



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 09:02 AM UTC

PDB ID : 5TZS / pdb_00005tzs
EMDB ID : EMD-8473
Title : Architecture of the yeast small subunit processome
Authors : Chaker-Margot, M.; Barandun, J.; Hunziker, M.; Klinge, S.
Deposited on : 2016-11-22
Resolution : 5.10 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

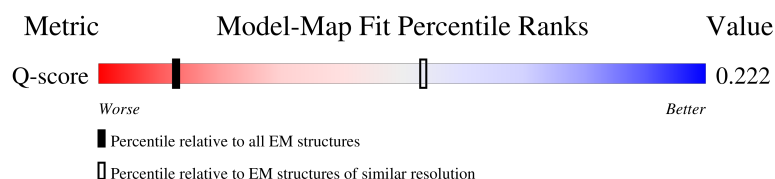
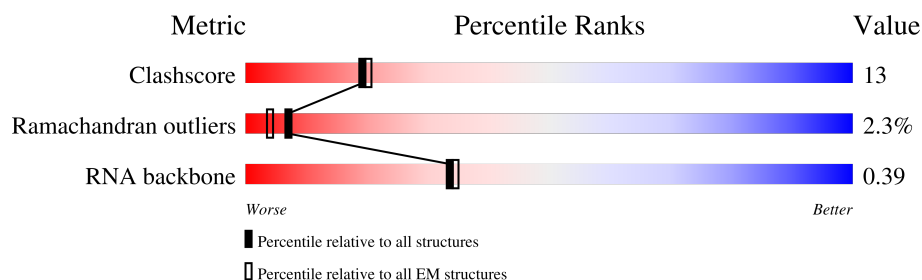
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 5.10 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
RNA backbone	8273	3508	-
Q-score	-	25397	844 (4.60 - 5.60)

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	0	364	21% 92% 8%
2	1	1800	12% 15% 10% 71%
3	2	126	12% 21% 40% 37%
4	3	236	79% 75% 15% 8%

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Mol	Chain	Length	Quality of chain
5	5	261	
6	6	225	
7	7	190	
8	8	200	
9	9	197	
10	A	39	
11	B	108	
12	C	143	
13	D	156	
14	E	130	
15	F	135	
16	G	67	
17	H	544	
18	I	176	
19	J	107	
19	K	107	
20	M	258	
21	N	545	
22	O	638	
23	P	306	
24	Q	710	
25	R	717	
26	S	250	
27	T	781	
28	U	284	

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Mol	Chain	Length	Quality of chain
29	V	263	
30	W	104	
31	X	640	
32	Y	641	
33	Z	151	
34	a	312	
35	b	341	
36	c	221	
37	d	216	
38	e	126	
38	f	126	
39	g	573	
40	h	367	
41	i	511	
42	j	252	
42	k	252	
43	l	124	
44	m	156	
45	n	160	
46	o	175	
47	p	924	
48	q	372	
49	r	145	
50	s	290	
50	t	290	

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Mol	Chain	Length	Quality of chain
50	u	290	9% 85% 10% 6%
51	v	580	15% 95% ...
52	y	507	15% 87% 7% 7%
53	z	76	32% 92% 8%

2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 98451 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 5' external transcribed spacer.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	364	Total	C	N	O	P	0	0
			4476	1871	43	2198	364		

- Molecule 2 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	515	Total	C	N	O	P	0	0
			10978	4908	1957	3598	515		

- Molecule 3 is a RNA chain called U3 snoRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	126	Total	C	N	O	P	0	0
			2468	1095	388	859	126		

- Molecule 4 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	3	216	Total	C	N	O	0	0
			1063	631	216	216		

- Molecule 5 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	5	241	Total	C	N	O	0	0
			1185	703	241	241		

- Molecule 6 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	6	202	Total	C	N	O	0	0
			1000	596	202	202		

- Molecule 7 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	7	186	Total	C	N	O	0	0
			923	551	186	186		

- Molecule 8 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	8	173	Total	C	N	O	0	0
			849	503	173	173		

- Molecule 9 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	9	185	Total	C	N	O	0	0
			915	545	185	185		

- Molecule 10 is a DNA chain called 5' domain-associated.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	A	39	Total	C	O	P	0	0
			468	195	234	39		

- Molecule 11 is a DNA chain called 3' domain-associated.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	B	108	Total	C	O	P	0	0
			1296	540	648	108		

- Molecule 12 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	C	115	Total	C	N	O	0	0
			566	336	115	115		

- Molecule 13 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	D	146	Total	C	N	O	0	0
			721	429	146	146		

- Molecule 14 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	E	127	Total	C	N	O	0	0
			624	370	127	127		

- Molecule 15 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	F	90	Total	C	N	O	0	0
			444	264	90	90		

- Molecule 16 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	G	62	Total	C	N	O	0	0
			306	182	62	62		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	17	ALA	GLY	conflict	UNP Q3E7X9

- Molecule 17 is a protein called Utp4.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	H	544	Total	C	N	O	0	0
			2680	1592	544	544		

- Molecule 18 is a protein called UtpA_CTD1.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	I	176	Total	C	N	O	0	0
			880	528	176	176		

- Molecule 19 is a protein called UtpA_CTD2.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	J	107	Total	C	N	O	0	0
			535	321	107	107		
19	K	105	Total	C	N	O	0	0
			525	315	105	105		

- Molecule 20 is a protein called Beta-propeller 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	M	258	Total	C	N	O	0	0
			1275	759	258	258		

- Molecule 21 is a protein called Utp17.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	N	545	Total	C	N	O	0	0
			2678	1588	545	545		

- Molecule 22 is a protein called Utp1.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	O	638	Total	C	N	O	0	0
			3153	1877	638	638		

- Molecule 23 is a protein called Utp6.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	P	306	Total	C	N	O	0	0
			1530	918	306	306		

- Molecule 24 is a protein called Utp12.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	Q	710	Total	C	N	O	0	0
			3503	2083	710	710		

- Molecule 25 is a protein called Utp13.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	R	717	Total	C	N	O	0	0
			3539	2105	717	717		

- Molecule 26 is a protein called Utp18.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	S	250	Total	C	N	O	0	0
			1228	728	250	250		

- Molecule 27 is a protein called U3 small nucleolar RNA-associated protein 21,Utp21.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	T	749	Total	C	N	O	0	0
			3691	2193	749	749		

- Molecule 28 is a protein called Beta-propeller 5.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	U	284	Total	C	N	O	0	0
			1398	830	284	284		

- Molecule 29 is a protein called Enp2.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	V	263	Total	C	N	O	0	0
			1298	772	263	263		

- Molecule 30 is a protein called UtpA_CTD4.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	W	104	Total	C	N	O	0	0
			520	312	104	104		

- Molecule 31 is a protein called Kre33.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	X	640	Total	C	N	O	0	0
			3155	1875	640	640		

- Molecule 32 is a protein called Kre33.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	Y	641	Total	C	N	O	0	0
			3160	1878	641	641		

- Molecule 33 is a protein called Imp3.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	Z	151	Total	C	N	O	0	0
			748	446	151	151		

- Molecule 34 is a protein called Nop56.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	a	312	Total	C	N	O	0	0
			1544	920	312	312		

- Molecule 35 is a protein called Nop58.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	b	341	Total	C	N	O	0	0
			1687	1005	341	341		

- Molecule 36 is a protein called Nop1.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	c	221	Total	C	N	O	0	0
			1088	646	221	221		

- Molecule 37 is a protein called Nop1.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	d	216	Total	C	N	O	0	0
			1064	632	216	216		

- Molecule 38 is a protein called 13 kDa ribonucleoprotein-associated protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	e	122	Total	C	N	O	0	0
			606	362	122	122		
38	f	114	Total	C	N	O	0	0
			566	338	114	114		

- Molecule 39 is a protein called Ribosomal RNA-processing protein 9.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	g	365	Total	C	N	O	0	0
			1799	1069	365	365		

- Molecule 40 is a protein called RNA 3'-terminal phosphate cyclase-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	h	355	Total	C	N	O	0	0
			1742	1032	355	355		

- Molecule 41 is a protein called Bms1,Ribosome biogenesis protein BMS1,Bms1,Ribosome

biogenesis protein BMS1.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	i	475	Total	C	N	O	0	0
			2347	1398	475	474		

- Molecule 42 is a protein called Ribosomal RNA small subunit methyltransferase NEP1.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	j	211	Total	C	N	O	0	0
			1047	625	211	211		
42	k	218	Total	C	N	O	0	0
			1081	645	218	218		

- Molecule 43 is a protein called Utp24.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	l	124	Total	C	N	O	0	0
			613	365	124	124		

- Molecule 44 is a protein called Imp4.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	m	156	Total	C	N	O	0	0
			775	463	156	156		

- Molecule 45 is a protein called Utp30.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	n	160	Total	C	N	O	0	0
			791	471	160	160		

- Molecule 46 is a protein called Unassigned KH domain.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	o	173	Total	C	N	O	0	0
			858	512	173	173		

- Molecule 47 is a protein called Utp20.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	p	924	Total	C	N	O	0	0
			4620	2772	924	924		

- Molecule 48 is a protein called Repeat protein 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	q	372	Total	C	N	O	0	0
			1860	1116	372	372		

- Molecule 49 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	r	82	Total	C	N	O	0	0
			402	238	82	82		

- Molecule 50 is a protein called Beta-propeller 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	s	290	Total	C	N	O	0	0
			1429	849	290	290		
50	t	269	Total	C	N	O	0	0
			1076	538	269	269		
50	u	274	Total	C	N	O	0	0
			1346	798	274	274		

- Molecule 51 is a protein called Repeat protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	v	577	Total	C	N	O	0	0
			2885	1731	577	577		

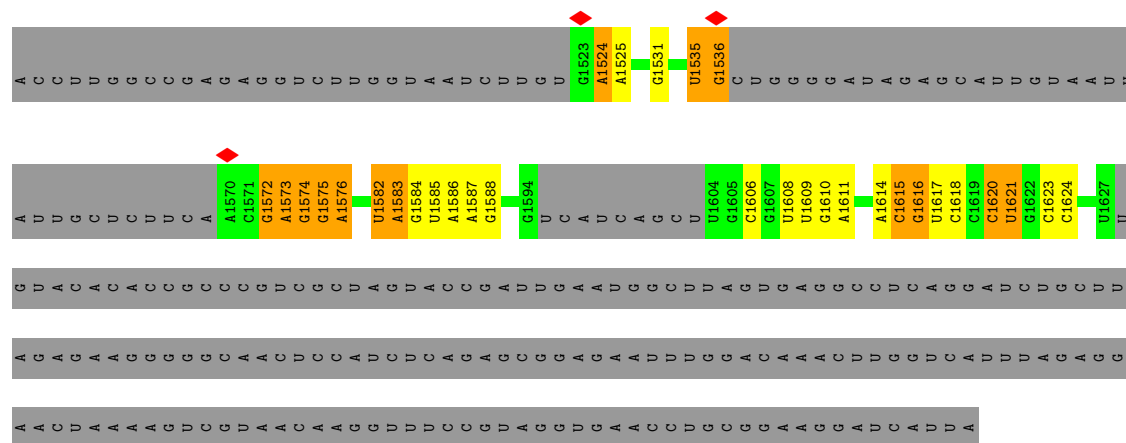
- Molecule 52 is a protein called Unassigned protein helices.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	y	507	Total	C	N	O	0	0
			2535	1521	507	507		

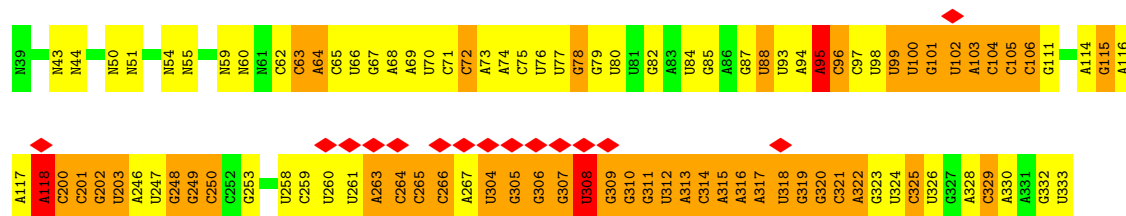
- Molecule 53 is a DNA chain called Unassigned RNA helices.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	z	76	Total	C	O	P	0	0
			912	380	456	76		

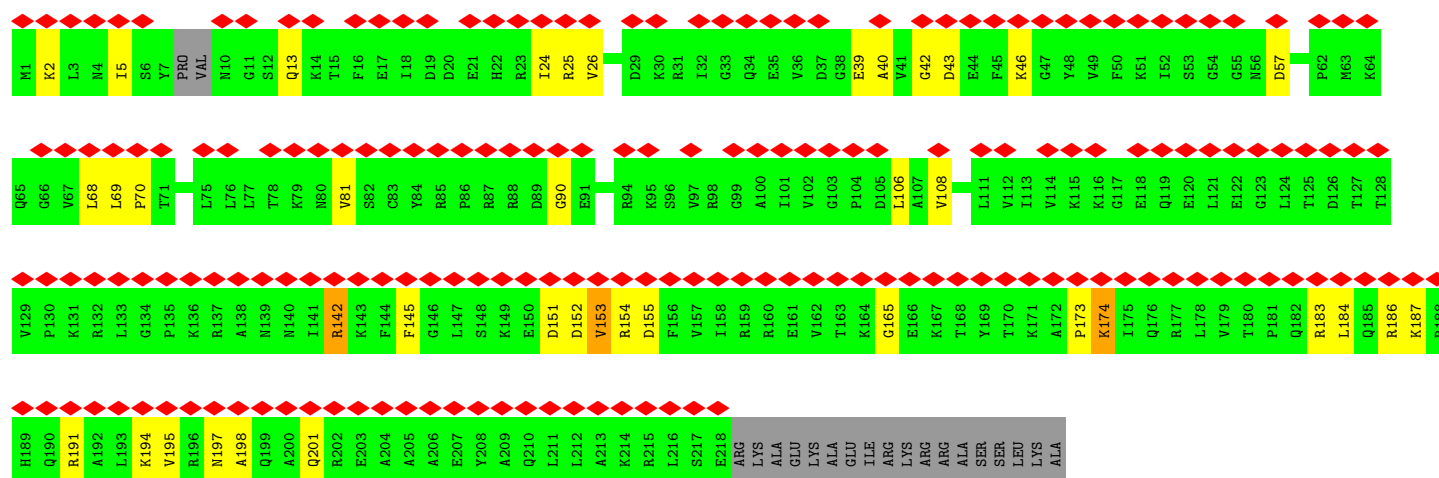
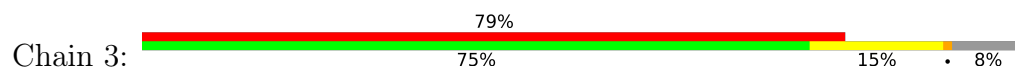




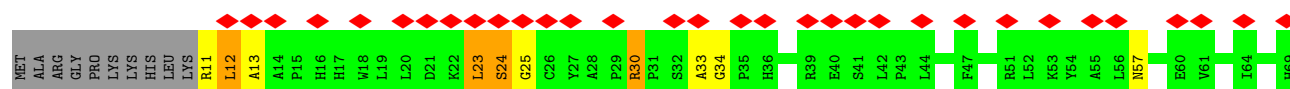
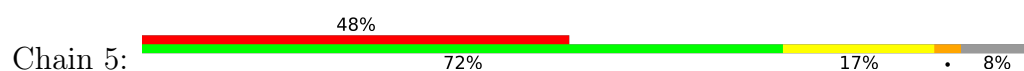
• Molecule 3: U3 snoRNA

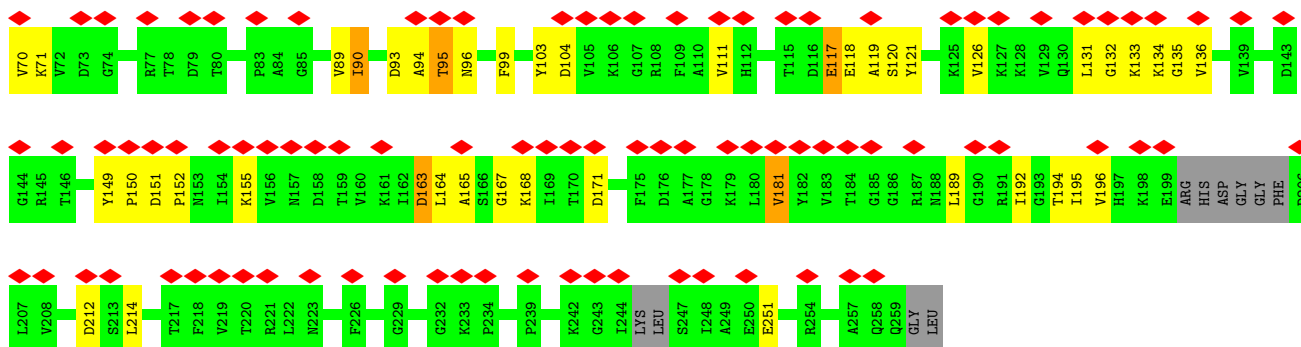


• Molecule 4: 40S ribosomal protein S6-A



• Molecule 5: 40S ribosomal protein S4-A

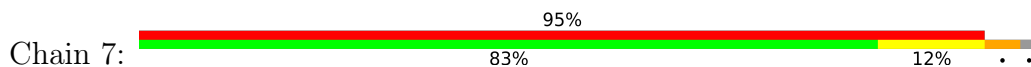




• Molecule 6: 40S ribosomal protein S5

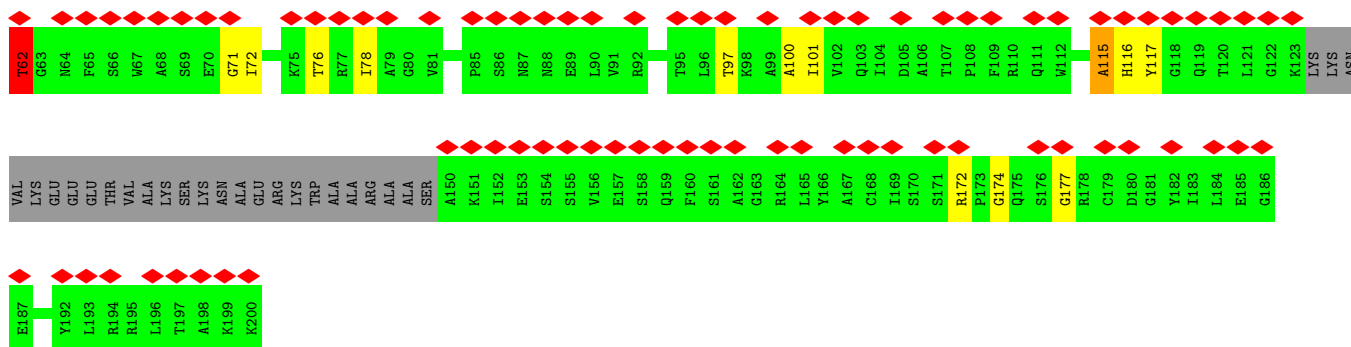


• Molecule 7: 40S ribosomal protein S7-A

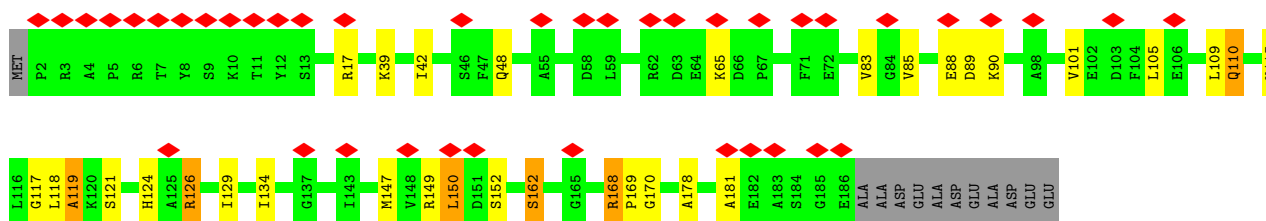
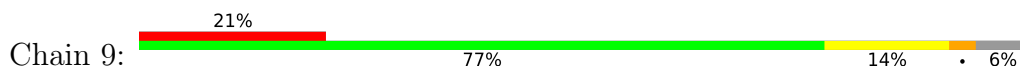


