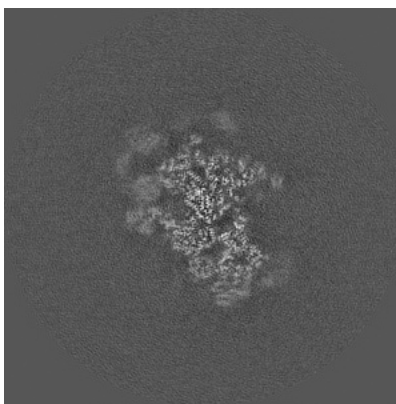
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

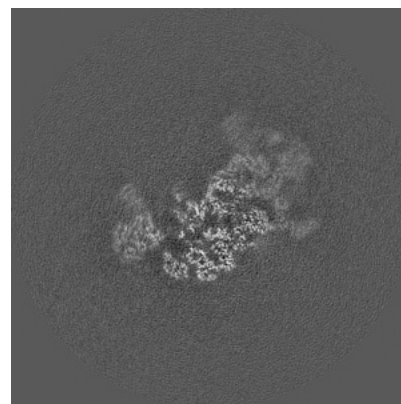
6.3.1 Primary map



X Index: 190



Y Index: 173

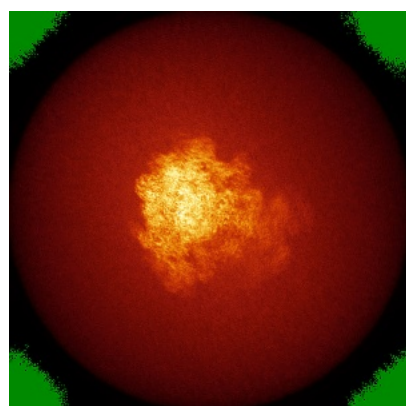


Z Index: 217

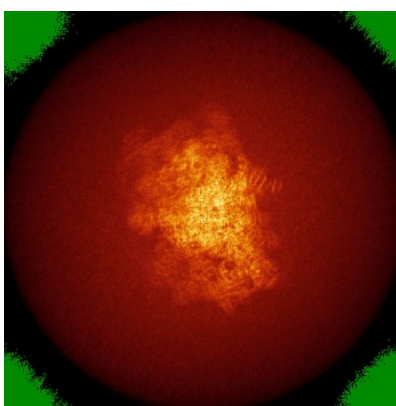
The images above show the largest variance slices of the map in three orthogonal directions.

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

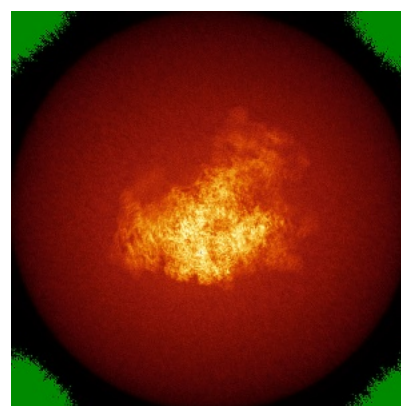
6.4.1 Primary map



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

This section was not generated.

