



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 04:11 PM UTC

PDB ID : 6YLX / pdb_00006ylx
EMDB ID : EMD-10841
Title : pre-60S State NE1 (TAP-Flag-Nop53)
Authors : Kater, L.; Beckmann, R.
Deposited on : 2020-04-07
Resolution : 3.90 Å(reported)
Based on initial models : 3JCT, 6ELZ, 6N8J

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:

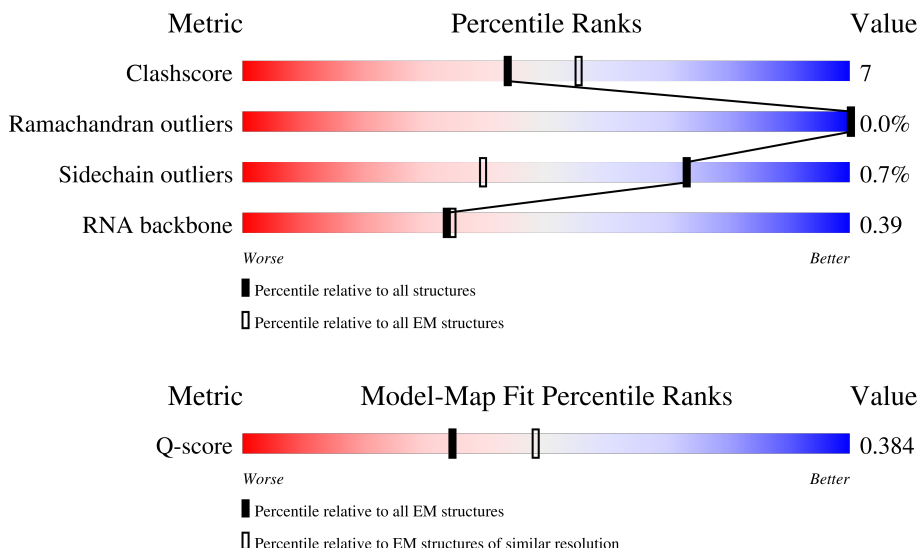
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.90 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.



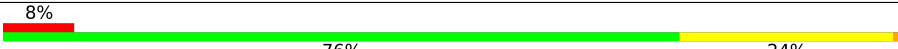
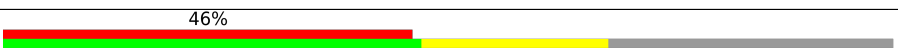
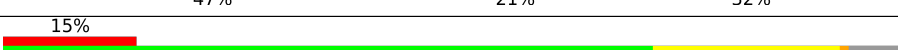
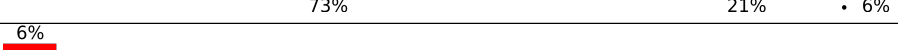
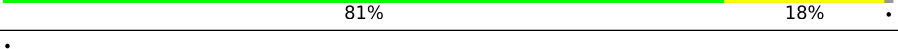
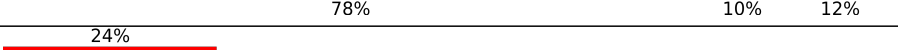
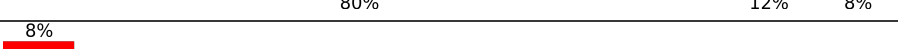
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8855 (3.40 - 4.40)

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	B	387	13% 75% 25%
2	C	362	83% 15%
3	E	176	5% 70% 18% 11%

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Mol	Chain	Length	Quality of chain
4	F	244	
5	G	256	
6	H	191	
7	K	376	
8	L	199	
9	M	138	
10	N	204	
11	O	199	
12	P	184	
13	Q	186	
14	R	189	
15	S	172	
16	T	160	
17	U	121	
18	V	137	
19	W	236	
20	X	142	
21	Y	127	
22	Z	136	
23	a	149	
24	b	647	
25	c	105	
26	d	113	
27	e	130	
28	f	107	

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Mol	Chain	Length	Quality of chain
29	g	121	
30	h	120	
31	i	100	
32	j	88	
33	k	78	
34	l	51	
35	n	605	
36	o	220	
37	q	455	
38	r	261	
39	s	520	
40	t	322	
41	u	199	
42	y	245	
43	z	106	
44	1	3396	
45	2	158	
46	6	232	
47	w	841	

2 Entry composition

There are 47 unique types of molecules in this entry. The entry contains 118882 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 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	386	Total	C	N	O	S	0	0
			3081	1956	584	533	8		

- Molecule 2 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	361	Total	C	N	O	S	0	0
			2749	1730	522	494	3		

- Molecule 3 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	156	Total	C	N	O	S	0	0
			1239	800	222	216	1		

- Molecule 4 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	F	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 5 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	192	Total	C	N	O	S	0	0
			1515	974	267	272	2		

- Molecule 6 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	H	191	Total	C	N	O	S	0	0
			1518	963	274	277	4		

- Molecule 7 is a protein called Proteasome-interacting protein CIC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	K	256	Total	C	N	O	S	0	0
			2064	1332	342	387	3		

- Molecule 8 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L	187	Total	C	N	O	S	0	0
			1499	934	307	258			

- Molecule 9 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	M	137	Total	C	N	O	S	0	0
			1059	678	200	179	2		

- Molecule 10 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	N	180	Total	C	N	O	S	0	0
			1543	968	325	249	1		

- Molecule 11 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	O	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 12 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	P	176	Total	C	N	O	S	0	0
			1397	868	279	250			

- Molecule 13 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Q	134	Total	C	N	O	S	0	0
			1035	659	196	179	1		

- Molecule 14 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	R	156	Total	C	N	O	0	0
			1258	781	265	212		

- Molecule 15 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	S	171	Total	C	N	O	S	0	0
			1437	925	266	243	3		

- Molecule 16 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	T	56	Total	C	N	O	S	0	0
			434	268	86	79	1		

- Molecule 17 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	U	106	Total	C	N	O	0	0
			844	545	138	161		

- Molecule 18 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	V	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 19 is a protein called Ribosome assembly factor MRT4.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	W	234	Total	C	N	O	S	0	0
			1885	1194	323	362	6		

- Molecule 20 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	X	141	Total	C	N	O	S	0	0
			1100	705	196	197	2		

- Molecule 21 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	Y	126	Total	C	N	O	0	0
			993	625	192	176		

- Molecule 22 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	Z	135	Total	C	N	O	0	0
			1092	710	202	180		

- Molecule 23 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	a	93	Total	C	N	O	S	0	0
			735	479	130	125	1		

- Molecule 24 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	b	470	Total	C	N	O	S	0	0
			3814	2424	663	709	18		

- Molecule 25 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	c	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 26 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	d	107	Total	C	N	O	S	0	0
			873	553	165	154	1		

- Molecule 27 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	e	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 28 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	f	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 29 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	g	112	Total	C	N	O	S	0	0
			881	546	179	152	4		

- Molecule 30 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	h	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 31 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	i	99	Total	C	N	O	S	0	0
			771	481	156	132	2		

- Molecule 32 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	j	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

- Molecule 33 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	k	77	Total	C	N	O	0	0
			612	391	115	106		

- Molecule 34 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	l	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 35 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	n	371	Total	C	N	O	S	0	0
			3030	1963	523	534	10		

- Molecule 36 is a protein called Ribosome biogenesis protein 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	o	133	Total	C	N	O	S	0	0
			1107	716	198	189	4		

- Molecule 37 is a protein called Ribosome biogenesis protein NOP53.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	q	87	Total	C	N	O	S	0	0
			723	450	129	143	1		

- Molecule 38 is a protein called Ribosome biogenesis protein NSA2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	r	217	Total	C	N	O	S	0	0
			1760	1110	334	309	7		

- Molecule 39 is a protein called Nuclear GTP-binding protein NUG1.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	s	36	Total	C	N	O	S	0	0
			301	184	69	46	2		

- Molecule 40 is a protein called Ribosome biogenesis protein RLP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	t	287	Total	C	N	O	S	0	0
			2306	1459	427	417	3		

- Molecule 41 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	u	123	Total	C	N	O	S	0	0
			1040	652	211	168	9		

- Molecule 42 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	y	244	Total	C	N	O	S	0	0
			1849	1146	319	377	7		

- Molecule 43 is a protein called UPF0642 protein YBL028C.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	z	55	Total	C	N	O	0	0
			444	273	88	83		

- Molecule 44 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	1	2534	Total	C	N	O	P	0	0
			54232	24220	9799	17679	2534		

- Molecule 45 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	2	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 46 is a RNA chain called ITS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	6	65	Total	C	N	O	P	0	0
			1370	614	228	463	65		

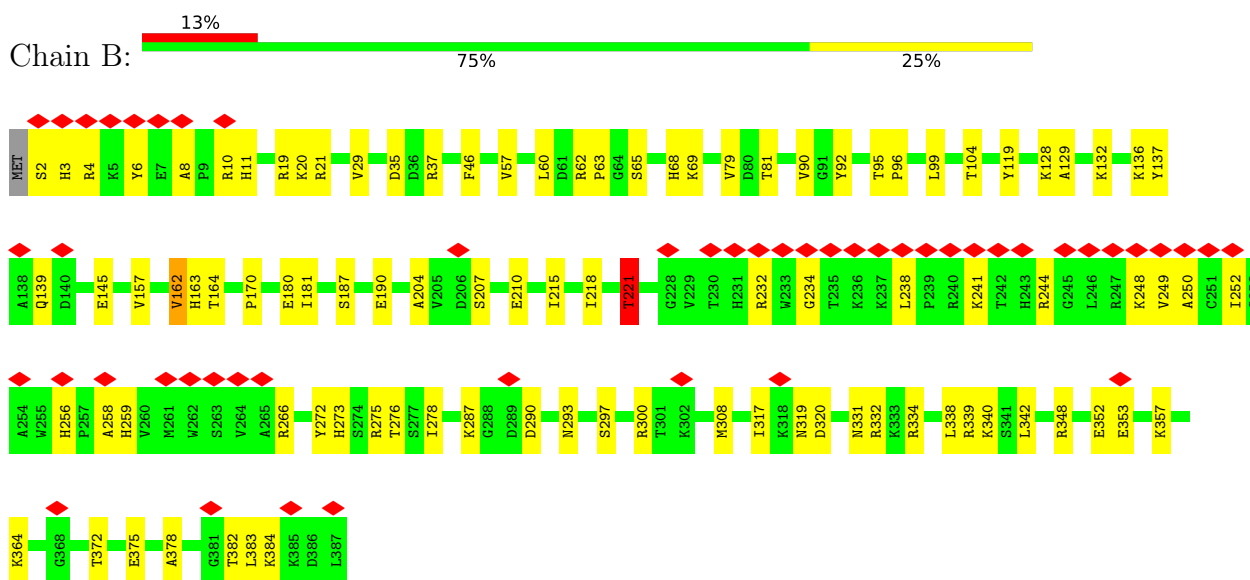
- Molecule 47 is a protein called 27S pre-rRNA (guanosine(2922)-2'-O)-methyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	w	360	Total	C	N	O	S	0	0
			2898	1860	507	516	15		

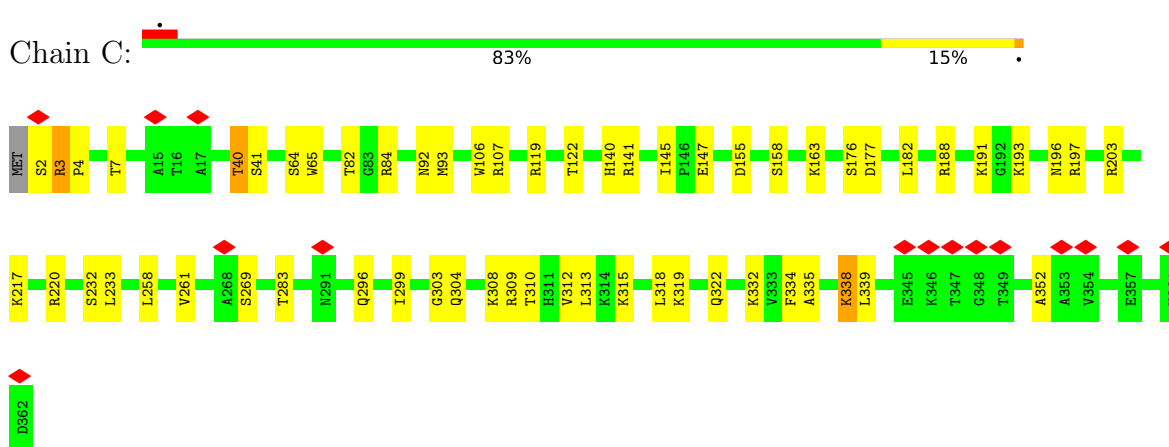
3 Residue-property plots

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: 60S ribosomal protein L3

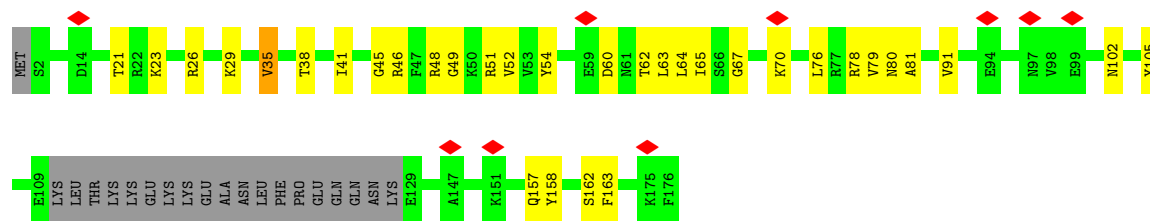


- Molecule 2: 60S ribosomal protein L4-A

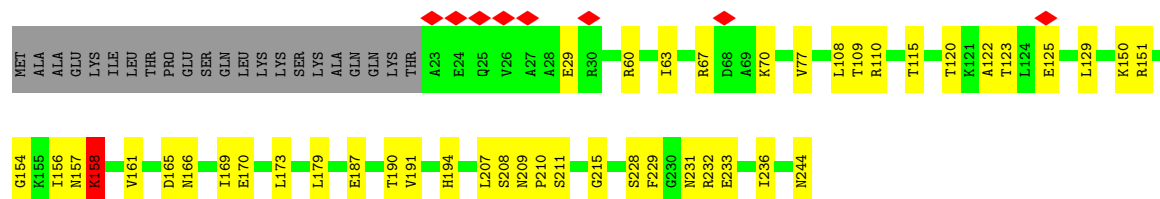


- Molecule 3: 60S ribosomal protein L6-A

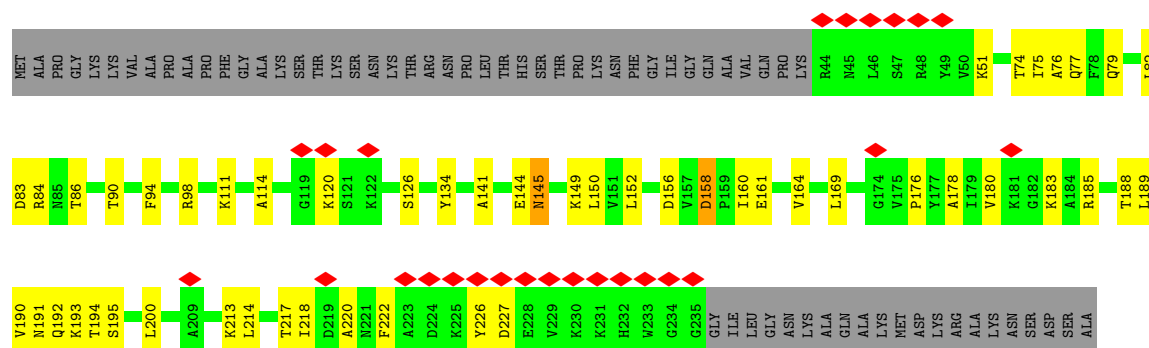




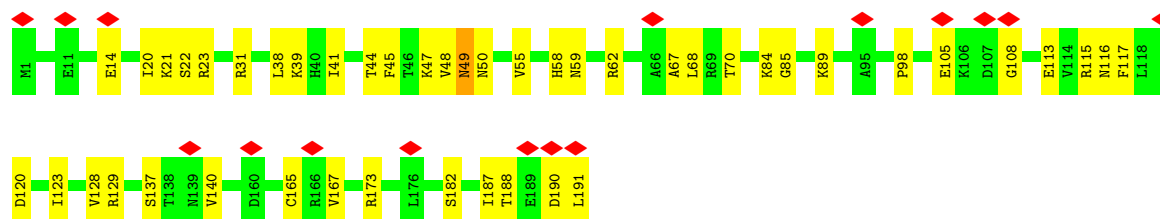
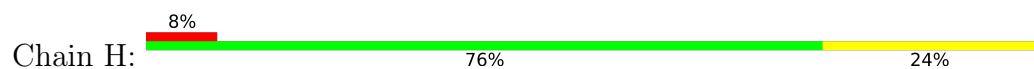
• Molecule 4: 60S ribosomal protein L7-A