• Molecule 8: 40S ribosomal protein S8-A





• Molecule 9: 40S ribosomal protein S9-A

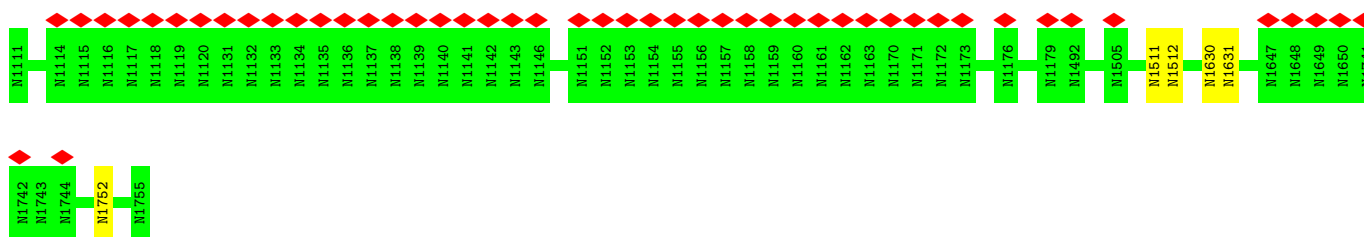


• Molecule 10: 5' domain-associated



There are no outlier residues recorded for this chain.

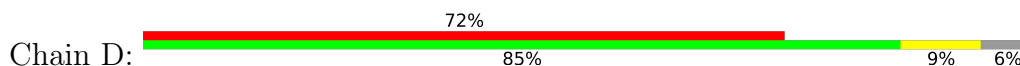
• Molecule 11: 3' domain-associated

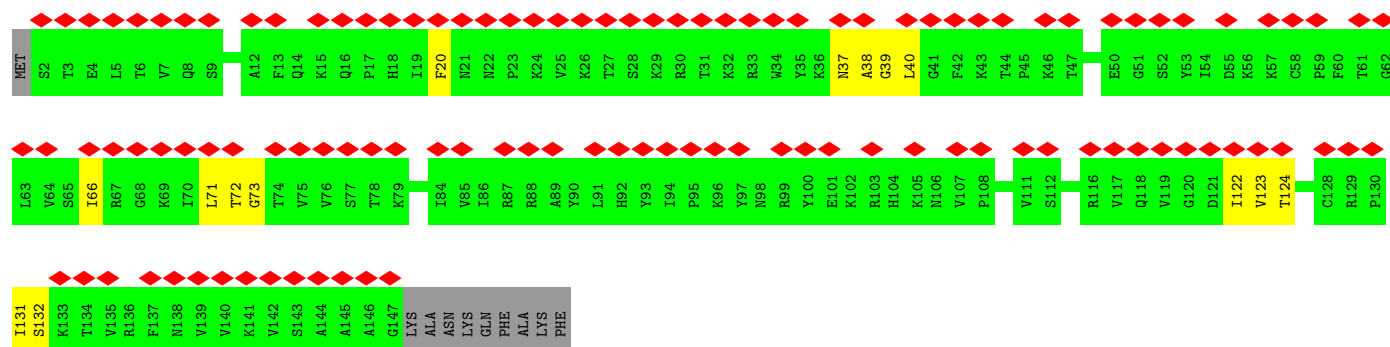


• Molecule 12: 40S ribosomal protein S16-A

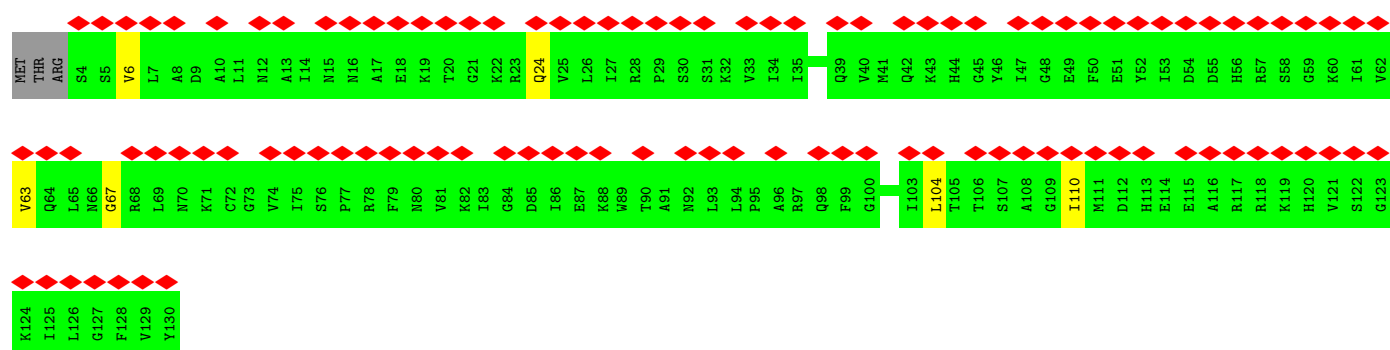
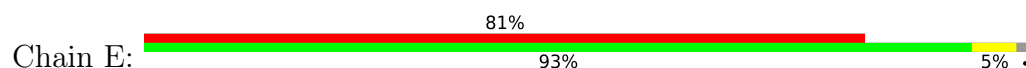


• Molecule 13: 40S ribosomal protein S11-A

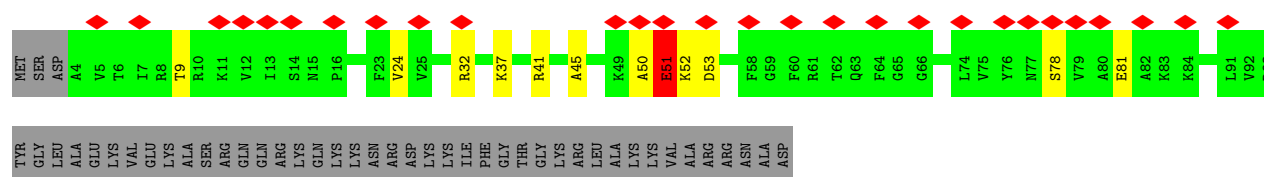




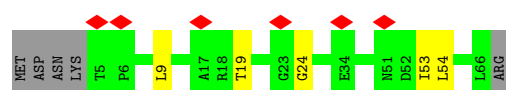
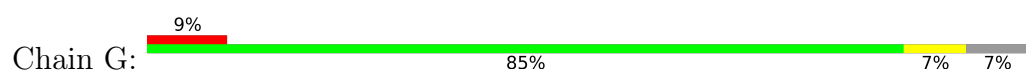
• Molecule 14: 40S ribosomal protein S22-A



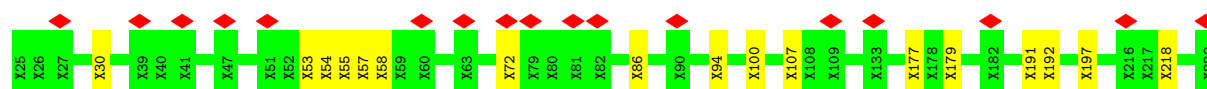
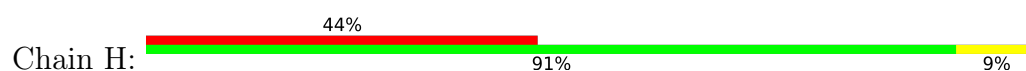
• Molecule 15: 40S ribosomal protein S24-A

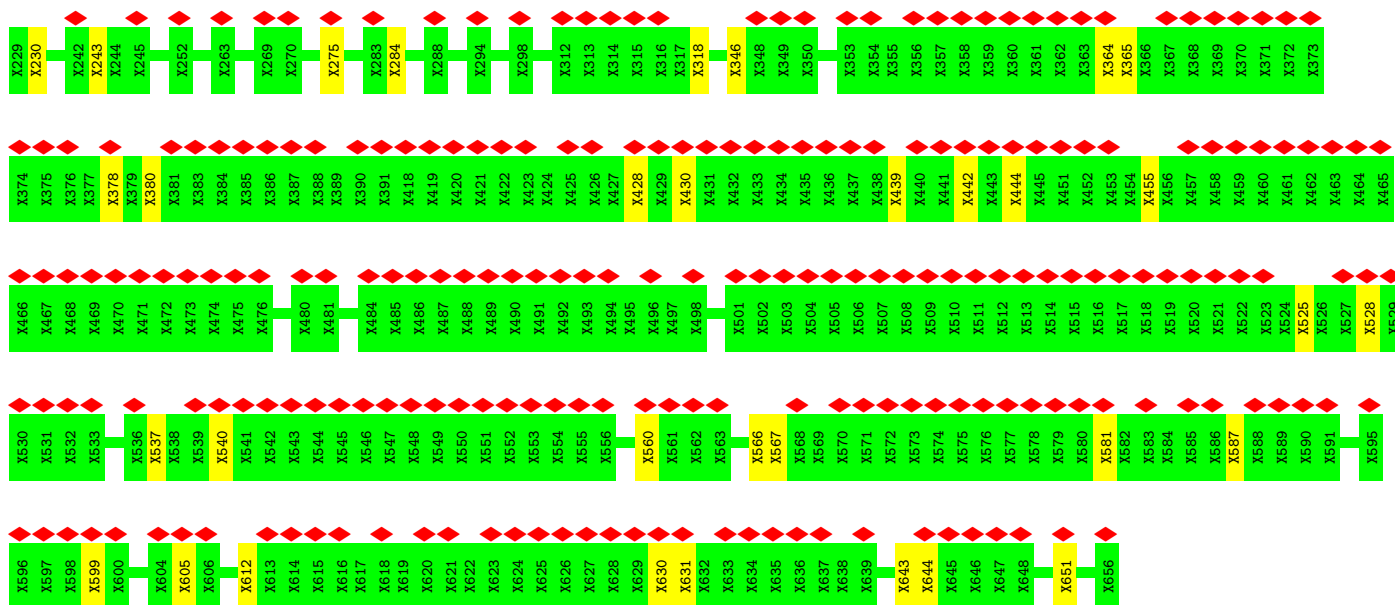


• Molecule 16: 40S ribosomal protein S28-A

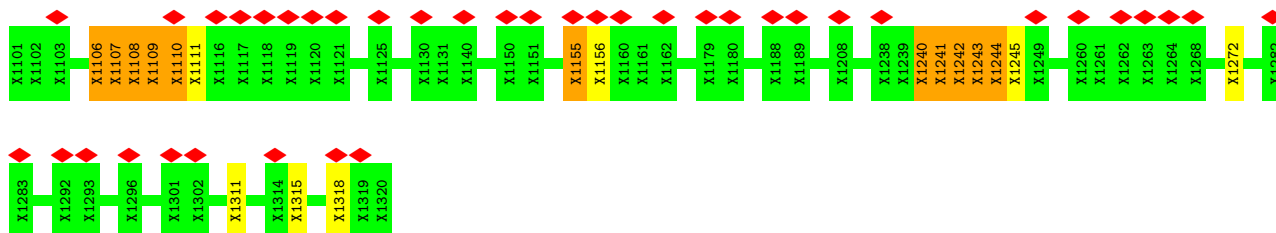


• Molecule 17: Utp4

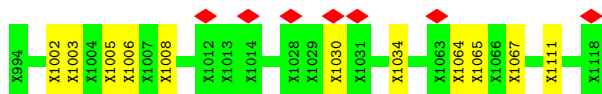
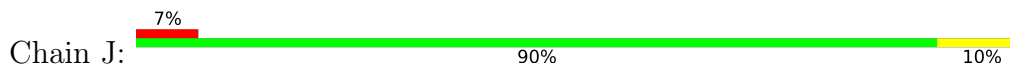




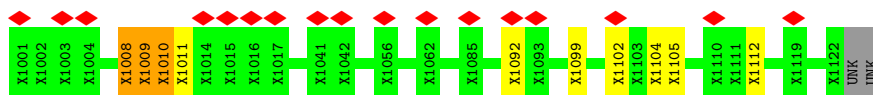
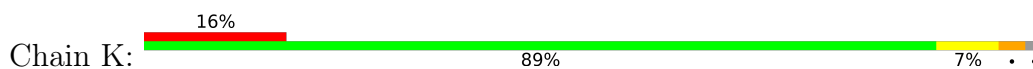
• Molecule 18: UtpA_CTD1



• Molecule 19: UtpA_CTD2

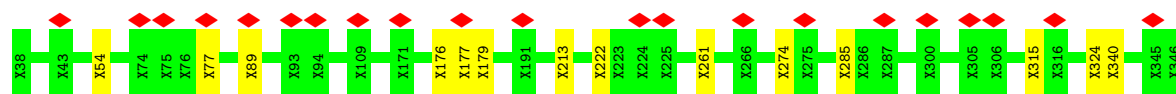


• Molecule 19: UtpA_CTD2

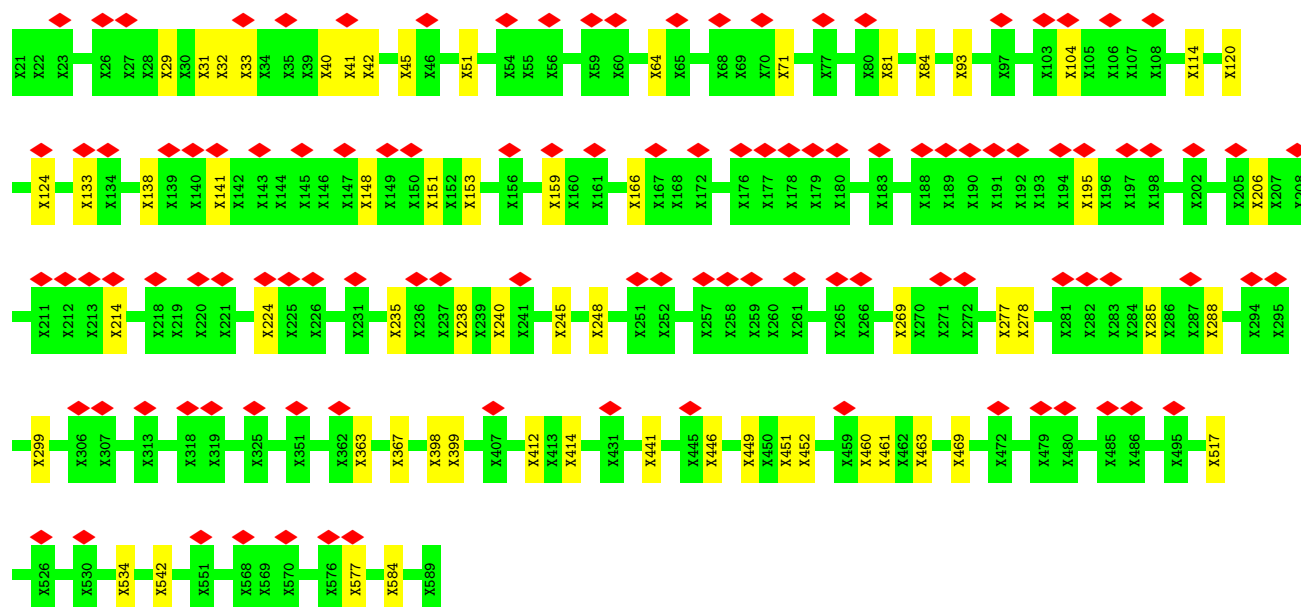
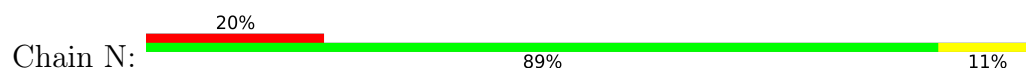


