



## wwPDB EM Validation Summary Report ⓘ

Nov 7, 2022 – 02:59 PM JST

PDB ID : 5WYJ  
EMDB ID : EMD-6695  
Title : Cryo-EM structure of the 90S small subunit pre-ribosome (Dhr1-depleted, Enp1-TAP, state 1)  
Authors : Ye, K.; Zhu, X.; Sun, Q.  
Deposited on : 2017-01-13  
Resolution : 8.70 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:

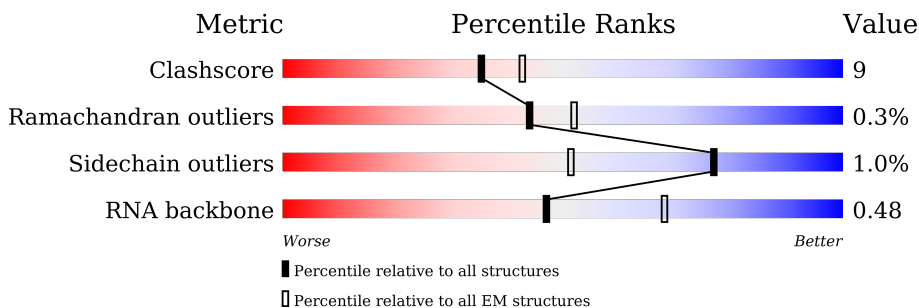
EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.2

# 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 8.70 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
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	3A	333	
2	3B	327	
2	3C	327	
3	3D	504	
4	3E	511	
5	3F	573	
6	3G	126	

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Mol	Chain	Length	Quality of chain
6	3H	126	18% 79% 17%
7	5A	700	26% 37% 25% 34%
8	AA	776	16% 62% 11% 27%
9	AB	643	17% 57% 5% 37%
10	AC	713	31% 62% 34%
11	AD	575	17% 82%
12	AE	1769	51% 75% 12% 13%
13	AF	513	10% 65% 8% 27%
14	AG	896	19% 60% 8% 32%
15	B1	1183	12% 35% 10% 55%
16	BA	923	20% 59% 22% 18%
17	BB	943	20% 61% 21% 17%
18	BC	817	40% 75% 20%
19	BD	594	20% 36% 18% 45%
20	BE	939	19% 57% 23% 20%
21	CA	297	32% 50% 15% 34%
22	CB	1237	41% 70% 19% 11%
23	E1	252	33% 65% 21% 14%
23	E2	252	31% 64% 21% 14%
24	E3	483	23% 42% 11% 46%
25	E4	707	13% 36% 5% 60%
26	K1	316	20% 44% 11% 45%
27	MA	183	13% 64% 8% 27%
28	MB	290	17% 49% 15% 37%
29	MC	593	7% 92%

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Mol	Chain	Length	Quality of chain
30	P1	274	15% 57% 6% 37%
31	R1	367	23% 80% 17%
32	R2	1729	15% 14% 84%
33	S1	489	10% 47% 11% 42%
34	SA	1812	9% 31% 23% 7% 38%
35	SC	255	29% 56% 26% 16%
36	SF	261	33% 64% 25% 9%
37	SG	225	18% 69% 21% 8%
38	SH	236	40% 57% 16% 26%
39	SI	190	34% 63% 23% 13%
40	SJ	200	34% 57% 27% 15%
41	SK	197	25% 70% 18% 11%
42	SM	156	44% 65% 23% 10%
43	SN	143	80% 69% 15% 13%
44	SO	151	28% 72% 17% 11%
45	SP	137	32% 69% 10% 20%
46	SR	143	20% 57% 28% 13%
47	SX	130	29% 73% 26%
48	SY	145	25% 51% 18% 29%
49	SZ	135	24% 59% 15% 25%
50	Sc	82	44% 96%
51	Sd	67	30% 90% 6%
52	Sf	63	48% 52%
53	Sg	152	34% 32% 66%
54	U1	554	6% 43% 8% 49%

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Mol	Chain	Length	Quality of chain
55	U2	250	
56	U3	2493	
57	U4	189	
58	U5	274	
59	UA	1615	
60	UB	987	
61	UC	1033	

## 2 Entry composition [i](#)

There are 61 unique types of molecules in this entry. The entry contains 173863 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
			Total	C	N	O	P		
1	3A	157	3327	1488	575	1107	157	0	0

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

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

- Molecule 3 is a protein called Nucleolar protein 56.

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

- Molecule 4 is a protein called Nucleolar protein 58.

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

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

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

- 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,Utp10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AE	1536	Total	C	N	O	S	0	0
			9970	6261	1772	1918	19		

- Molecule 13 is a protein called Utp15.

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

- Molecule 14 is a protein called Utp17.

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

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

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

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

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

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

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

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

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

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

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

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



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

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

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

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

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

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

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

- Molecule 24 is a protein called Essential nuclear protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	E3	260	2114	1378	359	374	3	0	0

- Molecule 25 is a protein called Enp2.

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

- Molecule 26 is a protein called KRR1 small subunit processome component.

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

- Molecule 27 is a protein called U3 small nucleolar ribonucleoprotein protein IMP3.

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

- Molecule 28 is a protein called U3 small nucleolar ribonucleoprotein protein IMP4.

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

- Molecule 29 is a protein called Mpp10,U3 small nucleolar RNA-associated protein MPP10.

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

- Molecule 30 is a protein called Pre-rRNA-processing protein PNO1.

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

- Molecule 31 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

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

- Molecule 32 is a protein called rRNA biogenesis protein RRP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	R2	272	2228	1433	374	416	5	0	0

- Molecule 33 is a protein called Sof1.

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

- Molecule 34 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
34	SA	1115	23759	10623	4225	7796	1115	0	0

- Molecule 35 is a protein called 40S ribosomal protein S1-A.

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

- Molecule 36 is a protein called 40S ribosomal protein S4-A.

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

- Molecule 37 is a protein called 40S ribosomal protein S5.

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

- Molecule 38 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	SH	174	1369	856	262	248	3	0	0

- Molecule 39 is a protein called 40S ribosomal protein S7-A.

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

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

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

- Molecule 41 is a protein called 40S ribosomal protein S9-A.

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

- Molecule 42 is a protein called 40S ribosomal protein S11-A.

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

- Molecule 43 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	SN	124	890	560	156	172	2	0	0

- Molecule 44 is a protein called 40S ribosomal protein S13.

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

- Molecule 45 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	SP	109	750	462	147	140	1	0	0

- Molecule 46 is a protein called 40S ribosomal protein S16-A.

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

- Molecule 47 is a protein called 40S ribosomal protein S22-A.

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

- Molecule 48 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 49 is a protein called 40S ribosomal protein S24-A.

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

- Molecule 50 is a protein called 40S ribosomal protein S27-A.

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

- Molecule 51 is a protein called 40S ribosomal protein S28-A.

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

- Molecule 52 is a protein called 40S ribosomal protein S30-A.

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

- Molecule 53 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	Sg	51	397	249	73	71	4	0	0

- Molecule 54 is a protein called Utp7.

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

- Molecule 55 is a protein called Utp11.

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

- Molecule 56 is a protein called Utp20.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
56	U3	1407	7035	4221	1407	1407	0	0

- Molecule 57 is a protein called rRNA-processing protein FCF1.

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

- Molecule 58 is a protein called Ribosome biogenesis protein UTP30.

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

- Molecule 59 is a protein called Helical domain protein.

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

- Molecule 60 is a protein called Helical domain protein.

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

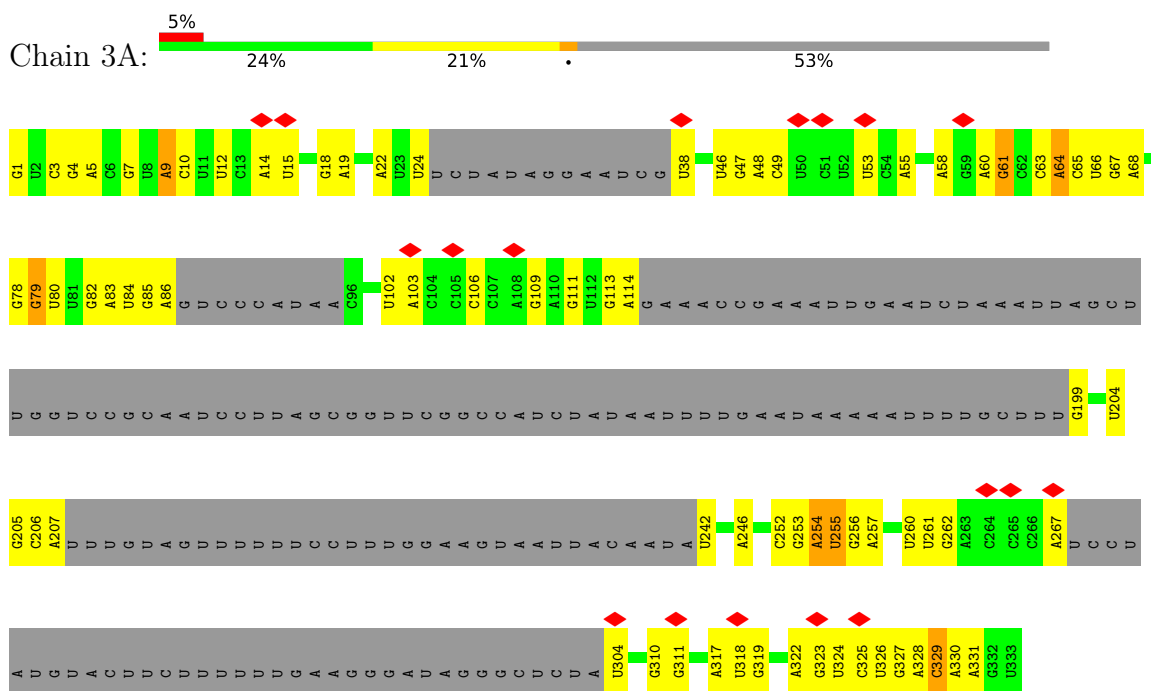
- Molecule 61 is a protein called Unassigned helices.