• Molecule 5: 60S ribosomal protein L8-A

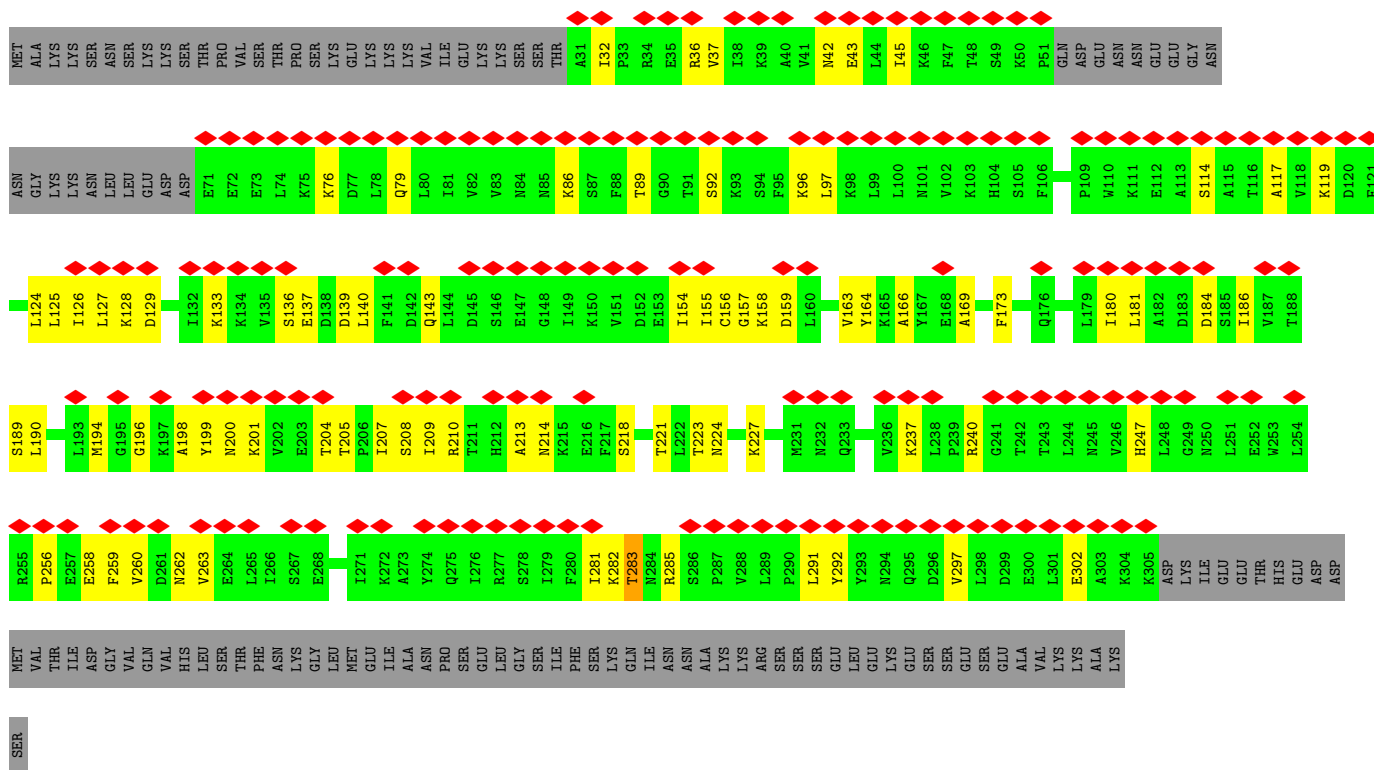


• Molecule 6: 60S ribosomal protein L9-A

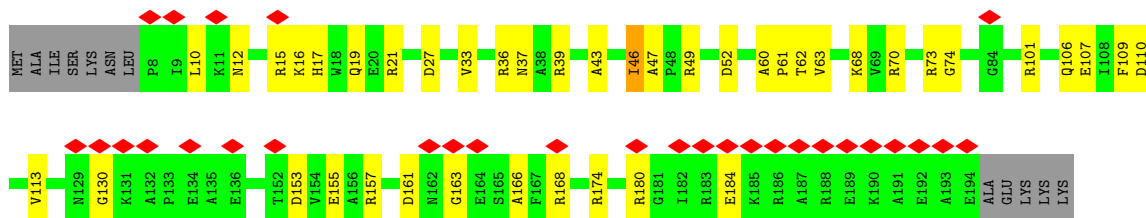


• Molecule 7: Proteasome-interacting protein CIC1

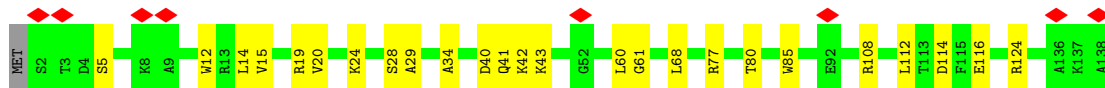
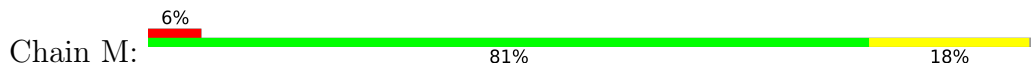




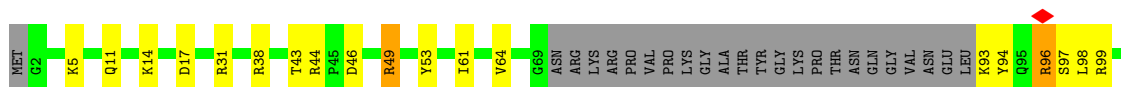
• Molecule 8: 60S ribosomal protein L13-A



• Molecule 9: 60S ribosomal protein L14-A



• Molecule 10: 60S ribosomal protein L15-A





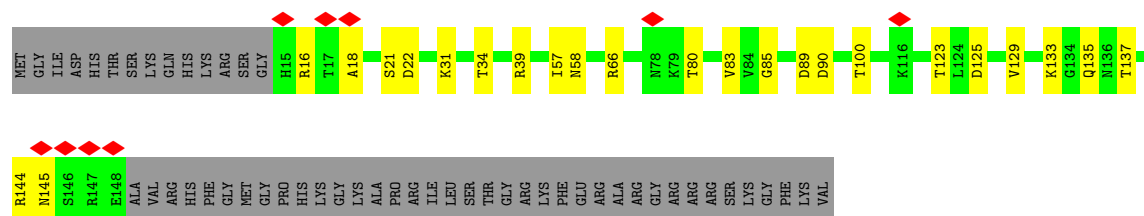
- Molecule 11: 60S ribosomal protein L16-A



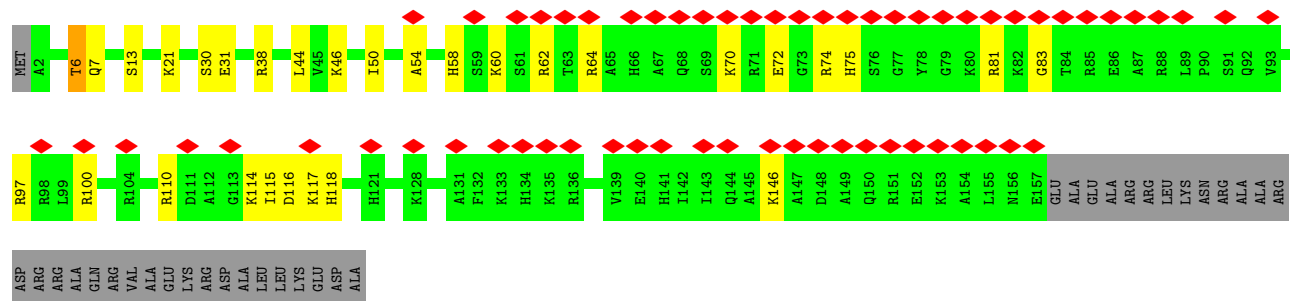
- Molecule 12: 60S ribosomal protein L17-A



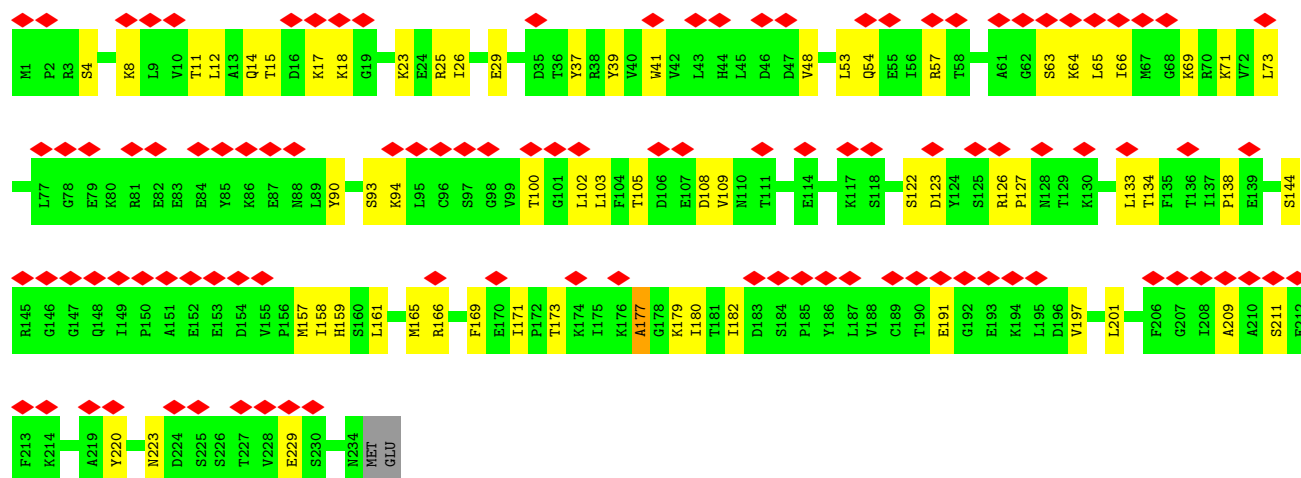
- Molecule 13: 60S ribosomal protein L18-A



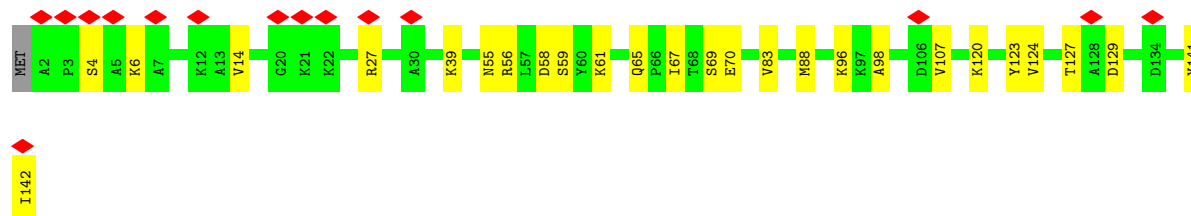
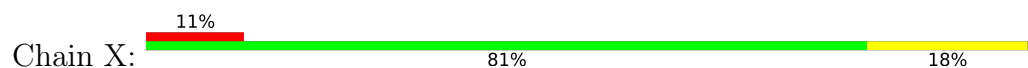
- Molecule 14: 60S ribosomal protein L19-A



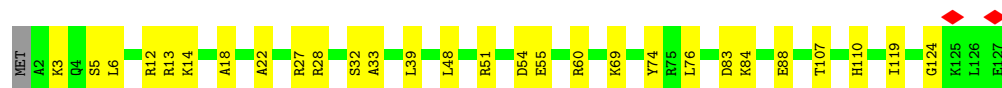
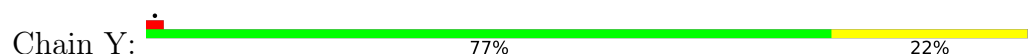
- Molecule 15: 60S ribosomal protein L20-A



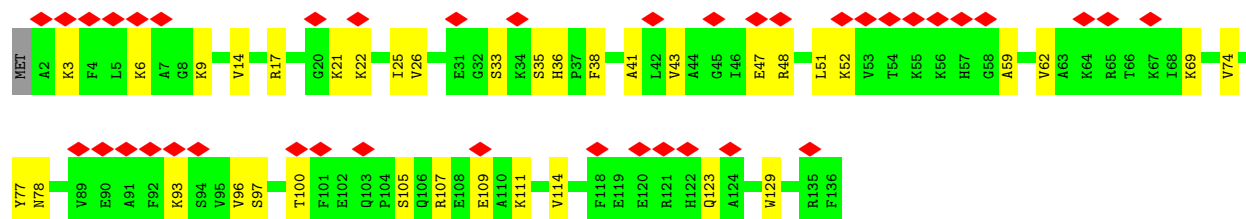
- Molecule 20: 60S ribosomal protein L25