• Molecule 20: Beta-propeller 2

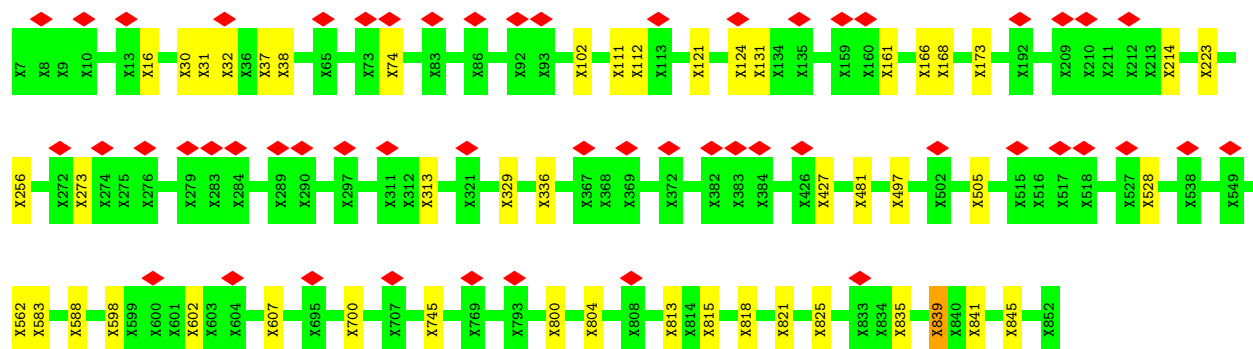




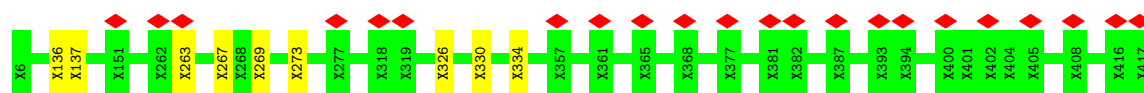
- Molecule 21: Utp17



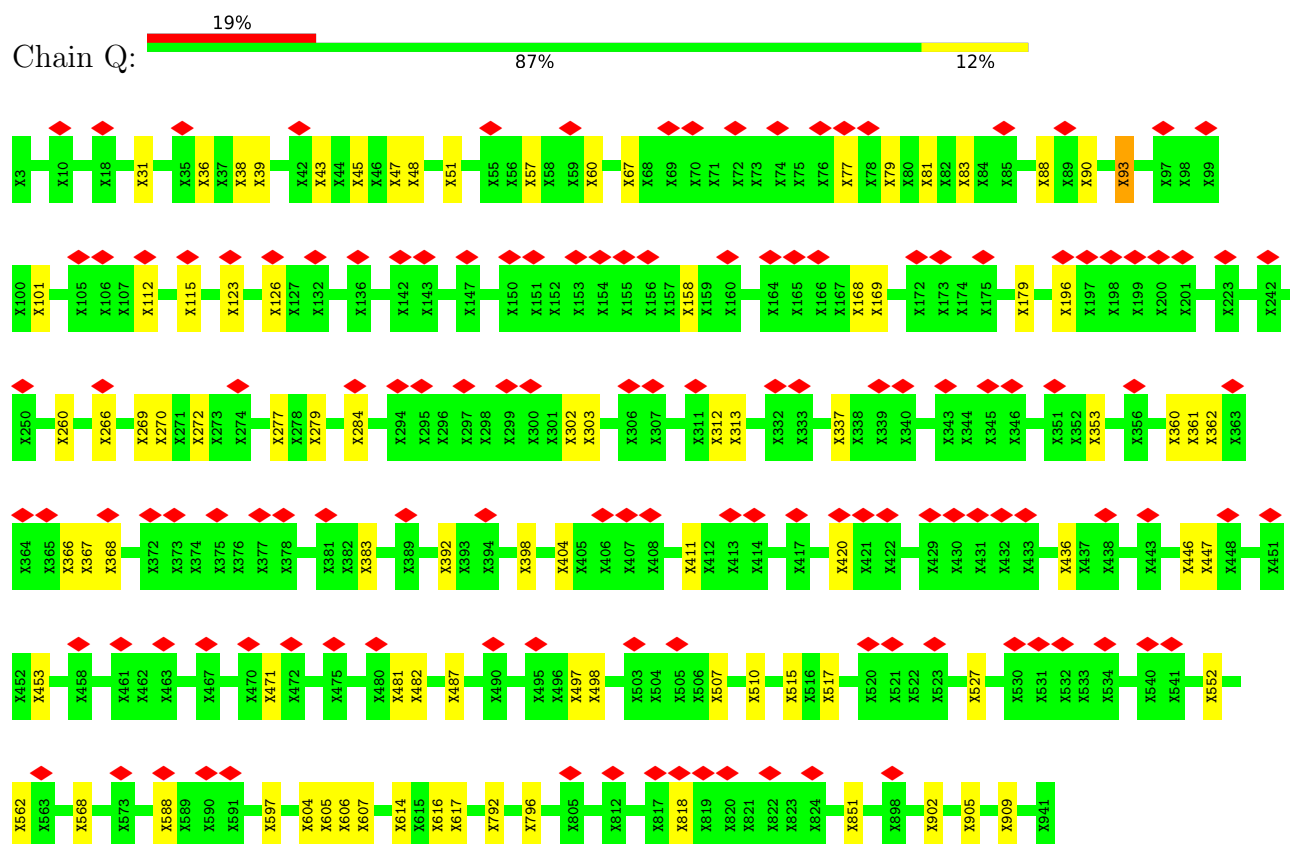
- Molecule 22: Utp1



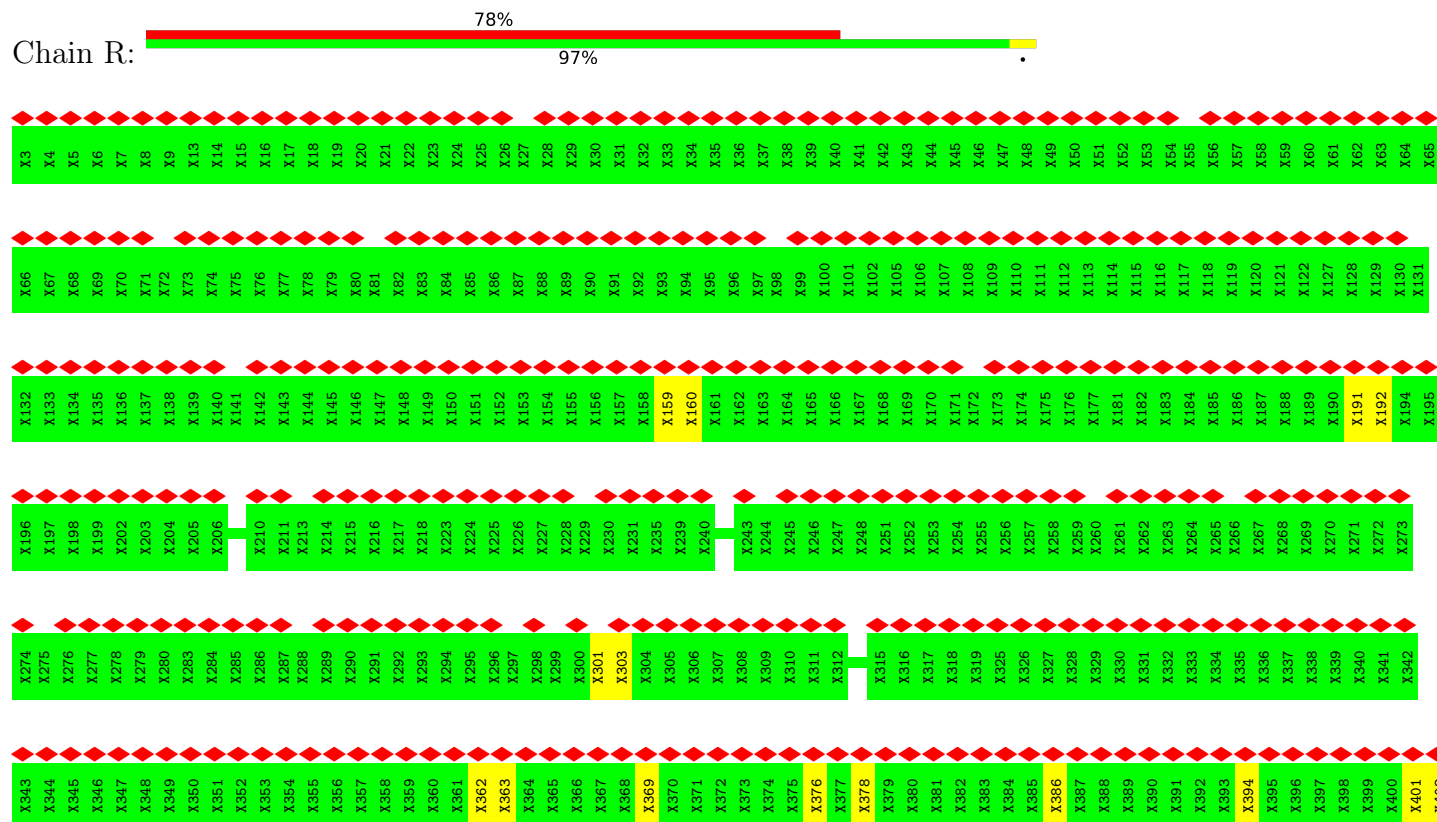
- Molecule 23: Utp6

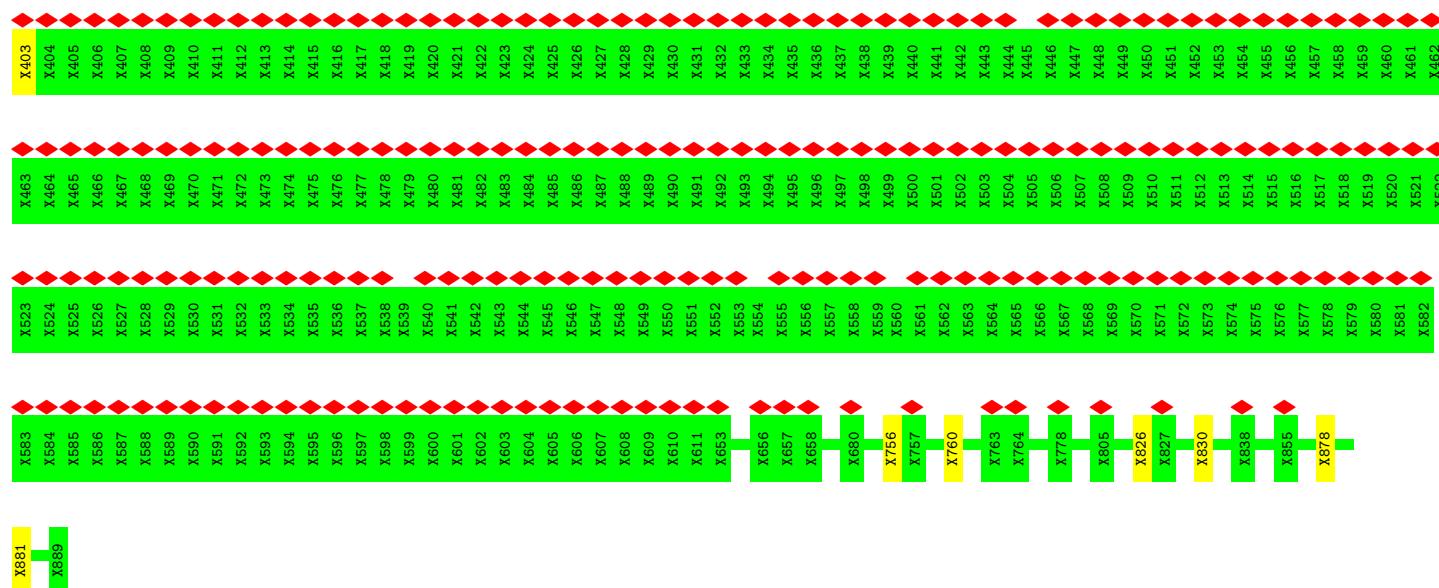


- Molecule 24: Utp12

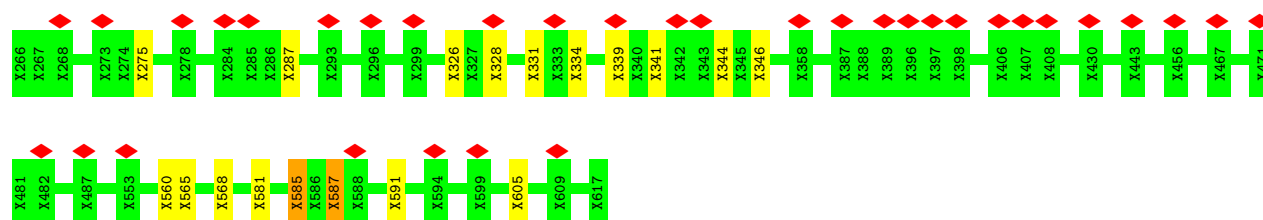


- Molecule 25: Utp13

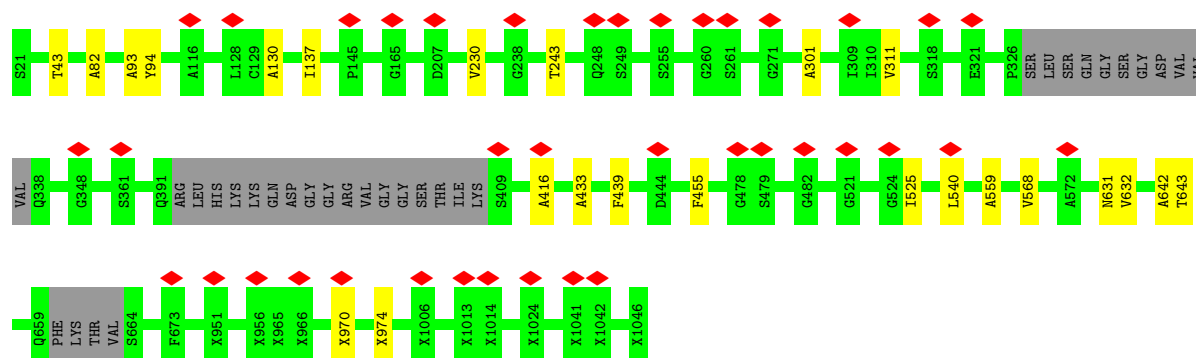




- Molecule 26: Utp18

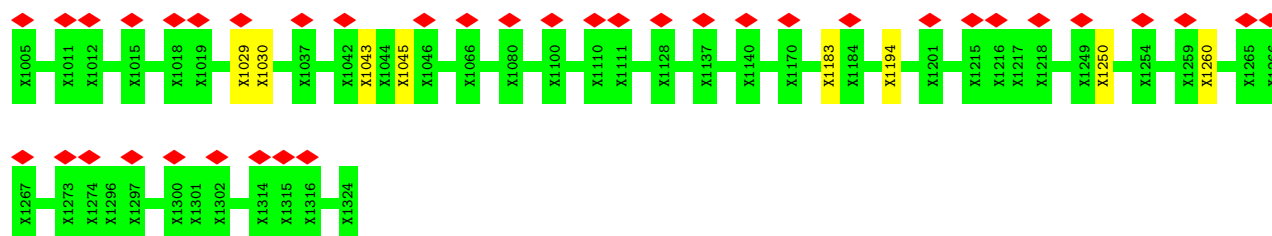


- Molecule 27: U3 small nucleolar RNA-associated protein 21, Utp21

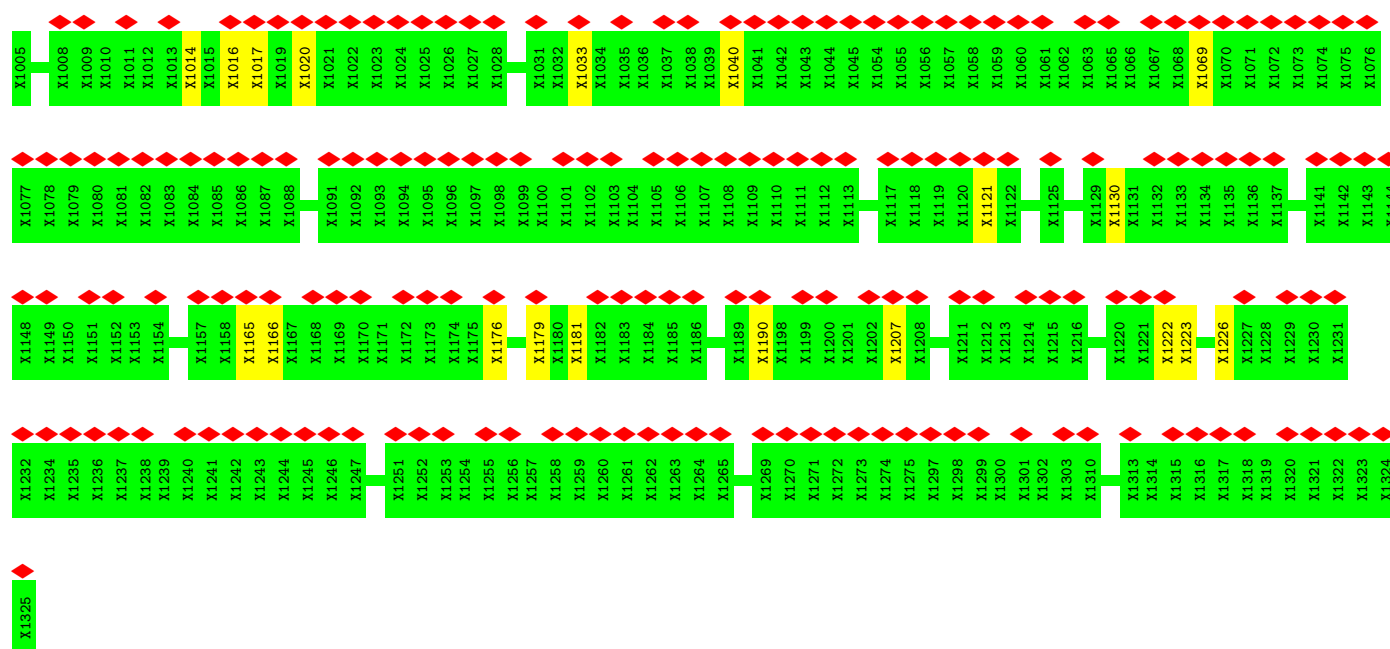
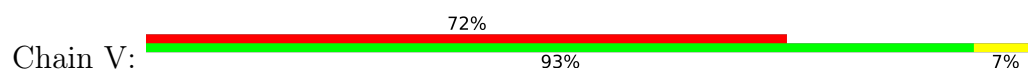


- Molecule 28: Beta-propeller 5

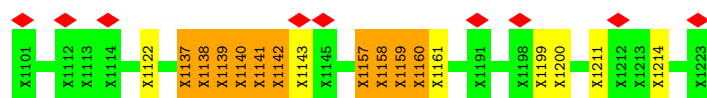
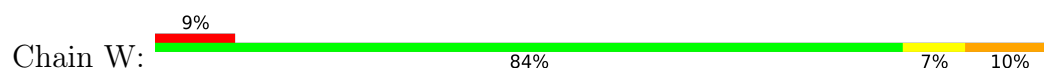