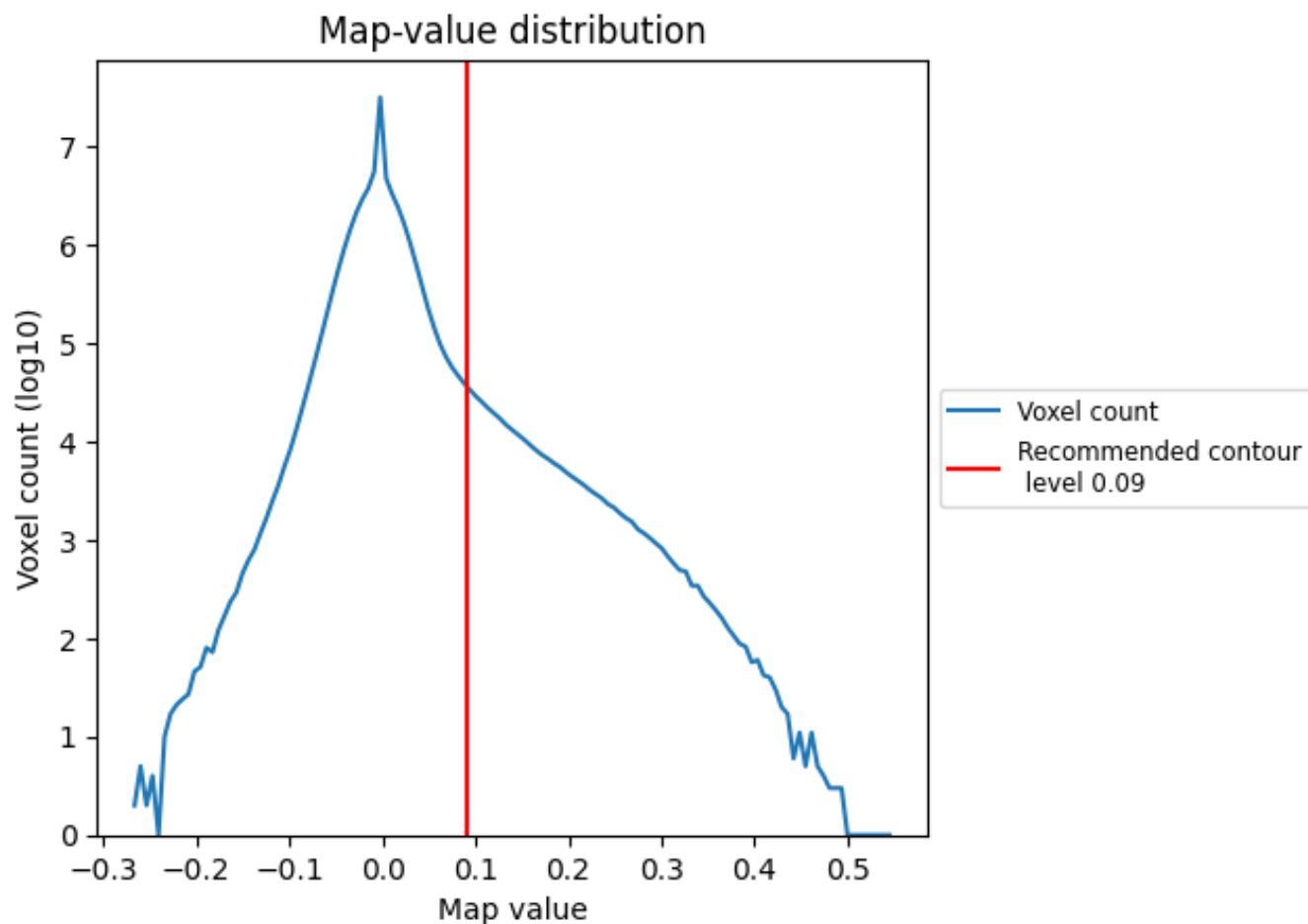
6.6 Mask visualisation

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

7 Map analysis [i](#)