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

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

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: U3 RNA





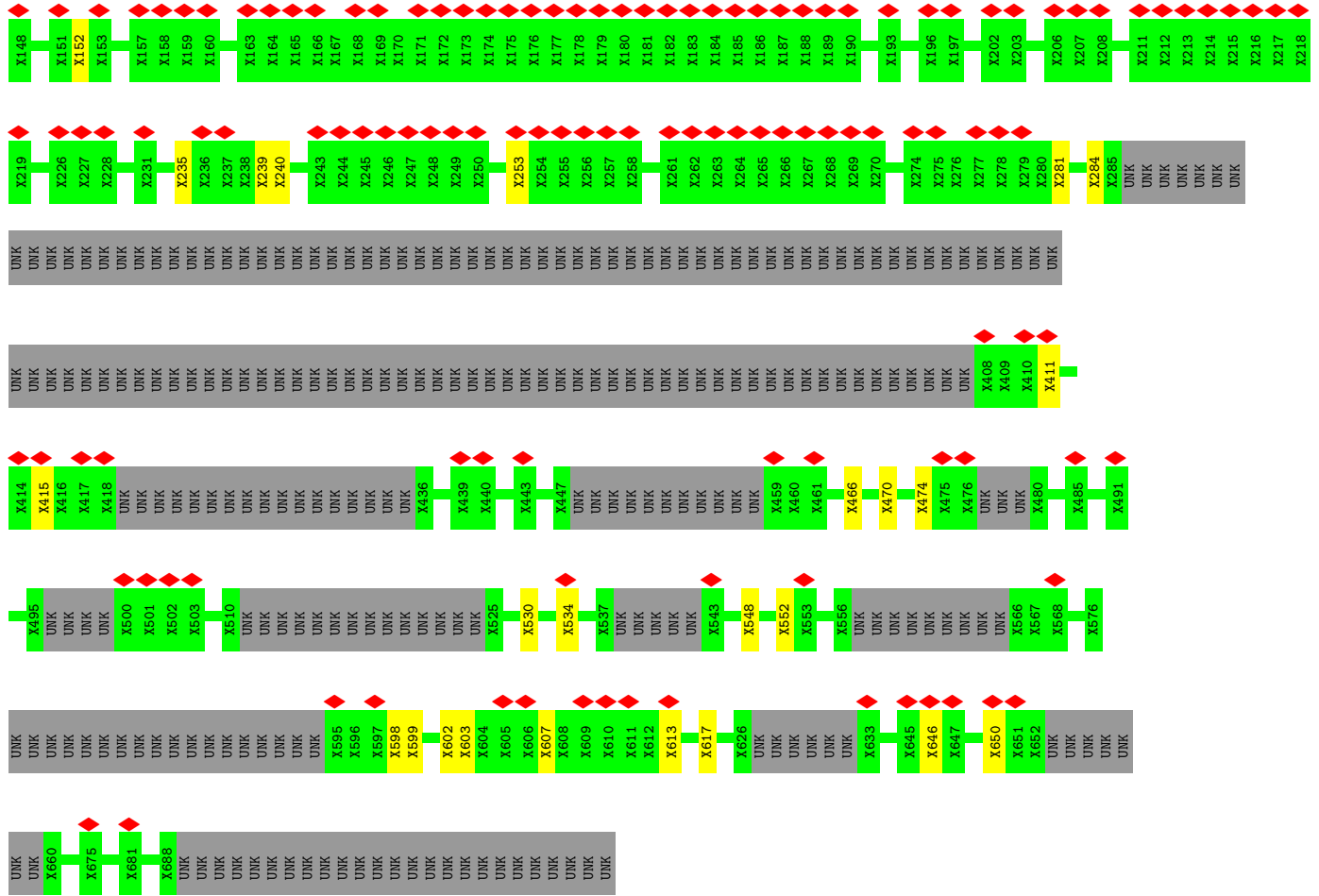




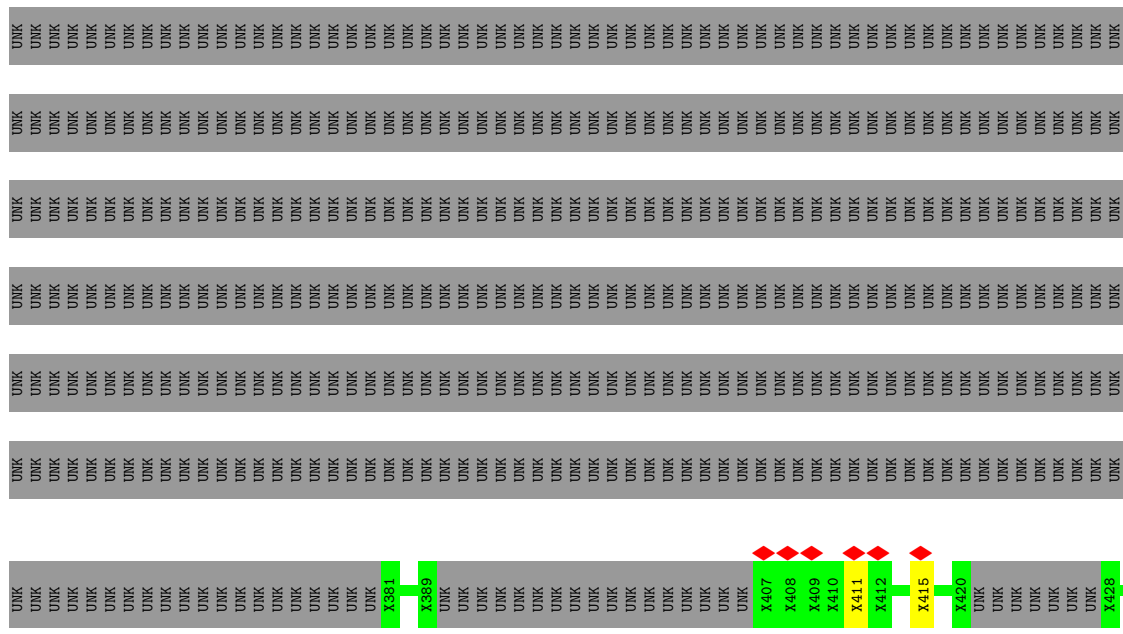


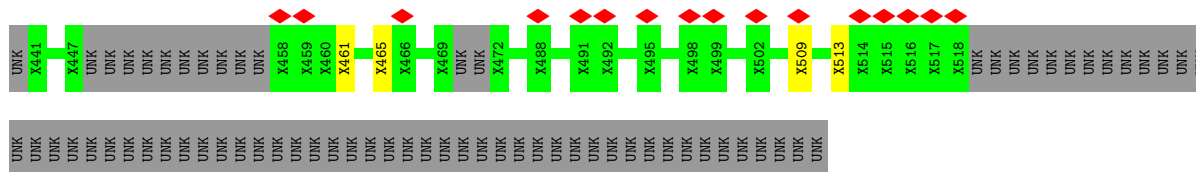




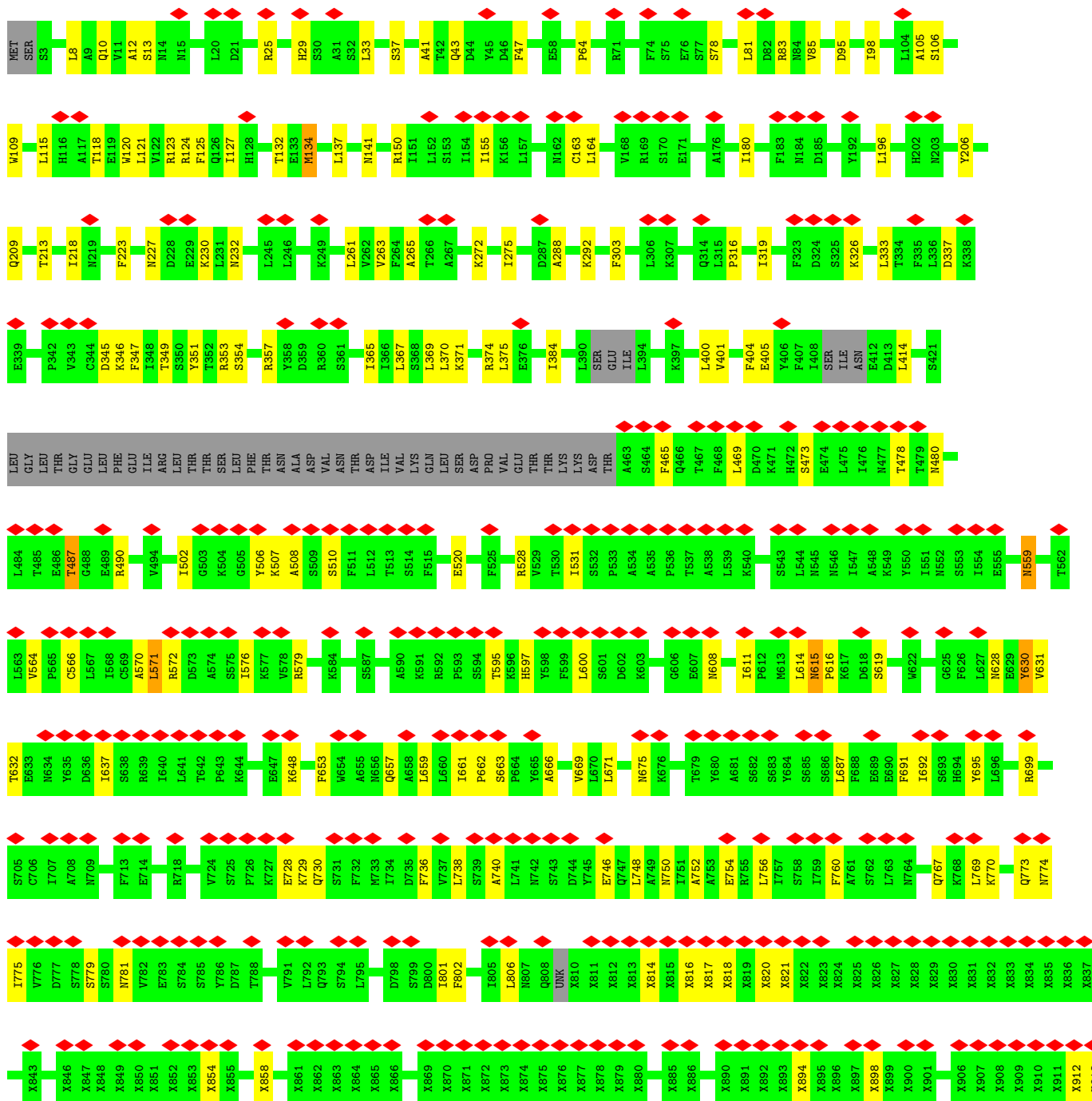
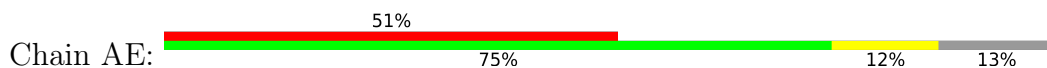