- Molecule 21: 60S ribosomal protein L26-A

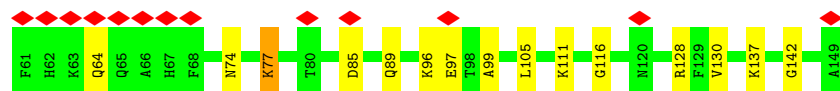


- Molecule 22: 60S ribosomal protein L27-A

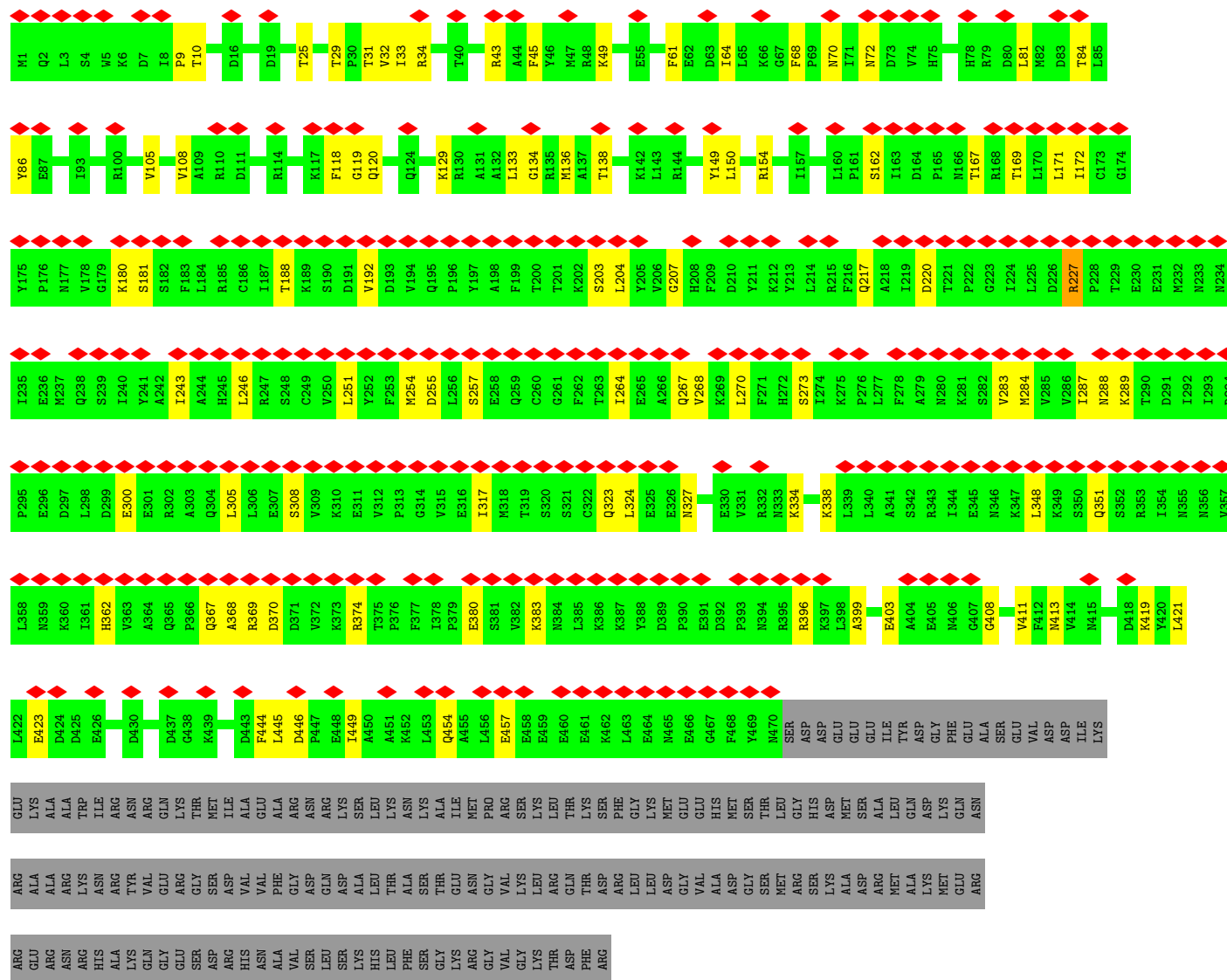
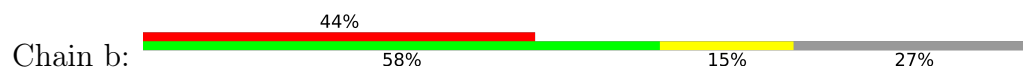


- Molecule 23: 60S ribosomal protein L28

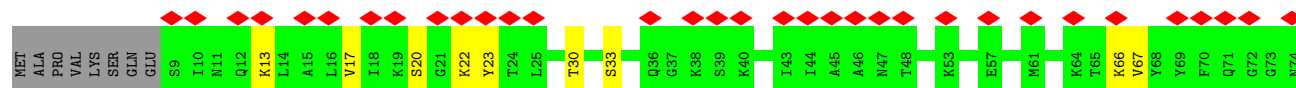
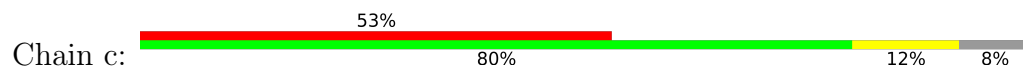


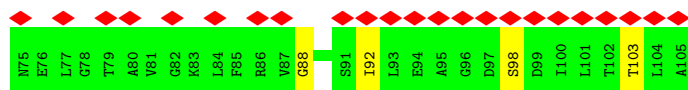


- Molecule 24: Nucleolar GTP-binding protein 1

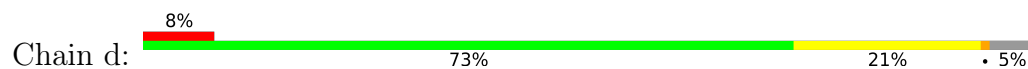


- Molecule 25: 60S ribosomal protein L30

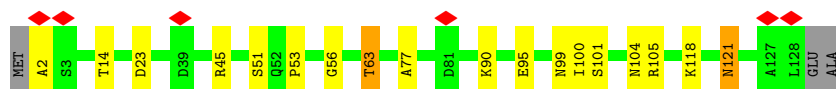
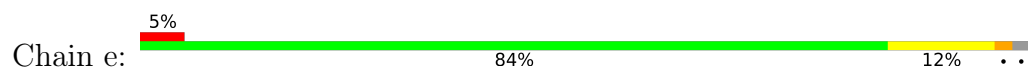




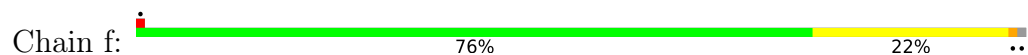
- Molecule 26: 60S ribosomal protein L31-A



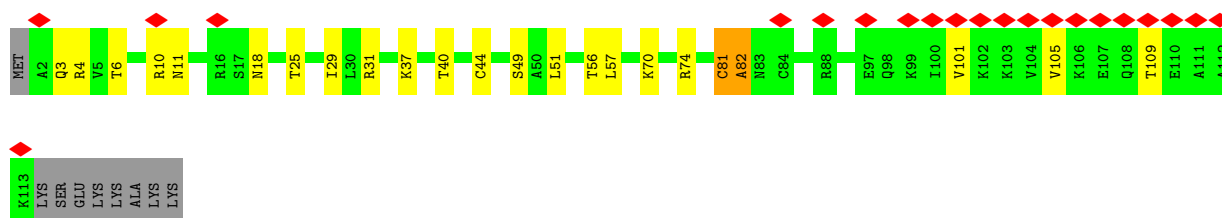
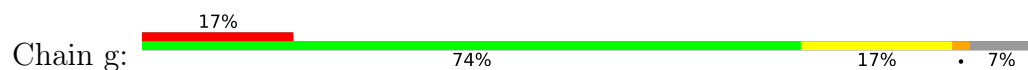
- Molecule 27: 60S ribosomal protein L32



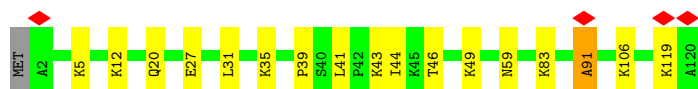
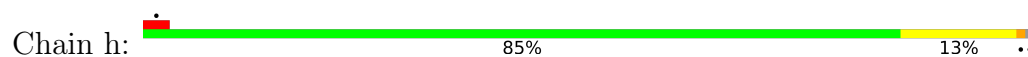
- Molecule 28: 60S ribosomal protein L33-A



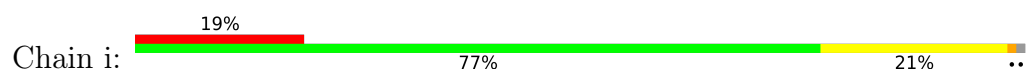
- Molecule 29: 60S ribosomal protein L34-A