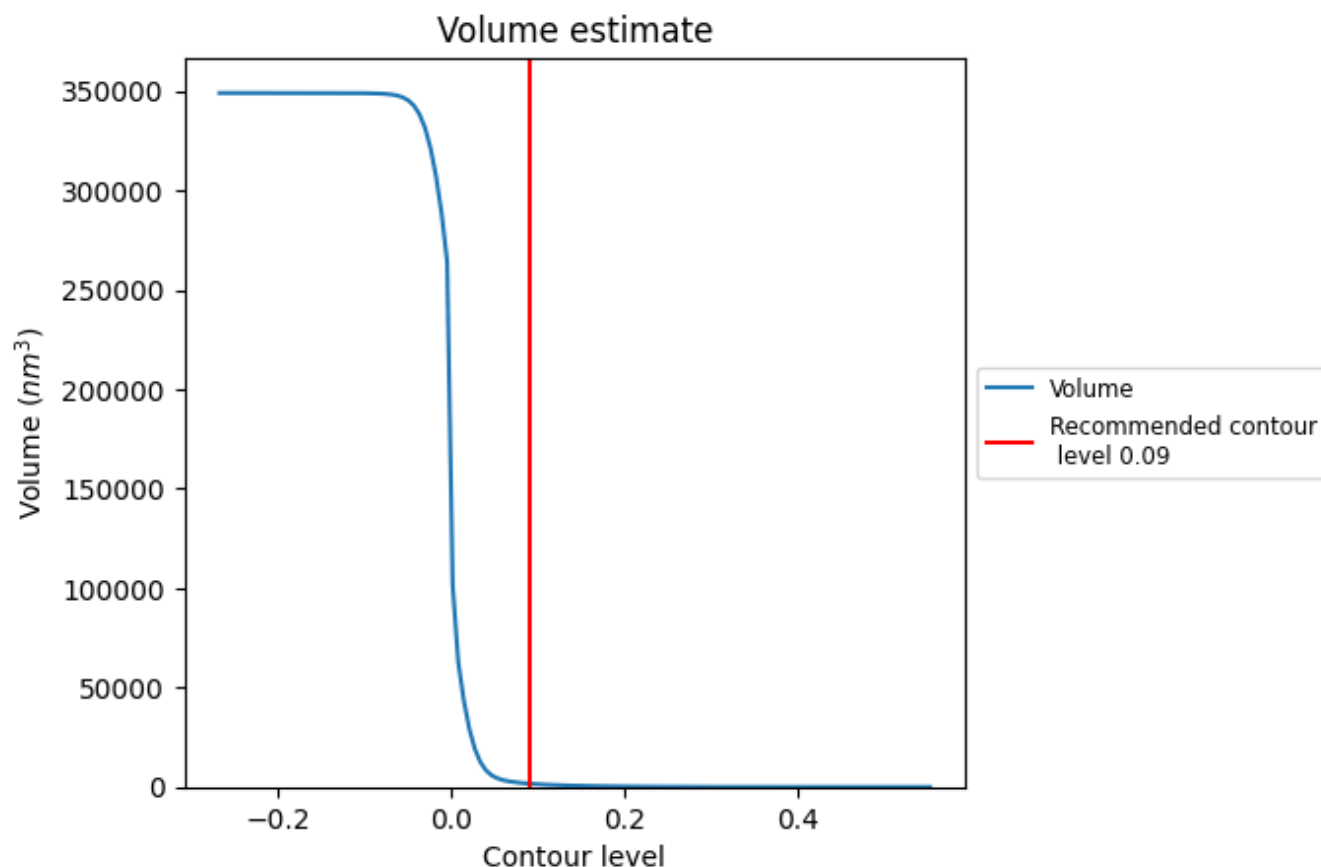
This section contains the results of statistical analysis of the map.

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.

