



wwPDB EM Validation Summary Report ⓘ

Nov 19, 2022 – 08:36 pm GMT

PDB ID : 5JPQ
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:

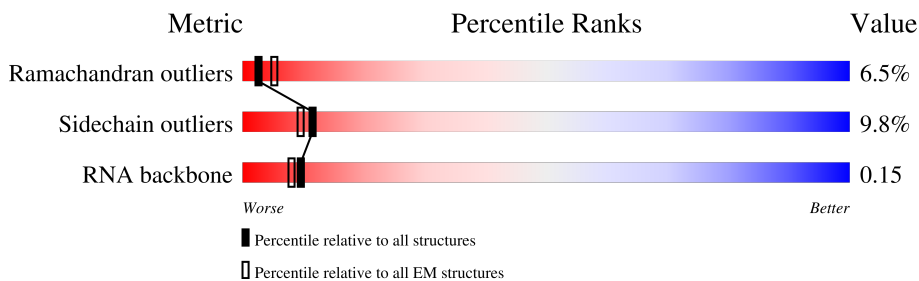
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

1 Overall quality at a glance 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)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 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	
1	B	1290	
1	C	1290	
1	D	1290	
1	E	1290	
1	F	1290	
1	J	1290	
1	K	1290	

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Mol	Chain	Length	Quality of chain
1	L	1290	9% 23% 77%
1	N	1290	18% 23% 77%
1	P	1290	11% 23% 77%
1	l	1290	9% 23% 77%
1	n	1290	13% 23% 77%
2	G	1802	14% 15% 84%
3	H	920	19% 34% 63%
4	I	939	21% 68% 32%
5	M	870	12% 36% 64%
5	O	870	32% 36% 64%
5	m	870	16% 36% 64%
6	Q	456	32% 82% 18%
7	R	560	15% 59% 41%
8	S	412	42% 88% 11%
8	T	412	49% 89% 11%
9	U	130	62% 92% 6%
9	V	130	61% 92% 6%
10	W	232	59% 96% ..
10	X	232	53% 96% ..
11	Y	573	30% 64% 36%
12	Z	367	38% 97% .
13	a	1183	5% 95%
14	b	183	45% 76% 7% 16%
15	c	297	33% 56% 6% 35%
16	d	184	35% 52% 15% 33%

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Mol	Chain	Length	Quality of chain
17	e	252	43% 84% 16%
17	f	252	42% 86% 13%
18	g	322	36% 54% 46%
18	h	322	37% 54% 46%
19	i	1073	36% 57% 39%
19	j	1073	41% 58% 37%
20	k	391	21% 42% 53%
21	o	265	52% 66% 14% 19%
22	p	259	56% 81% 18%
23	q	225	50% 46% 28% 25%
24	r	293	38% 72% 7% 20%
25	s	197	60% 82% 11% 6%
26	t	208	45% 84% 15%
27	u	197	29% 51% 27% 20%
28	v	151	62% 56% 19% 23%
29	w	137	65% 66% 26% 7%
30	x	143	71% 63% 29% 6%
31	y	157	57% 83% 15%
32	z	130	68% 67% 28%
33	0	149	65% 87% 11%
34	1	67	40% 45% 25% 30%
35	2	1800	9% 16% 26% 53%
36	3	274	15% 26% 23% 11% 40%

2 Entry composition [i](#)

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
			Total	C	N	O		
1	A	300	1500	900	300	300	0	0
1	B	300	1500	900	300	300	0	0
1	C	300	1500	900	300	300	0	0
1	D	300	1500	900	300	300	0	0
1	E	300	1500	900	300	300	0	0
1	F	300	1500	900	300	300	0	0
1	J	300	1500	900	300	300	0	0
1	K	300	1500	900	300	300	0	0
1	L	300	1500	900	300	300	0	0
1	N	300	1500	900	300	300	0	0
1	P	300	1500	900	300	300	0	0
1	l	300	1500	900	300	300	0	0
1	n	300	1500	900	300	300	0	0

- Molecule 2 is a protein called UTP10.

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

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

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

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

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

- Molecule 5 is a protein called WD40 domain proteins.

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

- Molecule 6 is a protein called UTP6.

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

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

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

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

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

- 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
			Total	C	N	O		
16	d	124	616	368	124	124	0	0

- Molecule 17 is a protein called Emg1.

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

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

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

- Molecule 19 is a protein called Kre33.

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

- Molecule 20 is a protein called Utp30.

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

- Molecule 21 is a protein called eS1.

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

- Molecule 22 is a protein called eS4.

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

- Molecule 23 is a protein called uS7.

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

- Molecule 24 is a protein called eS6.

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

- Molecule 25 is a protein called eS7.

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

- Molecule 26 is a protein called eS8.

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

- Molecule 27 is a protein called uS4.

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

- Molecule 28 is a protein called uS15.

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

- 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.

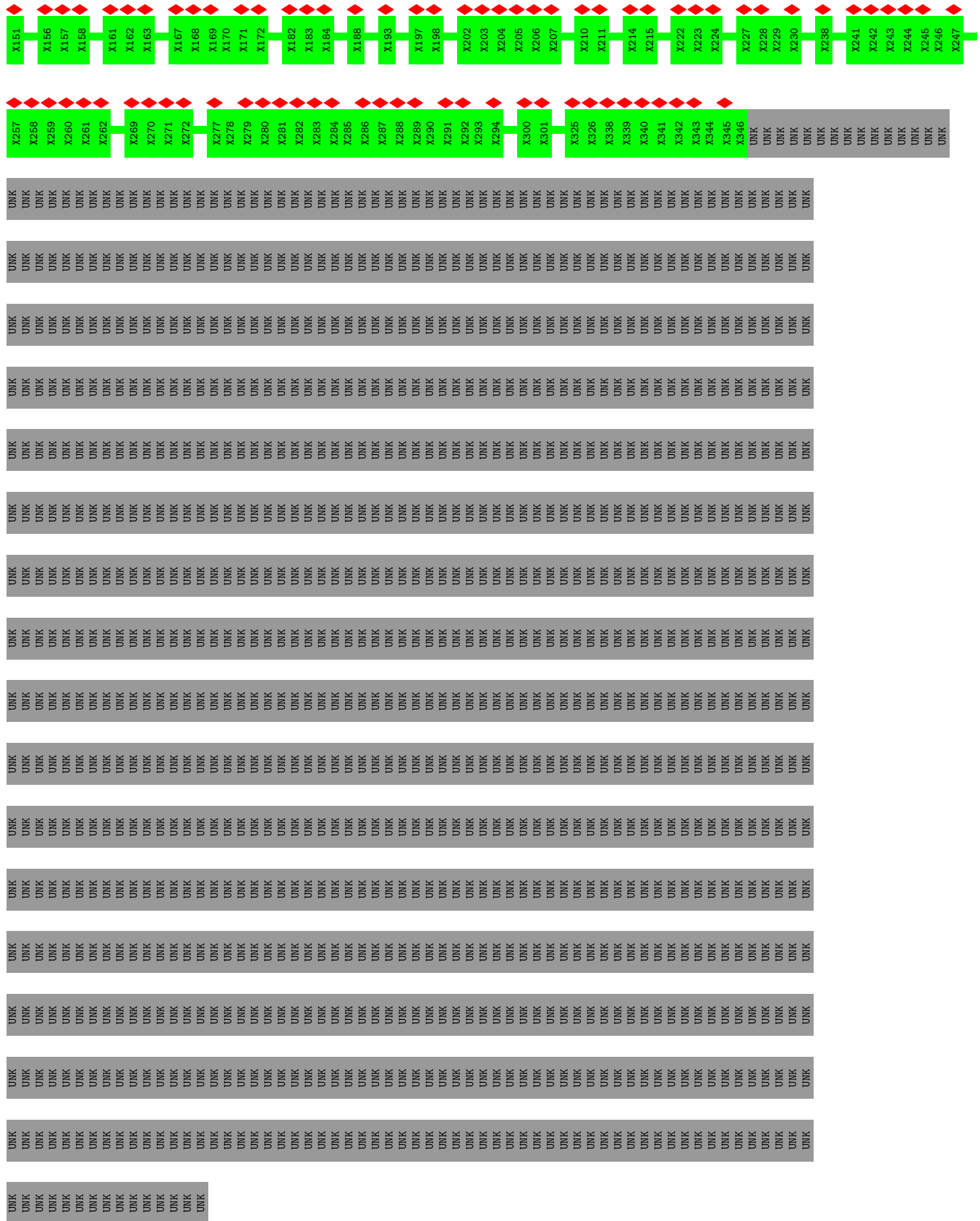
Mol	Chain	Residues	Atoms				AltConf	Trace
34	1	47	Total	C	N	O	0	0
			230	136	47	47		

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

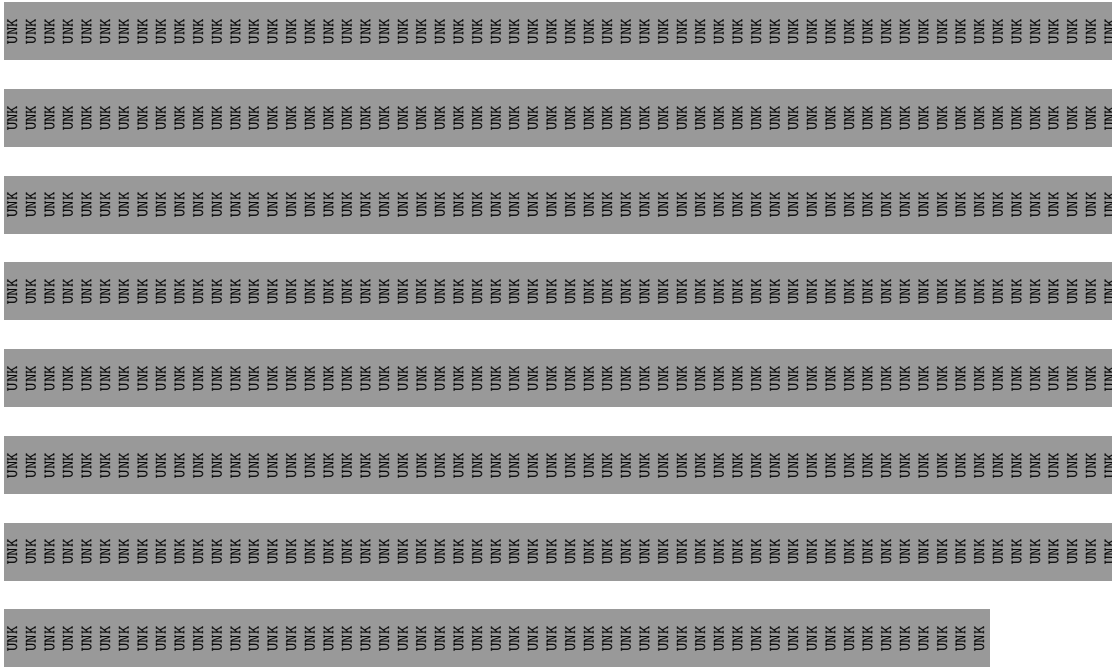
Mol	Chain	Residues	Atoms					AltConf	Trace
35	2	852	Total	C	N	O	P	0	0
			18149	8120	3229	5948	852		

- Molecule 36 is a RNA chain called U3 RNA.

