



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 11:48 PM UTC

PDB ID : 5JPQ / pdb_00005jpq
EMDB ID : EMD-8143
Title : Cryo-EM structure of the 90S pre-ribosome
Authors : Turk, M.; Cheng, J.; Berninghausen, O.; Kornprobst, M.; Flemming, D.; Kos-Braun, I.C.; Kos, M.; Thoms, M.; Hurt, E.; Beckmann, R.
Deposited on : 2016-05-04
Resolution : 7.30 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

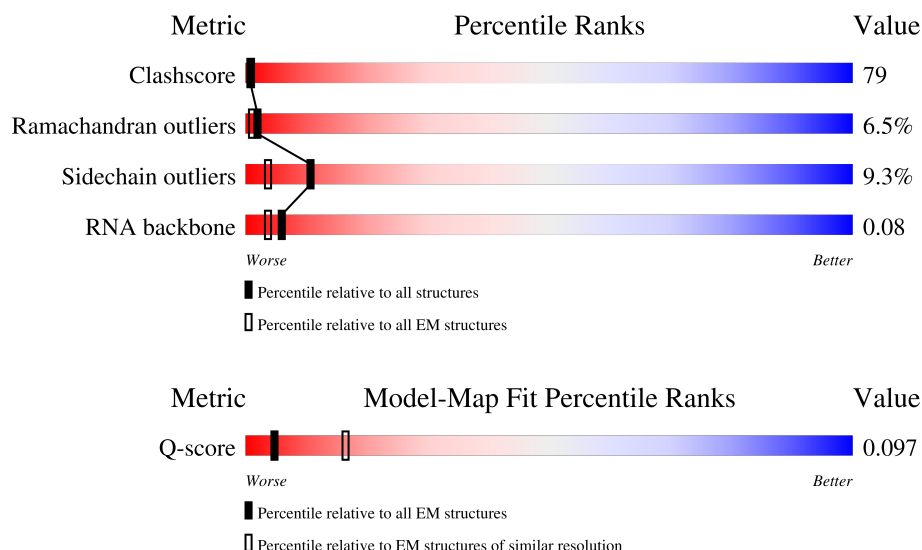
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 7.30 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	436 (6.80 - 7.80)

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	A	1290	8% 22% 77%
1	B	1290	9% 21% 77%
1	C	1290	11% 21% 77%

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Mol	Chain	Length	Quality of chain
1	D	1290	
1	E	1290	
1	F	1290	
1	J	1290	
1	K	1290	
1	L	1290	
1	N	1290	
1	P	1290	
1	l	1290	
1	n	1290	
2	G	1802	
3	H	920	
4	I	939	
5	M	870	
5	O	870	
5	m	870	
6	Q	456	
7	R	560	
8	S	412	
8	T	412	
9	U	130	
9	V	130	
10	W	232	
10	X	232	
11	Y	573	

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Mol	Chain	Length	Quality of chain
12	Z	367	
13	a	1183	
14	b	183	
15	c	297	
16	d	184	
17	e	252	
17	f	252	
18	g	322	
18	h	322	
19	i	1073	
19	j	1073	
20	k	391	
21	o	265	
22	p	259	
23	q	225	
24	r	293	
25	s	197	
26	t	208	
27	u	197	
28	v	151	
29	w	137	
30	x	143	
31	y	157	
32	z	130	
33	0	149	

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Mol	Chain	Length	Quality of chain
34	1	67	40% 34% 25% 10%
35	2	1800	9% 11% 34% 53%
36	3	274	15% 28% 28% 40%

2 Entry composition

There are 36 unique types of molecules in this entry. The entry contains 95839 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called WD40 domain proteins.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	300	Total	C	N	O	0	0
			1500	900	300	300		
1	B	300	Total	C	N	O	0	0
			1500	900	300	300		
1	C	300	Total	C	N	O	0	0
			1500	900	300	300		
1	D	300	Total	C	N	O	0	0
			1500	900	300	300		
1	E	300	Total	C	N	O	0	0
			1500	900	300	300		
1	F	300	Total	C	N	O	0	0
			1500	900	300	300		
1	J	300	Total	C	N	O	0	0
			1500	900	300	300		
1	K	300	Total	C	N	O	0	0
			1500	900	300	300		
1	L	300	Total	C	N	O	0	0
			1500	900	300	300		
1	N	300	Total	C	N	O	0	0
			1500	900	300	300		
1	P	300	Total	C	N	O	0	0
			1500	900	300	300		
1	l	300	Total	C	N	O	0	0
			1500	900	300	300		
1	n	300	Total	C	N	O	0	0
			1500	900	300	300		

- Molecule 2 is a protein called UTP10.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	G	283	Total	C	N	O	0	0
			1402	836	283	283		

- Molecule 3 is a protein called UTP-A oligomerization domain.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	H	343	Total	C	N	O	0	0
			1715	1029	343	343		

- Molecule 4 is a protein called U3 small nucleolar RNA-associated protein 21.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	I	634	Total	C	N	O	0	0
			3124	1856	634	634		

- Molecule 5 is a protein called WD40 domain proteins.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	M	309	Total	C	N	O	0	0
			1545	927	309	309		
5	O	309	Total	C	N	O	0	0
			1545	927	309	309		
5	m	309	Total	C	N	O	0	0
			1545	927	309	309		

- Molecule 6 is a protein called UTP6.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	Q	375	Total	C	N	O	0	0
			1875	1125	375	375		

- Molecule 7 is a protein called UTP-B oligomerisation domain.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	R	332	Total	C	N	O	0	0
			1660	996	332	332		

- Molecule 8 is a protein called Pre mRNA splicing protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	S	367	Total	C	N	O	0	0
			1815	1081	367	367		
8	T	367	Total	C	N	O	0	0
			1815	1081	367	367		

- Molecule 9 is a protein called Snu13.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	U	122	Total	C	N	O	0	0
			603	359	122	122		
9	V	122	Total	C	N	O	0	0
			603	359	122	122		

- Molecule 10 is a protein called Nop1.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	W	227	Total	C	N	O	0	0
			1124	670	227	227		
10	X	227	Total	C	N	O	0	0
			1124	670	227	227		

- Molecule 11 is a protein called rrp9.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	Y	365	Total	C	N	O	0	0
			1799	1069	365	365		

- Molecule 12 is a protein called Rcl1.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	Z	355	Total	C	N	O	0	0
			1742	1032	355	355		

- Molecule 13 is a protein called Bms1.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	a	54	Total	C	N	O	0	0
			267	160	54	53		

- Molecule 14 is a protein called Imp3.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	b	153	Total	C	N	O	0	0
			760	454	153	153		

- Molecule 15 is a protein called Putative U3 small nucleolar ribonucleoprotein.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	c	192	Total	C	N	O	0	0
			951	567	192	192		

- Molecule 16 is a protein called Utp24.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	d	124	Total	C	N	O	0	0
			616	368	124	124		

- Molecule 17 is a protein called Emg1.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	e	211	Total	C	N	O	0	0
			1047	625	211	211		
17	f	218	Total	C	N	O	0	0
			1081	645	218	218		

- Molecule 18 is a protein called KRR1 small subunit processome component.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	g	174	Total	C	N	O	0	0
			861	513	174	174		
18	h	174	Total	C	N	O	0	0
			861	513	174	174		

- Molecule 19 is a protein called Kre33.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	i	659	Total	C	N	O	0	0
			3254	1936	659	659		
19	j	677	Total	C	N	O	0	0
			3342	1988	677	677		

- Molecule 20 is a protein called Utp30.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	k	182	Total	C	N	O	0	0
			905	541	182	182		

- Molecule 21 is a protein called eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	o	215	Total	C	N	O	S	0	0
			1724	1090	314	316	4		

- Molecule 22 is a protein called eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	p	259	Total	C	N	O	S	0	0
			2079	1322	383	370	4		

- Molecule 23 is a protein called uS7.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	q	169	Total	C	N	O	0	0
			836	498	169	169		

- Molecule 24 is a protein called eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	r	235	Total	C	N	O	S	0	0
			1868	1184	347	326	11		

- Molecule 25 is a protein called eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	s	186	Total	C	N	O	S	0	0
			1539	989	271	278	1		

- Molecule 26 is a protein called eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	t	207	Total	C	N	O	S	0	0
			1693	1057	336	296	4		

- Molecule 27 is a protein called uS4.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	u	157	Total	C	N	O	0	0
			777	463	157	157		

- Molecule 28 is a protein called uS15.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	v	117	Total	C	N	O	0	0
			580	346	117	117		

- Molecule 29 is a protein called uS11.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	w	128	Total	C	N	O	0	0
			627	371	128	128		

- Molecule 30 is a protein called uS9.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	x	134	Total	C	N	O	0	0
			658	390	134	134		

- Molecule 31 is a protein called uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	y	157	Total	C	N	O	S	0	0
			1275	818	235	217	5		

- Molecule 32 is a protein called uS8.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	z	127	Total	C	N	O	0	0
			622	368	127	127		

- Molecule 33 is a protein called eS24.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	0	148	Total	C	N	O	0	0
			1197	763	221	213		

- Molecule 34 is a protein called eS28.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	1	47	Total	C	N	O	0	0
			230	136	47	47		

- Molecule 35 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	2	852	Total	C	N	O	P	0	0
			18149	8120	3229	5948	852		

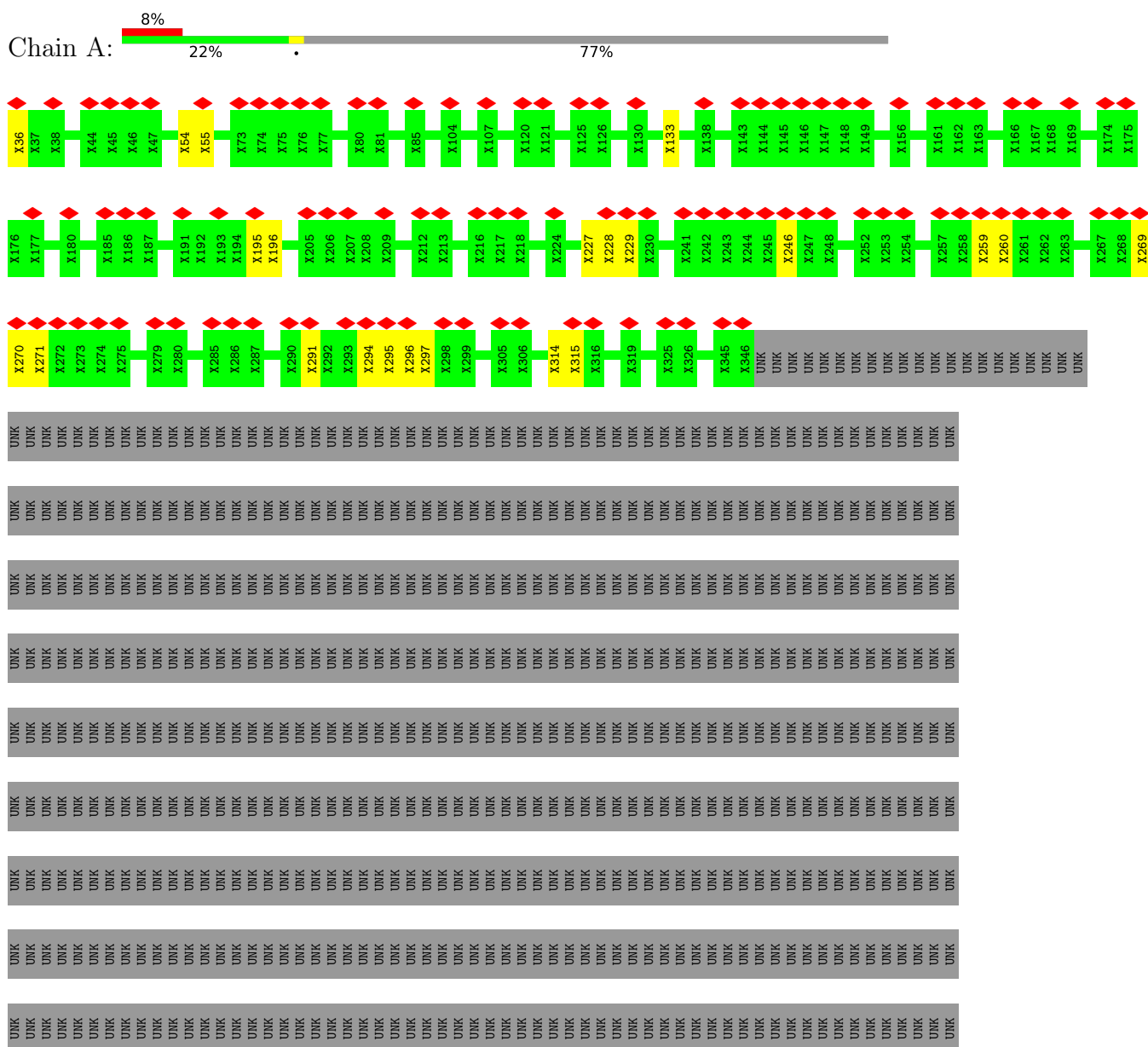
- Molecule 36 is a RNA chain called U3 RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
36	3	164	3504	1560	626	1154	164	0	0

3 Residue-property plots

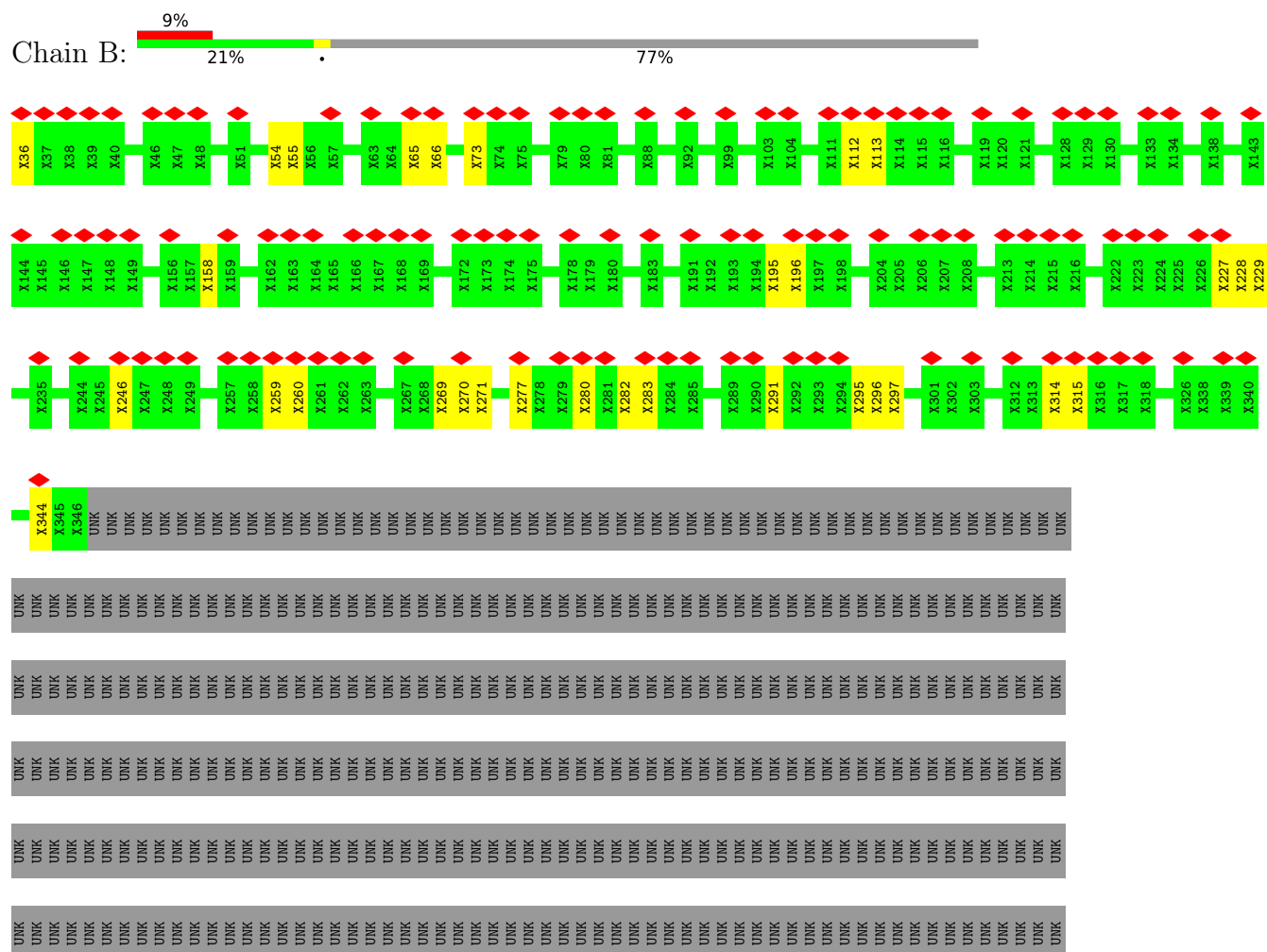
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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.

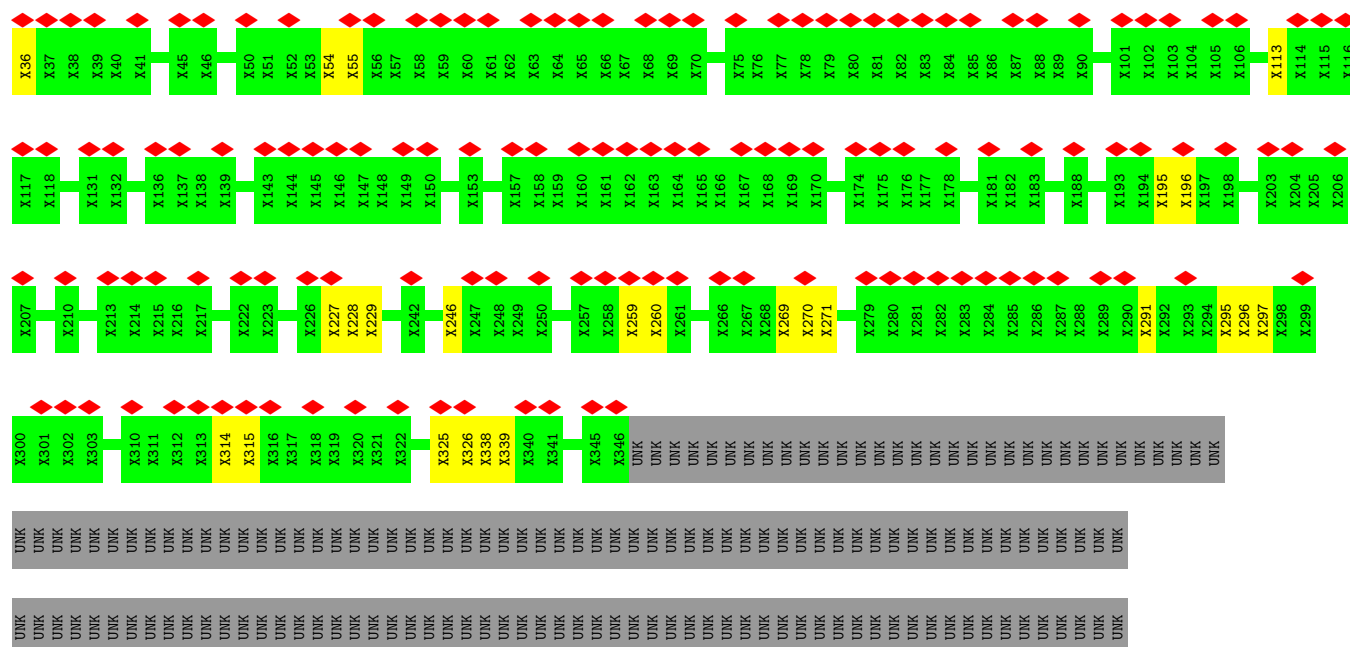
- Molecule 1: WD40 domain proteins



[illegible]

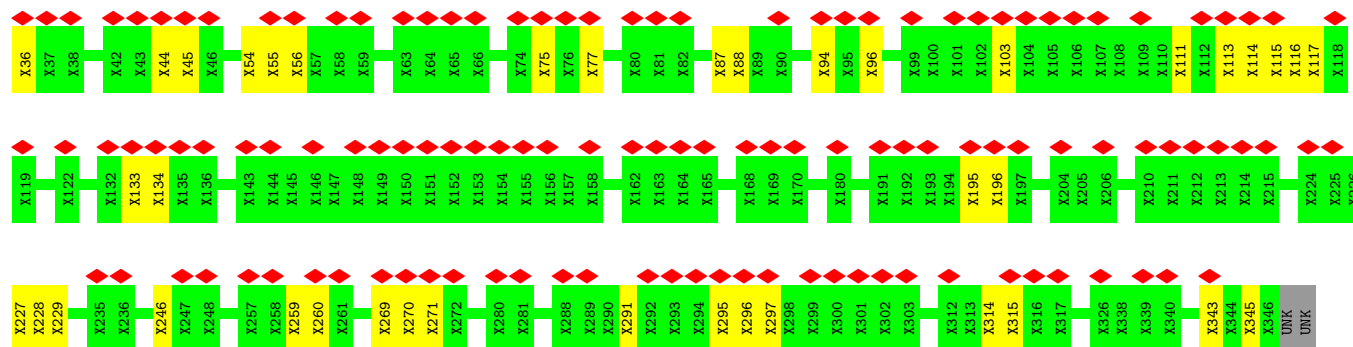
- Molecule 1: WD40 domain proteins





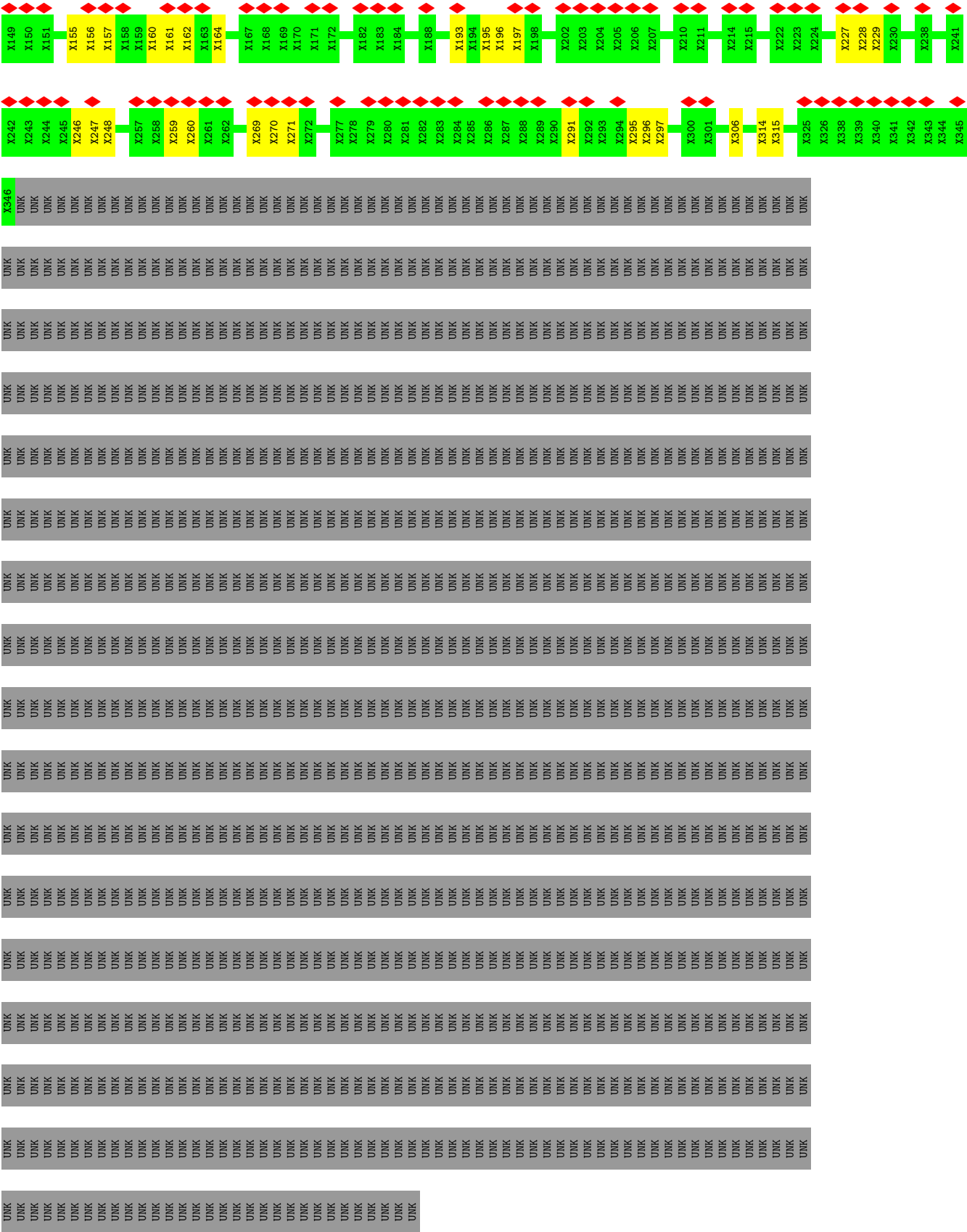
[illegible]