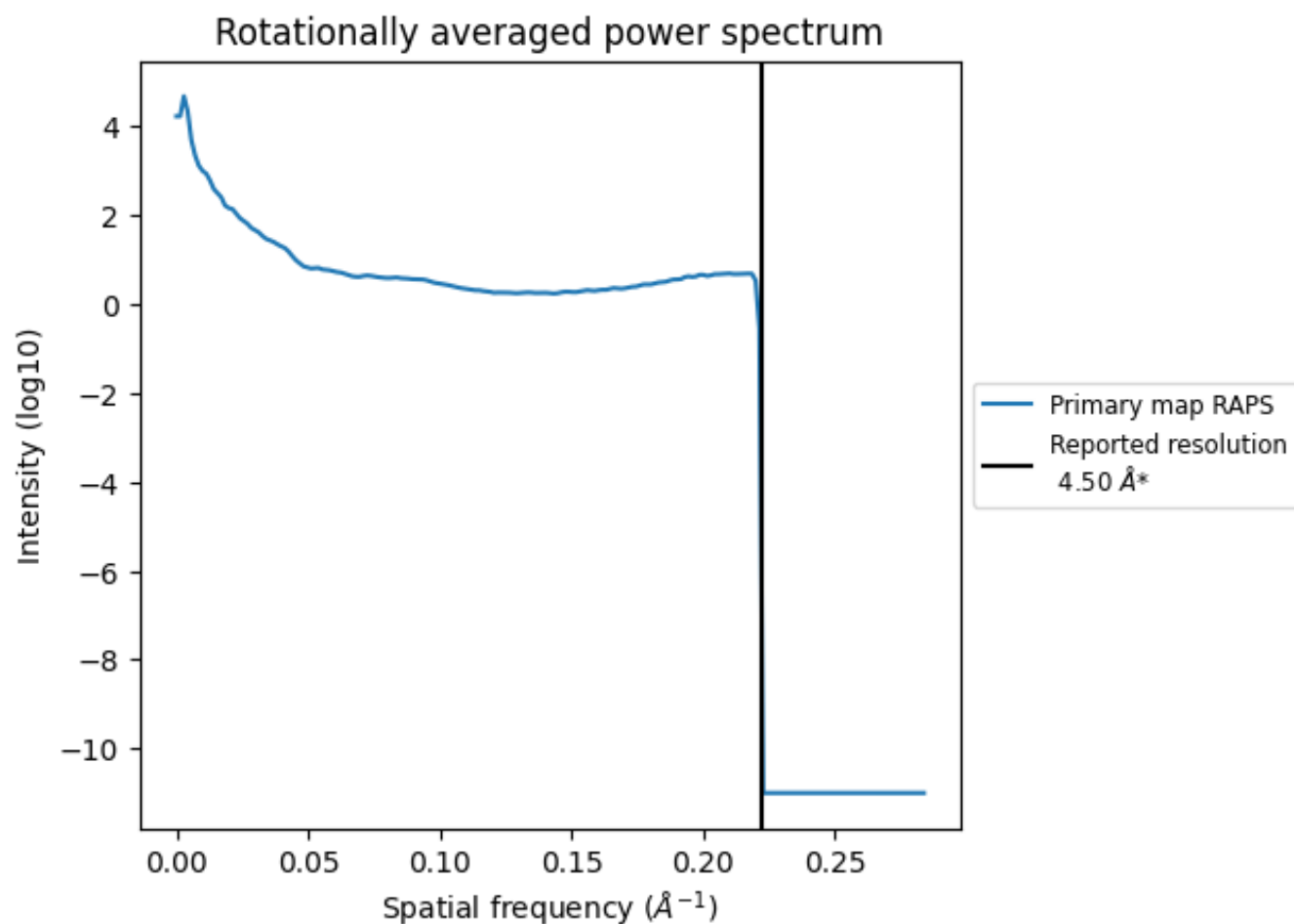
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1678 nm^3 ; this corresponds to an approximate mass of 1516 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 ⓘ

