



wwPDB EM Validation Summary Report ⓘ

Jul 8, 2024 – 03:56 pm BST

PDB ID : 7QWS
EMDB ID : EMD-14193
Title : Structure of ribosome translating beta-tubulin in complex with TTC5 and NAC
Authors : Jomaa, A.; Gamerding, M.; Hsieh, H.; Wallisch, A.; Chandrasekaran, V.; Ulusoy, Z.; Scaiola, A.; Hegde, R.; Shan, S.; Ban, N.; Deuerling, E.
Deposited on : 2022-01-25
Resolution : 3.40 Å (reported)
Based on initial model : 7OBR

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.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.37.1

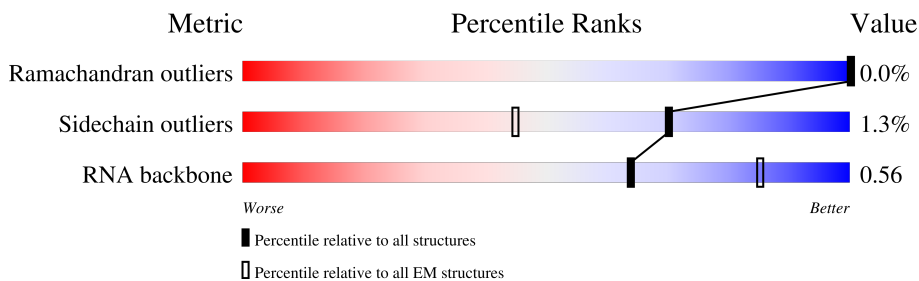
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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	s	24	100% 100%
2	t	215	30% 31% 69%
3	u	162	65% 66% 33%
4	A	245	87% 98%
5	b	223	25% 33% 66%
6	B	403	78% 97%
7	c	115	63% 81% 18%
8	C	413	66% 86% 12%

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Mol	Chain	Length	Quality of chain
9	d	125	66% 82% 14%
10	D	297	65% 97%
11	e	157	66% 82% 18%
12	E	291	67% 79% 19%
13	f	110	79% 97%
14	F	225	78% 100%
15	g	129	74% 86% 12%
16	G	319	57% 75% 24%
17	h	123	72% 97%
18	H	192	84% 97%
19	i	102	75% 97%
20	I	214	75% 95% 5%
21	j	97	71% 89% 11%
22	J	178	71% 95% 5%
23	k	69	75% 99%
24	L	210	73% 100%
25	l	51	90% 96%
26	M	218	47% 62% 37%
27	m	128	30% 41% 59%
28	N	204	80% 100%
29	n	25	76% 92% 8%
30	O	500	30% 39% 60%
31	o	141	60% 74% 26%
32	P	153	81% 100%
33	p	92	75% 96%

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Mol	Chain	Length	Quality of chain
34	Q	187	83% 98%
35	r	137	73% 91% 9%
36	R	196	73% 92% 8%
37	S	175	79% 98%
38	T	160	82% 98% ..
39	U	105	68% 97%
40	V	140	82% 93% 6%
41	W	157	34% 40% 60%
42	5	4754	47% 58% 15% 27%
43	X	156	62% 76% 24%
44	7	120	35% 88% 12%
45	Y	145	74% 91% 8%
46	8	156	68% 76% 24%
47	K	440	88% 96% ..
48	Z	136	71% 99% ..
49	a	148	76% 99%

2 Entry composition i

There are 51 unique types of molecules in this entry. The entry contains 137913 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 Nascent chain tubulin beta.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	s	24	120	72	24	24	0	0

- Molecule 2 is a protein called Nascent polypeptide-associated complex subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	t	67	531	335	97	98	1	0	0

- Molecule 3 is a protein called Transcription factor BTF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	u	108	837	523	155	156	3	0	0

- Molecule 4 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	A	244	1868	1171	382	309	6	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	46	LYS	-	insertion	UNP A0A5F9D5B2
A	47	ASP	-	insertion	UNP A0A5F9D5B2
A	48	ILE	-	insertion	UNP A0A5F9D5B2
A	49	ILE	-	insertion	UNP A0A5F9D5B2
A	50	HIS	-	insertion	UNP A0A5F9D5B2
A	51	ASP	-	insertion	UNP A0A5F9D5B2
A	52	PRO	-	insertion	UNP A0A5F9D5B2
A	53	GLY	-	insertion	UNP A0A5F9D5B2
A	54	ARG	-	insertion	UNP A0A5F9D5B2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	55	GLY	-	insertion	UNP A0A5F9D5B2
A	56	ALA	-	insertion	UNP A0A5F9D5B2
A	57	PRO	-	insertion	UNP A0A5F9D5B2
A	58	LEU	-	insertion	UNP A0A5F9D5B2
A	59	ALA	-	insertion	UNP A0A5F9D5B2
A	60	LYS	-	insertion	UNP A0A5F9D5B2
A	61	VAL	-	insertion	UNP A0A5F9D5B2
A	62	VAL	-	insertion	UNP A0A5F9D5B2
A	63	PHE	-	insertion	UNP A0A5F9D5B2
A	64	ARG	-	insertion	UNP A0A5F9D5B2
A	65	ASP	-	insertion	UNP A0A5F9D5B2
A	66	PRO	-	insertion	UNP A0A5F9D5B2
A	67	TYR	-	insertion	UNP A0A5F9D5B2
A	68	ARG	-	insertion	UNP A0A5F9D5B2
A	69	PHE	-	insertion	UNP A0A5F9D5B2

- Molecule 5 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	b	75	609	378	130	98	3	0	0

- Molecule 6 is a protein called Ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	B	394	3148	2007	591	537	13	0	0

- Molecule 7 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	c	94	732	465	130	131	6	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
c	34	THR	SER	conflict	UNP G1TDL2

- Molecule 8 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	C	362	2883	1812	577	480	14	0	0

- Molecule 9 is a protein called Ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	d	107	888	560	171	155	2	0	0

- Molecule 10 is a protein called Ribosomal_L18_c domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	D	292	2386	1509	437	426	14	0	0

- Molecule 11 is a protein called Ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	e	128	1053	667	216	165	5	0	0

- Molecule 12 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	E	236	1898	1215	362	318	3	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	126	ARG	LYS	conflict	UNP G1SKF7
E	217	GLN	LYS	conflict	UNP G1SKF7

- Molecule 13 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	f	109	876	555	174	143	4	0	0

- Molecule 14 is a protein called uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	F	225	1870	1202	358	301	9	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	175	ALA	THR	conflict	UNP G1SV32
F	185	GLY	ASN	conflict	UNP G1SV32
F	202	ARG	HIS	conflict	UNP G1SV32
F	233	GLU	GLY	conflict	UNP G1SV32

- Molecule 15 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	g	114	906	566	187	147	6	0	0

- Molecule 16 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	G	241	1934	1233	371	326	4	0	0

- Molecule 17 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	h	122	1013	640	204	168	1	0	0

- Molecule 18 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	H	190	1516	954	284	272	6	0	0

- Molecule 19 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	i	102	830	520	176	129	5	0	0

- Molecule 20 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	I	204	1655	1051	319	272	13	0	0

- Molecule 21 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	j	86	705	434	155	111	5	0	0

- Molecule 22 is a protein called Ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	J	169	1353	855	252	240	6	0	0

- Molecule 23 is a protein called Ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	k	69	569	366	103	99	1	0	0

- Molecule 24 is a protein called Ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	L	210	1703	1065	354	280	4	0	0

- Molecule 25 is a protein called Ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	l	50	444	281	98	64	1	0	0

- Molecule 26 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	M	138	1137	727	221	182	7	0	0

- Molecule 27 is a protein called Ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	m	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 28 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	N	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 29 is a protein called 60s ribosomal protein l41.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	n	23	Total	C	N	O	S	0	0
			222	134	61	25	2		

- Molecule 30 is a protein called Ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	O	199	Total	C	N	O	S	0	0
			1638	1056	321	256	5		

- Molecule 31 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	o	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 32 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	P	153	Total	C	N	O	S	0	0
			1242	777	241	215	9		

- Molecule 33 is a protein called eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	p	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 34 is a protein called Ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Q	187	Total	C	N	O	S	0	0
			1506	941	311	249	5		

- Molecule 35 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	r	125	Total	C	N	O	S	0	0
			1001	621	206	168	6		

- Molecule 36 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	R	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 37 is a protein called Ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	S	175	Total	C	N	O	S	0	0
			1454	925	284	235	10		

- Molecule 38 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	T	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 39 is a protein called Ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	U	105	Total	C	N	O	S	0	0
			859	547	150	160	2		

- Molecule 40 is a protein called Ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	V	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 41 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	W	63	Total	C	N	O	S	0	0
			528	337	103	85	3		

- Molecule 42 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	5	3493	Total	C	N	O	P	0	0
			74854	33335	13681	24346	3492		

- Molecule 43 is a protein called Ribosomal_L23eN domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	X	119	Total	C	N	O	S	0	0
			976	624	183	168	1		

- Molecule 44 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 45 is a protein called Ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Y	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 46 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 47 is a protein called Tetratricopeptide repeat protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	K	426	Total	C	N	O	S	0	0
			3337	2097	580	647	13		

- Molecule 48 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	Z	135	1107	714	208	182	3	0	0

- Molecule 49 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	a	147	1162	734	239	185	4	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	1	MET	-	initiating methionine	UNP G1SNY0

- Molecule 50 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
50	g	1	Total	Zn	0
			1	1	
50	j	1	Total	Zn	0
			1	1	
50	m	1	Total	Zn	0
			1	1	
50	o	1	Total	Zn	0
			1	1	
50	p	1	Total	Zn	0
			1	1	

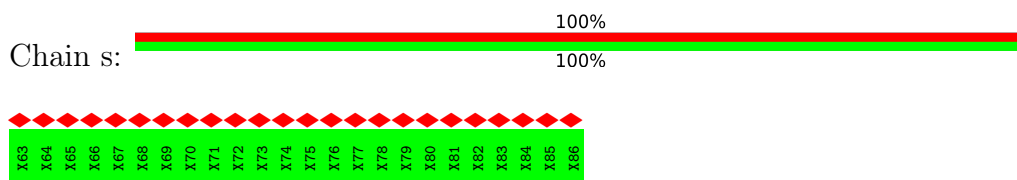
- Molecule 51 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
51	5	97	Total	Mg	0
			97	97	

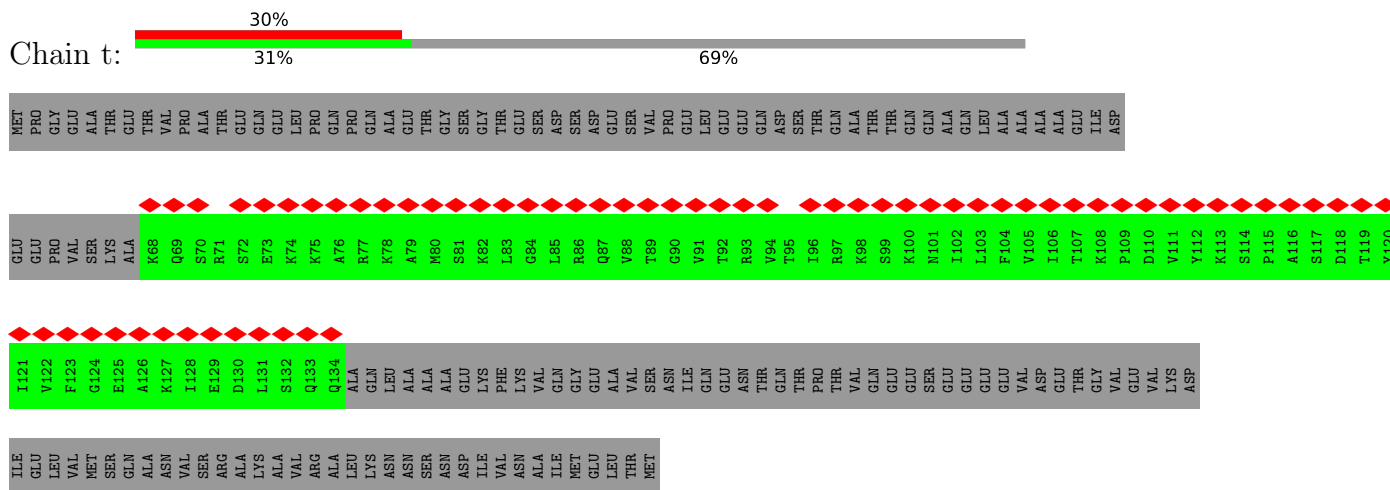
3 Residue-property plots

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.

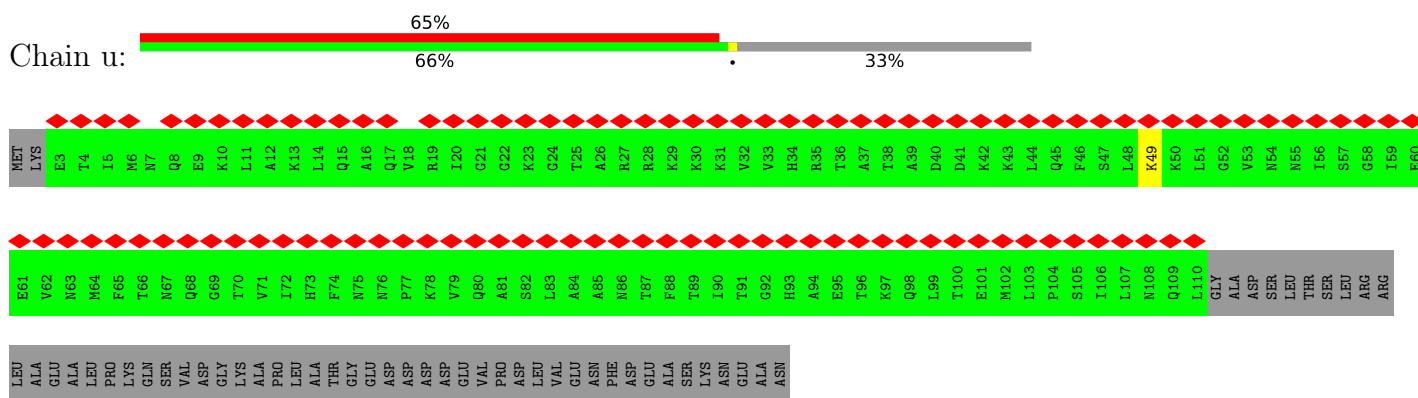
- Molecule 1: Nascent chain tubulin beta



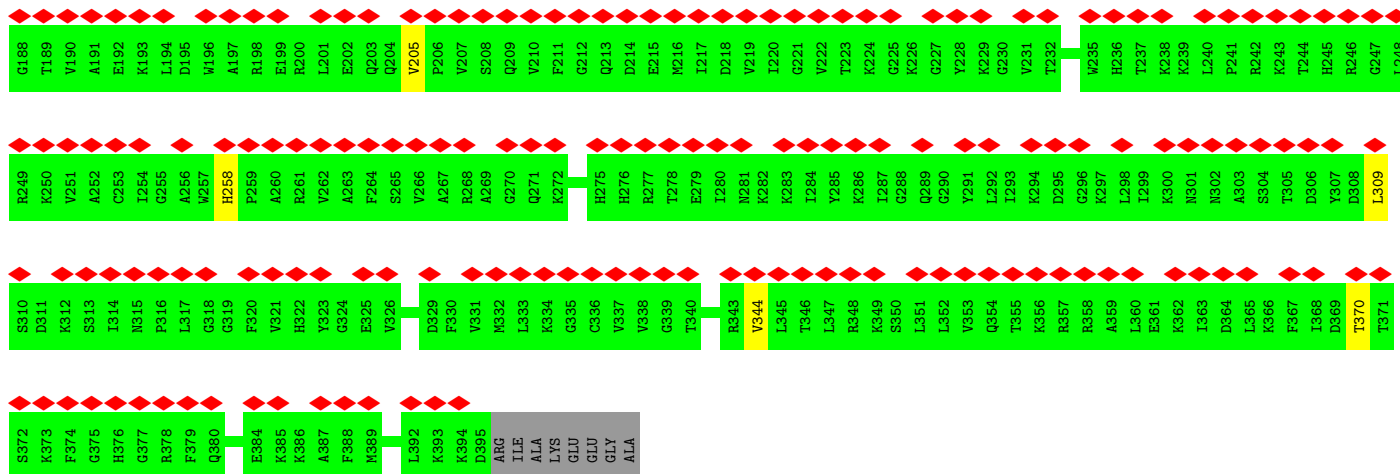
- Molecule 2: Nascent polypeptide-associated complex subunit alpha



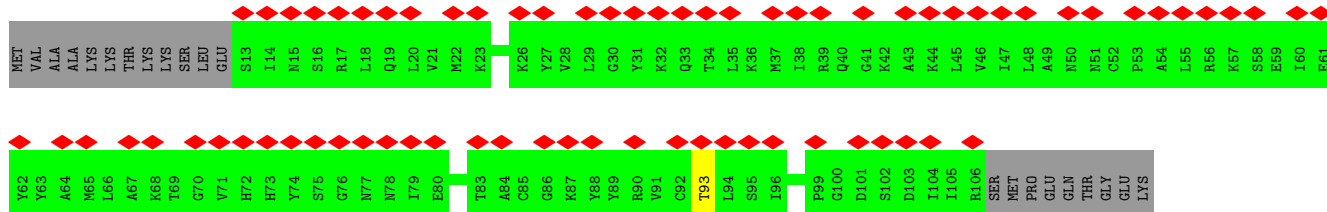
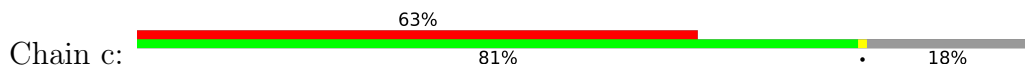
- Molecule 3: Transcription factor BTF3



