Full wwPDB EM Validation Report ⓘ

Mar 17, 2022 – 07:29 pm GMT

PDB ID	:	7QWS
EMDB ID	:	EMD-14193
Title	:	Structure of ribosome translating beta-tubulin in complex with TTC5 and NAC
Authors	:	Jomaa, A.; Gamerdinger, 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

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

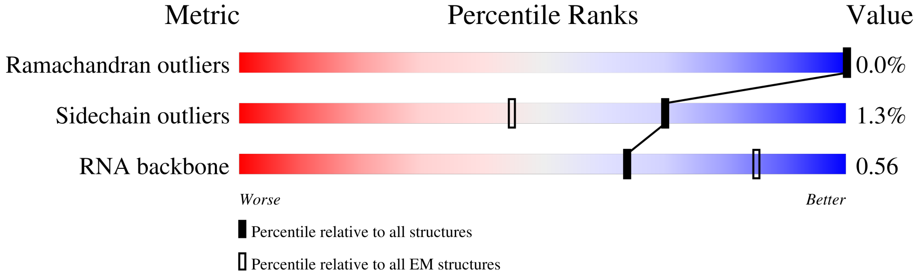
EMDB validation analysis	:	0.0.0.dev97
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.27

1 Overall quality at a glance ⓘ

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

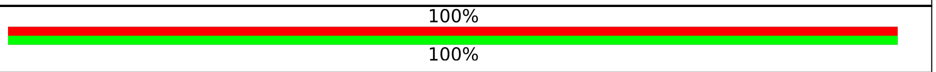
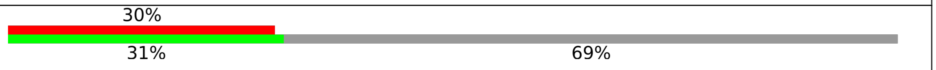
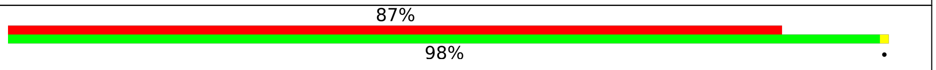
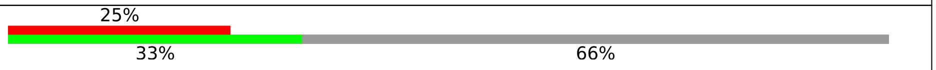
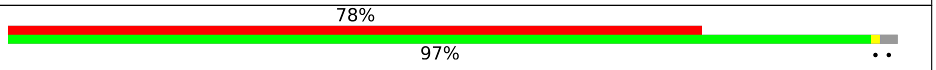
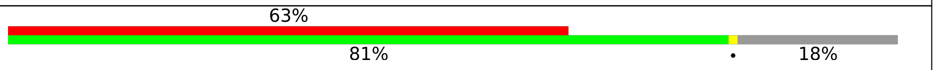
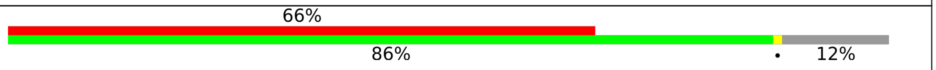
The reported resolution of this entry is 3.40 Å.

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 <=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	
2	t	215	
3	u	162	
4	A	245	
5	b	223	
6	B	403	
7	c	115	
8	C	413	