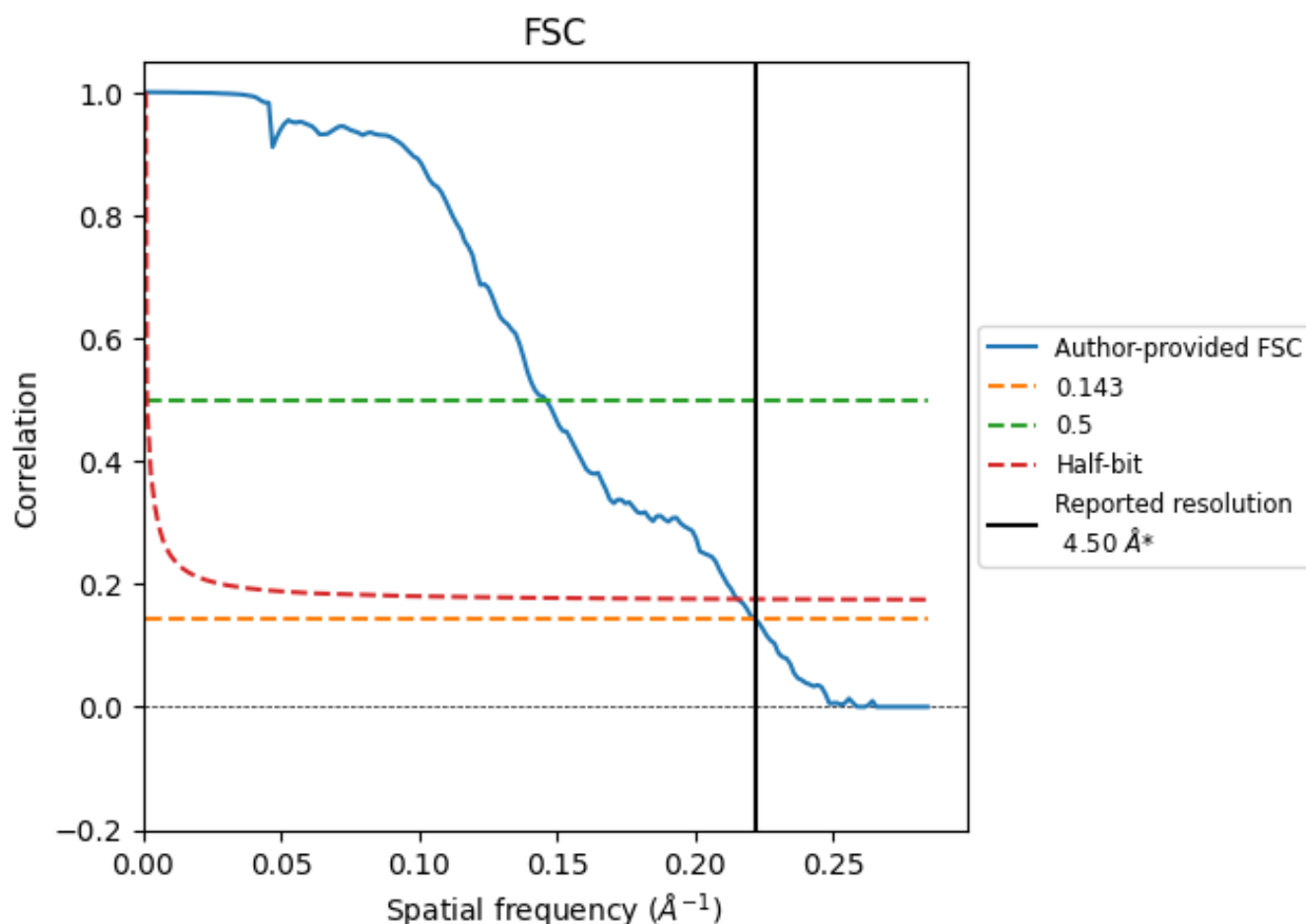


*Reported resolution corresponds to spatial frequency of 0.222 Å⁻¹

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 0.222 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.50	-	-
Author-provided FSC curve	4.52	6.86	4.64
Unmasked-calculated*	-	-	-

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

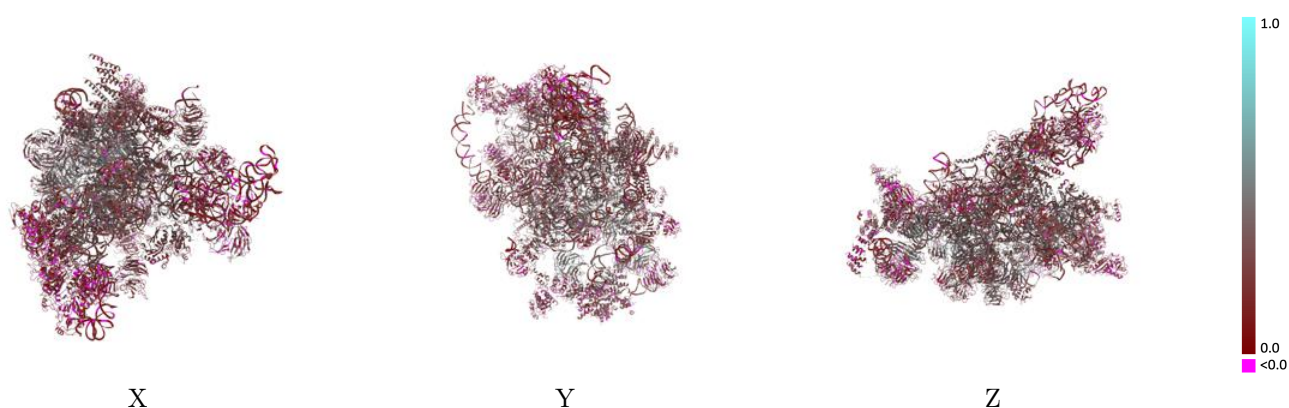
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-6696 and PDB model 5WYK. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)