• Molecule 11: Utp9



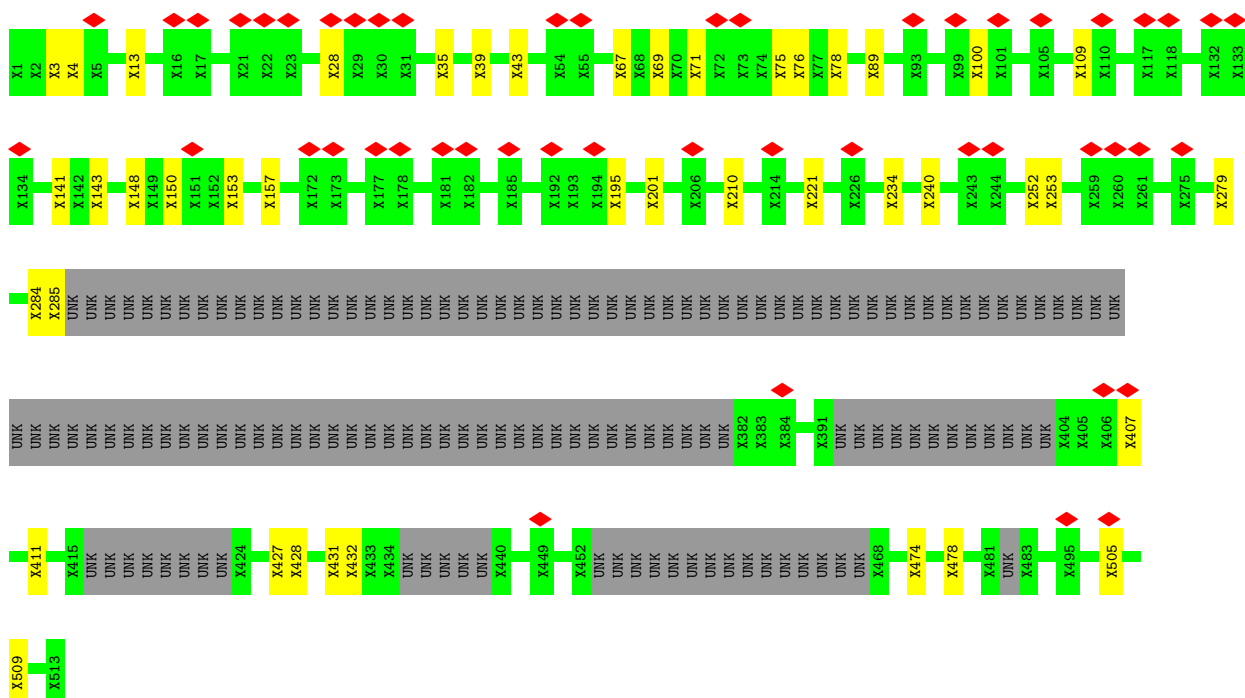


• Molecule 12: U3 small nucleolar RNA-associated protein 10,Utp10

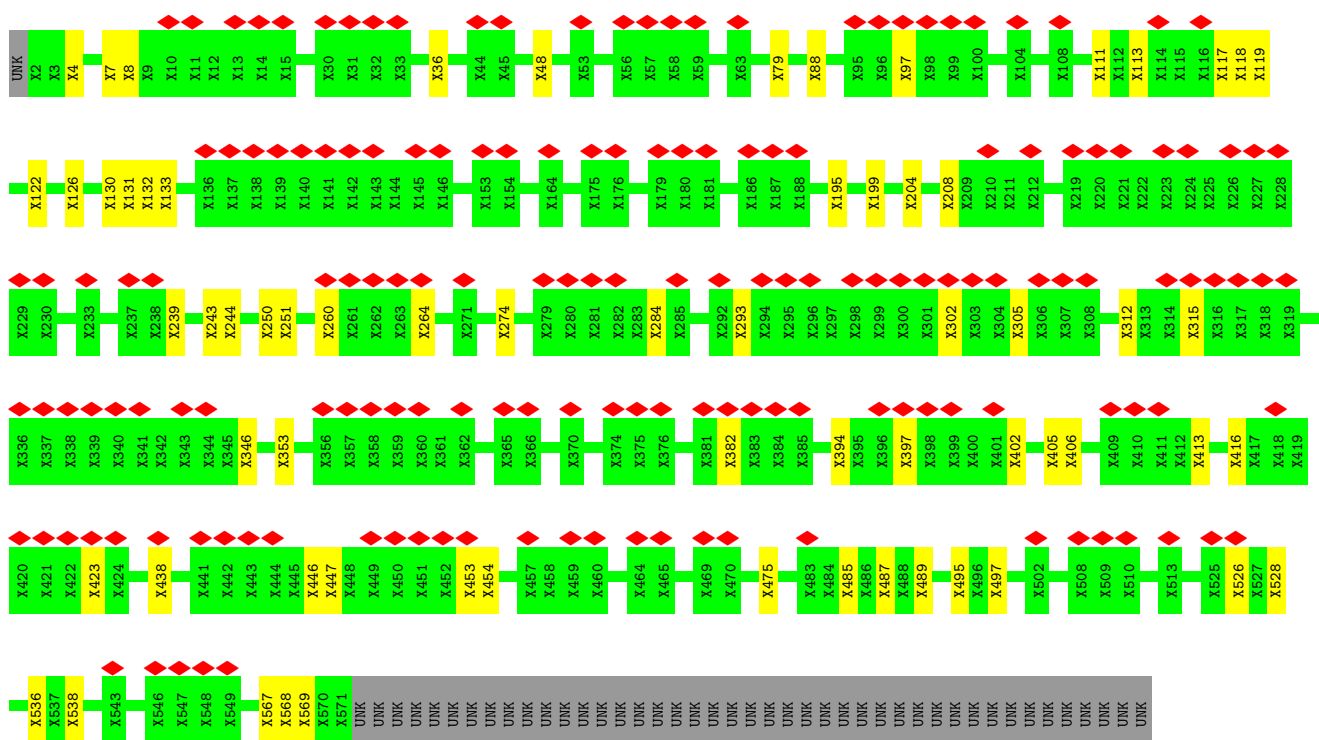




• Molecule 13: Utp15

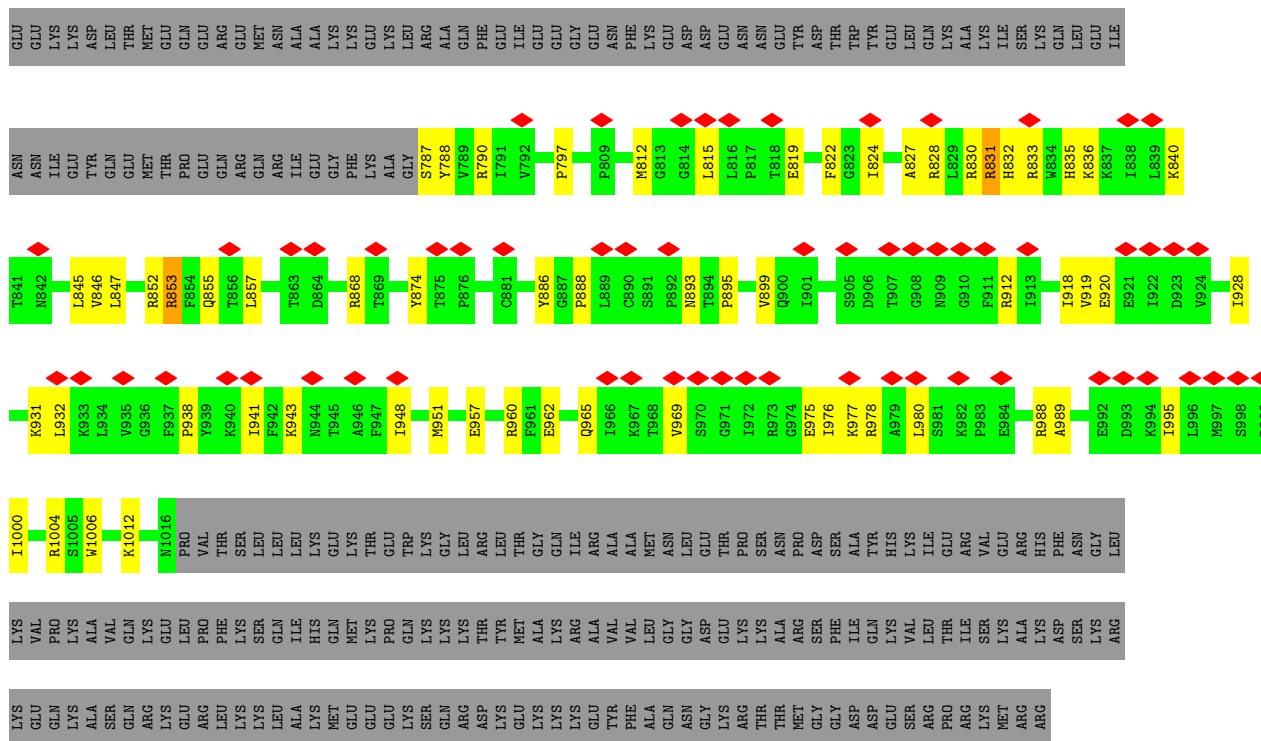


• Molecule 14: Utp17

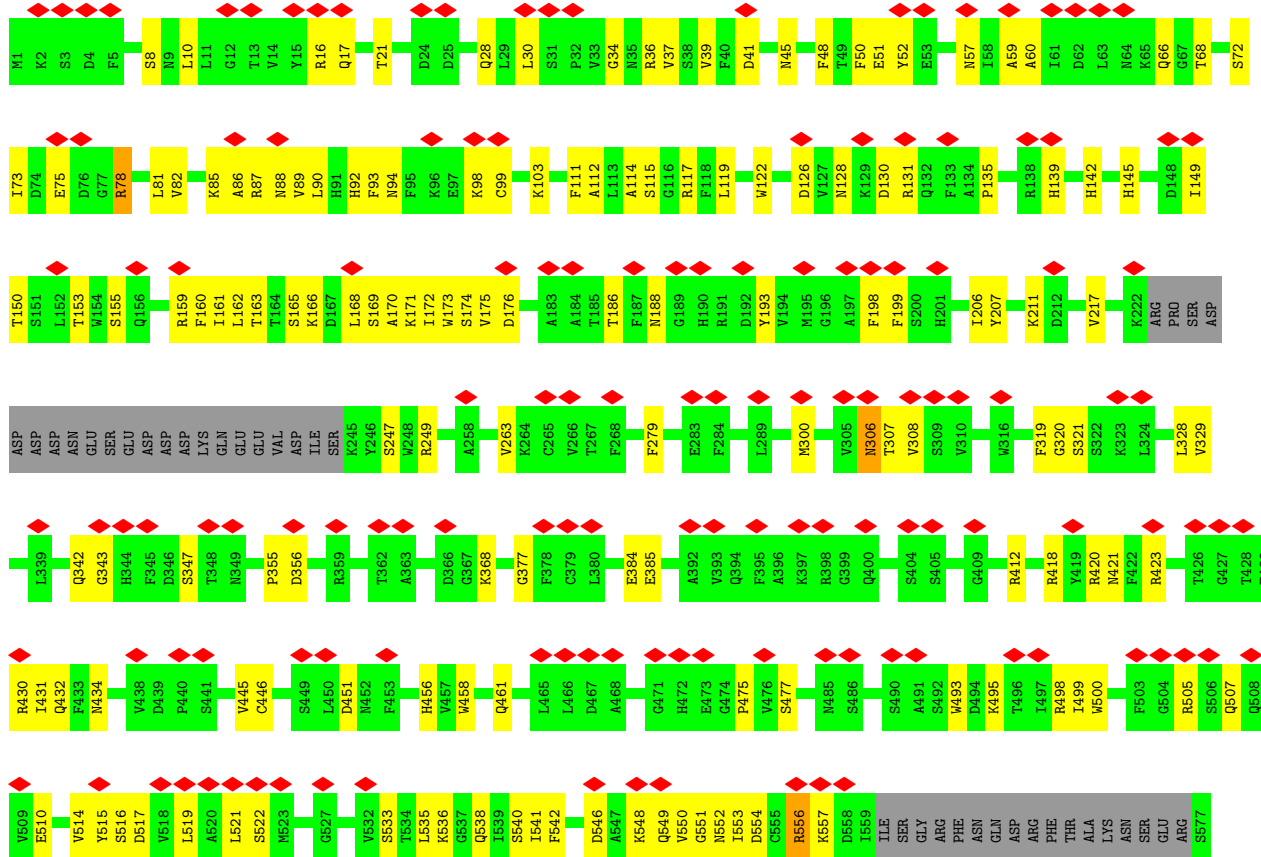


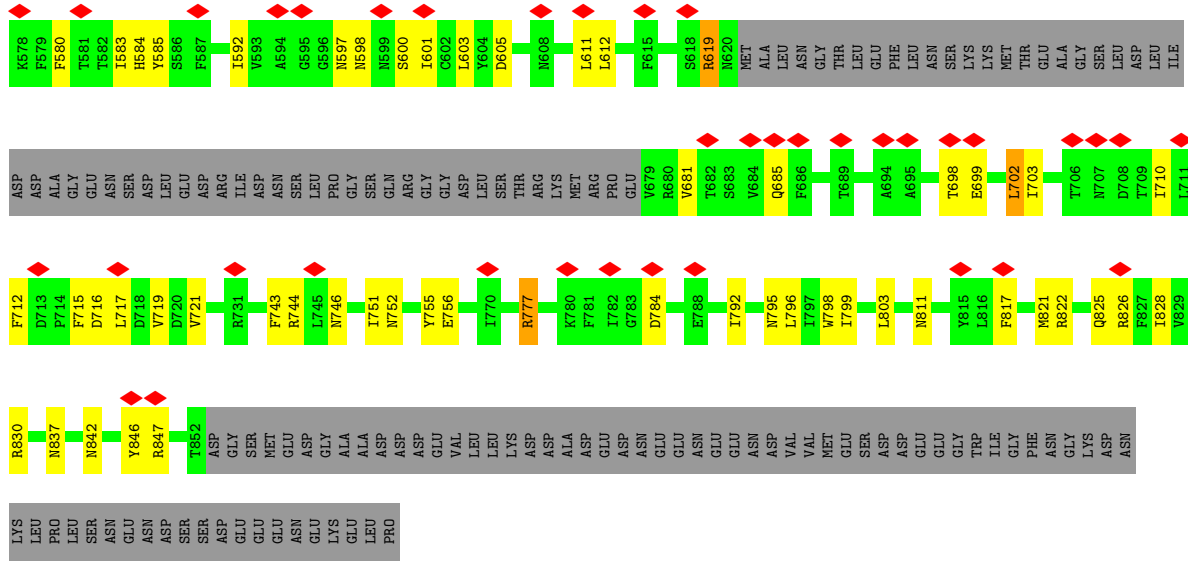




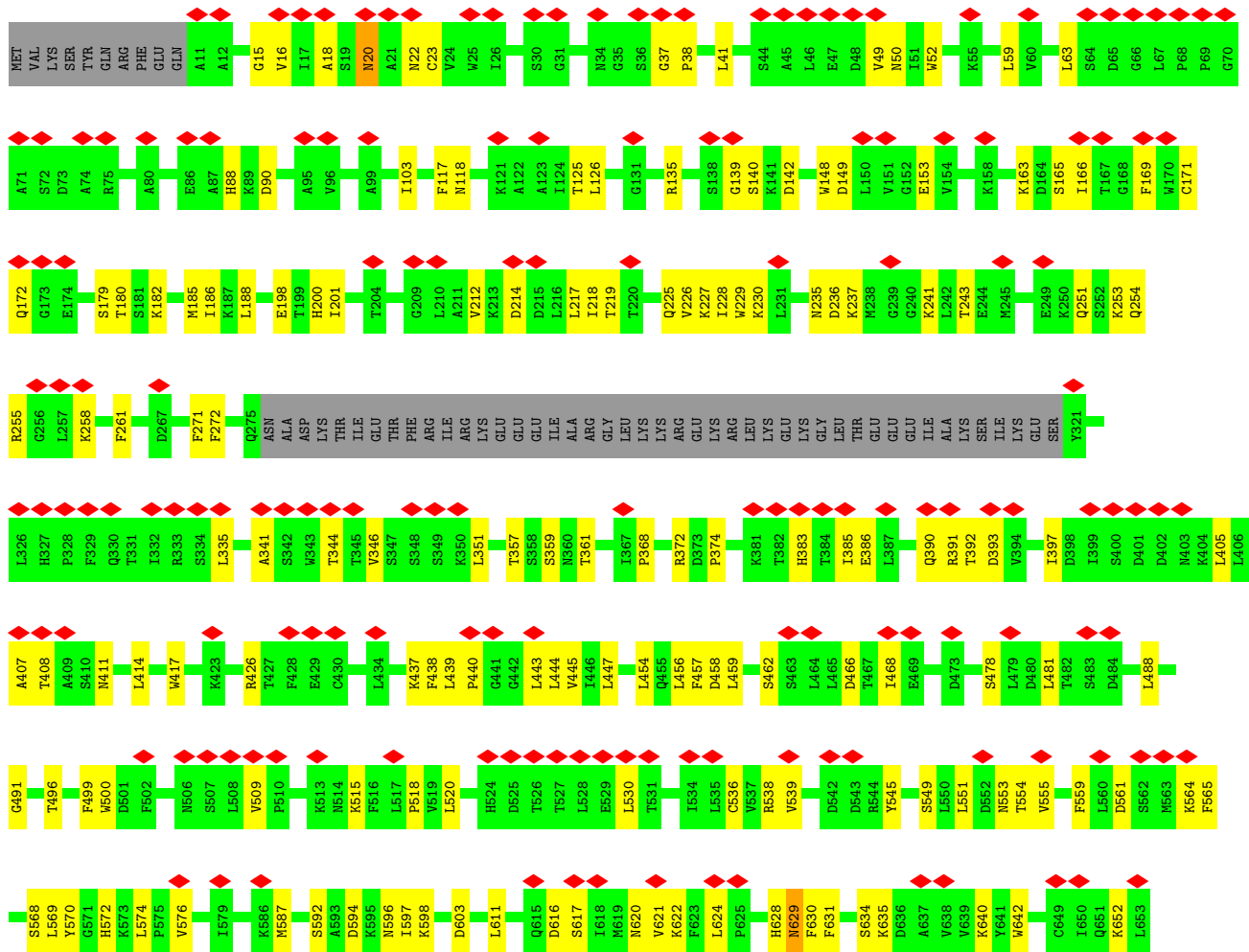


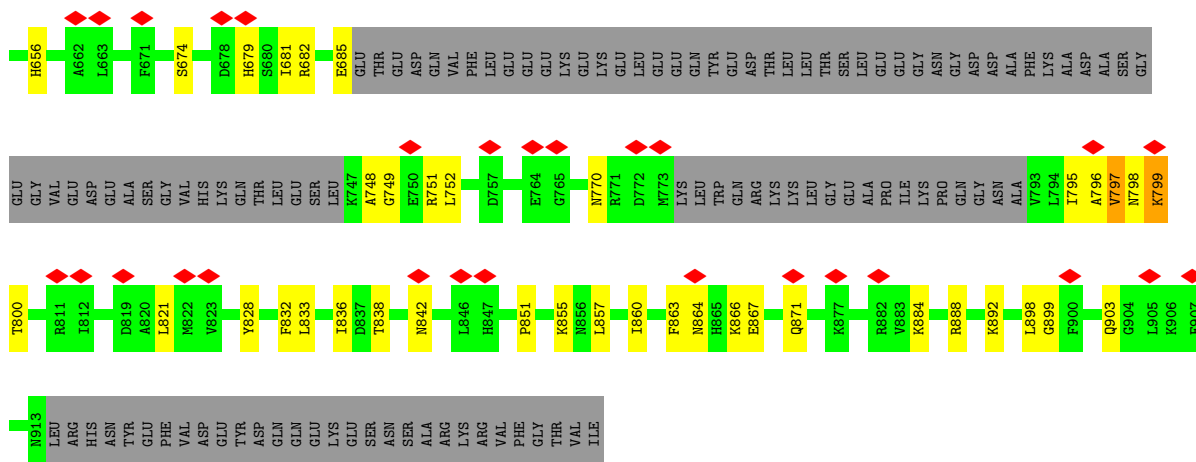
● Molecule 16: Periodic tryptophan protein 2



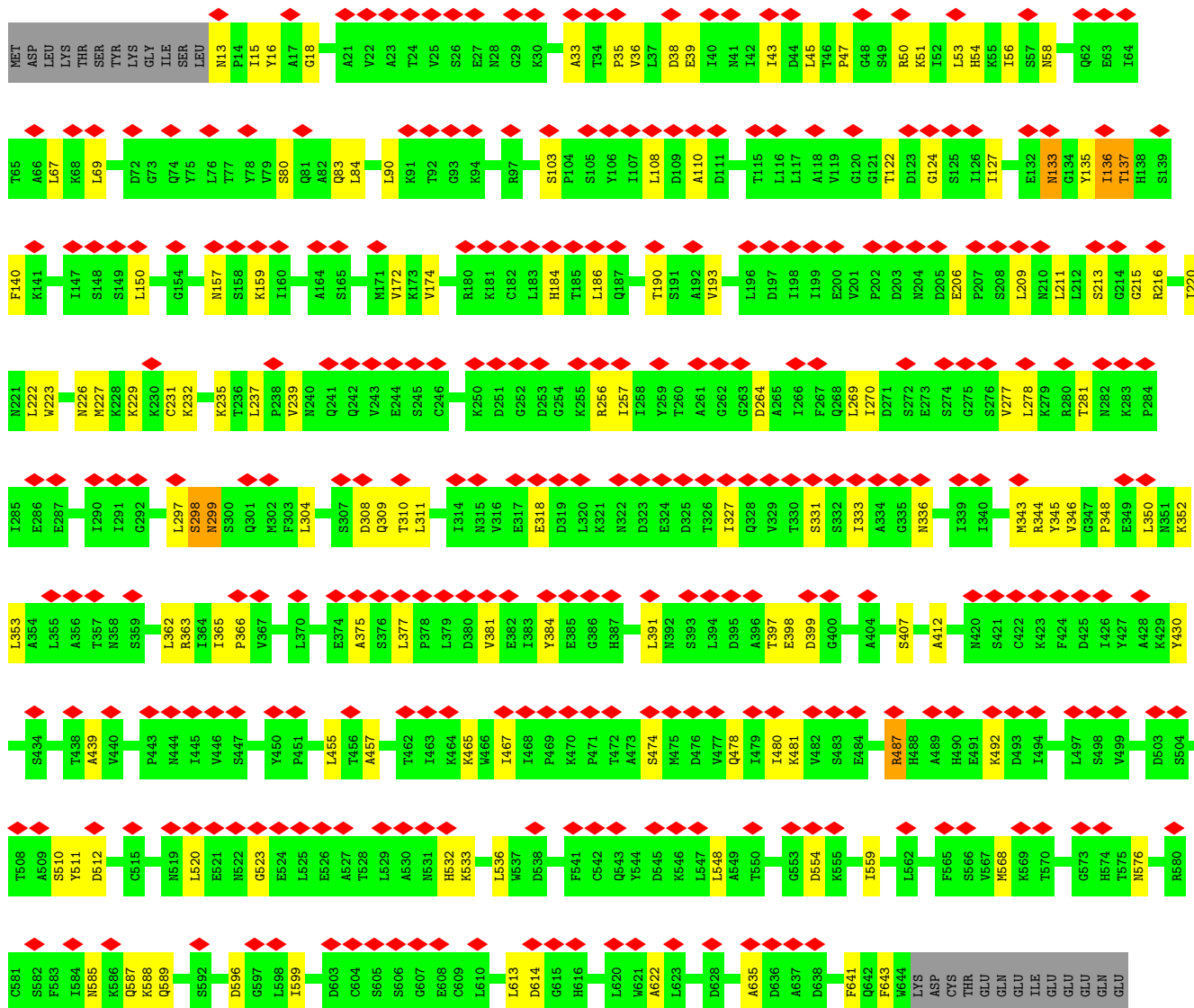
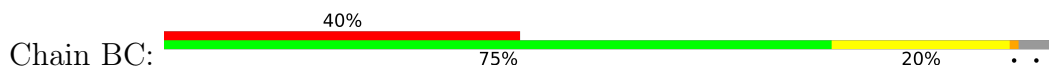


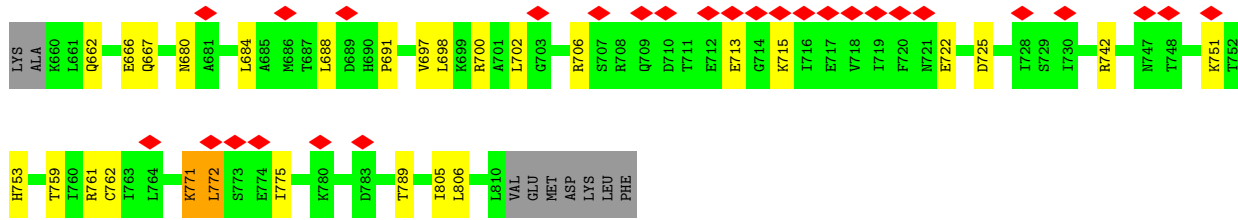
• Molecule 17: U3 small nucleolar RNA-associated protein 12



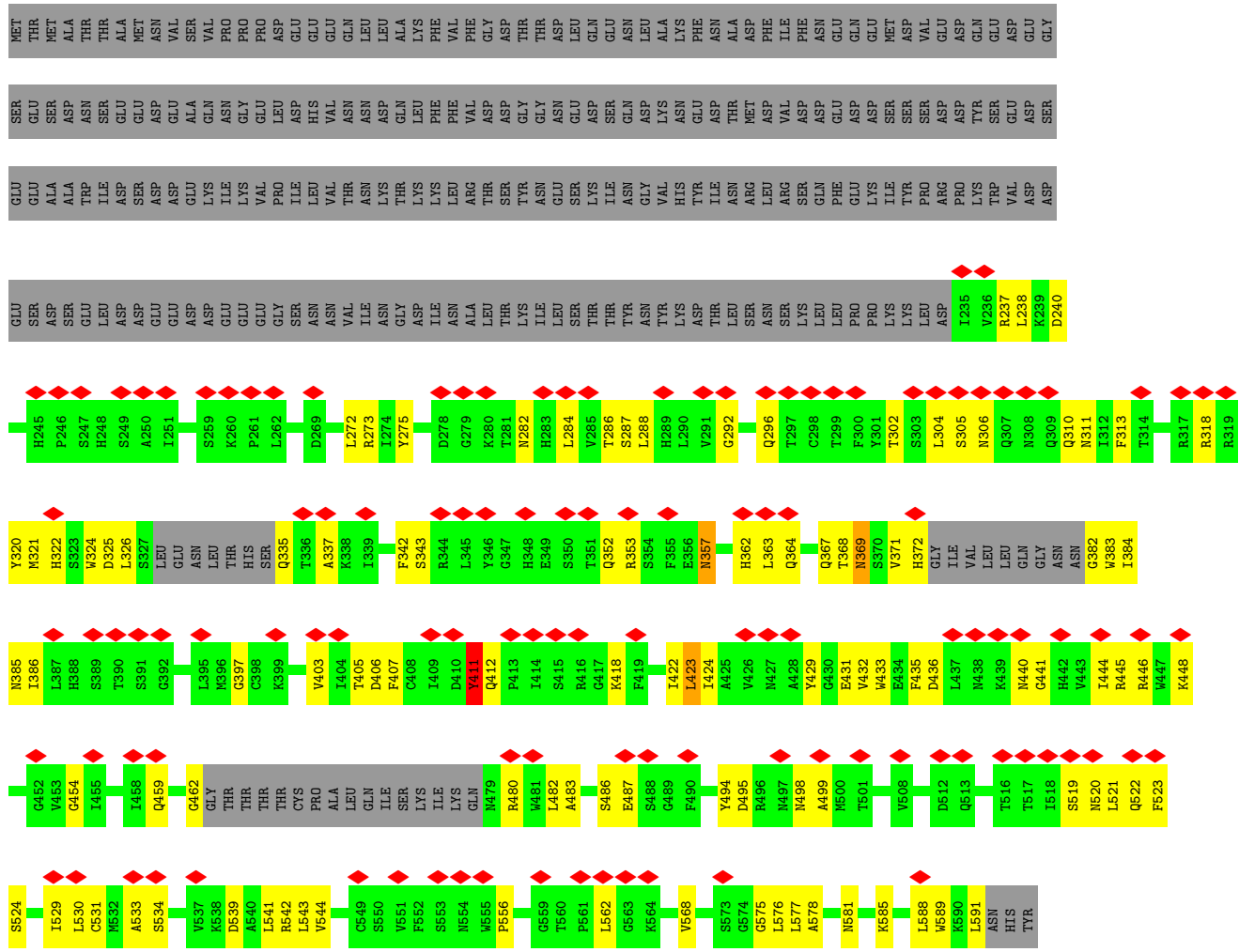
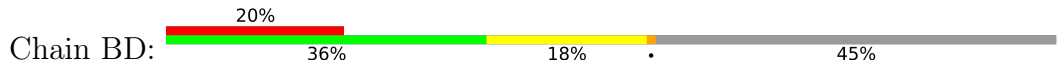