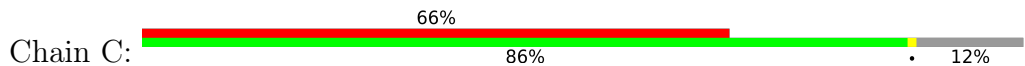
- Molecule 4: 60S ribosomal protein L8

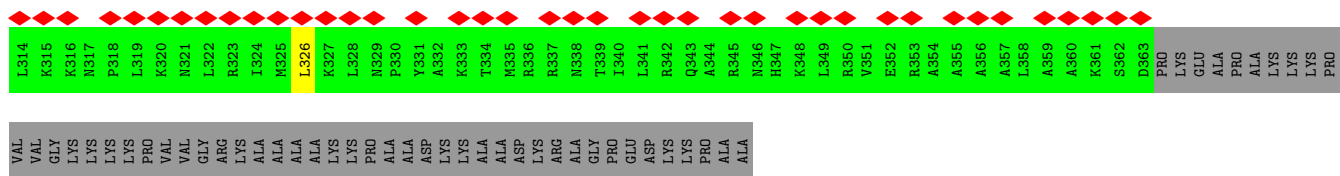


• Molecule 7: 60S ribosomal protein L30

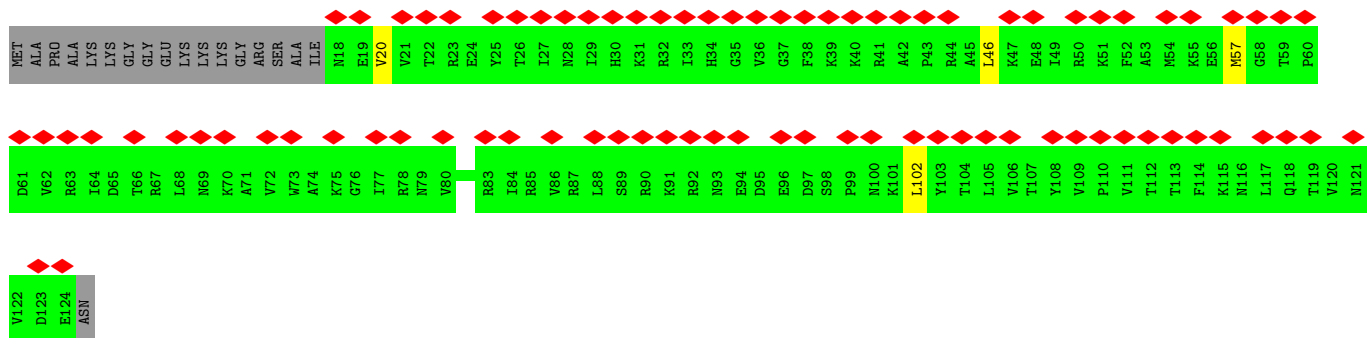
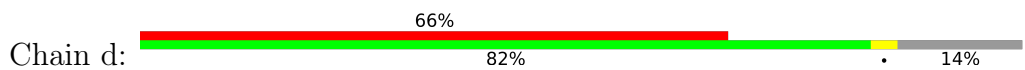


• Molecule 8: 60S ribosomal protein L4

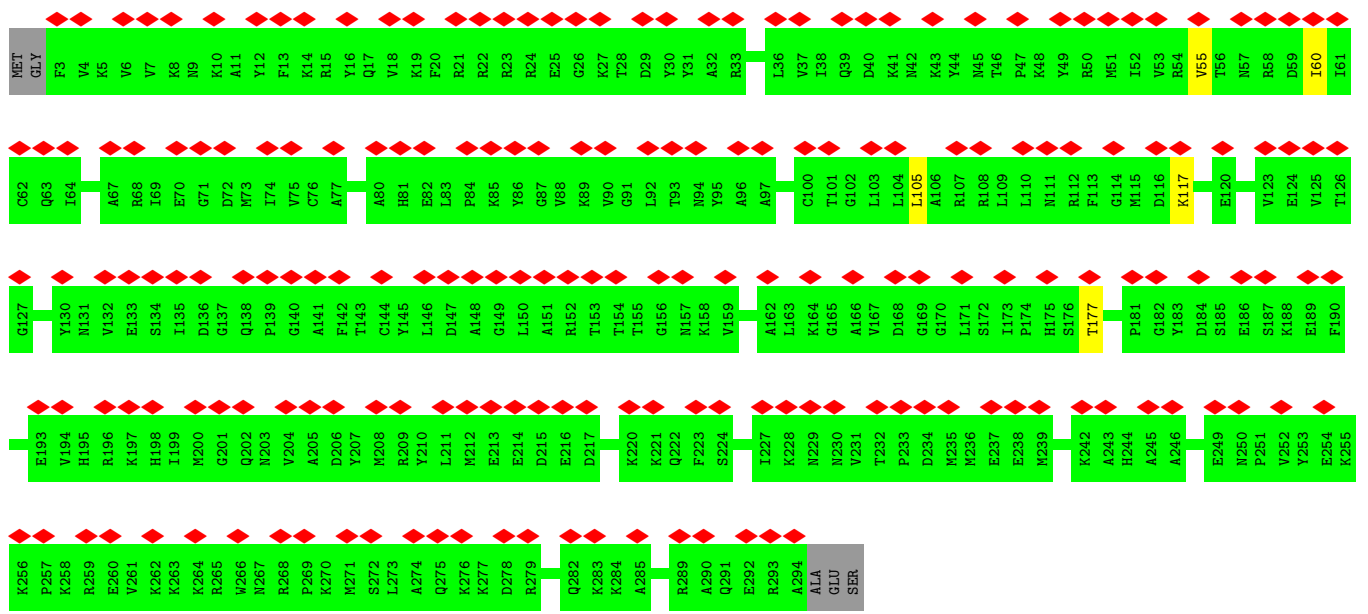




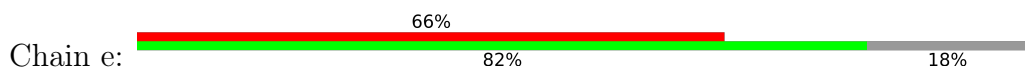
• Molecule 9: Ribosomal protein L31

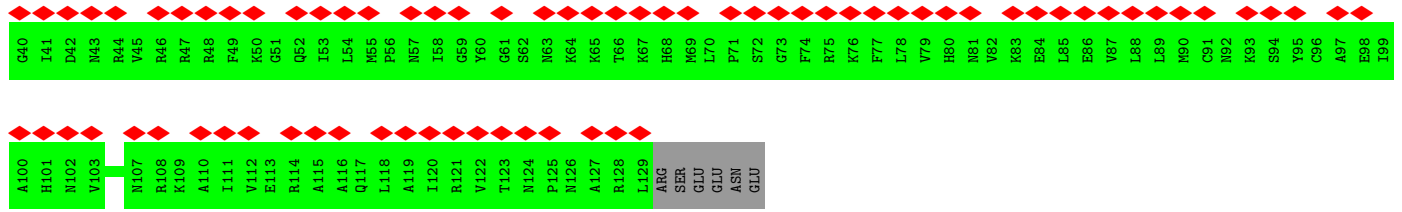


• Molecule 10: Ribosomal_L18_c domain-containing protein

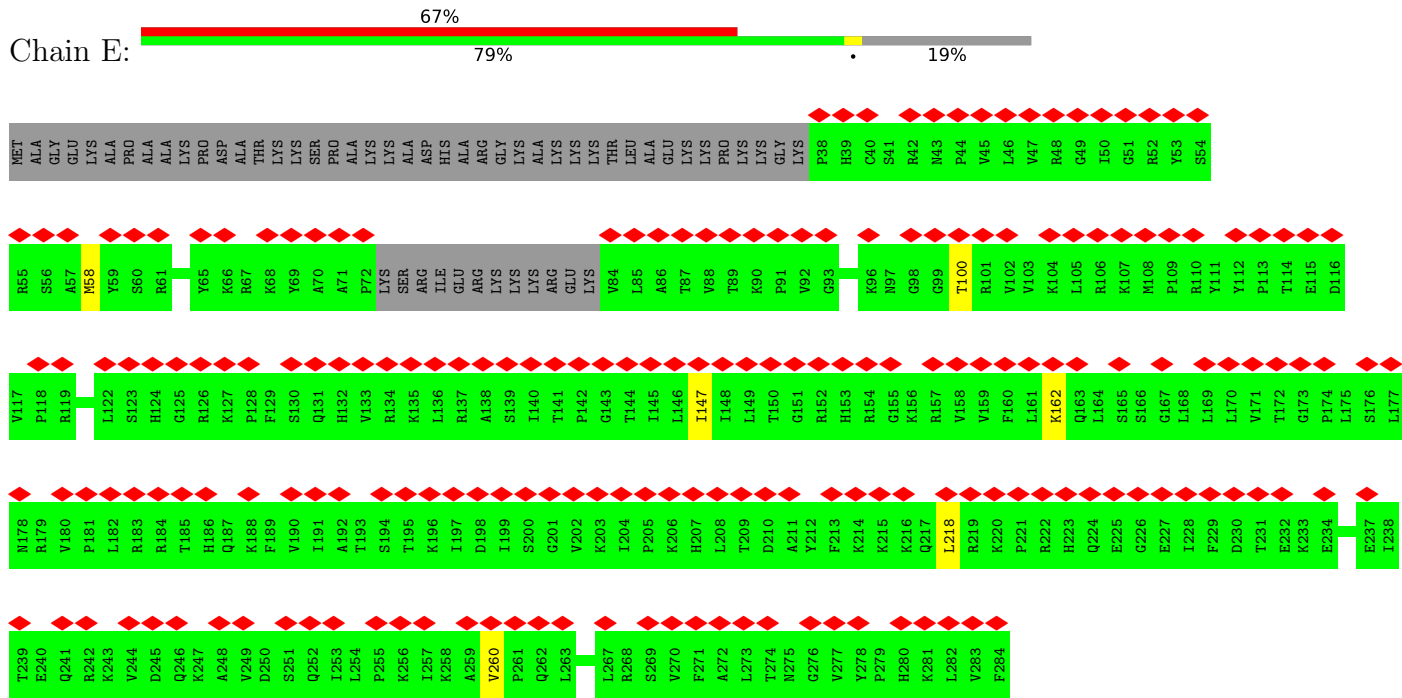


• Molecule 11: Ribosomal protein L32

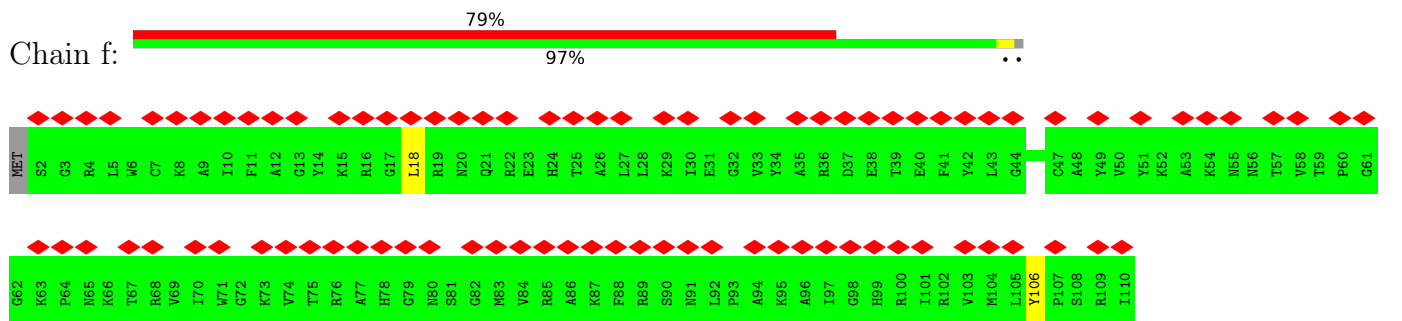




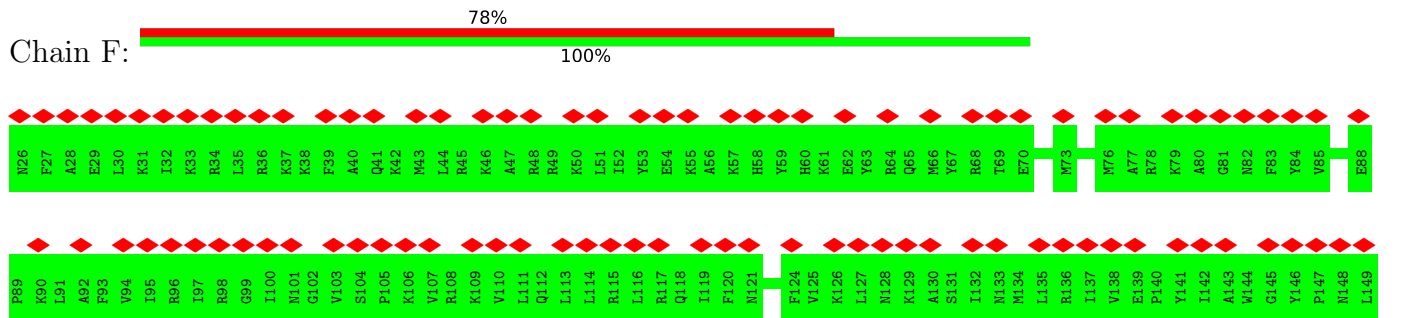
● Molecule 12: 60S ribosomal protein L6

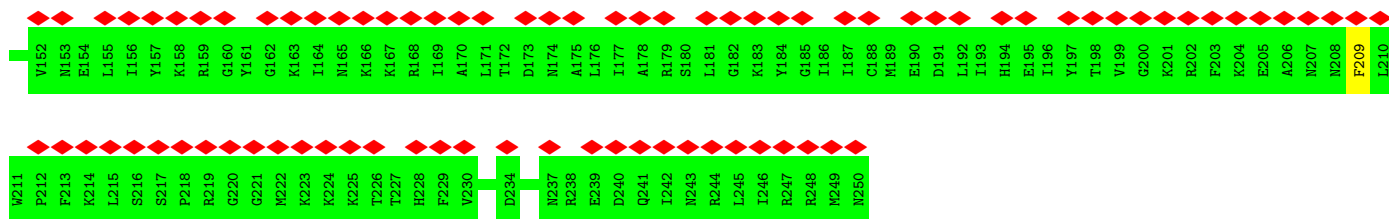


● Molecule 13: 60S ribosomal protein L35a

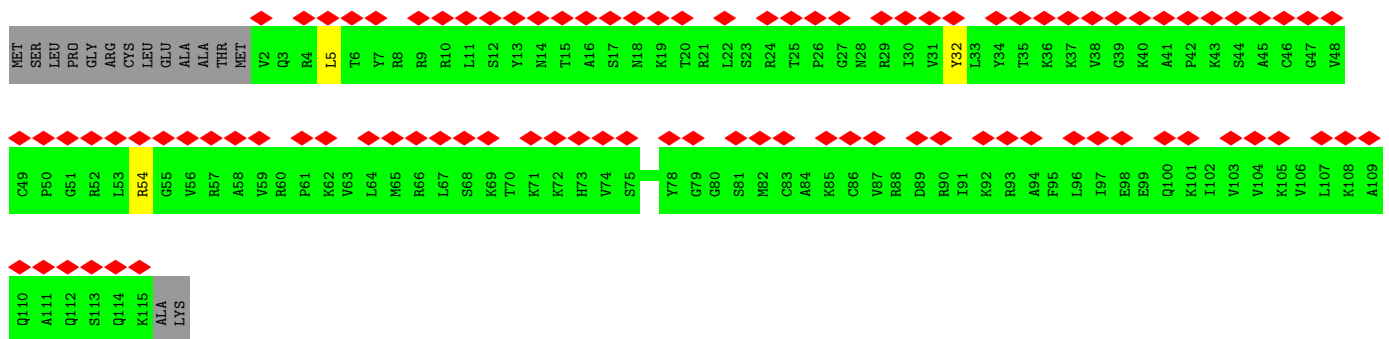
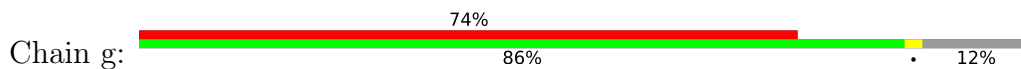


● Molecule 14: uL30

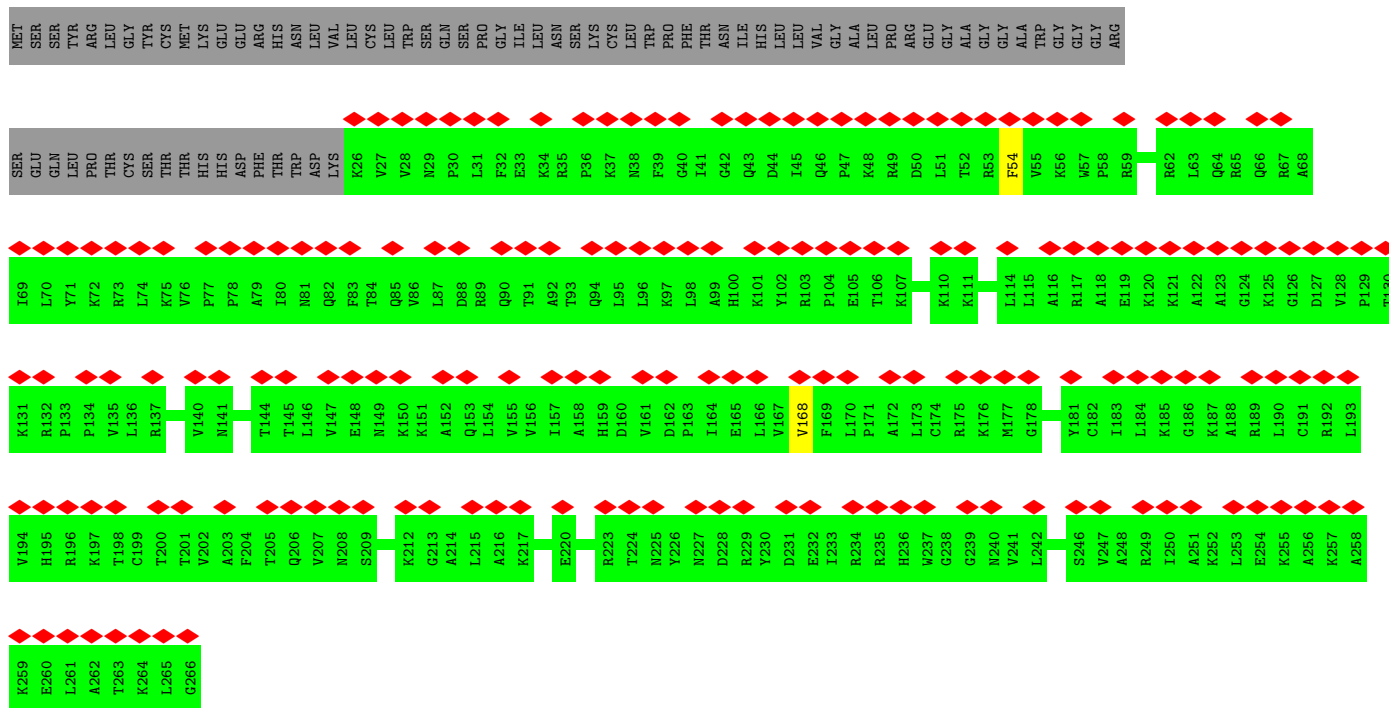
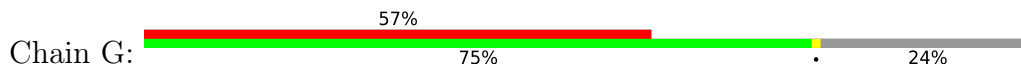