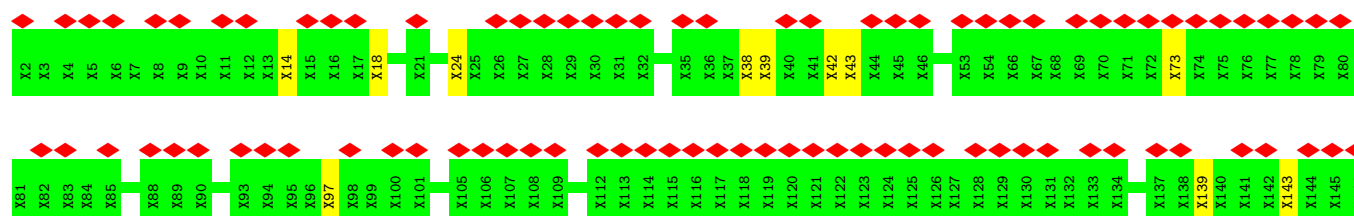
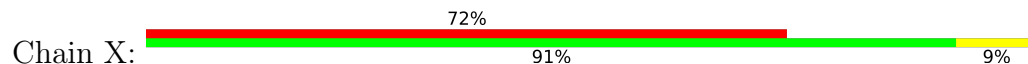
• Molecule 29: Enp2

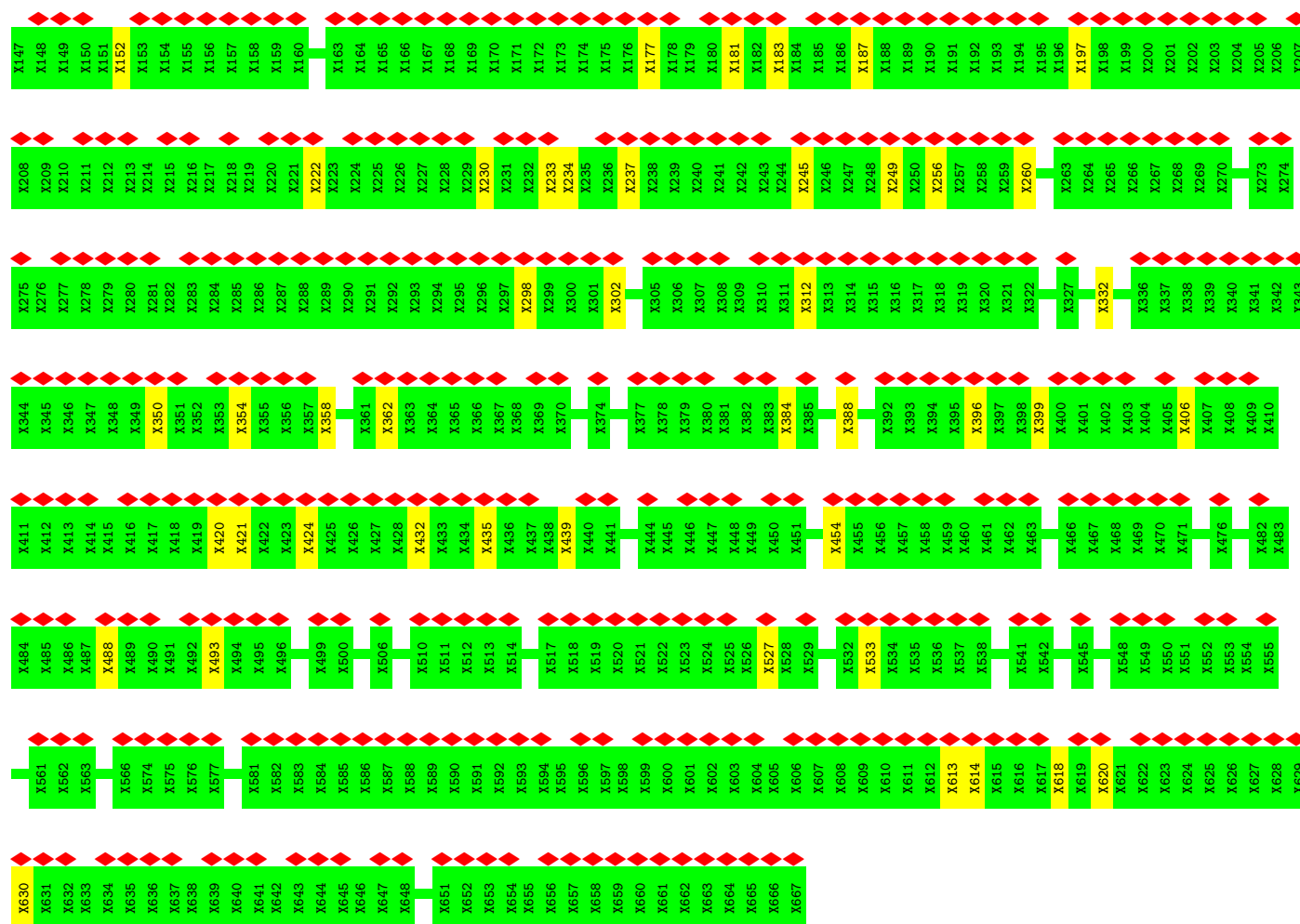


• Molecule 30: UtpA_CTD4



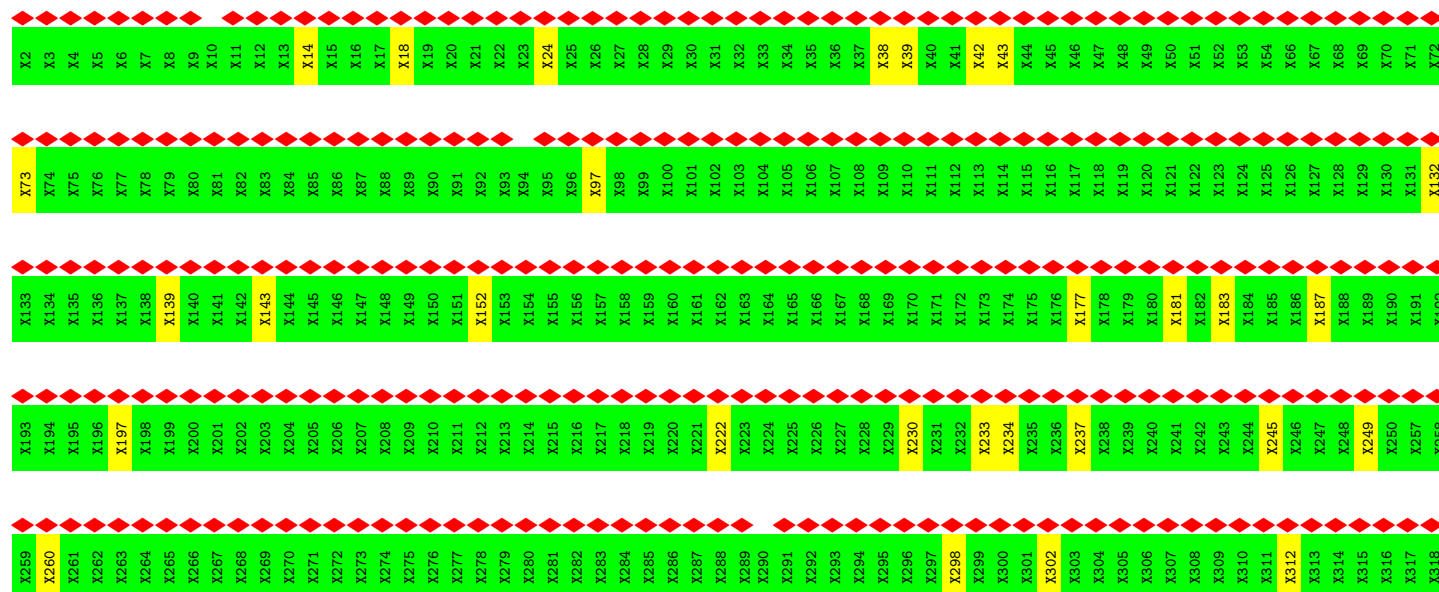
• Molecule 31: Kre33

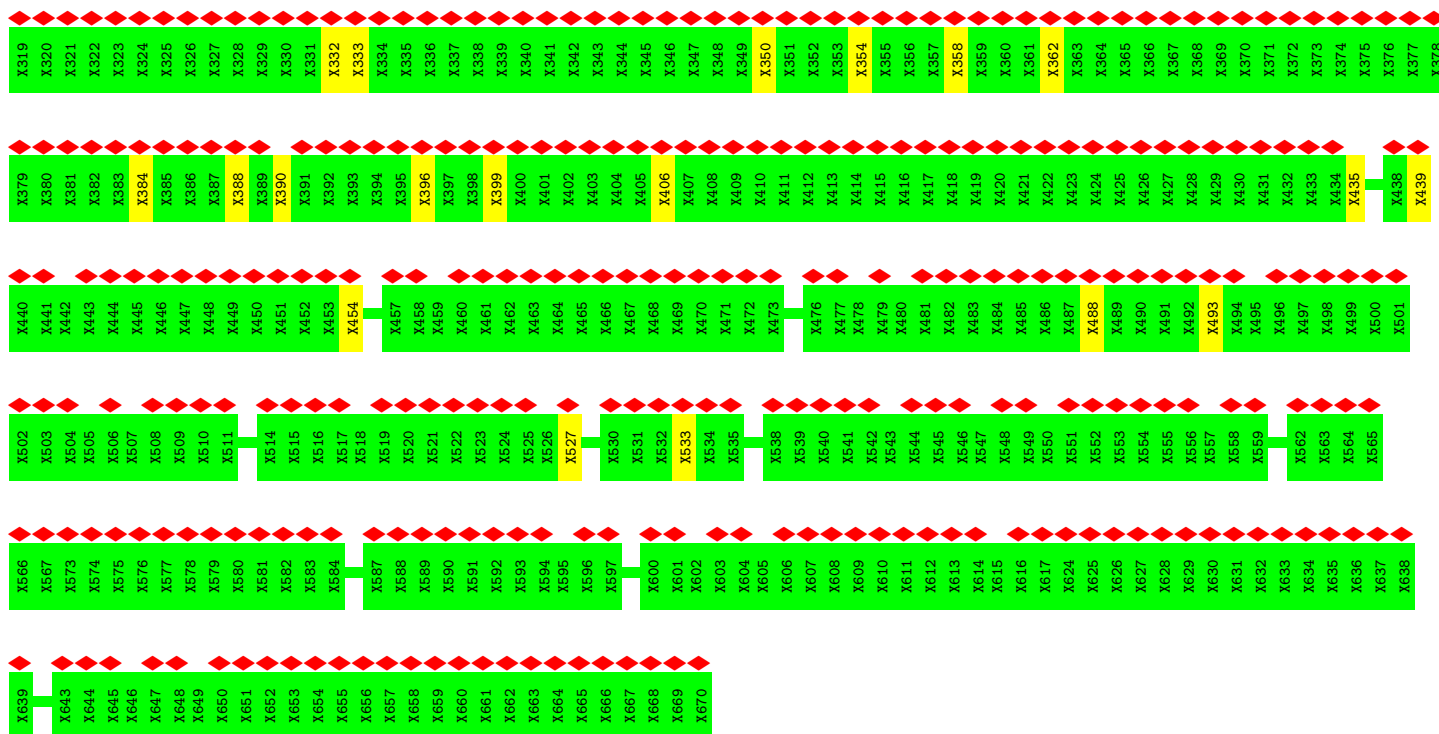




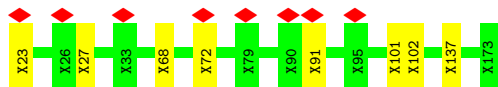
• Molecule 32: Kre33

Chain Y: 93% 7%

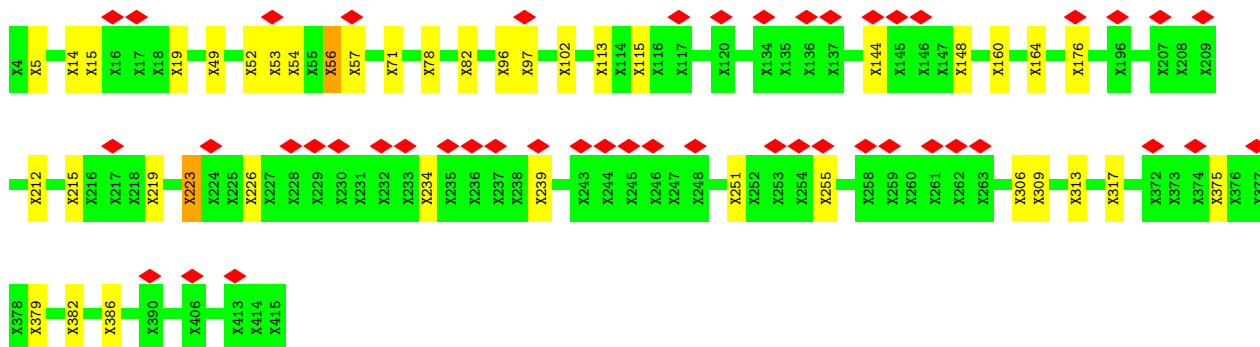
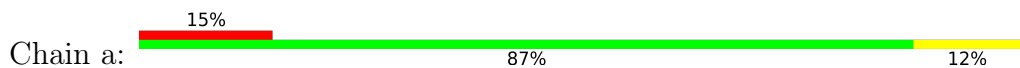




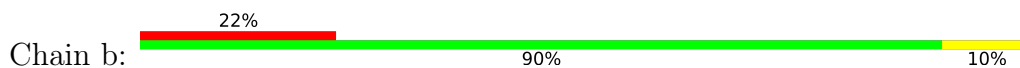
- Molecule 33: Imp3

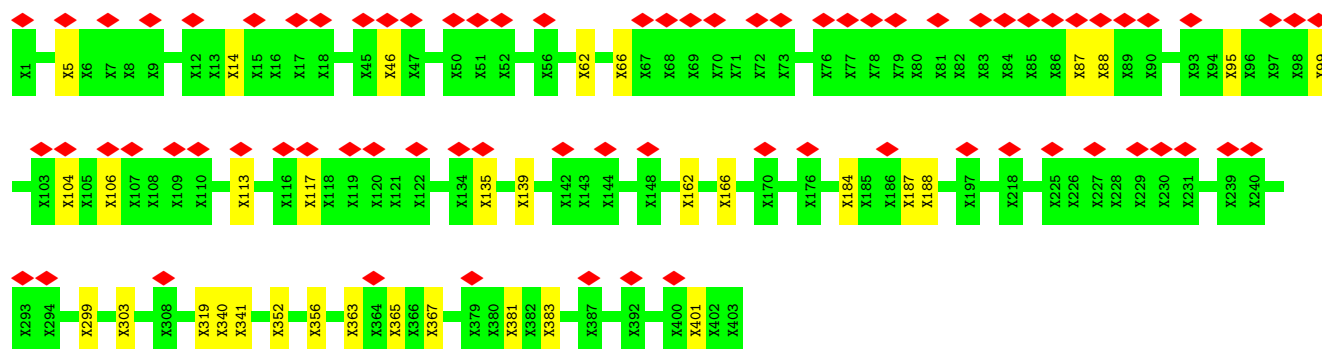


- Molecule 34: Nop56



- Molecule 35: Nop58

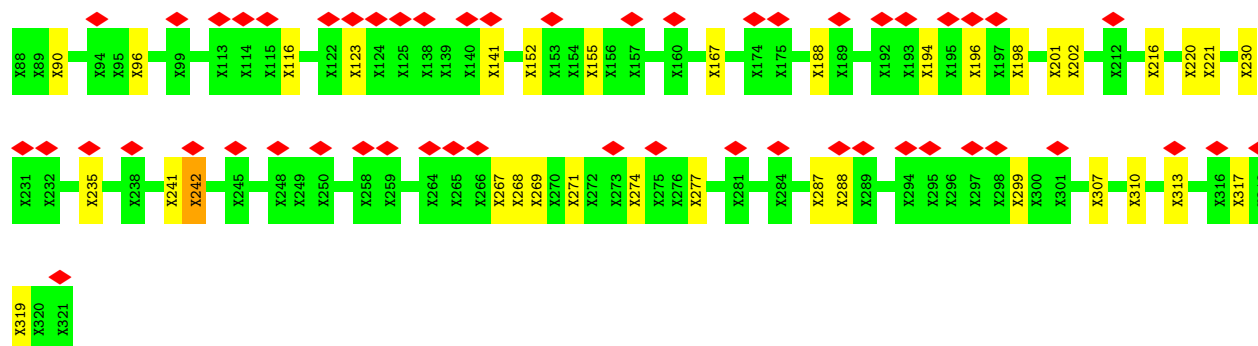
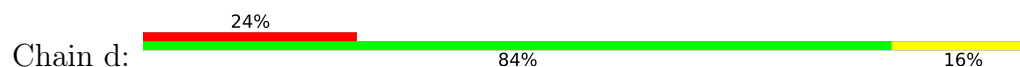