● Molecule 18: U3 small nucleolar RNA-associated protein 13

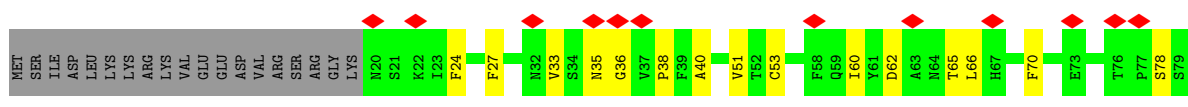




• Molecule 19: U3 small nucleolar RNA-associated protein 18



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



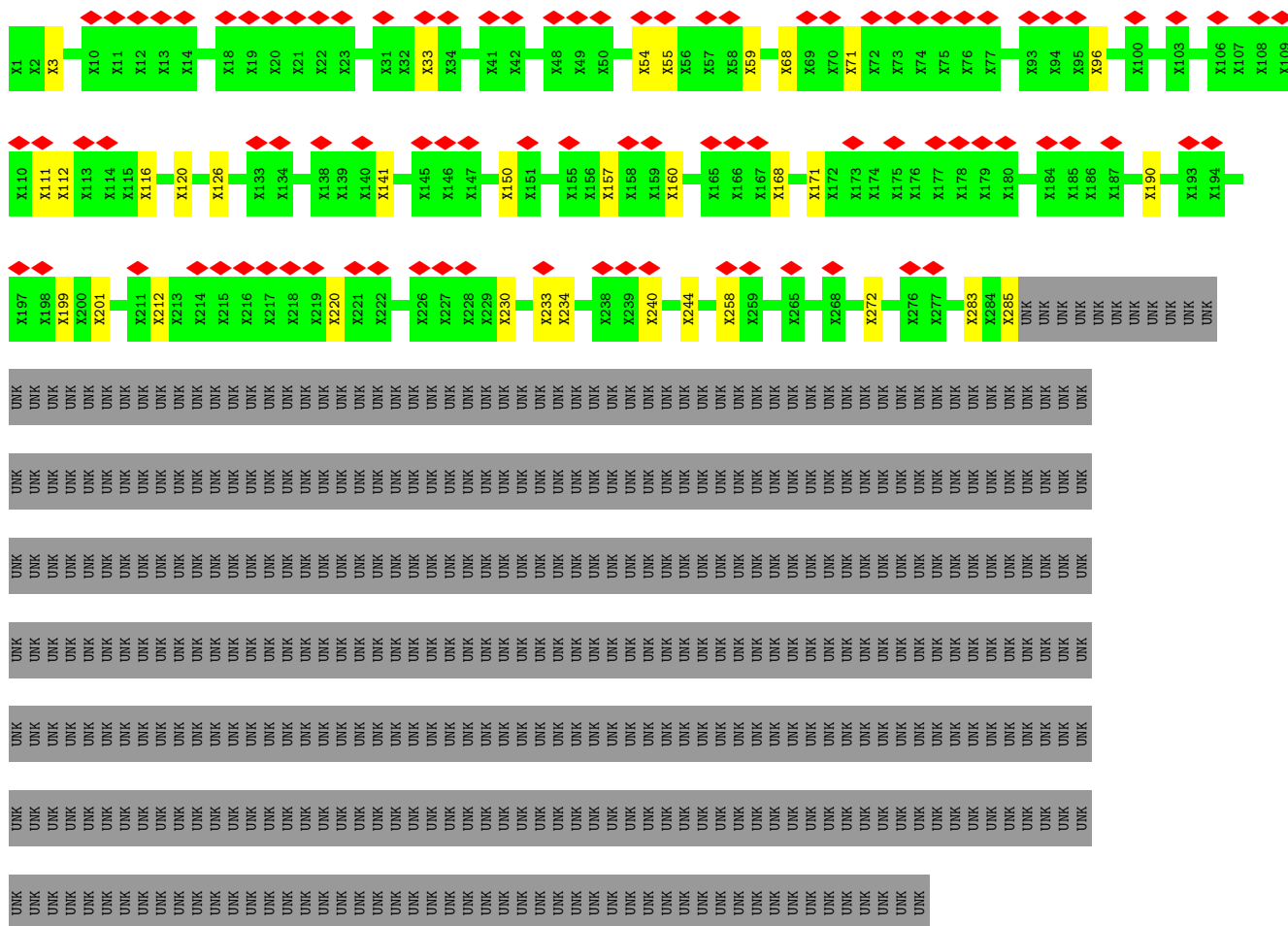




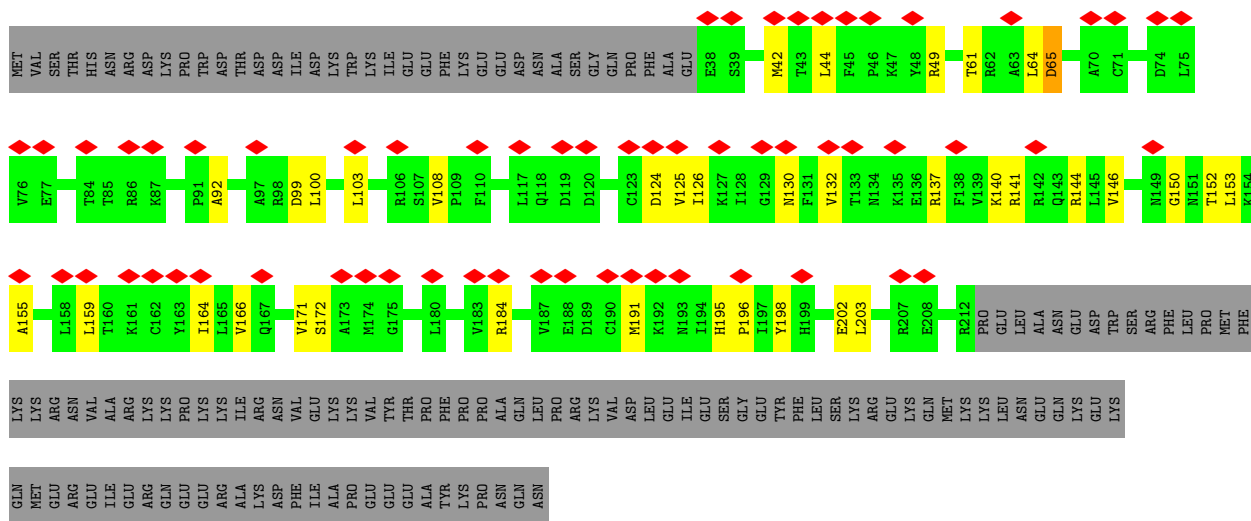
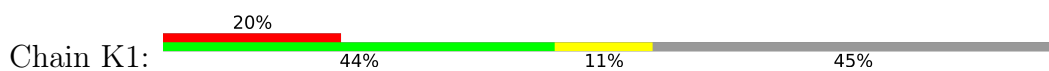




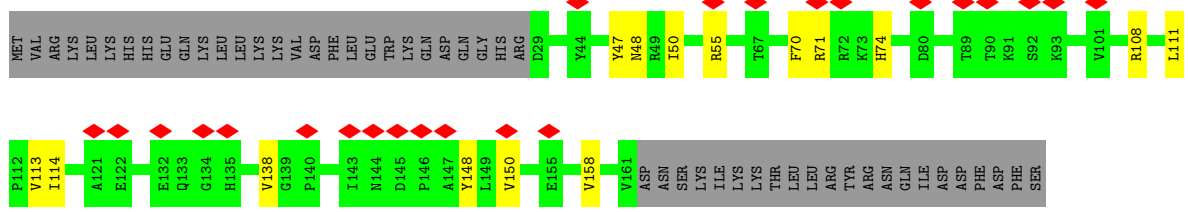




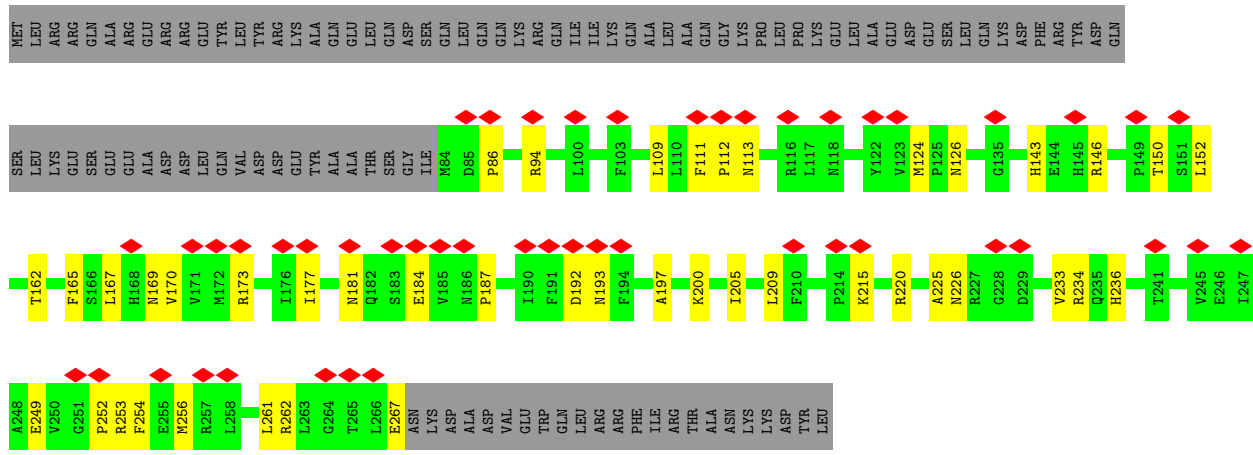
• Molecule 26: KRR1 small subunit processome component



• Molecule 27: U3 small nucleolar ribonucleoprotein protein IMP3



• Molecule 28: U3 small nucleolar ribonucleoprotein protein IMP4

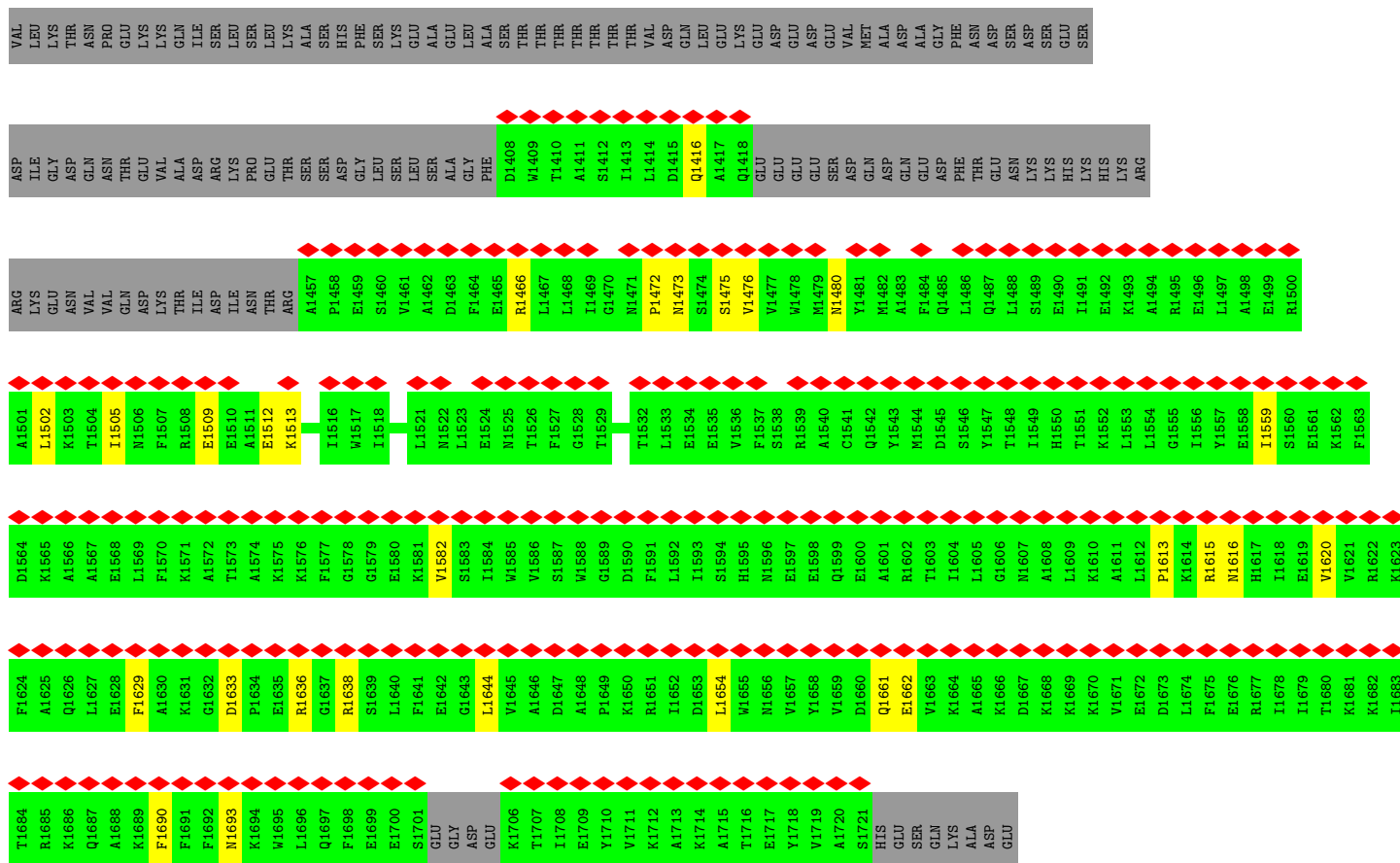


• Molecule 29: Mpp10,U3 small nucleolar RNA-associated protein MPP10

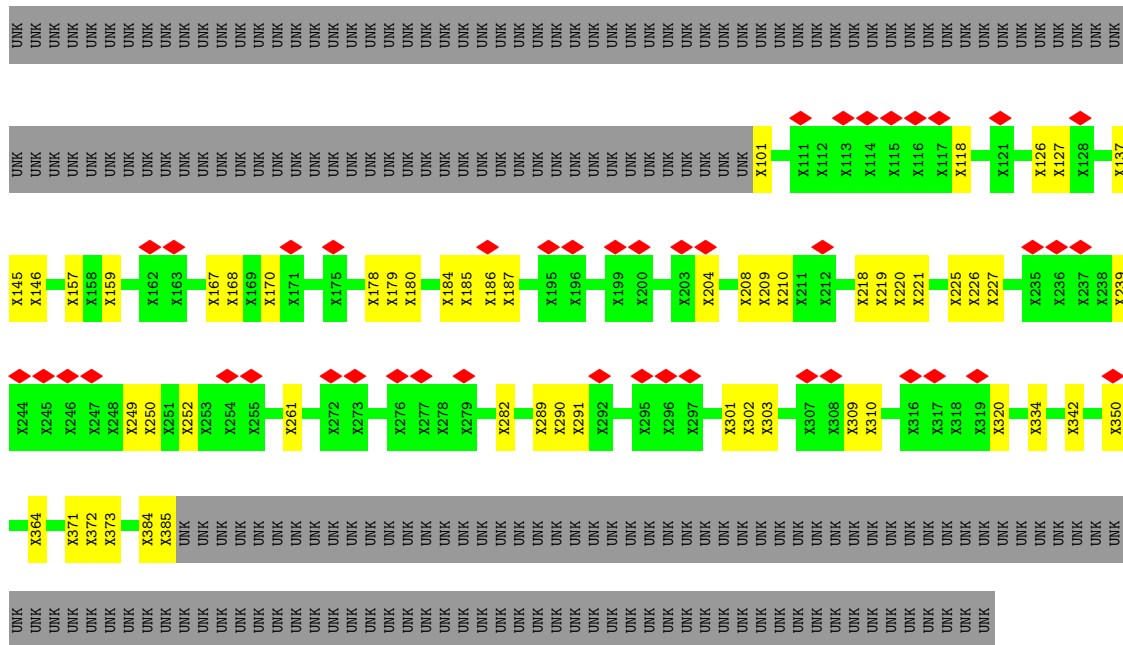




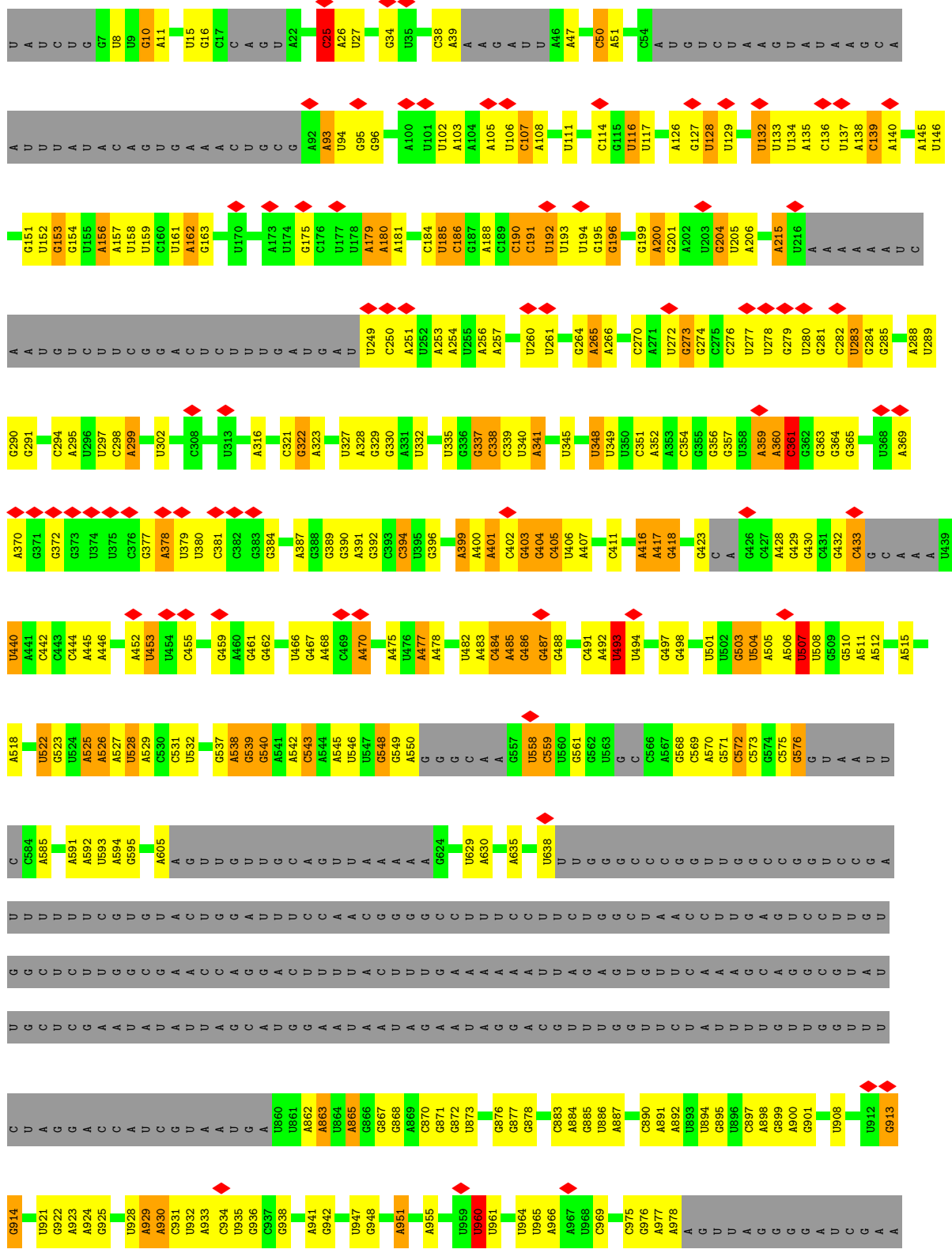
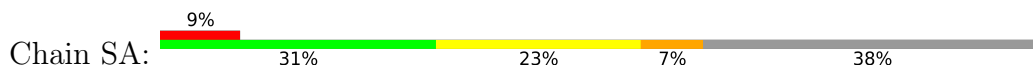