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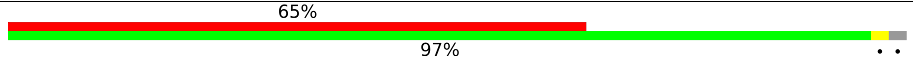
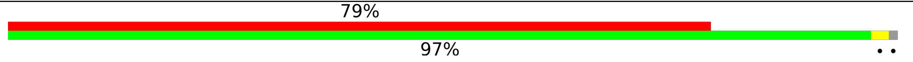
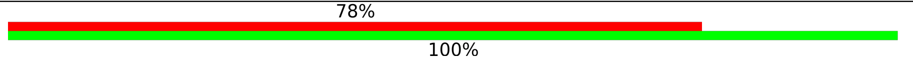
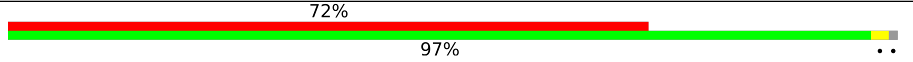
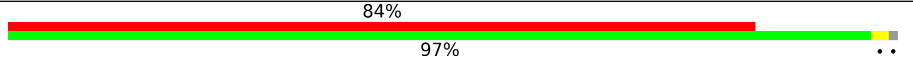
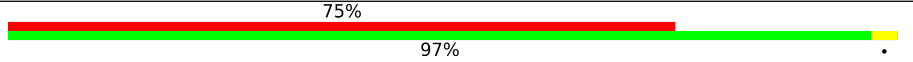
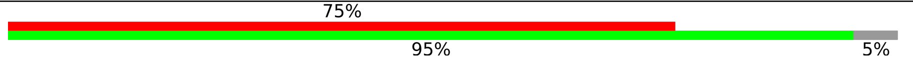
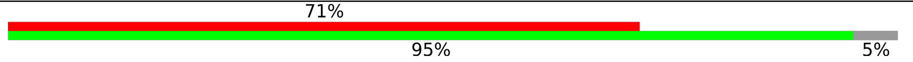
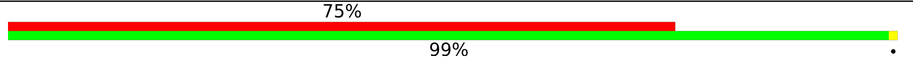
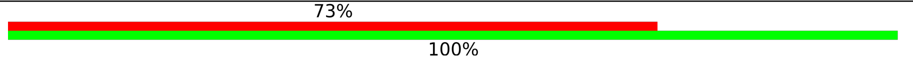
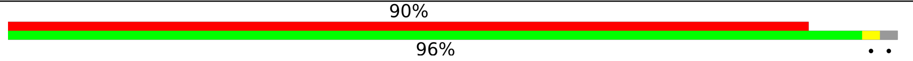
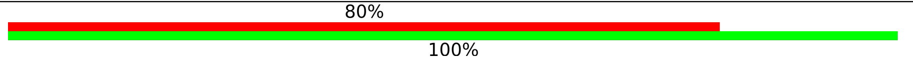
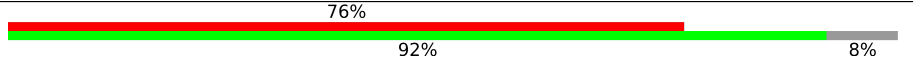
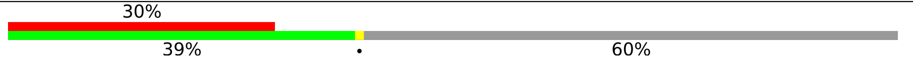
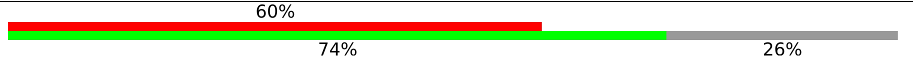
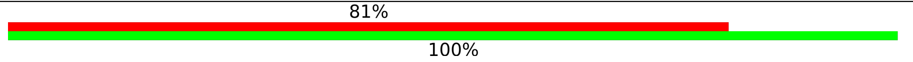
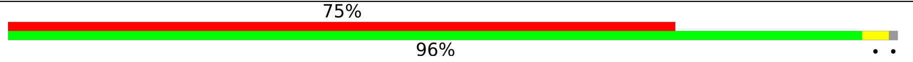
Mol	Chain	Length	Quality of chain
9	d	125	
10	D	297	
11	e	157	
12	E	291	
13	f	110	
14	F	225	
15	g	129	
16	G	319	
17	h	123	
18	H	192	
19	i	102	
20	I	214	
21	j	97	
22	J	178	
23	k	69	
24	L	210	
25	l	51	
26	M	218	
27	m	128	
28	N	204	
29	n	25	
30	O	500	
31	o	141	
32	P	153	
33	p	92	

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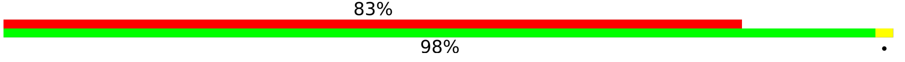
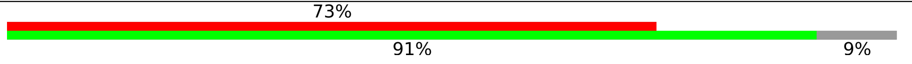
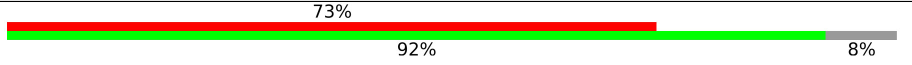
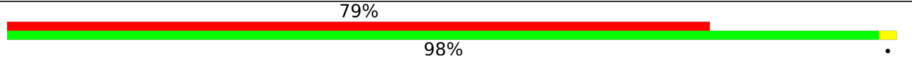
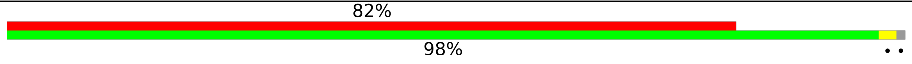
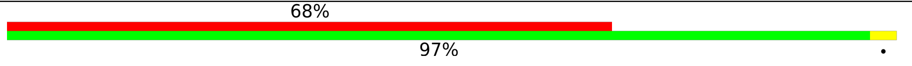
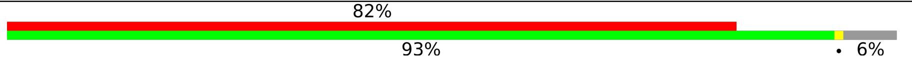
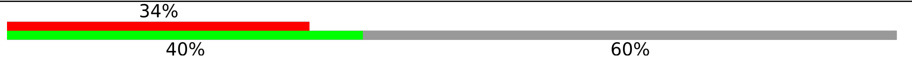
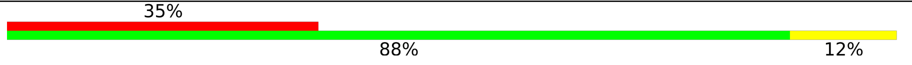
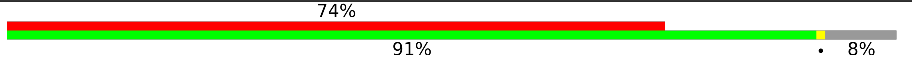
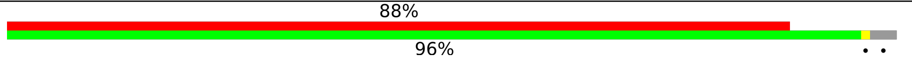
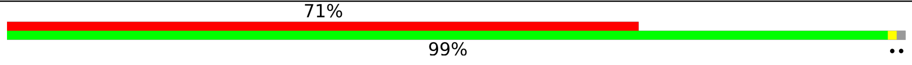
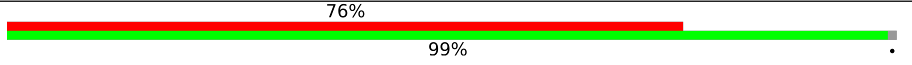
Mol	Chain	Length	Quality of chain
34	Q	187	
35	r	137	
36	R	196	
37	S	175	
38	T	160	
39	U	105	
40	V	140	
41	W	157	
42	5	4754	
43	X	156	
44	7	120	
45	Y	145	
46	8	156	
47	K	440	
48	Z	136	
49	a	148	