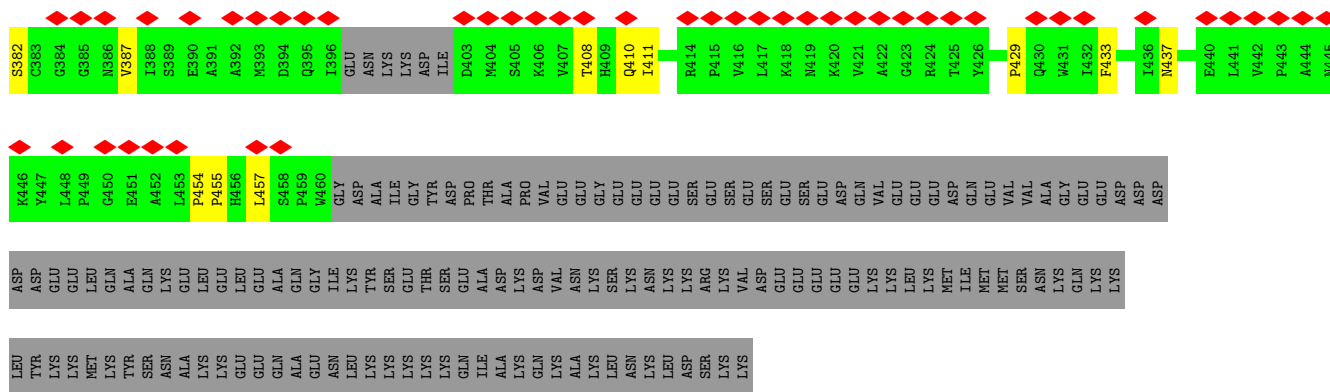


- Molecule 30: 60S ribosomal protein L35-A

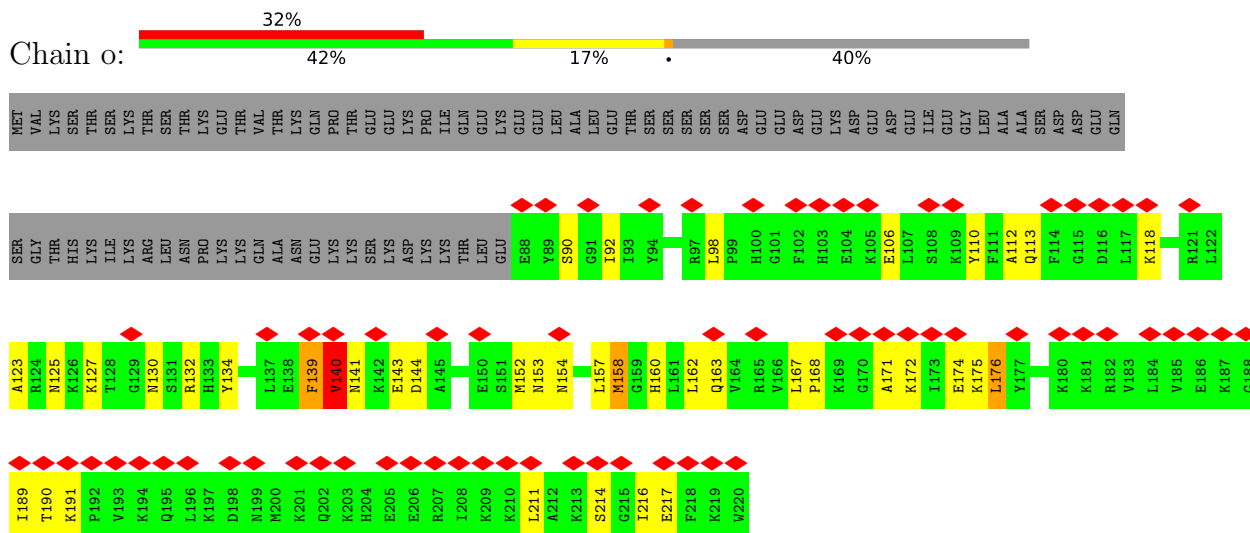


- Molecule 31: 60S ribosomal protein L36-A

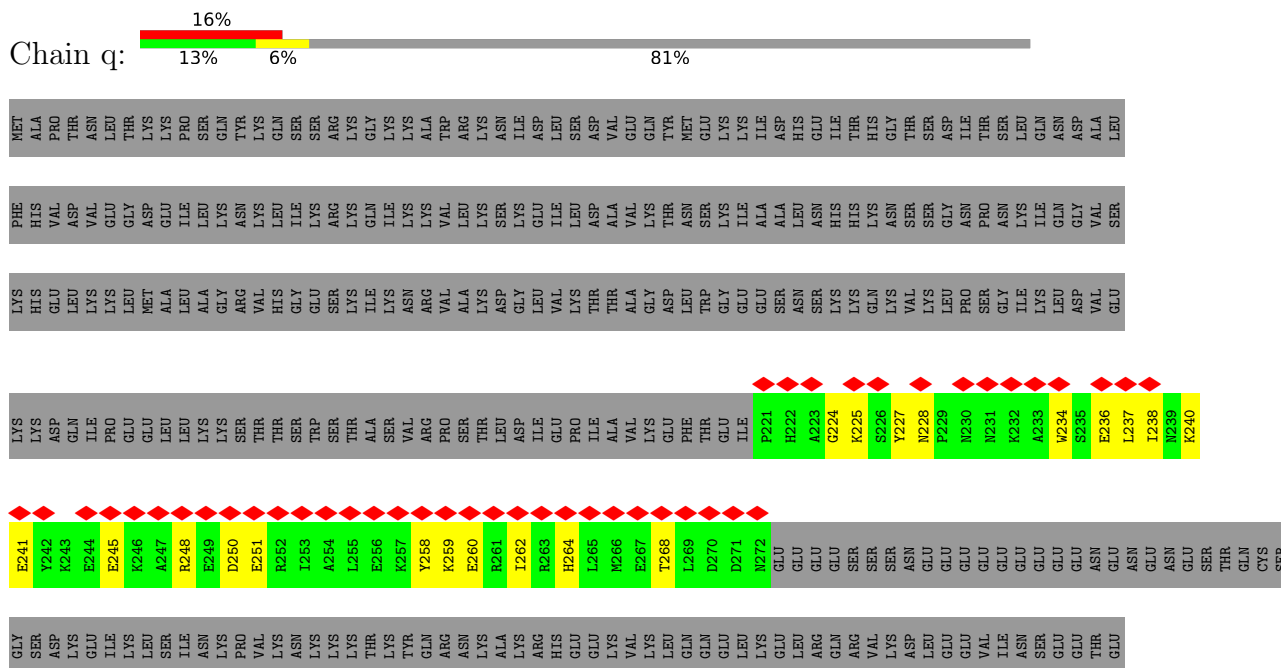




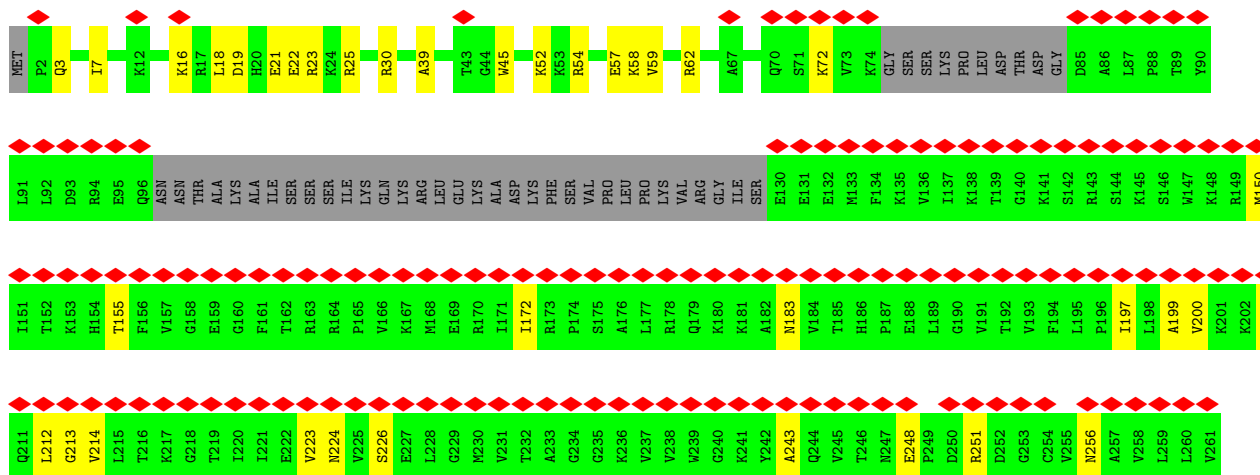
- Molecule 36: Ribosome biogenesis protein 15



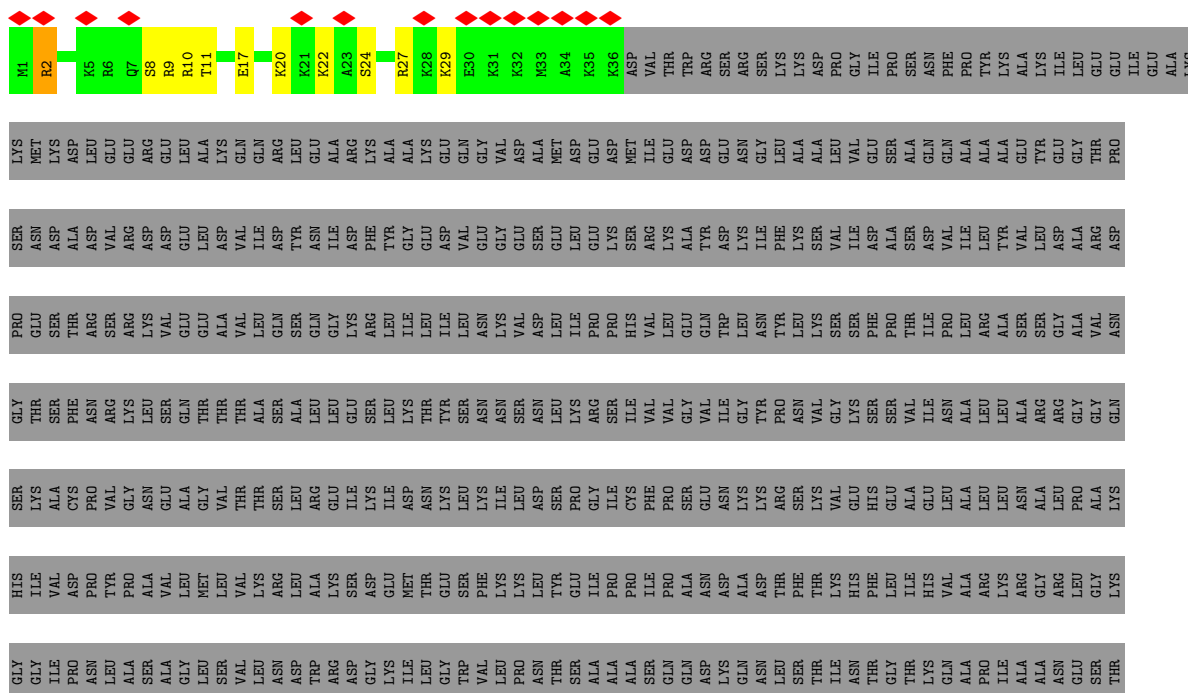
- Molecule 37: Ribosome biogenesis protein NOP53



- Molecule 38: Ribosome biogenesis protein NSA2



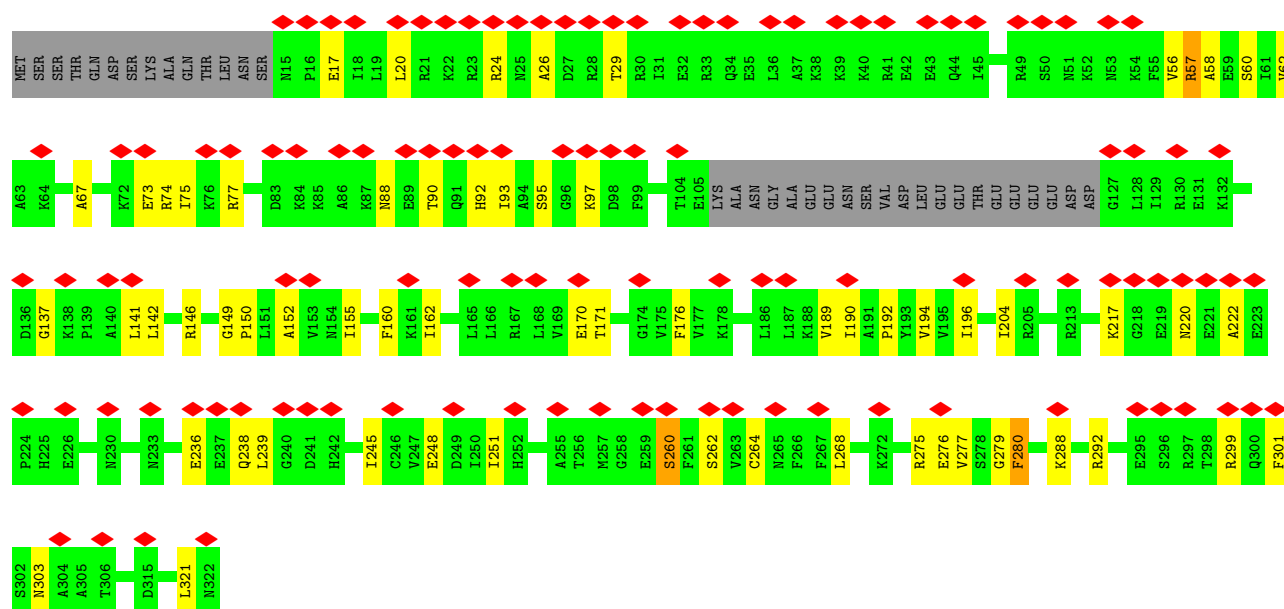
- Molecule 39: Nuclear GTP-binding protein NUG1



ILE VAL SER GLU THR TRP SER LYS PHE ASP LEU ASP GLY LEU PHE SER SER LEU ASP LYS ASP ALA THR MET MET GLU

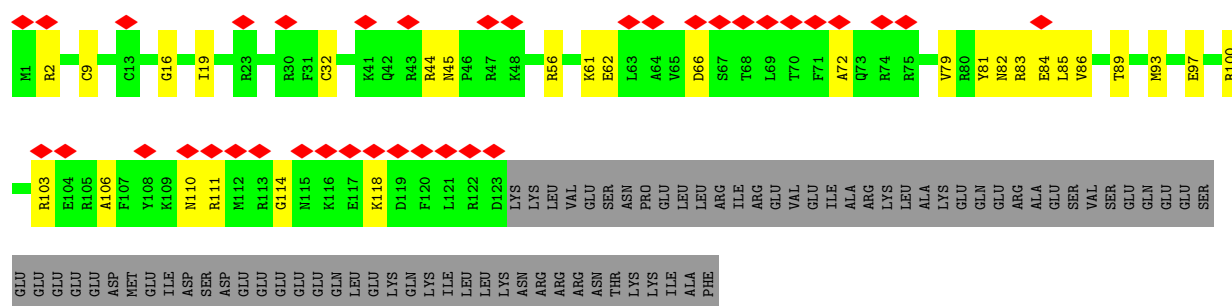
• Molecule 40: Ribosome biogenesis protein RLP7

Chain t: 



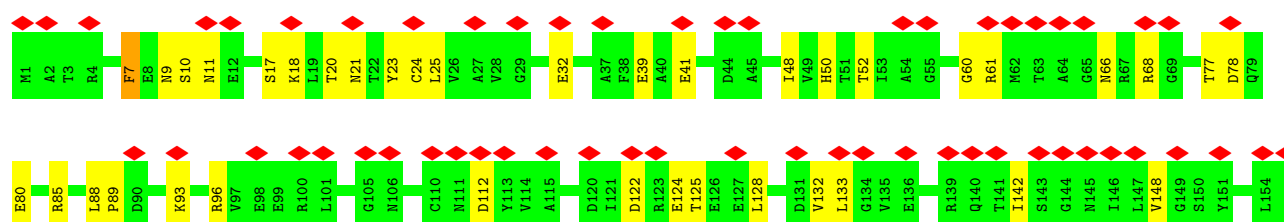
• Molecule 41: Ribosome biogenesis protein RLP24

Chain u: 



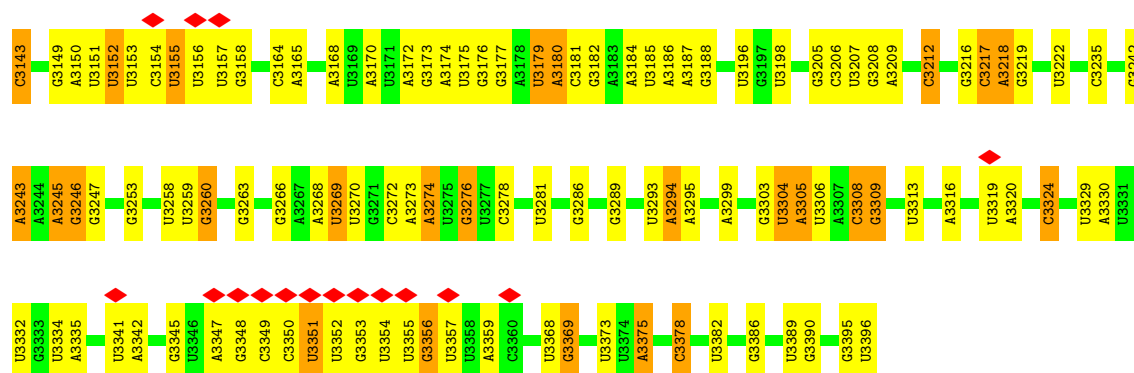
• Molecule 42: Eukaryotic translation initiation factor 6

Chain y: 

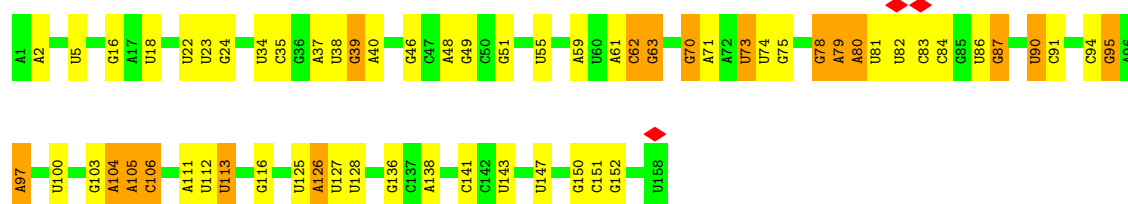




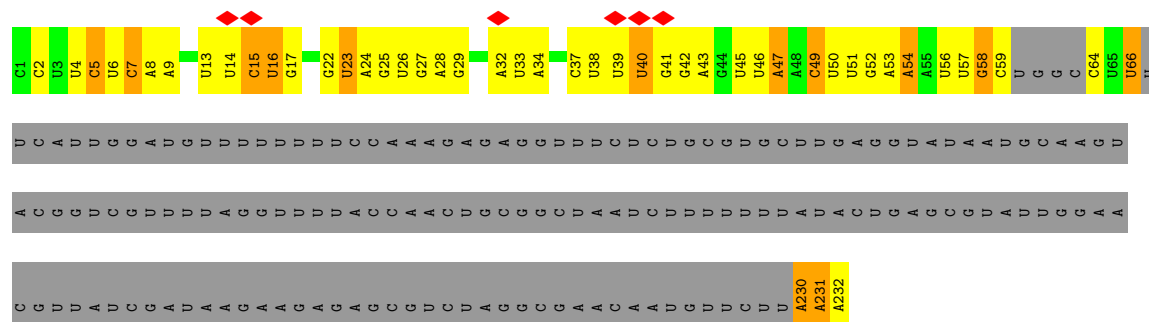




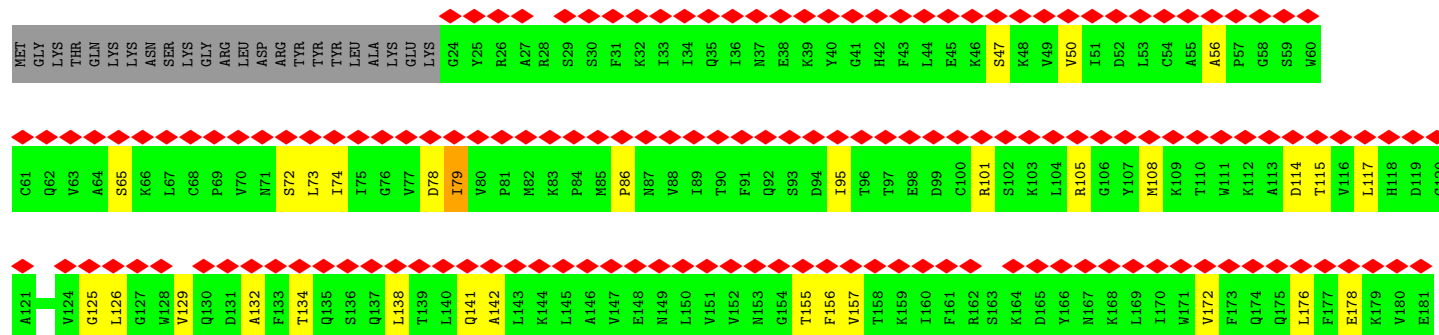
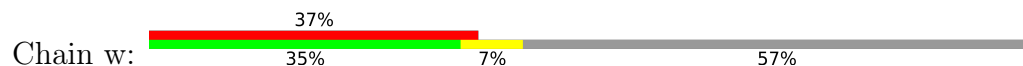
• Molecule 45: 5.8S rRNA