• Molecule 33: Sof1



• Molecule 34: 18S ribosomal RNA

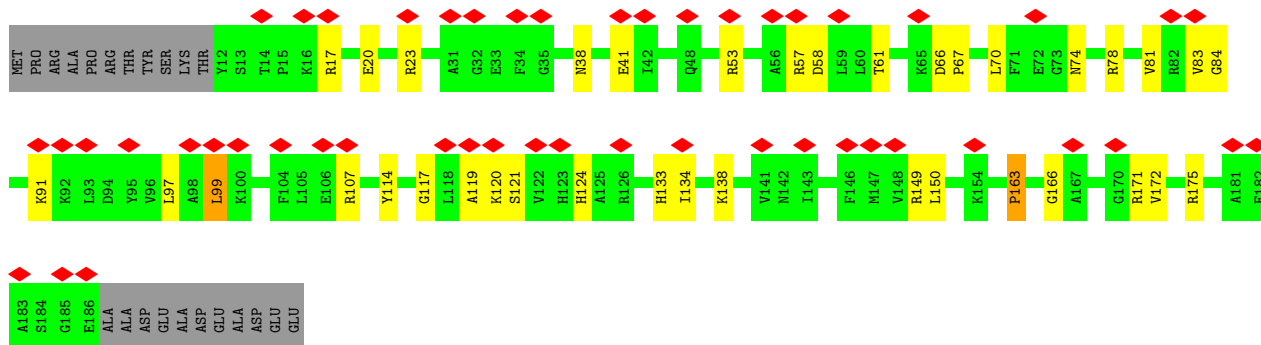




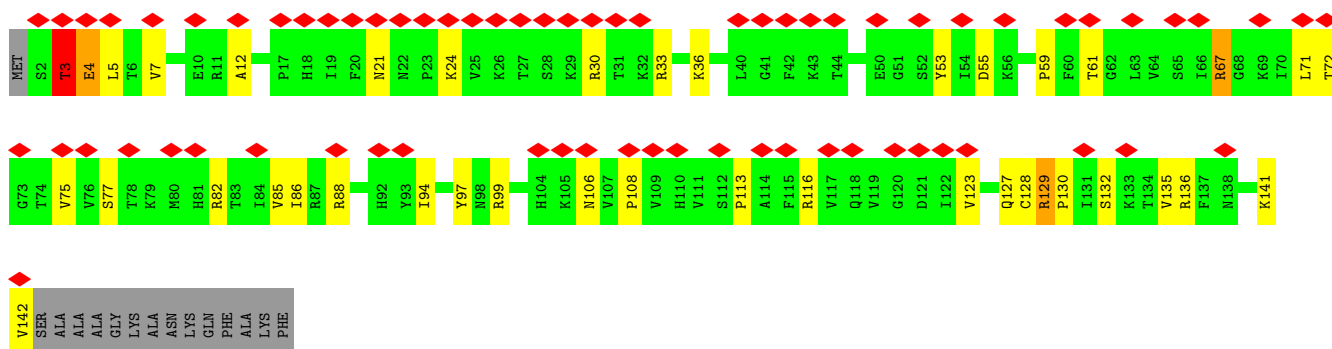




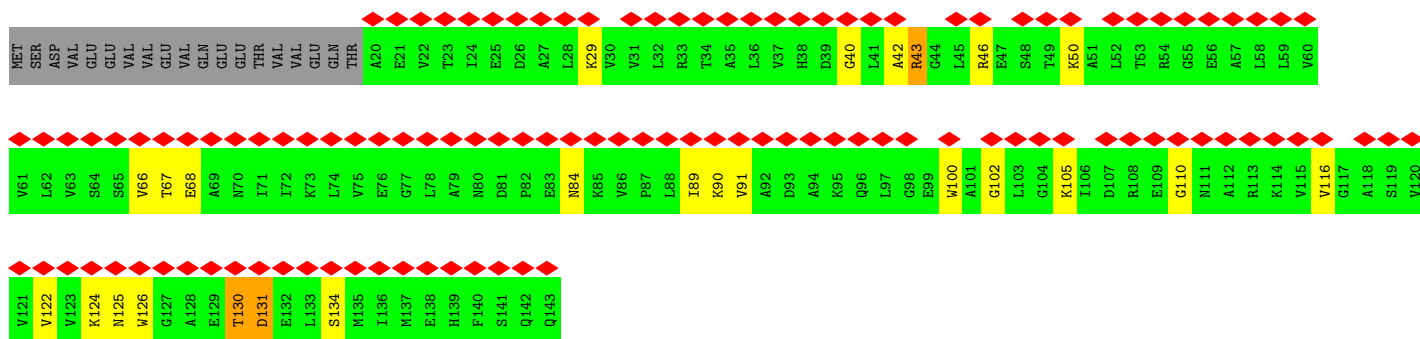
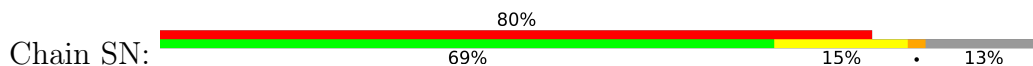




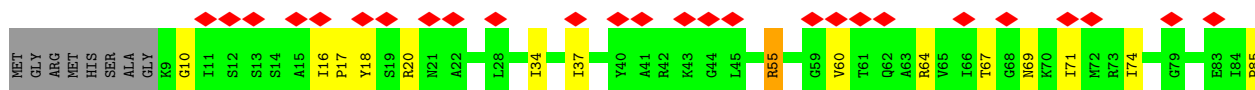
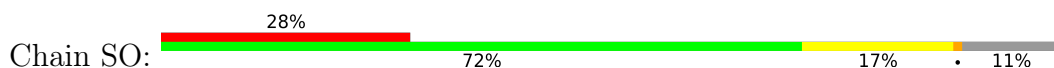
• Molecule 42: 40S ribosomal protein S11-A



• Molecule 43: 40S ribosomal protein S12



• Molecule 44: 40S ribosomal protein S13

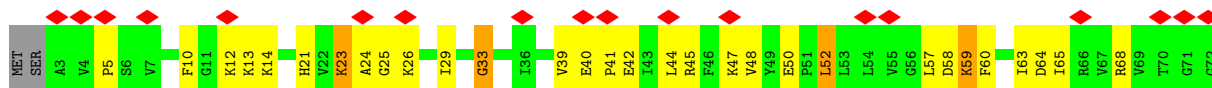




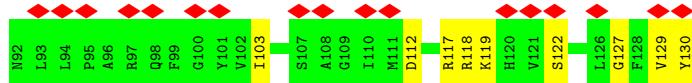
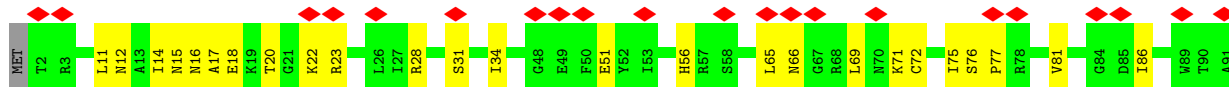
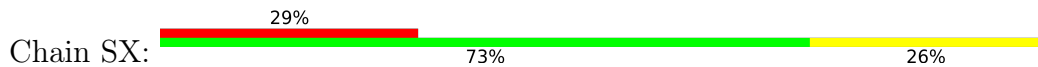
• Molecule 45: 40S ribosomal protein S14-A



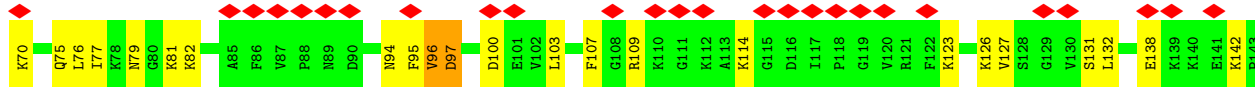
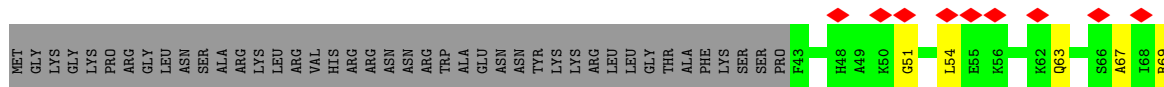
• Molecule 46: 40S ribosomal protein S16-A



• Molecule 47: 40S ribosomal protein S22-A

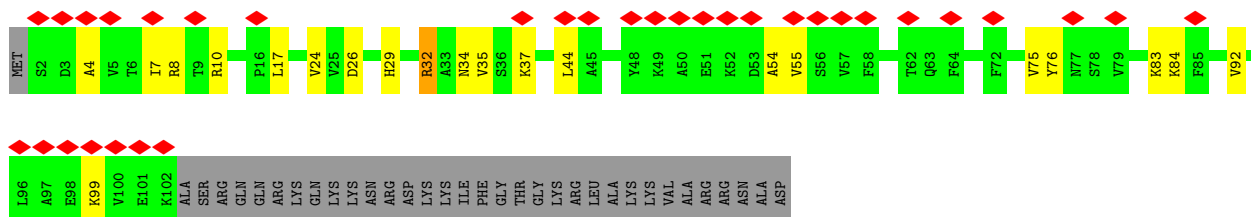


• Molecule 48: 40S ribosomal protein S23-A

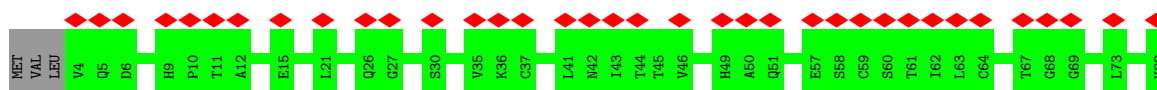
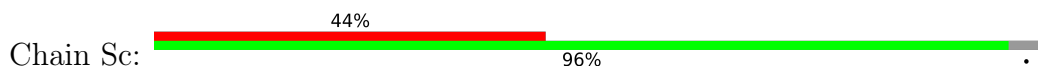




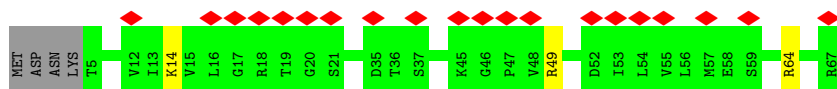
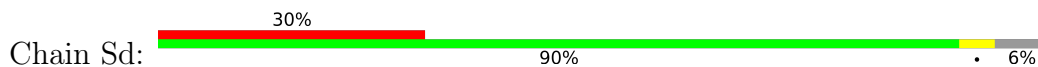
• Molecule 49: 40S ribosomal protein S24-A



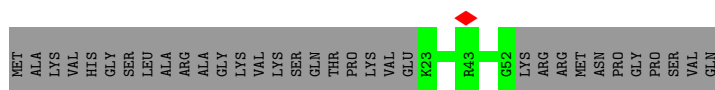
• Molecule 50: 40S ribosomal protein S27-A



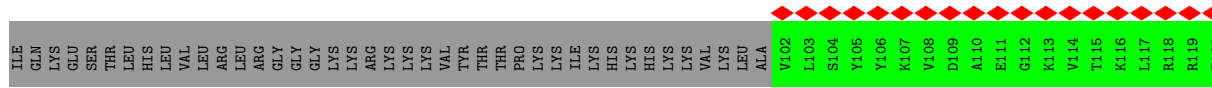
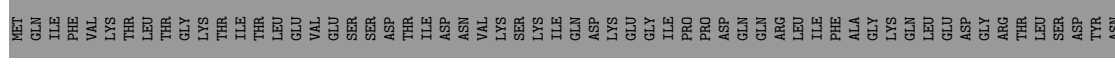
• Molecule 51: 40S ribosomal protein S28-A



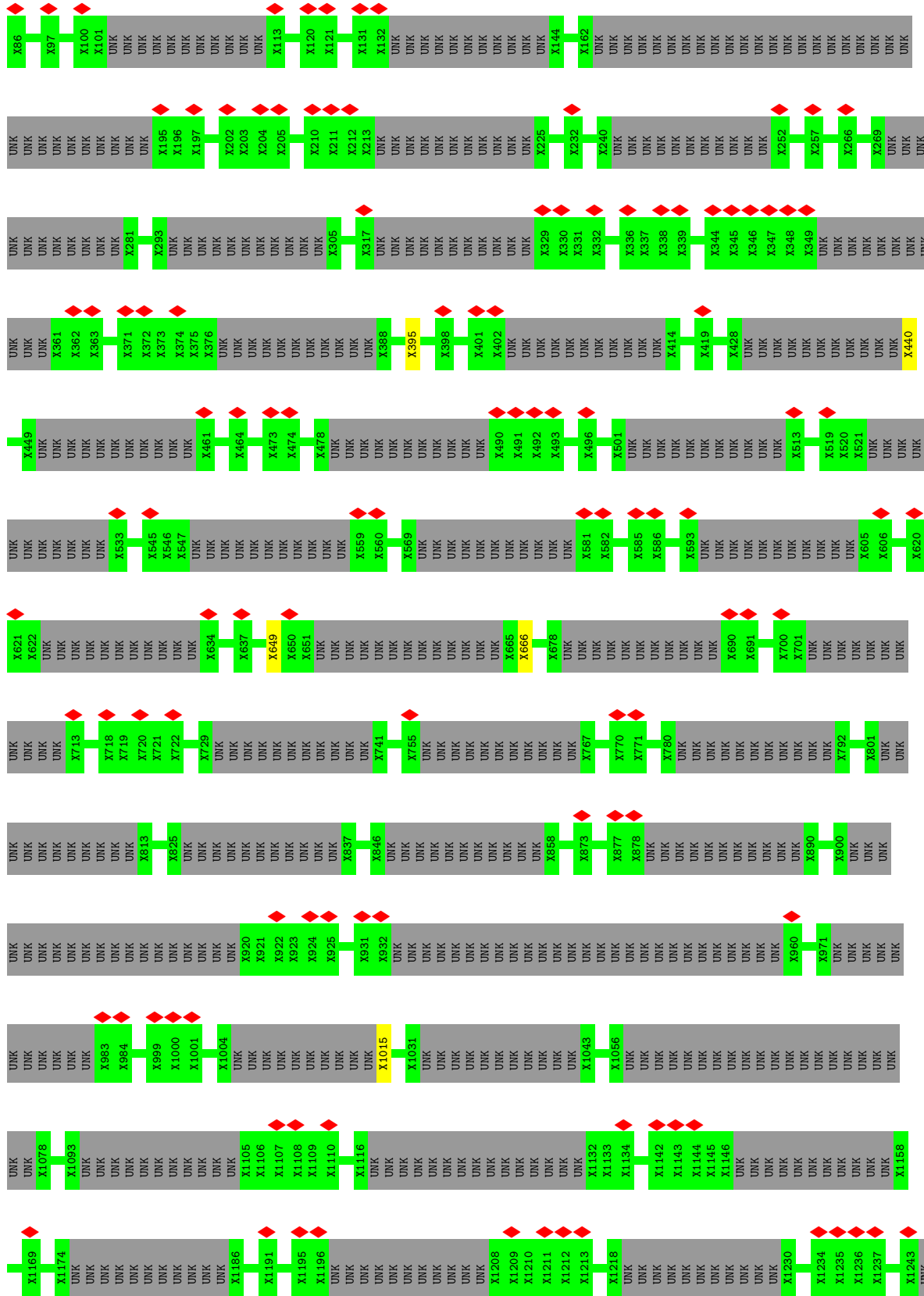
• Molecule 52: 40S ribosomal protein S30-A