2 Entry composition ⓘ

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
5	b	75	Total 609	C 378	N 130	O 98	S 3	0	0

- Molecule 6 is a protein called Ribosomal protein L3.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	c	94	Total 732	C 465	N 130	O 131	S 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
20	I	204	Total 1655	C 1051	N 319	O 272	S 13	0	0

- Molecule 21 is a protein called Ribosomal protein L37.

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

- Molecule 22 is a protein called Ribosomal protein L11.

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

- Molecule 23 is a protein called Ribosomal protein L38.

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

- Molecule 24 is a protein called Ribosomal protein L13.

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

- Molecule 25 is a protein called Ribosomal protein L39.

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

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

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

- Molecule 27 is a protein called Ribosomal protein L40.

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

- Molecule 28 is a protein called Ribosomal protein L15.

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

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

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

- Molecule 30 is a protein called Ribosomal protein L13a.

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

- Molecule 31 is a protein called eL42.

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

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

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

- Molecule 33 is a protein called eL43.

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

- Molecule 34 is a protein called Ribosomal protein L18.

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

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

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

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

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

- Molecule 37 is a protein called Ribosomal protein L18a.

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

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

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

- Molecule 39 is a protein called Ribosomal protein L22.

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

- Molecule 40 is a protein called Ribosomal protein L23.

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

- Molecule 41 is a protein called Ribosomal protein L24.

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

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

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

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

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

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

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

- Molecule 45 is a protein called Ribosomal protein L26.

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

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

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

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

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

- 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
			Total	Zn	
50	g	1	1	1	0
50	j	1	1	1	0
50	m	1	1	1	0
50	o	1	1	1	0
50	p	1	1	1	0

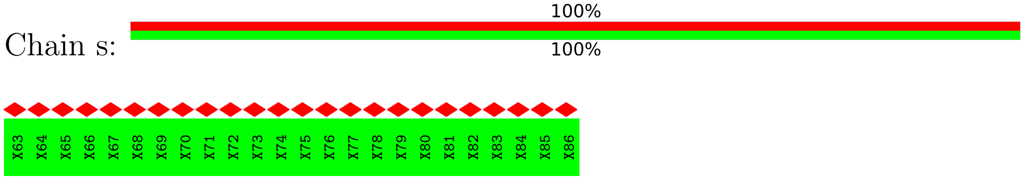
- Molecule 51 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