• Molecule 15: 60S ribosomal protein L34

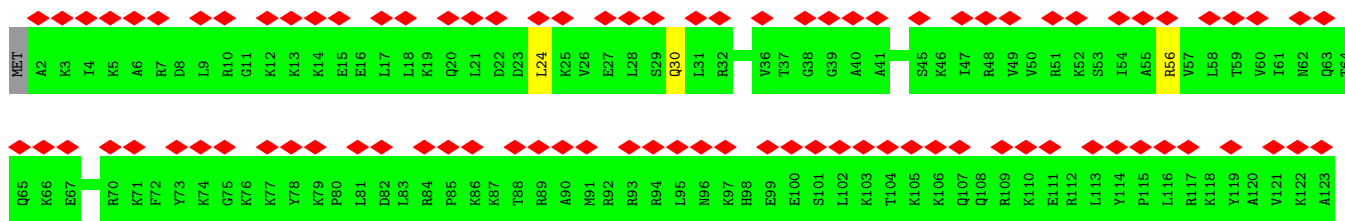


• Molecule 16: 60S ribosomal protein L7a

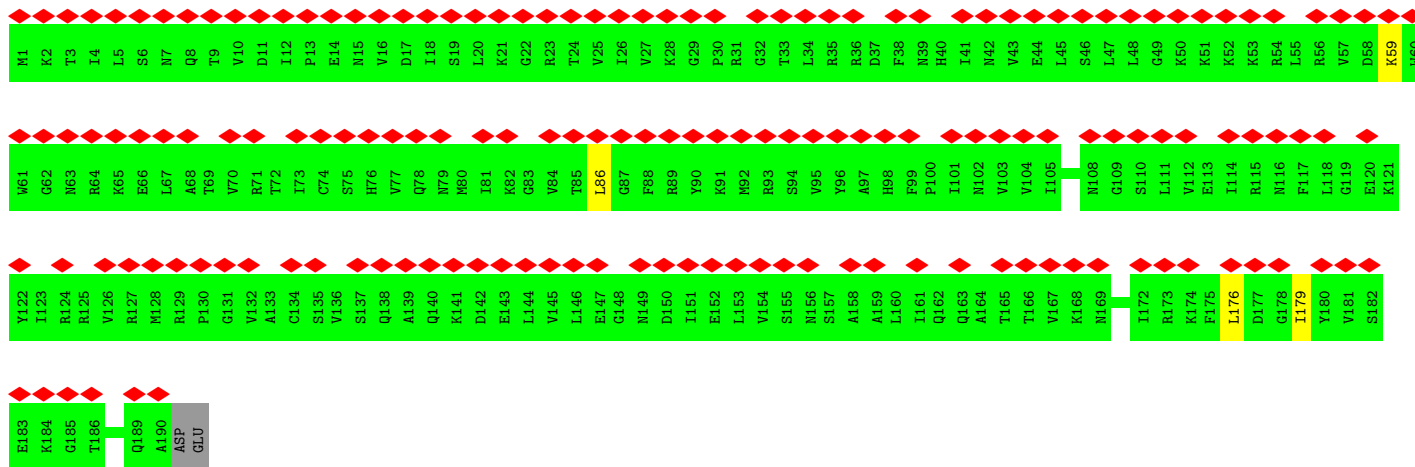
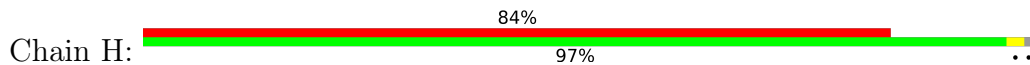


• Molecule 17: 60S ribosomal protein L35

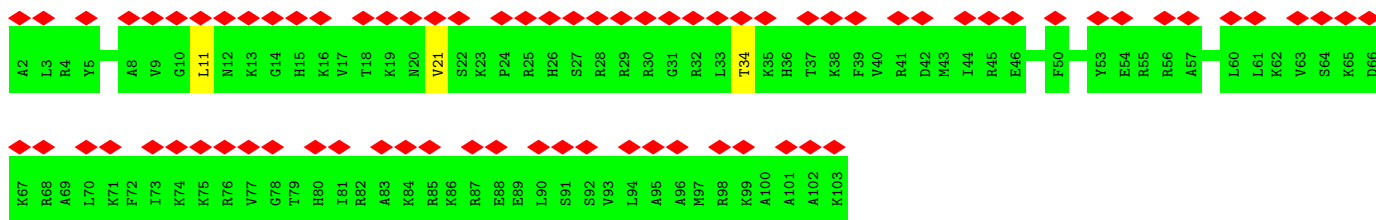
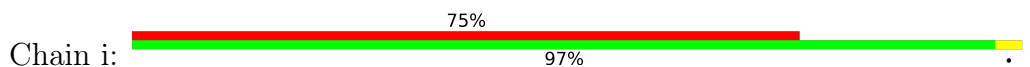




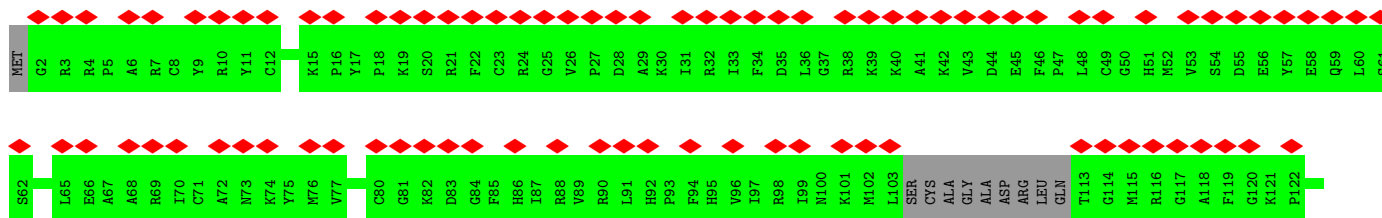
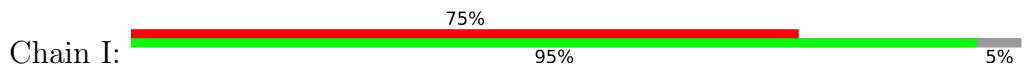
• Molecule 18: 60S ribosomal protein L9

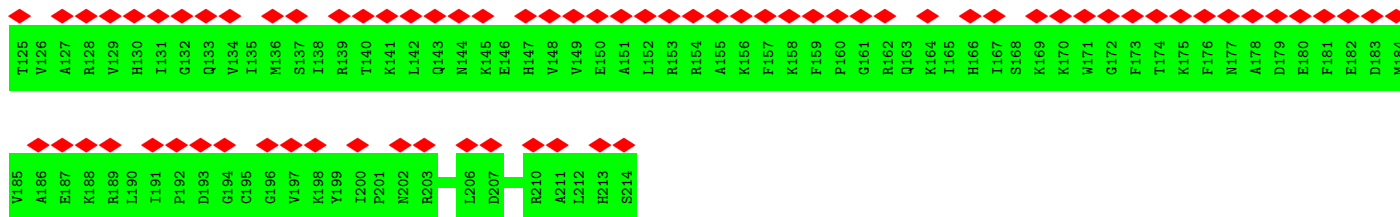


• Molecule 19: 60S ribosomal protein L36

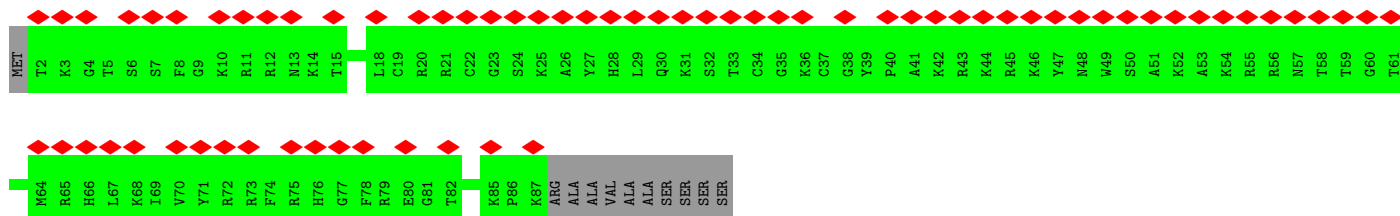
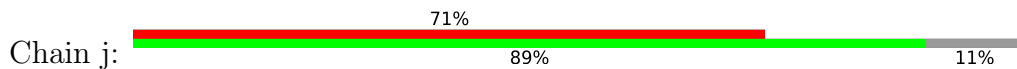


• Molecule 20: 60S ribosomal protein L10

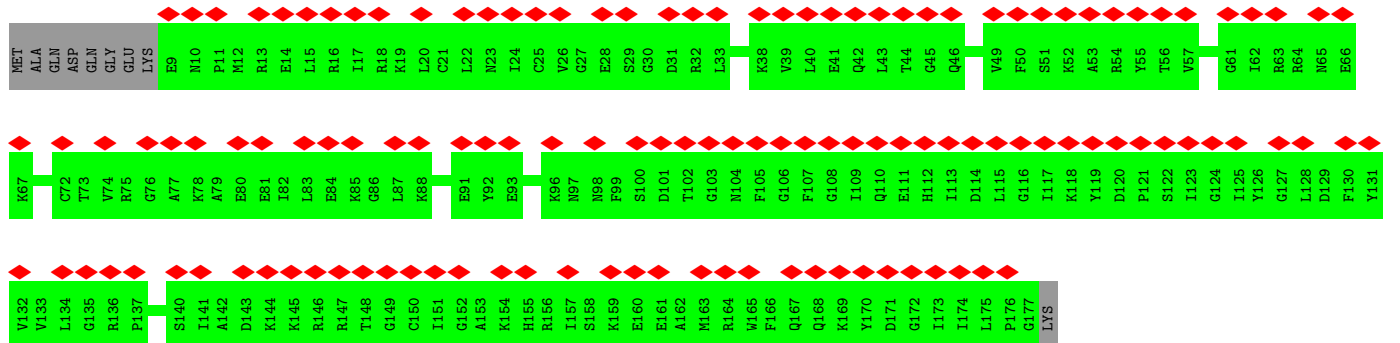




• Molecule 21: Ribosomal protein L37



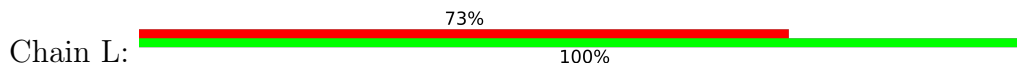
• Molecule 22: Ribosomal protein L11



• Molecule 23: Ribosomal protein L38

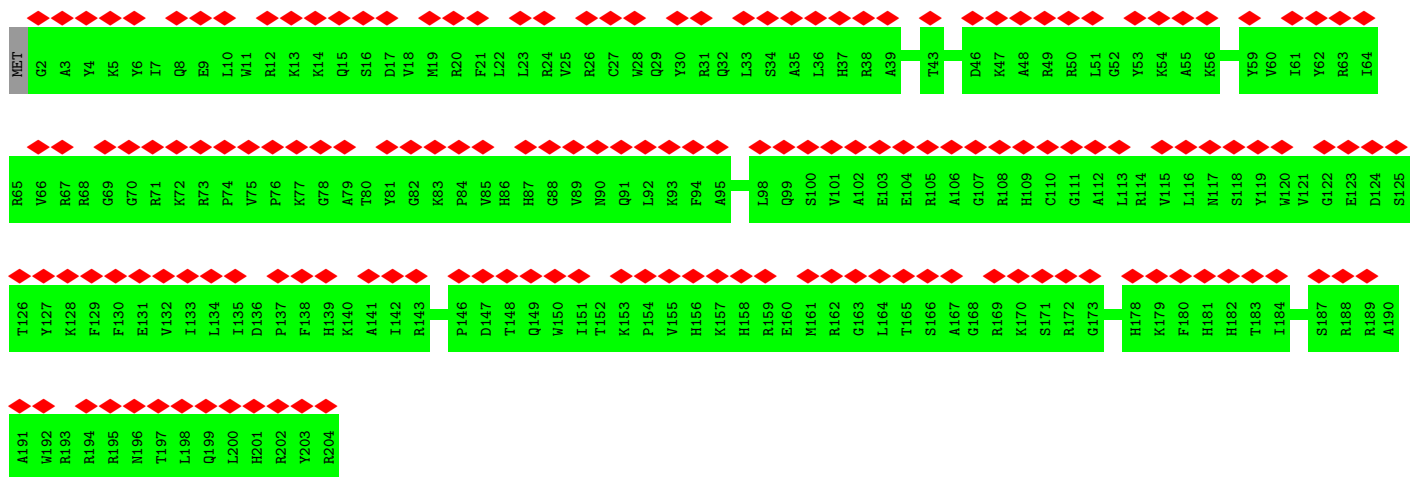
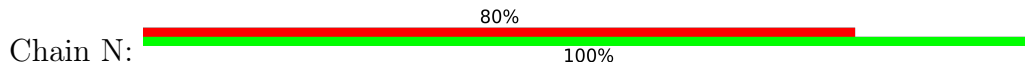


• Molecule 24: Ribosomal protein L13

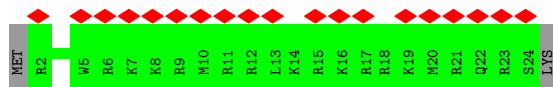
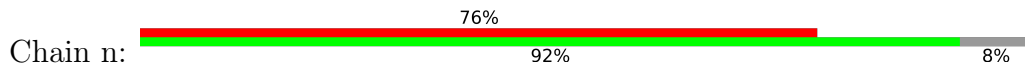


◆ ◆ ◆ ◆ ◆
R122 P123 K124
K125 K126 V127 K128

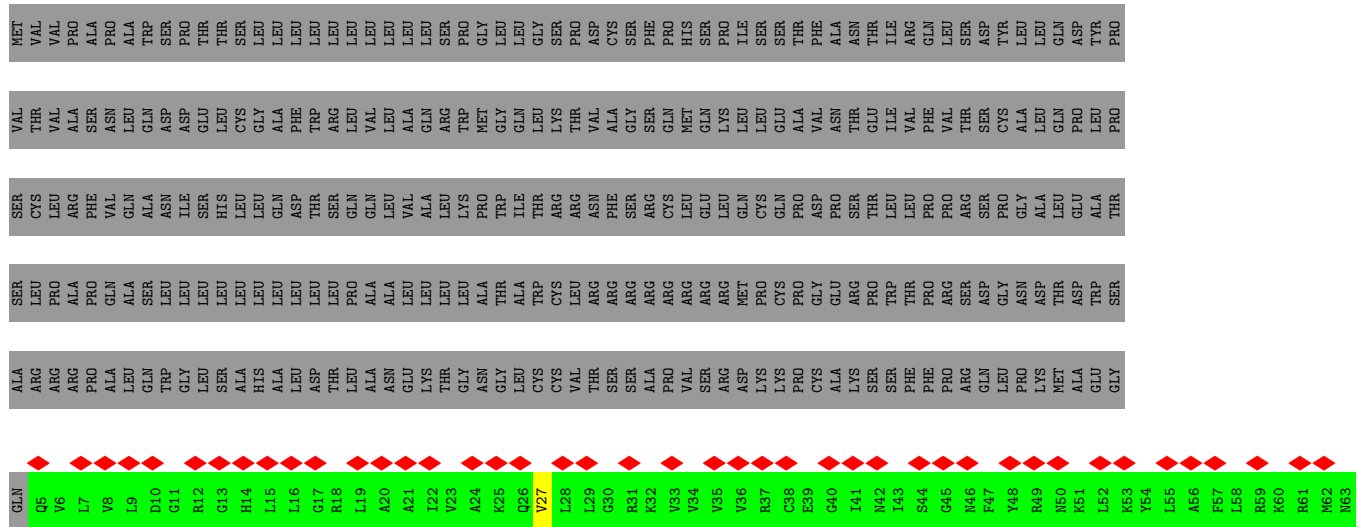
- Molecule 28: Ribosomal protein L15

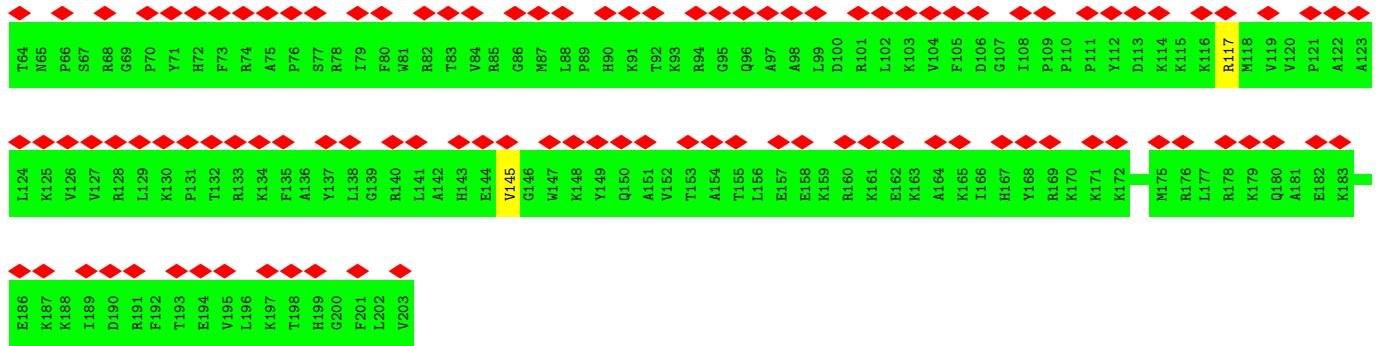


- Molecule 29: 60s ribosomal protein l41

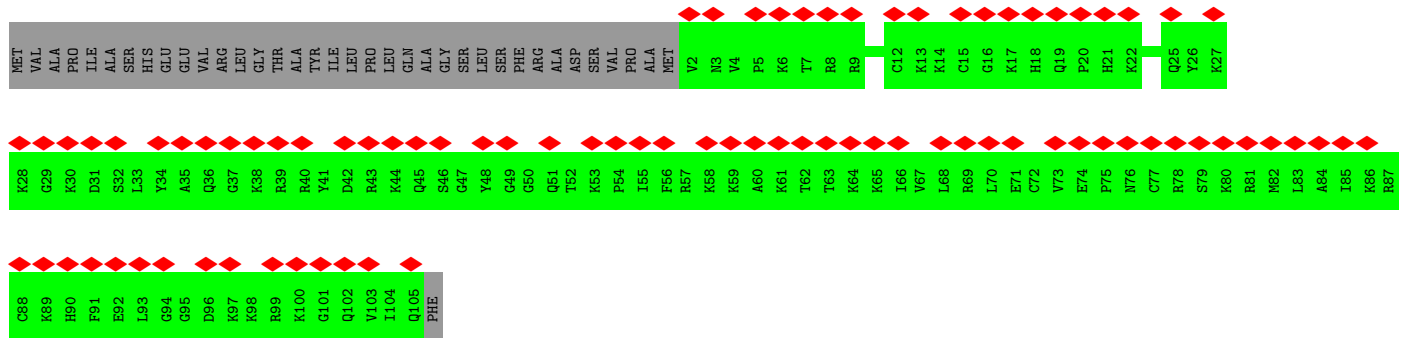
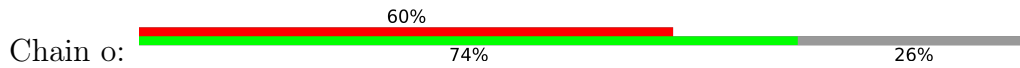