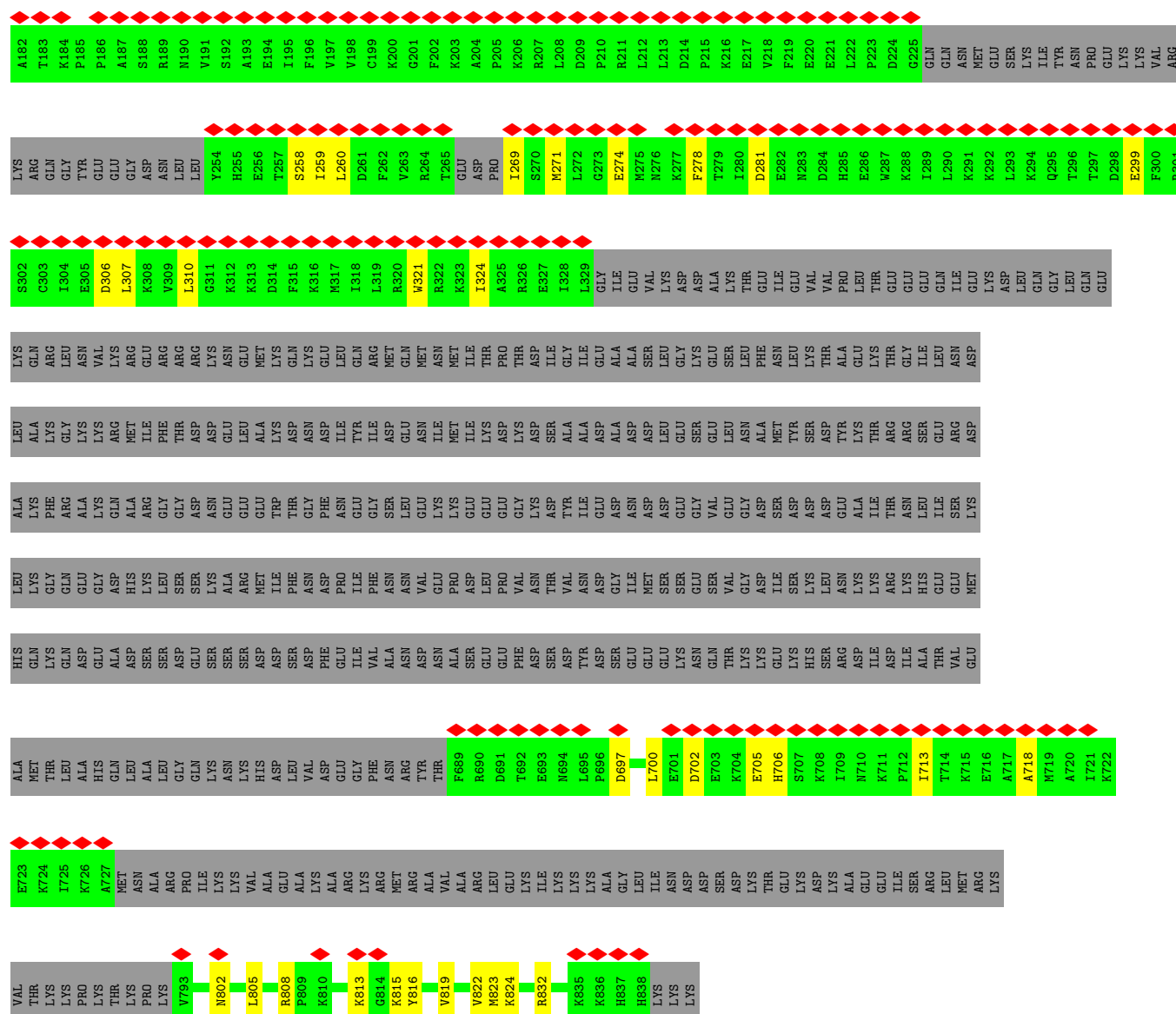


• Molecule 46: ITS2



• Molecule 47: 27S pre-rRNA (guanosine(2922)-2'-O)-methyltransferase





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	29163	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 ($e^-/\text{\AA}^2$)	24	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	0.483	Depositor
Minimum map value	-0.257	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.055	Depositor
Map size ($\text{\AA}$)	416.25598, 416.25598, 416.25598	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.084, 1.084, 1.084	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	B	1.10	1/3152 (0.0%)	0.96	1/4239 (0.0%)
2	C	1.36	1/2801 (0.0%)	1.03	4/3792 (0.1%)
3	E	0.98	0/1260	0.85	1/1694 (0.1%)
4	F	1.22	2/1821 (0.1%)	1.03	6/2451 (0.2%)
5	G	0.91	0/1542	0.89	3/2083 (0.1%)
6	H	0.88	0/1539	0.93	2/2073 (0.1%)
7	K	0.44	0/2098	0.77	4/2830 (0.1%)
8	L	1.12	0/1524	0.97	2/2046 (0.1%)
9	M	1.07	0/1074	0.89	0/1446
10	N	1.47	3/1575 (0.2%)	1.06	1/2106 (0.0%)
11	O	1.53	1/1585 (0.1%)	0.95	0/2128
12	P	1.34	3/1419 (0.2%)	0.94	0/1904
13	Q	1.13	0/1050	0.91	0/1419
14	R	0.74	1/1275 (0.1%)	0.78	0/1702
15	S	0.97	0/1473	0.92	0/1980
16	T	0.44	0/440	0.85	0/594
17	U	0.52	0/861	0.71	0/1167
18	V	0.69	0/1018	0.80	0/1369
19	W	0.48	0/1918	0.76	2/2586 (0.1%)
20	X	1.13	0/1116	0.84	0/1503
21	Y	1.19	0/1004	0.97	0/1341
22	Z	0.51	0/1118	0.74	0/1497
23	a	0.87	0/751	0.90	2/1013 (0.2%)
24	b	0.54	0/3885	0.82	0/5242
25	c	0.41	0/751	0.66	0/1008
26	d	1.02	0/887	0.90	4/1191 (0.3%)
27	e	1.43	2/1041 (0.2%)	1.00	1/1394 (0.1%)
28	f	1.71	4/868 (0.5%)	1.07	3/1168 (0.3%)
29	g	0.84	0/891	0.90	2/1191 (0.2%)
30	h	1.20	0/978	0.96	2/1301 (0.2%)
31	i	0.78	0/778	0.79	0/1034
32	j	1.44	2/696 (0.3%)	1.06	1/923 (0.1%)
33	k	0.64	0/618	0.78	0/826
34	l	0.70	0/443	0.92	0/588

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	n	0.74	0/3101	0.91	4/4187 (0.1%)
36	o	0.53	0/1129	0.89	4/1502 (0.3%)
37	q	0.42	0/733	0.80	0/977
38	r	0.64	0/1789	0.87	2/2389 (0.1%)
39	s	0.75	0/301	0.97	0/386
40	t	0.57	0/2333	0.89	3/3128 (0.1%)
41	u	0.73	1/1061 (0.1%)	0.97	2/1410 (0.1%)
42	y	0.54	0/1872	0.75	0/2548
43	z	0.67	0/445	0.89	0/585
44	1	0.91	1/60703 (0.0%)	0.75	3/94630 (0.0%)
45	2	1.16	0/3746	0.87	0/5832
46	6	0.46	0/1527	0.59	0/2371
47	w	0.43	0/2952	0.68	1/3965 (0.0%)
All	All	0.93	22/126942 (0.0%)	0.81	60/184739 (0.0%)

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
1	B	0	7
2	C	0	6
4	F	0	2
5	G	0	5
6	H	0	3
7	K	0	1
8	L	0	5
9	M	0	1
10	N	0	1
12	P	0	1
14	R	0	1
15	S	0	2
18	V	0	1
19	W	0	2
20	X	0	1
23	a	0	2
24	b	0	3
26	d	0	1
27	e	0	1
28	f	0	2
29	g	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
30	h	0	3
31	i	0	2
33	k	0	2
35	n	0	11
36	o	0	5
37	q	0	1
38	r	0	1
39	s	0	1
40	t	0	5
41	u	0	2
42	y	0	1
47	w	0	2
All	All	0	86

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	N	146	ALA	CA-C	-8.06	1.38	1.52
28	f	102	LEU	C-N	-7.29	1.16	1.33
1	B	96	PRO	C-N	-6.53	1.24	1.33
10	N	153	ASP	C-N	-6.45	1.26	1.34
28	f	104	PRO	CB-CG	-6.41	1.26	1.51

The worst 5 of 60 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	156	ILE	CA-C-N	9.47	139.63	121.54
4	F	156	ILE	C-N-CA	9.47	139.63	121.54
35	n	5	LYS	N-CA-C	7.26	119.41	110.91
3	E	35	VAL	N-CA-C	-6.92	103.52	109.19
4	F	157	ASN	CA-C-N	6.73	134.40	121.54

There are no chirality outliers.

5 of 86 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	170	PRO	Peptide
1	B	221	THR	Peptide
1	B	241	LYS	Peptide
1	B	35	ASP	Peptide
1	B	37	ARG	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	3081	0	3165	70	0
2	C	2749	0	2863	40	0
3	E	1239	0	1326	20	0
4	F	1784	0	1862	29	0
5	G	1515	0	1596	31	0
6	H	1518	0	1587	31	0
7	K	2064	0	2156	57	0
8	L	1499	0	1558	27	0
9	M	1059	0	1154	18	0
10	N	1543	0	1594	29	0
11	O	1555	0	1659	17	0
12	P	1397	0	1436	23	0
13	Q	1035	0	1115	16	0
14	R	1258	0	1342	25	0
15	S	1437	0	1475	17	0
16	T	434	0	450	14	0
17	U	844	0	855	11	0
18	V	1003	0	1048	19	0
19	W	1885	0	1921	49	0
20	X	1100	0	1187	18	0
21	Y	993	0	1081	22	0
22	Z	1092	0	1155	24	0
23	a	735	0	776	9	0
24	b	3814	0	3875	71	0
25	c	743	0	797	11	0
26	d	873	0	914	17	0
27	e	1020	0	1090	15	0
28	f	850	0	880	12	0
29	g	881	0	945	17	0
30	h	969	0	1078	9	0
31	i	771	0	849	16	0
32	j	681	0	687	15	0
33	k	612	0	682	5	0
34	l	436	0	475	15	0
35	n	3030	0	3107	37	0
36	o	1107	0	1159	35	0
37	q	723	0	722	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	r	1760	0	1850	25	0
39	s	301	0	359	9	0
40	t	2306	0	2454	40	0
41	u	1040	0	1067	20	0
42	y	1849	0	1836	46	0
43	z	444	0	478	13	0
44	1	54232	0	26854	497	0
45	2	3353	0	1655	31	0
46	6	1370	0	692	42	0
47	w	2898	0	3002	39	0
All	All	118882	0	91868	1303	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 7.

The worst 5 of 1303 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)
45:2:39:G:N2	45:2:106:C:N3	1.99	1.09
44:1:1392:G:N3	44:1:1418:A:N6	2.16	0.92
44:1:1538:G:H21	44:1:1583:A:H62	1.18	0.90
44:1:1449:A:H62	44:1:2355:G:H21	1.14	0.89
44:1:1392:G:H21	44:1:1418:A:H62	1.26	0.81

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	
1	B	384/387 (99%)	363 (94%)	21 (6%)	0	100	100
2	C	359/362 (99%)	338 (94%)	20 (6%)	1 (0%)	36	69

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	E	152/176 (86%)	150 (99%)	2 (1%)	0	100	100
4	F	220/244 (90%)	206 (94%)	14 (6%)	0	100	100
5	G	190/256 (74%)	183 (96%)	7 (4%)	0	100	100
6	H	189/191 (99%)	182 (96%)	6 (3%)	1 (0%)	24	59
7	K	252/376 (67%)	242 (96%)	10 (4%)	0	100	100
8	L	185/199 (93%)	176 (95%)	8 (4%)	1 (0%)	24	59
9	M	135/138 (98%)	133 (98%)	2 (2%)	0	100	100
10	N	176/204 (86%)	167 (95%)	9 (5%)	0	100	100
11	O	195/199 (98%)	191 (98%)	4 (2%)	0	100	100
12	P	172/184 (94%)	167 (97%)	5 (3%)	0	100	100
13	Q	132/186 (71%)	132 (100%)	0	0	100	100
14	R	154/189 (82%)	152 (99%)	2 (1%)	0	100	100
15	S	169/172 (98%)	165 (98%)	4 (2%)	0	100	100
16	T	54/160 (34%)	53 (98%)	1 (2%)	0	100	100
17	U	104/121 (86%)	103 (99%)	1 (1%)	0	100	100
18	V	134/137 (98%)	133 (99%)	1 (1%)	0	100	100
19	W	232/236 (98%)	229 (99%)	3 (1%)	0	100	100
20	X	139/142 (98%)	136 (98%)	3 (2%)	0	100	100
21	Y	124/127 (98%)	122 (98%)	2 (2%)	0	100	100
22	Z	133/136 (98%)	132 (99%)	1 (1%)	0	100	100
23	a	91/149 (61%)	87 (96%)	4 (4%)	0	100	100
24	b	468/647 (72%)	451 (96%)	17 (4%)	0	100	100
25	c	95/105 (90%)	95 (100%)	0	0	100	100
26	d	105/113 (93%)	103 (98%)	2 (2%)	0	100	100
27	e	125/130 (96%)	123 (98%)	2 (2%)	0	100	100
28	f	104/107 (97%)	102 (98%)	2 (2%)	0	100	100
29	g	110/121 (91%)	107 (97%)	3 (3%)	0	100	100
30	h	117/120 (98%)	110 (94%)	7 (6%)	0	100	100
31	i	97/100 (97%)	94 (97%)	3 (3%)	0	100	100
32	j	85/88 (97%)	82 (96%)	3 (4%)	0	100	100
33	k	75/78 (96%)	74 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	l	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
35	n	365/605 (60%)	339 (93%)	26 (7%)	0	100	100
36	o	131/220 (60%)	123 (94%)	8 (6%)	0	100	100
37	q	83/455 (18%)	80 (96%)	3 (4%)	0	100	100
38	r	211/261 (81%)	200 (95%)	11 (5%)	0	100	100
39	s	34/520 (6%)	31 (91%)	3 (9%)	0	100	100
40	t	283/322 (88%)	267 (94%)	16 (6%)	0	100	100
41	u	121/199 (61%)	115 (95%)	6 (5%)	0	100	100
42	y	242/245 (99%)	240 (99%)	2 (1%)	0	100	100
43	z	53/106 (50%)	52 (98%)	1 (2%)	0	100	100
47	w	350/841 (42%)	347 (99%)	3 (1%)	0	100	100
All	All	7377/10105 (73%)	7124 (97%)	250 (3%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	339	LEU
8	L	63	VAL
6	H	50	ASN