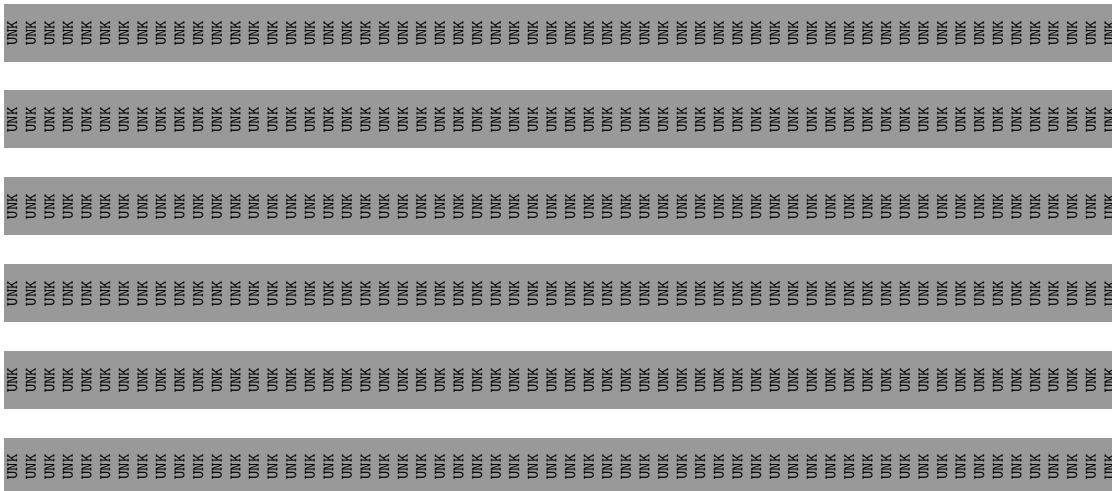
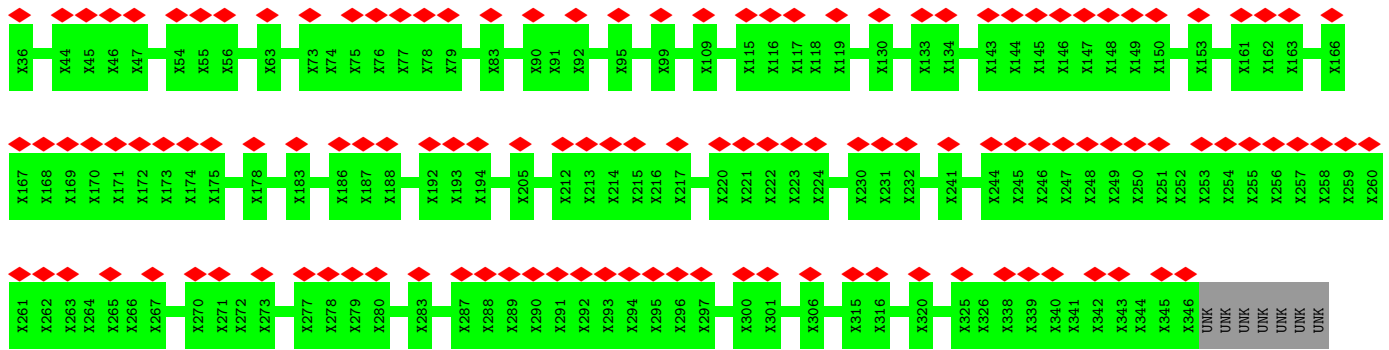
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
36	3	164	3504	1560	626	1154	164	0	0

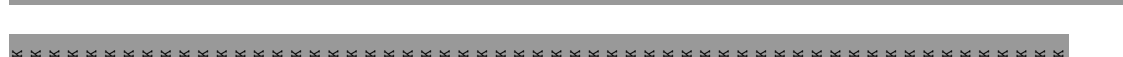
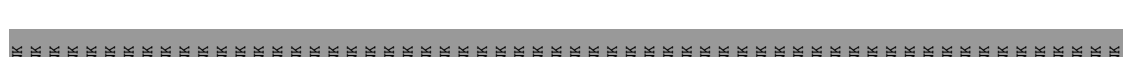
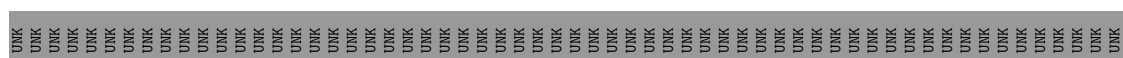
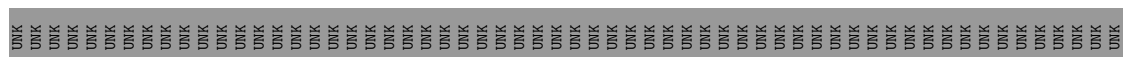
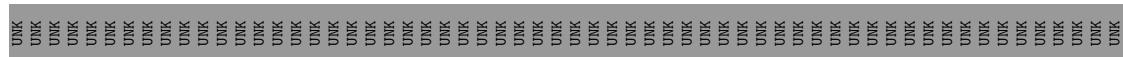
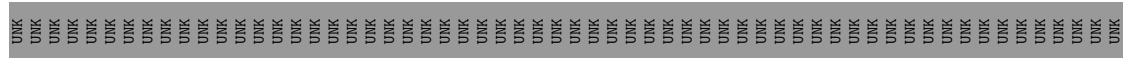
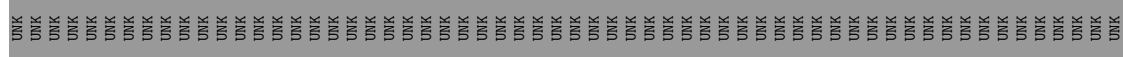
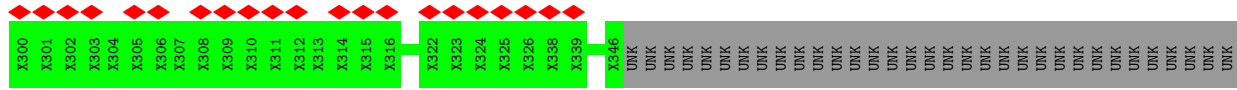
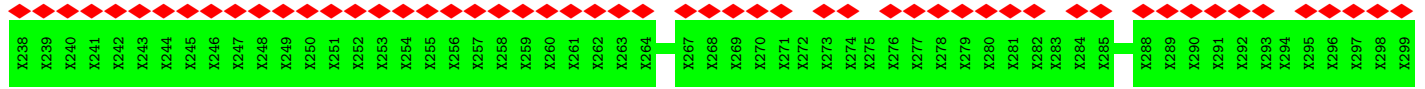


- Molecule 1: WD40 domain proteins



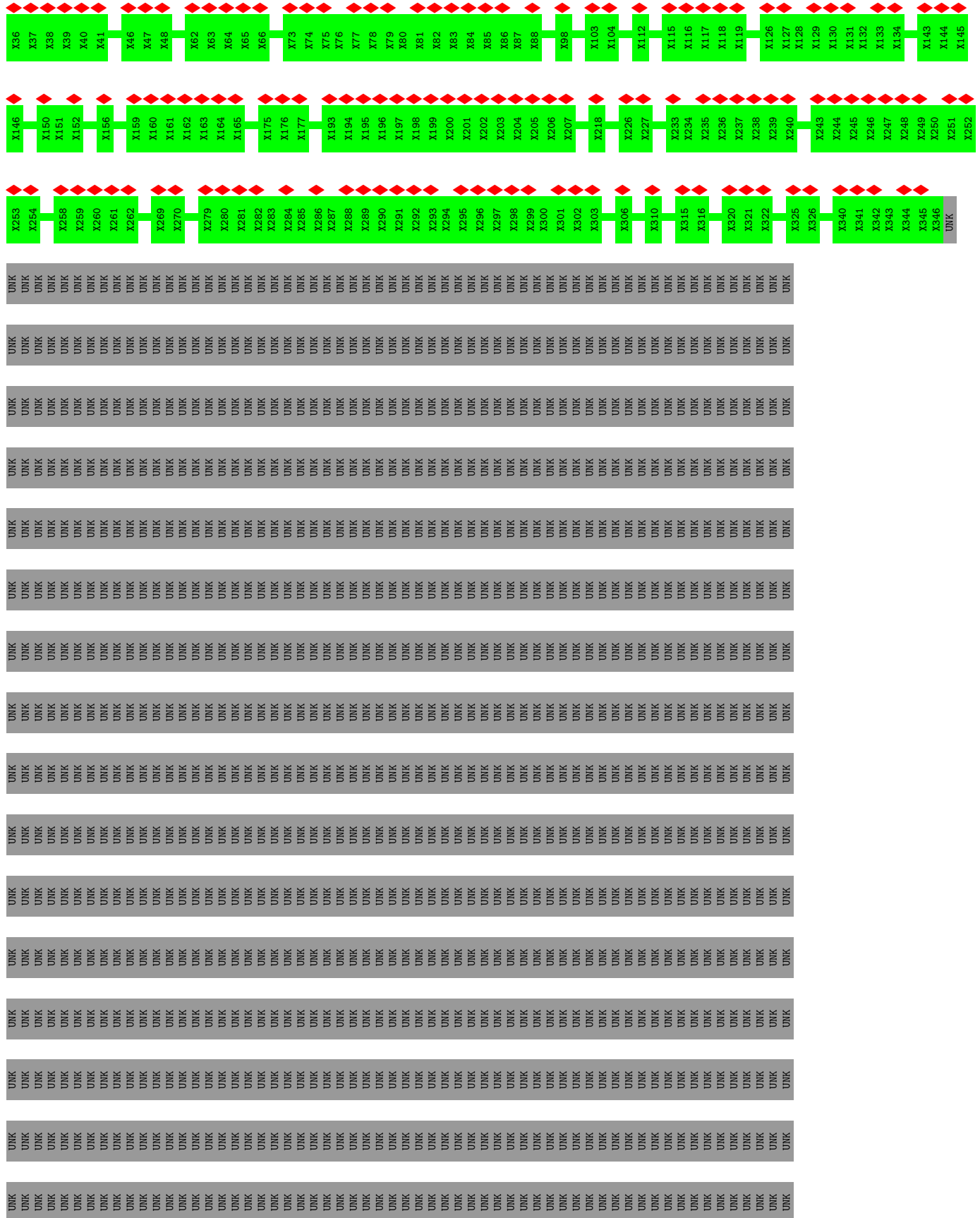
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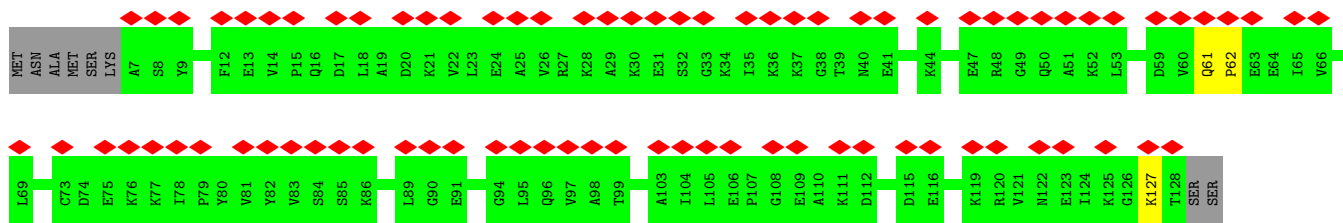




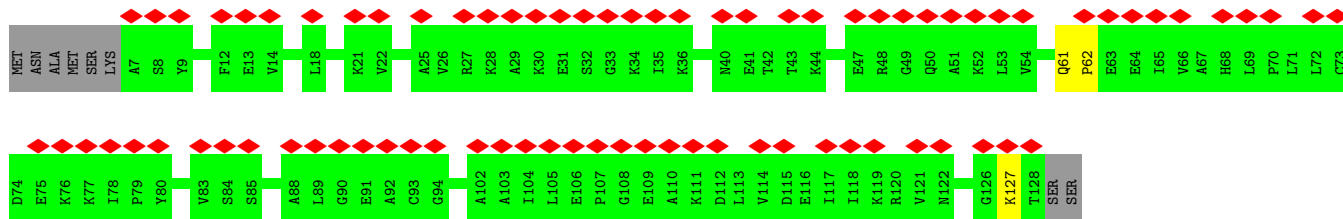
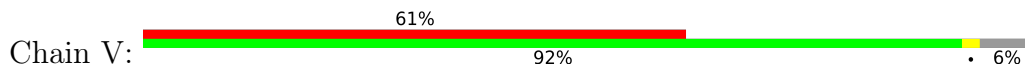
● Molecule 1: WD40 domain proteins