- Molecule 30: Ribosomal protein L13a

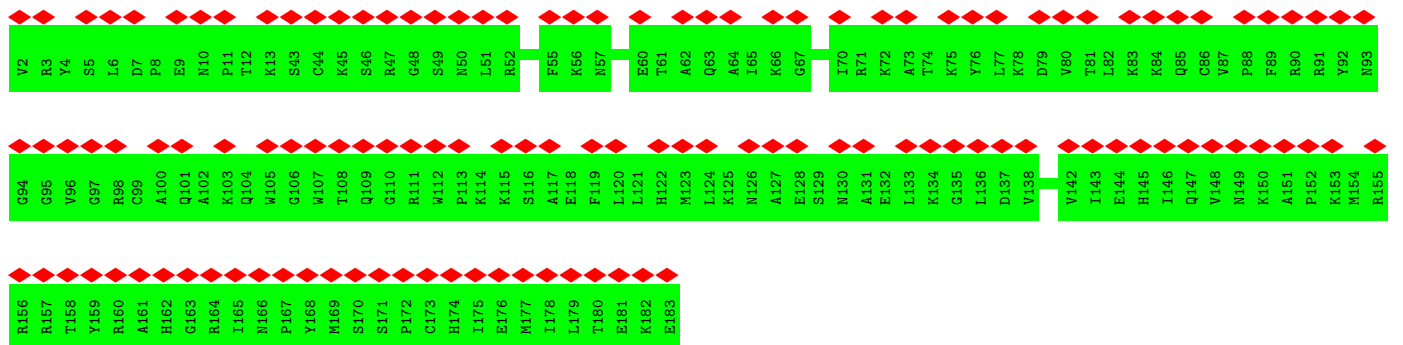
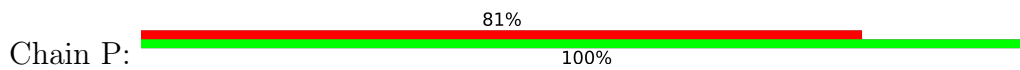




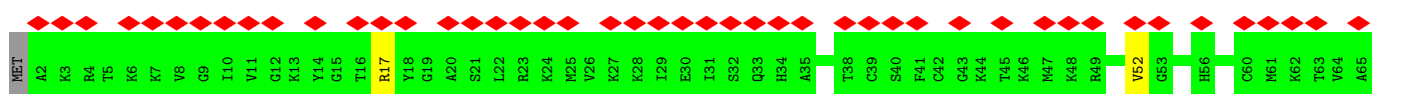
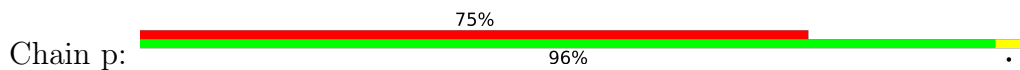
• Molecule 31: eL42

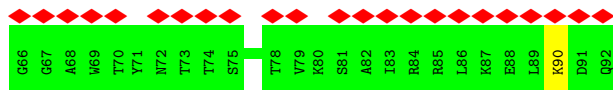


• Molecule 32: 60S ribosomal protein L17

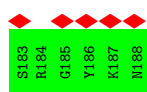
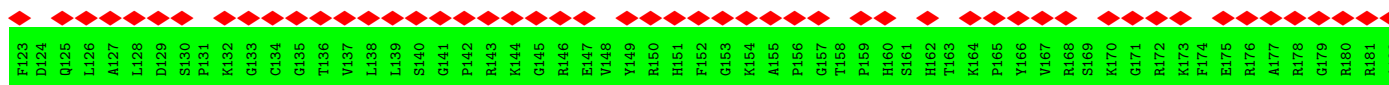
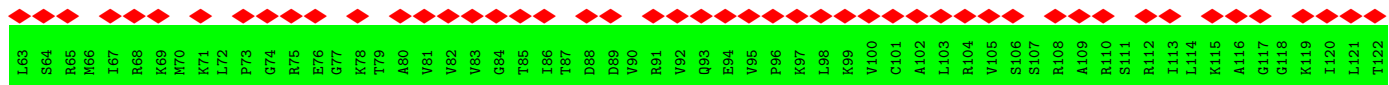
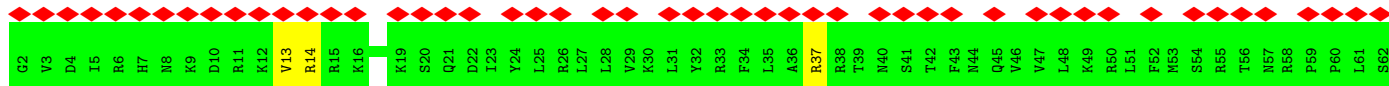


• Molecule 33: eL43

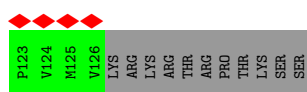
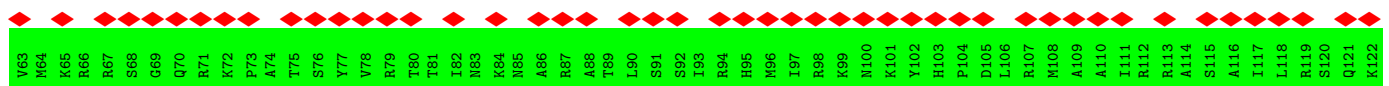
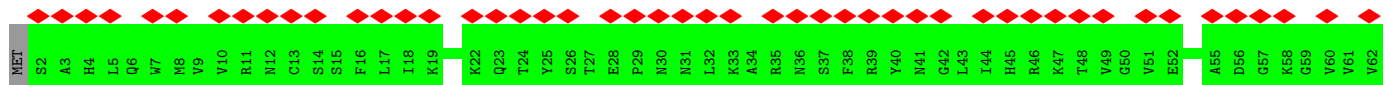
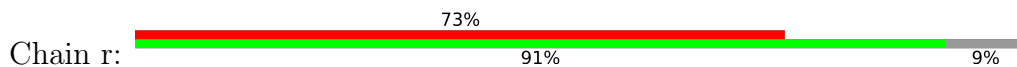




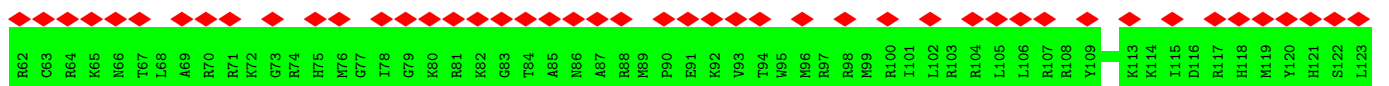
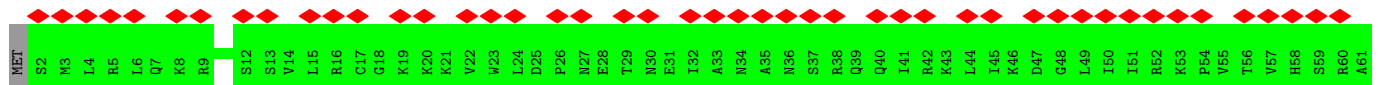
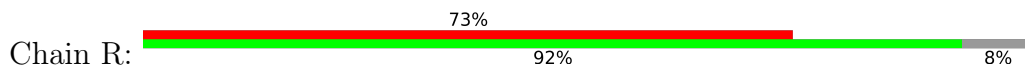
• Molecule 34: Ribosomal protein L18