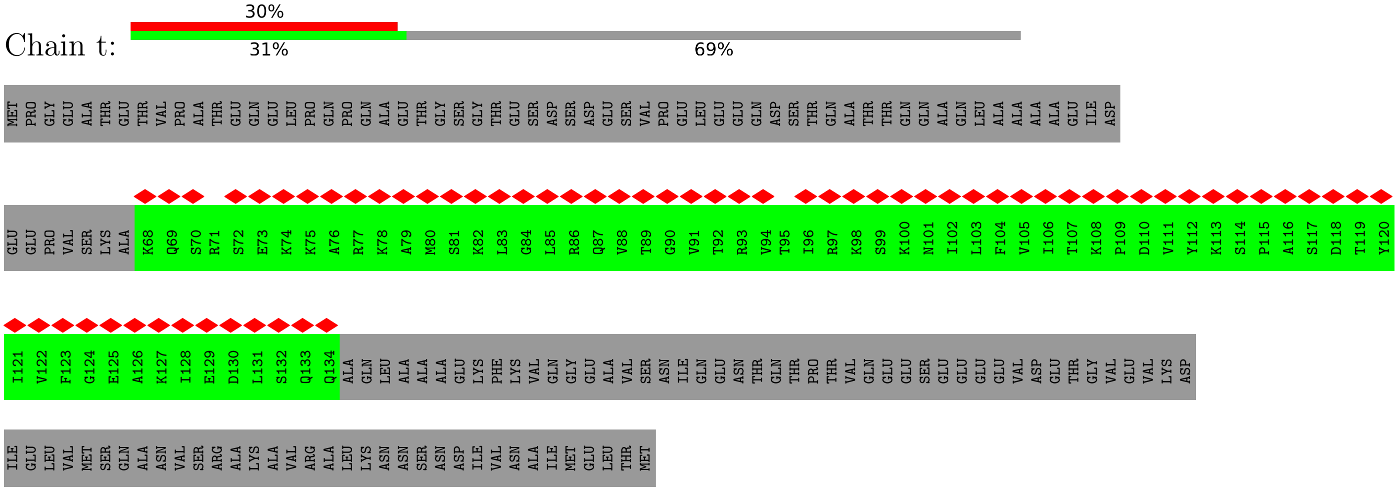
3 Residue-property plots ⓘ

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

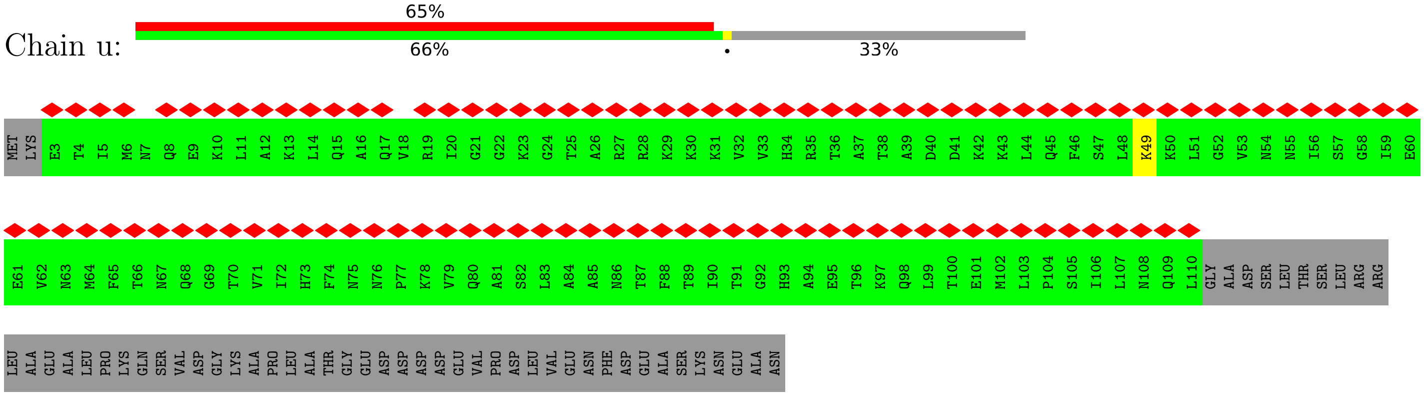
- Molecule 1: Nascent chain tubulin beta



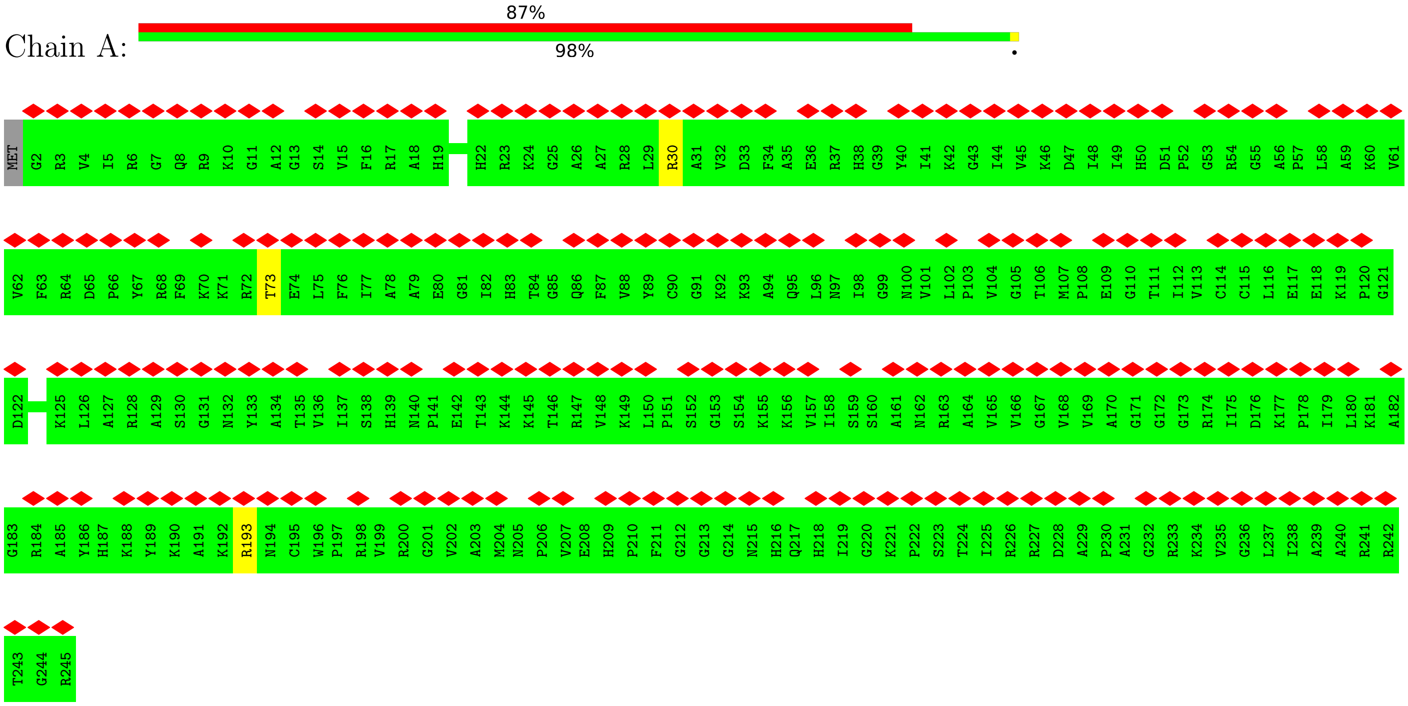
- Molecule 2: Nascent polypeptide-associated complex subunit alpha