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	
1	B	322/323 (100%)	318 (99%)	4 (1%)	63	72
2	C	288/289 (100%)	286 (99%)	2 (1%)	76	78
3	E	134/153 (88%)	132 (98%)	2 (2%)	57	70
4	F	186/205 (91%)	185 (100%)	1 (0%)	81	82
5	G	159/208 (76%)	157 (99%)	2 (1%)	61	71
6	H	171/171 (100%)	171 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	K	236/346 (68%)	236 (100%)	0	100	100
8	L	149/159 (94%)	148 (99%)	1 (1%)	76	78
9	M	108/109 (99%)	108 (100%)	0	100	100
10	N	156/176 (89%)	147 (94%)	9 (6%)	18	44
11	O	160/162 (99%)	159 (99%)	1 (1%)	78	80
12	P	142/146 (97%)	140 (99%)	2 (1%)	59	71
13	Q	110/151 (73%)	110 (100%)	0	100	100
14	R	129/154 (84%)	128 (99%)	1 (1%)	73	77
15	S	155/156 (99%)	154 (99%)	1 (1%)	78	80
16	T	45/137 (33%)	45 (100%)	0	100	100
17	U	93/107 (87%)	93 (100%)	0	100	100
18	V	104/105 (99%)	102 (98%)	2 (2%)	50	66
19	W	211/213 (99%)	211 (100%)	0	100	100
20	X	117/118 (99%)	116 (99%)	1 (1%)	70	75
21	Y	109/110 (99%)	109 (100%)	0	100	100
22	Z	115/116 (99%)	114 (99%)	1 (1%)	70	75
23	a	76/119 (64%)	75 (99%)	1 (1%)	61	71
24	b	424/573 (74%)	423 (100%)	1 (0%)	87	87
25	c	81/88 (92%)	81 (100%)	0	100	100
26	d	94/97 (97%)	92 (98%)	2 (2%)	47	65
27	e	109/111 (98%)	107 (98%)	2 (2%)	51	67
28	f	90/91 (99%)	89 (99%)	1 (1%)	65	74
29	g	95/103 (92%)	94 (99%)	1 (1%)	65	74
30	h	104/105 (99%)	104 (100%)	0	100	100
31	i	81/82 (99%)	81 (100%)	0	100	100
32	j	70/71 (99%)	70 (100%)	0	100	100
33	k	68/69 (99%)	68 (100%)	0	100	100
34	l	45/46 (98%)	45 (100%)	0	100	100
35	n	334/548 (61%)	332 (99%)	2 (1%)	78	80
36	o	118/199 (59%)	118 (100%)	0	100	100
37	q	80/420 (19%)	80 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	r	191/229 (83%)	191 (100%)	0	100	100
39	s	32/445 (7%)	32 (100%)	0	100	100
40	t	256/287 (89%)	256 (100%)	0	100	100
41	u	108/180 (60%)	107 (99%)	1 (1%)	70	75
42	y	210/211 (100%)	210 (100%)	0	100	100
43	z	48/95 (50%)	48 (100%)	0	100	100
47	w	319/745 (43%)	318 (100%)	1 (0%)	86	85
All	All	6432/8728 (74%)	6390 (99%)	42 (1%)	73	78

5 of 42 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
20	X	124	VAL
27	e	63	THR
22	Z	14	VAL
26	d	16	LEU
29	g	51	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 42 such sidechains are listed below:

Mol	Chain	Res	Type
30	h	59	ASN
38	r	183	ASN
33	k	40	GLN
35	n	437	ASN
40	t	300	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
44	1	2523/3396 (74%)	689 (27%)	34 (1%)
45	2	157/158 (99%)	46 (29%)	3 (1%)
46	6	63/232 (27%)	29 (46%)	0
All	All	2743/3786 (72%)	764 (27%)	37 (1%)

5 of 764 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
44	1	2	U
44	1	3	U
44	1	7	C
44	1	13	A
44	1	14	U

5 of 37 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
44	1	2317	A
45	2	73	U
44	1	2920	U
44	1	3350	C
44	1	761	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
28	f	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	f	102:LEU	C	103:TYR	N	1.16

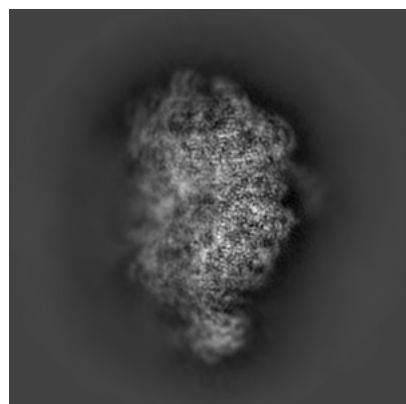
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10841. These allow visual inspection of the internal detail of the map and identification of artifacts.

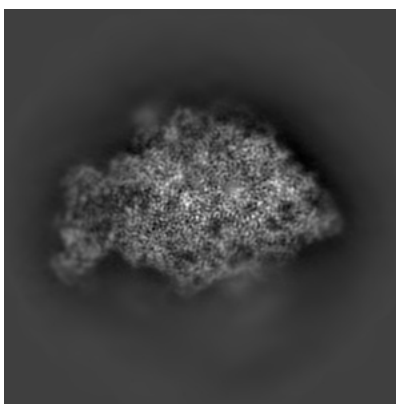
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

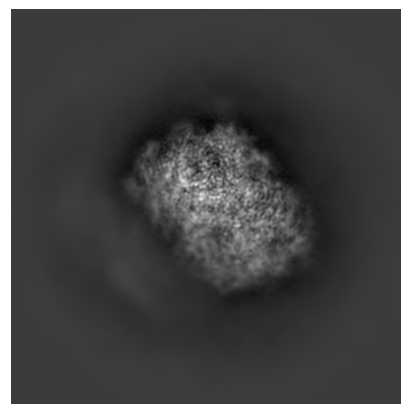
6.1.1 Primary map



X

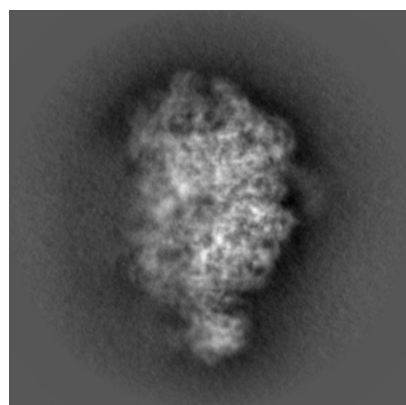


Y

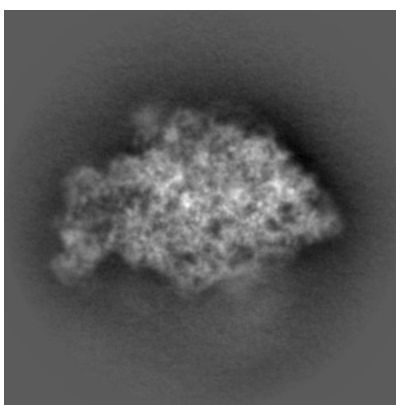


Z

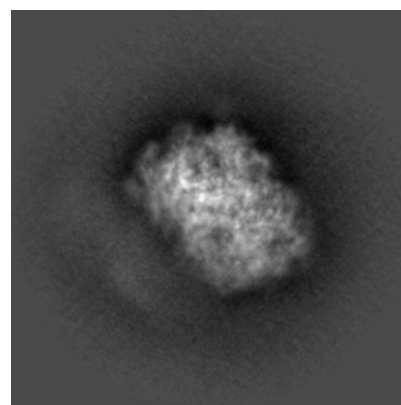
6.1.2 Raw map



X



Y

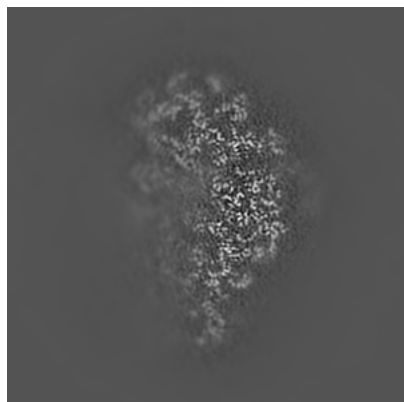


Z

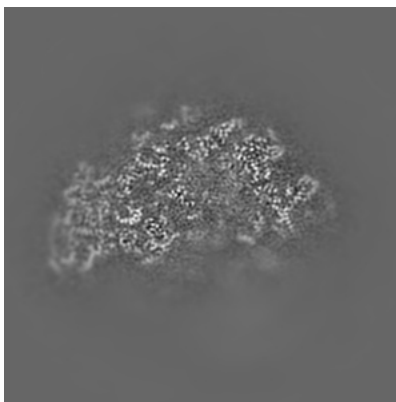
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

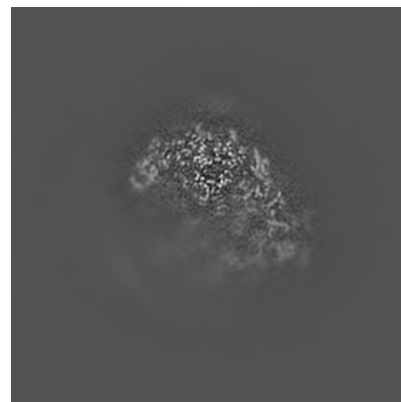
6.2.1 Primary map



X Index: 192

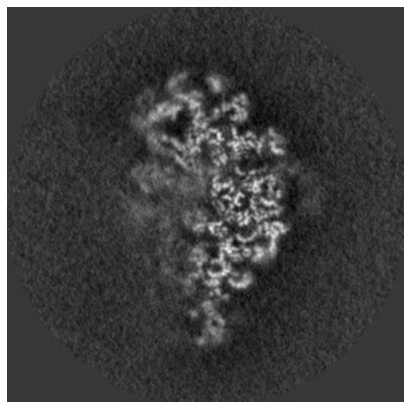


Y Index: 192

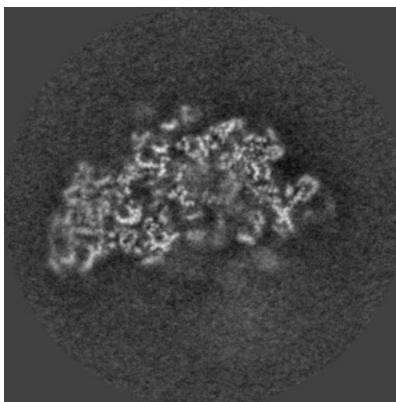


Z Index: 192

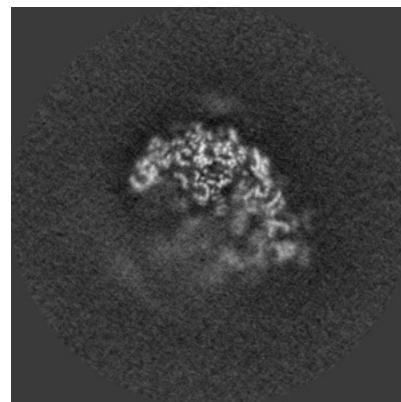
6.2.2 Raw map



X Index: 192



Y Index: 192

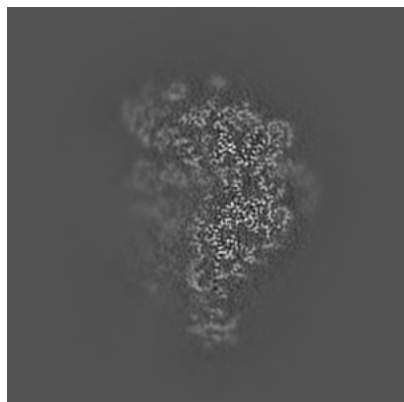


Z Index: 192

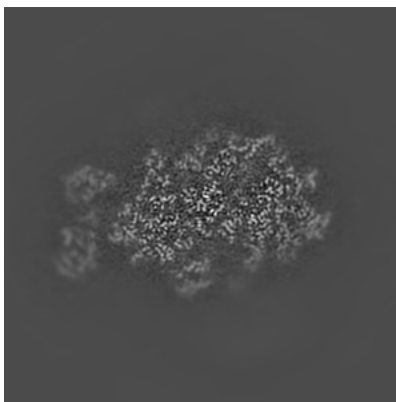
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

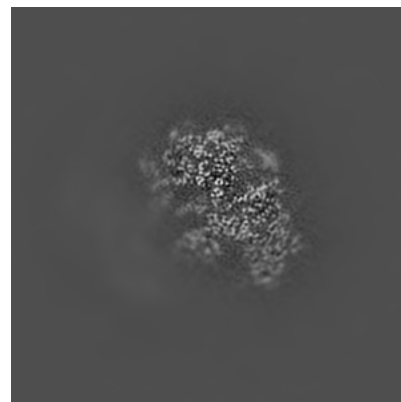
6.3.1 Primary map



X Index: 201

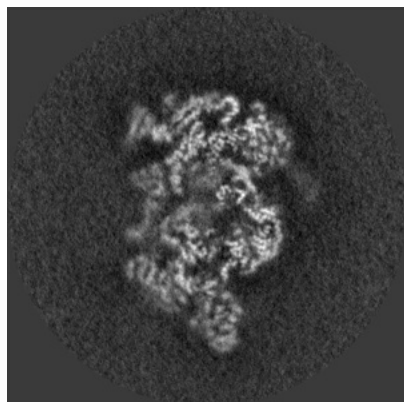


Y Index: 216

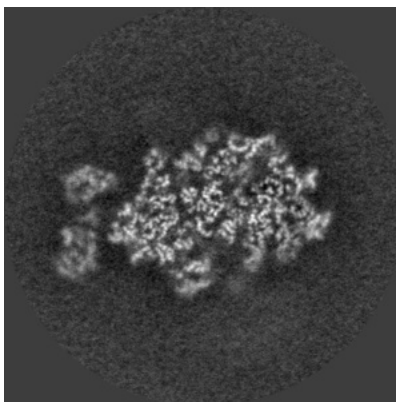


Z Index: 245

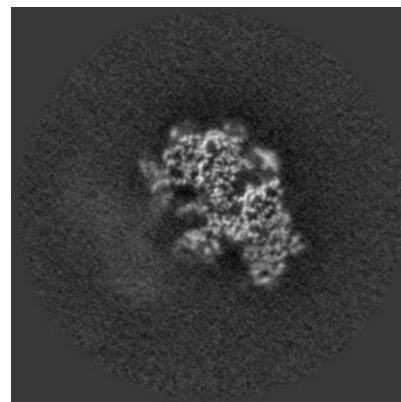
6.3.2 Raw map



X Index: 217



Y Index: 216

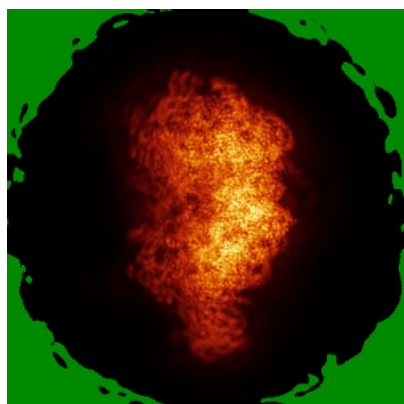


Z Index: 244

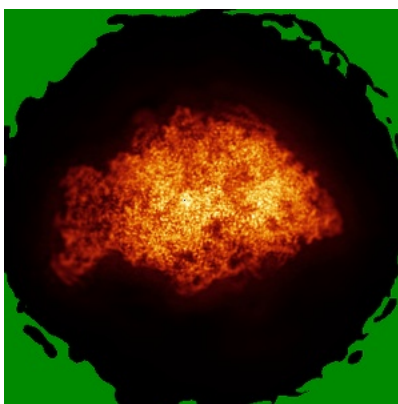
The images above show the largest variance slices of the map in three orthogonal directions.