• Molecule 53: Ubiquitin-40S ribosomal protein S31





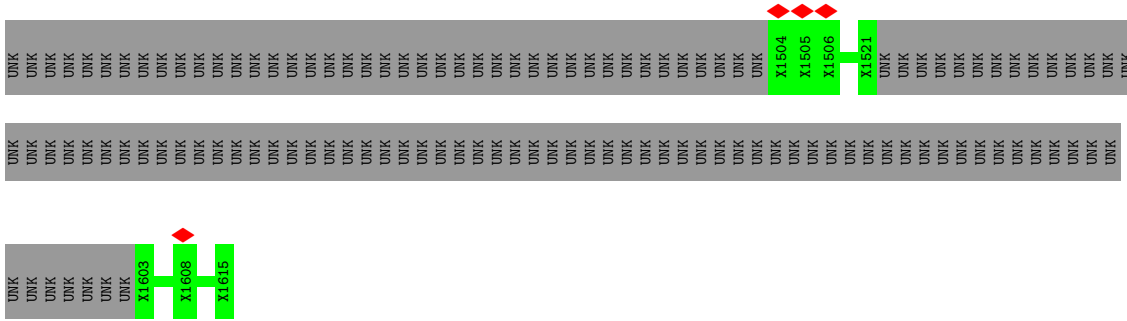




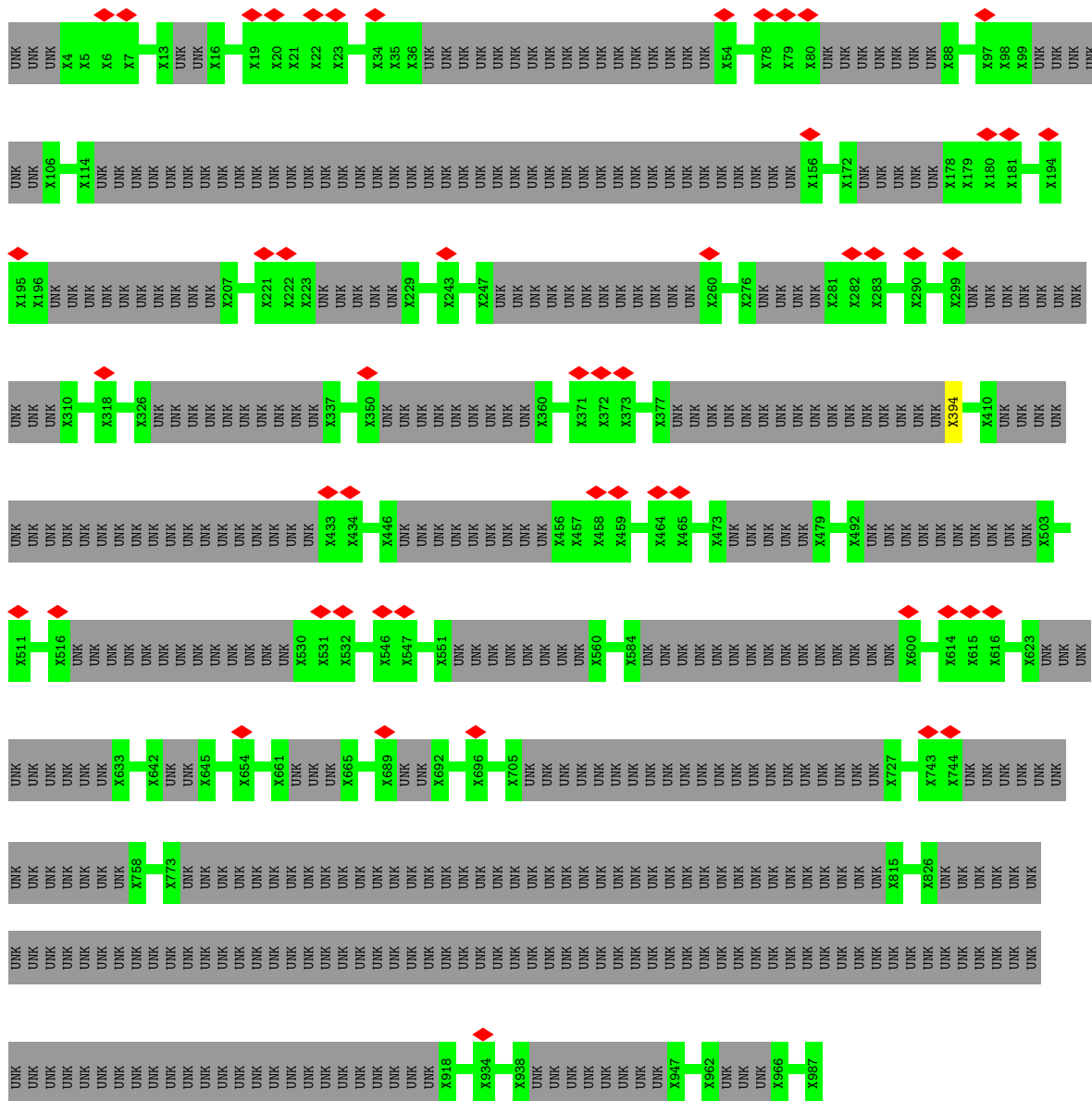




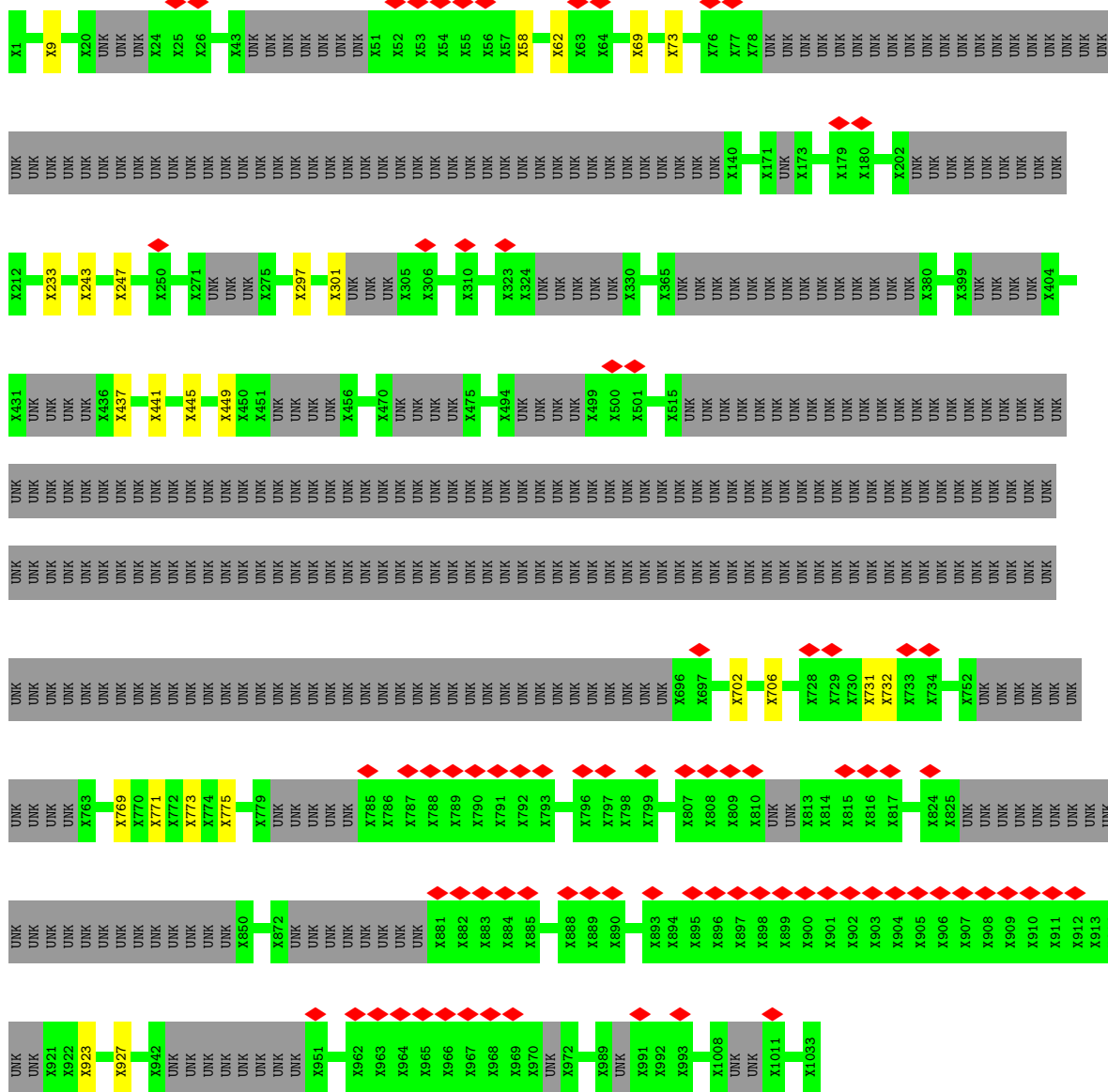




• Molecule 60: Helical domain protein



• Molecule 61: Unassigned helices



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	30995	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)	2000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	79545	Depositor
Image detector	OTHER	Depositor
Maximum map value	0.342	Depositor
Minimum map value	-0.265	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.018	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 i

### 5.1 Standard geometry i

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	3A	0.34	0/3710	1.04	6/5763 (0.1%)
2	3B	0.31	0/1903	0.53	0/2572
2	3C	0.28	0/1903	0.52	1/2572 (0.0%)
3	3D	0.30	0/2960	0.52	0/3987
4	3E	0.27	0/2970	0.46	0/4004
5	3F	0.30	0/2975	0.56	0/4008
6	3G	0.28	0/936	0.51	0/1273
6	3H	0.27	0/936	0.50	0/1273
7	5A	0.31	0/11029	1.07	51/17170 (0.3%)
12	AE	0.41	1/6194 (0.0%)	0.58	5/8384 (0.1%)
15	B1	0.30	0/4431	0.56	0/5988
16	BA	0.31	0/6164	0.58	4/8349 (0.0%)
17	BB	0.29	0/6264	0.59	0/8473
18	BC	0.29	0/6226	0.60	2/8442 (0.0%)
19	BD	0.46	4/2597 (0.2%)	0.64	4/3520 (0.1%)
20	BE	0.30	0/6056	0.56	0/8189
21	CA	0.27	0/1621	0.45	0/2196
22	CB	0.28	0/9081	0.47	0/12283
23	E1	0.25	0/1716	0.47	0/2319
23	E2	0.26	0/1721	0.48	0/2323
24	E3	0.29	0/2168	0.51	1/2942 (0.0%)
26	K1	0.29	0/1432	0.53	1/1926 (0.1%)
27	MA	0.27	0/1117	0.47	0/1509
28	MB	0.30	0/1496	0.53	0/2025
29	MC	0.26	0/209	0.50	0/282
30	P1	0.27	0/1394	0.51	0/1881
31	R1	0.28	0/2793	0.49	0/3774
32	R2	0.26	0/2271	0.44	0/3054
34	SA	0.70	9/26553 (0.0%)	1.17	165/41320 (0.4%)
35	SC	0.31	0/1735	0.72	1/2335 (0.0%)
36	SF	0.30	0/1920	0.64	3/2589 (0.1%)
37	SG	0.34	0/1629	0.62	0/2202
38	SH	0.28	0/1385	0.58	1/1851 (0.1%)
39	SI	0.33	0/1343	0.64	1/1808 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
40	SJ	0.28	0/1373	0.60	1/1834 (0.1%)
41	SK	0.29	0/1434	0.62	1/1920 (0.1%)
42	SM	0.35	0/1169	0.57	0/1576
43	SN	0.31	0/898	0.79	1/1220 (0.1%)
44	SO	0.28	0/1109	0.54	0/1495
45	SP	0.28	0/758	0.58	0/1028
46	SR	0.31	0/990	0.66	0/1335
47	SX	0.28	0/1038	0.58	0/1395
48	SY	0.30	0/796	0.67	0/1062
49	SZ	0.31	0/814	0.53	0/1093
50	Sc	0.28	0/605	0.56	0/817
51	Sd	0.26	0/499	0.55	0/670
52	Sf	0.29	0/255	0.54	0/339
53	Sg	0.29	0/404	0.56	0/542
57	U4	0.28	0/1007	0.54	0/1357
58	U5	0.27	0/2043	0.52	0/2747
All	All	0.41	14/144030 (0.0%)	0.78	249/203016 (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
3	3D	0	2
5	3F	0	2
12	AE	0	1
15	B1	0	3
16	BA	0	2
17	BB	0	7
18	BC	0	6
19	BD	0	3
20	BE	0	4
21	CA	0	1
22	CB	0	1
34	SA	0	1
35	SC	0	2
36	SF	0	2
37	SG	0	7
38	SH	0	1
39	SI	0	3
41	SK	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
42	SM	0	1
43	SN	0	4
45	SP	0	1
46	SR	0	3
48	SY	0	1
53	Sg	0	1
58	U5	0	1
61	UC	0	2
All	All	0	65

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	SA	283	U	C2-N3	53.18	1.75	1.37
34	SA	283	U	N3-C4	40.53	1.75	1.38
34	SA	283	U	N1-C2	39.84	1.74	1.38
34	SA	283	U	N1-C6	36.49	1.70	1.38
34	SA	283	U	C4-C5	32.43	1.72	1.43

The worst 5 of 249 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	SA	487	G	C5-C6-O6	38.33	151.60	128.60
34	SA	487	G	N1-C6-O6	-33.63	99.72	119.90
34	SA	493	U	C5-C4-O4	25.11	140.96	125.90
34	SA	493	U	N3-C4-O4	-20.41	105.11	119.40
34	SA	487	G	C4-C5-N7	-19.97	102.81	110.80

There are no chirality outliers.

5 of 65 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	3D	392	TYR	Peptide
3	3D	91	SER	Peptide
5	3F	342	ARG	Peptide
5	3F	437	ARG	Peptide
12	AE	64	PRO	Peptide



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

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	3A	3327	0	1687	58	0
2	3B	1866	0	1904	30	0
2	3C	1866	0	1904	20	0
3	3D	2915	0	2930	43	0
4	3E	2935	0	3033	48	0
5	3F	2916	0	2947	82	0
6	3G	924	0	975	20	0
6	3H	924	0	975	17	0
7	5A	9867	0	4954	82	0
8	AA	2845	0	658	47	0
9	AB	2015	0	454	19	0
10	AC	2360	0	534	17	0
11	AD	505	0	116	3	0
12	AE	9970	0	7056	161	0
13	AF	1880	0	425	23	0
14	AG	3060	0	707	36	0
15	B1	4325	0	4434	83	0
16	BA	6026	0	5940	129	0
17	BB	6138	0	6163	116	0
18	BC	6117	0	6141	98	0
19	BD	2539	0	2520	69	0
20	BE	5936	0	5882	137	0
21	CA	1582	0	1528	35	0
22	CB	8870	0	8975	149	0
23	E1	1689	0	1738	34	0
23	E2	1695	0	1757	38	0
24	E3	2114	0	2154	55	0
25	E4	1425	0	322	18	0
26	K1	1410	0	1503	27	0
27	MA	1097	0	1130	7	0
28	MB	1465	0	1486	31	0
29	MC	307	0	231	2	0
30	P1	1368	0	1436	9	0
31	R1	2742	0	2829	40	0
32	R2	2228	0	2228	15	0
33	S1	1425	0	334	35	0
34	SA	23759	0	11991	338	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
35	SC	1709	0	1784	47	0
36	SF	1881	0	1958	50	0
37	SG	1609	0	1675	41	0
38	SH	1369	0	1414	69	0
39	SI	1322	0	1394	29	0
40	SJ	1350	0	1374	41	0
41	SK	1412	0	1486	22	0
42	SM	1143	0	1210	26	0
43	SN	890	0	887	12	0
44	SO	1087	0	1152	16	0
45	SP	750	0	728	9	0
46	SR	973	0	1029	37	0
47	SX	1021	0	1060	27	0
48	SY	785	0	840	20	0
49	SZ	801	0	828	13	0
50	Sc	595	0	613	0	0
51	Sd	497	0	535	0	0
52	Sf	251	0	277	0	0
53	Sg	397	0	399	0	0
54	U1	1425	0	329	23	0
55	U2	365	0	75	0	0
56	U3	7035	0	1590	5	0
57	U4	990	0	1054	13	0
58	U5	2009	0	2130	16	0
59	UA	1690	0	370	0	0
60	UB	2775	0	620	1	0
61	UC	3300	0	727	12	0
All	All	173863	0	129519	2467	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 9.

The worst 5 of 2467 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)
12:AE:630:TYR:CE1	12:AE:637:ILE:CD1	1.86	1.56
34:SA:283:U:N3	34:SA:283:U:C2	1.75	1.54
34:SA:283:U:N1	34:SA:283:U:C6	1.70	1.54
34:SA:283:U:N3	34:SA:283:U:C4	1.74	1.53
34:SA:283:U:C2	34:SA:283:U:N1	1.74	1.52

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%)	227 (96%)	10 (4%)	0	100	100
2	3C	237/327 (72%)	216 (91%)	21 (9%)	0	100	100
3	3D	366/504 (73%)	343 (94%)	23 (6%)	0	100	100
4	3E	378/511 (74%)	358 (95%)	20 (5%)	0	100	100
5	3F	353/573 (62%)	334 (95%)	19 (5%)	0	100	100
6	3G	120/126 (95%)	114 (95%)	6 (5%)	0	100	100
6	3H	120/126 (95%)	118 (98%)	2 (2%)	0	100	100
12	AE	751/1769 (42%)	703 (94%)	48 (6%)	0	100	100
15	B1	528/1183 (45%)	481 (91%)	47 (9%)	0	100	100
16	BA	747/923 (81%)	669 (90%)	76 (10%)	2 (0%)	41	77
17	BB	770/943 (82%)	682 (89%)	86 (11%)	2 (0%)	41	77
18	BC	779/817 (95%)	678 (87%)	96 (12%)	5 (1%)	25	66
19	BD	317/594 (53%)	278 (88%)	39 (12%)	0	100	100
20	BE	741/939 (79%)	699 (94%)	42 (6%)	0	100	100
21	CA	190/297 (64%)	180 (95%)	10 (5%)	0	100	100
22	CB	1086/1237 (88%)	1059 (98%)	27 (2%)	0	100	100
23	E1	213/252 (84%)	209 (98%)	4 (2%)	0	100	100
23	E2	210/252 (83%)	204 (97%)	6 (3%)	0	100	100
24	E3	256/483 (53%)	242 (94%)	12 (5%)	2 (1%)	19	60
26	K1	173/316 (55%)	167 (96%)	6 (4%)	0	100	100
27	MA	131/183 (72%)	128 (98%)	3 (2%)	0	100	100
28	MB	182/290 (63%)	168 (92%)	14 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	MC	24/593 (4%)	24 (100%)	0	0	100	100
30	P1	171/274 (62%)	161 (94%)	10 (6%)	0	100	100
31	R1	353/367 (96%)	348 (99%)	5 (1%)	0	100	100
32	R2	266/1729 (15%)	262 (98%)	4 (2%)	0	100	100
35	SC	212/255 (83%)	170 (80%)	37 (18%)	5 (2%)	6	33
36	SF	235/261 (90%)	210 (89%)	24 (10%)	1 (0%)	34	72
37	SG	204/225 (91%)	181 (89%)	21 (10%)	2 (1%)	15	55
38	SH	170/236 (72%)	159 (94%)	11 (6%)	0	100	100
39	SI	161/190 (85%)	142 (88%)	18 (11%)	1 (1%)	25	66
40	SJ	166/200 (83%)	146 (88%)	19 (11%)	1 (1%)	25	66
41	SK	173/197 (88%)	157 (91%)	15 (9%)	1 (1%)	25	66
42	SM	139/156 (89%)	124 (89%)	13 (9%)	2 (1%)	11	46
43	SN	122/143 (85%)	83 (68%)	35 (29%)	4 (3%)	4	26
44	SO	132/151 (87%)	129 (98%)	3 (2%)	0	100	100
45	SP	107/137 (78%)	95 (89%)	12 (11%)	0	100	100
46	SR	123/143 (86%)	113 (92%)	8 (6%)	2 (2%)	9	44
47	SX	127/130 (98%)	115 (91%)	12 (9%)	0	100	100
48	SY	101/145 (70%)	82 (81%)	16 (16%)	3 (3%)	4	28
49	SZ	99/135 (73%)	88 (89%)	11 (11%)	0	100	100
50	Sc	77/82 (94%)	67 (87%)	10 (13%)	0	100	100
51	Sd	61/67 (91%)	57 (93%)	4 (7%)	0	100	100
52	Sf	28/63 (44%)	28 (100%)	0	0	100	100
53	Sg	49/152 (32%)	37 (76%)	12 (24%)	0	100	100
57	U4	124/189 (66%)	115 (93%)	8 (6%)	1 (1%)	19	60
58	U5	246/274 (90%)	229 (93%)	17 (7%)	0	100	100
All	All	12555/19466 (64%)	11579 (92%)	942 (8%)	34 (0%)	44	77

5 of 34 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
18	BC	298	SER
24	E3	306	ALA
35	SC	207	LEU

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Mol	Chain	Res	Type
35	SC	209	ASN
37	SG	50	GLU