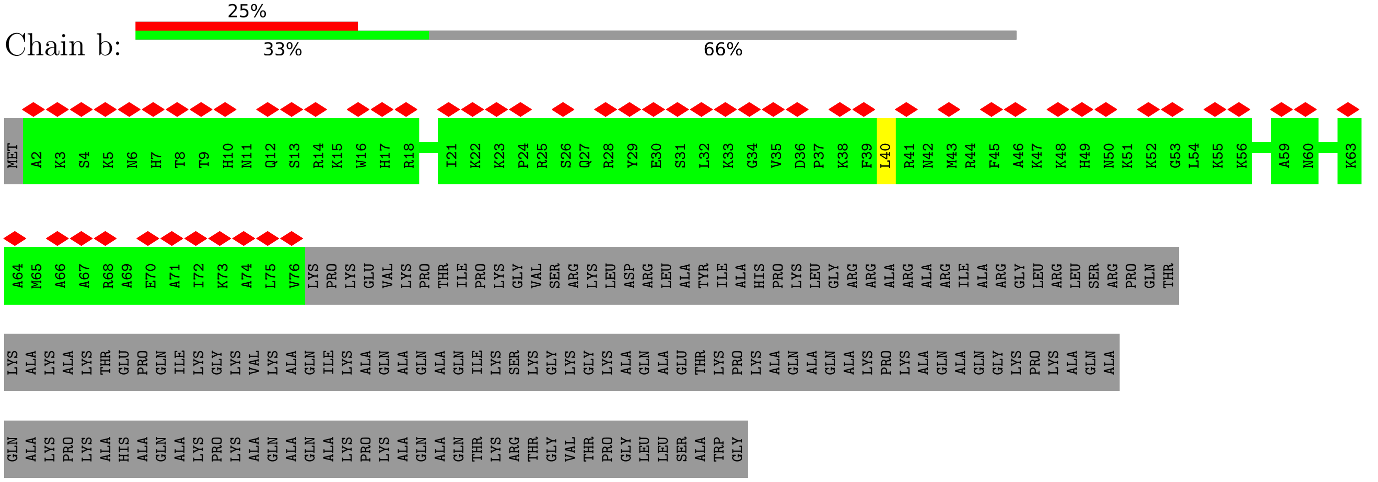
- Molecule 3: Transcription factor BTF3



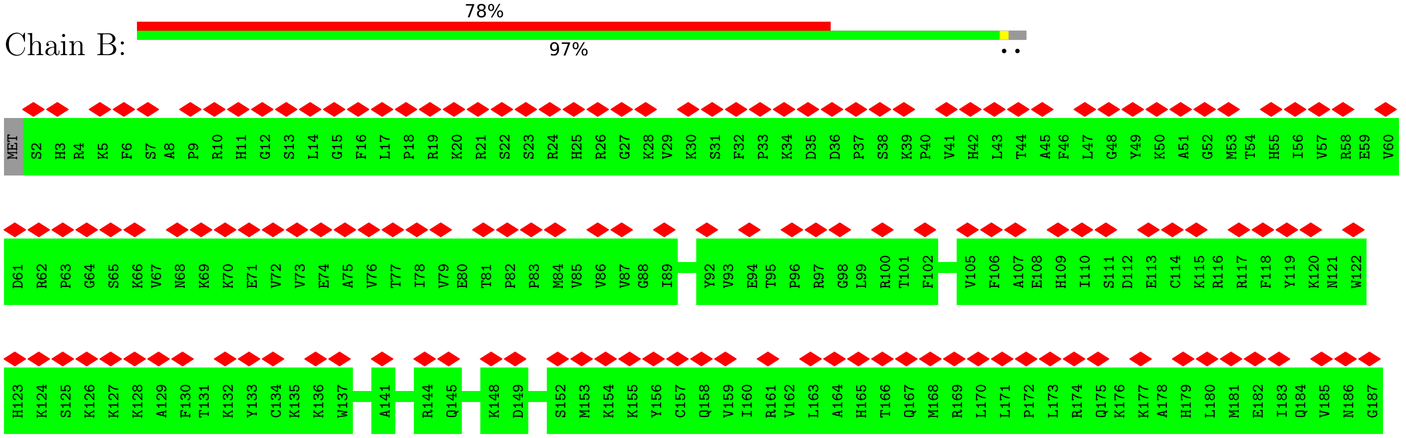
- Molecule 4: 60S ribosomal protein L8

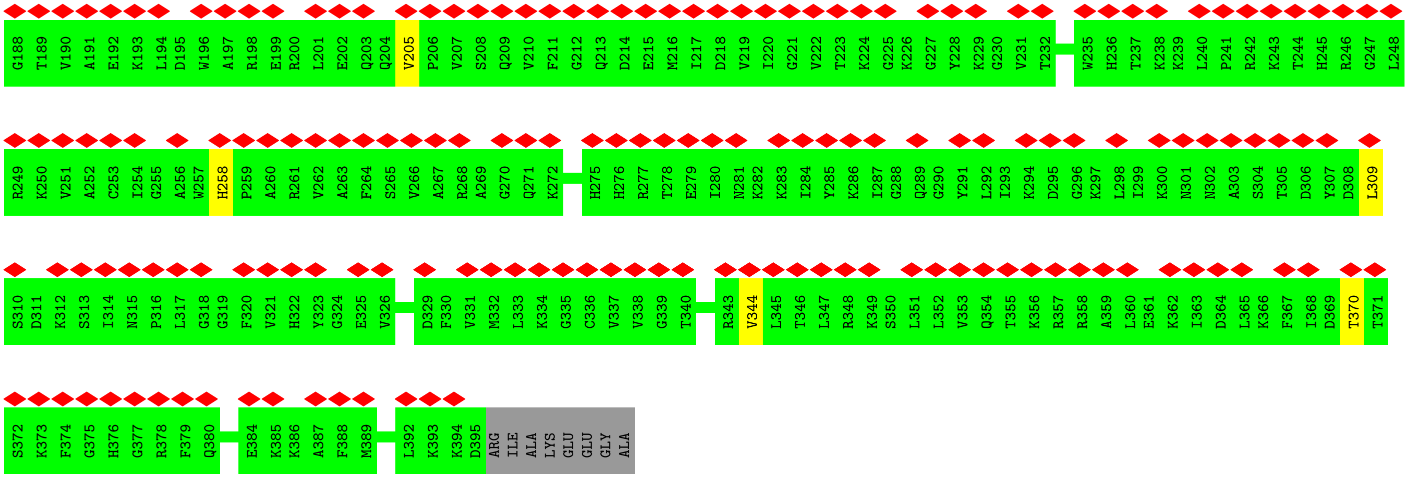


- Molecule 5: 60S ribosomal protein L29