- Molecule 1: WD40 domain proteins



- Molecule 1: WD40 domain proteins

Category	Item Count
X36	1
X43	1
X44	1
X45	1
X46	1
X47	1
X54	1
X55	1
X56	1
X63	1
X68	1
X73	1
X74	1
X75	1
X79	1
X80	1
X92	1
X93	1
X94	1
X95	1
X96	1
X103	1
X104	1
X105	1
X106	1
X107	1
X113	1
X114	1
X115	1
X116	1
X117	1
X118	1
X121	1
X122	1
X130	1
X131	1
X132	1
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X137	1
X138	1
X139	1
X143	1
X144	1
X145	1



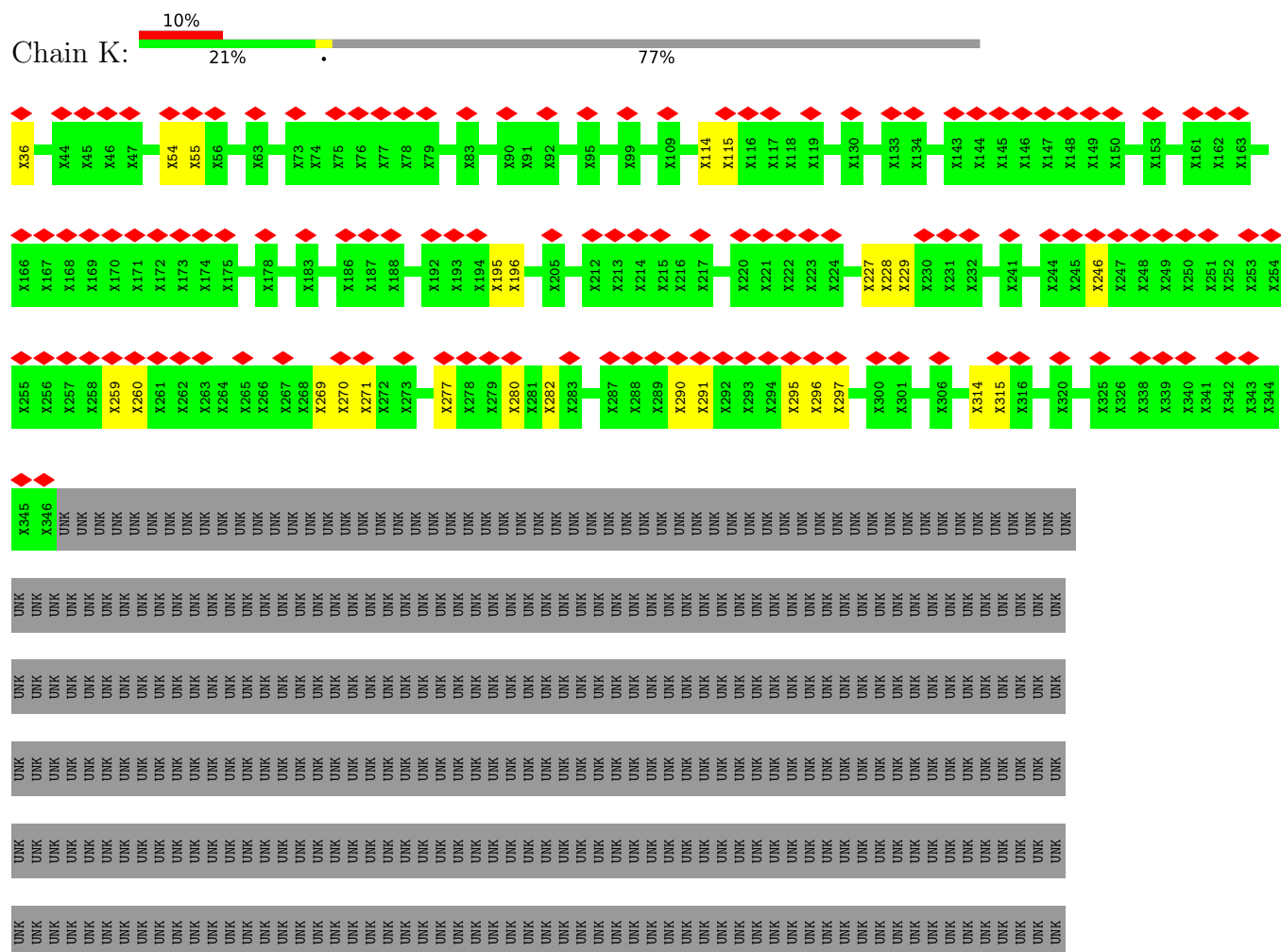
● Molecule 1: WD40 domain proteins

- Molecule 1: WD40 domain proteins



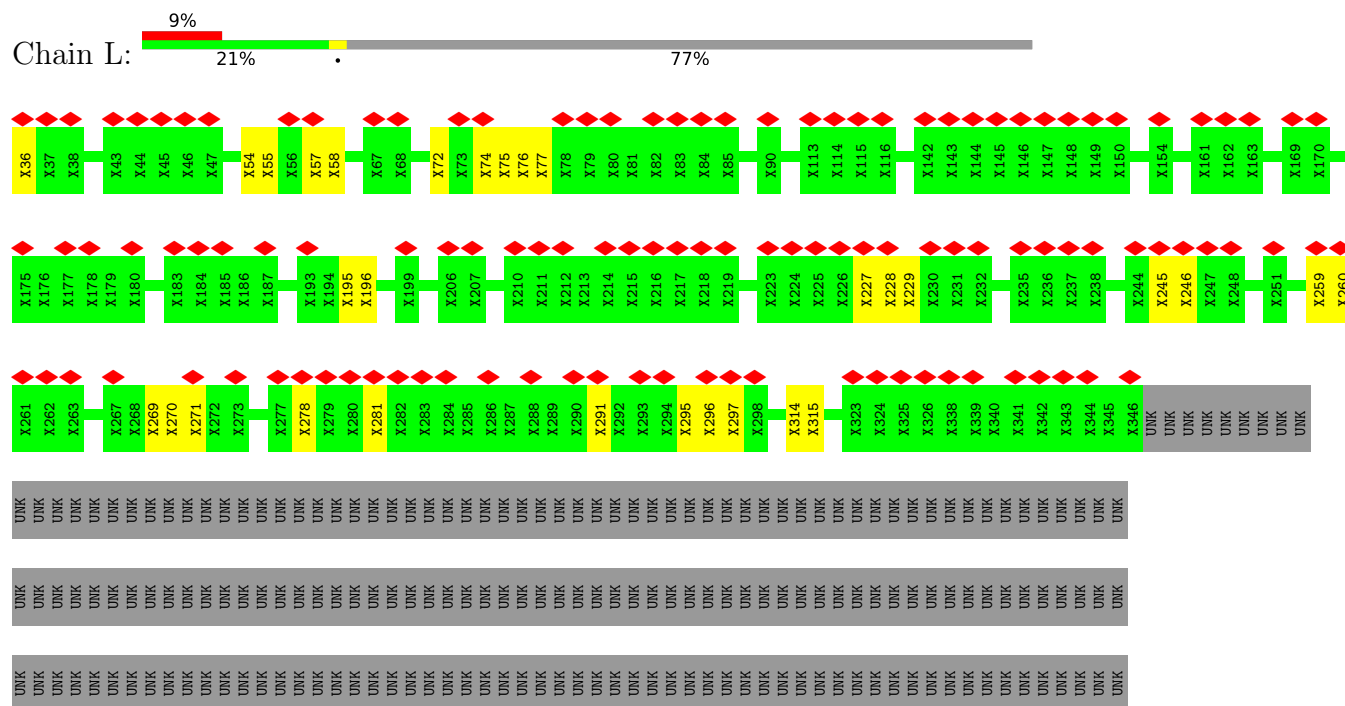
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- Molecule 1: WD40 domain proteins

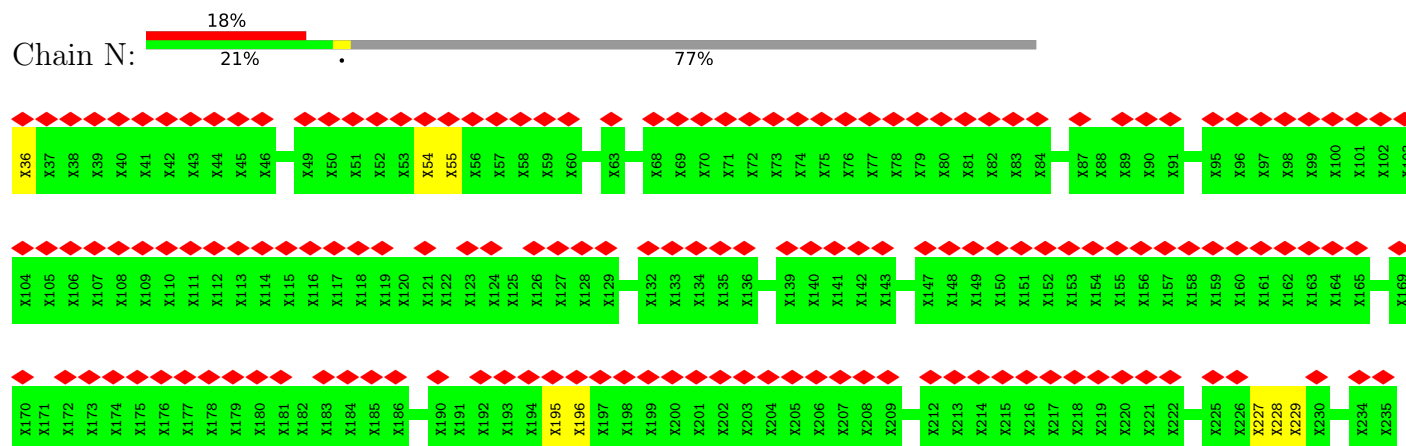


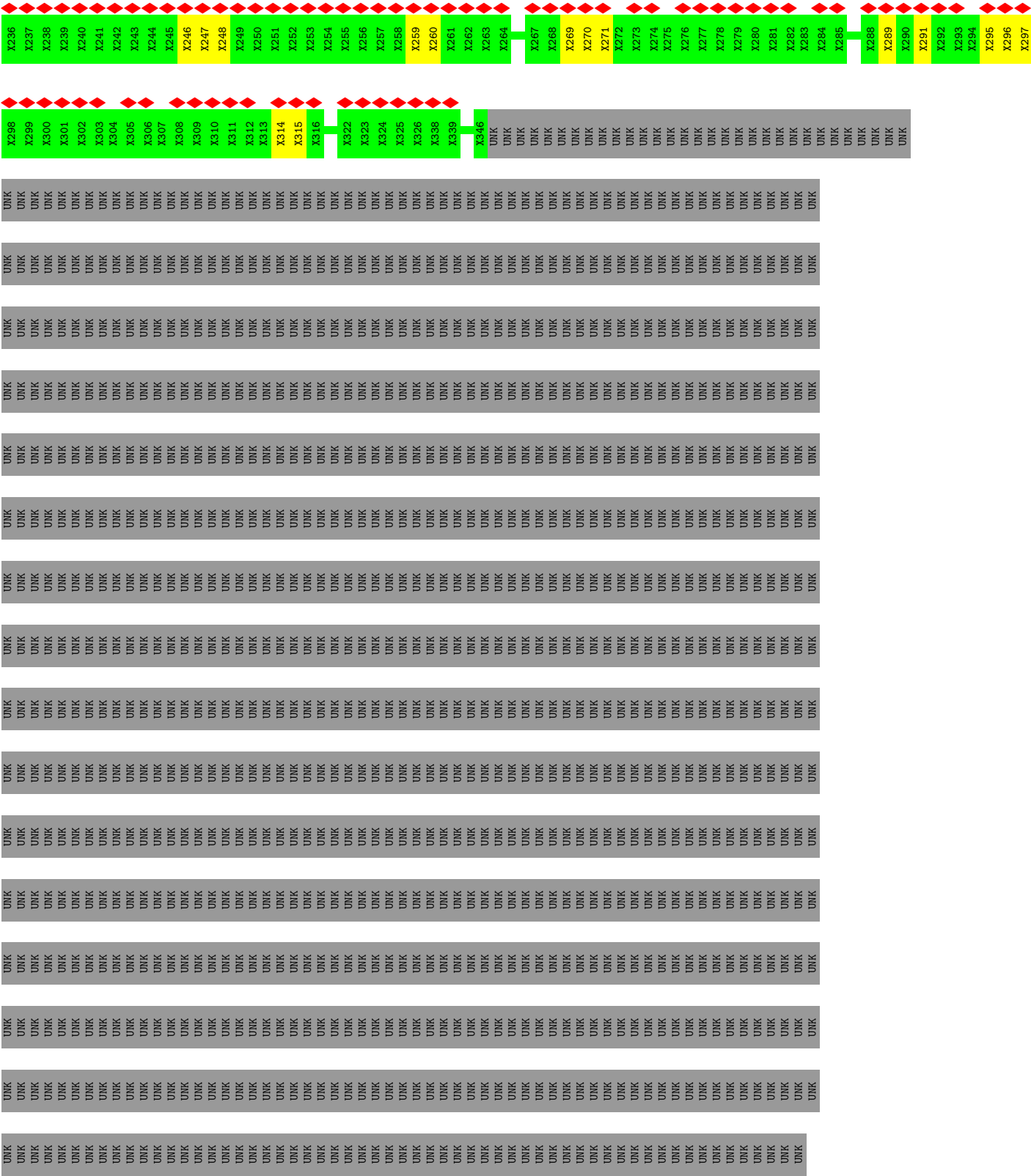
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- Molecule 1: WD40 domain proteins