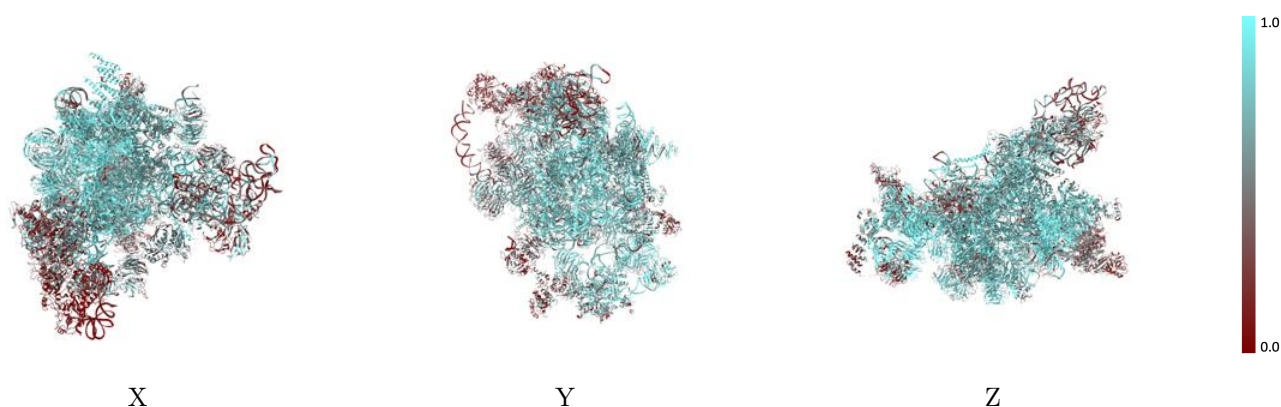
This section was not generated.

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



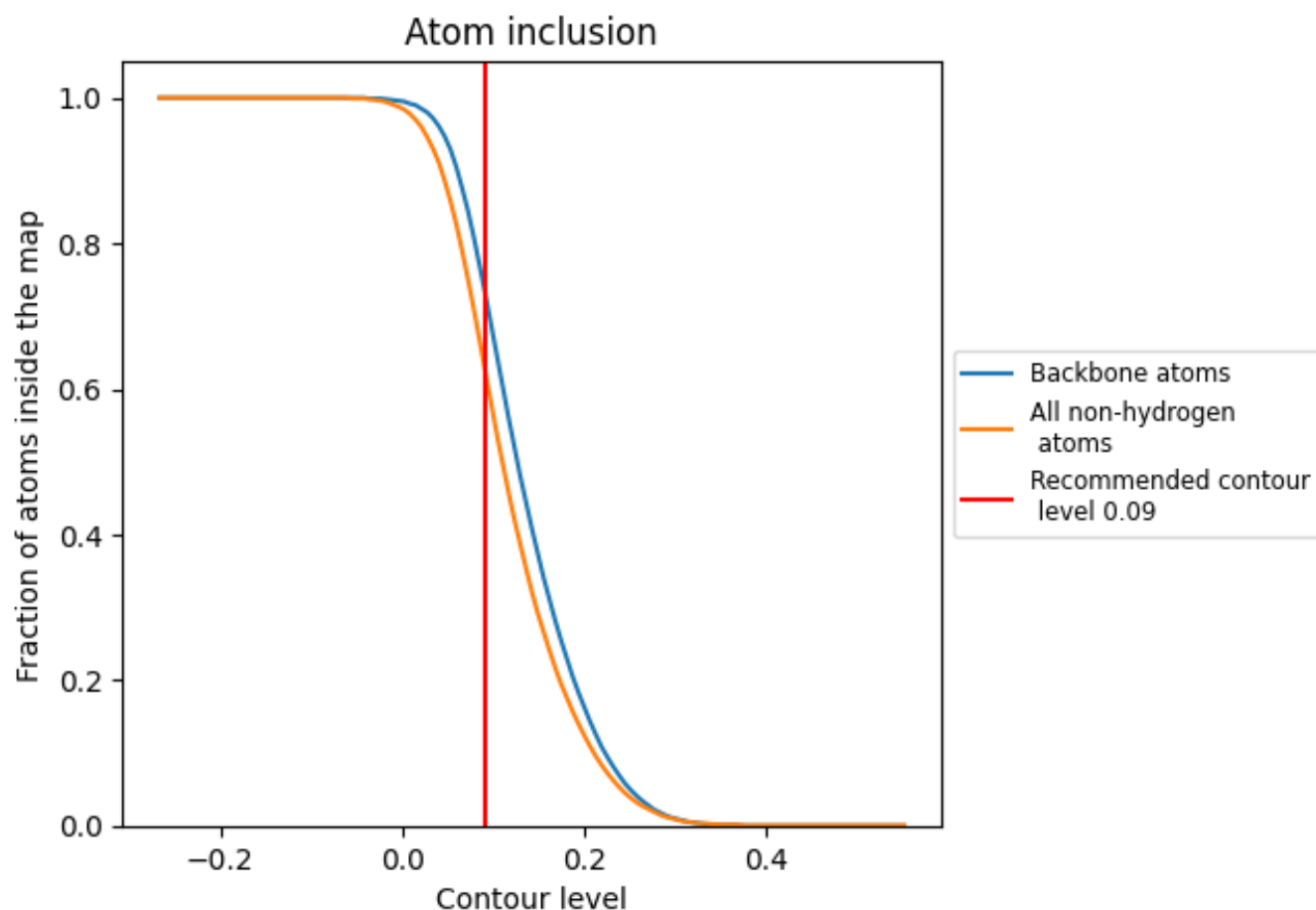
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.09).