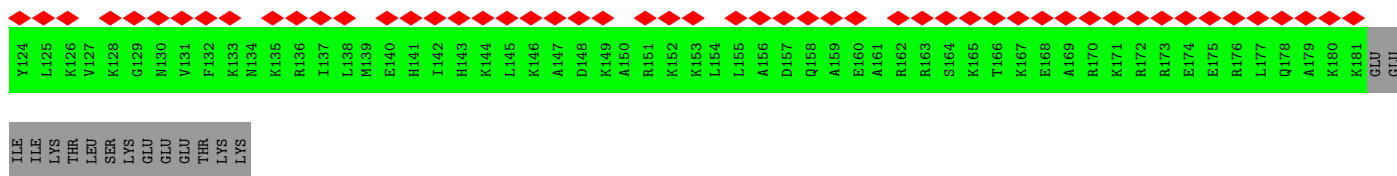


• Molecule 35: 60S ribosomal protein L28

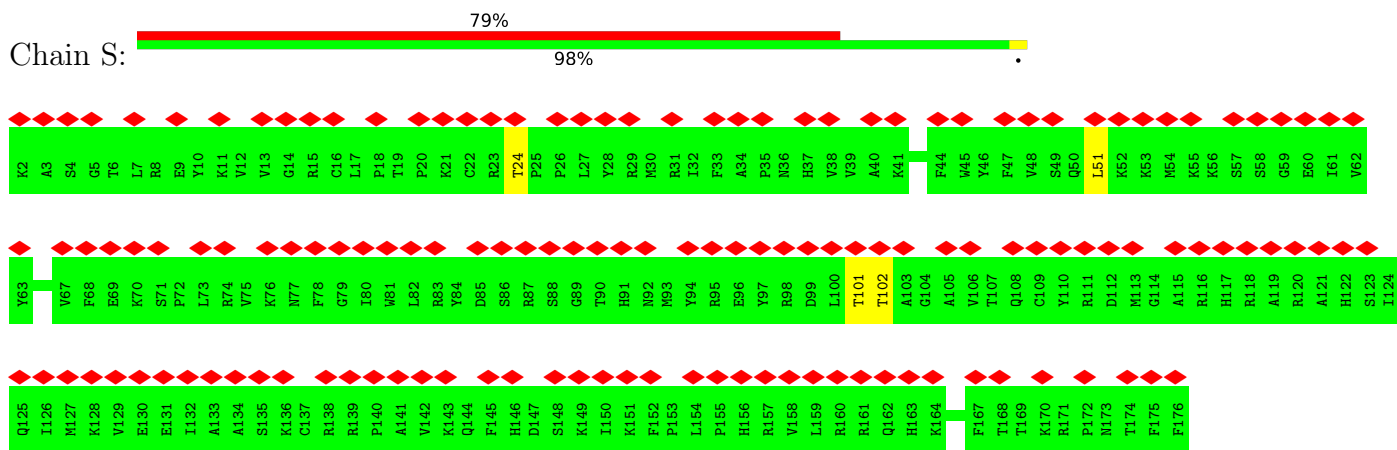


• Molecule 36: 60S ribosomal protein L19

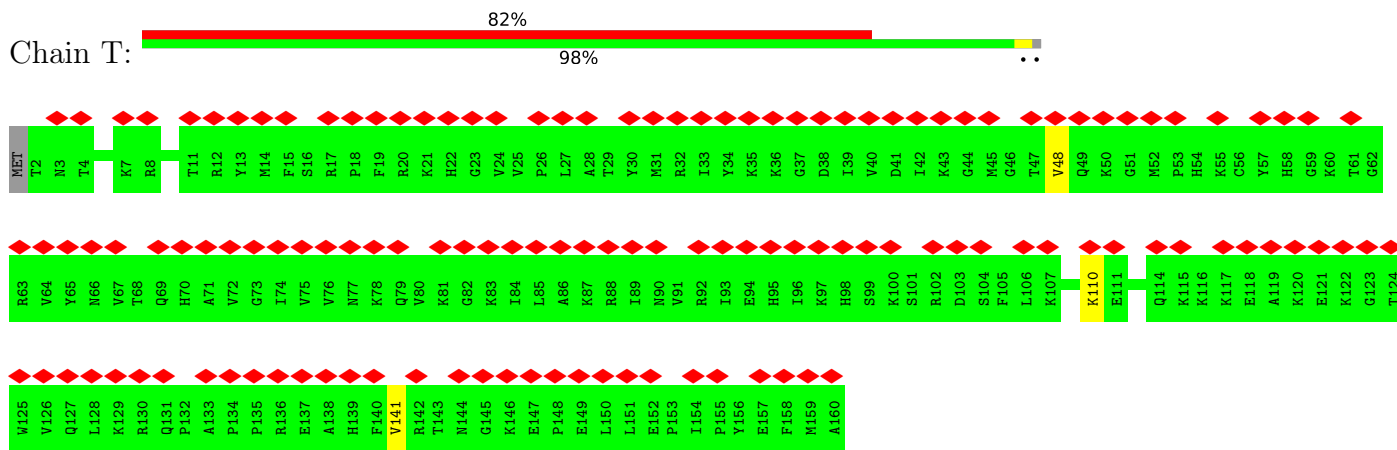




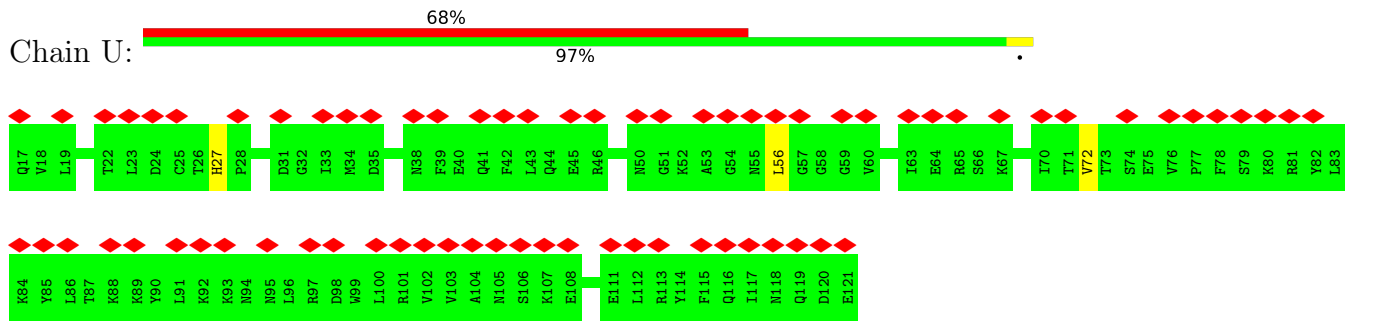
• Molecule 37: Ribosomal protein L18a



• Molecule 38: 60S ribosomal protein L21

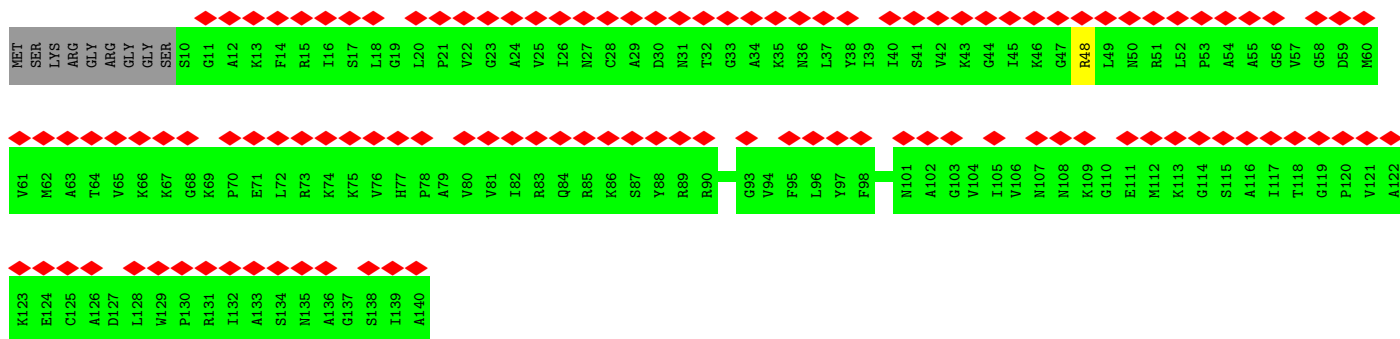


• Molecule 39: Ribosomal protein L22

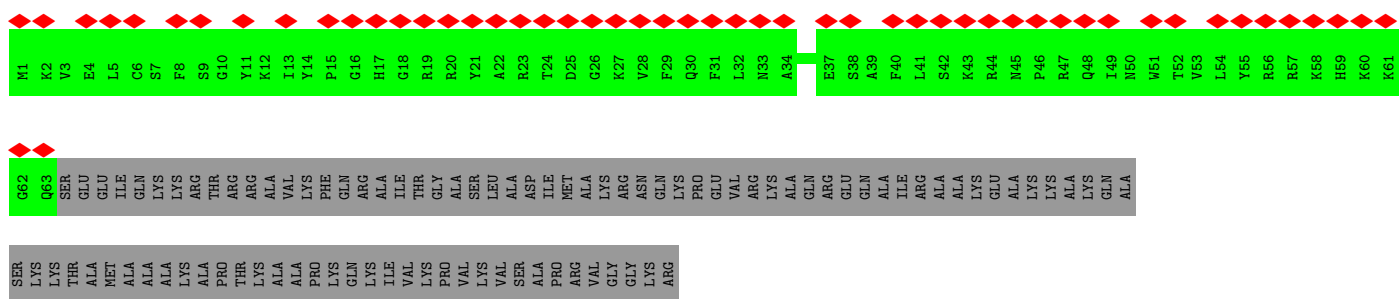


• Molecule 40: Ribosomal protein L23

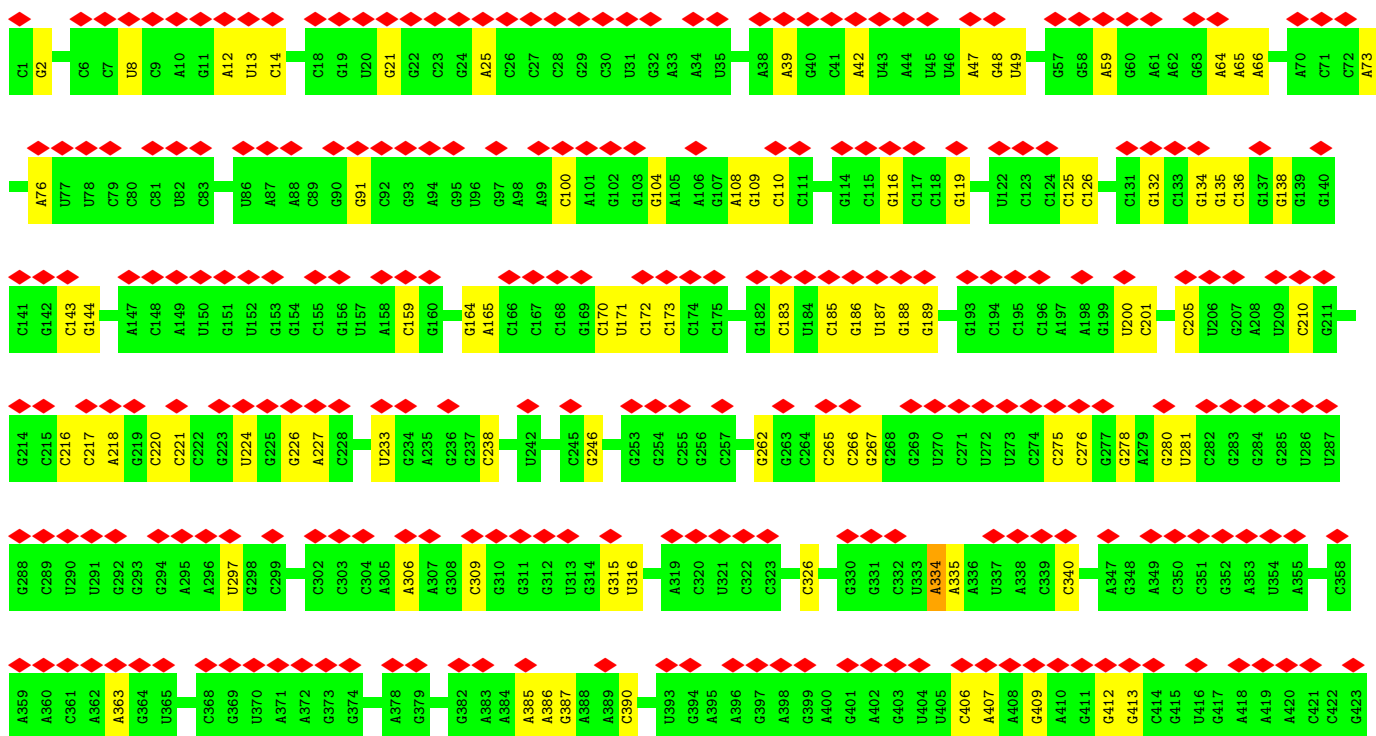


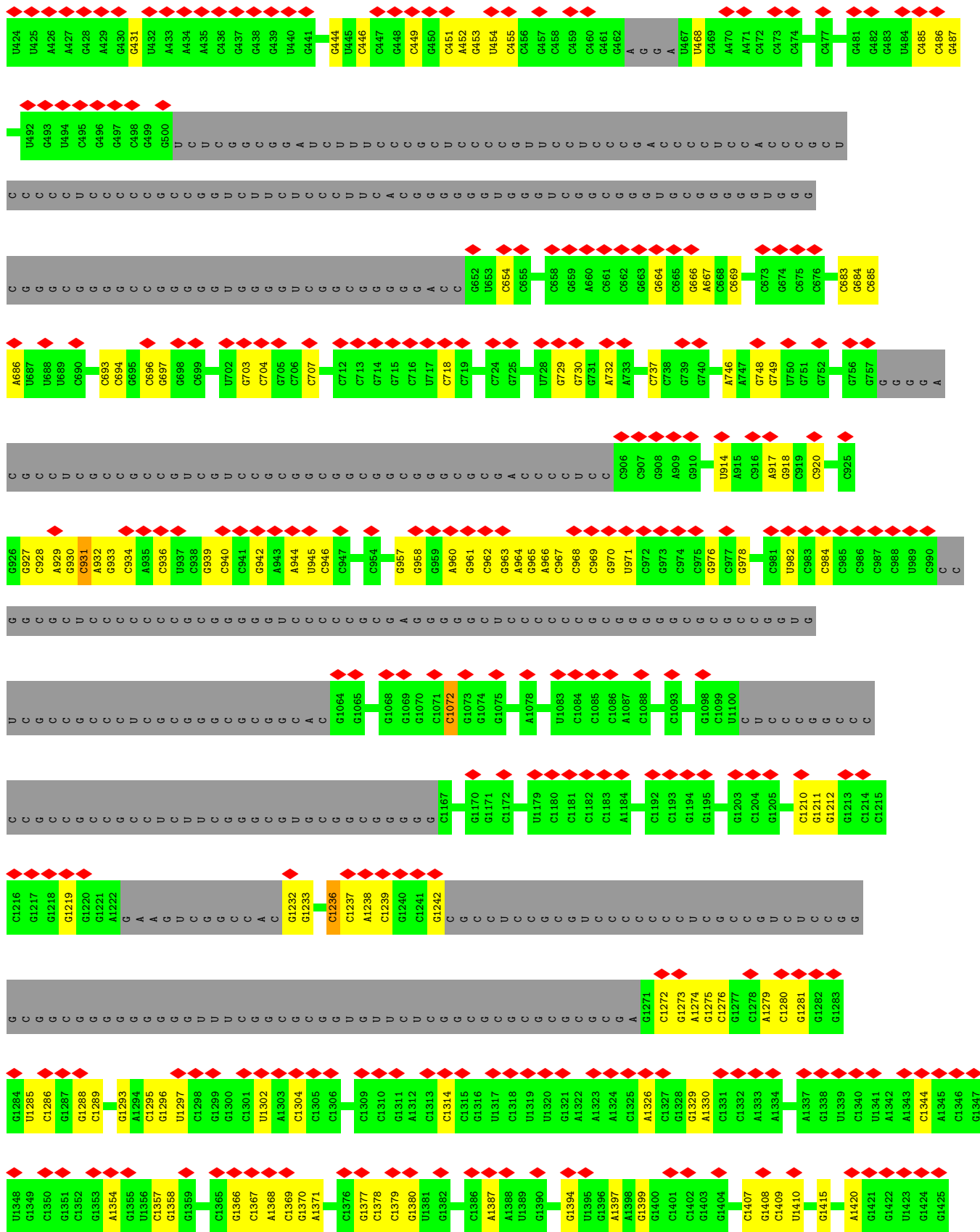


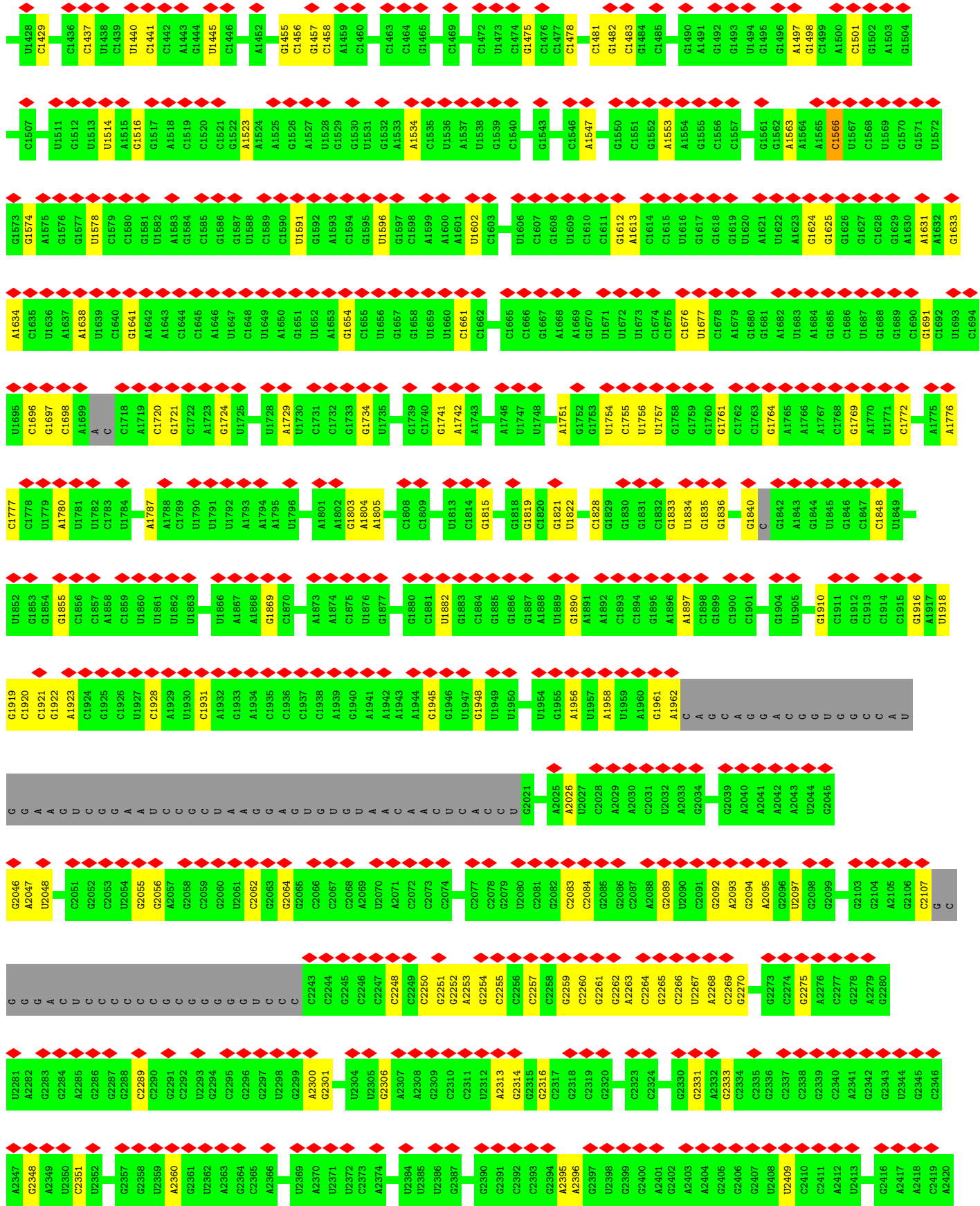
• Molecule 41: Ribosomal protein L24

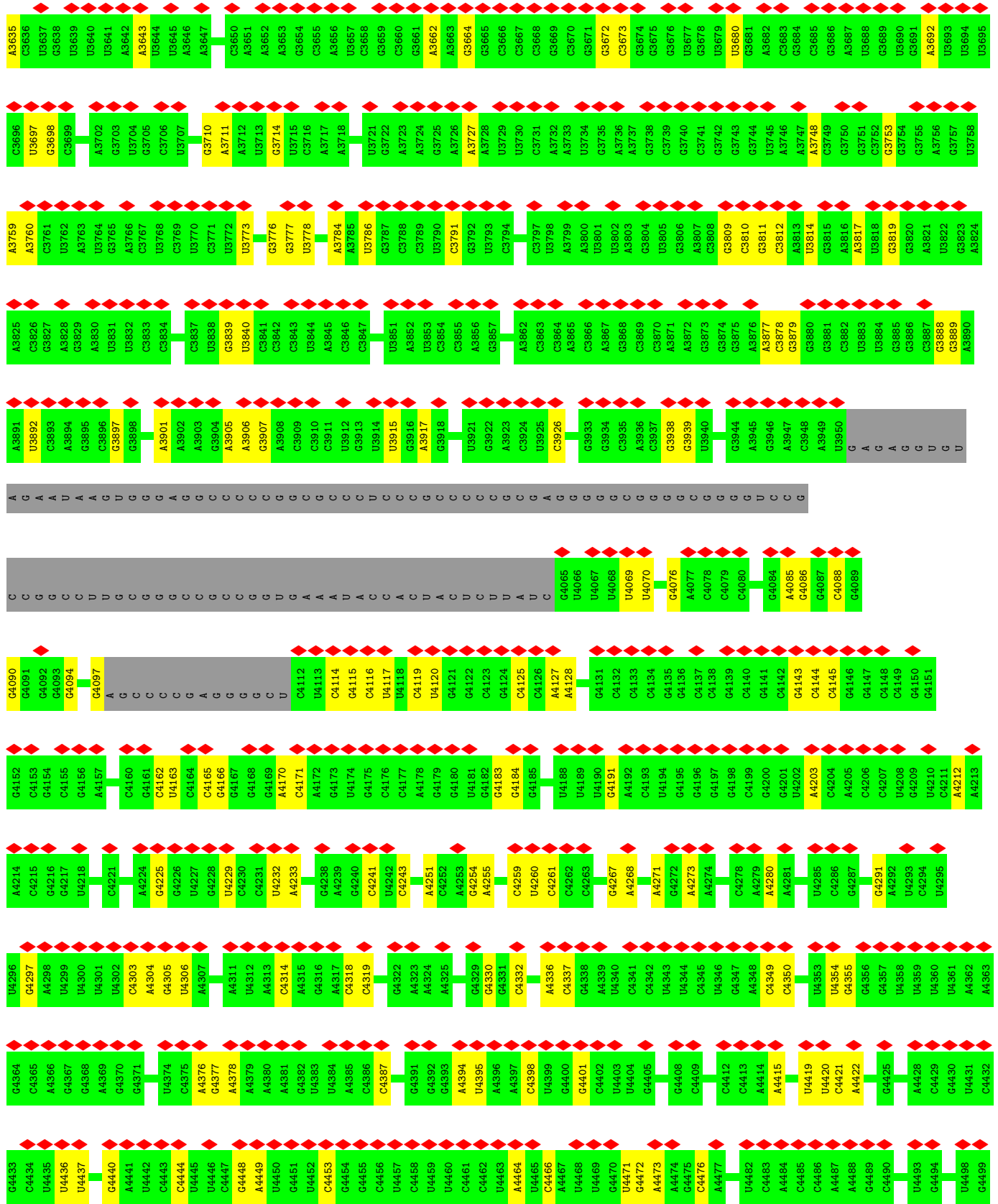


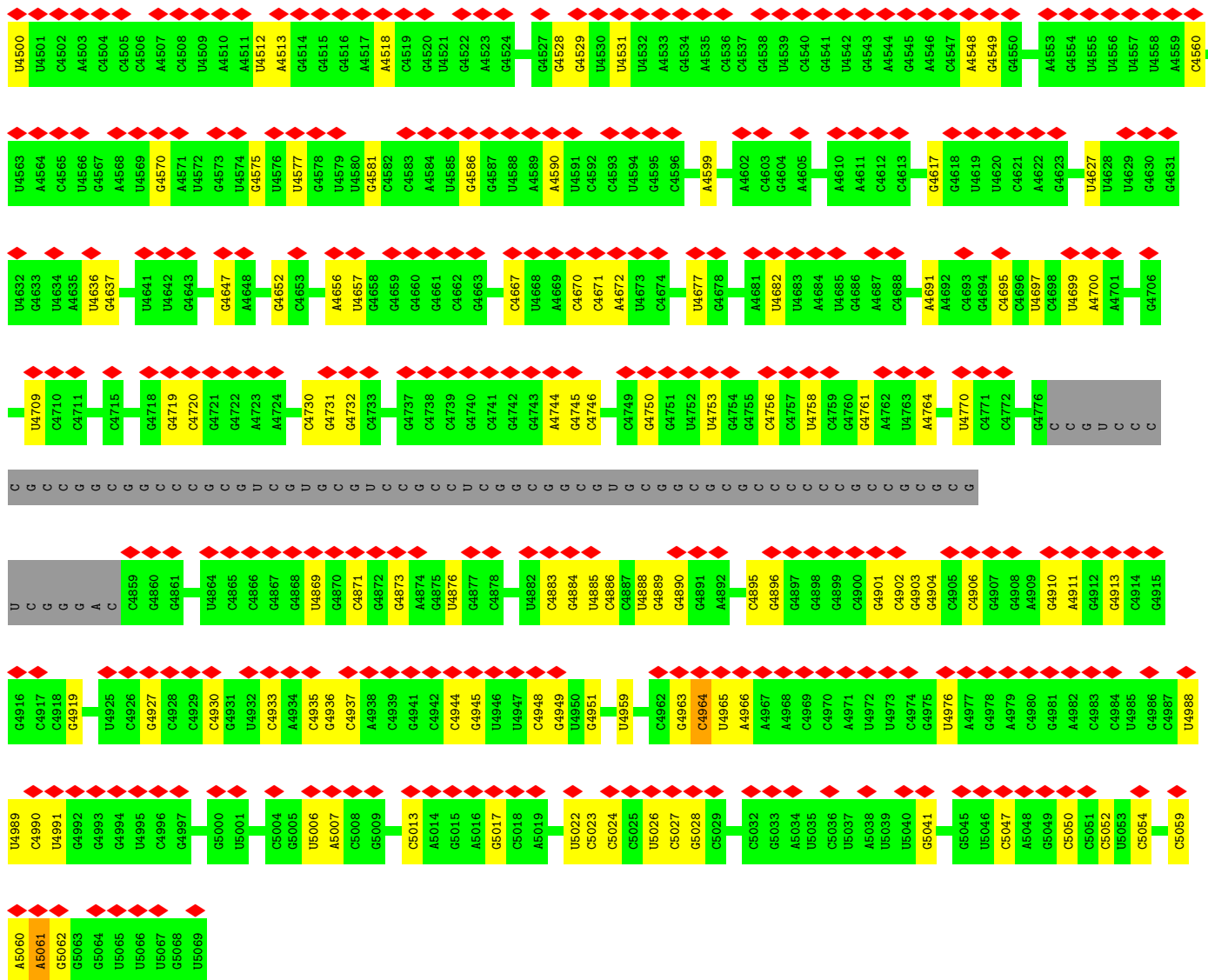
• Molecule 42: 28S rRNA



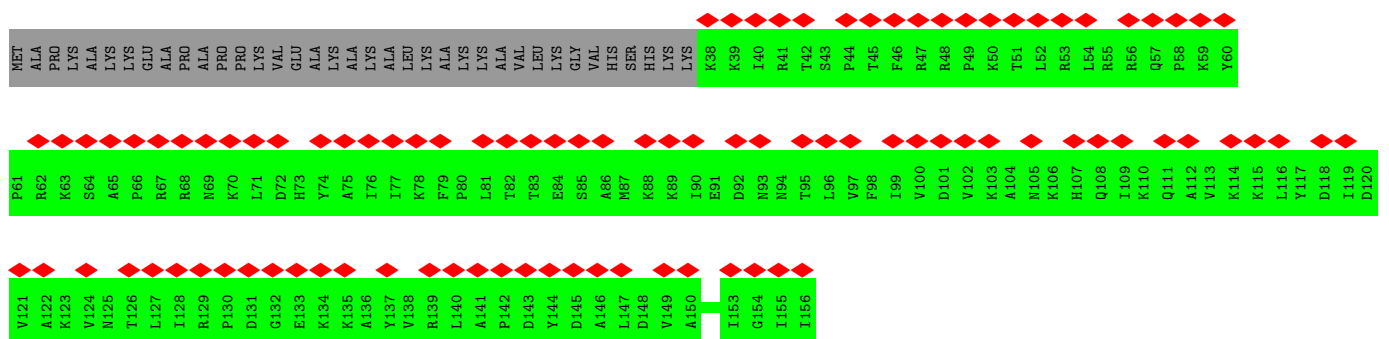
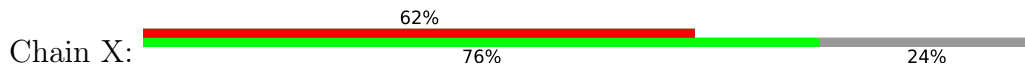