- Molecule 1: WD40 domain proteins



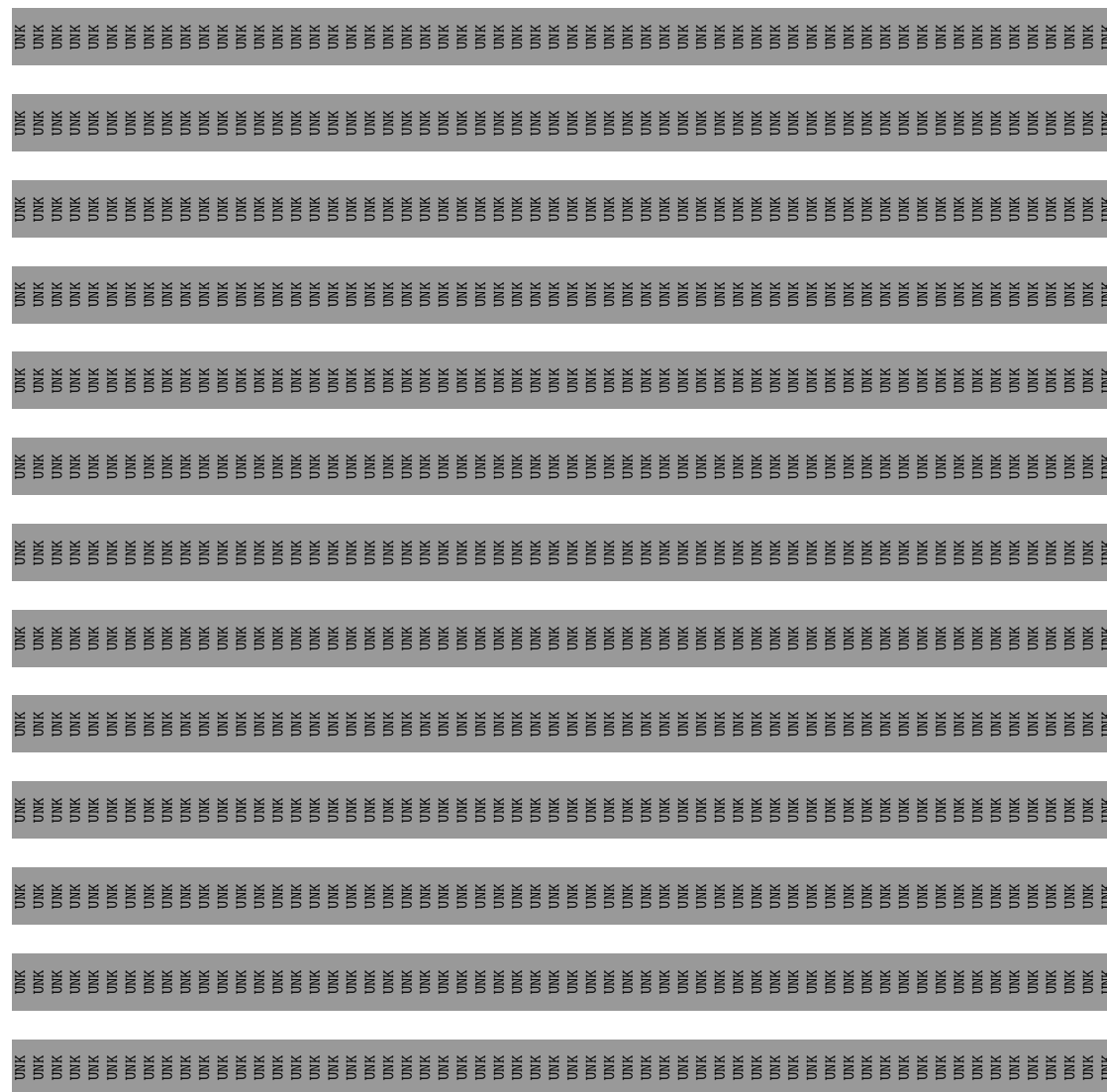


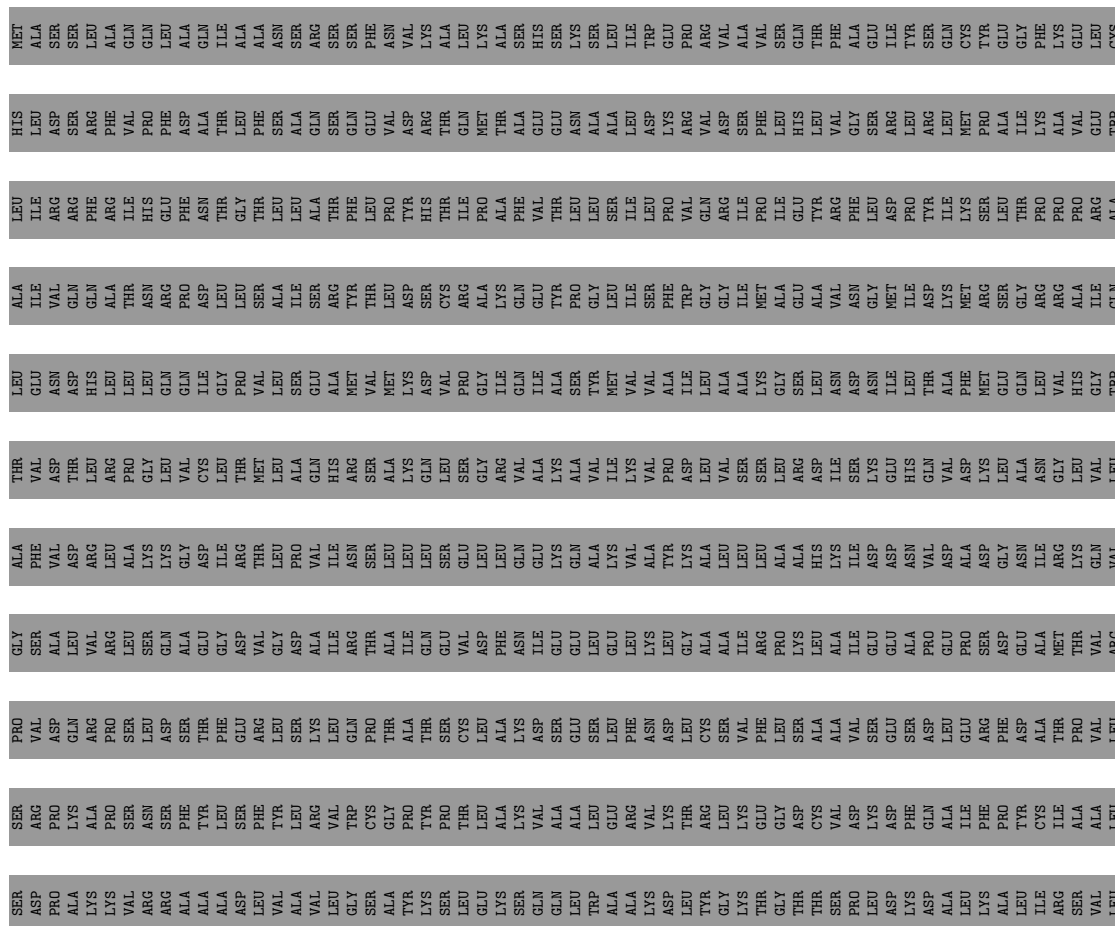
● Molecule 1: WD40 domain proteins





- Molecule 1: WD40 domain proteins

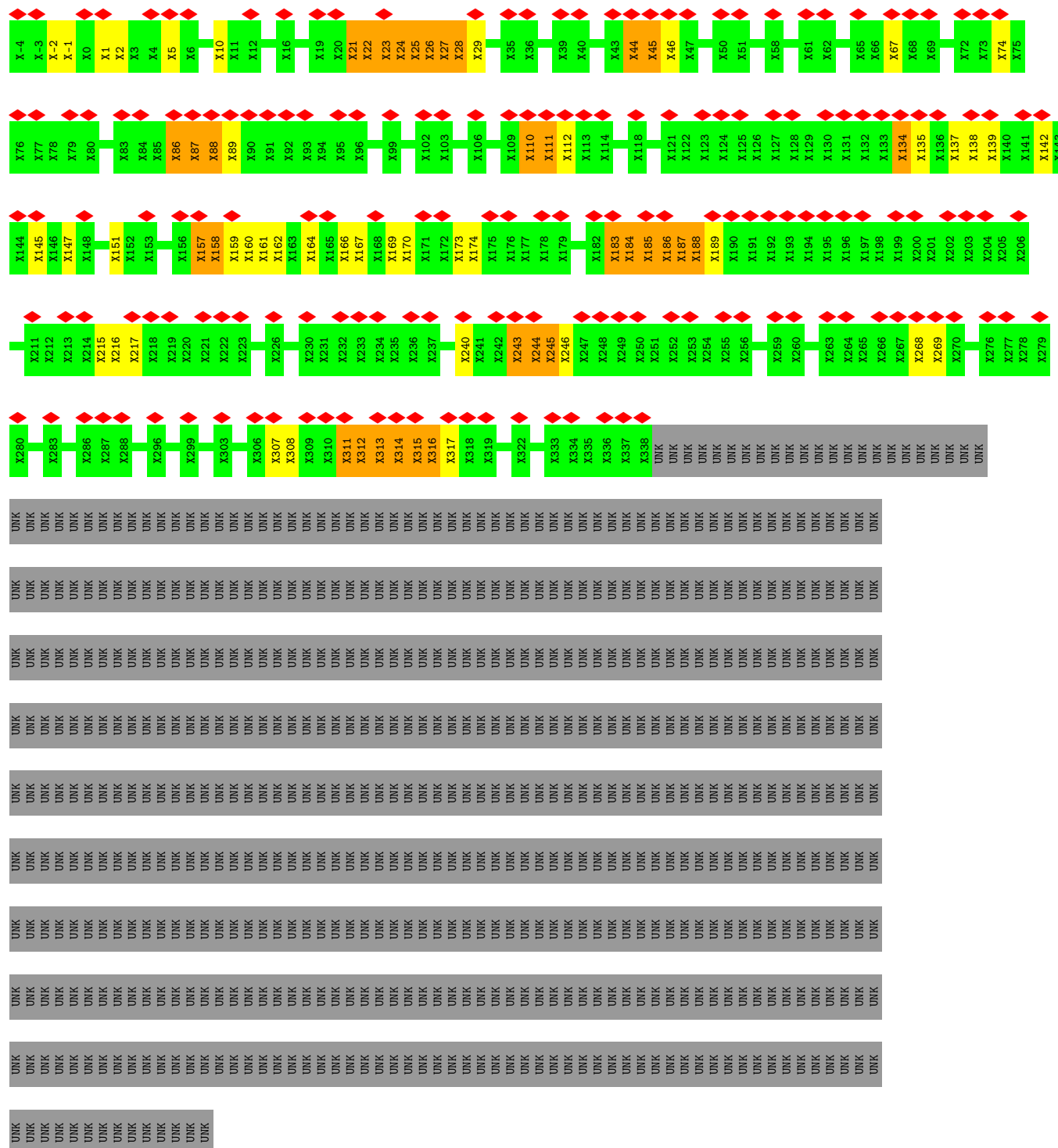




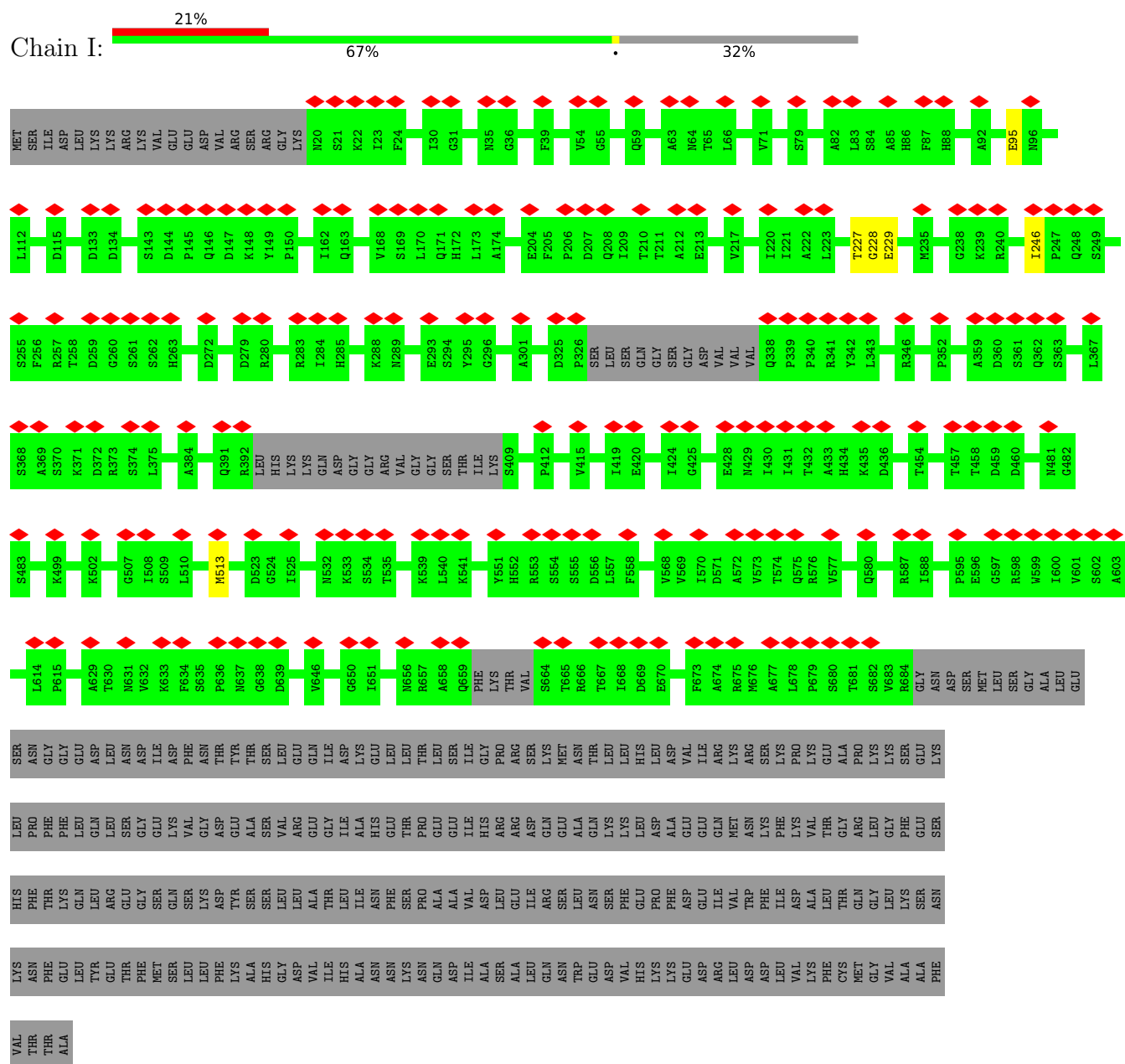




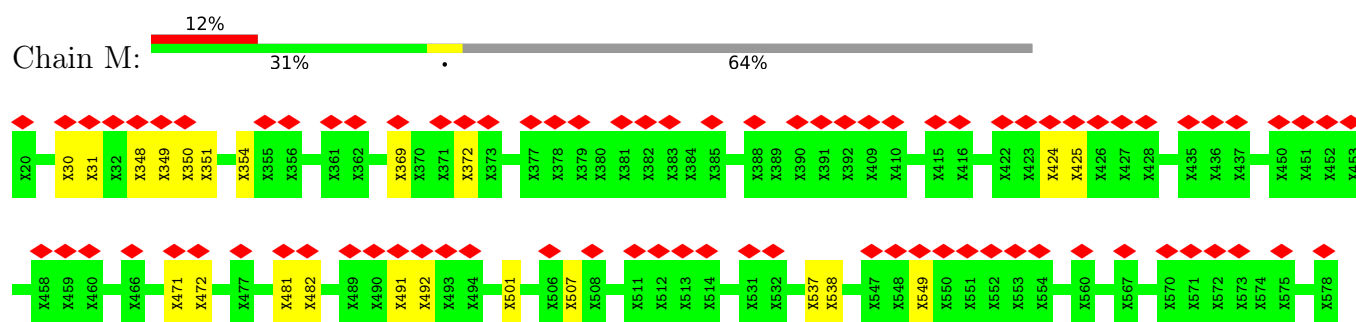
• Molecule 3: UTP-A oligomerization domain



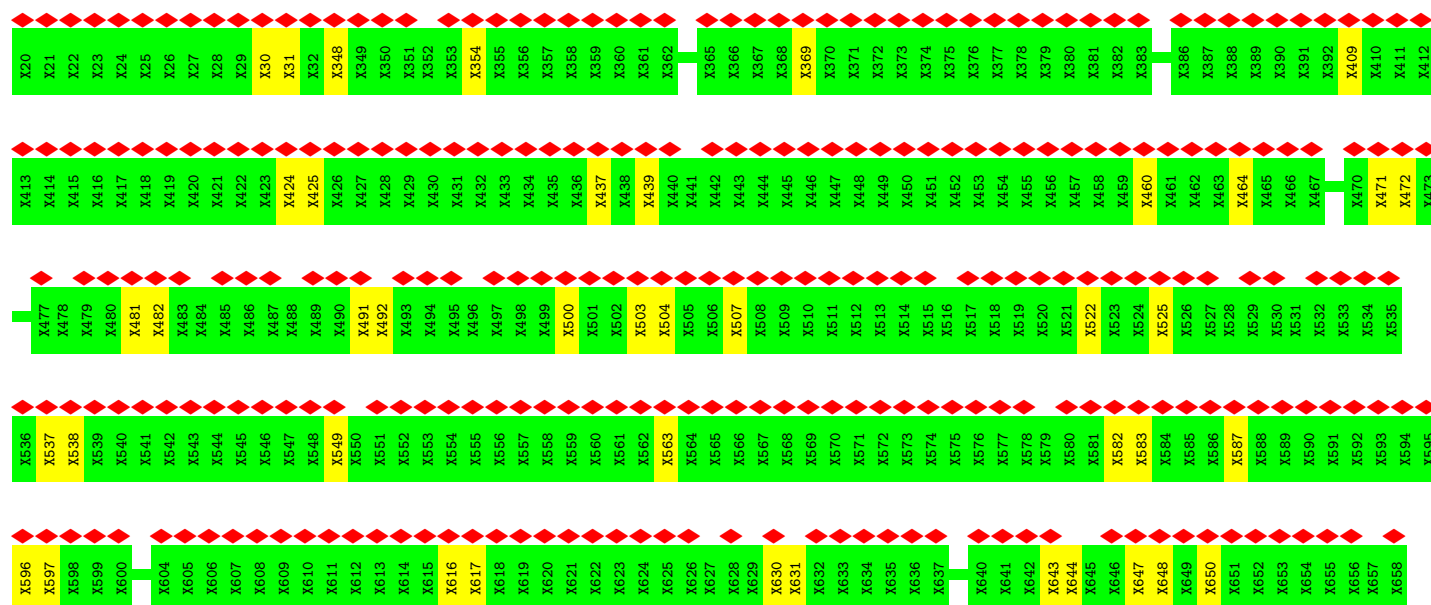
- Molecule 4: U3 small nucleolar RNA-associated protein 21

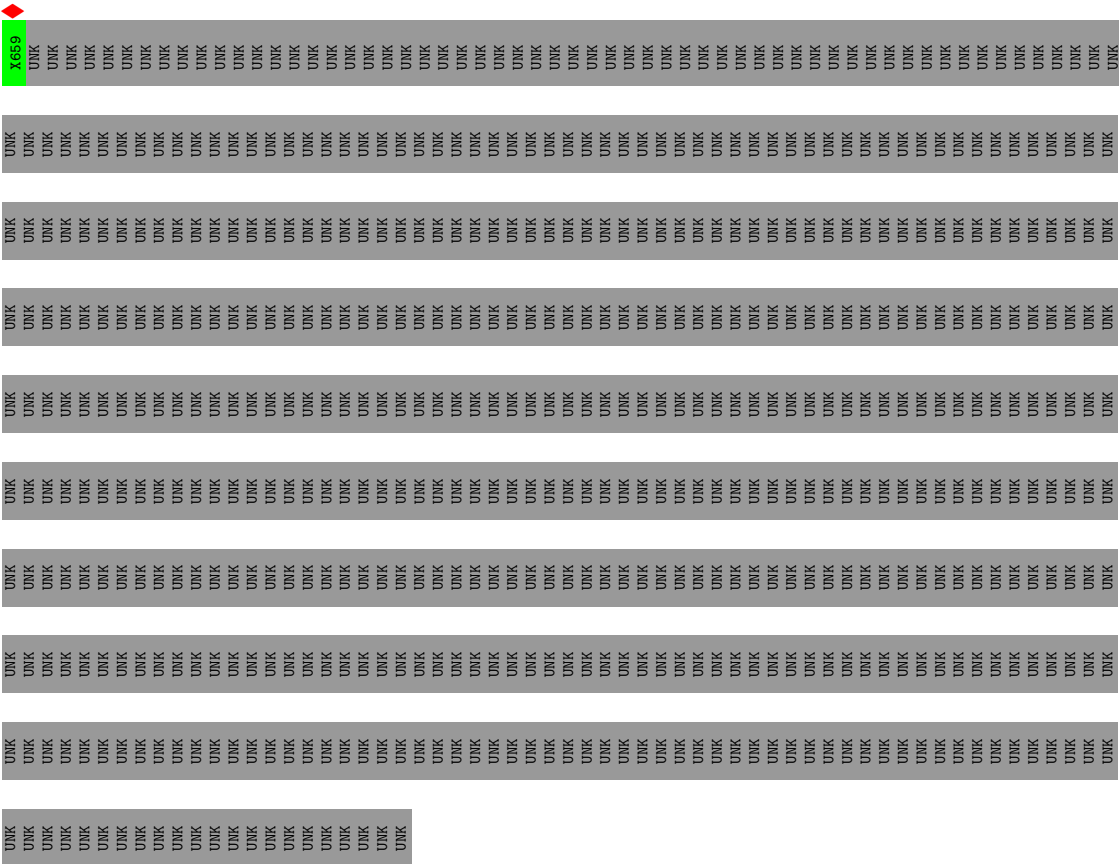


- Molecule 5: WD40 domain proteins

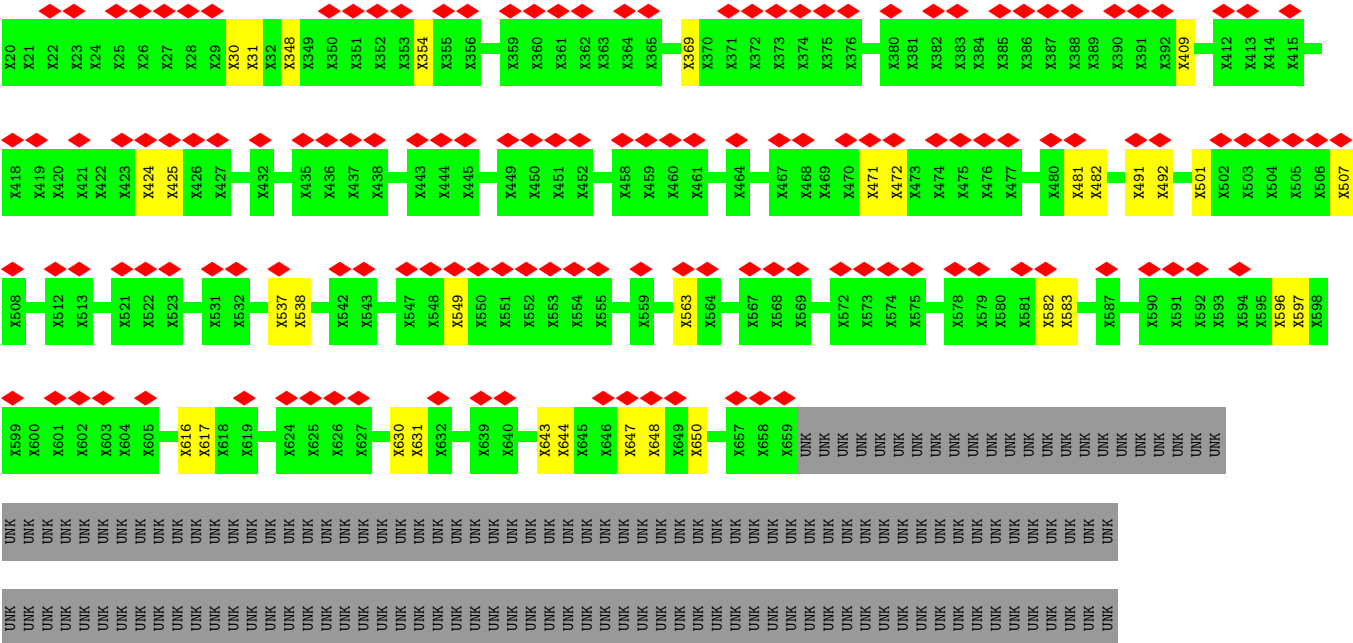


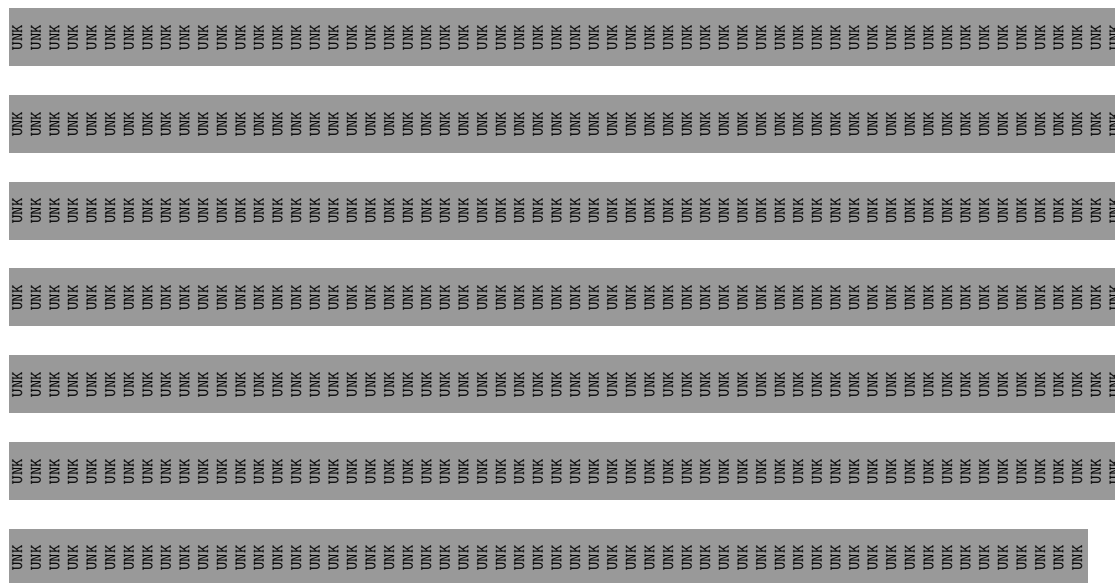
- Molecule 5: WD40 domain proteins



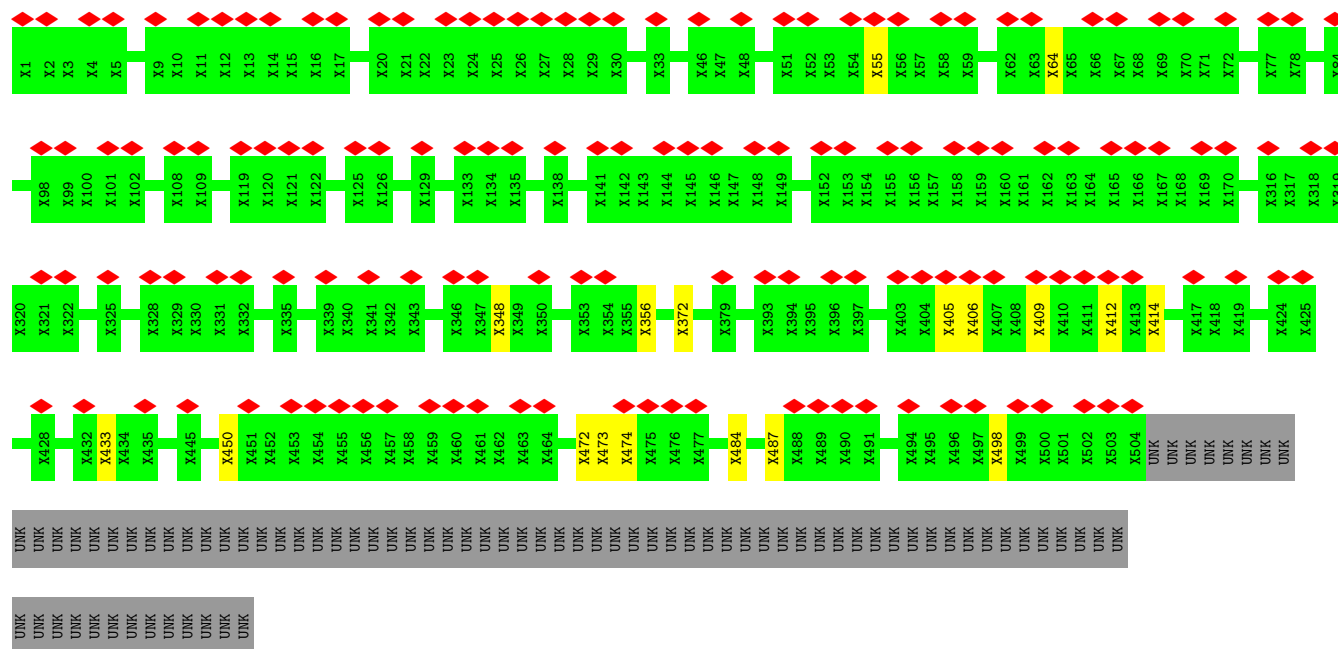
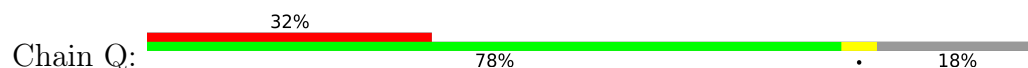