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

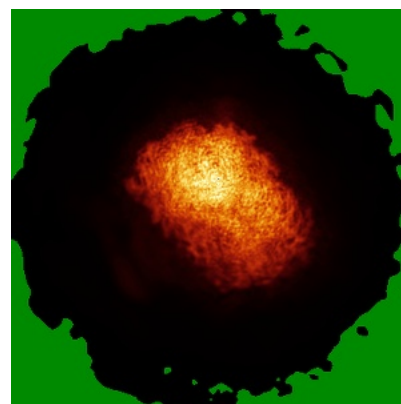
6.4.1 Primary map



X

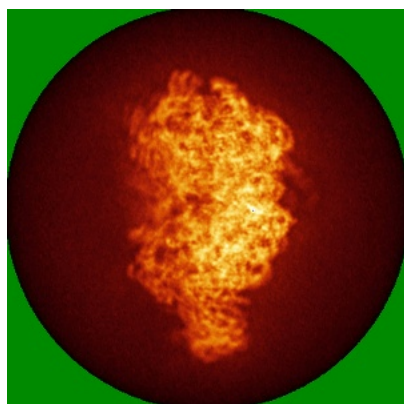


Y

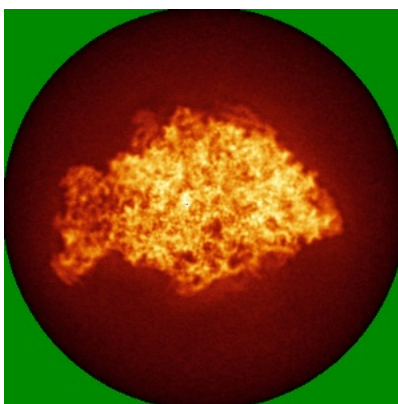


Z

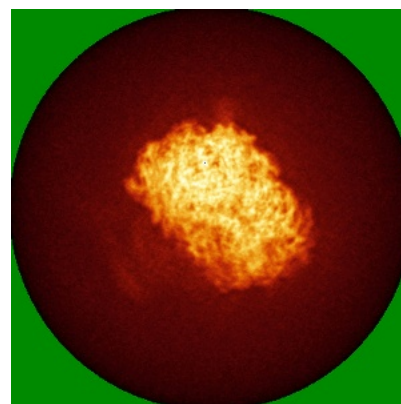
6.4.2 Raw map



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

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

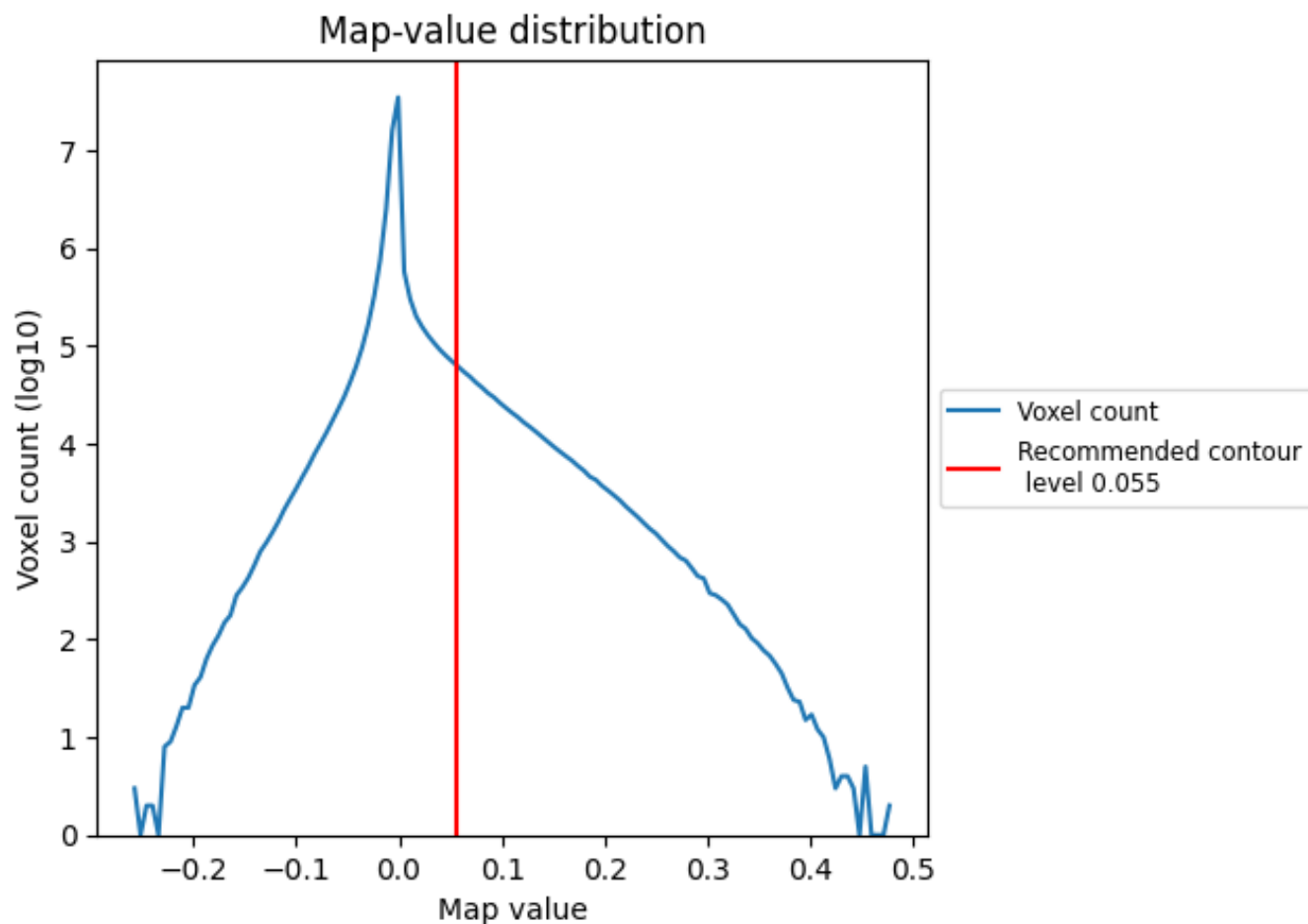
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

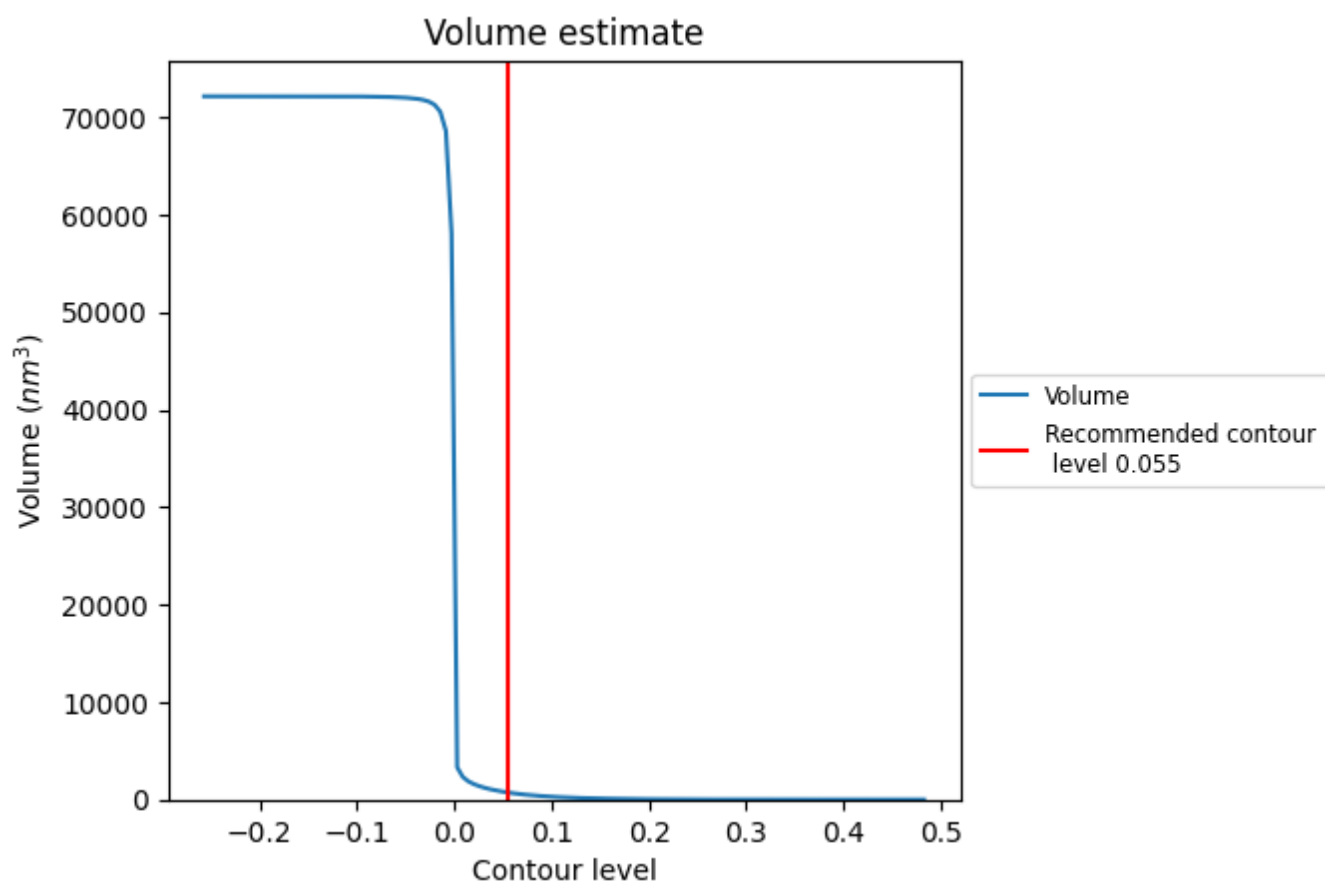
This section contains the results of statistical analysis of the map.

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.

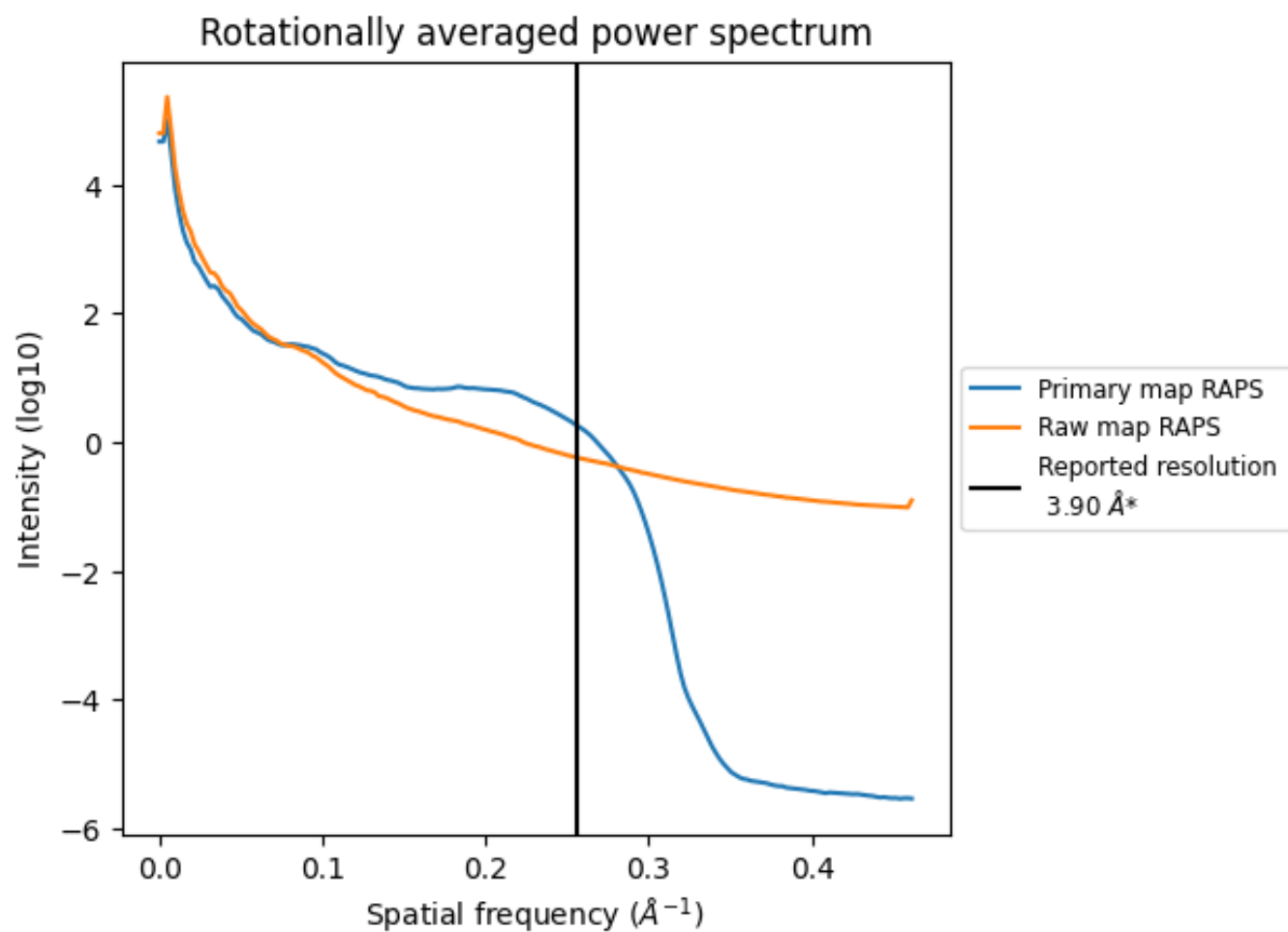
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 727 nm³; this corresponds to an approximate mass of 656 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 ⓘ