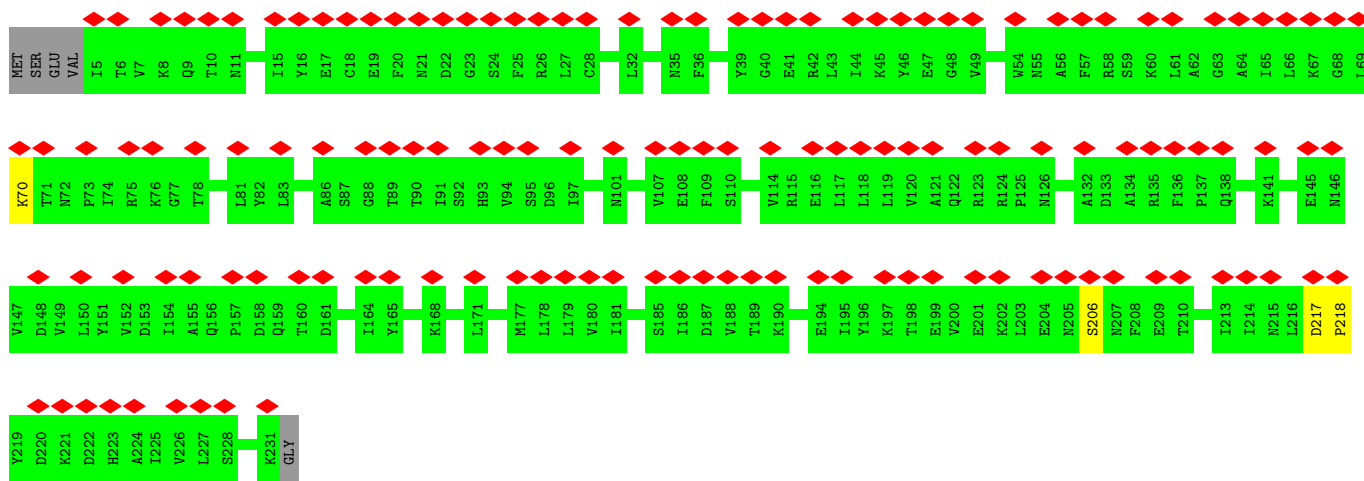




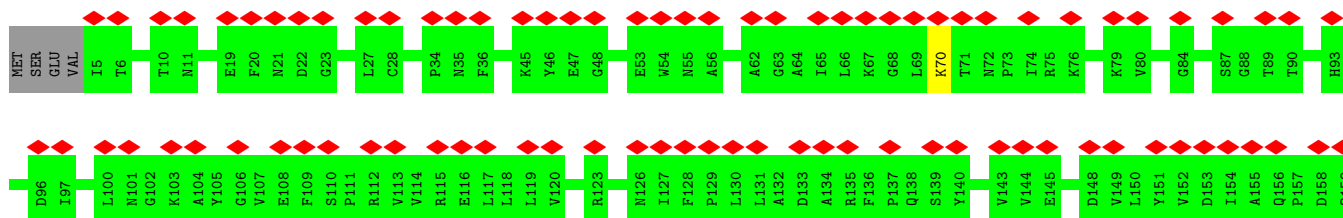
• Molecule 9: Smu13

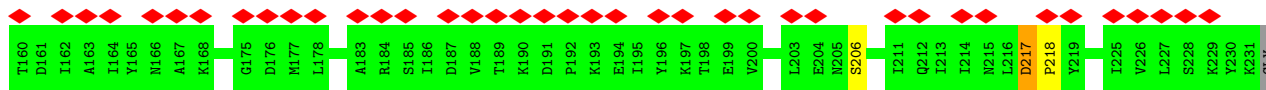


• Molecule 10: Nop1



• Molecule 10: Nop1

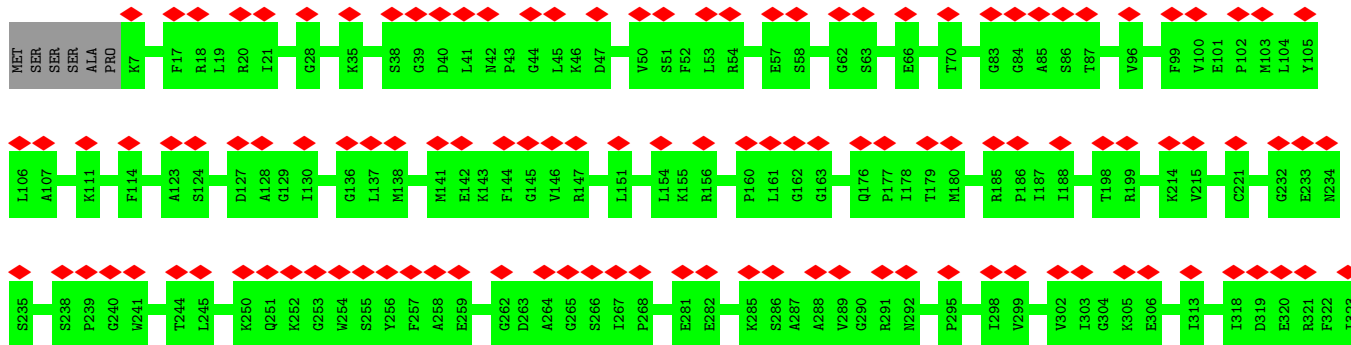


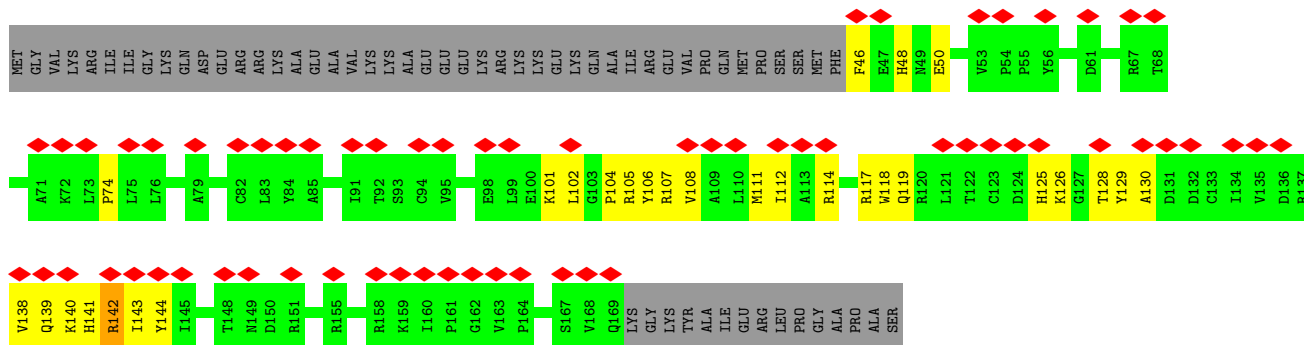


• Molecule 11: rrp9

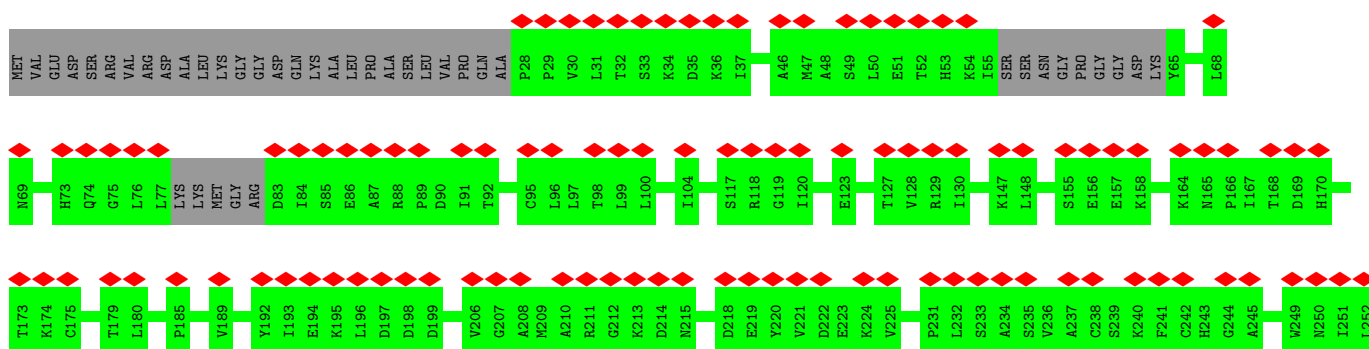
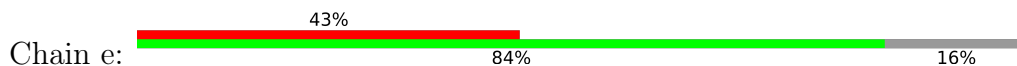


• Molecule 12: Rcl1

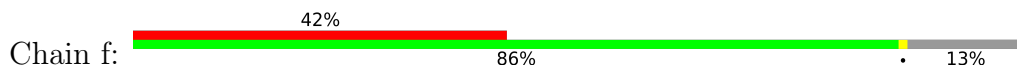




• Molecule 17: Emg1

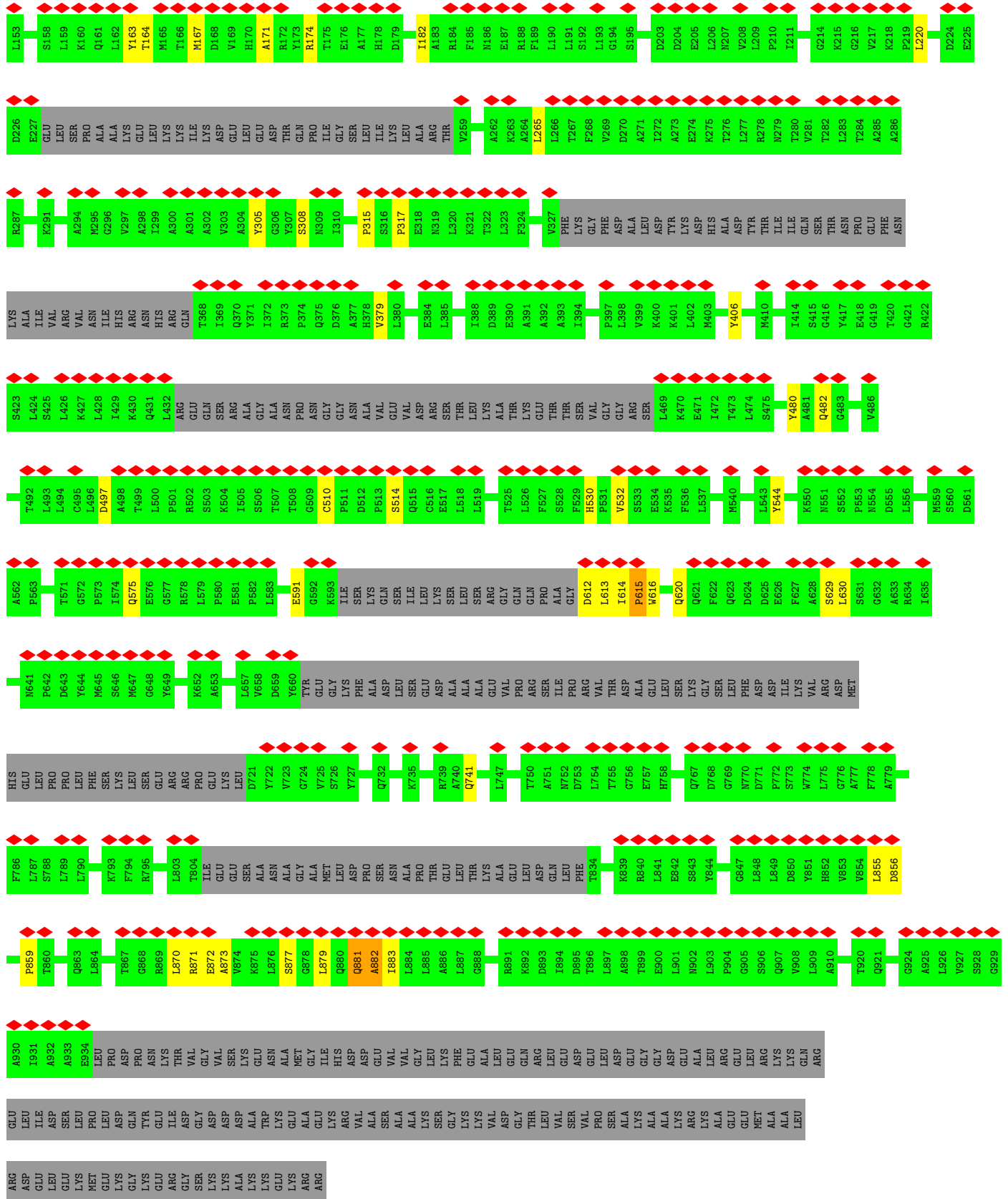


• Molecule 17: Emg1



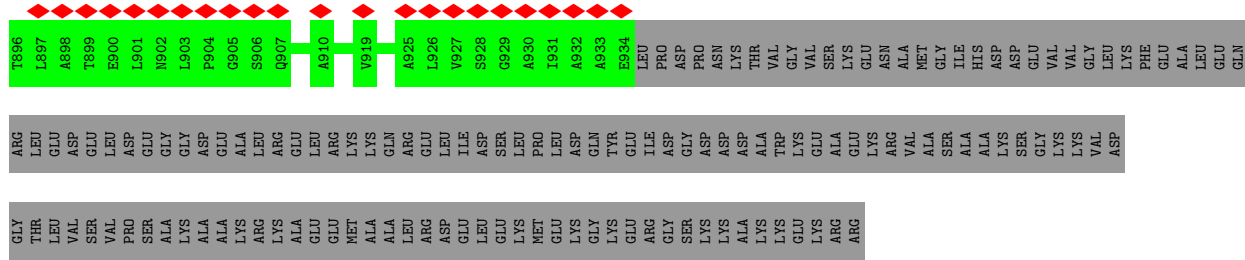
• Molecule 18: KRR1 small subunit processome component