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

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	3B	202/240 (84%)	200 (99%)	2 (1%)	76	86
2	3C	202/240 (84%)	202 (100%)	0	100	100
3	3D	317/435 (73%)	315 (99%)	2 (1%)	86	92
4	3E	314/433 (72%)	312 (99%)	2 (1%)	86	92
5	3F	317/503 (63%)	316 (100%)	1 (0%)	92	95
6	3G	101/104 (97%)	100 (99%)	1 (1%)	76	86
6	3H	101/104 (97%)	100 (99%)	1 (1%)	76	86
12	AE	698/744 (94%)	688 (99%)	10 (1%)	67	80
15	B1	471/1039 (45%)	466 (99%)	5 (1%)	73	84
16	BA	663/812 (82%)	653 (98%)	10 (2%)	65	80
17	BB	687/832 (83%)	676 (98%)	11 (2%)	62	79
18	BC	687/719 (96%)	683 (99%)	4 (1%)	86	92
19	BD	281/529 (53%)	277 (99%)	4 (1%)	67	80
20	BE	657/819 (80%)	654 (100%)	3 (0%)	88	93
21	CA	178/274 (65%)	177 (99%)	1 (1%)	86	92
22	CB	1000/1125 (89%)	994 (99%)	6 (1%)	86	92
23	E1	191/222 (86%)	191 (100%)	0	100	100
23	E2	193/222 (87%)	193 (100%)	0	100	100
24	E3	232/424 (55%)	228 (98%)	4 (2%)	60	78
26	K1	158/289 (55%)	158 (100%)	0	100	100
27	MA	123/172 (72%)	121 (98%)	2 (2%)	62	79
28	MB	164/258 (64%)	164 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	MC	24/148 (16%)	24 (100%)	0	100	100
30	P1	151/238 (63%)	150 (99%)	1 (1%)	84	90
31	R1	302/312 (97%)	301 (100%)	1 (0%)	92	95
32	R2	235/1544 (15%)	233 (99%)	2 (1%)	78	87
35	SC	191/224 (85%)	191 (100%)	0	100	100
36	SF	203/222 (91%)	199 (98%)	4 (2%)	55	74
37	SG	173/191 (91%)	171 (99%)	2 (1%)	71	83
38	SH	141/201 (70%)	138 (98%)	3 (2%)	53	72
39	SI	146/170 (86%)	146 (100%)	0	100	100
40	SJ	138/161 (86%)	137 (99%)	1 (1%)	84	90
41	SK	149/166 (90%)	145 (97%)	4 (3%)	44	65
42	SM	128/137 (93%)	123 (96%)	5 (4%)	32	56
43	SN	88/119 (74%)	85 (97%)	3 (3%)	37	60
44	SO	117/128 (91%)	115 (98%)	2 (2%)	60	78
45	SP	66/105 (63%)	66 (100%)	0	100	100
46	SR	105/119 (88%)	103 (98%)	2 (2%)	57	75
47	SX	110/111 (99%)	110 (100%)	0	100	100
48	SY	85/120 (71%)	84 (99%)	1 (1%)	71	83
49	SZ	85/113 (75%)	83 (98%)	2 (2%)	49	69
50	Sc	68/71 (96%)	68 (100%)	0	100	100
51	Sd	56/60 (93%)	53 (95%)	3 (5%)	22	47
52	Sf	27/54 (50%)	27 (100%)	0	100	100
53	Sg	43/135 (32%)	42 (98%)	1 (2%)	50	70
57	U4	110/169 (65%)	110 (100%)	0	100	100
58	U5	231/256 (90%)	229 (99%)	2 (1%)	78	87
All	All	11109/15813 (70%)	11001 (99%)	108 (1%)	77	86

5 of 108 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
22	CB	155	ASN
32	R2	1466	ARG
48	SY	144	ARG

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Mol	Chain	Res	Type
22	CB	216	LYS
24	E3	304	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 149 such sidechains are listed below:

Mol	Chain	Res	Type
32	R2	1661	GLN
57	U4	57	GLN
35	SC	146	GLN
39	SI	147	ASN
17	BB	20	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3A	151/333 (45%)	31 (20%)	1 (0%)
34	SA	1091/1812 (60%)	268 (24%)	22 (2%)
7	5A	452/700 (64%)	102 (22%)	4 (0%)
All	All	1694/2845 (59%)	401 (23%)	27 (1%)

5 of 401 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	3A	9	A
1	3A	14	A
1	3A	15	U
1	3A	22	A
1	3A	24	U

5 of 27 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
34	SA	503	G
34	SA	929	A
34	SA	1441	C
34	SA	913	G
34	SA	1083	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](#)

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.



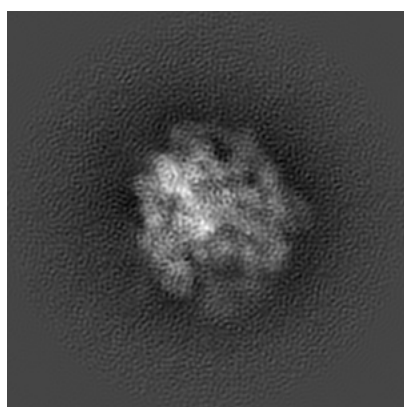
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6695. These allow visual inspection of the internal detail of the map and identification of artifacts.

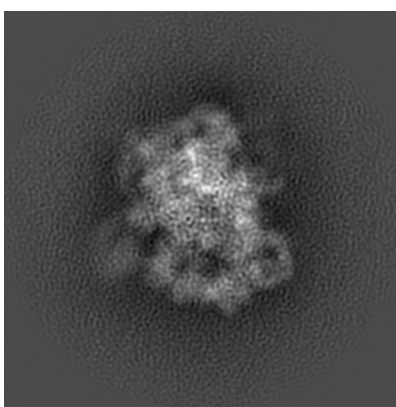
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

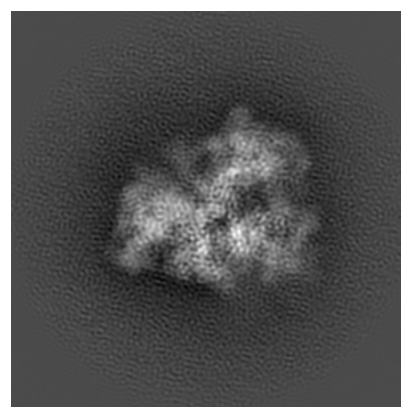
#### 6.1.1 Primary map



X



Y

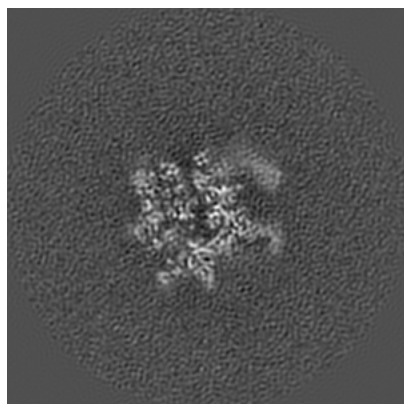


Z

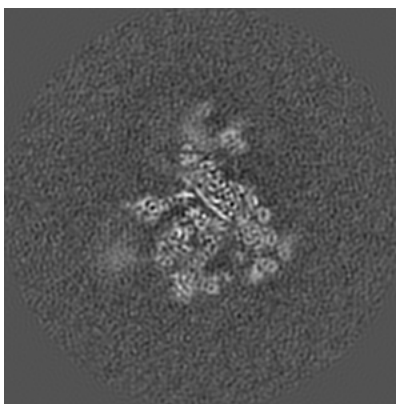
The images above show the map projected in three orthogonal directions.

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

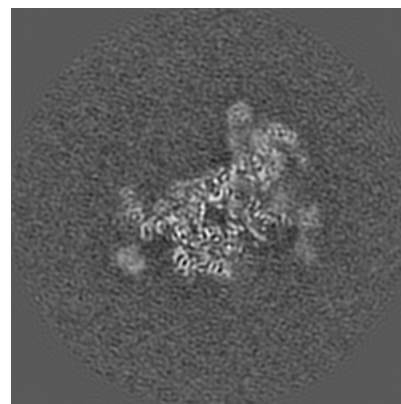
#### 6.2.1 Primary map



X Index: 200



Y Index: 200

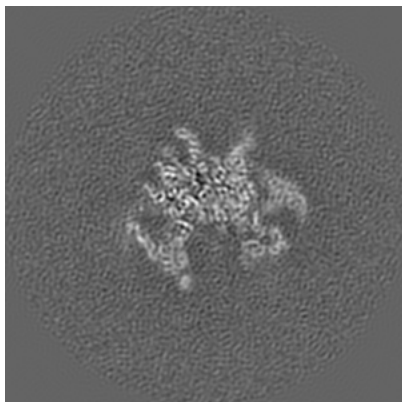


Z Index: 200

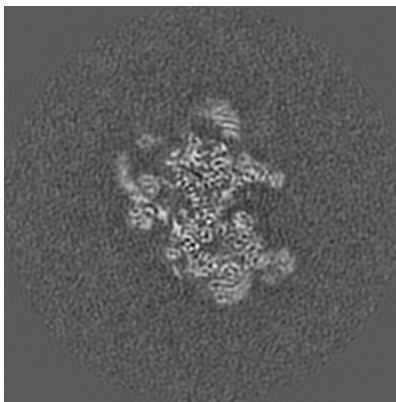
The images above show central slices of the map in three orthogonal directions.

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

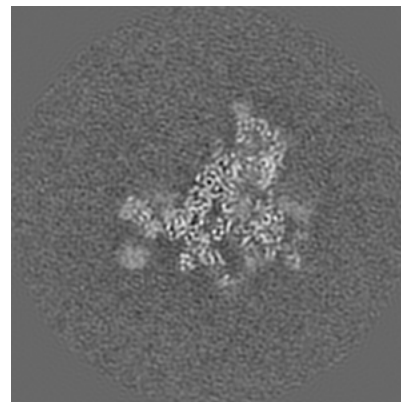
### 6.3.1 Primary map



X Index: 221



Y Index: 178



Z Index: 187

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

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

### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.09. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

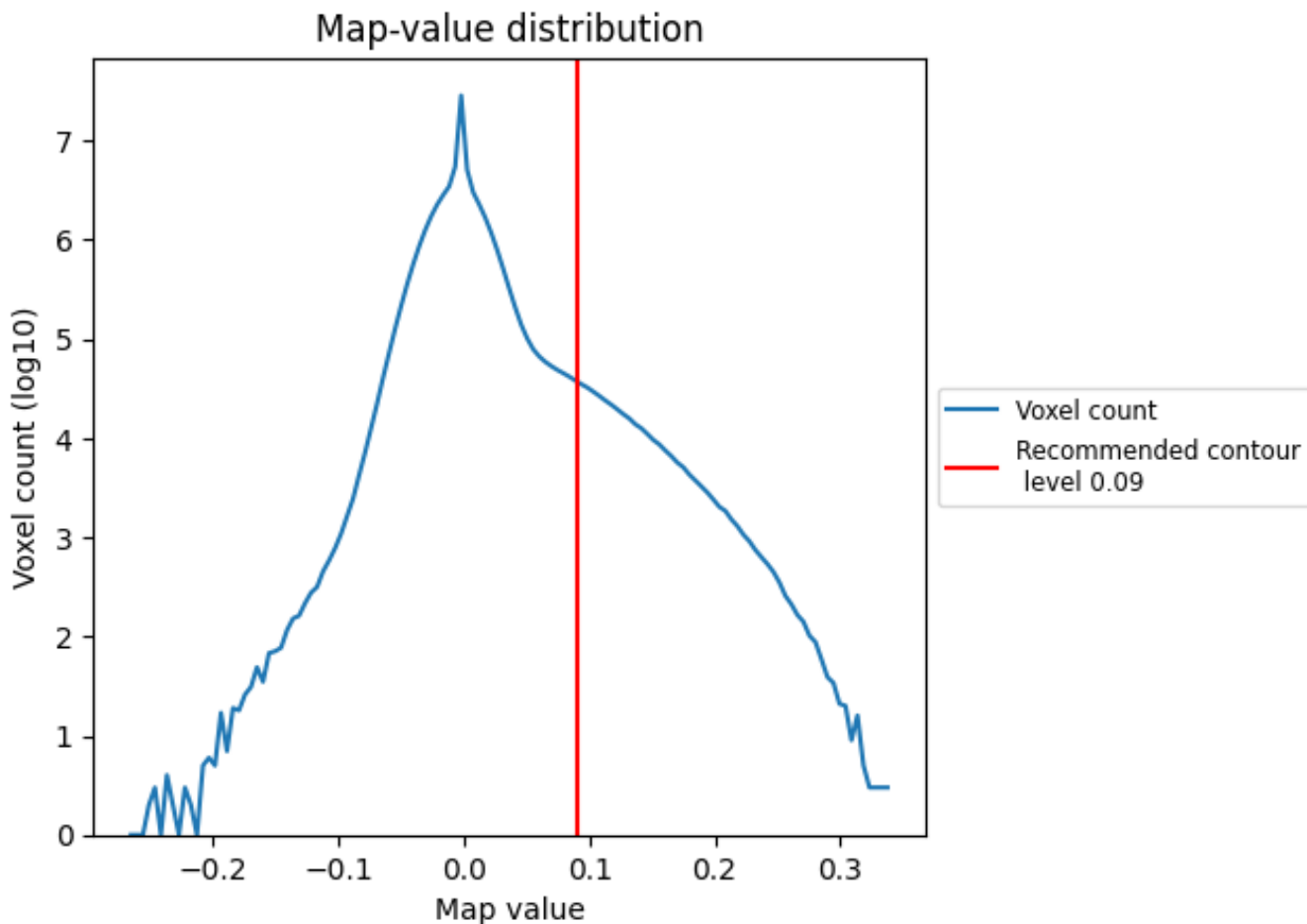
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

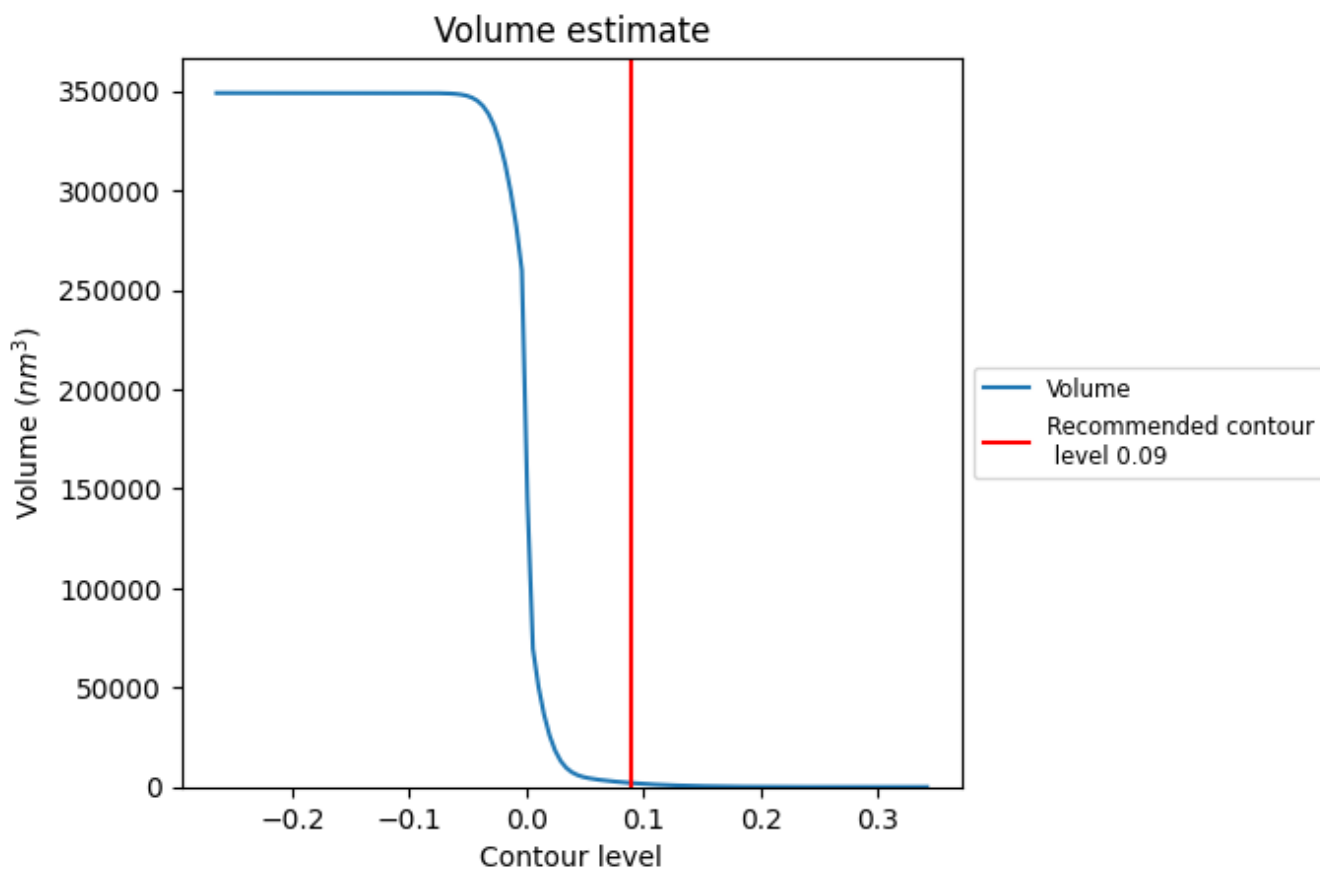
This section contains the results of statistical analysis of the map.