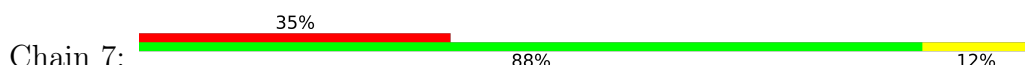


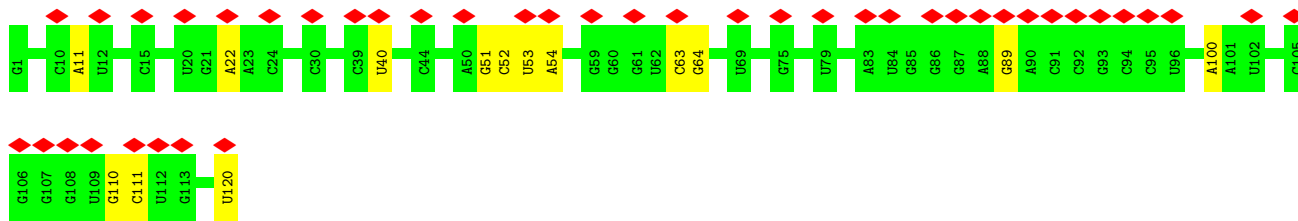


● Molecule 43: Ribosomal_L23eN domain-containing protein

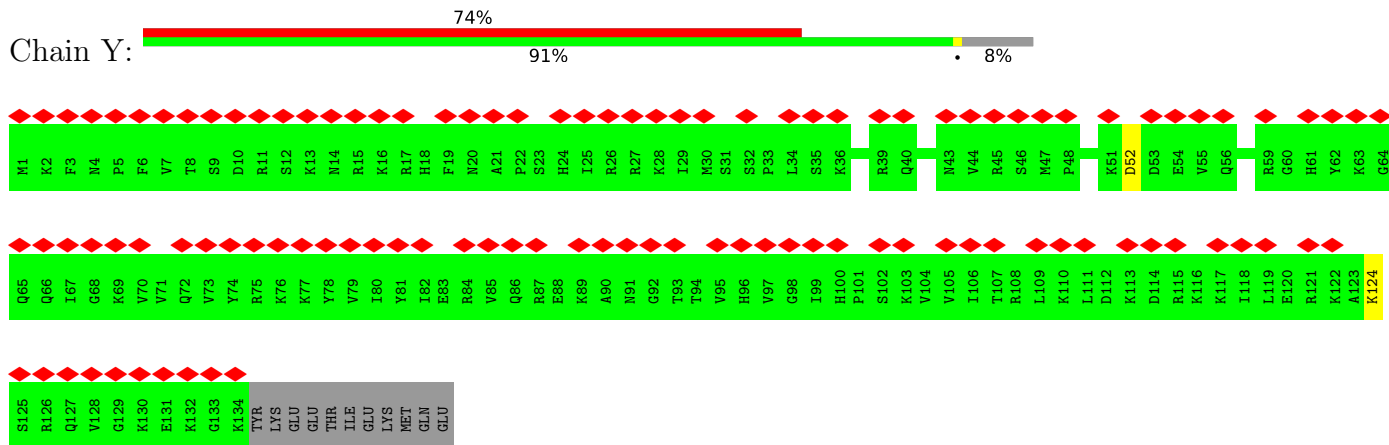


● Molecule 44: 5S rRNA

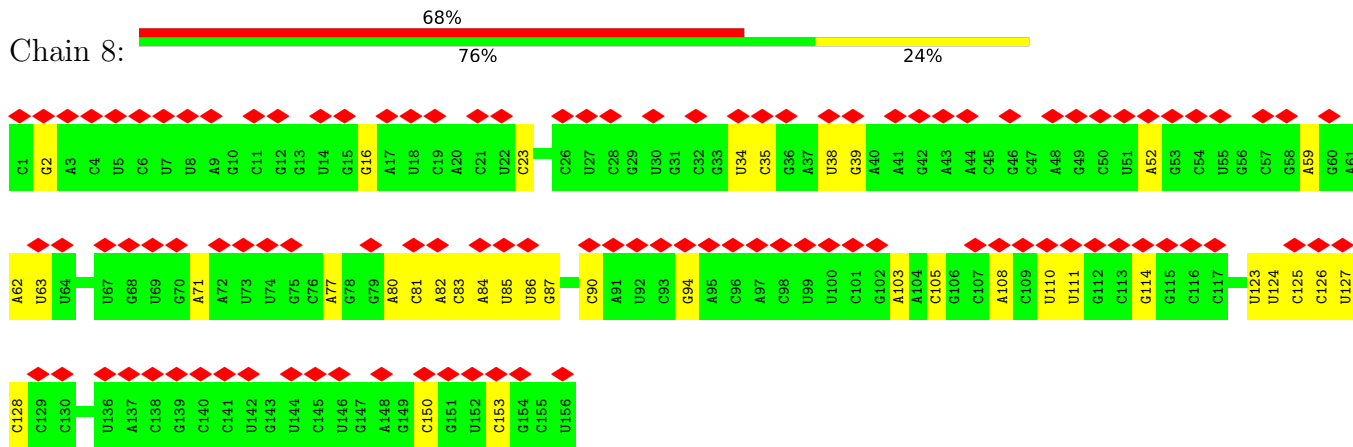




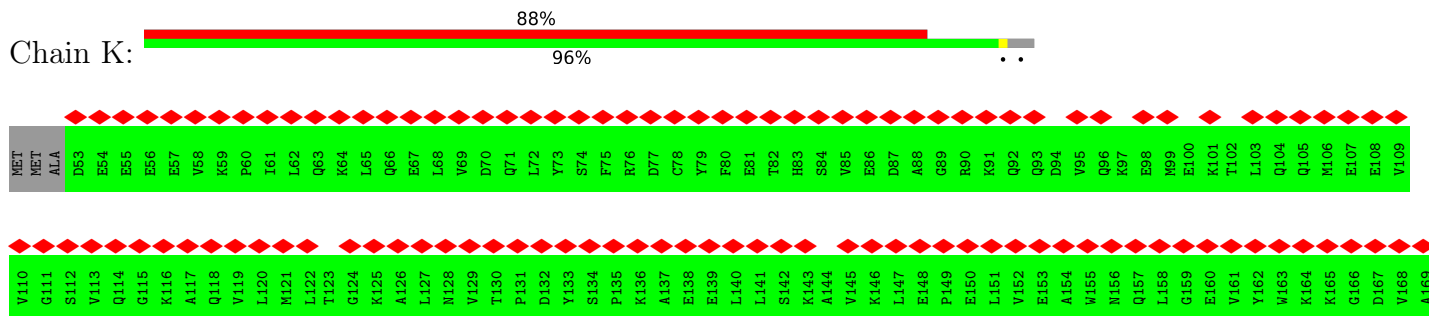
• Molecule 45: Ribosomal protein L26

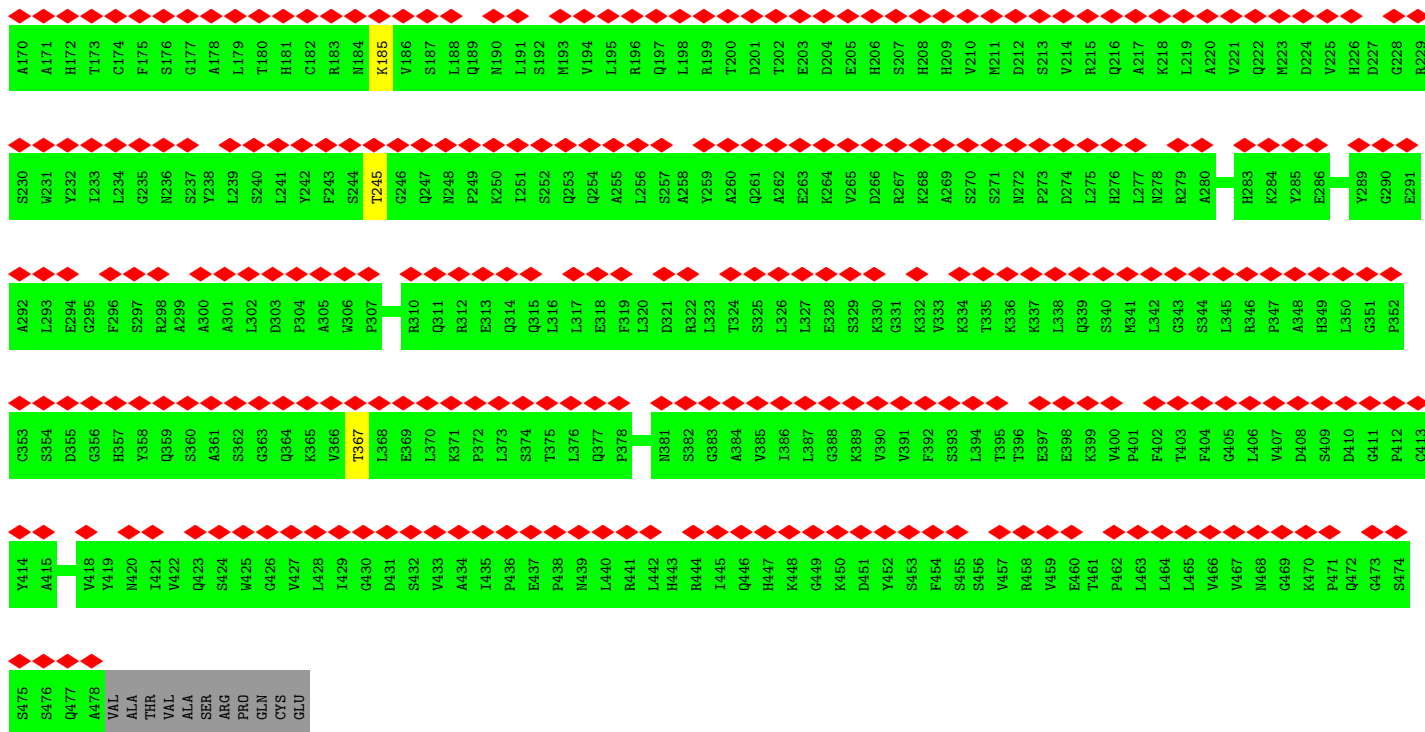


• Molecule 46: 5.8S rRNA



• Molecule 47: Tetratricopeptide repeat protein 5

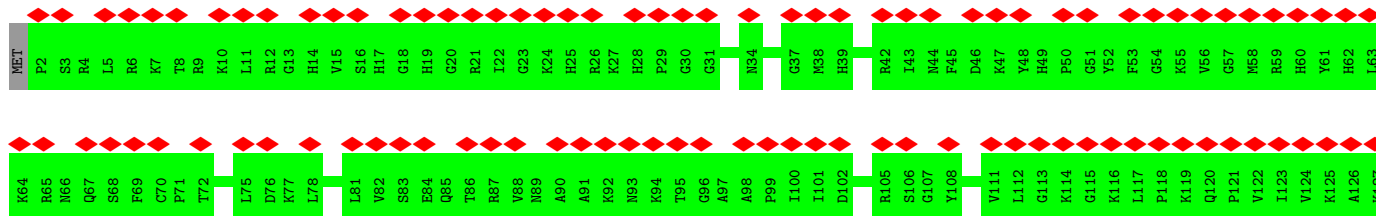
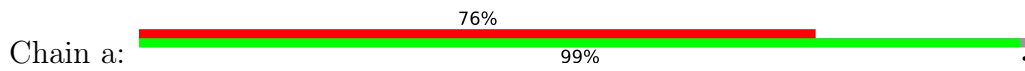




• Molecule 48: 60S ribosomal protein L27



• Molecule 49: 60S ribosomal protein L27a



F128	F129	S130	R131	R132	A133	E134	E135	K136	I137	K138	G139	V140	G141	G142	A143	C144	V145	L146	V147	A148
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	83053	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.381	Depositor
Minimum map value	-0.210	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.019	Depositor
Recommended contour level	0.05	Depositor
Map size (\AA)	535.6, 535.6, 535.6	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.339, 1.339, 1.339	Depositor

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN

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	t	0.23	0/536	0.48	0/715
3	u	0.25	0/845	0.46	0/1134
4	A	0.25	0/1906	0.55	0/2556
5	b	0.23	0/619	0.45	0/818
6	B	0.25	0/3216	0.50	0/4311
7	c	0.24	0/742	0.45	0/996
8	C	0.23	0/2937	0.52	0/3946
9	d	0.24	0/903	0.53	0/1216
10	D	0.25	0/2432	0.50	0/3257
11	e	0.23	0/1071	0.50	0/1429
12	E	0.24	0/1936	0.55	0/2600
13	f	0.25	0/895	0.55	0/1198
14	F	0.25	0/1905	0.50	0/2539
15	g	0.24	0/916	0.55	0/1220
16	G	0.24	0/1967	0.50	0/2647
17	h	0.23	0/1021	0.51	0/1348
18	H	0.24	0/1535	0.51	0/2063
19	i	0.24	0/841	0.53	0/1112
20	I	0.25	0/1693	0.51	0/2260
21	j	0.24	0/720	0.58	0/952
22	J	0.24	0/1376	0.52	0/1841
23	k	0.23	0/575	0.48	0/761
24	L	0.24	0/1734	0.55	0/2317
25	l	0.24	0/454	0.58	0/599
26	M	0.24	0/1158	0.51	0/1547
27	m	0.25	0/435	0.53	0/575
28	N	0.24	0/1746	0.55	0/2338
29	n	0.21	0/223	0.68	0/284
30	O	0.25	0/1671	0.51	0/2234
31	o	0.25	0/864	0.53	0/1140
32	P	0.23	0/1268	0.49	0/1700
33	p	0.24	0/718	0.51	0/953

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
34	Q	0.24	0/1530	0.57	0/2041
35	r	0.24	0/1017	0.56	0/1364
36	R	0.23	0/1524	0.55	0/2013
37	S	0.25	0/1493	0.54	0/2002
38	T	0.25	0/1326	0.50	0/1770
39	U	0.25	0/873	0.49	0/1172
40	V	0.26	0/993	0.51	0/1332
41	W	0.25	0/541	0.50	0/720
42	5	0.20	0/83726	0.78	38/130593 (0.0%)
43	X	0.24	0/993	0.49	0/1334
44	7	0.17	0/2858	0.74	1/4455 (0.0%)
45	Y	0.24	0/1132	0.51	0/1504
46	8	0.18	0/3701	0.75	0/5766
47	K	0.24	0/3402	0.44	0/4603
48	Z	0.26	0/1130	0.51	0/1507
49	a	0.24	0/1191	0.51	0/1590
All	All	0.22	0/148288	0.70	39/218372 (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
13	f	0	1

There are no bond length outliers.