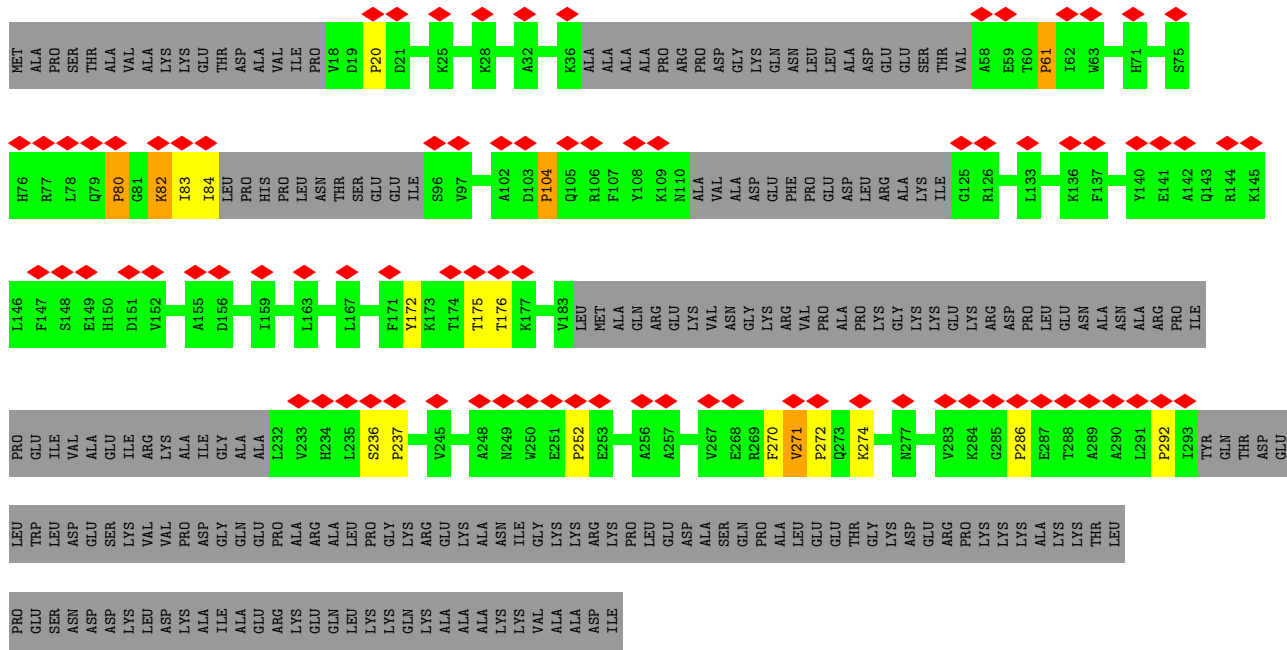
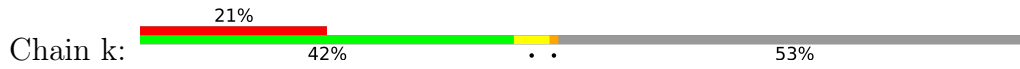


• Molecule 19: Kre33

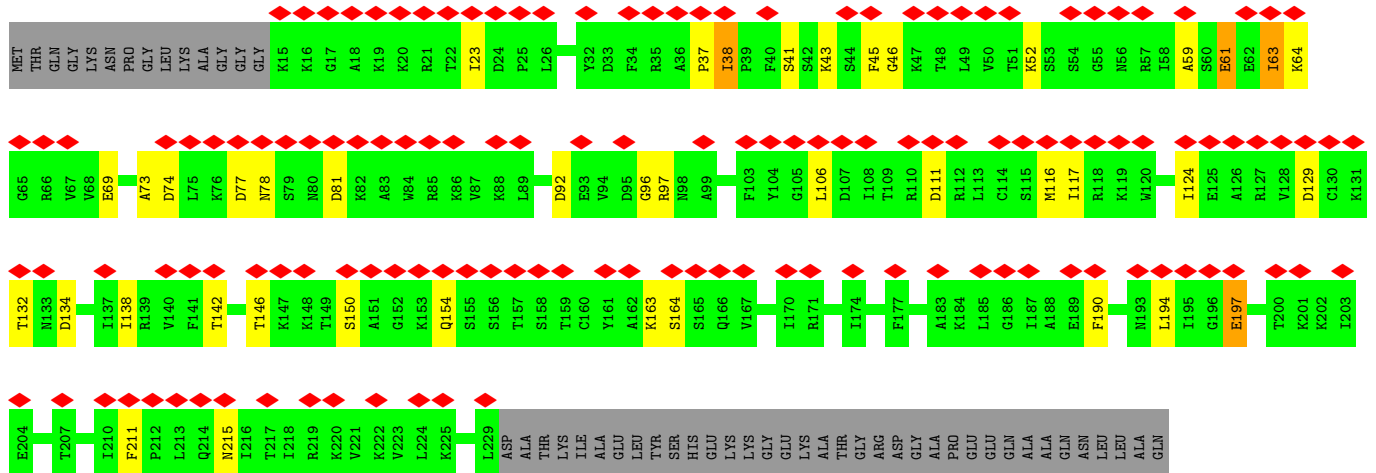




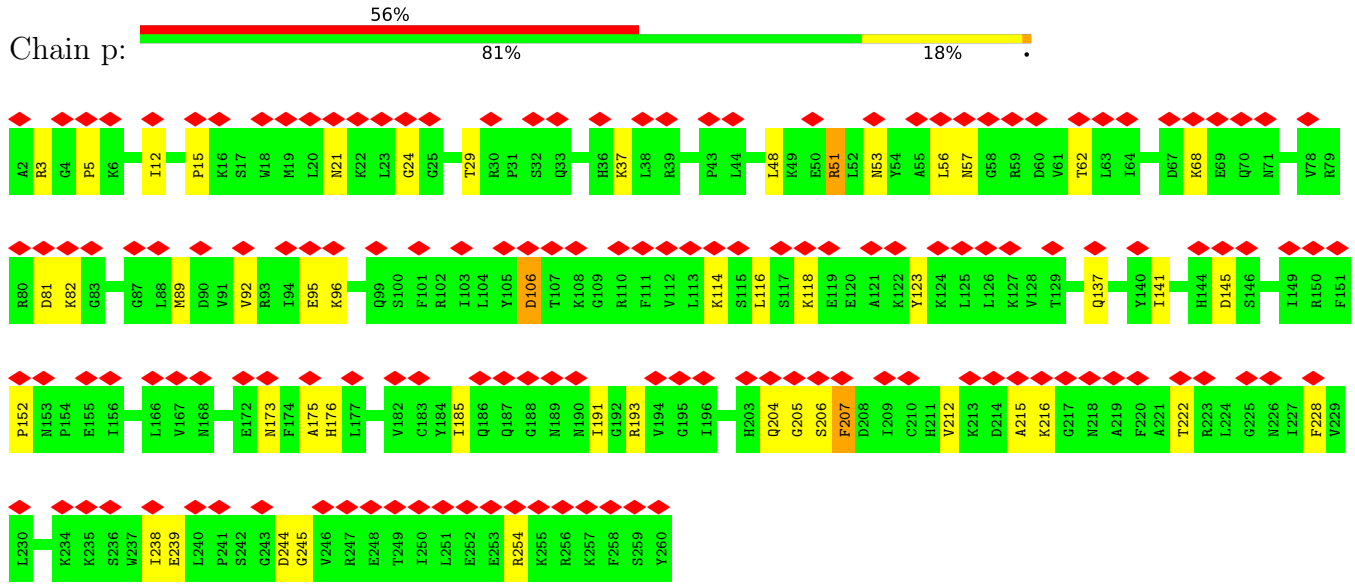
• Molecule 20: Utp30



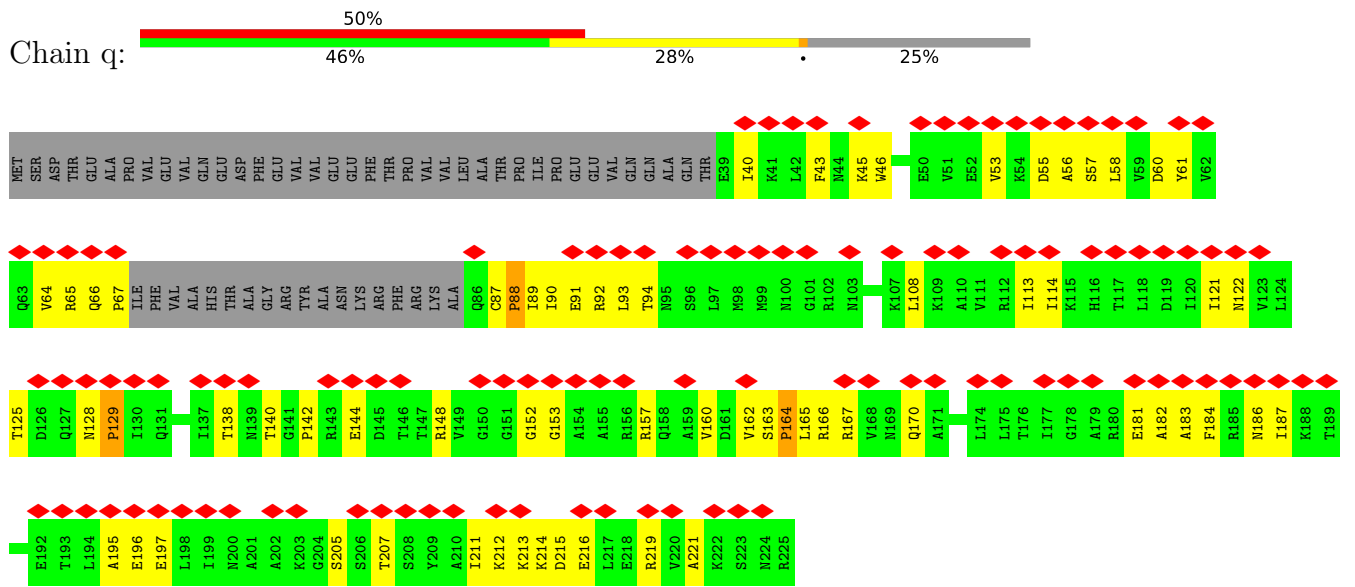
• Molecule 21: eS1



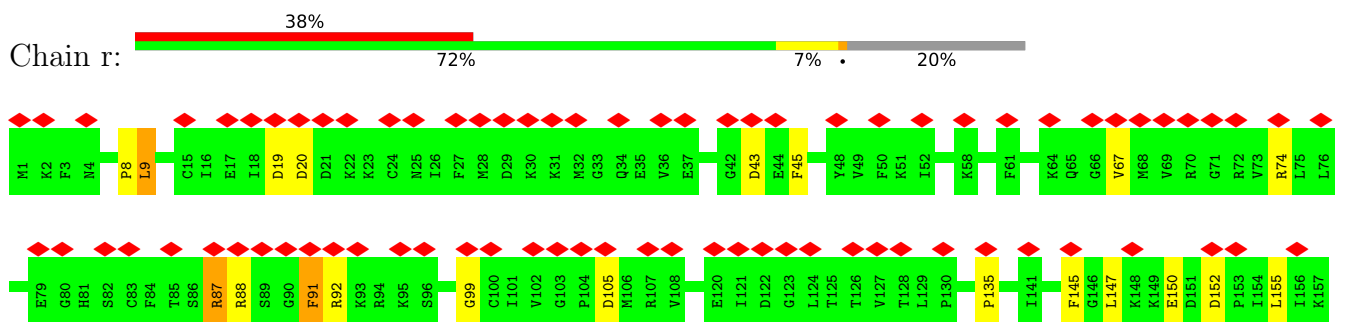
• Molecule 22: eS4

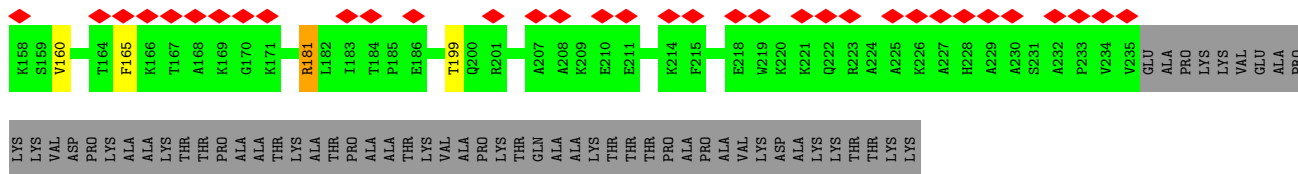


• Molecule 23: uS7

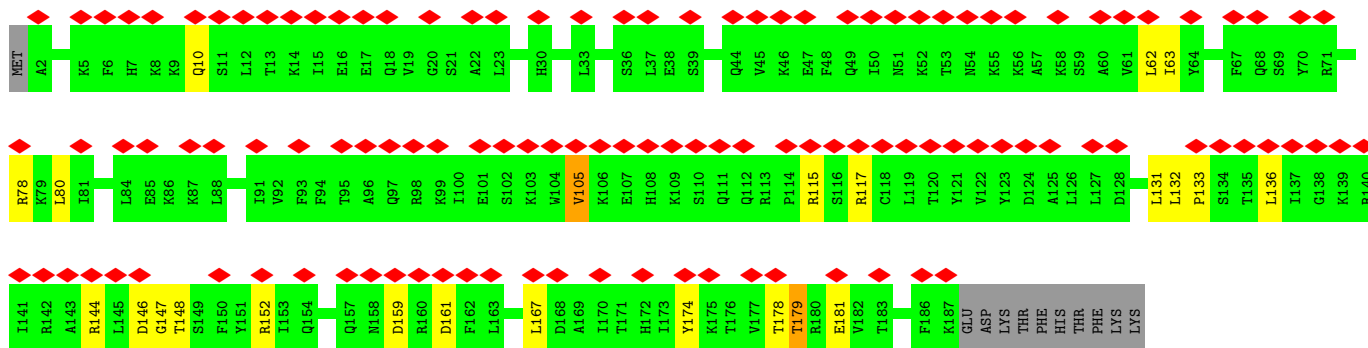
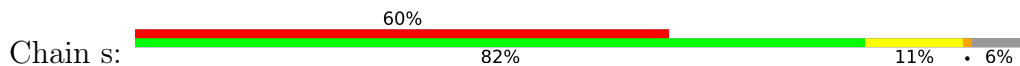