● Molecule 5: WD40 domain proteins

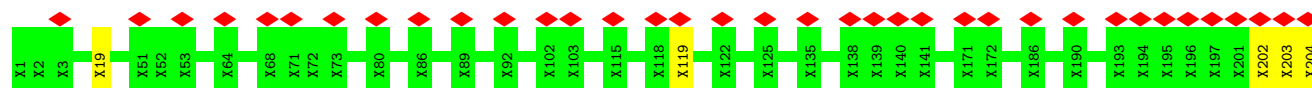


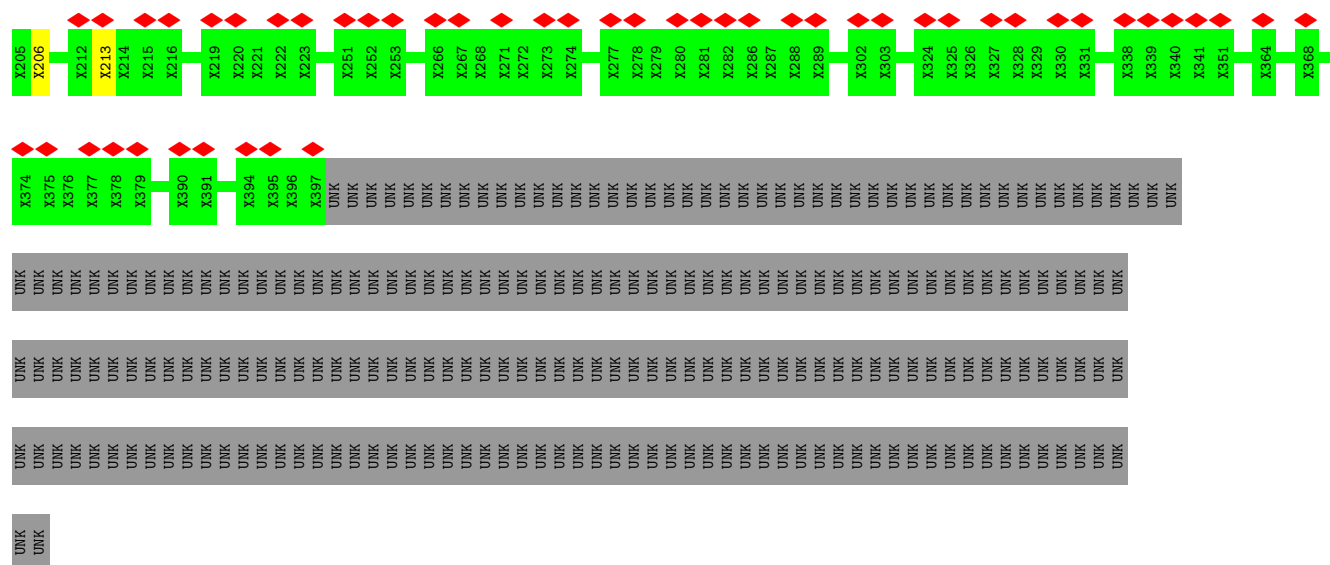


- Molecule 6: UTP6

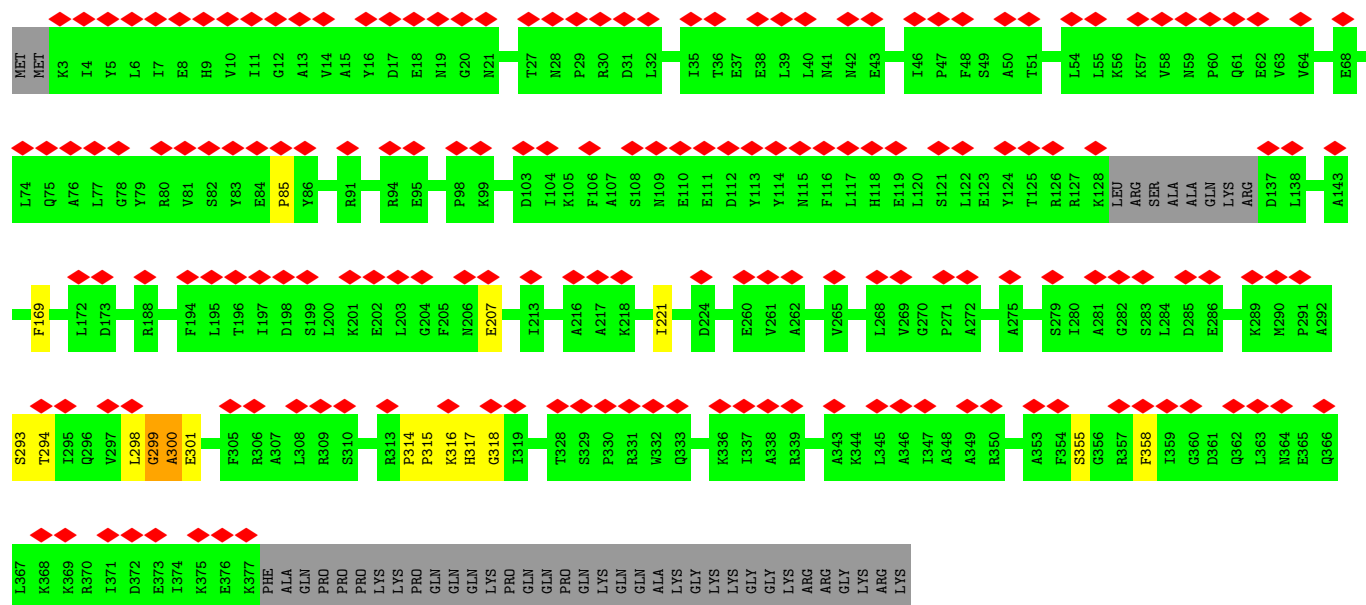
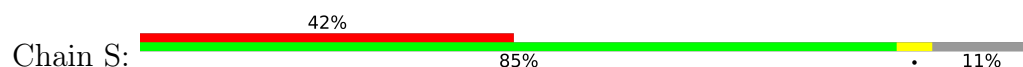


- Molecule 7: UTP-B oligomerisation domain

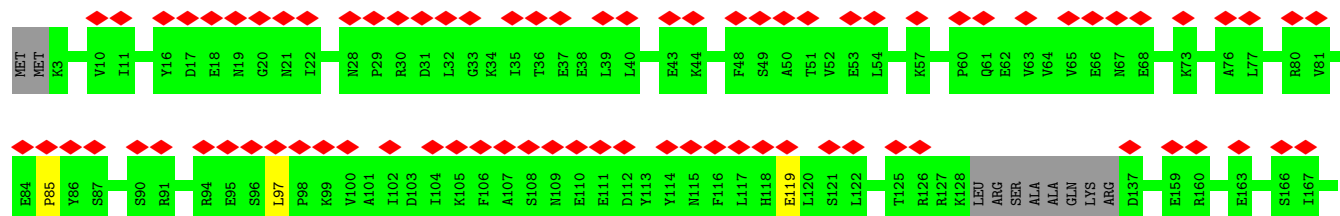
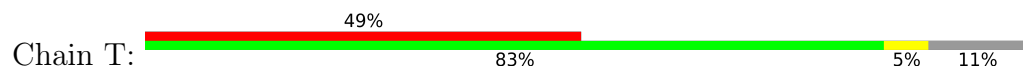


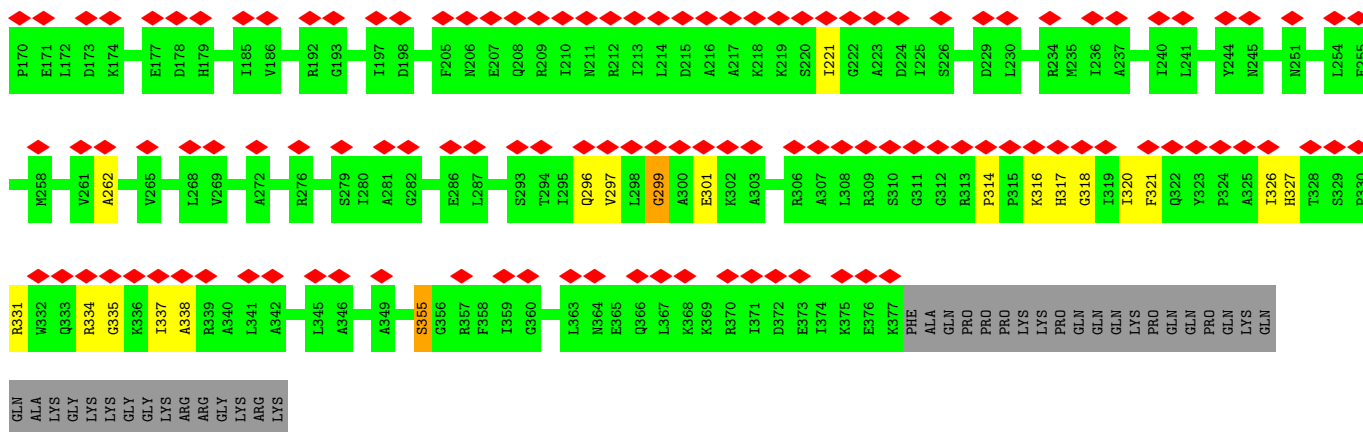


- Molecule 8: Pre mRNA splicing protein

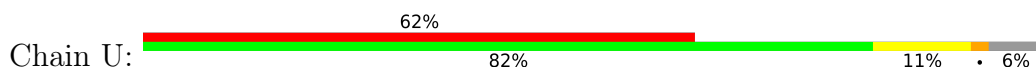


- Molecule 8: Pre mRNA splicing protein

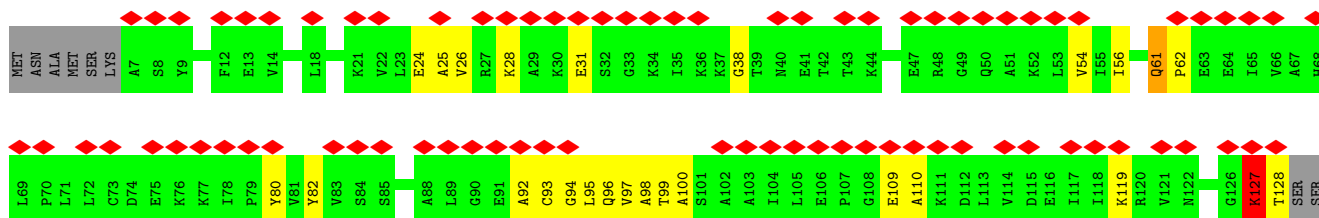
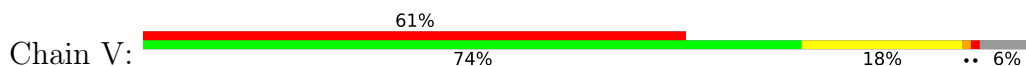




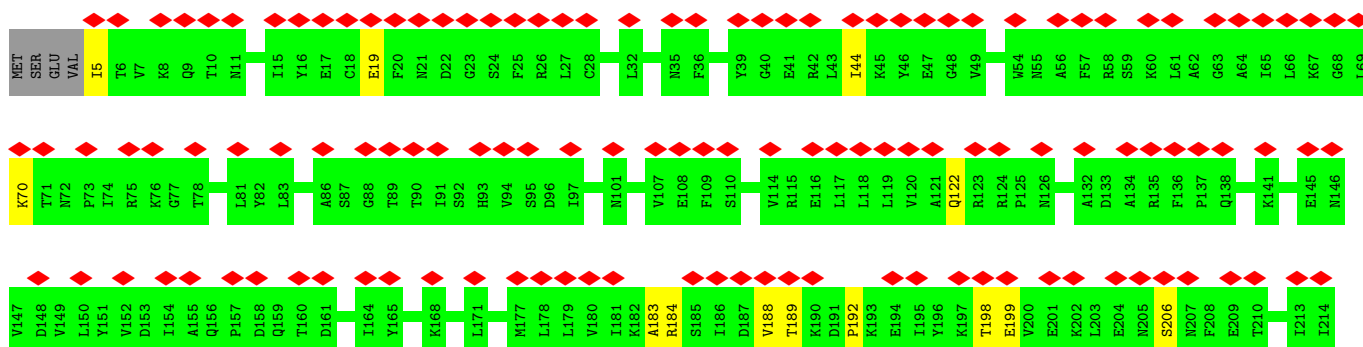
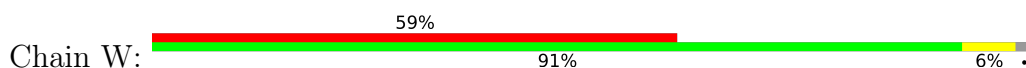
• Molecule 9: Snu13



• Molecule 9: Snu13



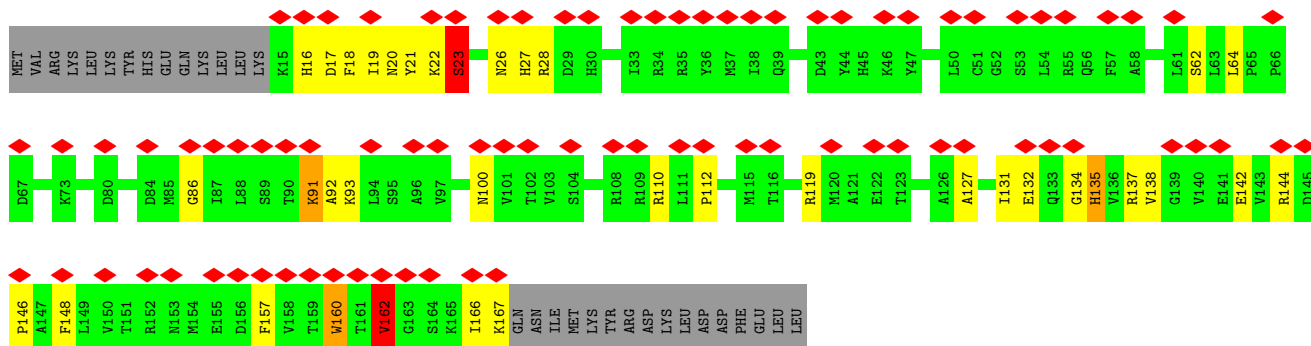
• Molecule 10: Nop1



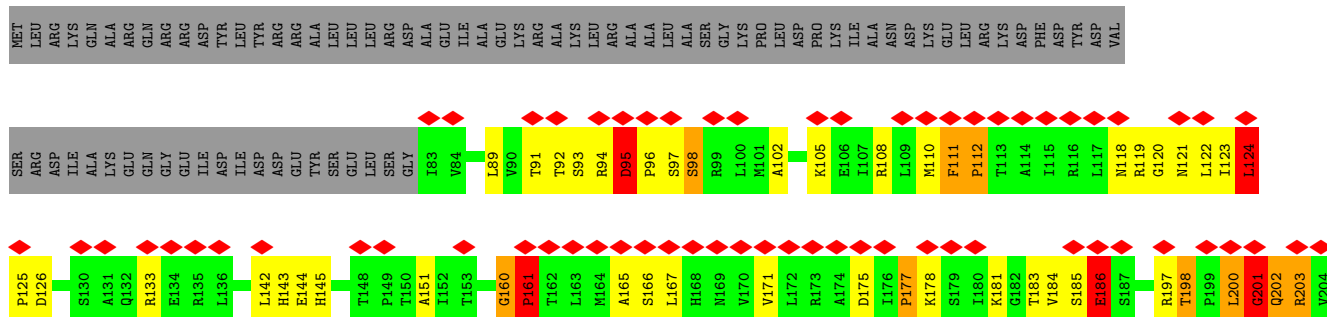
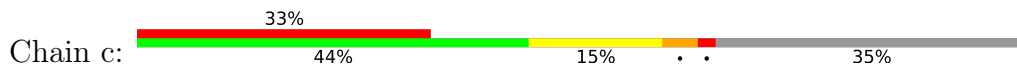


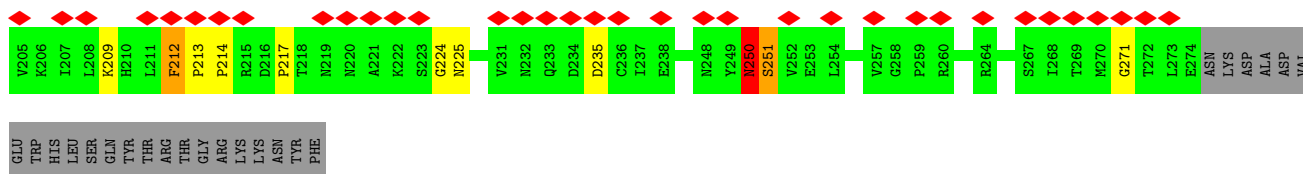
[illegible]

- Molecule 14: Imp3

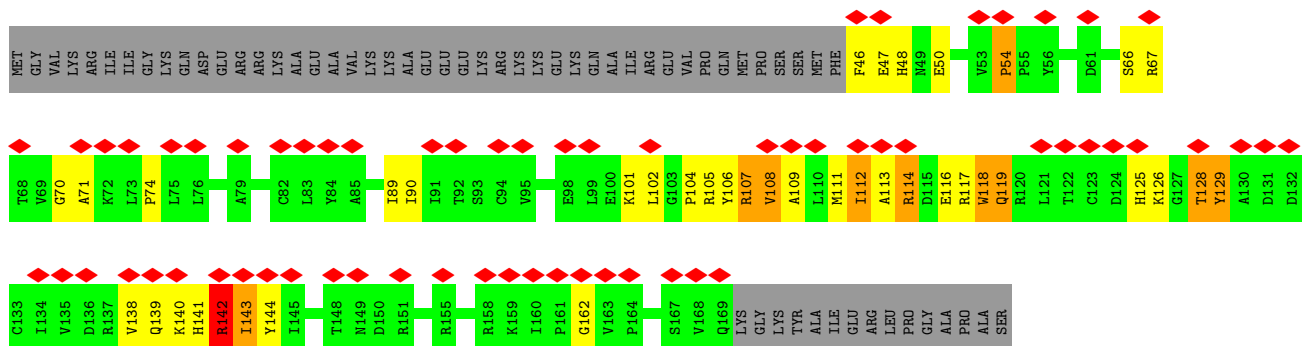


- Molecule 15: Putative U3 small nucleolar ribonucleoprotein

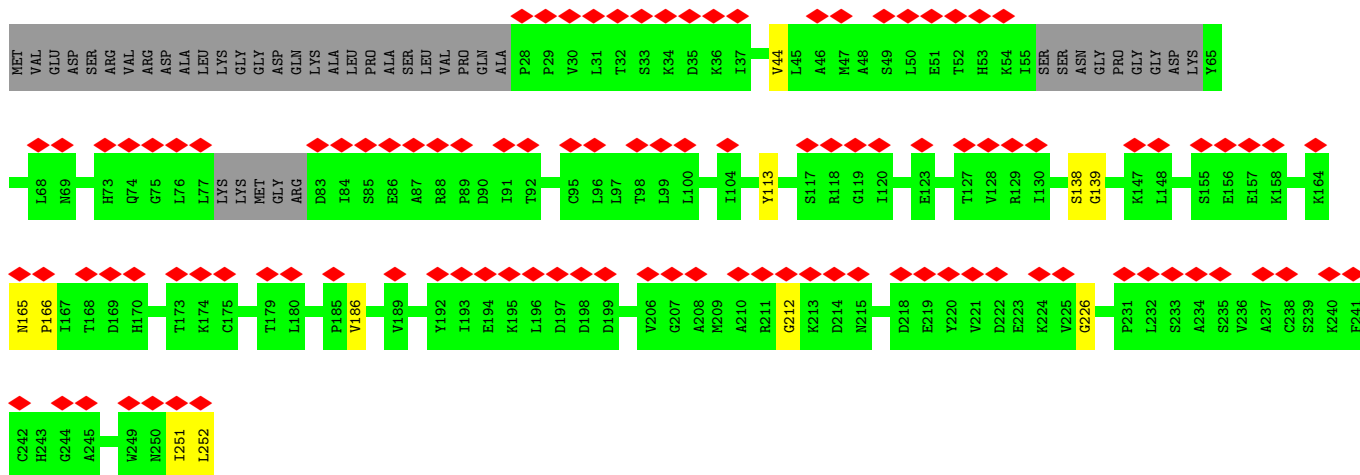
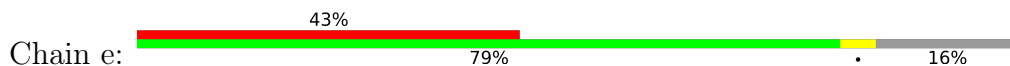




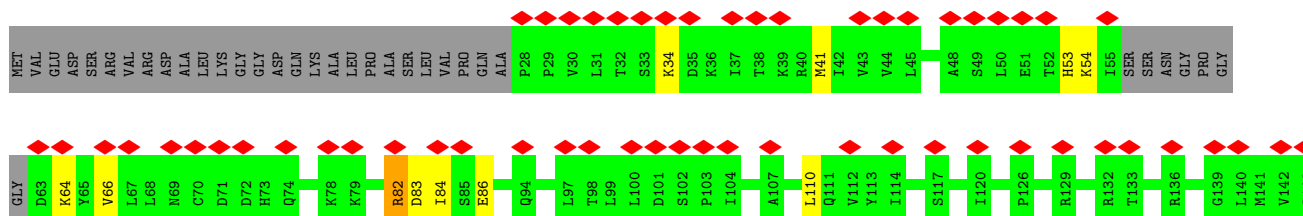
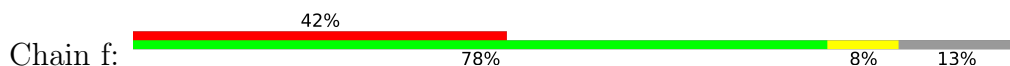
• Molecule 16: Utp24