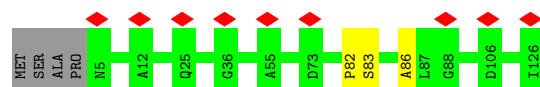
- Molecule 36: Nop1



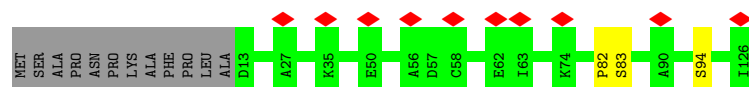
- Molecule 37: Nop1



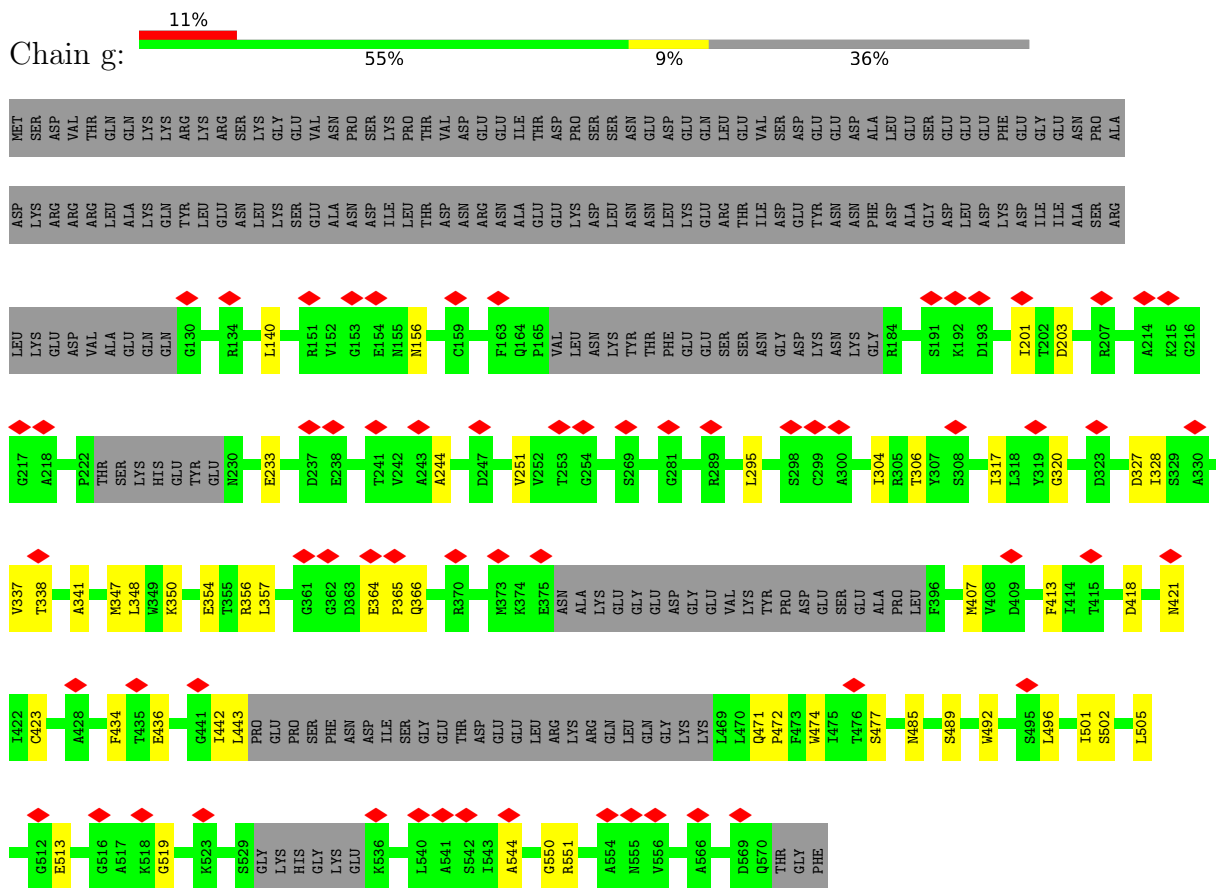
- Molecule 38: 13 kDa ribonucleoprotein-associated protein



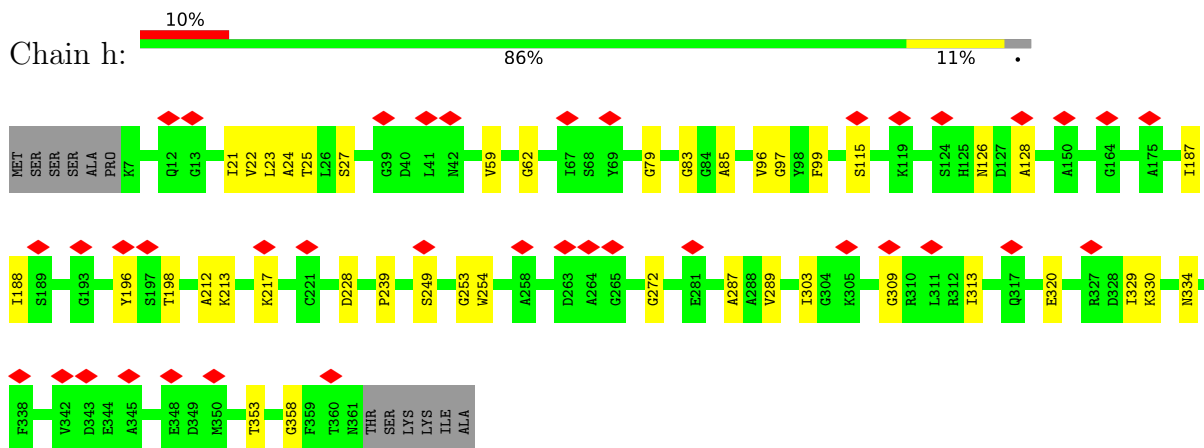
- Molecule 38: 13 kDa ribonucleoprotein-associated protein



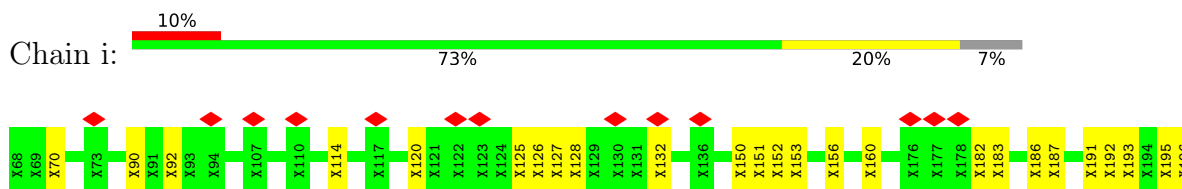
- Molecule 39: Ribosomal RNA-processing protein 9

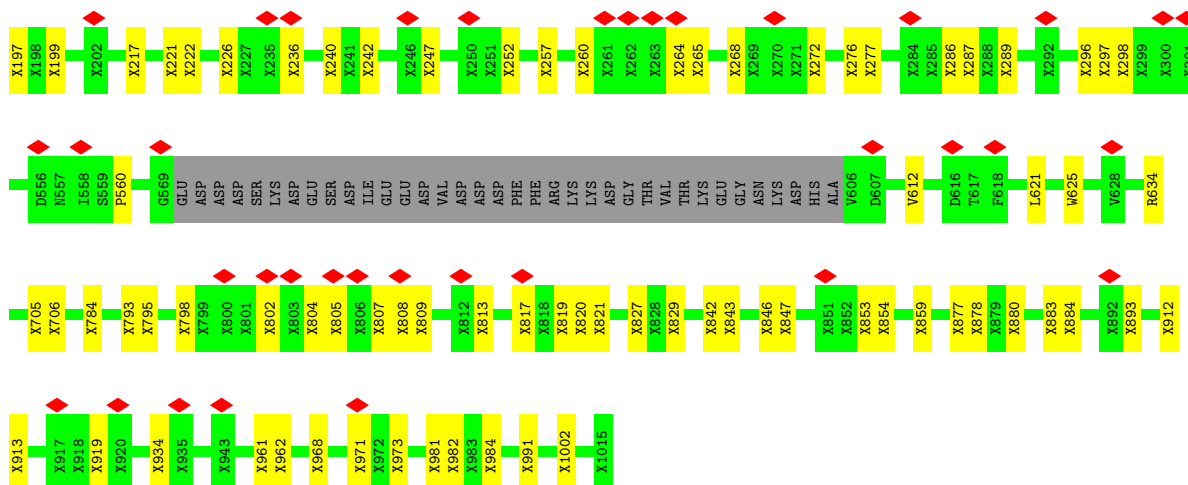


- Molecule 40: RNA 3'-terminal phosphate cyclase-like protein

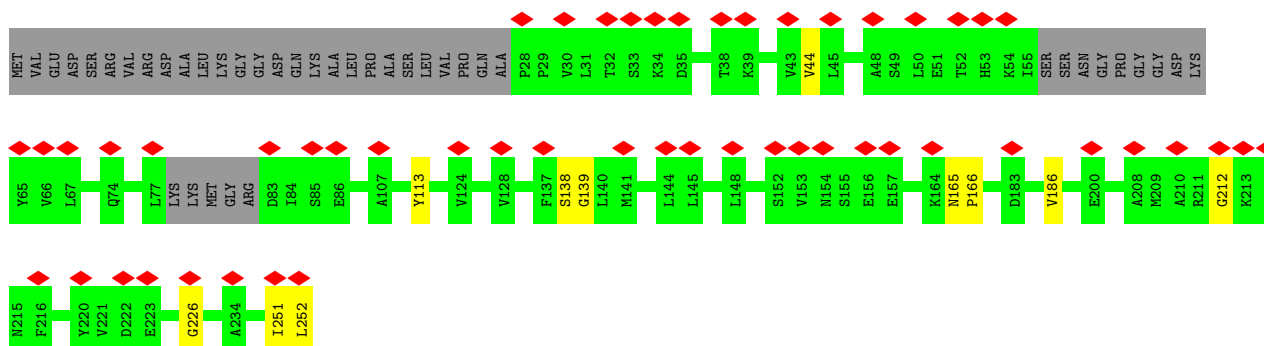
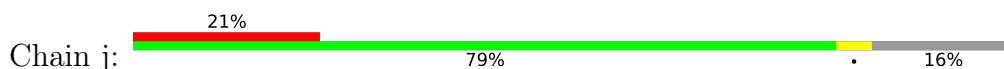


- Molecule 41: Bms1, Ribosome biogenesis protein BMS1, Bms1, Ribosome biogenesis protein BMS1

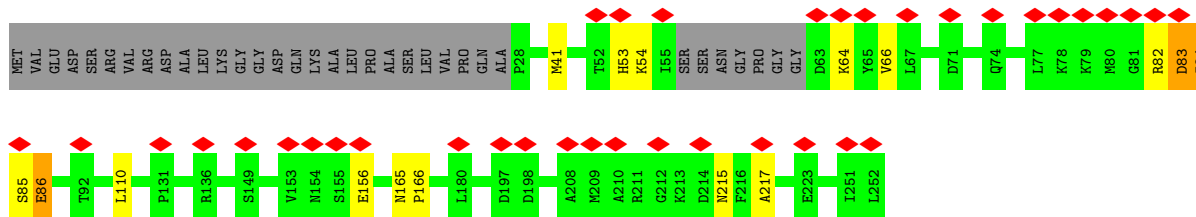
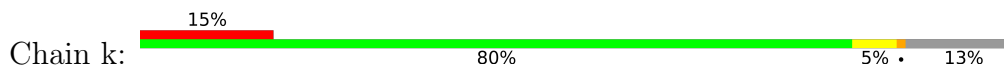




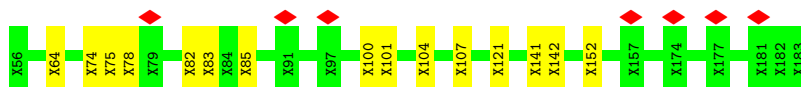
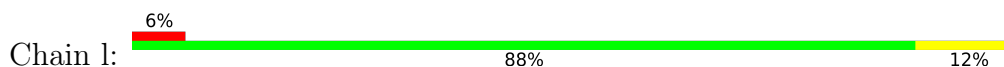
- Molecule 42: Ribosomal RNA small subunit methyltransferase NEP1



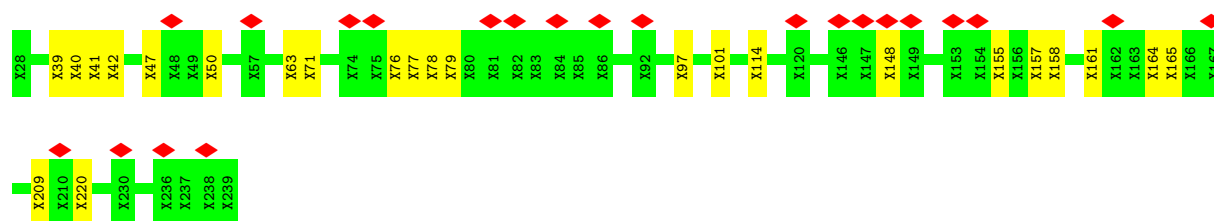
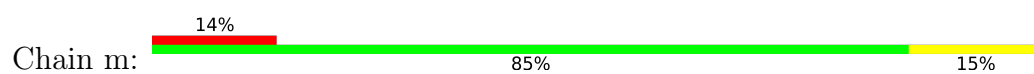
- Molecule 42: Ribosomal RNA small subunit methyltransferase NEP1



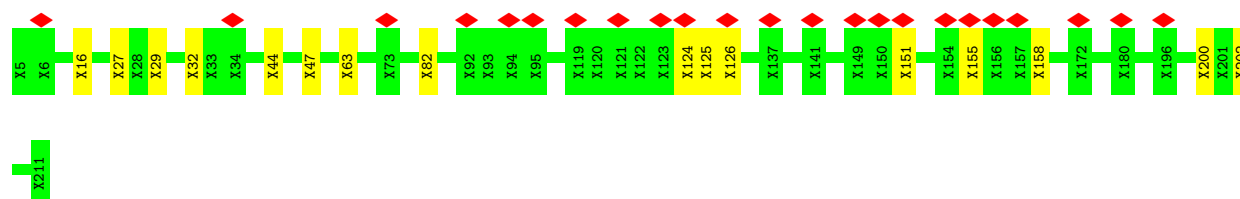
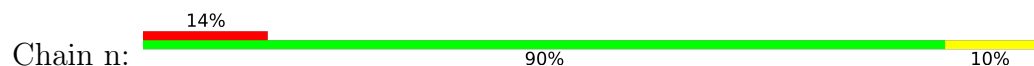
- Molecule 43: Utp24



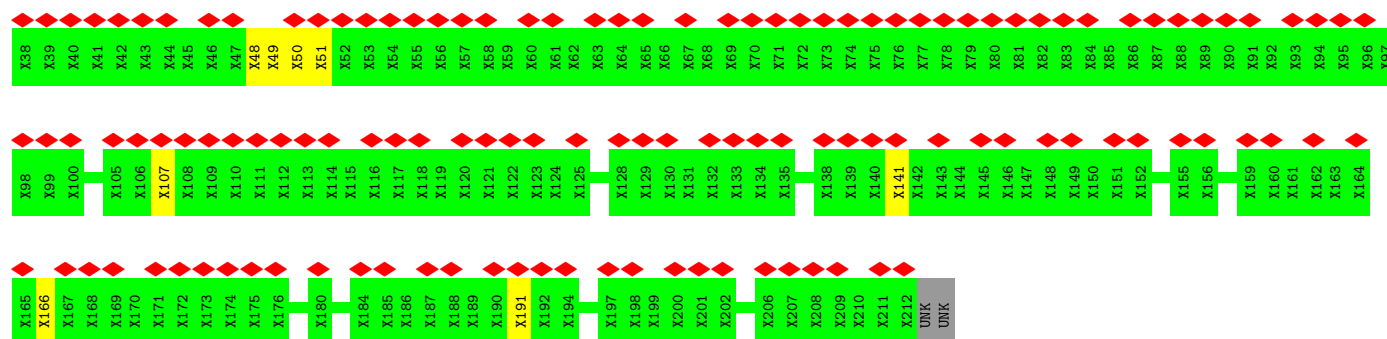
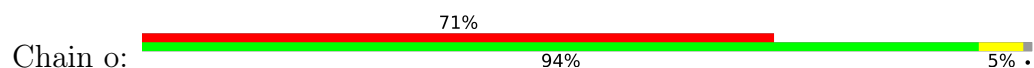
- Molecule 44: Imp4



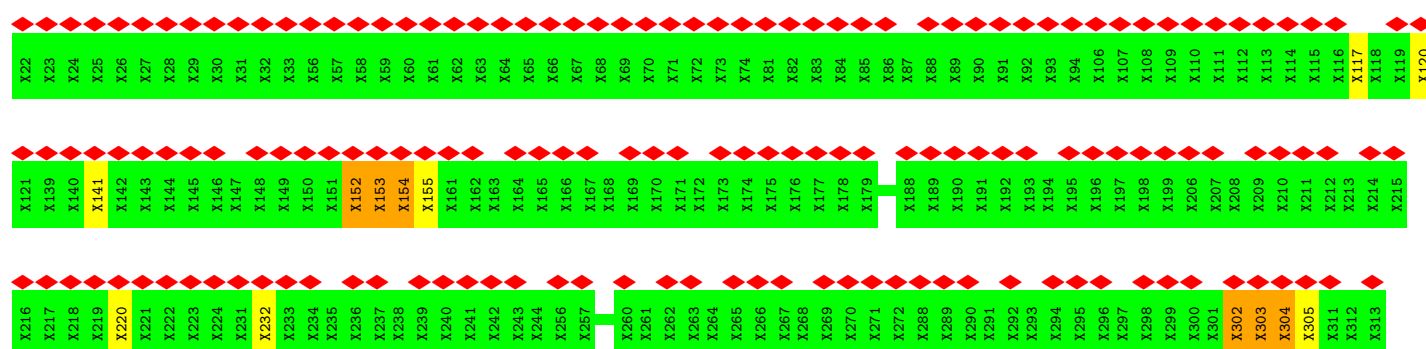
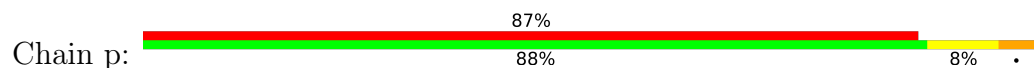
• Molecule 45: Utp30