• Molecule 24: eS6

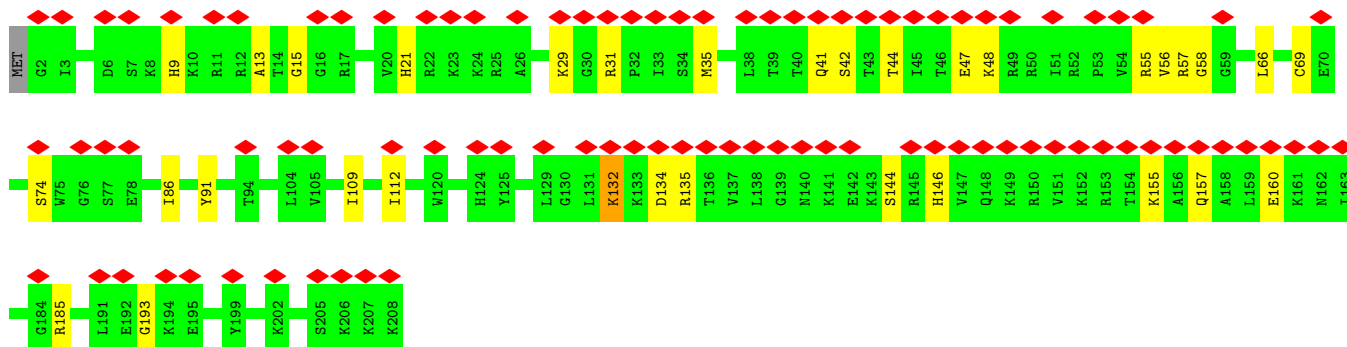
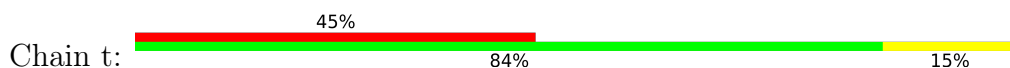




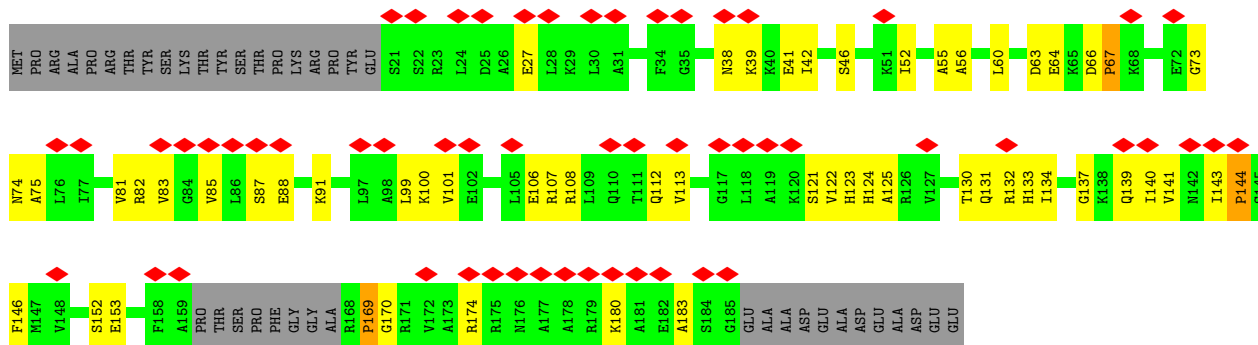
• Molecule 25: eS7



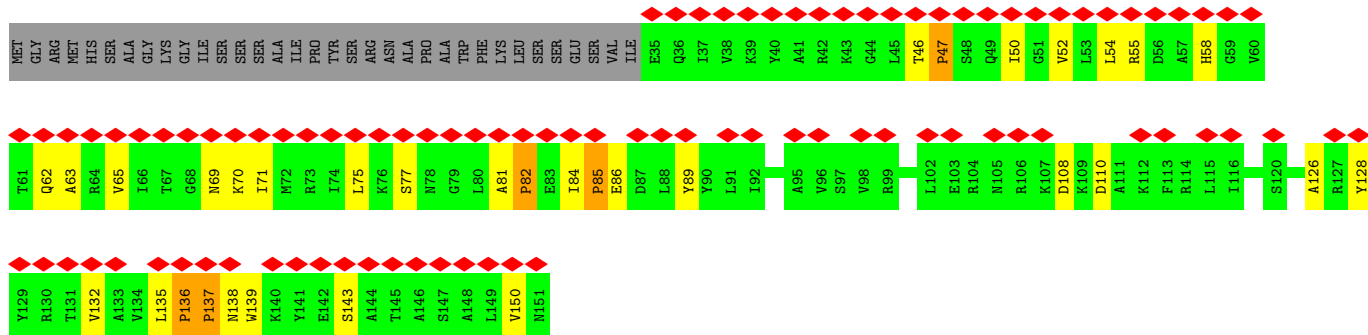
• Molecule 26: eS8



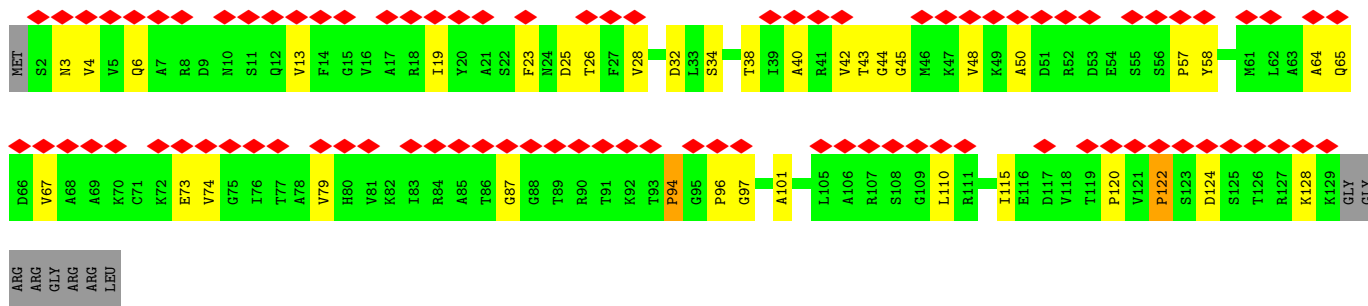
• Molecule 27: uS4



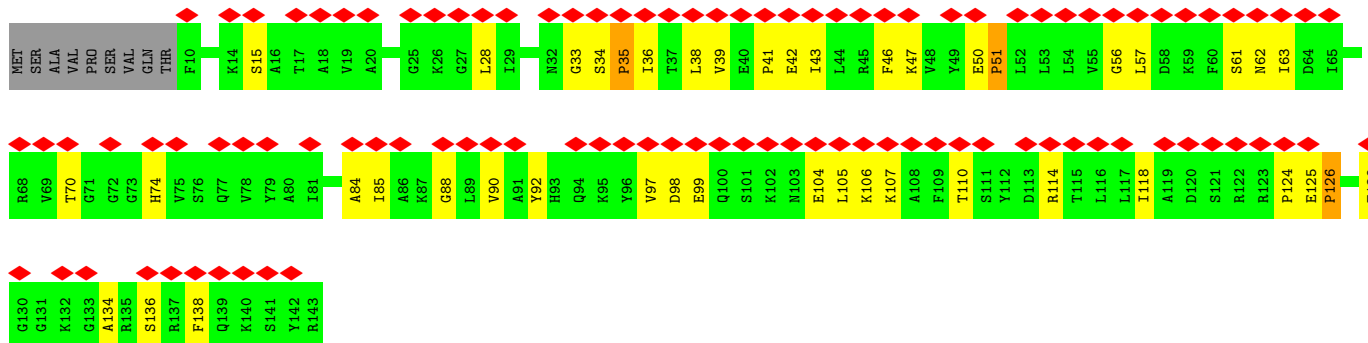
• Molecule 28: uS15



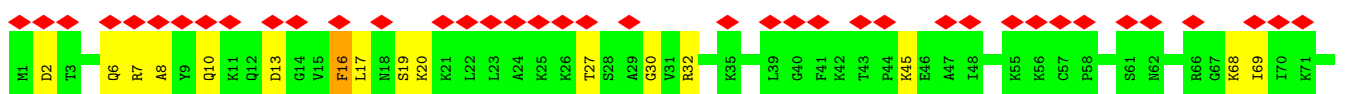
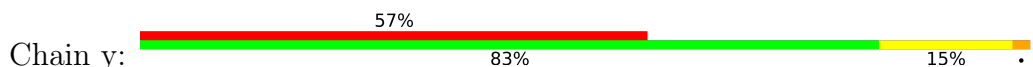
• Molecule 29: uS11

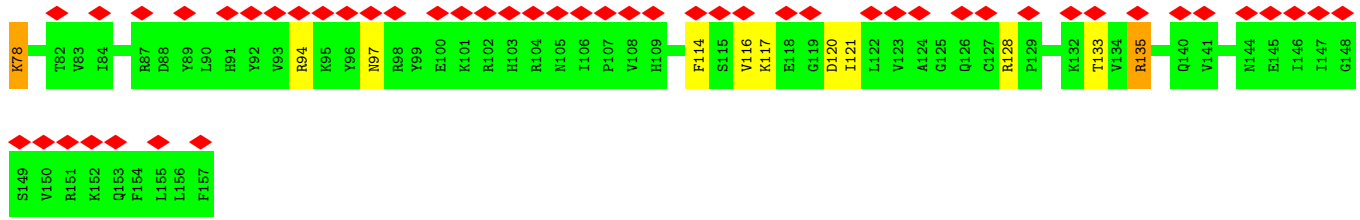


• Molecule 30: uS9



• Molecule 31: uS17

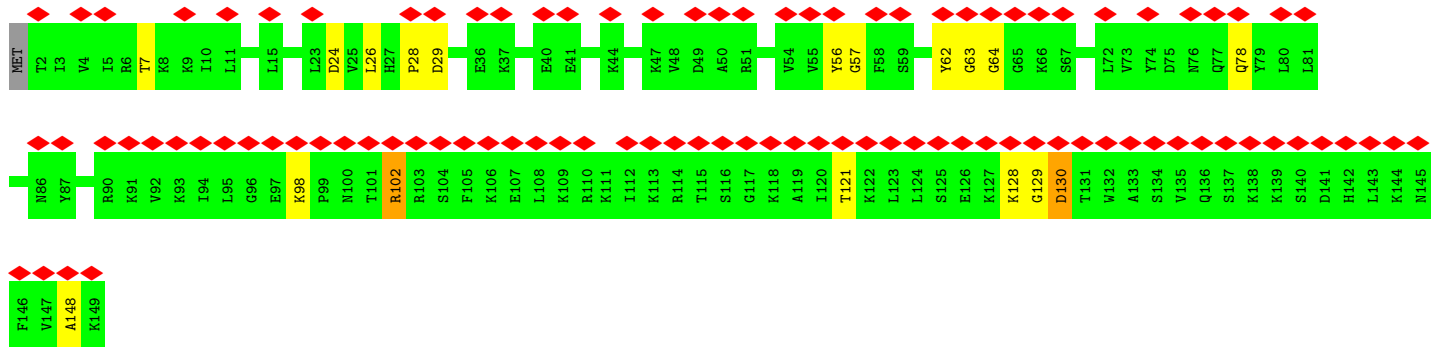
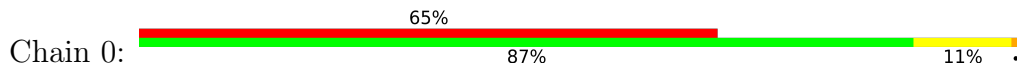




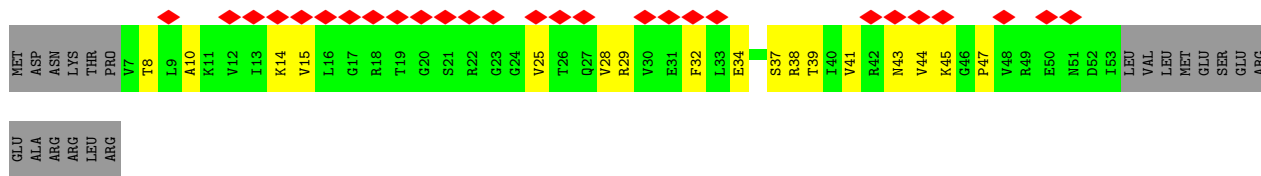
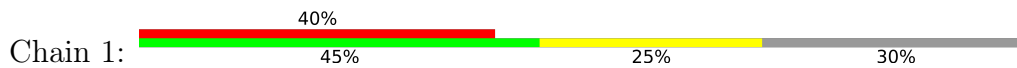
• Molecule 32: uS8



• 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 (\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 (\AA)	1.068, 1.068, 1.068	Depositor