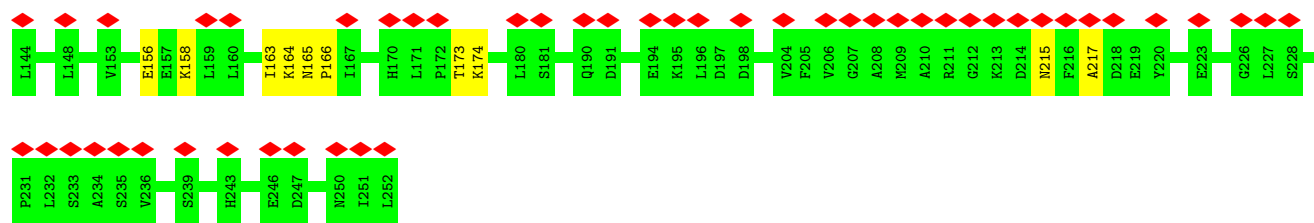


• Molecule 17: Emg1

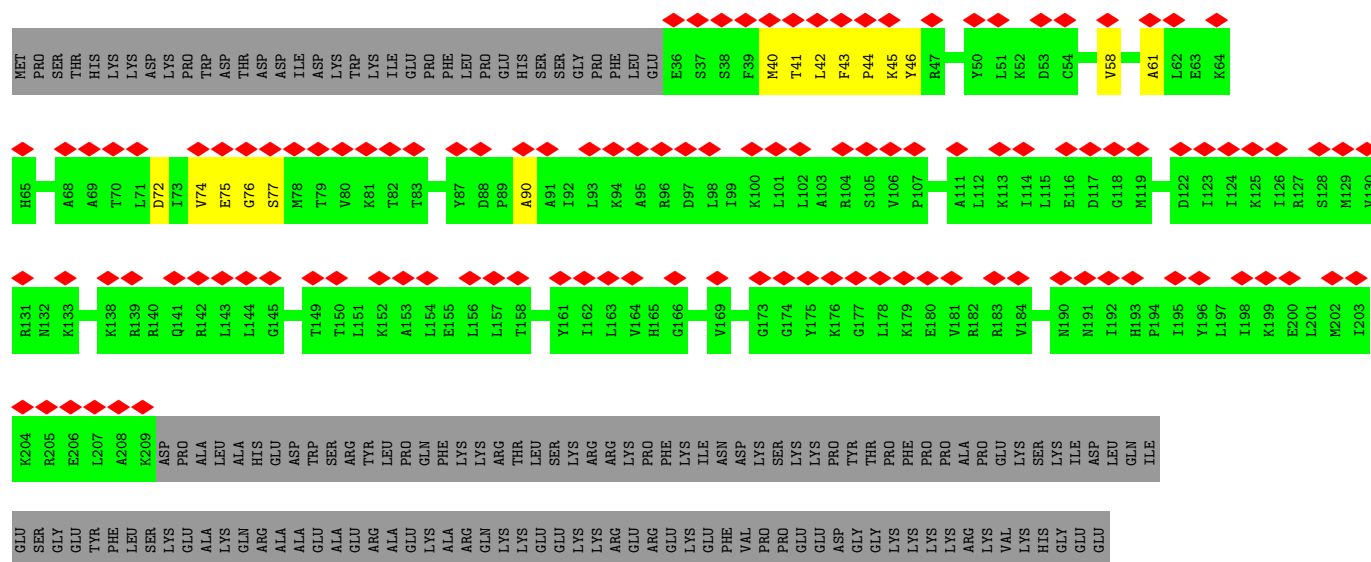


• Molecule 17: Emg1

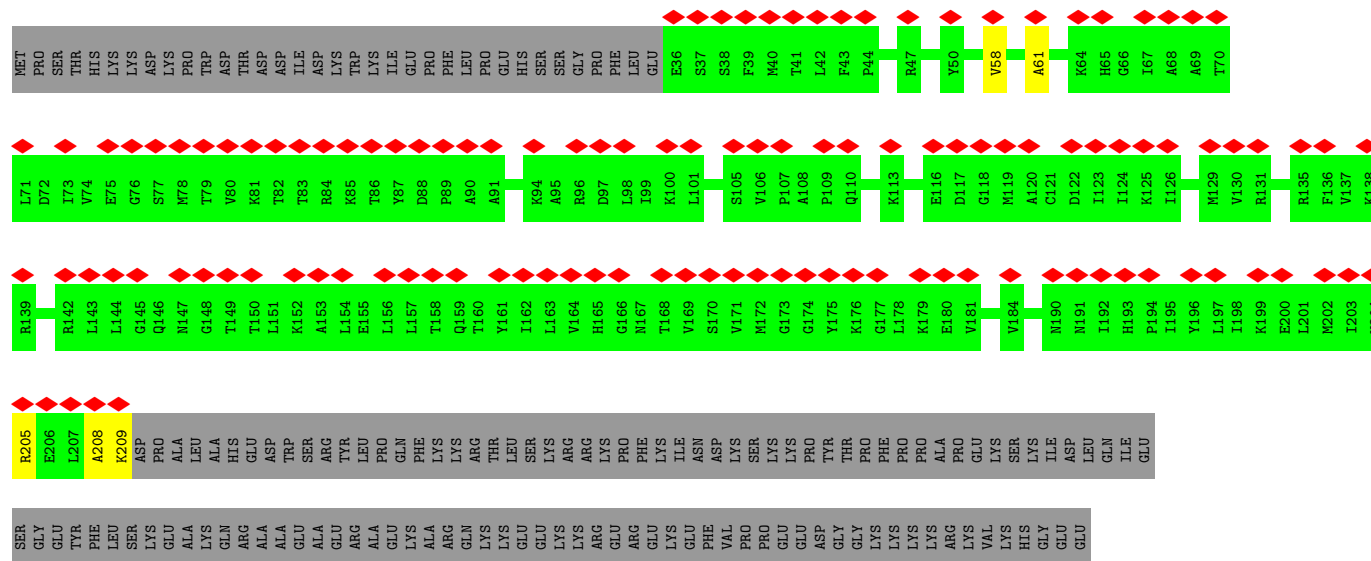




- Molecule 18: KRR1 small subunit processome component

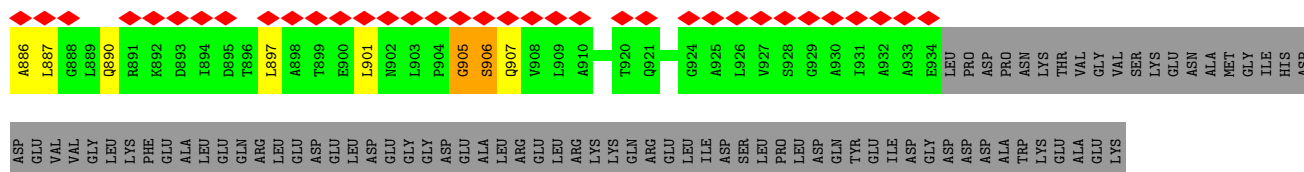


- Molecule 18: KRR1 small subunit processome component

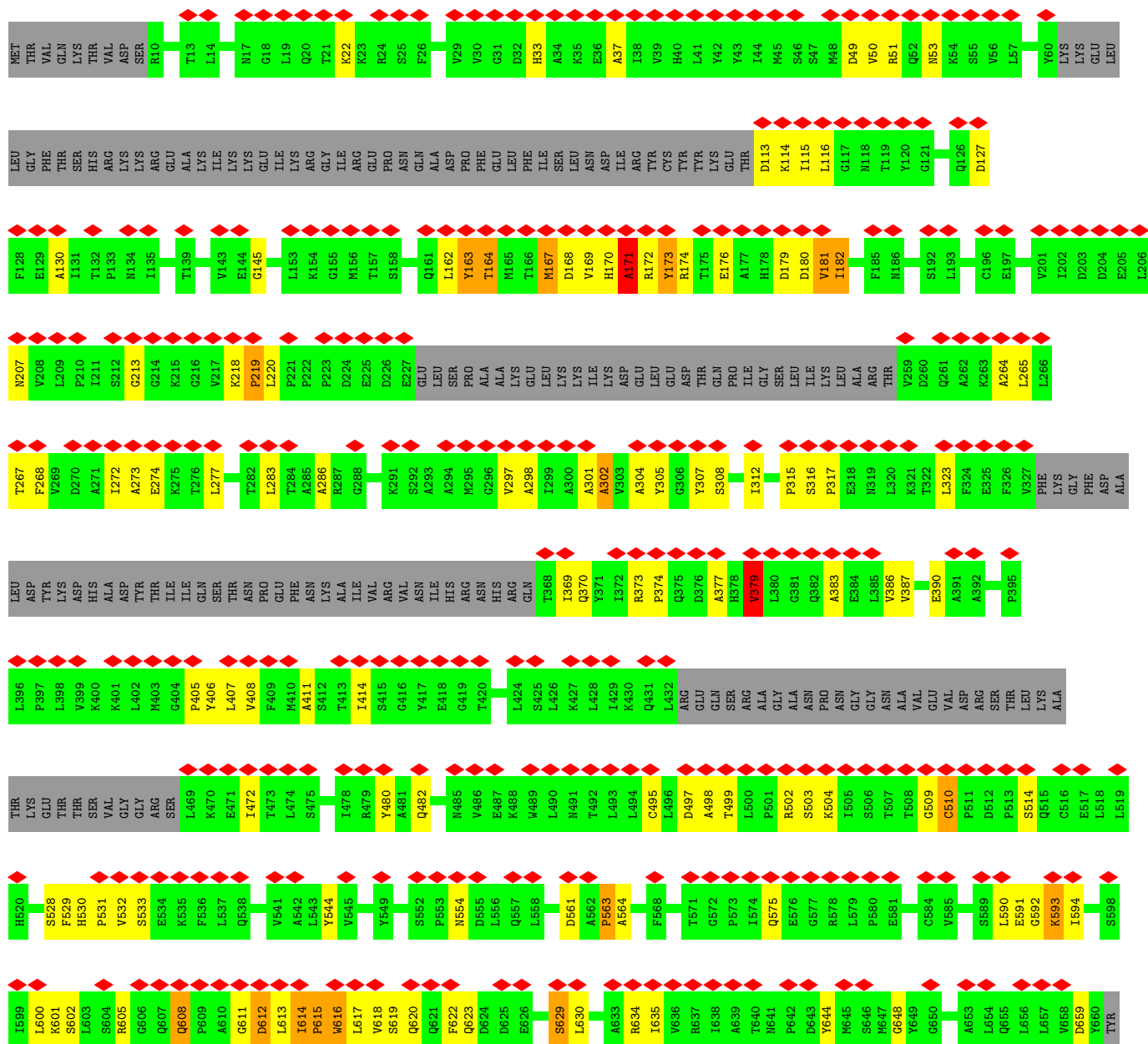
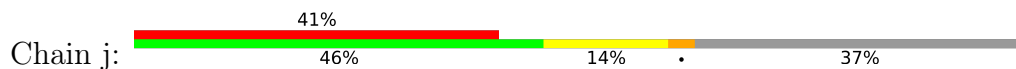


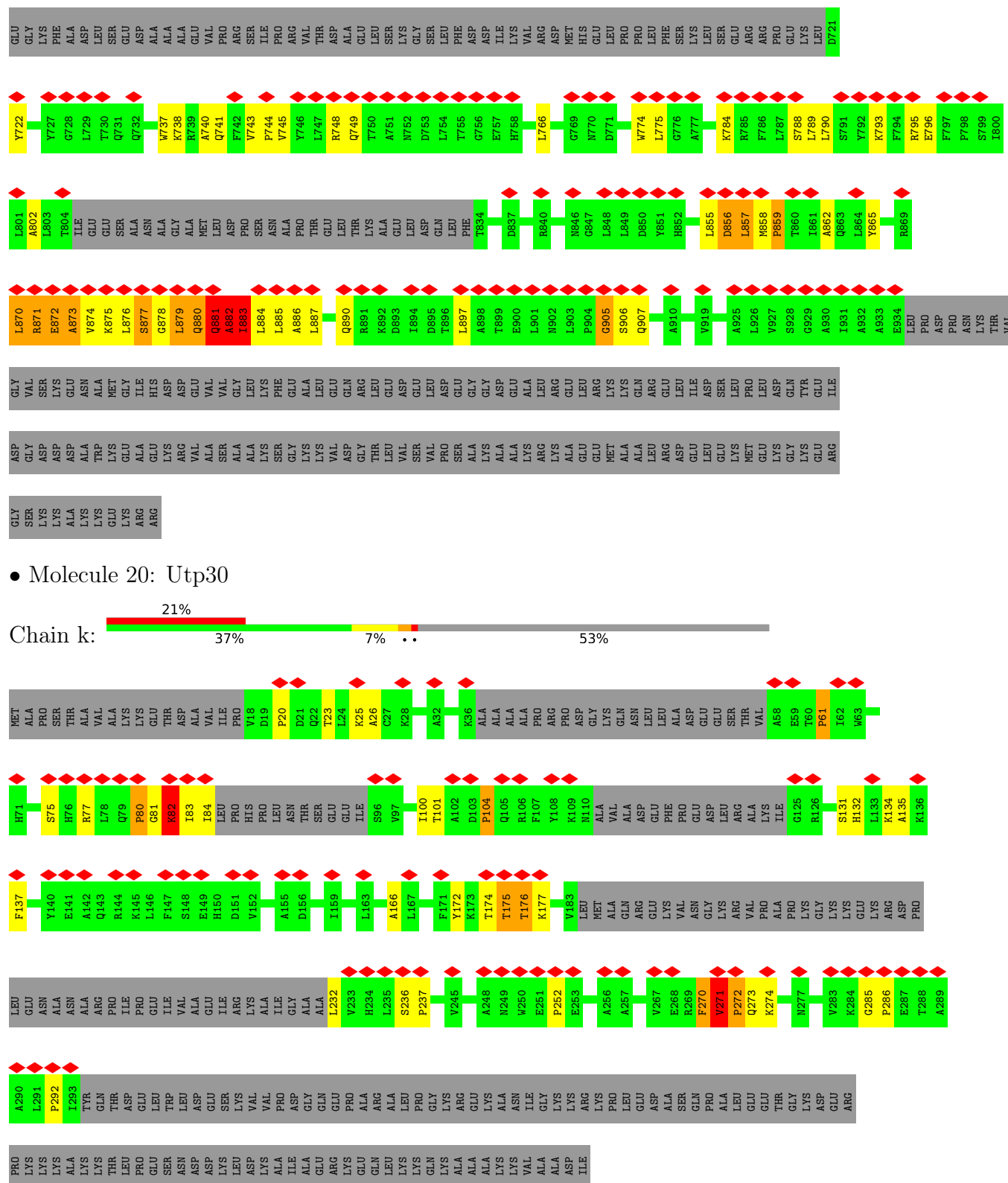
- Molecule 19: Kre33



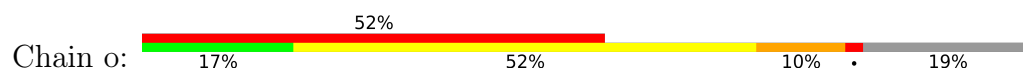


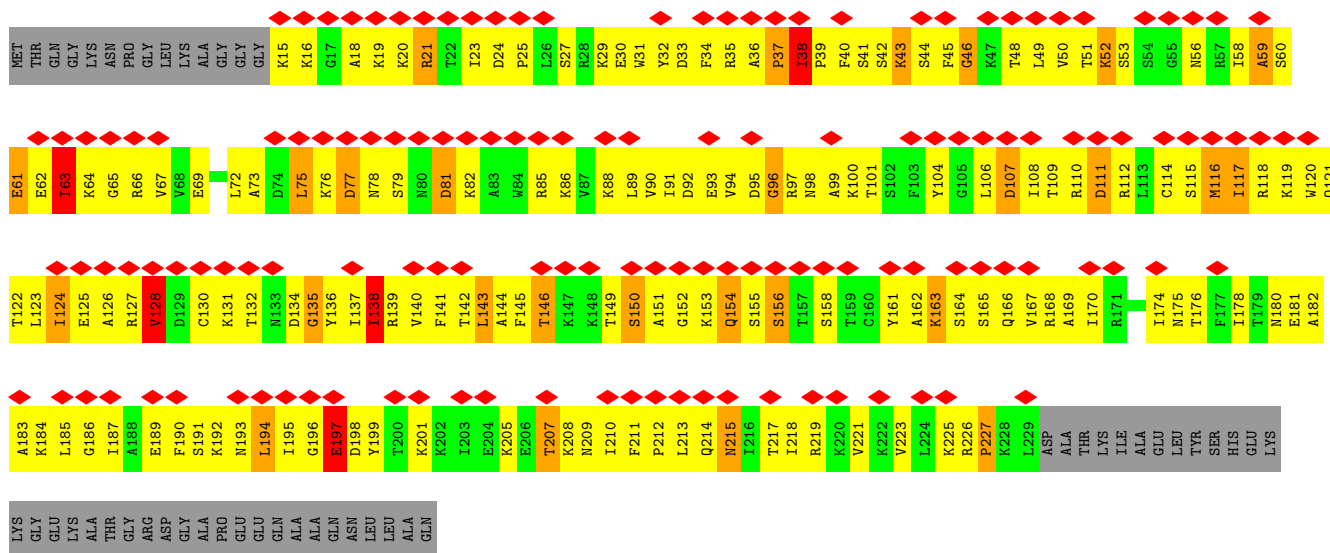
• Molecule 19: Kre33



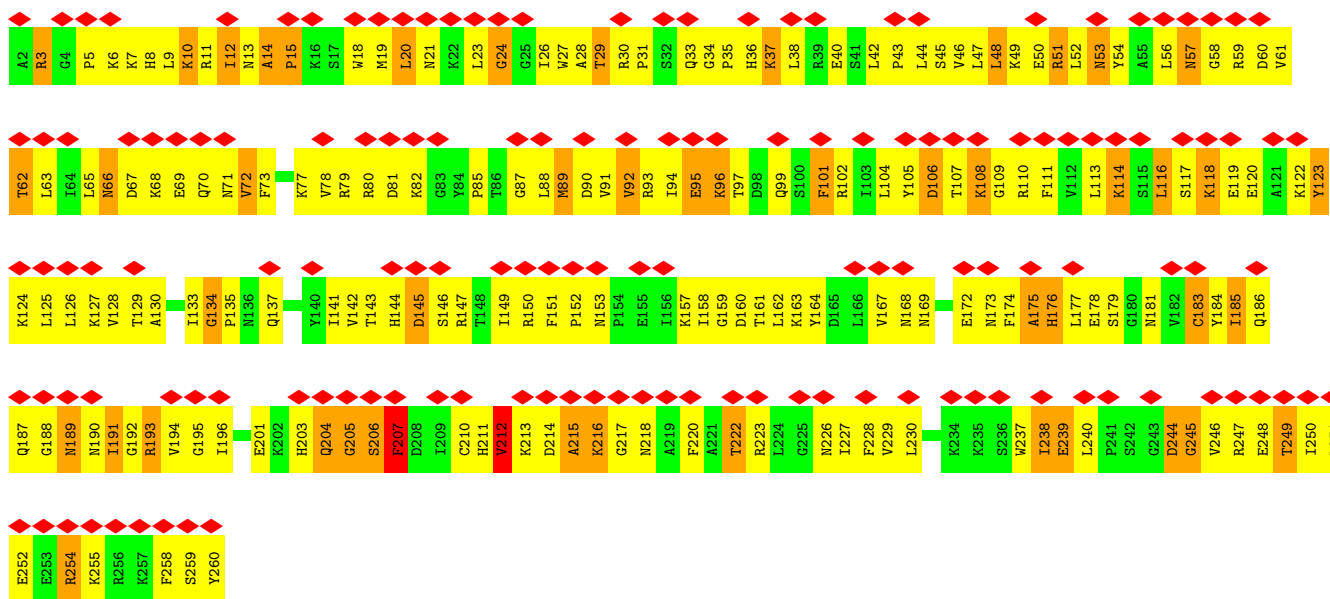


• Molecule 21: eS1

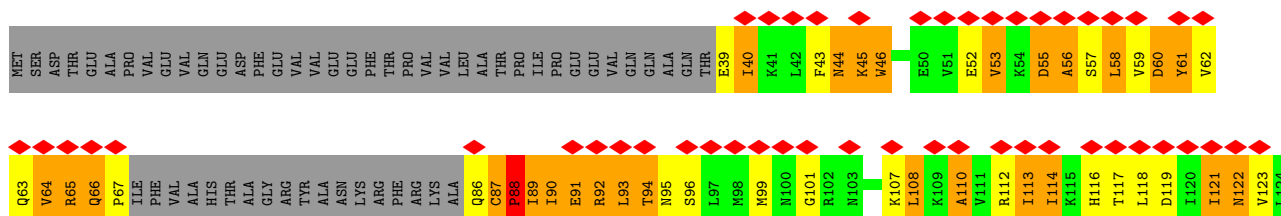


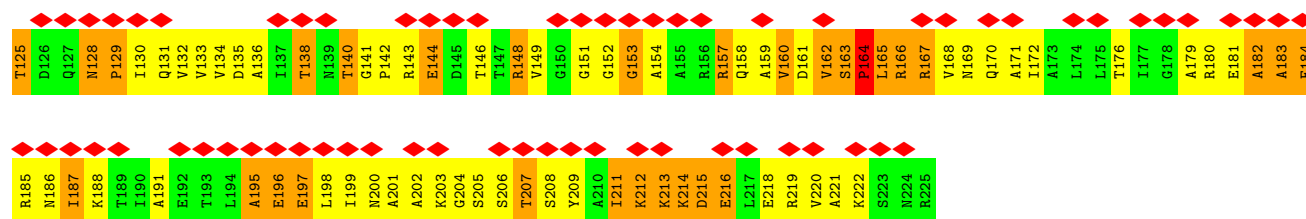


• Molecule 22: eS4

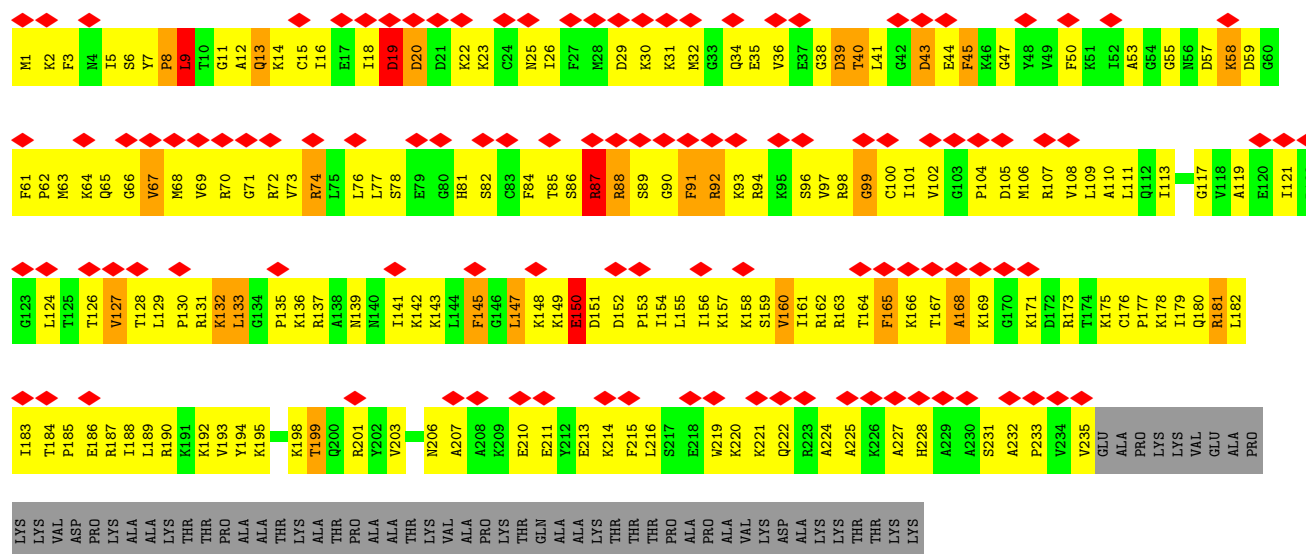
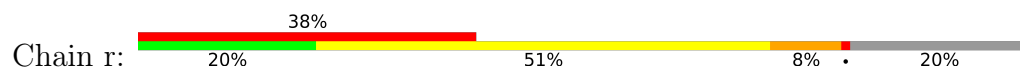