9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 63% 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 (0.09) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6320	 0.2670
3A	 0.8460	 0.2930
3B	 0.7530	 0.3650
3C	 0.5200	 0.2540
3D	 0.6770	 0.2700
3E	 0.5950	 0.2560
3F	 0.6560	 0.2770
3G	 0.6530	 0.2980
3H	 0.7600	 0.3610
5A	 0.8020	 0.2670
AA	 0.8980	 0.4020
AB	 0.7560	 0.2470
AC	 0.3220	 0.1820
AD	 0.6510	 0.2490
AE	 0.6370	 0.2990
AF	 0.8850	 0.3770
AG	 0.7770	 0.2860
B1	 0.6530	 0.2440
BA	 0.7520	 0.3380
BB	 0.5360	 0.2020
BC	 0.4180	 0.1770
BD	 0.6560	 0.2250
BE	 0.7950	 0.3440
CA	 0.2110	 0.1470
CB	 0.2360	 0.1710
E1	 0.3190	 0.1730
E2	 0.3860	 0.2460
E4	 0.3240	 0.2260
K1	 0.6680	 0.2960
MA	 0.7890	 0.3800
MB	 0.6160	 0.2880
MC	 0.8260	 0.3300
P1	 0.5380	 0.2240
R1	 0.5550	 0.2640
S1	 0.9380	 0.4440



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Chain	Atom inclusion	Q-score
SA	 0.6690	 0.2470
SC	 0.5390	 0.3150
SF	 0.4070	 0.1890
SG	 0.7440	 0.3370
SI	 0.5370	 0.2280
SJ	 0.3980	 0.1410
SK	 0.6720	 0.3060
SM	 0.3330	 0.1450
SO	 0.6800	 0.2970
SP	 0.6460	 0.3170
SR	 0.7670	 0.3800
SX	 0.6790	 0.3310
SY	 0.6210	 0.2950
SZ	 0.5610	 0.2310
Sc	 0.6350	 0.3410
Sd	 0.6580	 0.3410
Sf	 0.7220	 0.3220
U1	 0.9680	 0.4960
U2	 0.8520	 0.3830
U4	 0.7540	 0.3660
U5	 0.5610	 0.1850
UA	 0.8950	 0.3170
UB	 0.4490	 0.2530
UC	 0.9030	 0.3760