5 Model quality i

5.1 Standard geometry i

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	G	0.99	0/1393	1.23	7/1928 (0.4%)
4	I	0.23	0/3120	0.49	0/4334
8	S	0.36	0/1813	0.53	0/2523
8	T	0.38	0/1813	0.55	0/2523
9	U	0.35	0/602	0.57	0/837
9	V	0.39	0/602	0.59	0/837
10	W	0.40	0/1123	0.62	0/1564
10	X	0.35	0/1123	0.57	0/1564
11	Y	0.23	0/1793	0.52	0/2485
12	Z	0.45	0/1741	0.70	0/2416
13	a	0.48	0/265	0.70	0/367
14	b	0.72	0/759	1.01	2/1058 (0.2%)
15	c	0.74	3/950 (0.3%)	1.32	15/1323 (1.1%)
16	d	0.55	1/615 (0.2%)	2.34	41/857 (4.8%)
17	e	0.35	0/1044	0.61	0/1452
17	f	0.39	0/1079	0.58	0/1502
18	g	0.53	0/860	0.73	1/1197 (0.1%)
18	h	0.53	0/860	0.74	1/1197 (0.1%)
19	i	1.00	5/3246 (0.2%)	1.37	27/4507 (0.6%)
19	j	1.01	5/3335 (0.1%)	1.40	31/4632 (0.7%)
20	k	0.88	0/900	2.02	18/1249 (1.4%)
21	o	0.40	0/1748	0.71	1/2340 (0.0%)
22	p	0.42	0/2119	0.74	0/2849
23	q	0.45	0/834	0.71	5/1159 (0.4%)
24	r	0.38	0/1895	0.67	0/2523
25	s	0.41	0/1563	0.71	0/2100
26	t	0.38	0/1717	0.70	1/2288 (0.0%)
27	u	0.54	0/775	0.73	3/1077 (0.3%)
28	v	0.52	0/579	0.79	5/806 (0.6%)
29	w	0.44	0/626	0.72	4/867 (0.5%)
30	x	0.49	0/657	0.78	5/911 (0.5%)
31	y	0.46	0/1298	0.74	0/1741
32	z	0.56	0/621	0.85	3/860 (0.3%)
33	0	0.41	0/1215	0.70	0/1626

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
34	1	0.40	0/229	0.64	1/316 (0.3%)
35	2	2.02	729/20292 (3.6%)	2.64	2257/31586 (7.1%)
36	3	1.06	8/3912 (0.2%)	1.68	94/6092 (1.5%)
All	All	1.22	751/69116 (1.1%)	1.71	2522/99493 (2.5%)

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 751 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	2	407	A	N9-C4	-12.24	1.30	1.37
35	2	485	A	N9-C4	-12.21	1.30	1.37
35	2	328	A	N9-C4	-12.18	1.30	1.37
35	2	432	G	N7-C5	-12.13	1.31	1.39
35	2	503	G	N9-C4	-11.40	1.28	1.38

The worst 5 of 2522 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	k	272	PRO	N-CA-CB	37.92	148.80	103.30
16	d	104	PRO	N-CA-CB	37.74	148.58	103.30
20	k	82	LYS	O-C-N	-24.01	84.28	122.70
16	d	128	THR	N-CA-CB	23.81	155.54	110.30
35	2	381	C	N3-C4-N4	-22.05	102.57	118.00

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 [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	G	265/1802 (15%)	245 (92%)	11 (4%)	9 (3%)	3	26
4	I	626/939 (67%)	609 (97%)	17 (3%)	0	100	100
8	S	363/412 (88%)	344 (95%)	14 (4%)	5 (1%)	11	46
8	T	363/412 (88%)	341 (94%)	20 (6%)	2 (1%)	25	66
9	U	120/130 (92%)	111 (92%)	7 (6%)	2 (2%)	9	42
9	V	120/130 (92%)	112 (93%)	6 (5%)	2 (2%)	9	42
10	W	225/232 (97%)	206 (92%)	16 (7%)	3 (1%)	12	48
10	X	225/232 (97%)	204 (91%)	17 (8%)	4 (2%)	8	40
11	Y	353/573 (62%)	341 (97%)	11 (3%)	1 (0%)	41	77
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	17
15	c	190/297 (64%)	163 (86%)	12 (6%)	15 (8%)	1	12

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	d	122/184 (66%)	110 (90%)	8 (7%)	4 (3%)	4	26
17	e	205/252 (81%)	190 (93%)	15 (7%)	0	100	100
17	f	214/252 (85%)	201 (94%)	11 (5%)	2 (1%)	17	57
18	g	172/322 (53%)	163 (95%)	9 (5%)	0	100	100
18	h	172/322 (53%)	163 (95%)	9 (5%)	0	100	100
19	i	643/1073 (60%)	577 (90%)	38 (6%)	28 (4%)	2	22
19	j	663/1073 (62%)	591 (89%)	43 (6%)	29 (4%)	2	22
20	k	172/391 (44%)	151 (88%)	12 (7%)	9 (5%)	2	19
21	o	213/265 (80%)	161 (76%)	33 (16%)	19 (9%)	1	11
22	p	257/259 (99%)	193 (75%)	40 (16%)	24 (9%)	0	10
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	17
25	s	184/197 (93%)	151 (82%)	23 (12%)	10 (5%)	2	19
26	t	205/208 (99%)	147 (72%)	38 (18%)	20 (10%)	0	9
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%)	1	11
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	13
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	16

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 [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	o	191/225 (85%)	166 (87%)	25 (13%)	4	18
22	p	226/226 (100%)	197 (87%)	29 (13%)	4	18
24	r	201/244 (82%)	187 (93%)	14 (7%)	15	40
25	s	172/183 (94%)	156 (91%)	16 (9%)	9	28
26	t	184/185 (100%)	171 (93%)	13 (7%)	14	39
31	y	141/141 (100%)	125 (89%)	16 (11%)	6	21
33	0	133/134 (99%)	124 (93%)	9 (7%)	16	41
All	All	1248/1338 (93%)	1126 (90%)	122 (10%)	11	26

5 of 122 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
24	r	45	PHE
31	y	128	ARG
25	s	105	VAL
31	y	121	ILE
33	0	98	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 37 such sidechains are listed below:

Mol	Chain	Res	Type
31	y	36	ASN
33	0	27	HIS
31	y	62	ASN
31	y	109	HIS
24	r	34	GLN

5.3.3 RNA [i](#)

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
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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

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

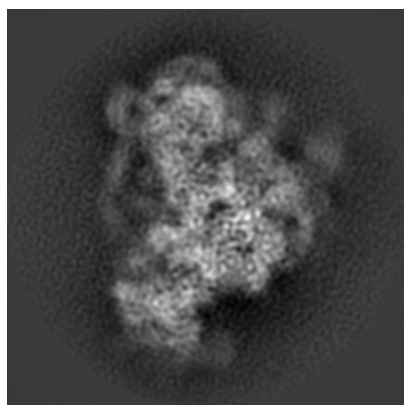
6 Map visualisation [i](#)

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.

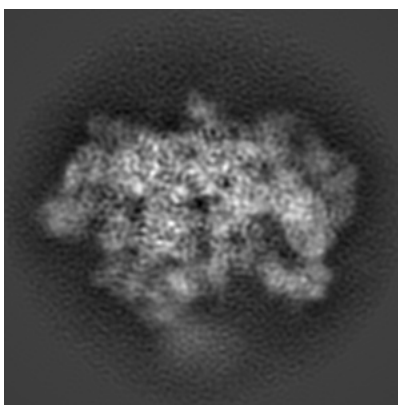
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

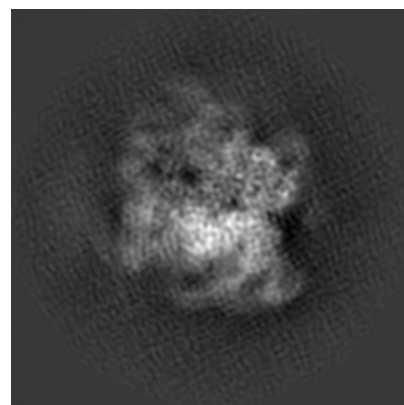
6.1.1 Primary map



X



Y

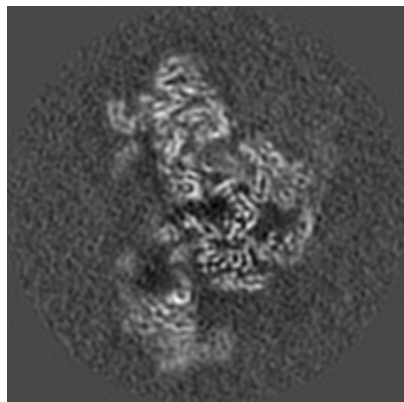


Z

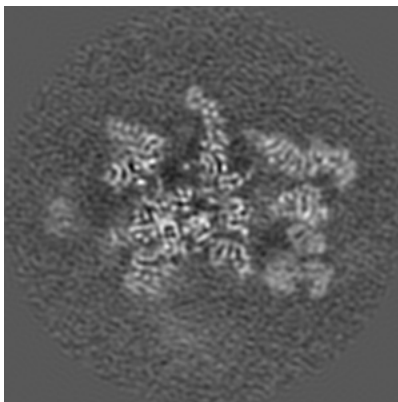
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

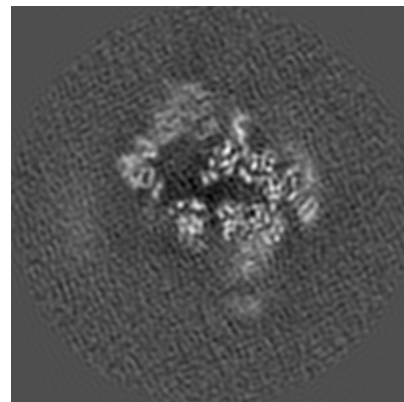
6.2.1 Primary map



X Index: 224



Y Index: 224

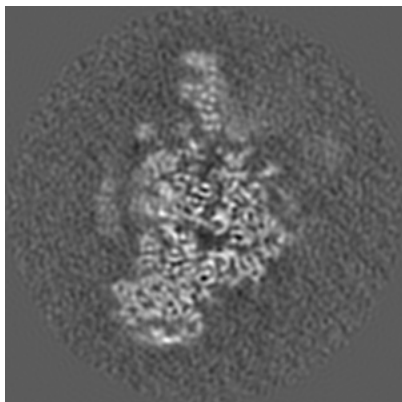


Z Index: 224

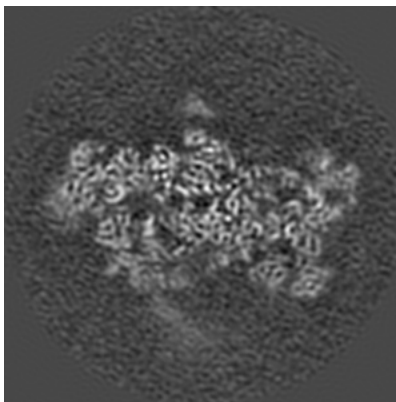
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

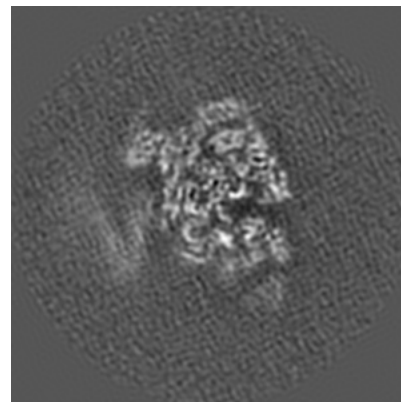
6.3.1 Primary map



X Index: 266



Y Index: 206



Z Index: 191

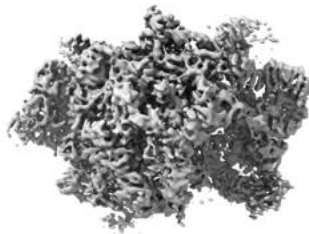
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