• Molecule 23: uS7

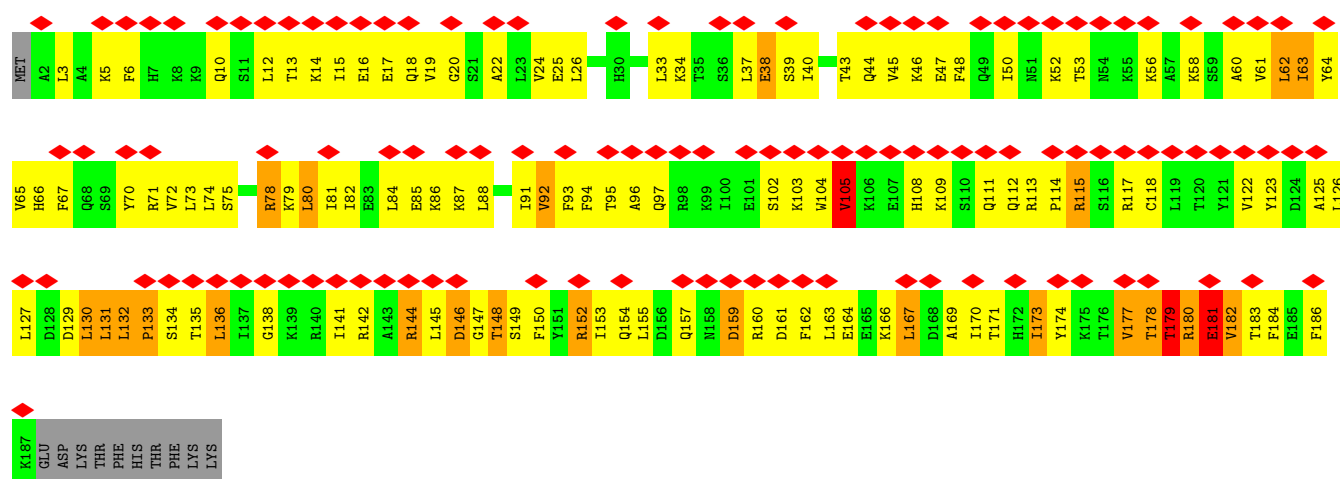




• Molecule 24: eS6

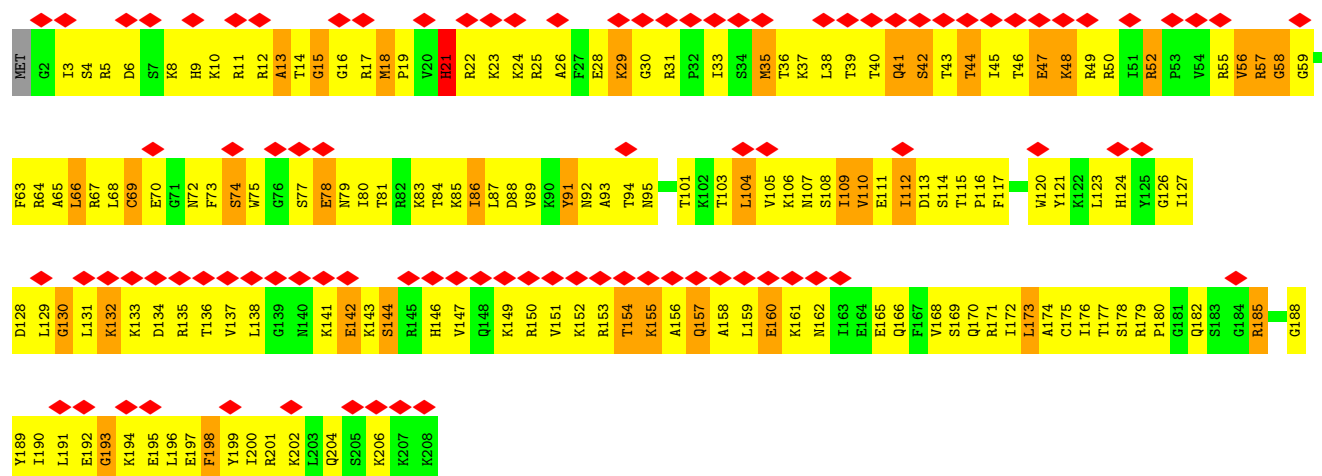


• Molecule 25: eS7

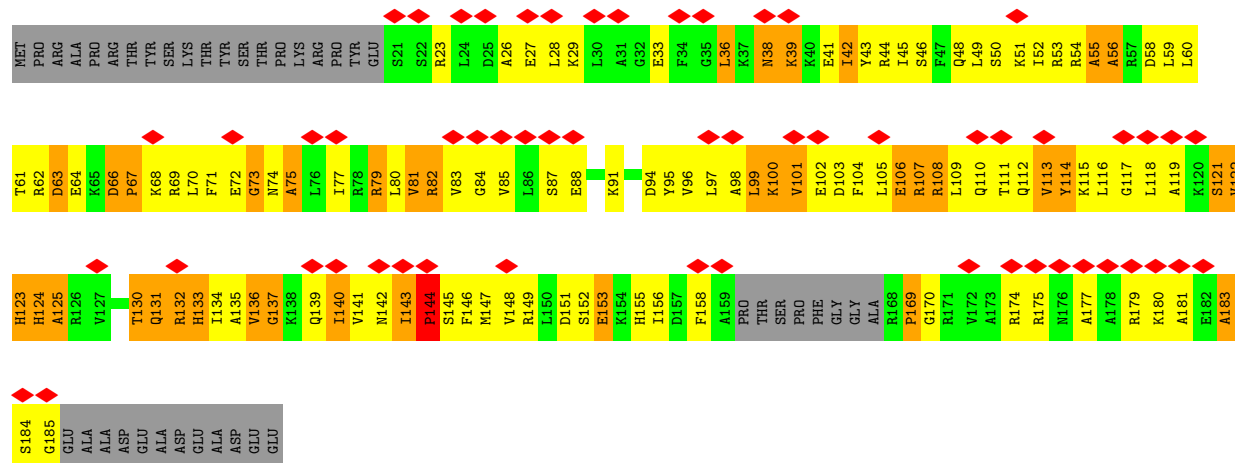
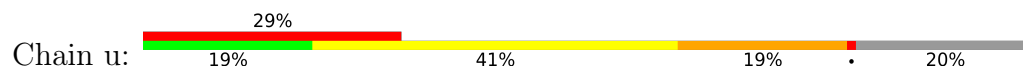


• Molecule 26: eS8

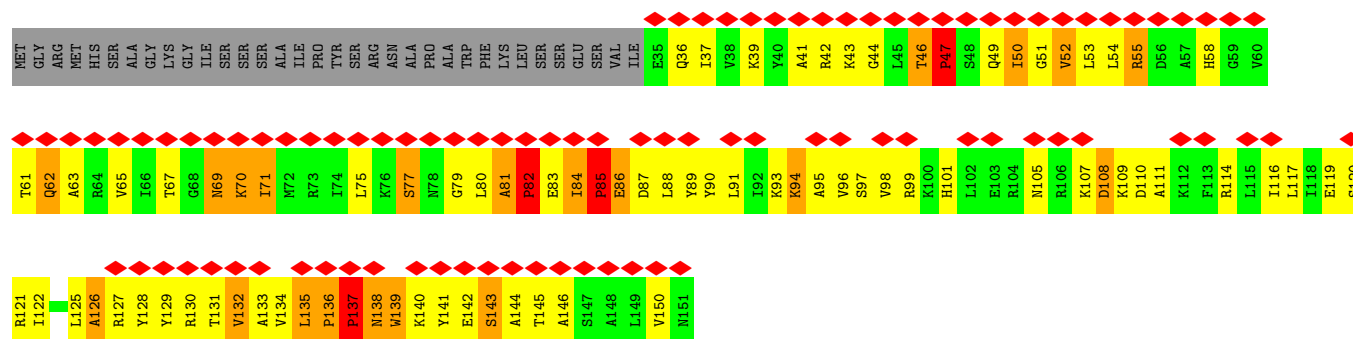
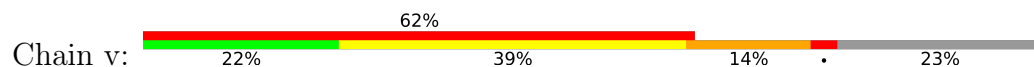




• Molecule 27: uS4

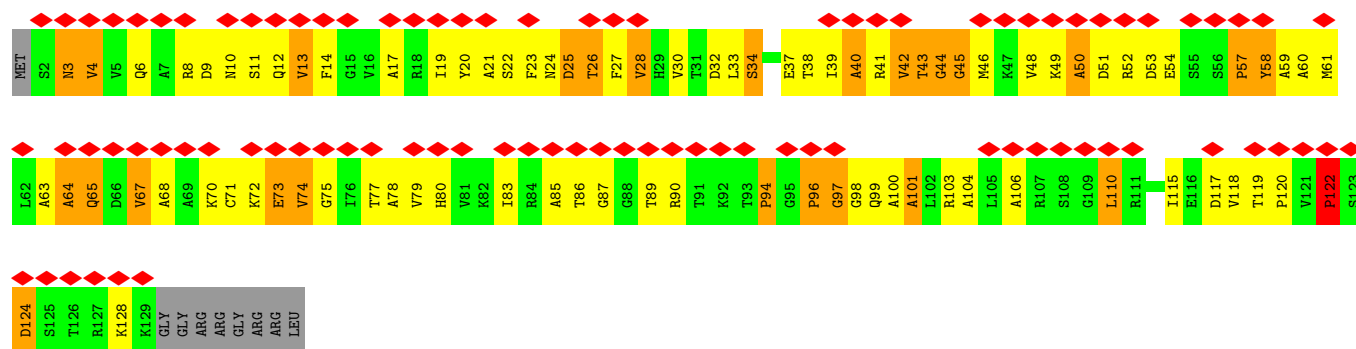


• Molecule 28: uS15

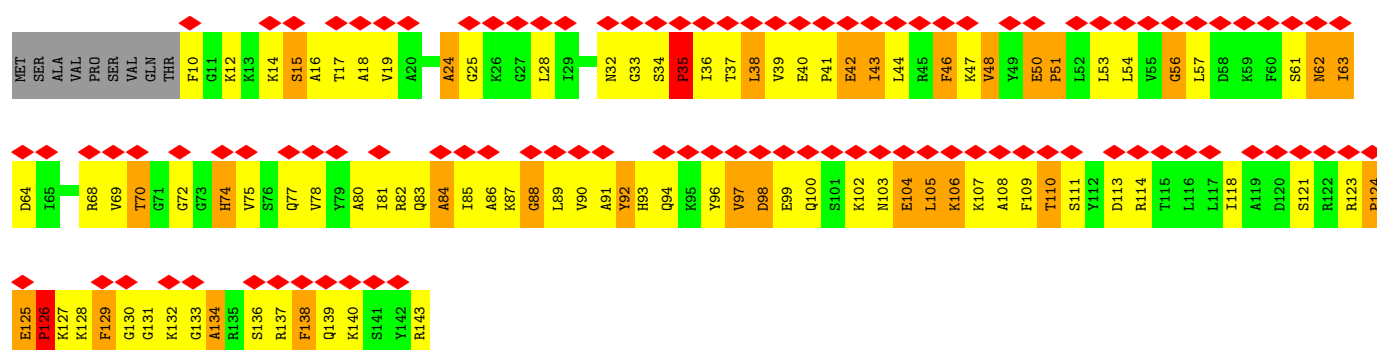


• Molecule 29: uS11

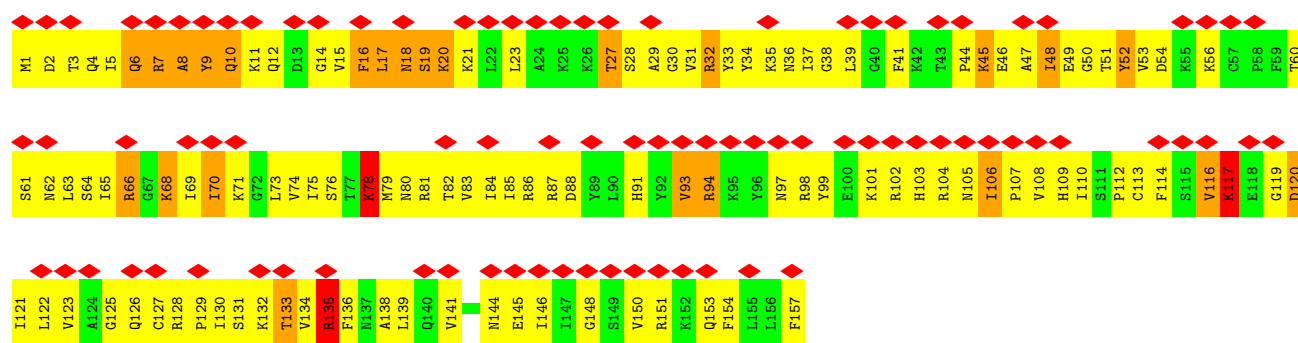




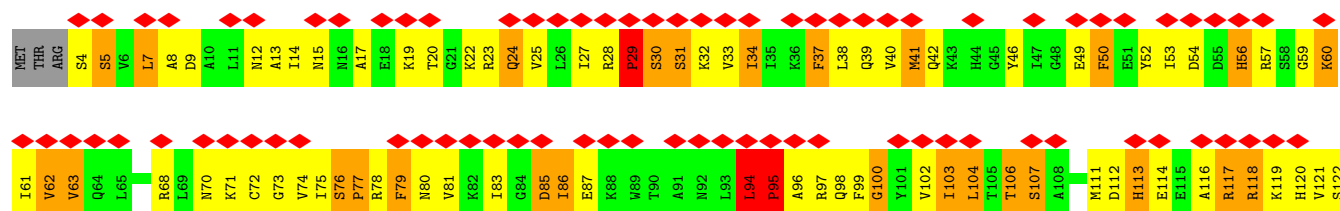
• Molecule 30: uS9



• Molecule 31: uS17

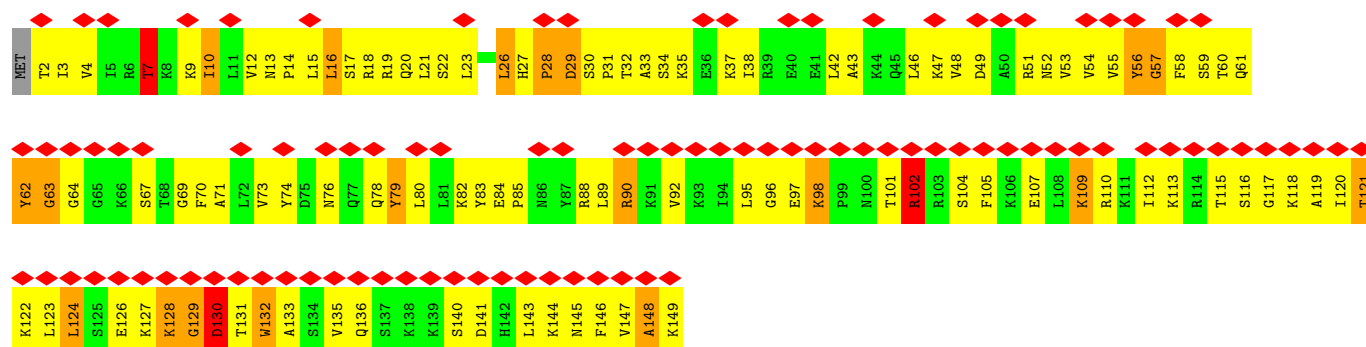


• Molecule 32: uS8

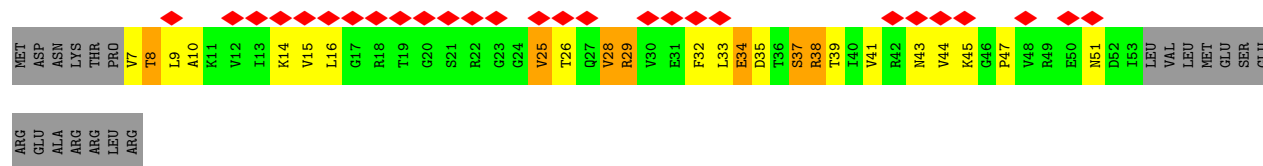
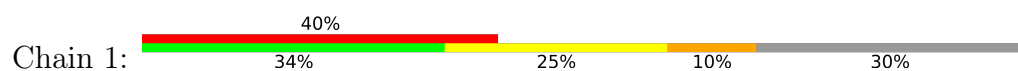




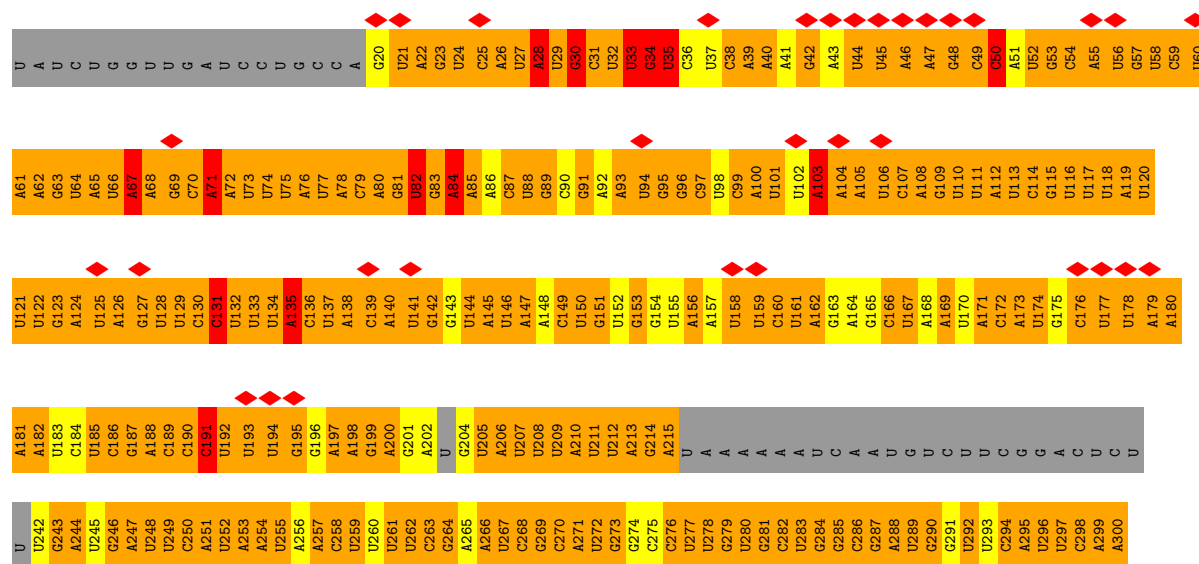
• Molecule 33: eS24



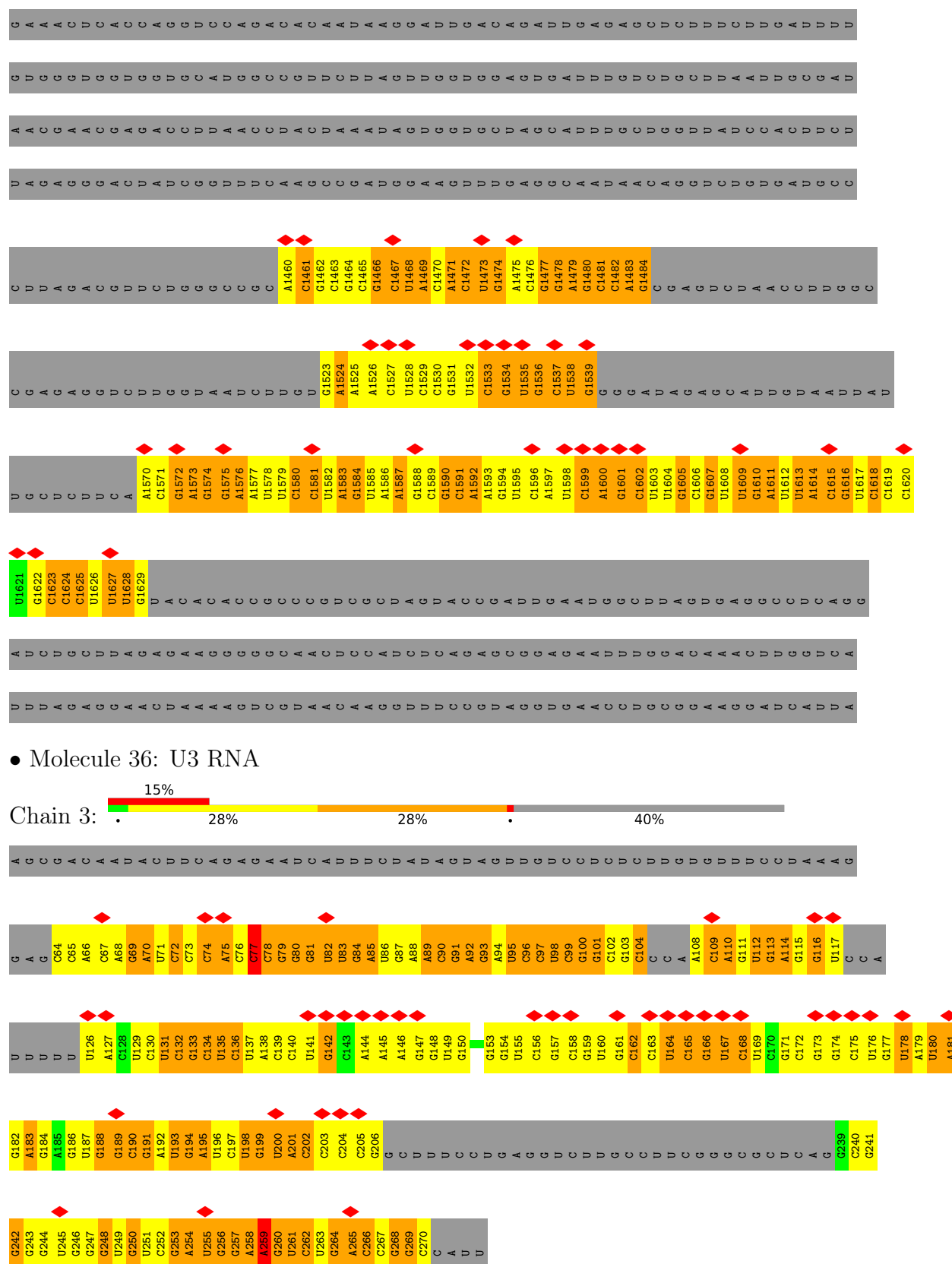
• Molecule 34: eS28



• Molecule 35: 18S ribosomal RNA







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	43000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	16	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.107	Depositor
Minimum map value	-0.056	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.025	Depositor
Map size ($\text{\AA}$)	478.464, 478.464, 478.464	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.068, 1.068, 1.068	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	$\# Z > 5$
2	G	1.67	12/1393 (0.9%)	2.07	34/1928 (1.8%)
4	I	0.37	0/3120	0.87	1/4334 (0.0%)
8	S	0.61	0/1813	1.08	3/2523 (0.1%)
8	T	0.64	0/1813	1.10	5/2523 (0.2%)
9	U	0.61	0/602	1.12	1/837 (0.1%)
9	V	0.67	0/602	1.10	2/837 (0.2%)
10	W	0.68	0/1123	1.14	3/1564 (0.2%)
10	X	0.60	0/1123	1.04	0/1564
11	Y	0.37	0/1793	0.94	2/2485 (0.1%)
12	Z	0.89	1/1741 (0.1%)	1.31	4/2416 (0.2%)
13	a	0.92	0/265	1.56	1/367 (0.3%)
14	b	1.23	5/759 (0.7%)	1.51	2/1058 (0.2%)
15	c	1.16	5/950 (0.5%)	1.92	38/1323 (2.9%)
16	d	0.83	1/615 (0.2%)	3.00	47/857 (5.5%)
17	e	0.59	0/1044	1.12	1/1452 (0.1%)
17	f	0.61	0/1079	1.06	1/1502 (0.1%)
18	g	0.93	0/860	1.30	0/1197
18	h	0.93	0/860	1.30	0/1197
19	i	1.66	14/3246 (0.4%)	2.23	138/4507 (3.1%)
19	j	1.68	19/3335 (0.6%)	2.29	154/4632 (3.3%)
20	k	1.45	1/900 (0.1%)	2.63	22/1249 (1.8%)
21	o	0.49	0/1748	1.05	15/2340 (0.6%)
22	p	0.52	0/2119	1.15	22/2849 (0.8%)
23	q	0.69	0/834	1.10	9/1159 (0.8%)
24	r	0.46	0/1895	1.07	9/2523 (0.4%)
25	s	0.47	0/1563	1.06	8/2100 (0.4%)
26	t	0.49	0/1717	1.05	10/2288 (0.4%)
27	u	0.81	0/775	1.13	9/1077 (0.8%)
28	v	0.80	0/579	1.32	9/806 (1.1%)
29	w	0.68	0/626	1.12	5/867 (0.6%)
30	x	0.75	0/657	1.21	11/911 (1.2%)
31	y	0.57	0/1298	1.13	14/1741 (0.8%)
32	z	0.89	0/621	1.40	11/860 (1.3%)
33	0	0.50	0/1215	1.08	8/1626 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
34	1	0.59	0/229	1.05	2/316 (0.6%)
35	2	0.95	0/20292	1.10	64/31586 (0.2%)
36	3	0.51	0/3912	0.70	3/6092 (0.0%)
All	All	0.93	58/69116 (0.1%)	1.33	668/99493 (0.7%)