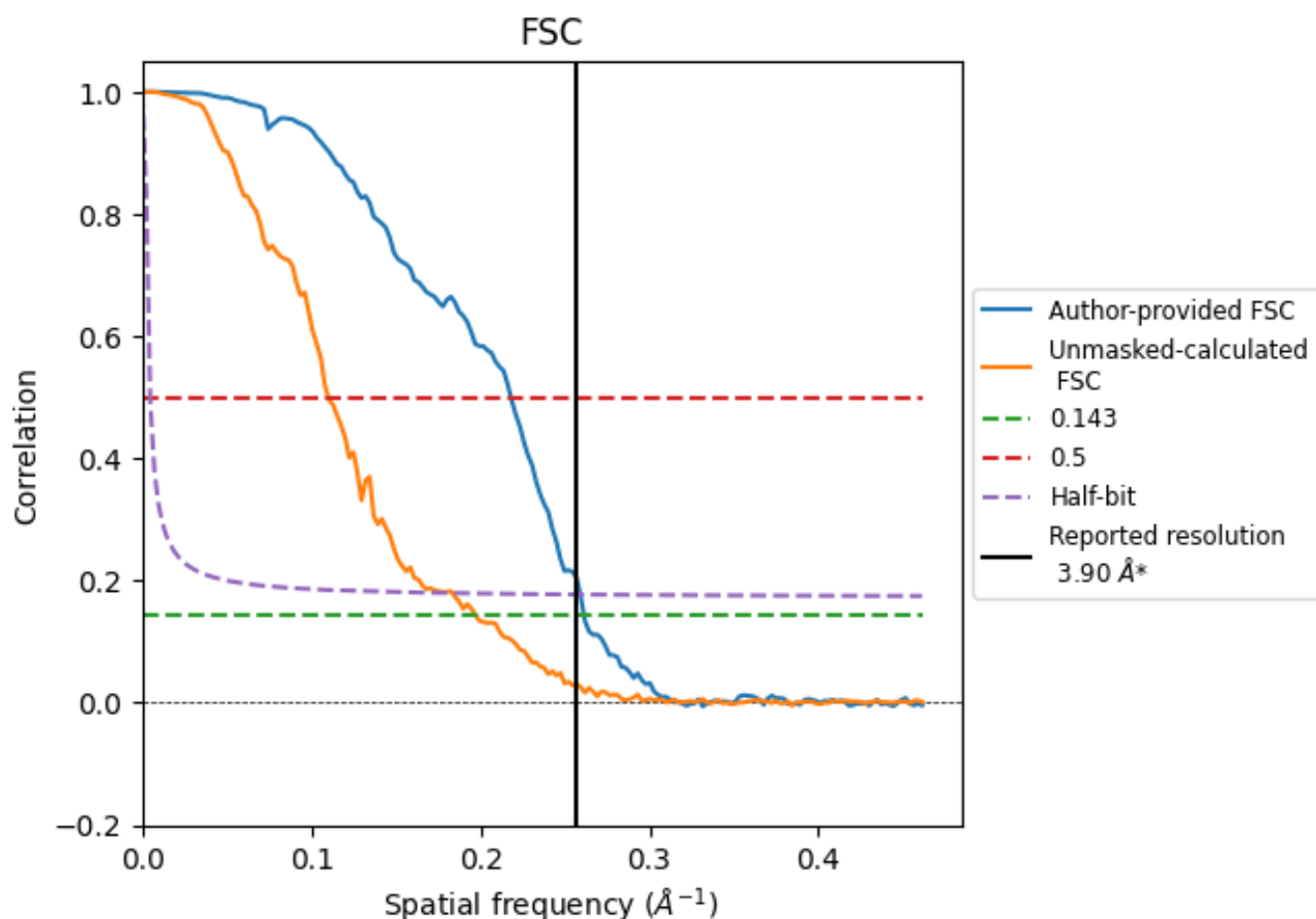


*Reported resolution corresponds to spatial frequency of 0.256 Å⁻¹

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 0.256 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

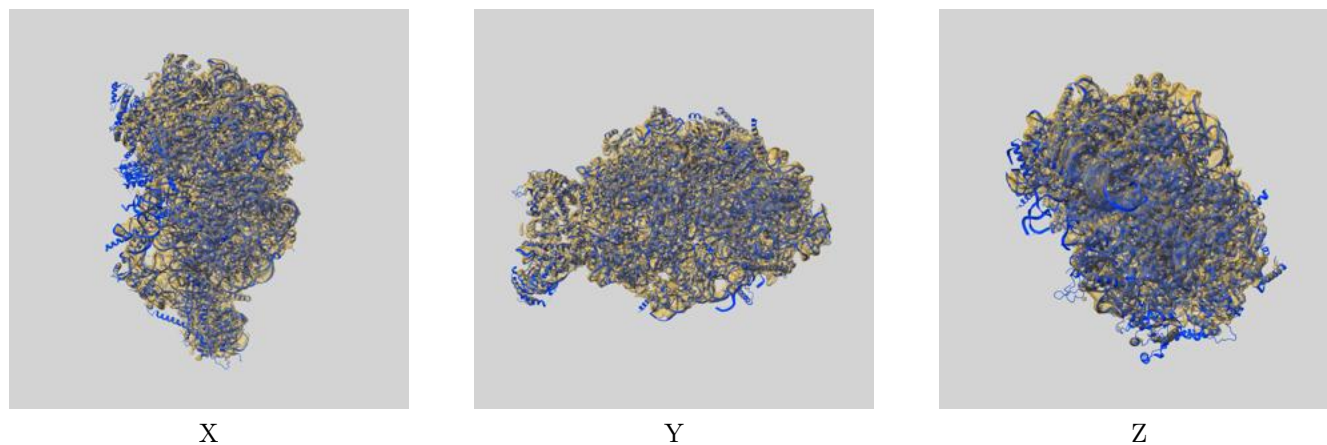
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	3.83	4.59	3.86
Unmasked-calculated*	5.07	9.08	5.45

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.07 differs from the reported value 3.9 by more than 10 %

9 Map-model fit [i](#)

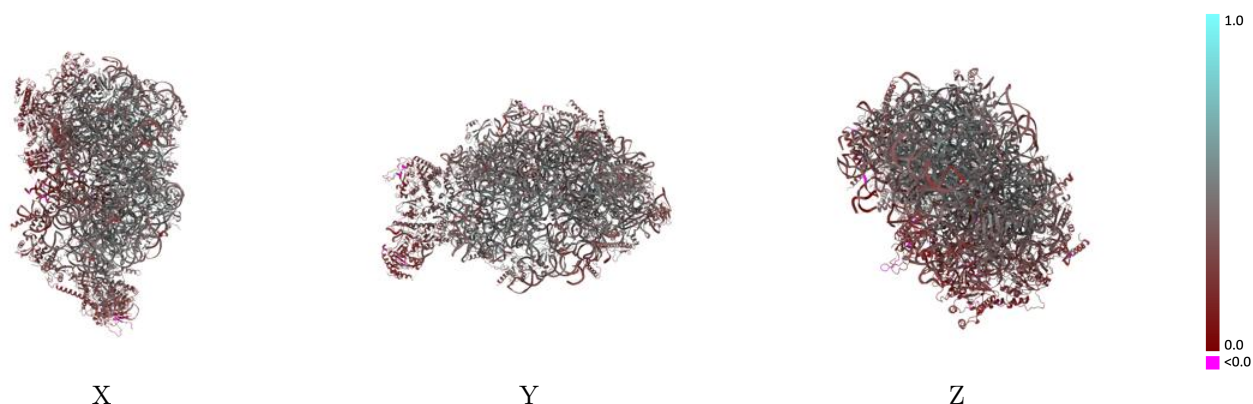
This section contains information regarding the fit between EMDB map EMD-10841 and PDB model 6YLX. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)



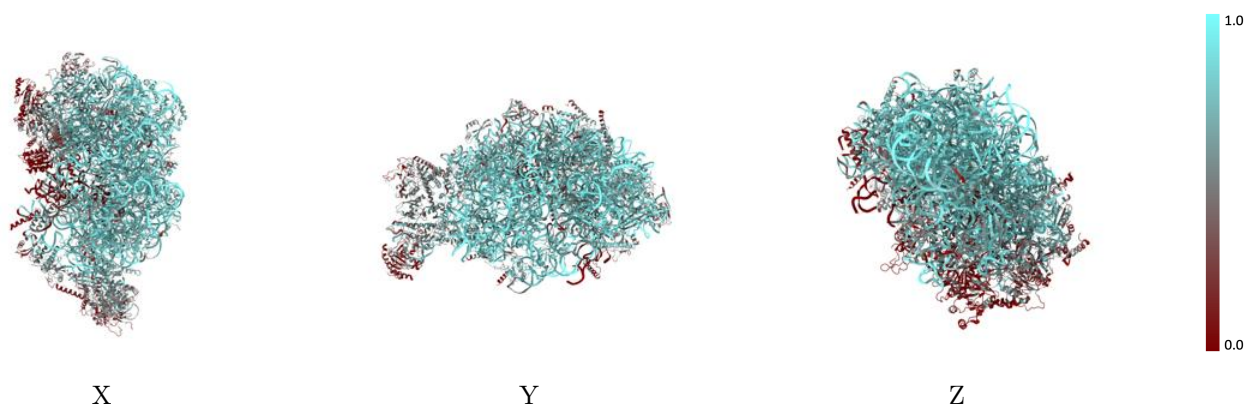
The images above show the 3D surface view of the map at the recommended contour level 0.055 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



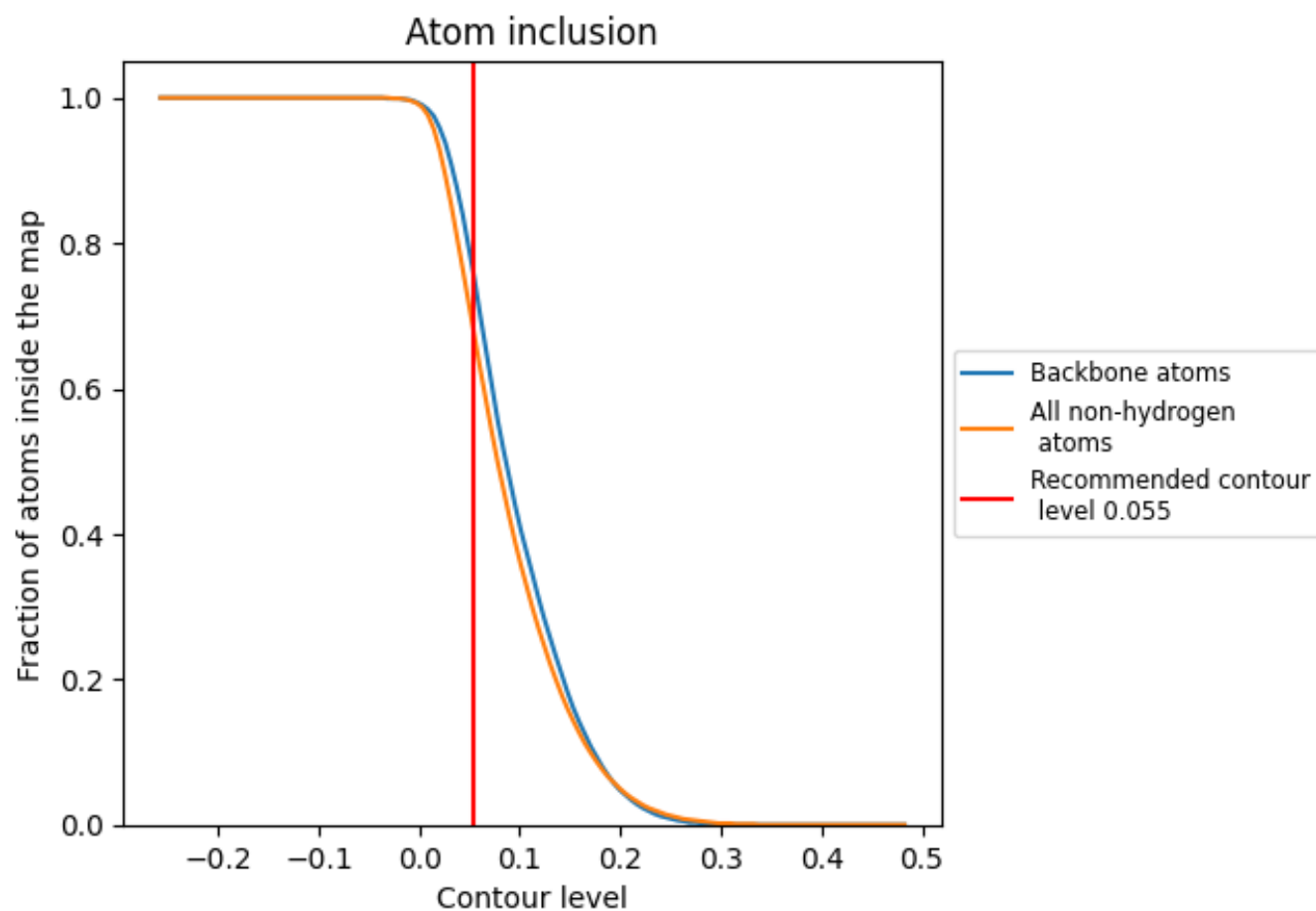
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.055).

9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 67% 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 (0.055) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6730	 0.3840
1	 0.7890	 0.3960
2	 0.8920	 0.4560
6	 0.6830	 0.3070
B	 0.6810	 0.4290
C	 0.7750	 0.4690
E	 0.7250	 0.4280
F	 0.7770	 0.4300
G	 0.6420	 0.3890
H	 0.6870	 0.4150
K	 0.2690	 0.2150
L	 0.6910	 0.4310
M	 0.7610	 0.4410
N	 0.8020	 0.4900
O	 0.8060	 0.4790
P	 0.7620	 0.4590
Q	 0.7510	 0.4440
R	 0.4550	 0.3430
S	 0.7070	 0.4280
T	 0.1880	 0.3110
U	 0.4610	 0.3320
V	 0.5390	 0.3800
W	 0.4070	 0.2770
X	 0.7080	 0.4430
Y	 0.7800	 0.4720
Z	 0.5030	 0.3200
a	 0.6190	 0.3960
b	 0.3230	 0.2730
c	 0.3410	 0.2580
d	 0.7040	 0.4430
e	 0.8010	 0.4980
f	 0.8390	 0.5110
g	 0.5810	 0.3980
h	 0.7410	 0.4570
i	 0.5930	 0.3700



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Chain	Atom inclusion	Q-score
j	 0.7500	 0.4660
k	 0.5410	 0.3910
l	 0.2800	 0.3650
n	 0.5320	 0.3380
o	 0.3760	 0.2480
q	 0.1930	 0.2420
r	 0.2480	 0.2720
s	 0.4770	 0.4100
t	 0.4620	 0.3010
u	 0.5330	 0.3480
w	 0.1110	 0.2630
y	 0.4430	 0.2890
z	 0.4560	 0.3770