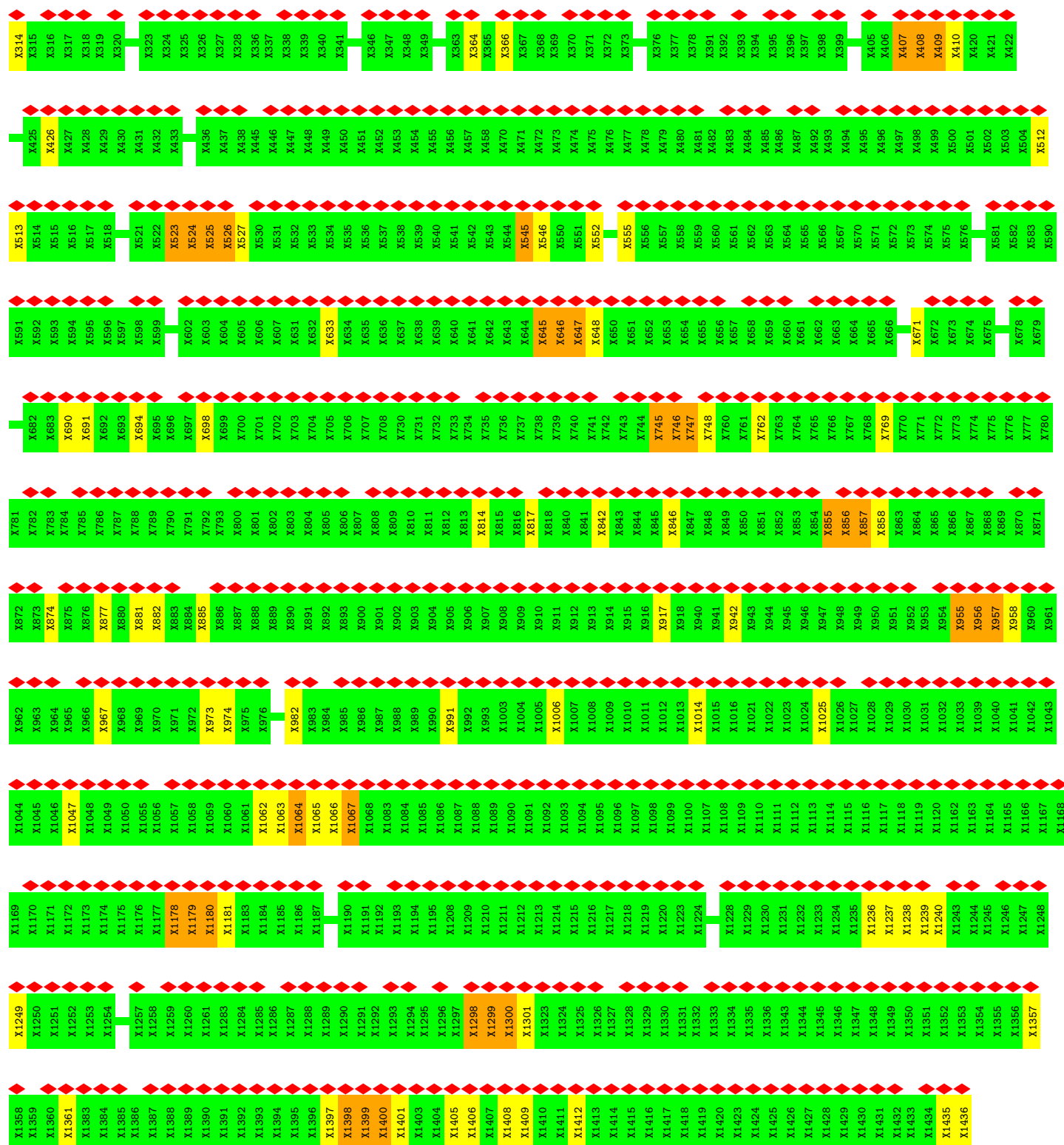


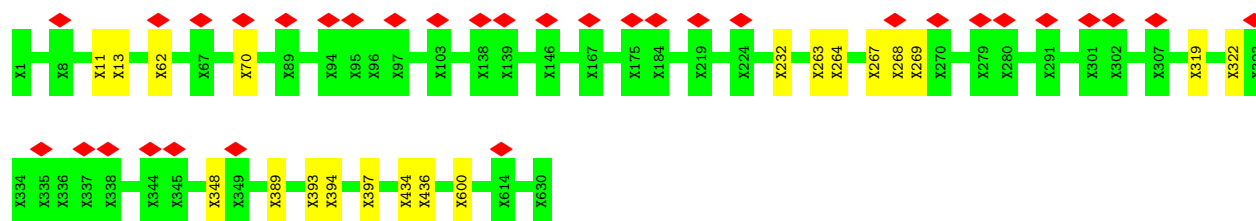
• Molecule 46: Unassigned KH domain



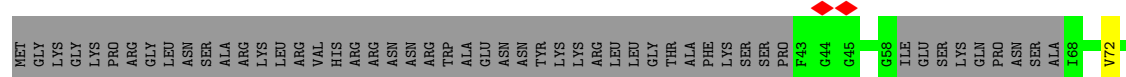
• Molecule 47: Utp20



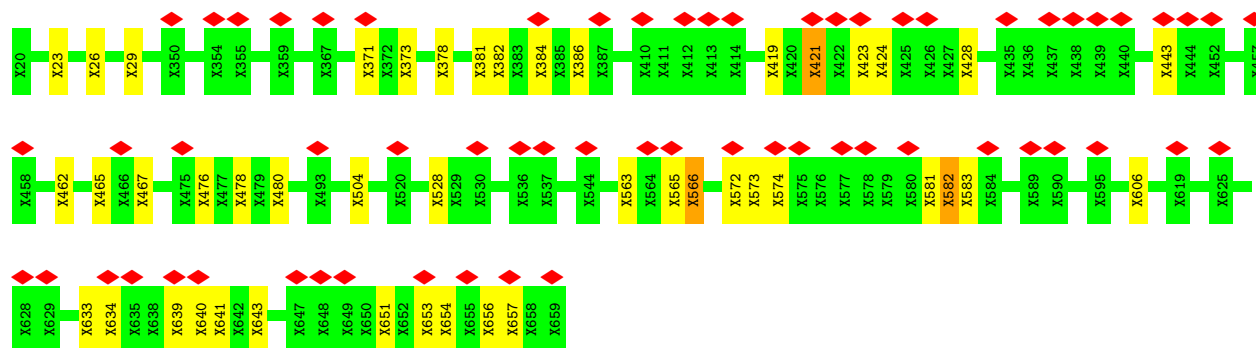
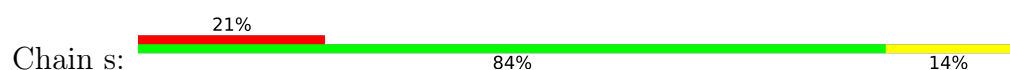




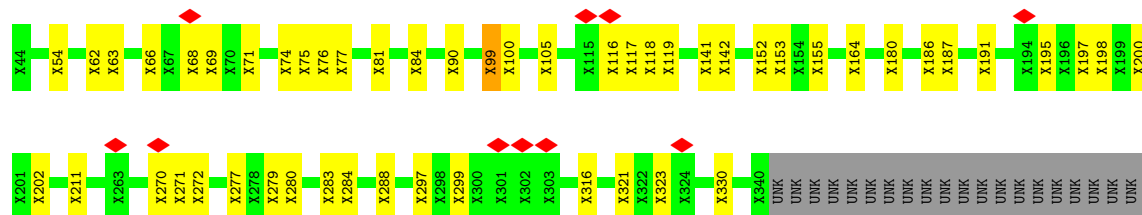
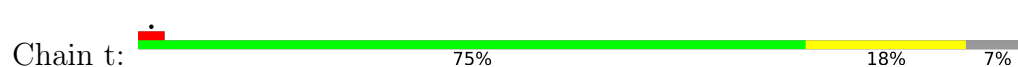
• Molecule 49: 40S ribosomal protein S23-A



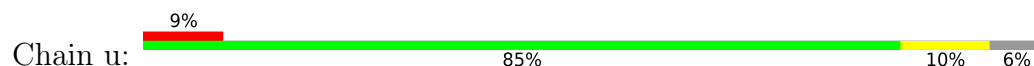
• Molecule 50: Beta-propeller 1

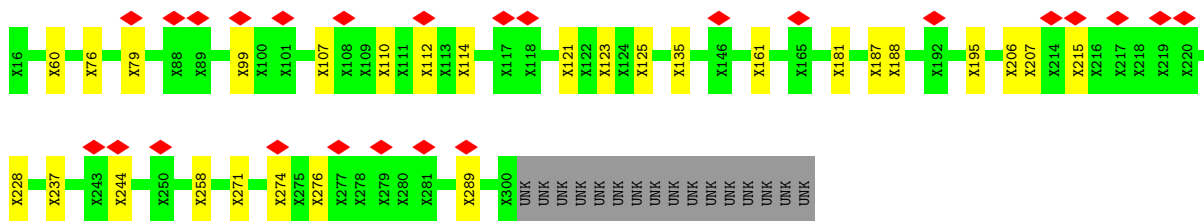


• Molecule 50: Beta-propeller 1

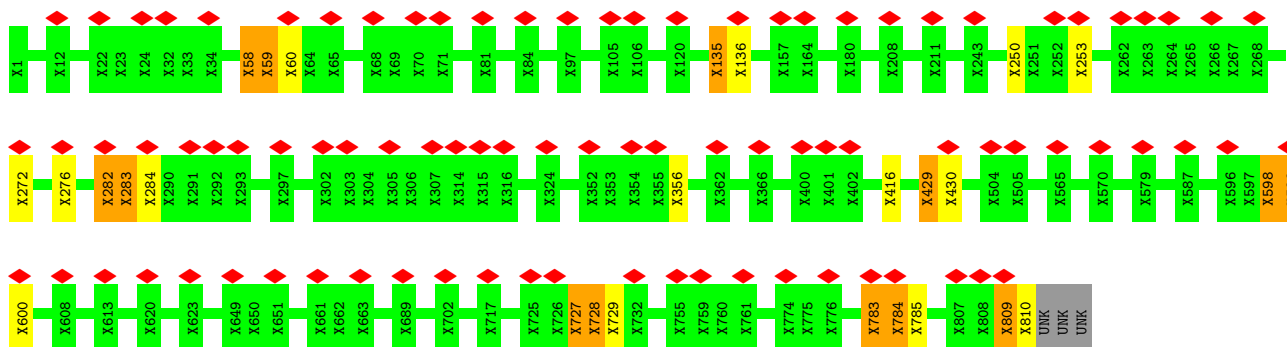


• Molecule 50: Beta-propeller 1

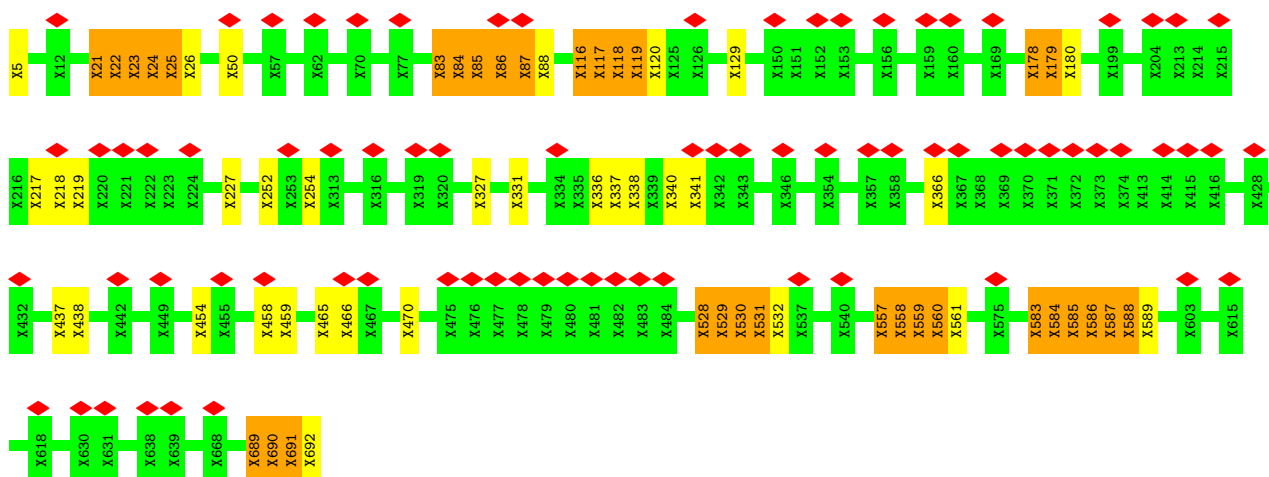
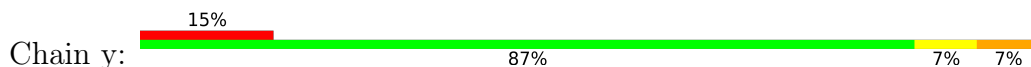




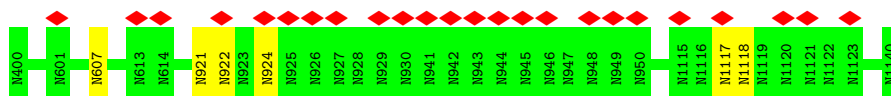
- Molecule 51: Repeat protein 1



- Molecule 52: Unassigned protein helices



- Molecule 53: Unassigned RNA helices



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	33813	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.56	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	22500	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.086	Depositor
Minimum map value	-0.043	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.018	Depositor
Map size ($\text{\AA}$)	503.50003, 503.50003, 503.50003	wwPDB
Map dimensions	380, 380, 380	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.325, 1.325, 1.325	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	0	0.52	0/268	0.52	0/417
2	1	0.74	4/12260 (0.0%)	0.68	6/19055 (0.0%)
3	2	1.36	27/2443 (1.1%)	1.30	32/3787 (0.8%)
4	3	0.92	0/1061	1.33	5/1472 (0.3%)
5	5	1.02	0/1182	1.49	17/1638 (1.0%)
6	6	1.16	3/998 (0.3%)	1.98	17/1388 (1.2%)
7	7	0.88	1/922 (0.1%)	1.46	13/1285 (1.0%)
8	8	1.04	0/847	1.53	7/1173 (0.6%)
9	9	0.91	0/914	1.45	9/1272 (0.7%)
12	C	0.67	0/565	1.19	3/784 (0.4%)
13	D	0.34	0/720	0.87	0/1001
14	E	0.34	0/623	0.78	2/864 (0.2%)
15	F	0.47	0/443	1.08	0/615
16	G	0.61	0/305	1.14	0/423
27	T	0.65	0/3055	0.90	0/4243
38	e	0.46	0/605	1.01	2/843 (0.2%)
38	f	0.46	0/565	1.02	2/787 (0.3%)
39	g	0.49	0/1793	0.94	6/2485 (0.2%)
40	h	0.48	0/1741	0.76	0/2416
41	i	0.35	0/265	0.61	0/367
42	j	0.60	0/1044	1.12	1/1452 (0.1%)
42	k	0.61	0/1079	1.05	1/1502 (0.1%)
49	r	0.41	0/399	0.81	0/549
All	All	0.79	35/34097 (0.1%)	1.02	123/49818 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
3	2	0	1
6	6	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
9	9	0	3
12	C	0	1
15	F	0	2
16	G	0	1
17	H	0	4
18	I	0	11
19	J	0	2
19	K	0	3
20	M	0	3
21	N	0	4
22	O	0	12
24	Q	0	4
26	S	0	4
27	T	0	2
28	U	0	1
30	W	0	10
31	X	0	2
33	Z	0	2
34	a	0	6
35	b	0	1
36	c	0	3
37	d	0	3
39	g	0	2
41	i	0	5
44	m	0	2
47	p	0	38
50	s	0	9
50	t	0	11
50	u	0	1
51	v	0	13
52	y	0	33
All	All	0	202

The worst 5 of 35 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	2	308	U	O3'-P	-51.07	0.84	1.61
2	1	1615	C	O3'-P	-33.55	1.10	1.61
6	6	145	ASP	C-N	-19.76	1.05	1.33
6	6	207	THR	C-N	-16.37	1.12	1.33
3	2	118	A	C1'-N9	-10.60	1.32	1.48

The worst 5 of 123 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	6	145	ASP	O-C-N	-31.24	87.17	123.10
6	6	207	THR	O-C-N	23.54	146.55	122.30
2	1	1615	C	OP2-P-O3'	-23.38	37.85	108.00
6	6	145	ASP	CA-C-N	21.50	152.50	122.19
6	6	145	ASP	C-N-CA	21.50	152.50	122.19

There are no chirality outliers.

5 of 202 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	2	118	A	Sidechain
6	6	145	ASP	Mainchain
6	6	44	ASN	Peptide
6	6	99	MET	Peptide
9	9	88	GLU	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	0	4476	0	2976	88	0
2	1	10978	0	5538	369	0
3	2	2468	0	1299	294	0
4	3	1063	0	481	38	0
5	5	1185	0	530	67	0
6	6	1000	0	473	26	0
7	7	923	0	406	7	0
8	8	849	0	407	55	0
9	9	915	0	421	13	0
10	A	468	0	318	0	0
11	B	1296	0	874	9	0
12	C	566	0	265	9	0
13	D	721	0	316	28	0
14	E	624	0	285	2	0
15	F	444	0	206	6	0
16	G	306	0	134	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	H	2680	0	588	25	0
18	I	880	0	200	15	0
19	J	535	0	118	8	0
19	K	525	0	117	10	0
20	M	1275	0	303	15	0
21	N	2678	0	575	30	0
22	O	3153	0	715	19	0
23	P	1530	0	339	9	0
24	Q	3503	0	746	45	0
25	R	3539	0	778	12	0
26	S	1228	0	295	9	0
27	T	3691	0	1493	11	0
28	U	1398	0	303	4	0
29	V	1298	0	300	11	0
30	W	520	0	116	13	0
31	X	3155	0	637	37	0
32	Y	3160	0	638	27	0
33	Z	748	0	151	6	0
34	a	1544	0	319	27	0
35	b	1687	0	344	20	0
36	c	1088	0	213	9	0
37	d	1064	0	215	19	0
38	e	606	0	291	2	0
38	f	566	0	271	12	0
39	g	1799	0	805	33	0
40	h	1742	0	785	25	0
41	i	2347	0	569	57	0
42	j	1047	0	454	6	0
42	k	1081	0	470	11	0
43	l	613	0	129	10	0
44	m	775	0	180	28	0
45	n	791	0	173	13	0
46	o	858	0	176	21	0
47	p	4620	0	1041	136	0
48	q	1860	0	419	31	0
49	r	402	0	178	7	0
50	s	1429	0	317	28	0
50	t	1076	0	45	29	0
50	u	1346	0	300	18	0
51	v	2885	0	641	16	0
52	y	2535	0	545	69	0
53	z	912	0	610	33	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	98451	0	32831	1652	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 13.