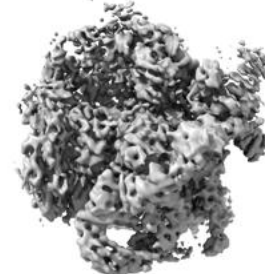
6.4.1 Primary map



X



Y



Z

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

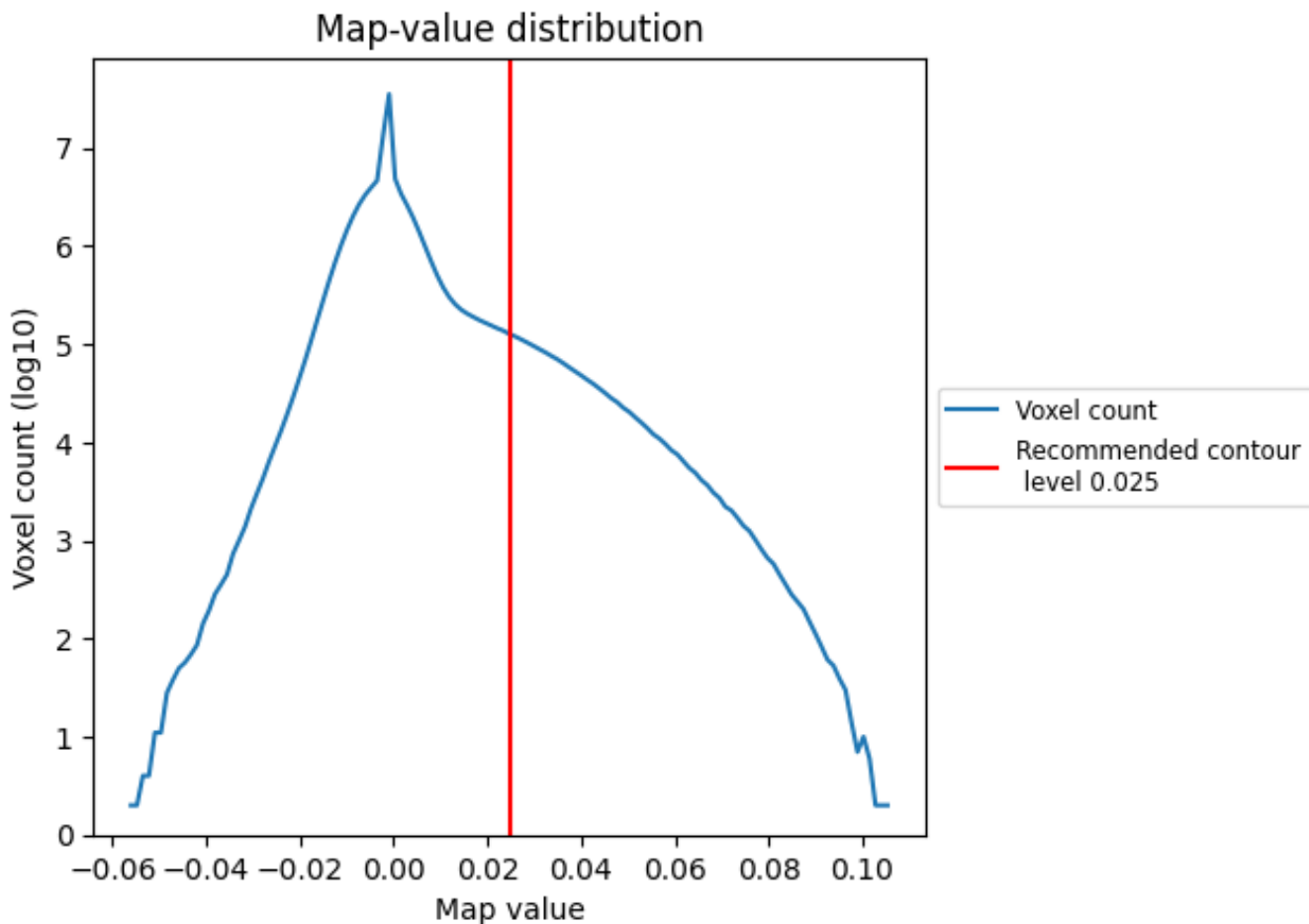
6.5 Mask visualisation

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

7 Map analysis [i](#)

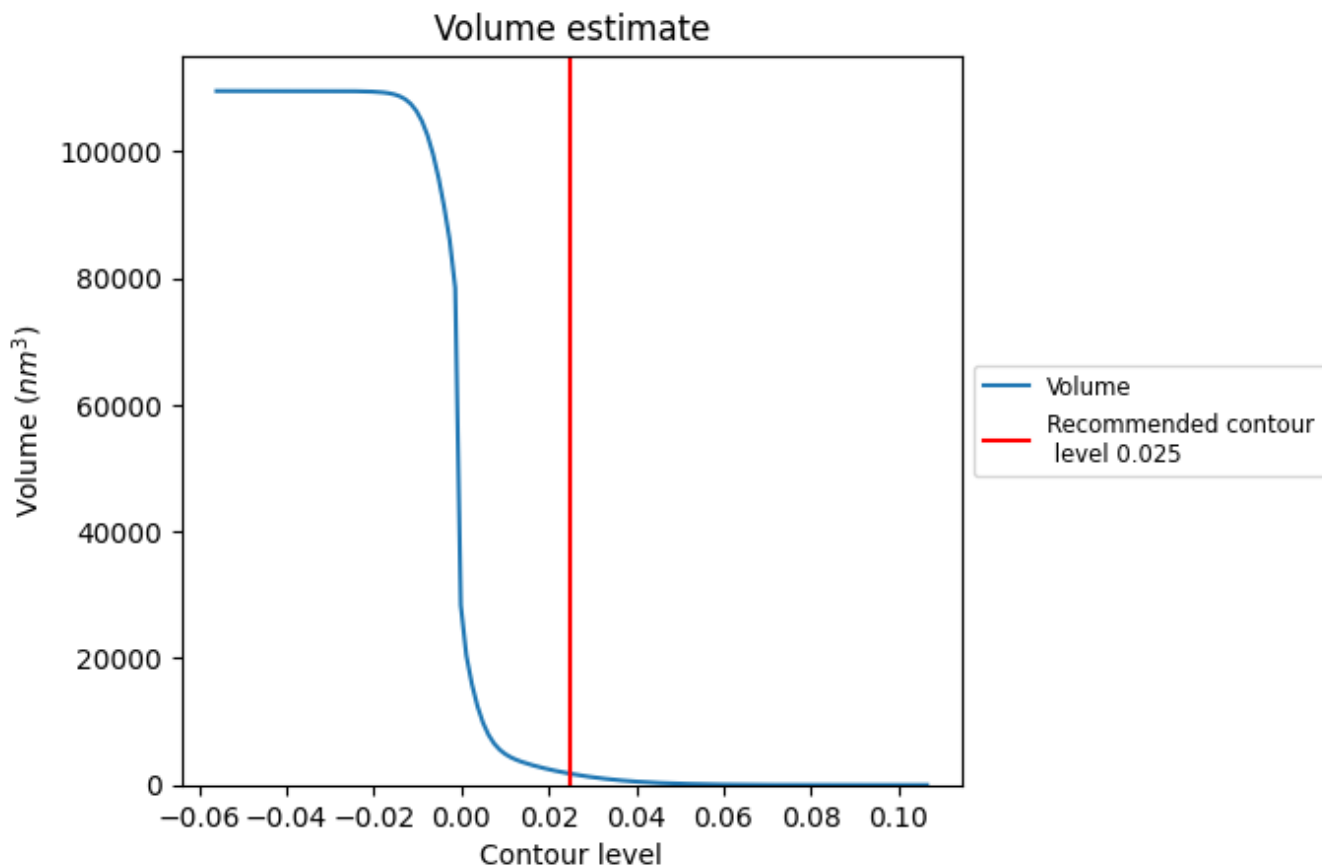
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

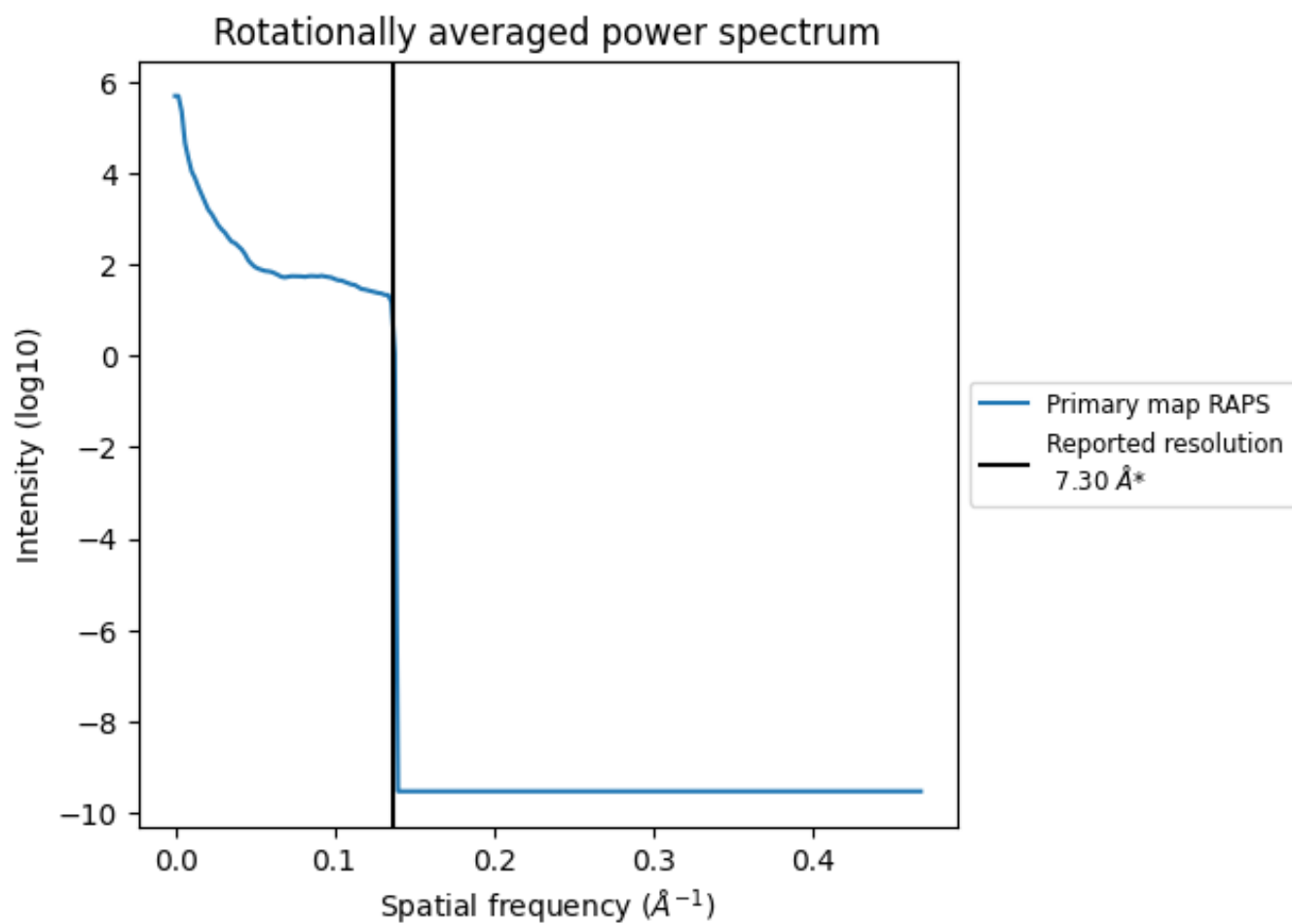
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 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 [\(i\)](#)