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	H	0	33
8	T	0	1
9	U	0	1
9	V	0	1
10	W	0	1
10	X	0	1
14	b	0	5
15	c	0	7
16	d	0	2
19	i	0	3
19	j	0	3
20	k	0	1
All	All	0	59

The worst 5 of 58 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	j	612	ASP	CA-C	-12.33	1.36	1.52
19	i	616	TRP	N-CA	11.30	1.59	1.46
19	j	616	TRP	N-CA	11.28	1.59	1.46
15	c	161	PRO	C-O	-10.63	1.10	1.24
19	j	882	ALA	CA-C	-10.58	1.38	1.52

The worst 5 of 668 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	k	272	PRO	N-CA-CB	42.72	148.80	103.52
16	d	104	PRO	N-CA-CB	41.84	148.58	103.39
20	k	82	LYS	O-C-N	-28.80	84.28	122.59
16	d	128	THR	N-CA-CB	27.50	155.54	110.16
20	k	272	PRO	CB-CA-C	-24.33	76.59	112.11

There are no chirality outliers.

5 of 59 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	H	21	UNK	Mainchain
3	H	22	UNK	Mainchain
3	H	23	UNK	Mainchain
3	H	24	UNK	Mainchain
3	H	25	UNK	Mainchain

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	A	1500	0	326	24	0
1	B	1500	0	326	35	0
1	C	1500	0	326	28	0
1	D	1500	0	321	84	0
1	E	1500	0	321	85	0
1	F	1500	0	326	26	0
1	J	1500	0	323	32	0
1	K	1500	0	326	43	0
1	L	1500	0	325	47	0
1	N	1500	0	324	20	0
1	P	1500	0	326	72	0
1	l	1500	0	325	28	0
1	n	1500	0	325	79	0
2	G	1402	0	649	79	0
3	H	1715	0	364	121	0
4	I	3124	0	1397	6	0
5	M	1545	0	333	45	0
5	O	1545	0	331	43	0
5	m	1545	0	334	31	0
6	Q	1875	0	432	18	0
7	R	1660	0	362	13	0
8	S	1815	0	842	39	0
8	T	1815	0	841	69	0
9	U	603	0	287	53	0
9	V	603	0	288	71	0
10	W	1124	0	497	37	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	X	1124	0	497	12	0
11	Y	1799	0	805	4	0
12	Z	1742	0	785	5	0
13	a	267	0	112	0	0
14	b	760	0	331	57	0
15	c	951	0	393	152	0
16	d	616	0	271	50	0
17	e	1047	0	454	6	0
17	f	1081	0	469	31	0
18	g	861	0	385	96	0
18	h	861	0	386	22	0
19	i	3254	0	1481	139	0
19	j	3342	0	1522	113	0
20	k	905	0	399	31	0
21	o	1724	0	1793	455	0
22	p	2079	0	2150	340	0
23	q	836	0	390	144	0
24	r	1868	0	1985	535	0
25	s	1539	0	1620	164	0
26	t	1693	0	1793	467	0
27	u	777	0	360	132	0
28	v	580	0	266	71	0
29	w	627	0	307	103	0
30	x	658	0	304	127	0
31	y	1275	0	1353	418	0
32	z	622	0	283	63	0
33	0	1197	0	1281	286	0
34	1	230	0	100	11	0
35	2	18149	0	9087	7048	0
36	3	3504	0	1769	656	0
All	All	95839	0	44308	10818	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 79.

The worst 5 of 10818 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)
1:E:248:UNK:CB	3:H:312:UNK:CA	1.75	1.64
1:l:338:UNK:CA	23:q:199:ILE:CB	1.74	1.63
3:H:1:UNK:CB	3:H:173:UNK:CA	1.77	1.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:t:14:THR:CG2	35:2:354:C:H5''	1.15	1.60
24:r:157:LYS:CD	35:2:78:A:C8	1.77	1.60

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	G	265/1802 (15%)	245 (92%)	11 (4%)	9 (3%)	3	21
4	I	626/939 (67%)	609 (97%)	17 (3%)	0	100	100
8	S	363/412 (88%)	344 (95%)	14 (4%)	5 (1%)	9	40
8	T	363/412 (88%)	341 (94%)	20 (6%)	2 (1%)	21	59
9	U	120/130 (92%)	111 (92%)	7 (6%)	2 (2%)	7	36
9	V	120/130 (92%)	112 (93%)	6 (5%)	2 (2%)	7	36
10	W	225/232 (97%)	206 (92%)	16 (7%)	3 (1%)	9	42
10	X	225/232 (97%)	204 (91%)	17 (8%)	4 (2%)	6	34
11	Y	353/573 (62%)	341 (97%)	11 (3%)	1 (0%)	36	72
12	Z	353/367 (96%)	347 (98%)	6 (2%)	0	100	100
13	a	50/1183 (4%)	49 (98%)	1 (2%)	0	100	100
14	b	151/183 (82%)	128 (85%)	14 (9%)	9 (6%)	1	13
15	c	190/297 (64%)	163 (86%)	12 (6%)	15 (8%)	1	9
16	d	122/184 (66%)	110 (90%)	8 (7%)	4 (3%)	3	21
17	e	205/252 (81%)	190 (93%)	15 (7%)	0	100	100
17	f	214/252 (85%)	201 (94%)	11 (5%)	2 (1%)	14	51
18	g	172/322 (53%)	163 (95%)	9 (5%)	0	100	100
18	h	172/322 (53%)	163 (95%)	9 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	i	643/1073 (60%)	577 (90%)	38 (6%)	28 (4%)	2	17
19	j	663/1073 (62%)	591 (89%)	43 (6%)	29 (4%)	2	17
20	k	172/391 (44%)	151 (88%)	12 (7%)	9 (5%)	1	15
21	o	213/265 (80%)	161 (76%)	33 (16%)	19 (9%)	0	8
22	p	257/259 (99%)	193 (75%)	40 (16%)	24 (9%)	0	8
23	q	165/225 (73%)	55 (33%)	46 (28%)	64 (39%)	0	0
24	r	233/293 (80%)	188 (81%)	31 (13%)	14 (6%)	1	13
25	s	184/197 (93%)	151 (82%)	23 (12%)	10 (5%)	1	15
26	t	205/208 (99%)	147 (72%)	38 (18%)	20 (10%)	0	7
27	u	153/197 (78%)	48 (31%)	49 (32%)	56 (37%)	0	0
28	v	115/151 (76%)	49 (43%)	33 (29%)	33 (29%)	0	0
29	w	126/137 (92%)	51 (40%)	39 (31%)	36 (29%)	0	0
30	x	132/143 (92%)	57 (43%)	33 (25%)	42 (32%)	0	0
31	y	155/157 (99%)	115 (74%)	26 (17%)	14 (9%)	0	8
32	z	125/130 (96%)	50 (40%)	35 (28%)	40 (32%)	0	0
33	0	146/149 (98%)	115 (79%)	20 (14%)	11 (8%)	1	10
34	1	45/67 (67%)	17 (38%)	12 (27%)	16 (36%)	0	0
All	All	8021/13339 (60%)	6743 (84%)	755 (9%)	523 (6%)	2	12

5 of 523 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	G	2992	ASN
2	G	3194	ASP
8	T	355	SER
9	U	62	PRO
9	V	62	PRO

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	
21	o	191/225 (85%)	171 (90%)	20 (10%)	6	21
22	p	226/226 (100%)	199 (88%)	27 (12%)	5	18
24	r	201/244 (82%)	187 (93%)	14 (7%)	14	35
25	s	172/183 (94%)	155 (90%)	17 (10%)	7	24
26	t	184/185 (100%)	168 (91%)	16 (9%)	9	29
31	y	141/141 (100%)	128 (91%)	13 (9%)	8	26
33	0	133/134 (99%)	124 (93%)	9 (7%)	14	36
All	All	1248/1338 (93%)	1132 (91%)	116 (9%)	11	26

5 of 116 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
24	r	150	GLU
33	0	56	TYR
25	s	148	THR
33	0	54	VAL
31	y	69	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 44 such sidechains are listed below:

Mol	Chain	Res	Type
26	t	124	HIS
31	y	80	ASN
26	t	182	GLN
31	y	12	GLN
31	y	109	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
35	2	842/1800 (46%)	640 (76%)	124 (14%)
36	3	160/274 (58%)	80 (50%)	11 (6%)
All	All	1002/2074 (48%)	720 (71%)	135 (13%)

5 of 720 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
35	2	21	U

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Mol	Chain	Res	Type
35	2	22	A
35	2	23	G
35	2	24	U
35	2	25	C

5 of 135 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
35	2	1472	C
35	2	1573	A
36	3	199	G
35	2	295	A
35	2	294	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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
6	Q	30
7	R	15
3	H	13

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Mol	Chain	Number of breaks
5	M	2
5	O	2
5	m	2
1	A	1
1	B	1
1	C	1
1	D	1
1	E	1
1	F	1
1	J	1
1	K	1
1	L	1
1	N	1
1	P	1
1	l	1
1	n	1

The worst 5 of 77 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Q	171:UNK	C	301:UNK	N	88.70
1	R	41:UNK	C	51:UNK	N	66.84
1	R	141:UNK	C	151:UNK	N	66.84
1	R	241:UNK	C	251:UNK	N	66.84
1	R	341:UNK	C	351:UNK	N	66.84

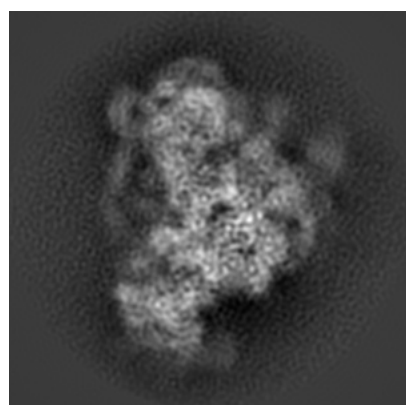
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8143. These allow visual inspection of the internal detail of the map and identification of artifacts.

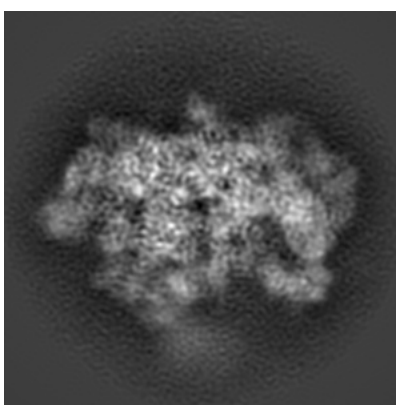
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

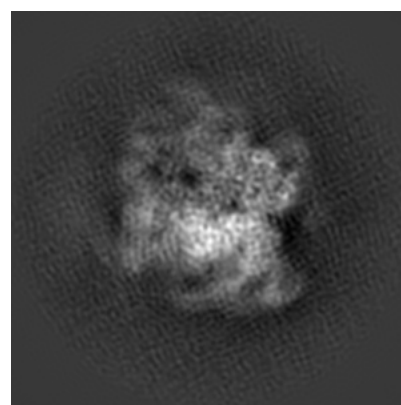
6.1.1 Primary map



X



Y

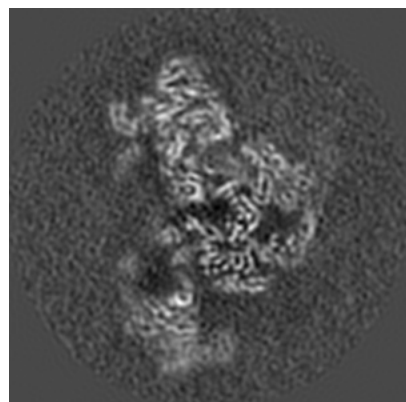


Z

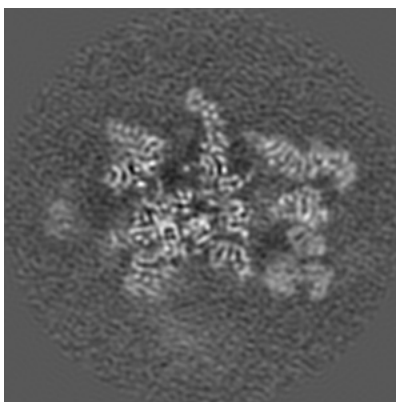
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

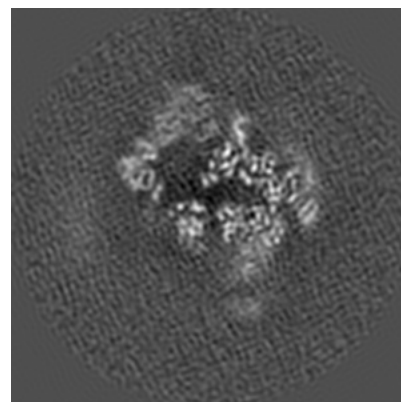
6.2.1 Primary map



X Index: 224



Y Index: 224

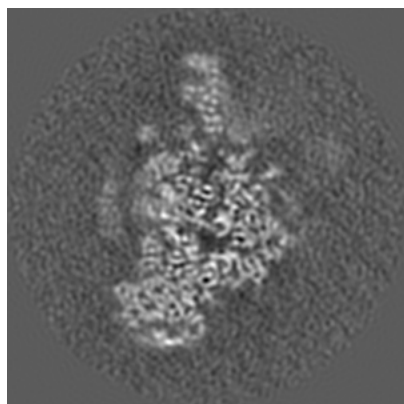


Z Index: 224

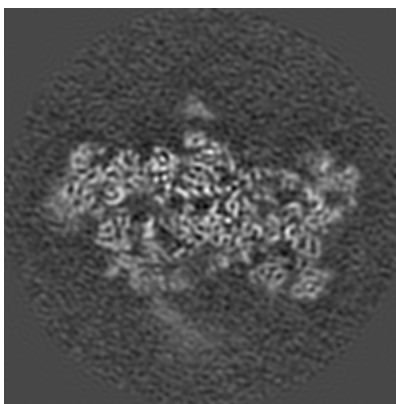
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

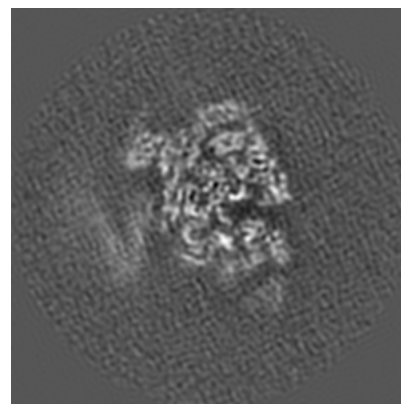
6.3.1 Primary map



X Index: 266



Y Index: 206

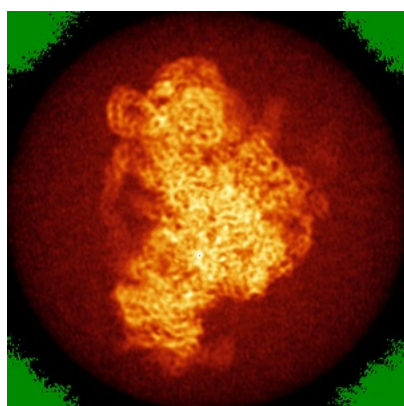


Z Index: 191

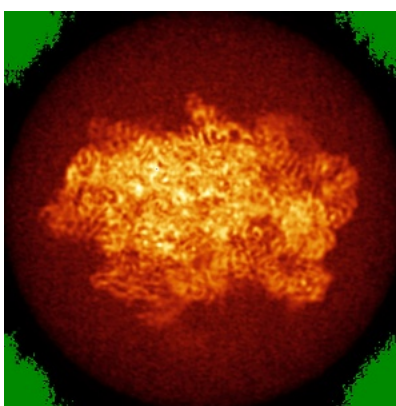
The images above show the largest variance slices of the map in three orthogonal directions.

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

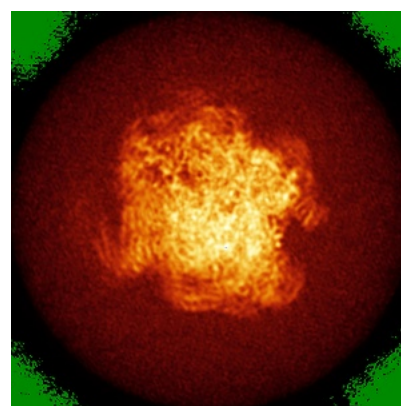
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.025. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

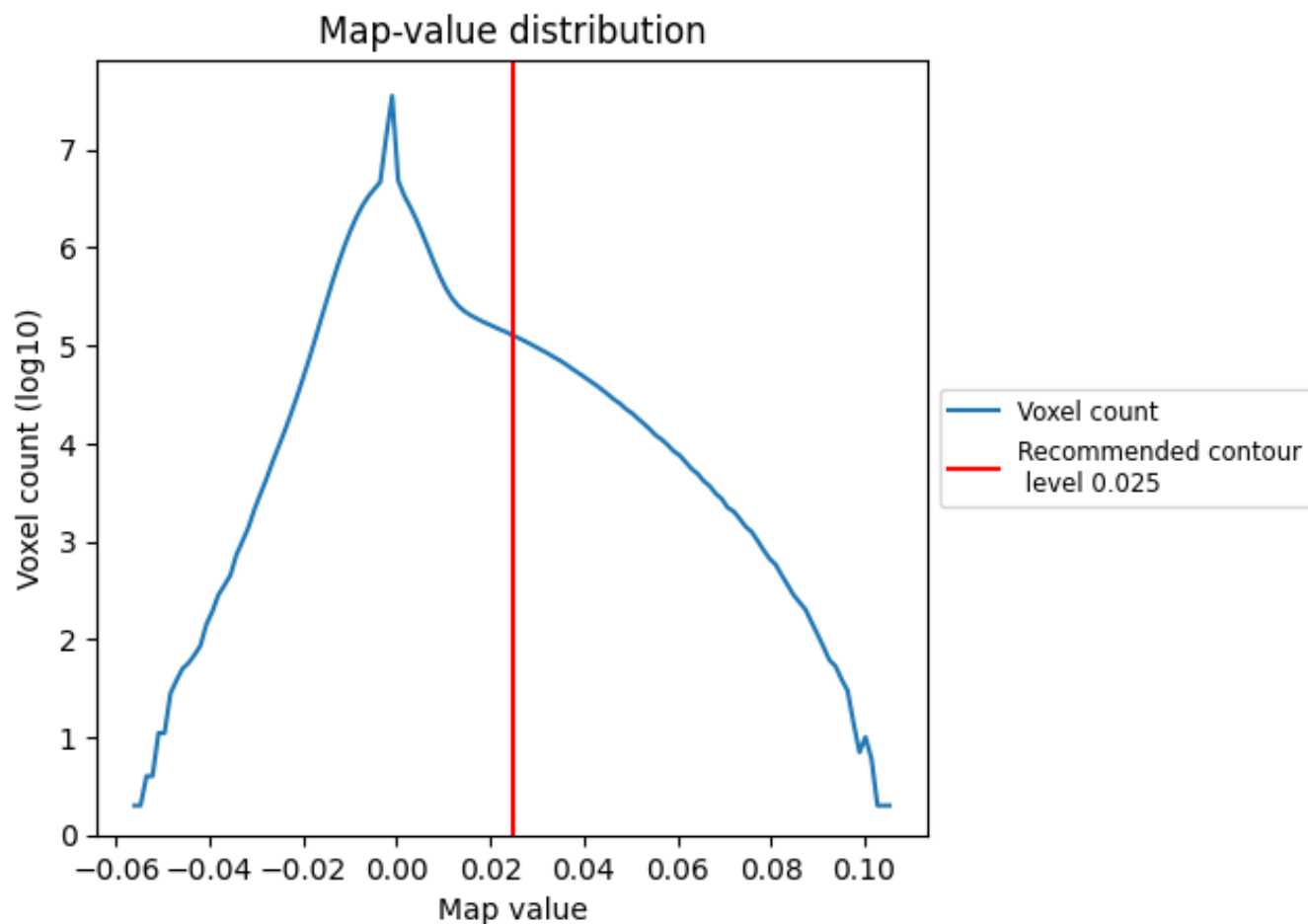
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