The worst 5 of 1652 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)
46:o:107:UNK:CB	53:z:922:N:H1'2	1.28	1.58
2:1:252:U:H5''	5:5:133:LYS:CA	1.32	1.56
47:p:220:UNK:CB	47:p:232:UNK:CB	1.76	1.56
47:p:117:UNK:HA	47:p:141:UNK:CB	1.35	1.52
47:p:691:UNK:HA	47:p:762:UNK:CB	1.39	1.49

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	
4	3	212/236 (90%)	180 (85%)	20 (9%)	12 (6%)	1	13
5	5	235/261 (90%)	199 (85%)	19 (8%)	17 (7%)	1	10
6	6	198/225 (88%)	148 (75%)	36 (18%)	14 (7%)	1	10
7	7	184/190 (97%)	143 (78%)	23 (12%)	18 (10%)	0	7
8	8	169/200 (84%)	150 (89%)	14 (8%)	5 (3%)	3	22
9	9	183/197 (93%)	152 (83%)	17 (9%)	14 (8%)	1	9
12	C	113/143 (79%)	107 (95%)	6 (5%)	0	100	100
13	D	144/156 (92%)	125 (87%)	19 (13%)	0	100	100
14	E	125/130 (96%)	113 (90%)	11 (9%)	1 (1%)	16	53

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	F	88/135 (65%)	72 (82%)	13 (15%)	3 (3%)	3	20
16	G	60/67 (90%)	53 (88%)	7 (12%)	0	100	100
27	T	613/781 (78%)	565 (92%)	48 (8%)	0	100	100
38	e	120/126 (95%)	118 (98%)	2 (2%)	0	100	100
38	f	112/126 (89%)	110 (98%)	2 (2%)	0	100	100
39	g	353/573 (62%)	337 (96%)	15 (4%)	1 (0%)	36	72
40	h	353/367 (96%)	340 (96%)	13 (4%)	0	100	100
41	i	50/511 (10%)	48 (96%)	2 (4%)	0	100	100
42	j	205/252 (81%)	190 (93%)	15 (7%)	0	100	100
42	k	214/252 (85%)	201 (94%)	11 (5%)	2 (1%)	14	50
49	r	76/145 (52%)	66 (87%)	9 (12%)	1 (1%)	9	40
All	All	3807/5073 (75%)	3417 (90%)	302 (8%)	88 (2%)	7	27

5 of 88 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	3	153	VAL
4	3	173	PRO
4	3	174	LYS
5	5	24	SER
5	5	95	THR

5.3.2 Protein sidechains ⓘ

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

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	0	10/364 (2%)	1 (10%)	0
2	1	497/1800 (27%)	124 (24%)	22 (4%)
3	2	95/126 (75%)	20 (21%)	3 (3%)
All	All	602/2290 (26%)	145 (24%)	25 (4%)

5 of 145 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	0	287	G
2	1	57	G
2	1	60	U
2	1	67	A
2	1	68	A

5 of 25 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	1	512	A
2	1	1572	G
3	2	318	U
2	1	1535	U
2	1	1573	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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
47	p	58
1	0	45
51	v	31

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Mol	Chain	Number of breaks
22	O	27
48	q	23
25	R	20
52	y	18
24	Q	18
41	i	16
17	H	16
23	P	15
26	S	13
21	N	11
18	I	11
29	V	11
20	M	11
45	n	10
11	B	9
3	2	8
2	1	8
53	z	7
34	a	7
44	m	7
31	X	7
32	Y	7
50	t	6
35	b	6
30	W	6
50	s	6
19	K	5
10	A	5
19	J	5
28	U	5
50	u	4
27	T	3
43	l	3
6	6	3
46	o	2
37	d	2
36	c	1

The worst 5 of 476 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	y	204:UNK	C	213:UNK	N	135.82
1	y	180:UNK	C	185:UNK	N	133.64

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	y	618:UNK	C	625:UNK	N	128.71
1	z	950:N	O3'	1110:N	P	127.24
1	y	144:UNK	C	150:UNK	N	117.41

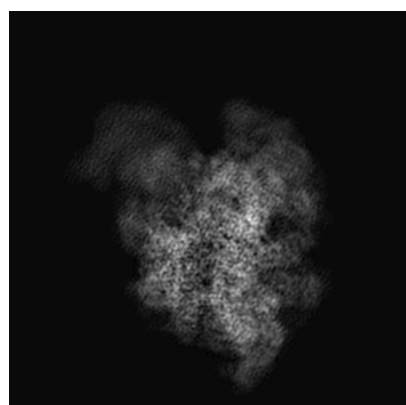
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8473. These allow visual inspection of the internal detail of the map and identification of artifacts.

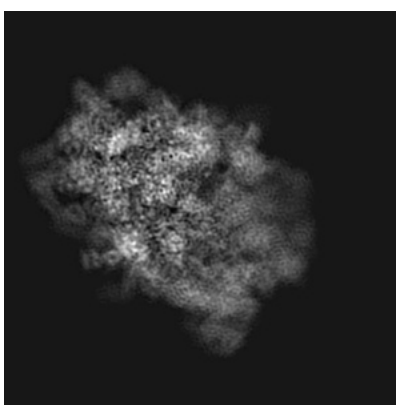
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

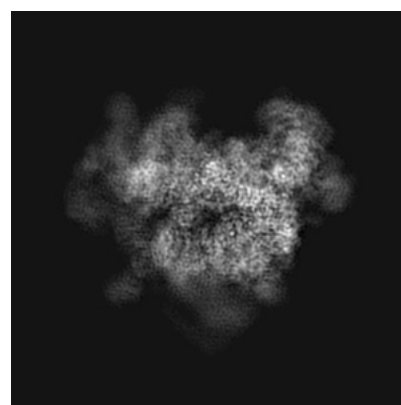
6.1.1 Primary map



X



Y

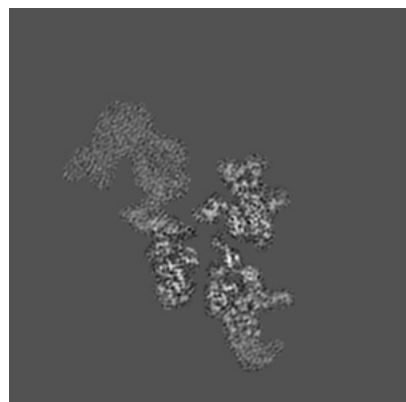


Z

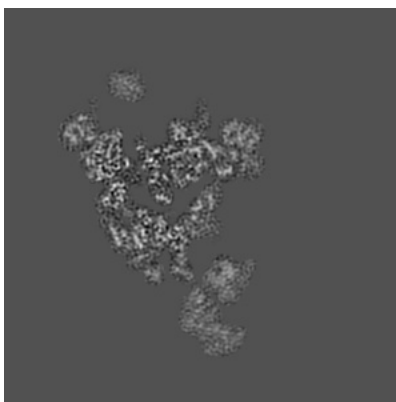
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

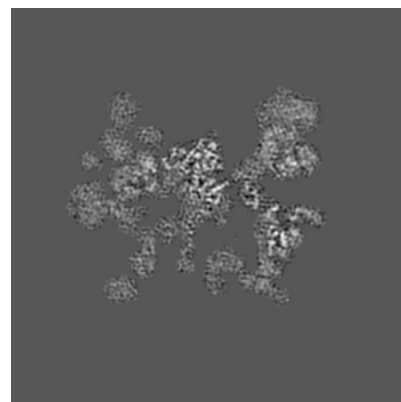
6.2.1 Primary map



X Index: 190



Y Index: 190

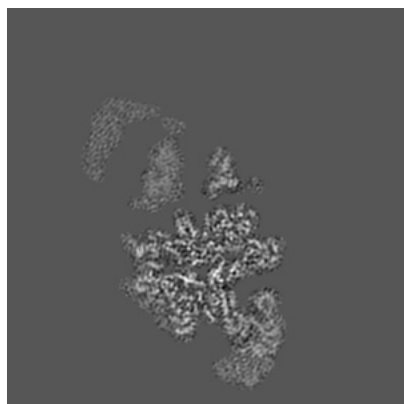


Z Index: 190

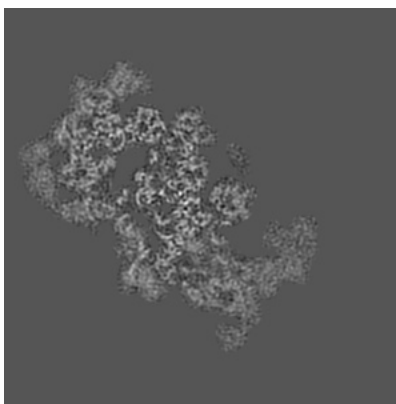
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

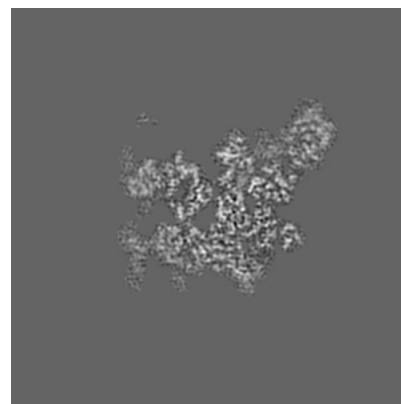
6.3.1 Primary map



X Index: 217



Y Index: 219

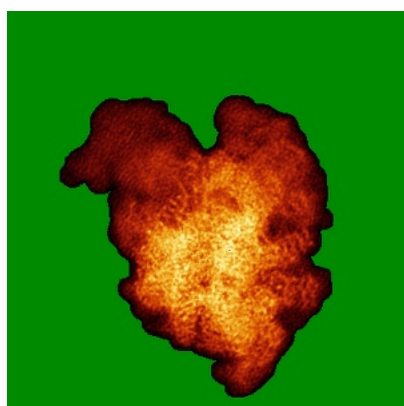


Z Index: 151

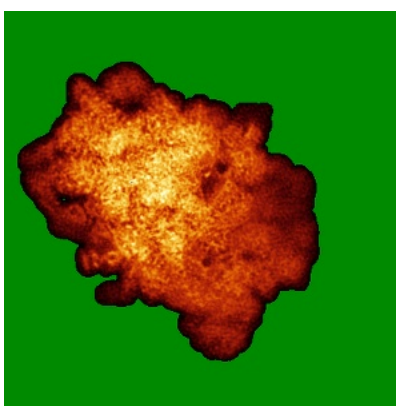
The images above show the largest variance slices of the map in three orthogonal directions.

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

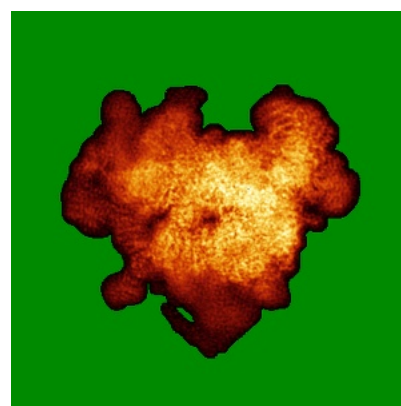
6.4.1 Primary map



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 0.018. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

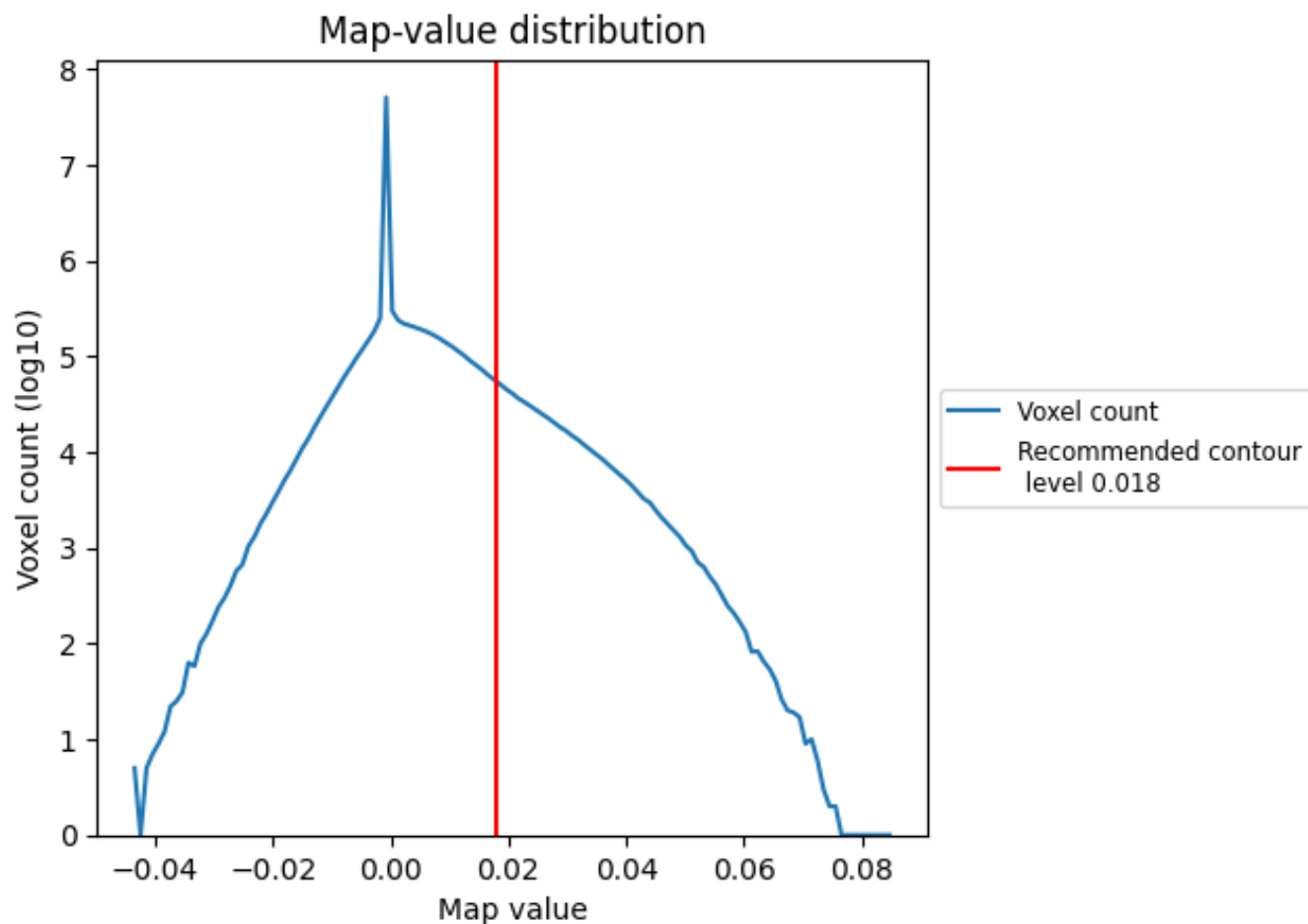
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

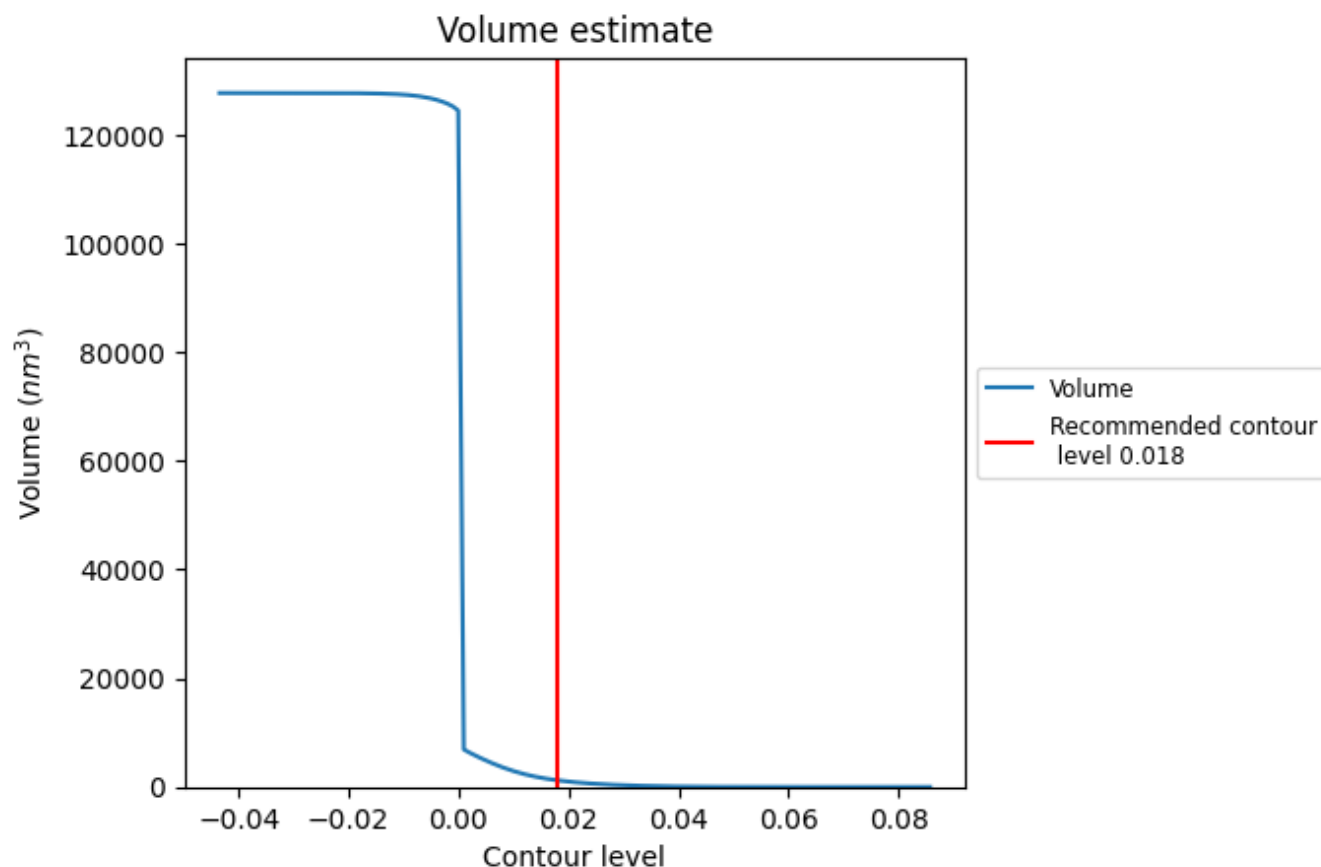
This section contains the results of statistical analysis of the map.

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.