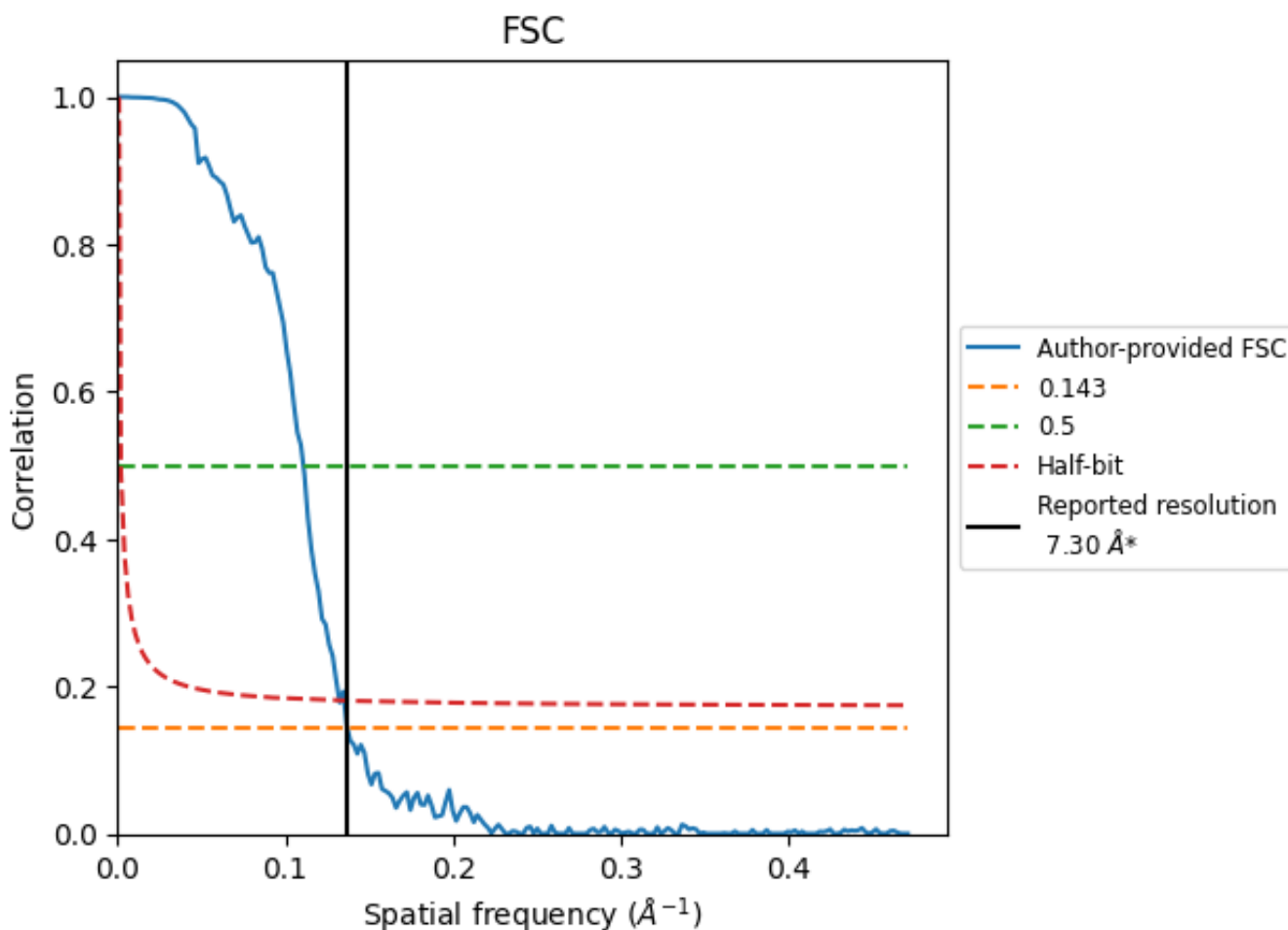


*Reported resolution corresponds to spatial frequency of 0.137 Å⁻¹

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 0.137 Å⁻¹

8.2 Resolution estimates [i](#)

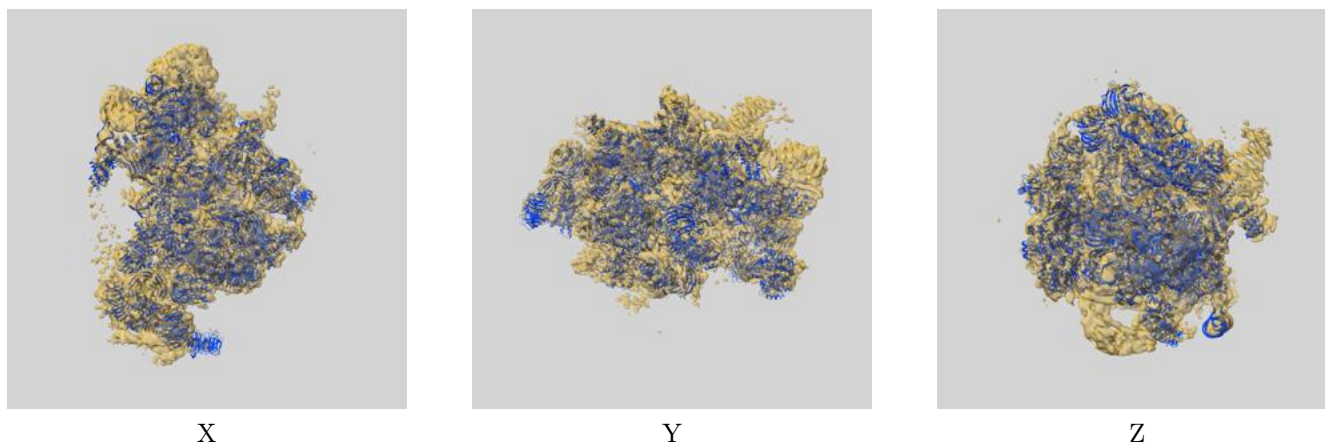
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.30	-	-
Author-provided FSC curve	7.30	9.03	7.56
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

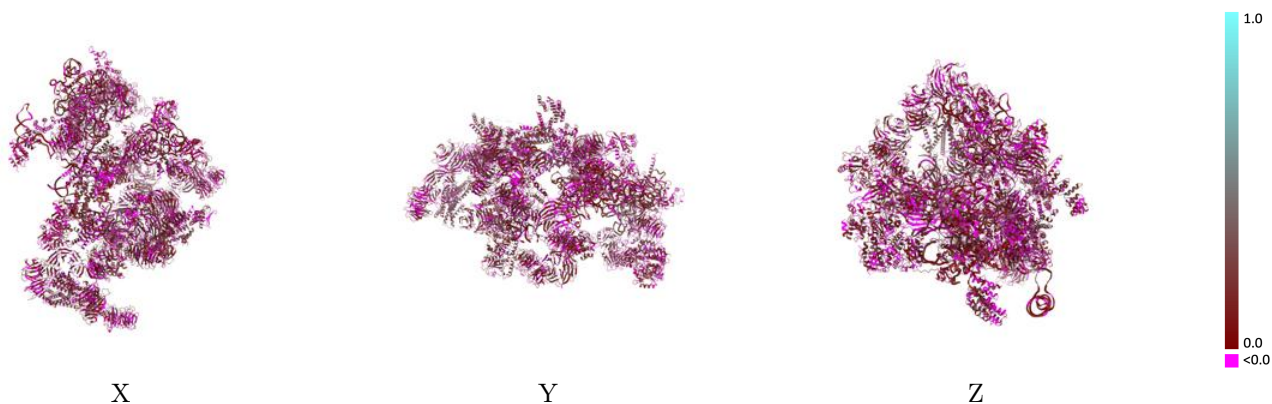
This section contains information regarding the fit between EMDB map EMD-8143 and PDB model 5JPQ. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)



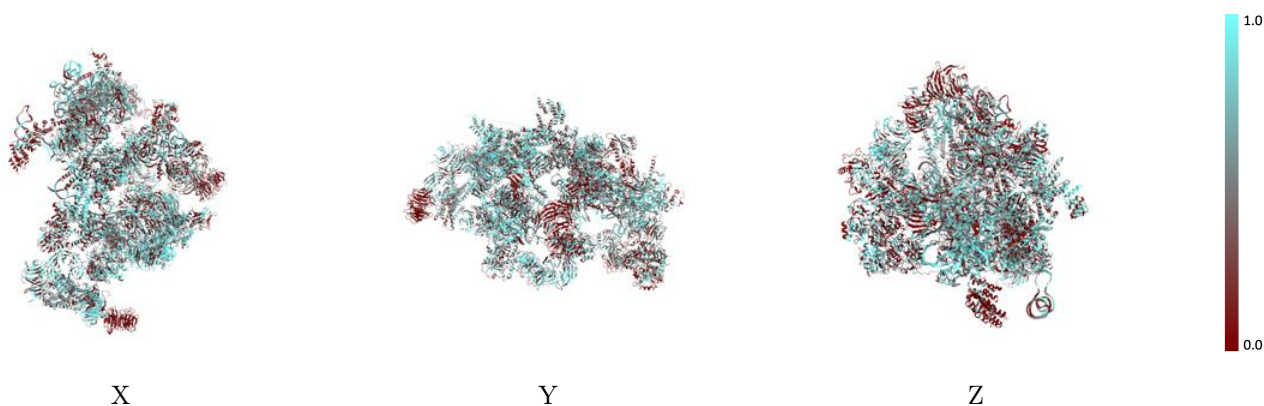
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



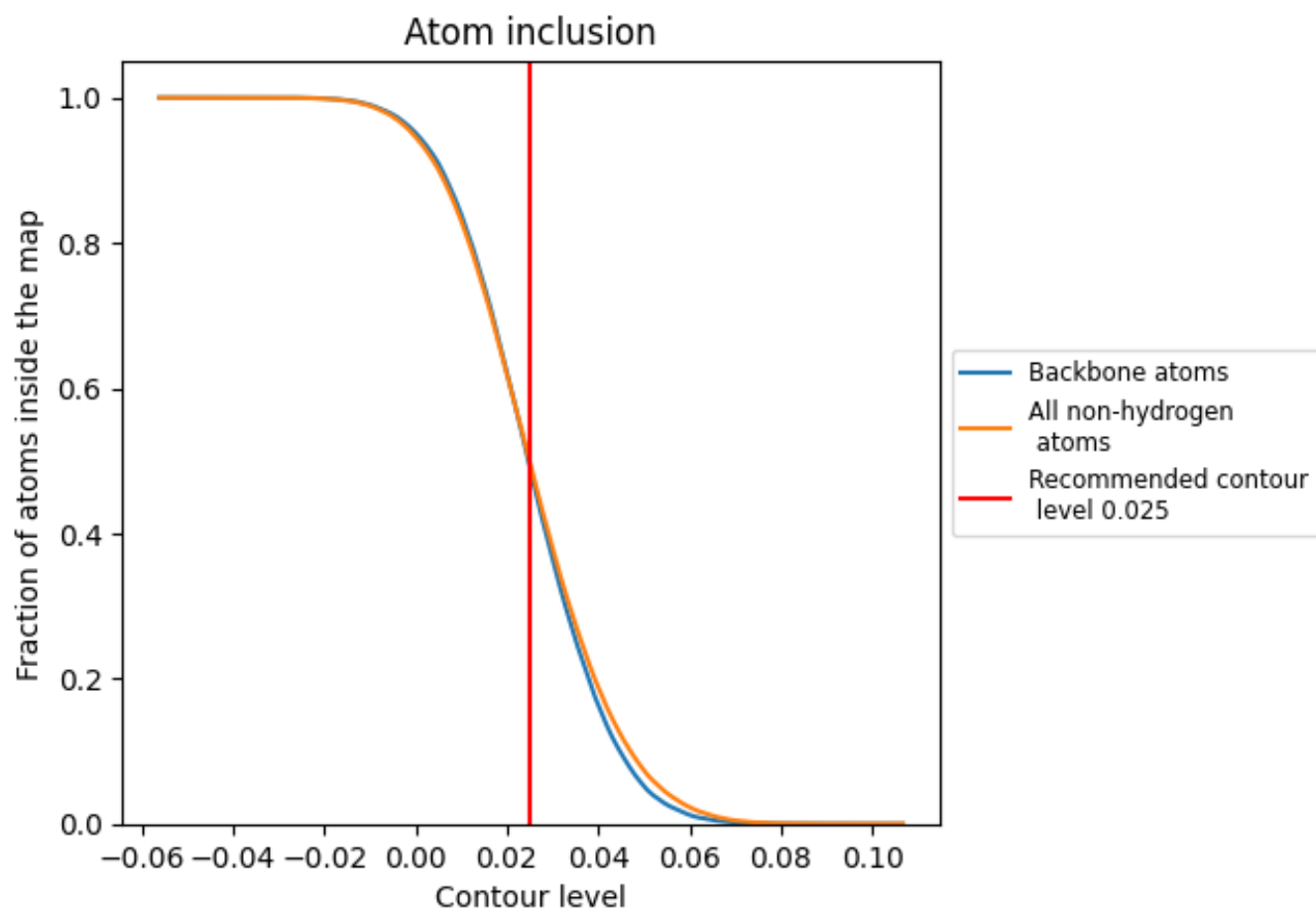
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	 0.4982	 0.0970
0	 0.3048	 0.0260
1	 0.4087	 0.0650
2	 0.6615	 0.1280
3	 0.6130	 0.1220
A	 0.6107	 0.0820
B	 0.5833	 0.0830
C	 0.5453	 0.0770
D	 0.6067	 0.0980
E	 0.5800	 0.0960
F	 0.0367	 0.0420
G	 0.1127	 0.0640
H	 0.4962	 0.1840
I	 0.6533	 0.1260
J	 0.4473	 0.1170
K	 0.5400	 0.0860
L	 0.5940	 0.1300
M	 0.6142	 0.1110
N	 0.2333	 0.0800
O	 0.1184	 0.0390
P	 0.5427	 0.1060
Q	 0.6011	 0.1280
R	 0.7247	 0.2060
S	 0.5240	 0.1050
T	 0.4567	 0.0770
U	 0.3582	 0.0160
V	 0.3449	 0.0050
W	 0.4004	 0.0570
X	 0.4600	 0.0650
Y	 0.5192	 0.0970
Z	 0.5695	 0.1350
a	 0.5281	 0.1590
b	 0.4855	 0.1190
c	 0.4658	 0.1190
d	 0.4562	 0.1080



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Chain	Atom inclusion	Q-score
e	 0.4718	 0.1430
f	 0.4801	 0.1490
g	 0.3554	 0.0620
h	 0.3438	 0.0650
i	 0.4084	 0.0800
j	 0.3612	 0.0740
k	 0.5392	 0.1430
l	 0.5987	 0.1410
m	 0.5476	 0.0940
n	 0.4407	 0.0680
o	 0.2979	 0.0530
p	 0.3622	 0.0230
q	 0.3373	 0.0210
r	 0.4370	 0.0780
s	 0.3024	 0.0230
t	 0.4474	 0.0610
u	 0.6242	 0.1790
v	 0.2138	 0.0690
w	 0.3270	 0.0790
x	 0.2401	 -0.0630
y	 0.3755	 0.0250
z	 0.3135	 0.0310