### 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.

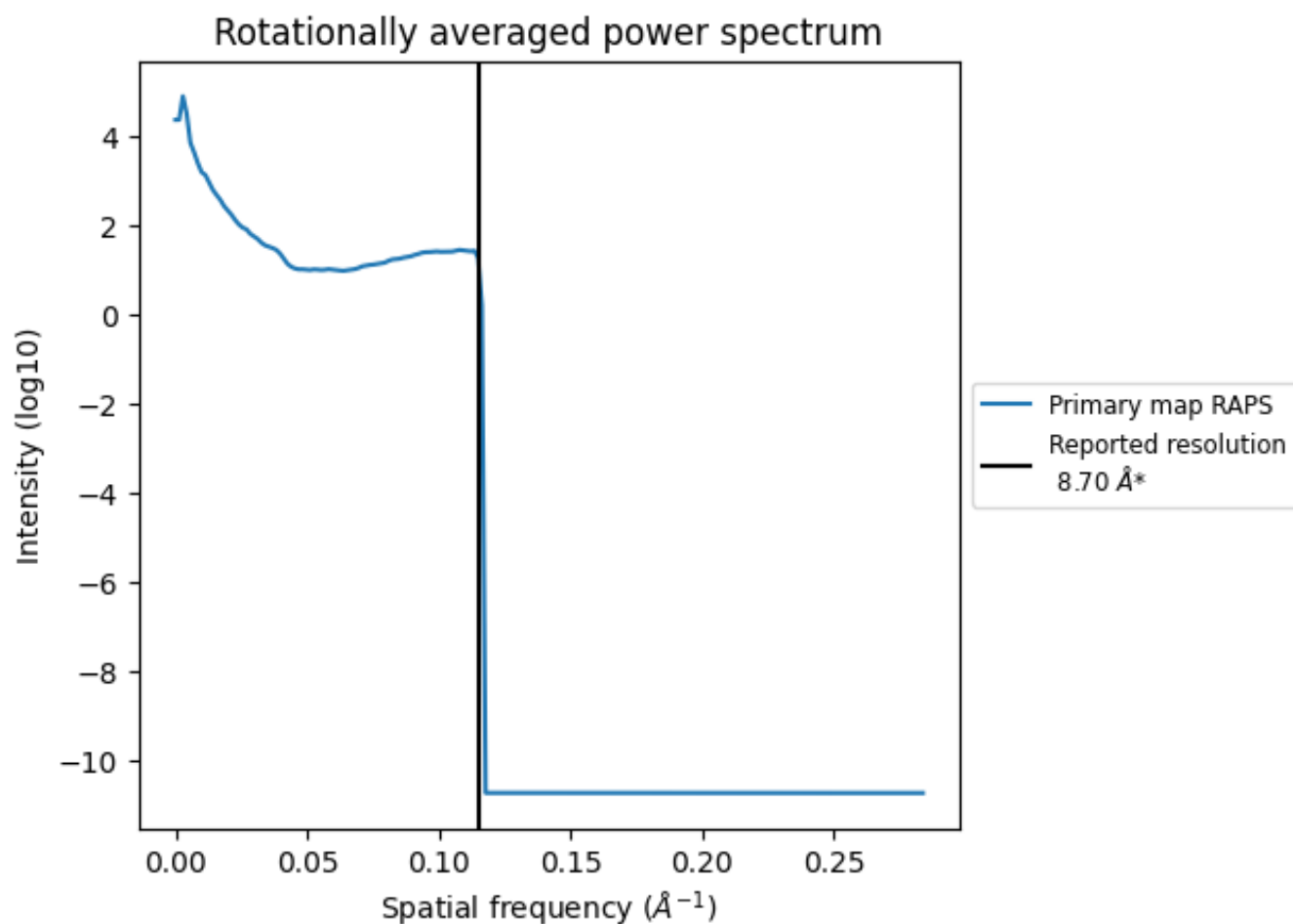
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1973  $\text{nm}^3$ ; this corresponds to an approximate mass of 1782 kDa.

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

### 7.3 Rotationally averaged power spectrum [\(i\)](#)

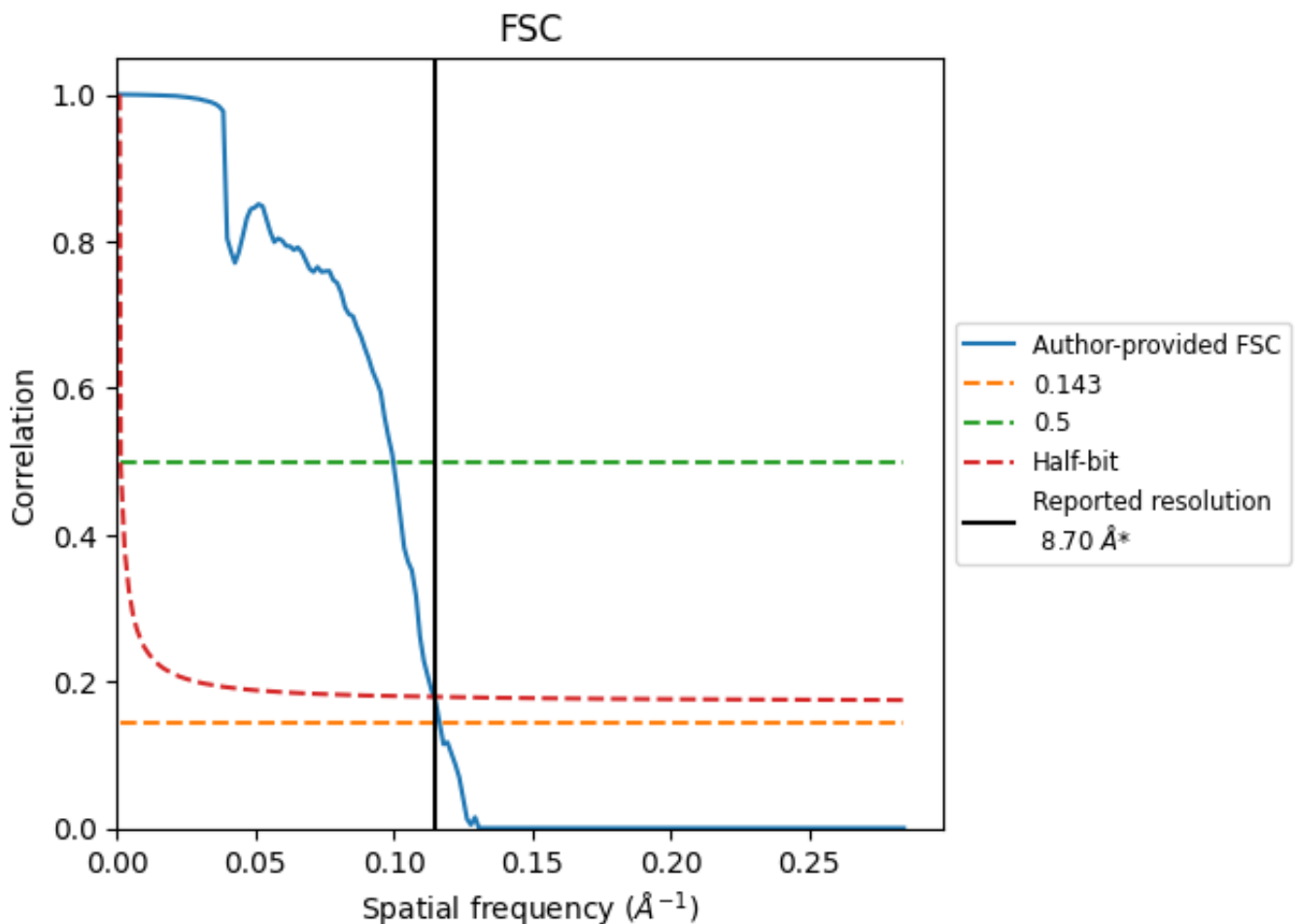


\*Reported resolution corresponds to spatial frequency of 0.115 Å<sup>-1</sup>

## 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 0.115 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	8.70	-	-
Author-provided FSC curve	8.58	10.02	8.74
Unmasked-calculated*	-	-	-

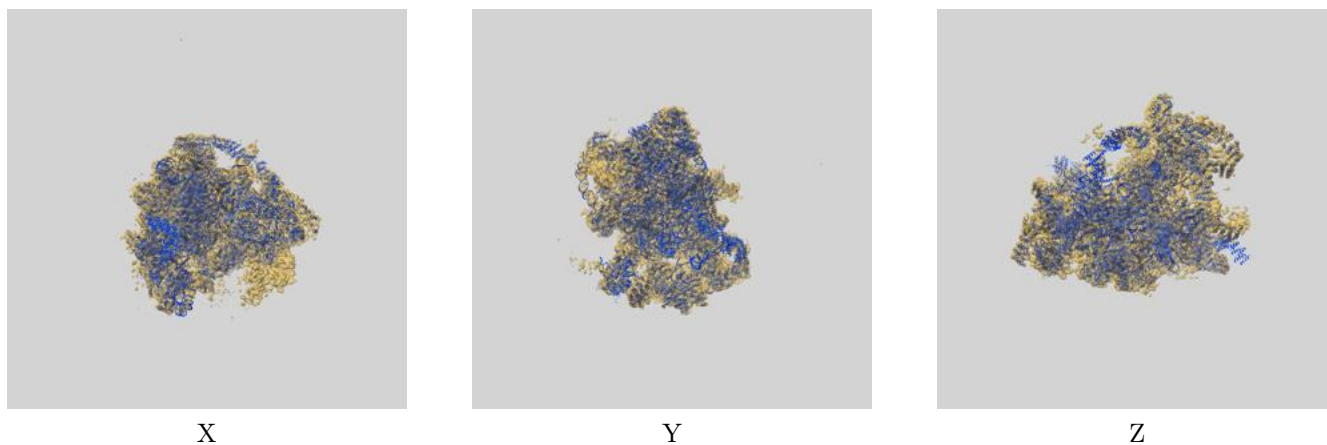
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.



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

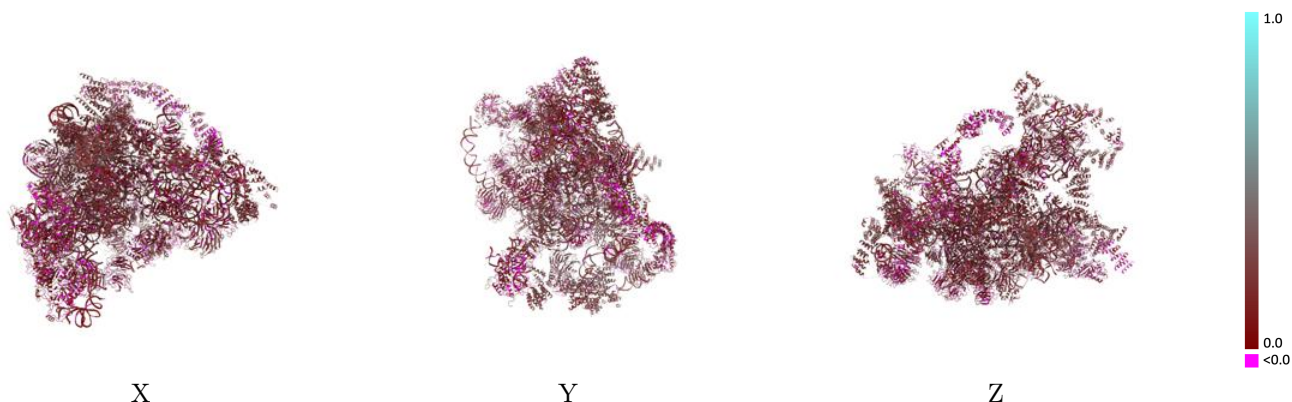
This section contains information regarding the fit between EMDB map EMD-6695 and PDB model 5WYJ. Per-residue inclusion information can be found in section [3](#) on page [15](#).

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



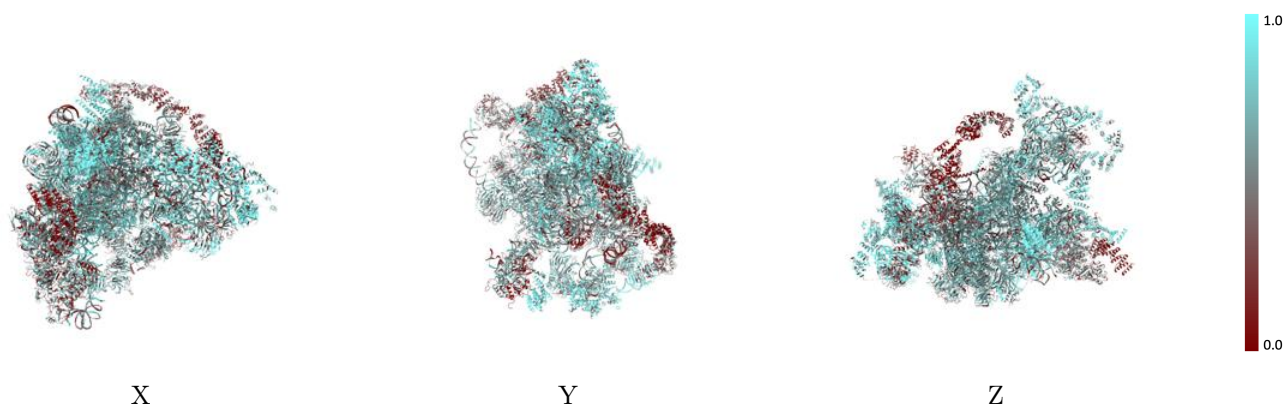
The images above show the 3D surface view of the map at the recommended contour level 0.09 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



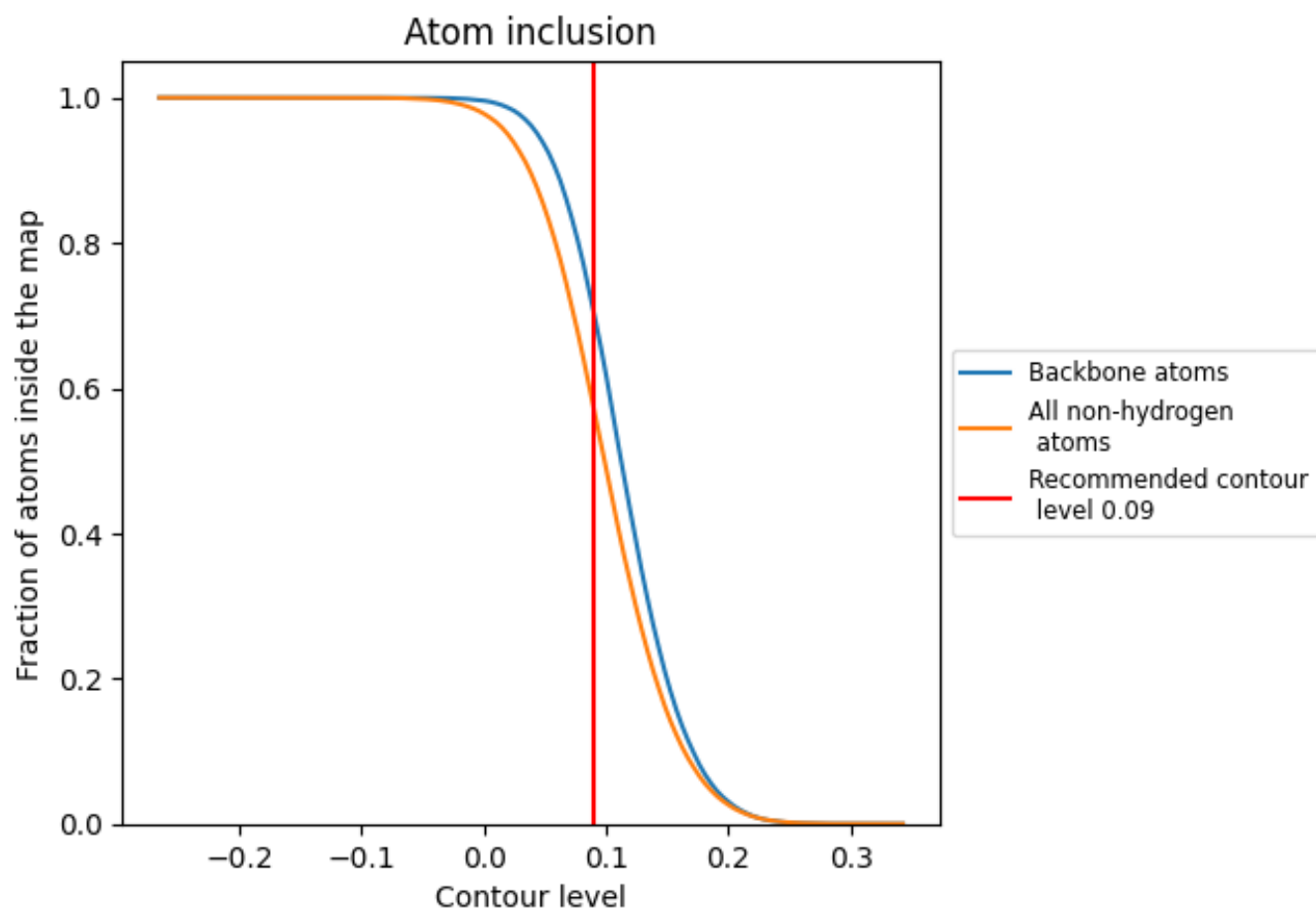
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 70% of all backbone atoms, 57% 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	 0.5717	 0.1600
3A	 0.7484	 0.1830
3B	 0.5458	 0.1630
3C	 0.3769	 0.1290
3D	 0.5854	 0.1550
3E	 0.5061	 0.1500
3F	 0.5810	 0.1410
3G	 0.5822	 0.1580
3H	 0.5548	 0.1590
5A	 0.4966	 0.1750
AA	 0.7525	 0.2230
AB	 0.6864	 0.1990
AC	 0.5123	 0.1480
AD	 0.7386	 0.2190
AE	 0.3774	 0.1220
AF	 0.8144	 0.2410
AG	 0.6980	 0.2000
B1	 0.5596	 0.1420
BA	 0.5864	 0.1550
BB	 0.5861	 0.1320
BC	 0.4752	 0.1160
BD	 0.5207	 0.1110
BE	 0.5976	 0.1430
CA	 0.3852	 0.1130
CB	 0.4158	 0.1210
E1	 0.4618	 0.1290
E2	 0.4841	 0.1330
E3	 0.4816	 0.1220
E4	 0.6484	 0.2180
K1	 0.4877	 0.1450
MA	 0.6006	 0.1550
MB	 0.5297	 0.1350
MC	 0.7115	 0.2100
P1	 0.5508	 0.1530
R1	 0.5599	 0.1470



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Chain	Atom inclusion	Q-score
R2	 0.0516	 0.1040
S1	 0.7818	 0.2440
SA	 0.7164	 0.1710
SC	 0.4735	 0.1580
SF	 0.5003	 0.1300
SG	 0.5640	 0.1610
SH	 0.3787	 0.1150
SI	 0.4751	 0.1500
SJ	 0.4862	 0.1320
SK	 0.5275	 0.1470
SM	 0.4038	 0.1150
SN	 0.0693	 0.0710
SO	 0.5171	 0.1480
SP	 0.5062	 0.1440
SR	 0.5839	 0.1490
SX	 0.5150	 0.1580
SY	 0.5013	 0.1190
SZ	 0.5134	 0.1450
Sc	 0.4317	 0.1560
Sd	 0.5178	 0.1400
Sf	 0.6432	 0.1490
Sg	 0.0181	 0.0120
U1	 0.8204	 0.2560
U2	 0.9068	 0.2620
U3	 0.7750	 0.2360
U4	 0.5397	 0.1660
U5	 0.1585	 0.1000
UA	 0.9189	 0.2650
UB	 0.8288	 0.2540
UC	 0.8200	 0.2700