The worst 5 of 39 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	5	1566	C	C6-N1-C2	13.51	125.70	120.30
42	5	4259	C	N3-C2-O2	-9.04	115.57	121.90
42	5	931	C	N1-C2-O2	8.76	124.16	118.90
42	5	931	C	C2-N1-C1'	8.74	128.42	118.80
42	5	1072	C	N1-C2-O2	8.50	124.00	118.90

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
13	f	106	TYR	Peptide

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	t	65/215 (30%)	63 (97%)	2 (3%)	0	100	100
3	u	106/162 (65%)	102 (96%)	4 (4%)	0	100	100
4	A	242/245 (99%)	223 (92%)	19 (8%)	0	100	100
5	b	73/223 (33%)	72 (99%)	1 (1%)	0	100	100
6	B	392/403 (97%)	384 (98%)	8 (2%)	0	100	100
7	c	92/115 (80%)	91 (99%)	1 (1%)	0	100	100
8	C	360/413 (87%)	347 (96%)	13 (4%)	0	100	100
9	d	105/125 (84%)	104 (99%)	1 (1%)	0	100	100
10	D	290/297 (98%)	280 (97%)	10 (3%)	0	100	100
11	e	126/157 (80%)	121 (96%)	5 (4%)	0	100	100
12	E	232/291 (80%)	205 (88%)	27 (12%)	0	100	100
13	f	107/110 (97%)	101 (94%)	6 (6%)	0	100	100
14	F	223/225 (99%)	218 (98%)	5 (2%)	0	100	100
15	g	112/129 (87%)	111 (99%)	1 (1%)	0	100	100
16	G	239/319 (75%)	225 (94%)	14 (6%)	0	100	100
17	h	120/123 (98%)	117 (98%)	3 (2%)	0	100	100
18	H	188/192 (98%)	181 (96%)	7 (4%)	0	100	100
19	i	100/102 (98%)	97 (97%)	2 (2%)	1 (1%)	15	46
20	I	200/214 (94%)	193 (96%)	7 (4%)	0	100	100
21	j	84/97 (87%)	81 (96%)	3 (4%)	0	100	100
22	J	167/178 (94%)	159 (95%)	8 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
23	k	67/69 (97%)	62 (92%)	5 (8%)	0	100	100
24	L	208/210 (99%)	196 (94%)	12 (6%)	0	100	100
25	l	48/51 (94%)	44 (92%)	4 (8%)	0	100	100
26	M	136/218 (62%)	128 (94%)	8 (6%)	0	100	100
27	m	50/128 (39%)	48 (96%)	2 (4%)	0	100	100
28	N	201/204 (98%)	192 (96%)	9 (4%)	0	100	100
29	n	21/25 (84%)	21 (100%)	0	0	100	100
30	O	197/500 (39%)	196 (100%)	1 (0%)	0	100	100
31	o	102/141 (72%)	96 (94%)	6 (6%)	0	100	100
32	P	151/153 (99%)	150 (99%)	1 (1%)	0	100	100
33	p	89/92 (97%)	87 (98%)	2 (2%)	0	100	100
34	Q	185/187 (99%)	181 (98%)	4 (2%)	0	100	100
35	r	123/137 (90%)	116 (94%)	7 (6%)	0	100	100
36	R	178/196 (91%)	175 (98%)	3 (2%)	0	100	100
37	S	173/175 (99%)	164 (95%)	9 (5%)	0	100	100
38	T	157/160 (98%)	153 (98%)	4 (2%)	0	100	100
39	U	103/105 (98%)	100 (97%)	3 (3%)	0	100	100
40	V	129/140 (92%)	127 (98%)	2 (2%)	0	100	100
41	W	61/157 (39%)	61 (100%)	0	0	100	100
43	X	117/156 (75%)	115 (98%)	2 (2%)	0	100	100
45	Y	132/145 (91%)	129 (98%)	3 (2%)	0	100	100
47	K	424/440 (96%)	417 (98%)	7 (2%)	0	100	100
48	Z	133/136 (98%)	125 (94%)	8 (6%)	0	100	100
49	a	145/148 (98%)	139 (96%)	6 (4%)	0	100	100
All	All	6953/8408 (83%)	6697 (96%)	255 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
19	i	11	LEU

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	t	60/183 (33%)	60 (100%)	0	100	100
3	u	92/136 (68%)	91 (99%)	1 (1%)	73	86
4	A	187/188 (100%)	184 (98%)	3 (2%)	62	81
5	b	62/170 (36%)	61 (98%)	1 (2%)	62	81
6	B	336/348 (97%)	331 (98%)	5 (2%)	65	82
7	c	79/98 (81%)	78 (99%)	1 (1%)	69	84
8	C	302/337 (90%)	296 (98%)	6 (2%)	55	77
9	d	98/110 (89%)	94 (96%)	4 (4%)	30	59
10	D	247/250 (99%)	242 (98%)	5 (2%)	55	77
11	e	114/141 (81%)	114 (100%)	0	100	100
12	E	208/251 (83%)	202 (97%)	6 (3%)	42	69
13	f	88/89 (99%)	87 (99%)	1 (1%)	73	86
14	F	194/195 (100%)	193 (100%)	1 (0%)	88	94
15	g	98/109 (90%)	95 (97%)	3 (3%)	40	68
16	G	206/273 (76%)	204 (99%)	2 (1%)	76	88
17	h	109/110 (99%)	106 (97%)	3 (3%)	43	70
18	H	169/171 (99%)	165 (98%)	4 (2%)	49	74
19	i	86/86 (100%)	84 (98%)	2 (2%)	50	74
20	I	174/181 (96%)	174 (100%)	0	100	100
21	j	73/80 (91%)	73 (100%)	0	100	100
22	J	142/149 (95%)	142 (100%)	0	100	100
23	k	64/64 (100%)	63 (98%)	1 (2%)	62	81
24	L	176/176 (100%)	175 (99%)	1 (1%)	86	94
25	l	47/48 (98%)	46 (98%)	1 (2%)	53	76
26	M	117/160 (73%)	114 (97%)	3 (3%)	46	72
27	m	48/116 (41%)	48 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	N	171/172 (99%)	171 (100%)	0	100	100
29	n	22/24 (92%)	22 (100%)	0	100	100
30	O	171/433 (40%)	168 (98%)	3 (2%)	59	79
31	o	92/121 (76%)	92 (100%)	0	100	100
32	P	134/134 (100%)	134 (100%)	0	100	100
33	p	74/75 (99%)	71 (96%)	3 (4%)	30	59
34	Q	163/163 (100%)	160 (98%)	3 (2%)	59	79
35	r	109/121 (90%)	109 (100%)	0	100	100
36	R	159/175 (91%)	159 (100%)	0	100	100
37	S	156/156 (100%)	152 (97%)	4 (3%)	46	72
38	T	139/140 (99%)	136 (98%)	3 (2%)	52	75
39	U	95/95 (100%)	92 (97%)	3 (3%)	39	67
40	V	101/107 (94%)	100 (99%)	1 (1%)	76	88
41	W	55/126 (44%)	55 (100%)	0	100	100
43	X	107/134 (80%)	107 (100%)	0	100	100
45	Y	124/135 (92%)	122 (98%)	2 (2%)	62	81
47	K	370/381 (97%)	367 (99%)	3 (1%)	81	91
48	Z	117/118 (99%)	116 (99%)	1 (1%)	78	90
49	a	119/120 (99%)	119 (100%)	0	100	100
All	All	6054/7149 (85%)	5974 (99%)	80 (1%)	70	84

5 of 80 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
33	p	17	ARG
39	U	56	LEU
33	p	90	LYS
37	S	101	THR
45	Y	124	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 114 such sidechains are listed below:

Mol	Chain	Res	Type
22	J	42	GLN

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Mol	Chain	Res	Type
47	K	468	ASN
28	N	109	HIS
47	K	443	HIS
41	W	59	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
42	5	3477/4754 (73%)	684 (19%)	65 (1%)
44	7	119/120 (99%)	13 (10%)	0
46	8	155/156 (99%)	36 (23%)	1 (0%)
All	All	3751/5030 (74%)	733 (19%)	66 (1%)

5 of 733 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
42	5	2	G
42	5	8	U
42	5	12	A
42	5	13	U
42	5	14	C

5 of 66 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
42	5	4889	G
42	5	4948	C
46	8	124	U
42	5	1236	C
42	5	1232	G

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 102 ligands modelled in this entry, 102 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

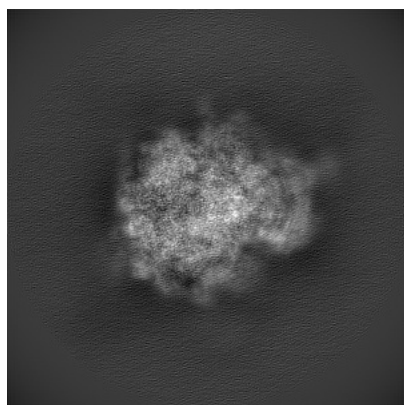
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14193. These allow visual inspection of the internal detail of the map and identification of artifacts.

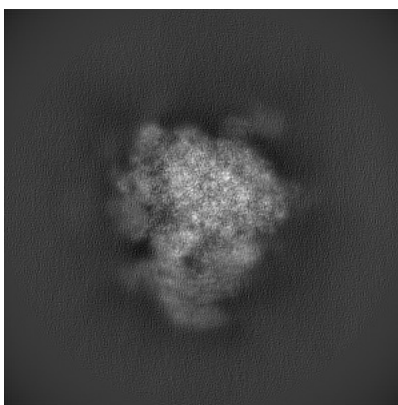
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

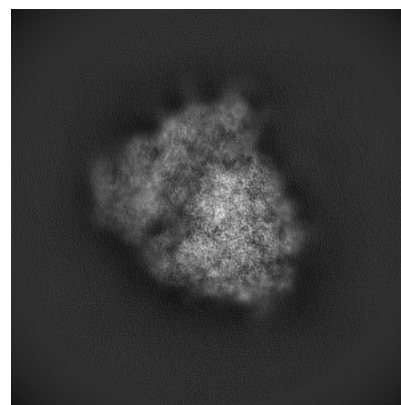
6.1.1 Primary map



X



Y

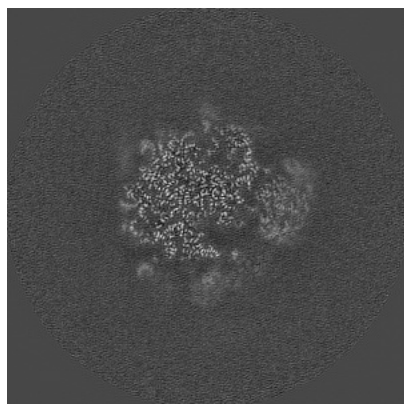


Z

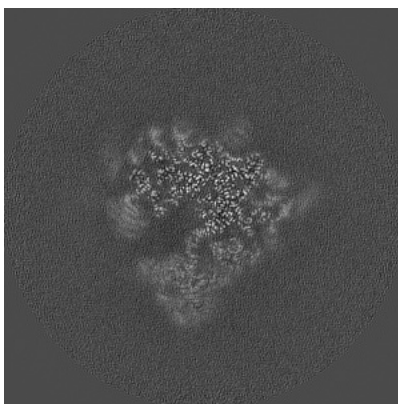
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

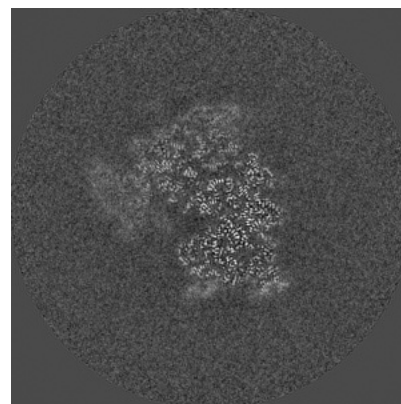
6.2.1 Primary map



X Index: 200



Y Index: 200

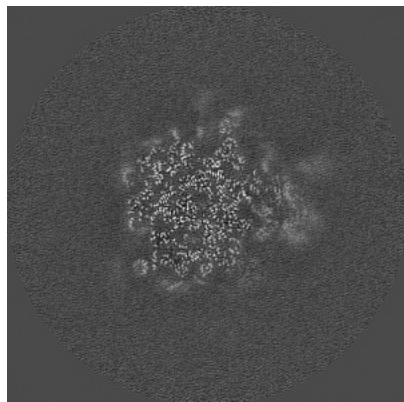


Z Index: 200

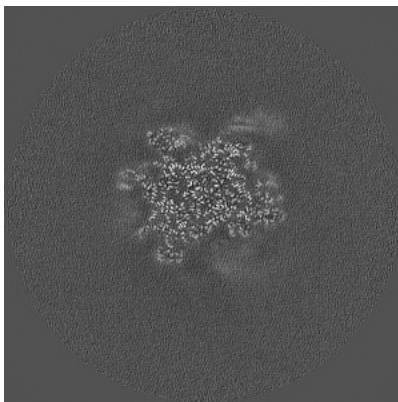
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

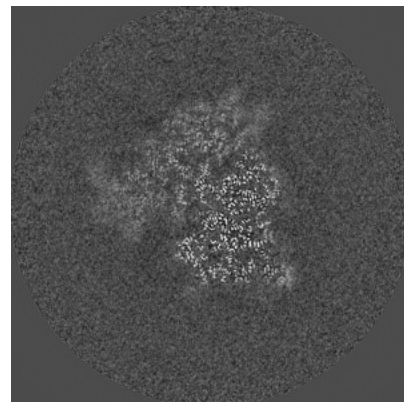
6.3.1 Primary map



X Index: 216



Y Index: 160

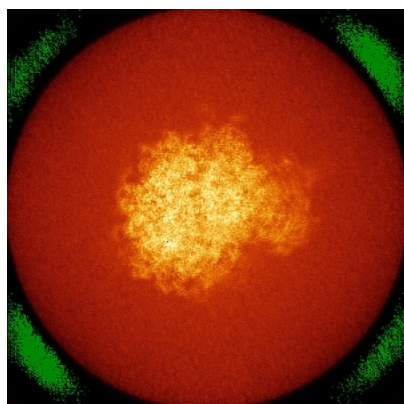


Z Index: 191

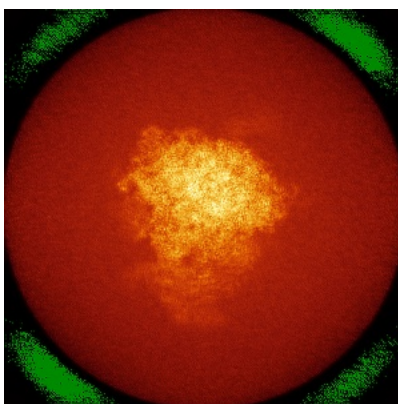
The images above show the largest variance slices of the map in three orthogonal directions.

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

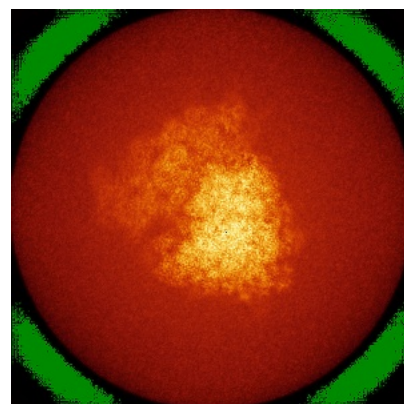
6.4.1 Primary map



X



Y

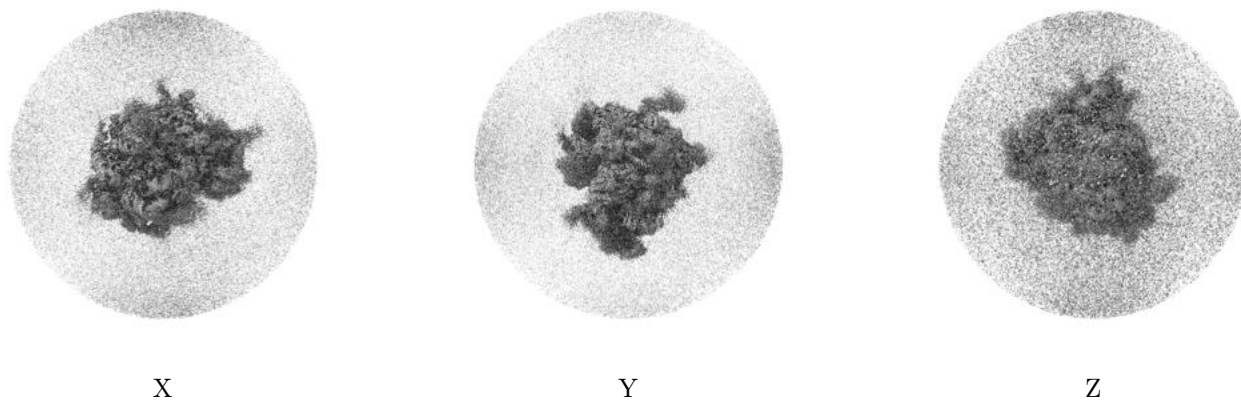


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

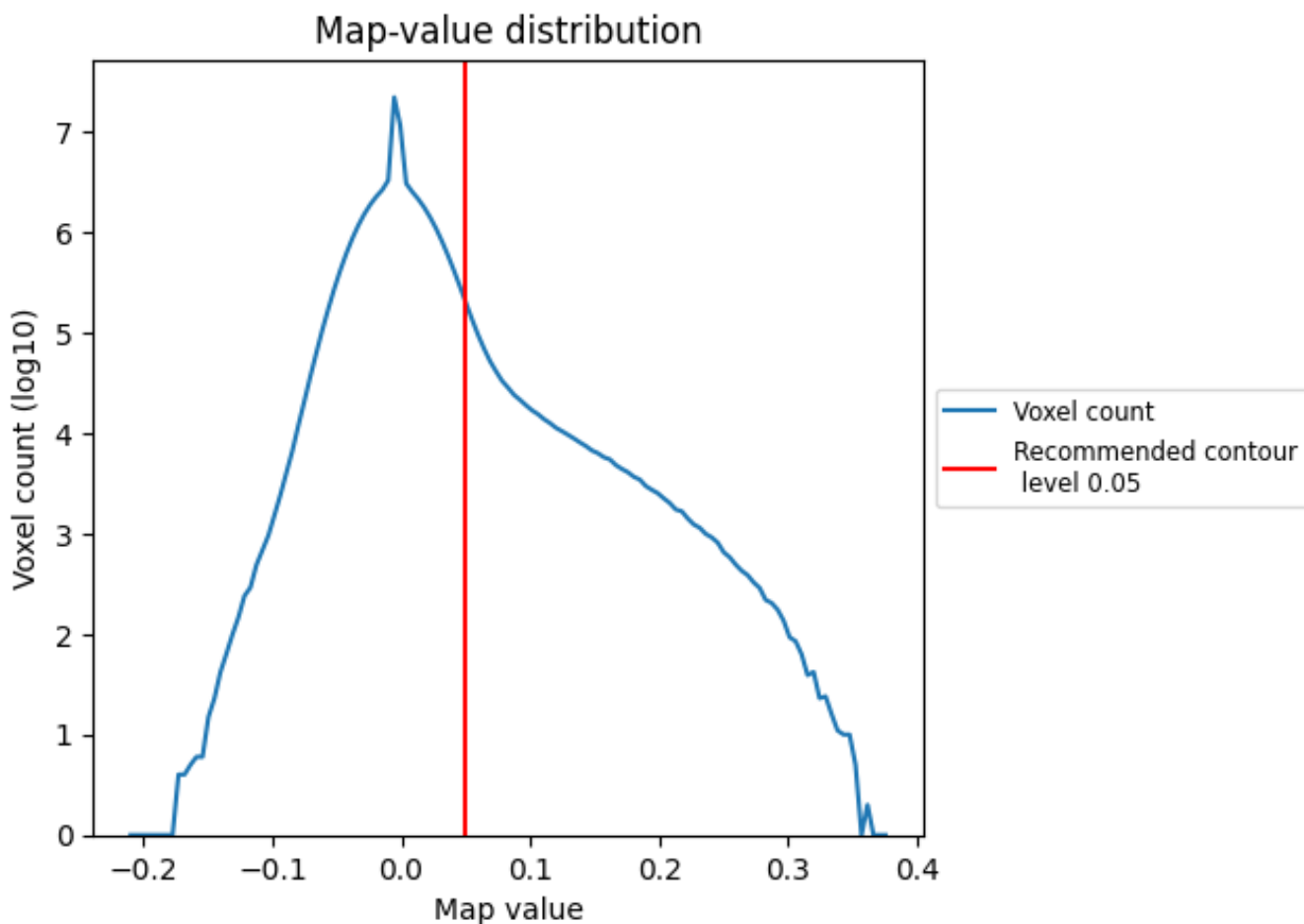
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