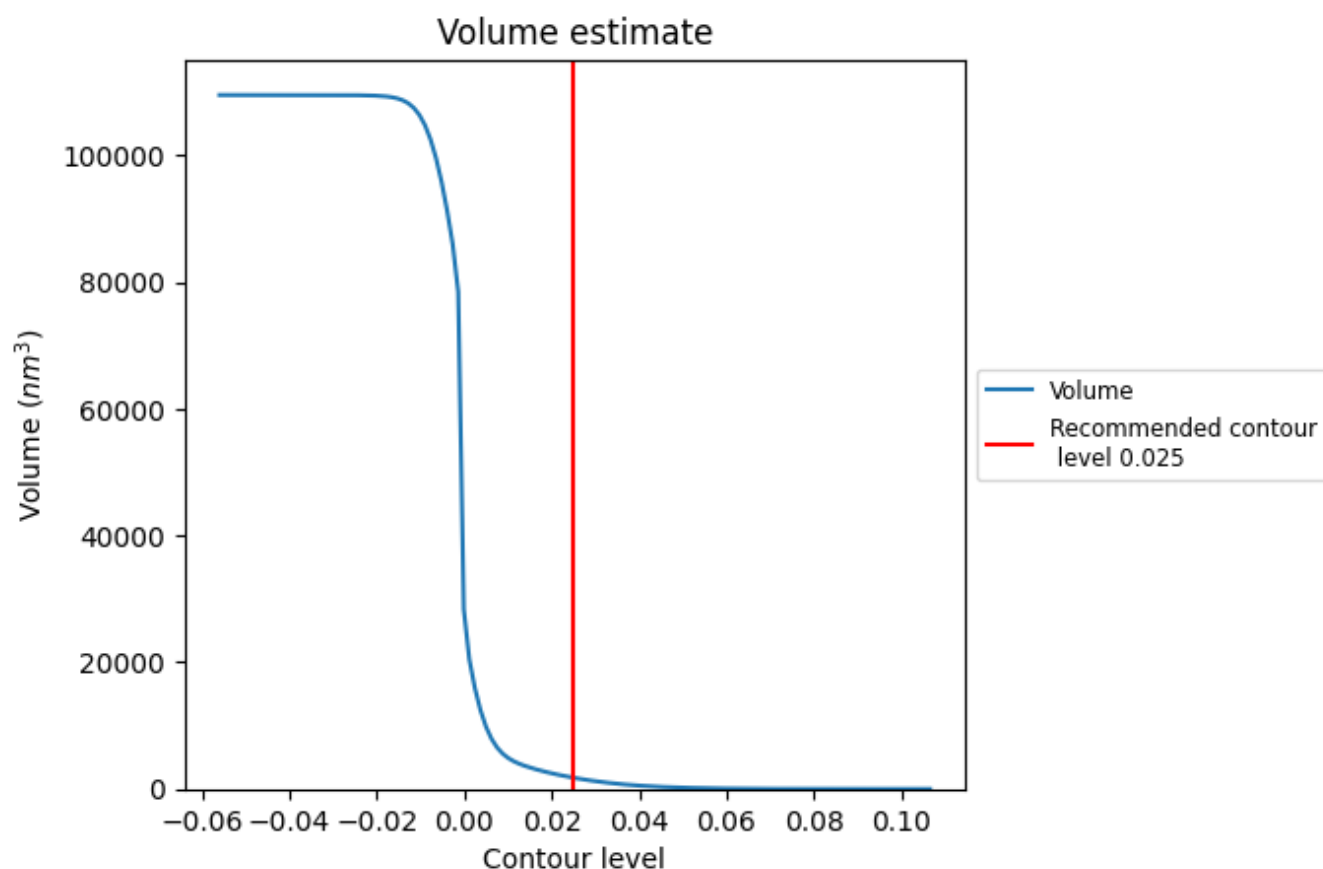
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

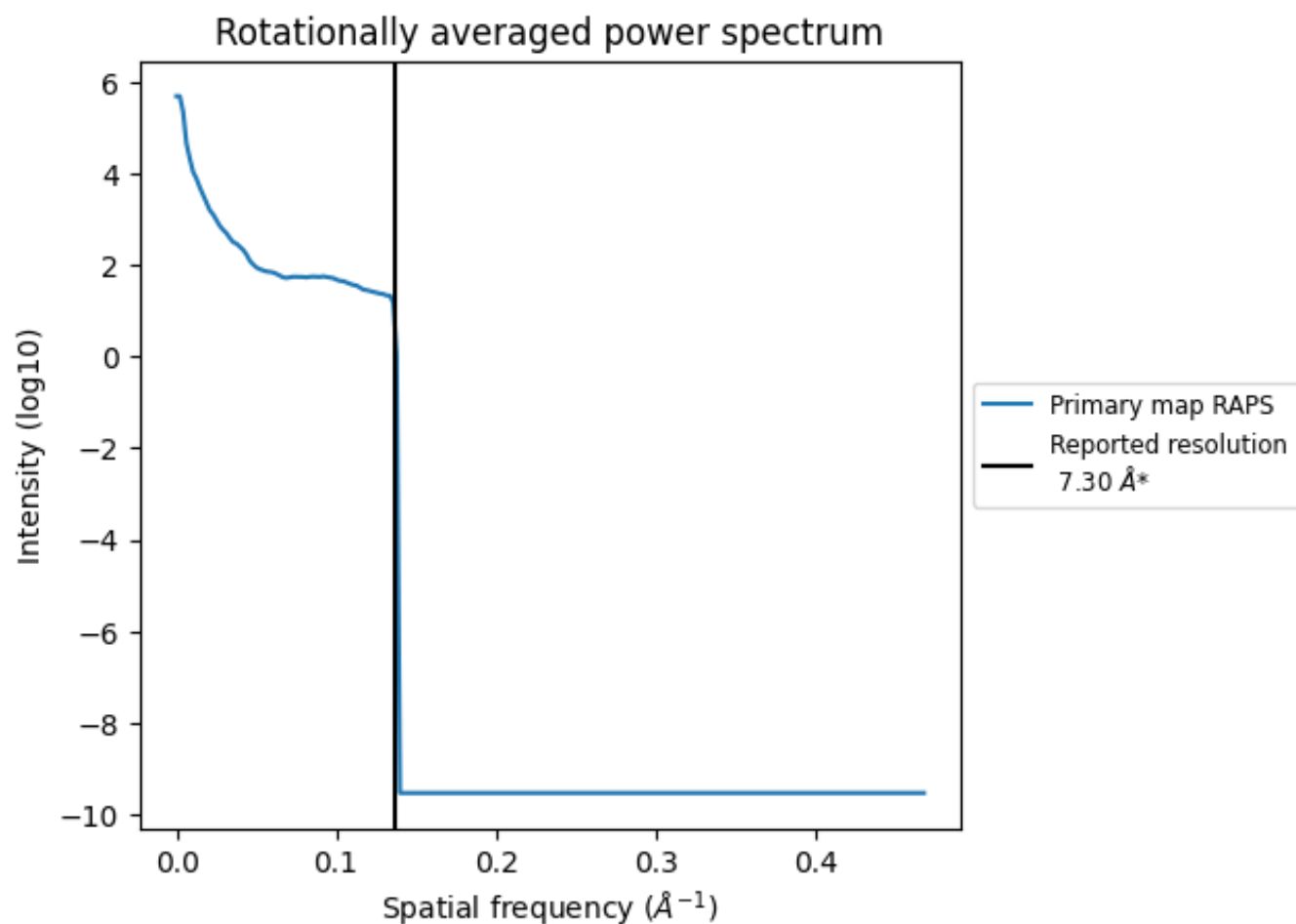
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1769 nm³; this corresponds to an approximate mass of 1598 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 ⓘ

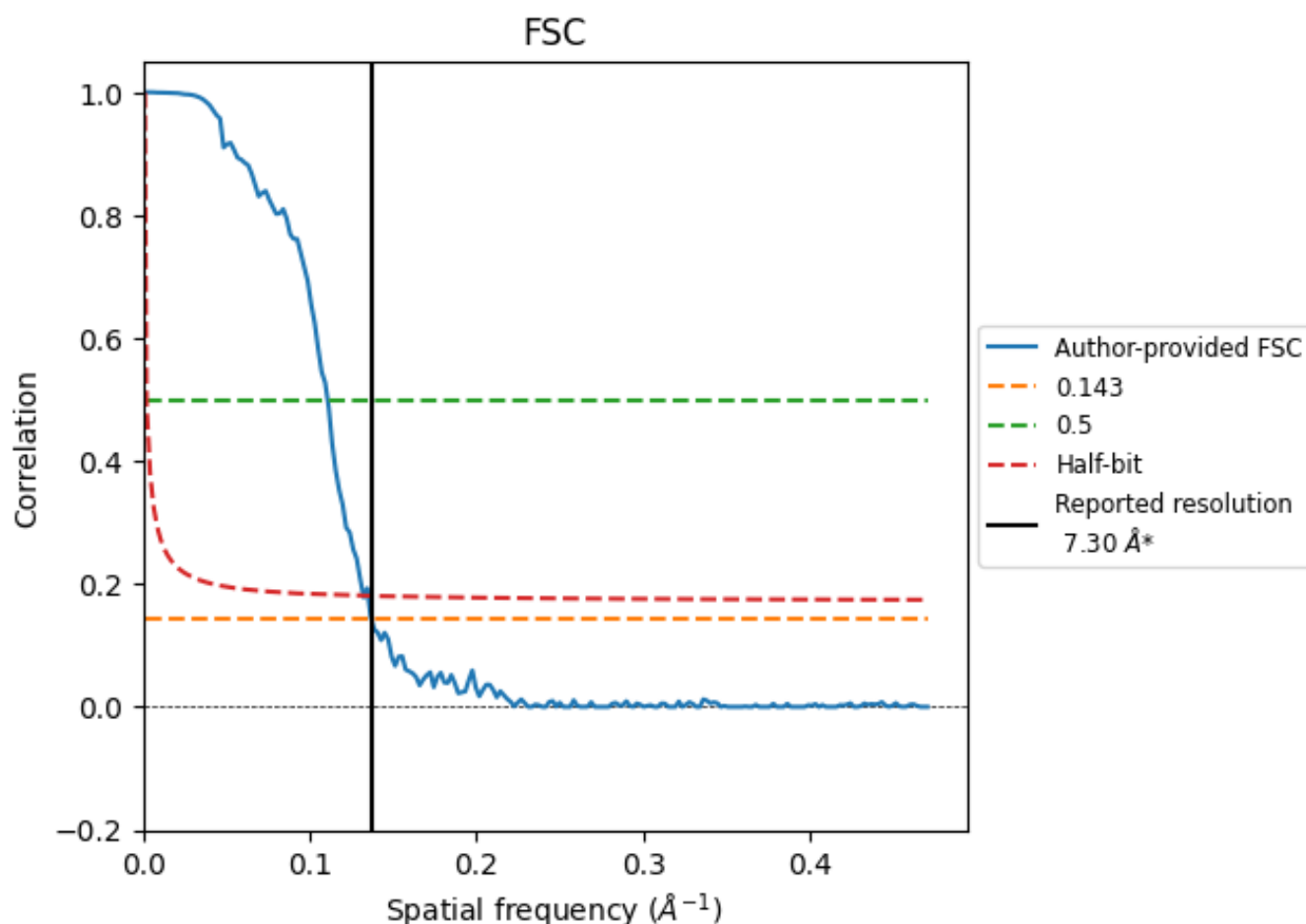


*Reported resolution corresponds to spatial frequency of 0.137 $\text{\AA}^{-1}$

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 $0.137 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

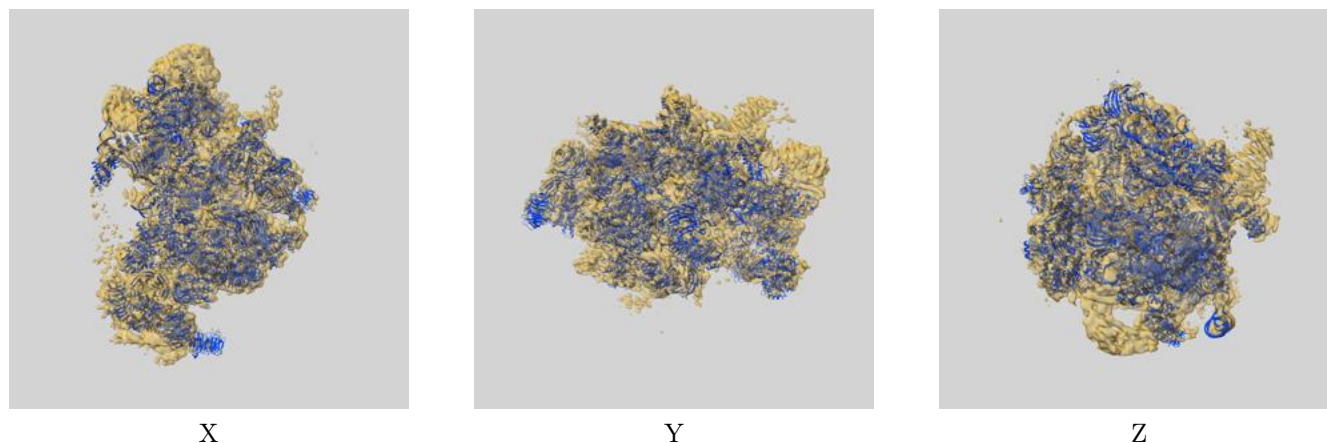
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.30	-	-
Author-provided FSC curve	7.30	9.03	7.56
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

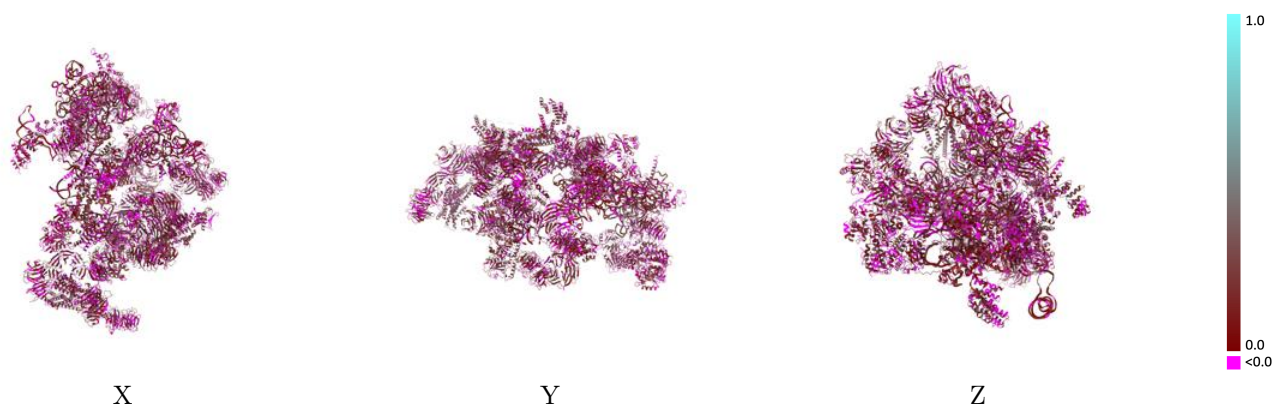
This section contains information regarding the fit between EMDB map EMD-8143 and PDB model 5JPQ. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



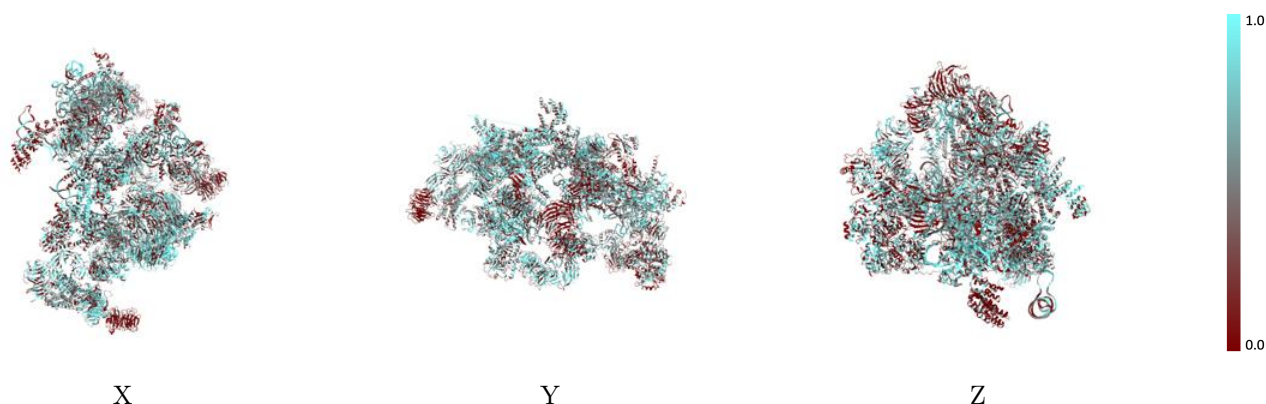
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



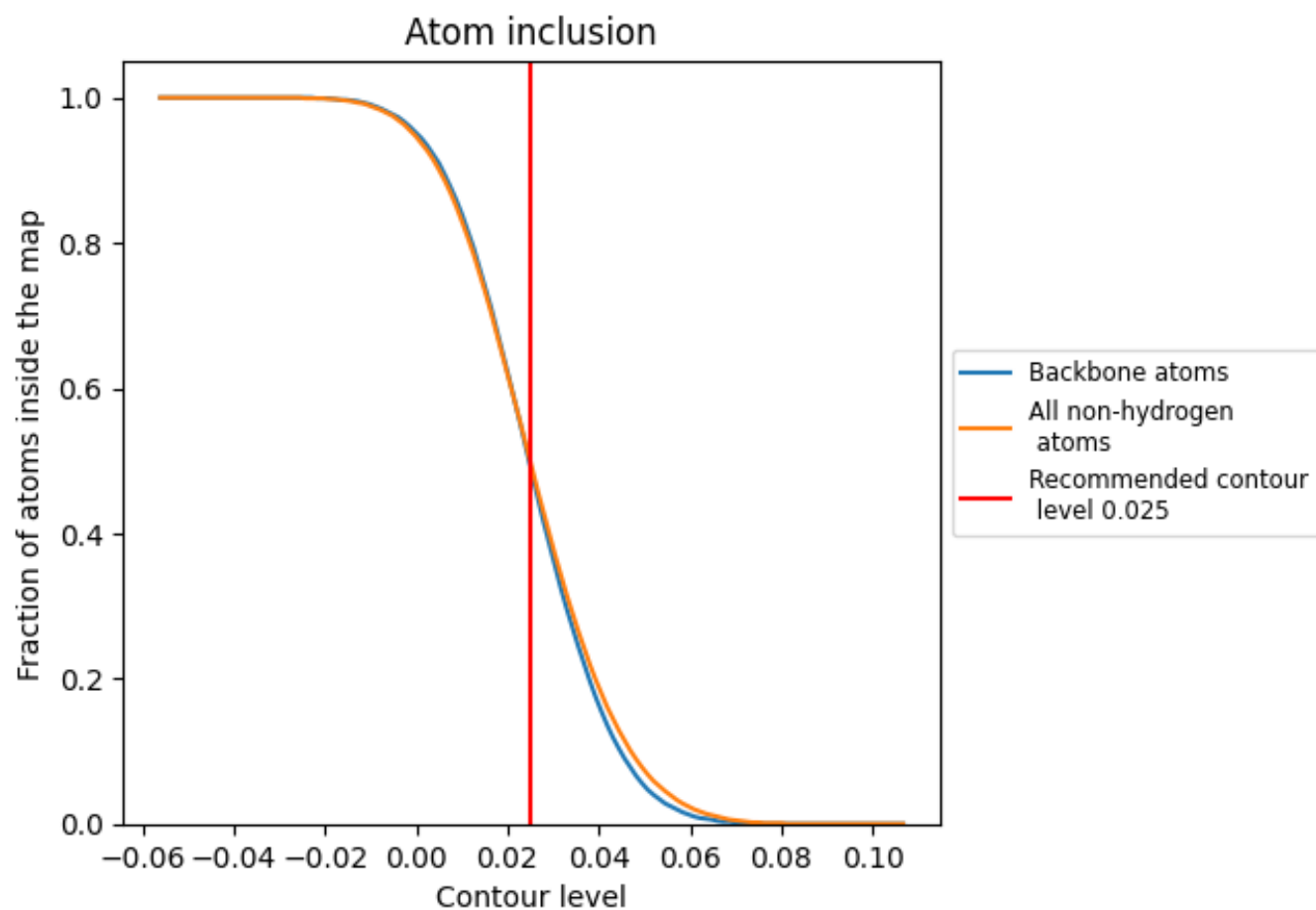
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.025).

9.4 Atom inclusion [i](#)



At the recommended contour level, 49% of all backbone atoms, 50% 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 (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4980	 0.0970
0	 0.3050	 0.0260
1	 0.4090	 0.0650
2	 0.6610	 0.1280
3	 0.6130	 0.1220
A	 0.6110	 0.0820
B	 0.5830	 0.0830
C	 0.5450	 0.0770
D	 0.6070	 0.0980
E	 0.5800	 0.0960
F	 0.0370	 0.0410
G	 0.1130	 0.0640
H	 0.4960	 0.1840
I	 0.6530	 0.1260
J	 0.4470	 0.1170
K	 0.5400	 0.0860
L	 0.5940	 0.1300
M	 0.6140	 0.1110
N	 0.2330	 0.0800
O	 0.1180	 0.0390
P	 0.5430	 0.1060
Q	 0.6010	 0.1280
R	 0.7250	 0.2060
S	 0.5240	 0.1050
T	 0.4570	 0.0770
U	 0.3580	 0.0160
V	 0.3450	 0.0050
W	 0.4000	 0.0570
X	 0.4600	 0.0650
Y	 0.5190	 0.0970
Z	 0.5700	 0.1350
a	 0.5280	 0.1590
b	 0.4850	 0.1190
c	 0.4660	 0.1190
d	 0.4560	 0.1080



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Chain	Atom inclusion	Q-score
e	 0.4720	 0.1430
f	 0.4800	 0.1490
g	 0.3550	 0.0620
h	 0.3440	 0.0650
i	 0.4080	 0.0800
j	 0.3610	 0.0740
k	 0.5390	 0.1430
l	 0.5990	 0.1410
m	 0.5480	 0.0940
n	 0.4410	 0.0680
o	 0.2980	 0.0530
p	 0.3620	 0.0230
q	 0.3370	 0.0210
r	 0.4370	 0.0780
s	 0.3020	 0.0230
t	 0.4470	 0.0610
u	 0.6240	 0.1790
v	 0.2140	 0.0690
w	 0.3270	 0.0790
x	 0.2400	 -0.0630
y	 0.3760	 0.0250
z	 0.3140	 0.0310