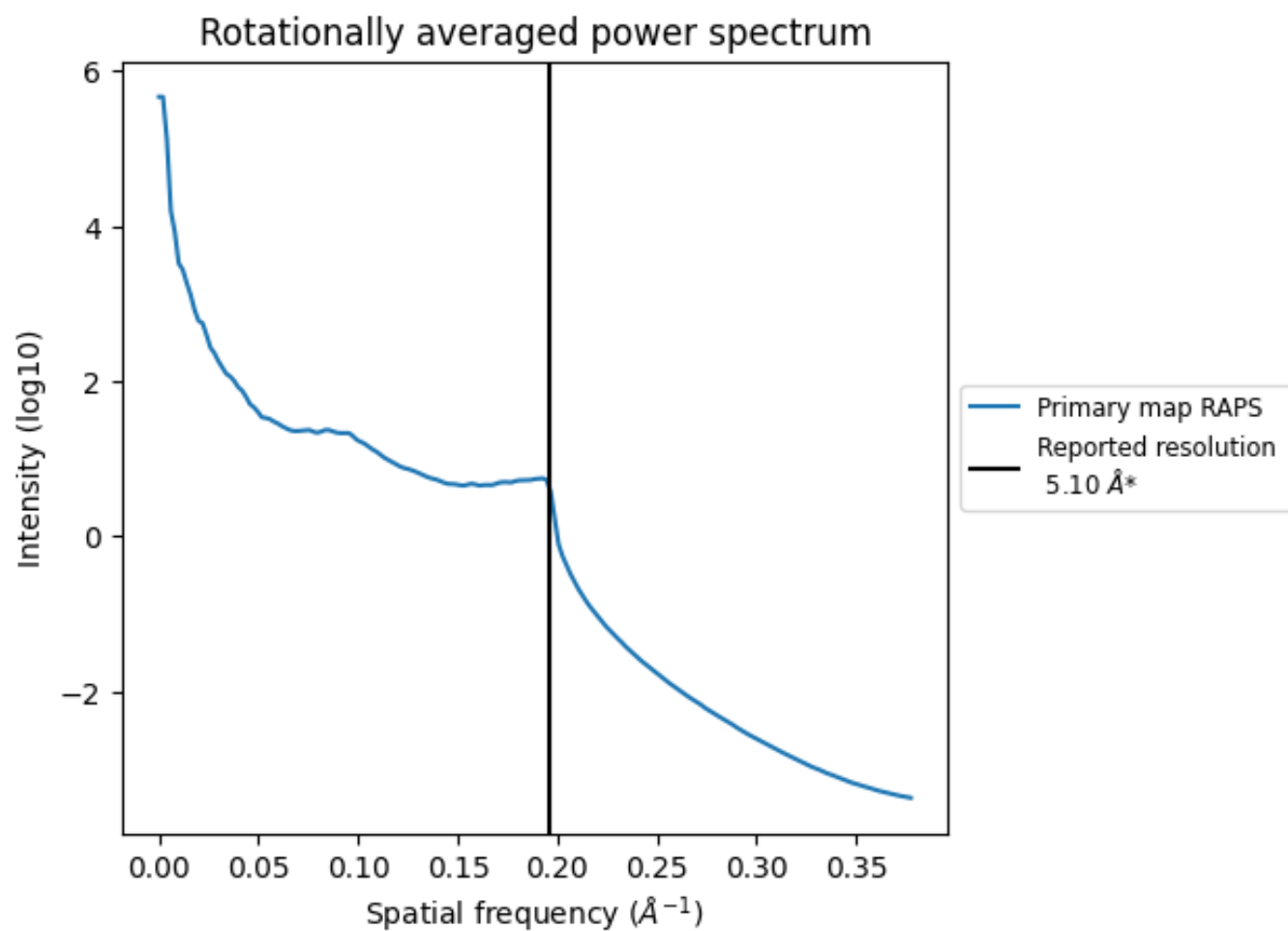
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1219 nm³; this corresponds to an approximate mass of 1101 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 ⓘ

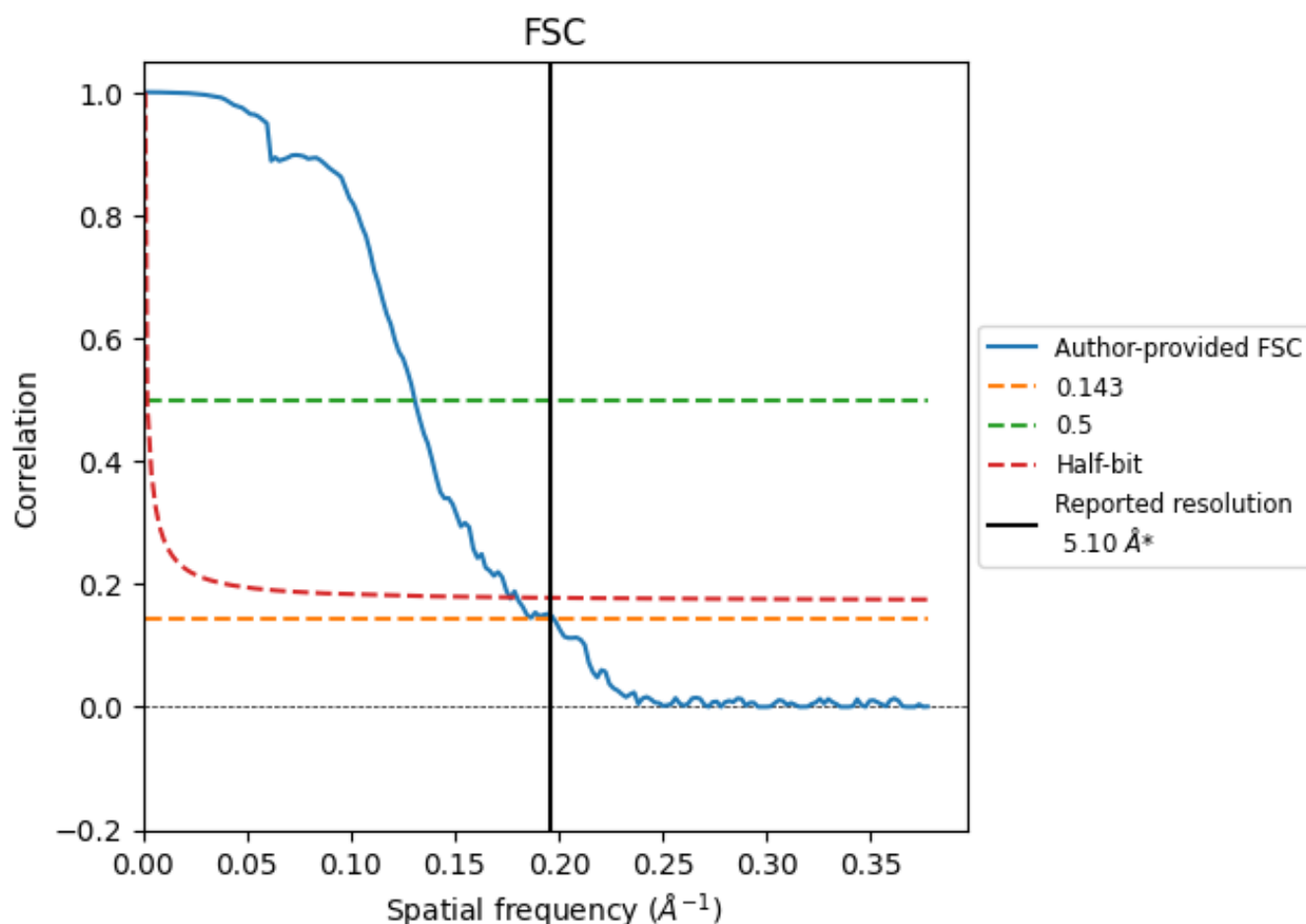


*Reported resolution corresponds to spatial frequency of 0.196 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.196 Å⁻¹

8.2 Resolution estimates [i](#)

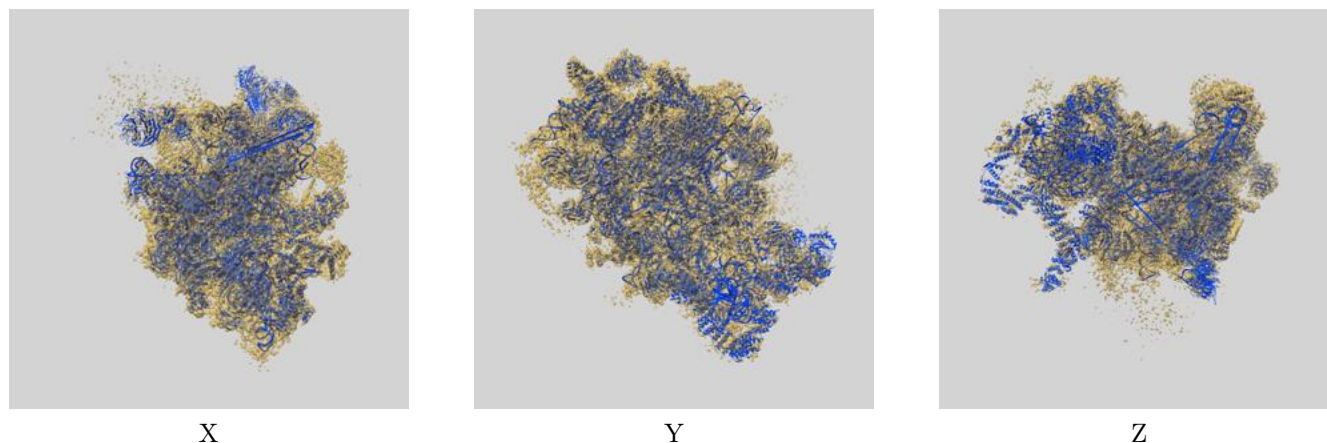
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.10	-	-
Author-provided FSC curve	5.06	7.66	5.67
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

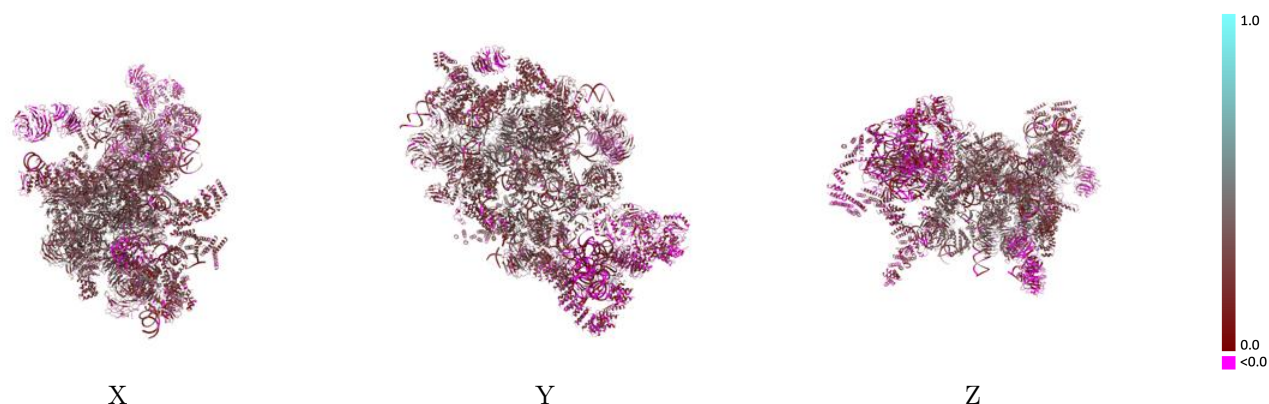
This section contains information regarding the fit between EMDB map EMD-8473 and PDB model 5TZS. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

9.1 Map-model overlay [i](#)



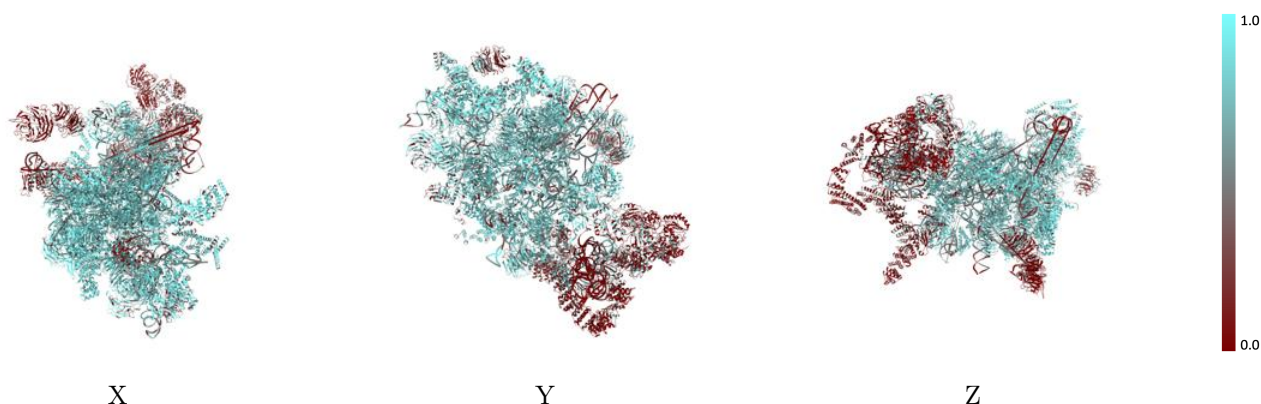
The images above show the 3D surface view of the map at the recommended contour level 0.018 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



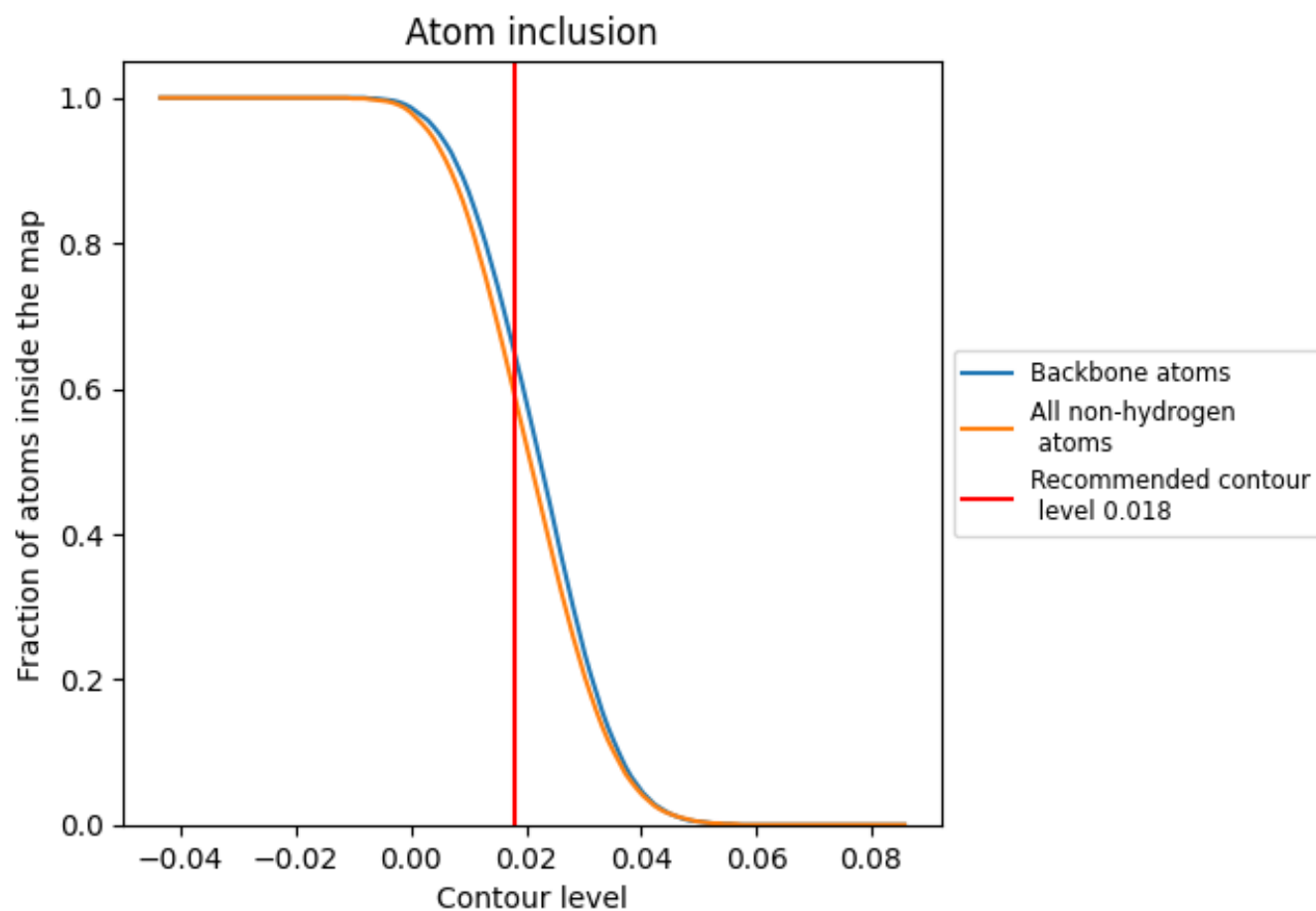
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.018).

9.4 Atom inclusion [i](#)



At the recommended contour level, 65% of all backbone atoms, 59% 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 (0.018) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5910	 0.2220
0	 0.6070	 0.2240
1	 0.4540	 0.1320
2	 0.7480	 0.2460
3	 0.1550	 0.0920
5	 0.4780	 0.2120
6	 0.7840	 0.3030
7	 0.0630	 0.1230
8	 0.2990	 0.1450
9	 0.6980	 0.2580
A	 0.7050	 0.2770
B	 0.4340	 0.1860
C	 0.8680	 0.3440
D	 0.2520	 0.0990
E	 0.2210	 0.2220
F	 0.6010	 0.2400
G	 0.8170	 0.3800
H	 0.5250	 0.1500
I	 0.7210	 0.2200
J	 0.8110	 0.2700
K	 0.7600	 0.2390
M	 0.8220	 0.3410
N	 0.7080	 0.2560
O	 0.8240	 0.3370
P	 0.8320	 0.2500
Q	 0.7260	 0.2480
R	 0.2290	 0.0620
S	 0.7890	 0.3220
T	 0.8460	 0.3420
U	 0.7640	 0.2990
V	 0.2930	 0.1150
W	 0.8270	 0.2800
X	 0.2850	 0.1060
Y	 0.0920	 0.0530
Z	 0.8280	 0.3300



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Chain	Atom inclusion	Q-score
a	 0.7590	 0.2500
b	 0.7180	 0.2690
c	 0.8280	 0.3400
d	 0.6760	 0.3030
e	 0.7920	 0.3070
f	 0.7830	 0.2920
g	 0.7400	 0.2740
h	 0.7830	 0.3100
i	 0.7840	 0.3150
j	 0.6710	 0.2490
k	 0.7150	 0.2920
l	 0.8550	 0.3440
m	 0.7830	 0.3260
n	 0.7660	 0.2590
o	 0.3090	 0.1520
p	 0.1710	 0.1420
q	 0.8020	 0.2450
r	 0.8010	 0.3590
s	 0.7180	 0.2400
t	 0.9130	 0.3770
u	 0.8100	 0.3320
v	 0.7580	 0.2380
y	 0.7500	 0.2570
z	 0.4700	 0.2040