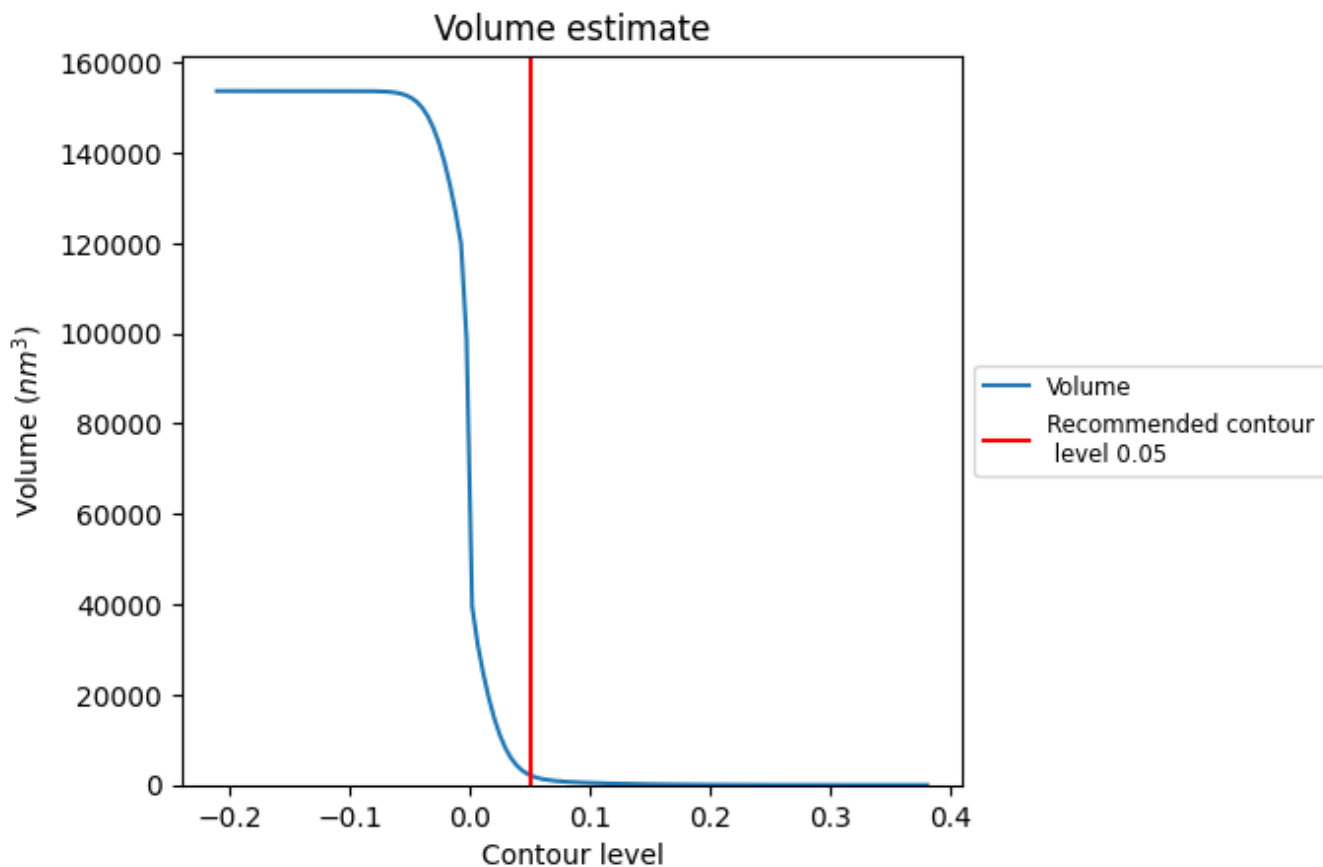
This section contains the results of statistical analysis of the map.

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.

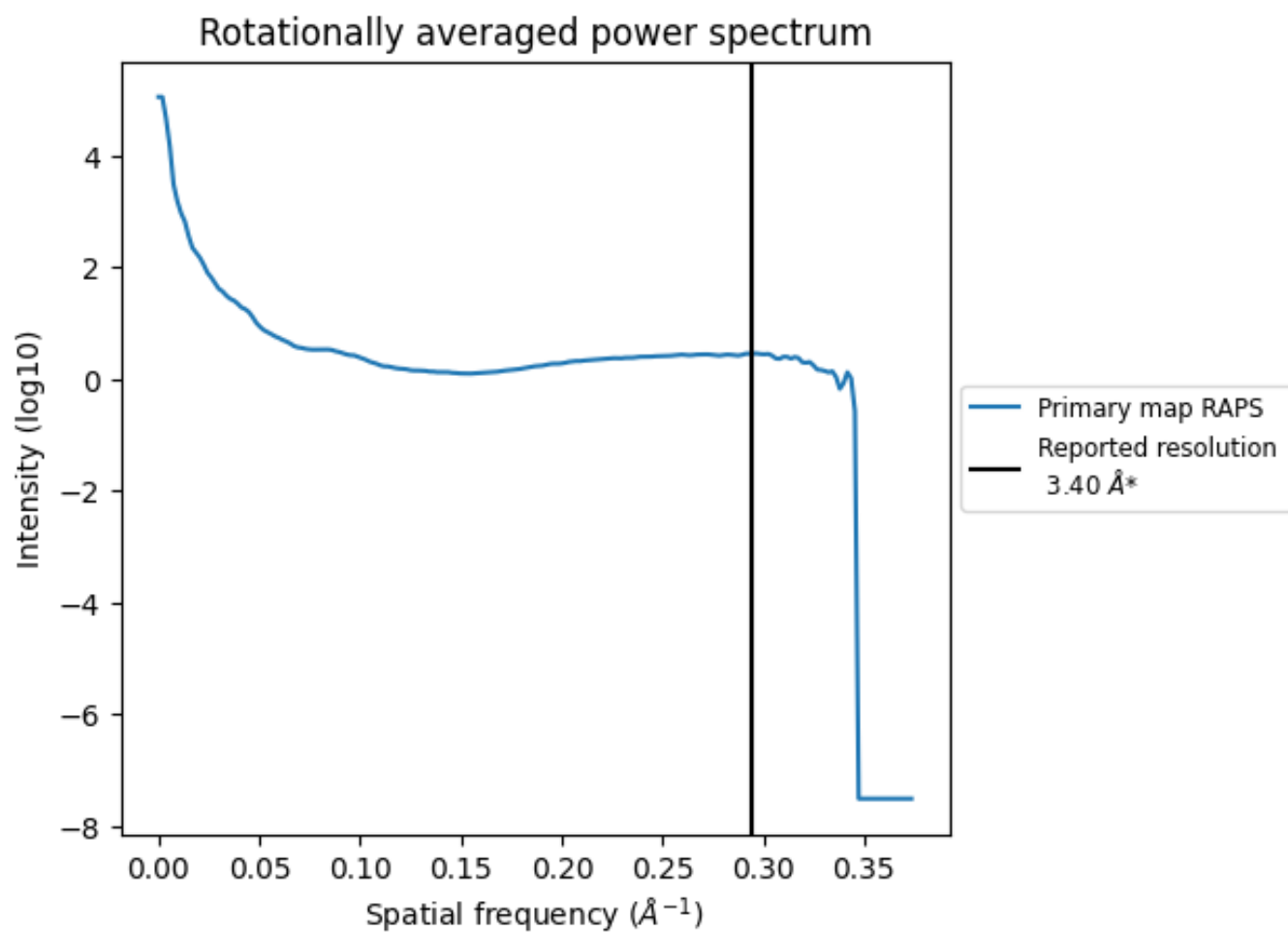
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 2230 nm³; this corresponds to an approximate mass of 2015 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 0.294 Å⁻¹

8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

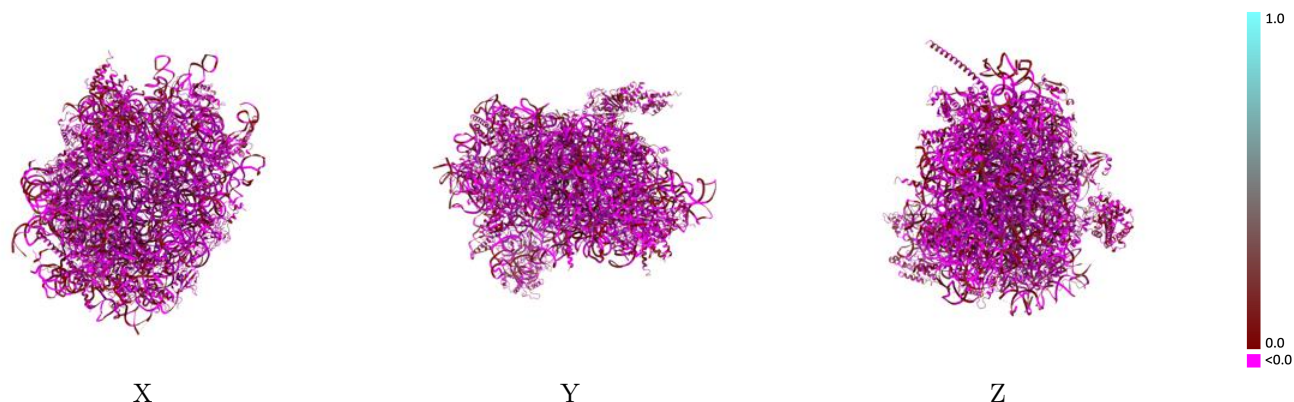
This section contains information regarding the fit between EMDB map EMD-14193 and PDB model 7QWS. Per-residue inclusion information can be found in section [3](#) on page [14](#).

9.1 Map-model overlay [i](#)



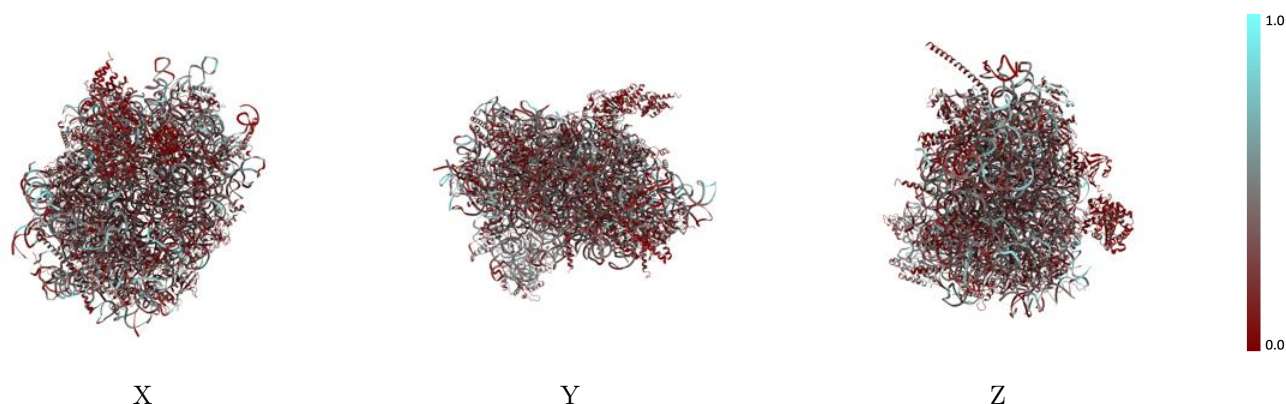
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



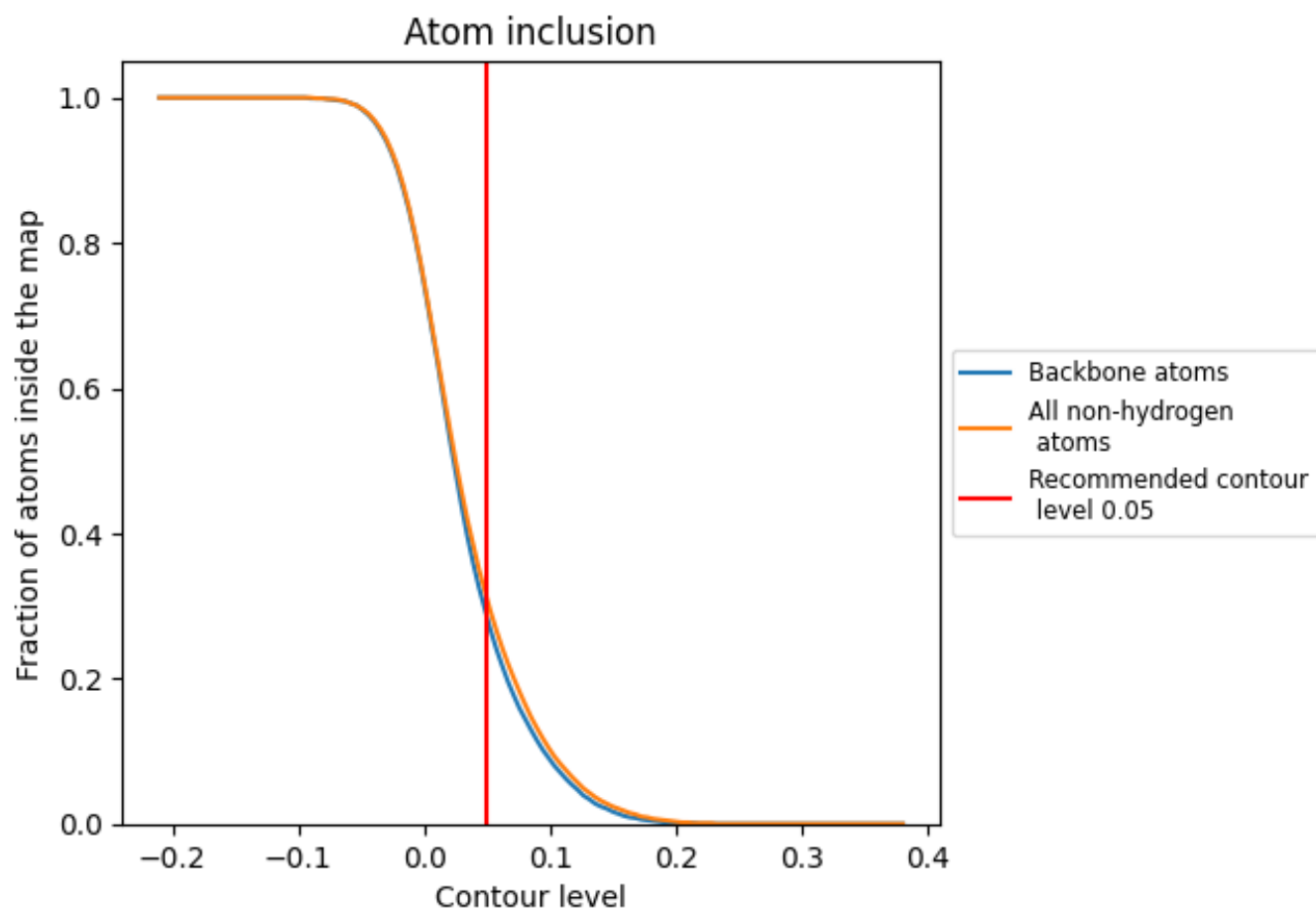
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 29% of all backbone atoms, 31% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3110	 -0.0540
5	 0.3640	 -0.0470
7	 0.4800	 -0.0430
8	 0.3490	 -0.0470
A	 0.1850	 -0.1200
B	 0.2390	 -0.0850
C	 0.2460	 -0.0870
D	 0.3320	 -0.0080
E	 0.2240	 -0.0540
F	 0.2520	 -0.0690
G	 0.2300	 -0.0470
H	 0.2020	 -0.0740
I	 0.2350	 -0.0640
J	 0.2660	 -0.0140
K	 0.1280	 0.0050
L	 0.2650	 -0.0490
M	 0.2820	 -0.0520
N	 0.2230	 -0.1060
O	 0.2550	 -0.0560
P	 0.2270	 -0.0920
Q	 0.2150	 -0.0930
R	 0.2220	 -0.0910
S	 0.2450	 -0.0600
T	 0.2210	 -0.0440
U	 0.3290	 0.0040
V	 0.1770	 -0.0990
W	 0.2120	 -0.0840
X	 0.2520	 -0.0870
Y	 0.2350	 -0.1150
Z	 0.2730	 -0.0520
a	 0.2430	 -0.0830
b	 0.2460	 -0.0350
c	 0.2460	 -0.0670
d	 0.2240	 -0.0750
e	 0.2160	 -0.1000



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Chain	Atom inclusion	Q-score
f	 0.2370	 -0.0820
g	 0.2070	 -0.0920
h	 0.2820	 -0.0570
i	 0.2550	 -0.0630
j	 0.2390	 -0.1050
k	 0.2530	 -0.0690
l	 0.1630	 -0.1180
m	 0.2070	 -0.0700
n	 0.1740	 -0.0650
o	 0.2200	 -0.0770
p	 0.2350	 -0.0670
r	 0.2400	 -0.1050
s	 0.0750	 0.0350
t	 0.0410	 0.0100
u	 0.0580	 0.0090