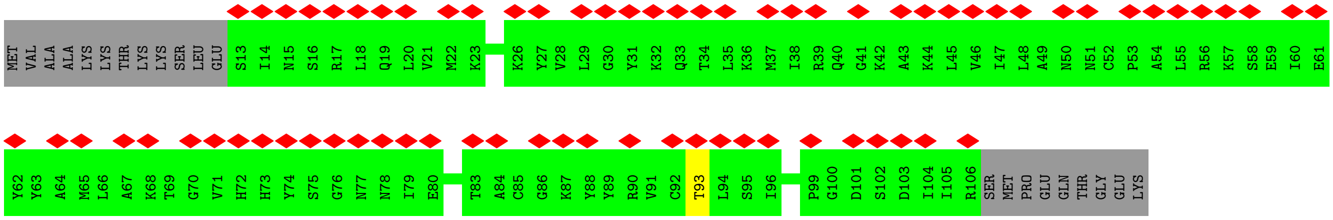
- Molecule 6: Ribosomal protein L3





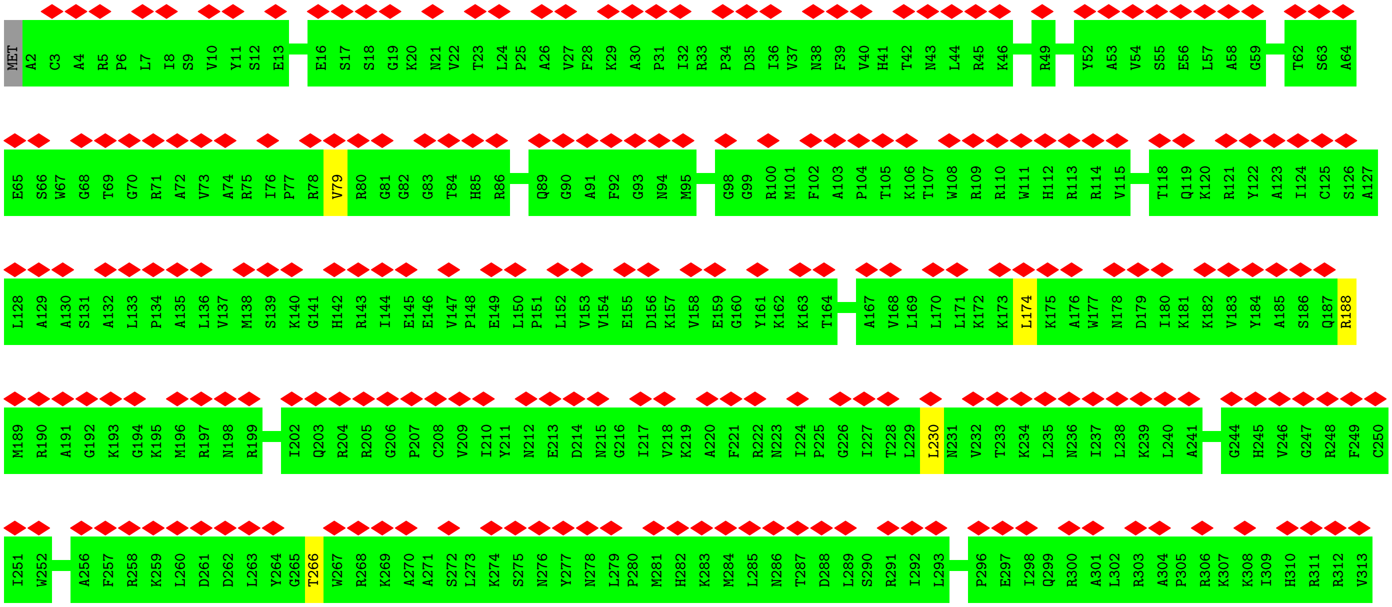
- Molecule 7: 60S ribosomal protein L30

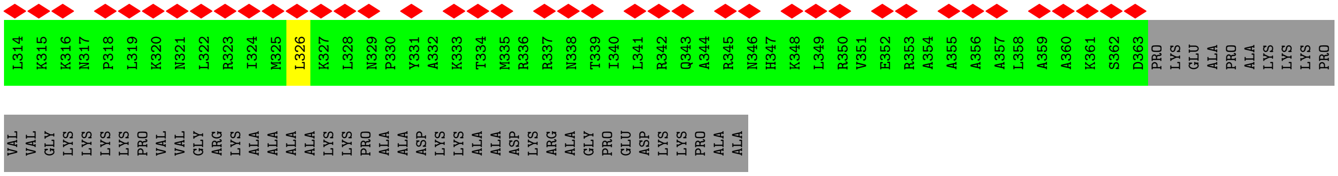
Chain c:



- Molecule 8: 60S ribosomal protein L4

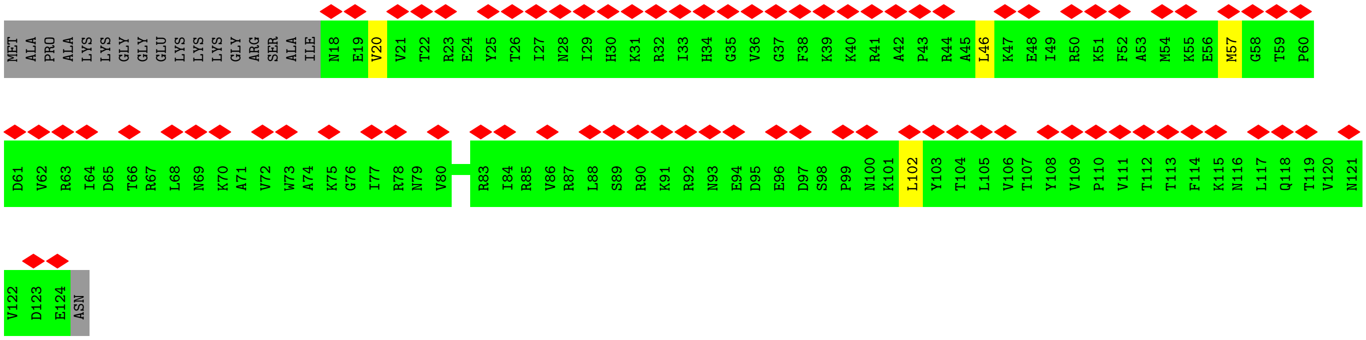
Chain C:





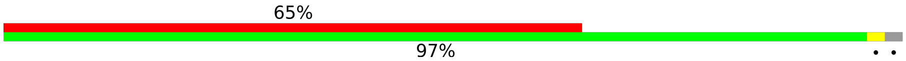
- Molecule 9: Ribosomal protein L31

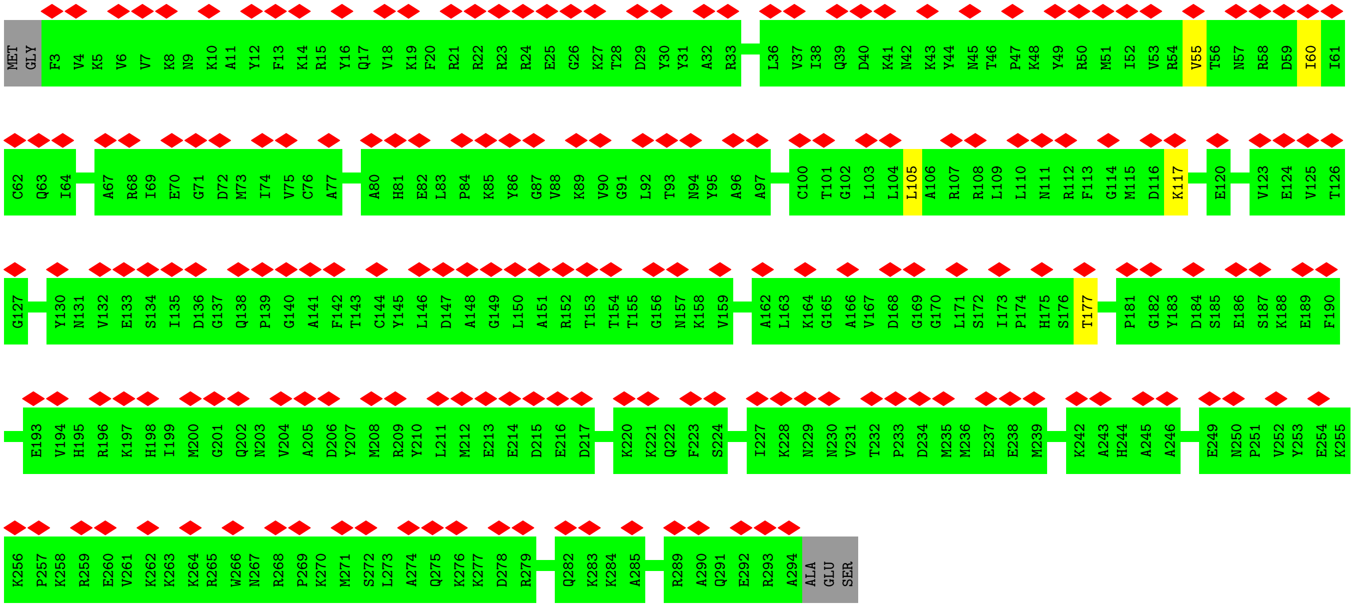
Chain d:



- Molecule 10: Ribosomal_L18_c domain-containing protein

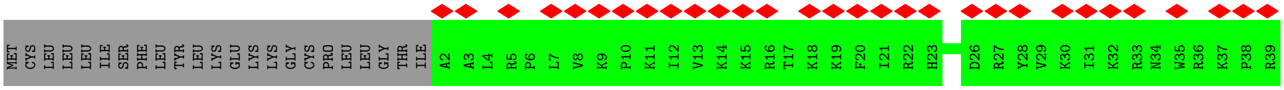
Chain D:

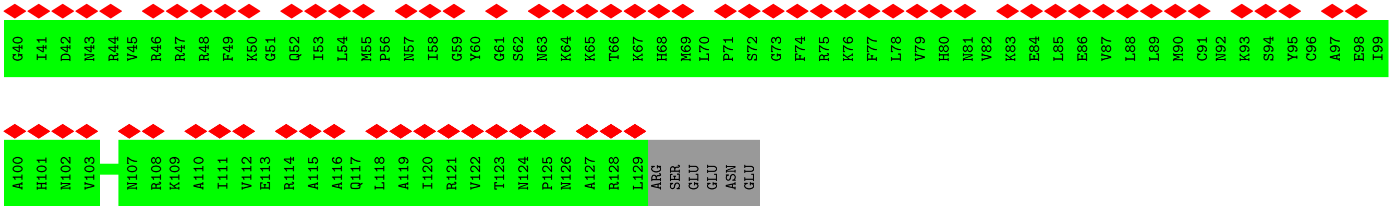




- Molecule 11: Ribosomal protein L32

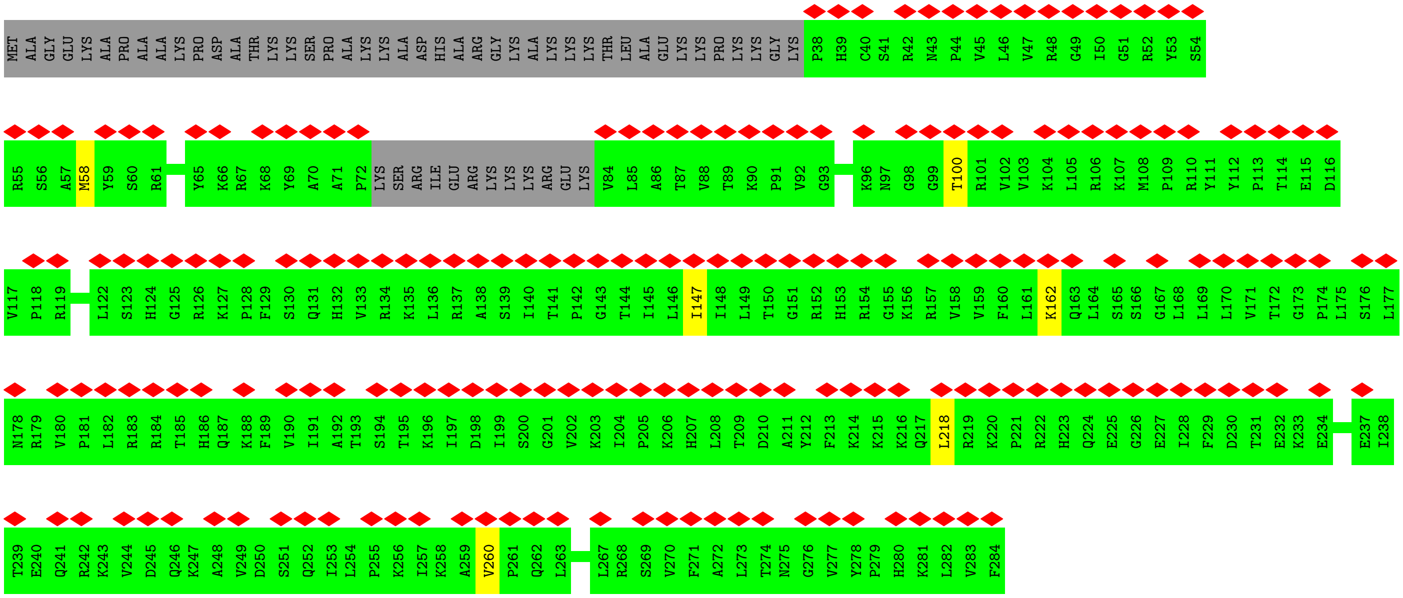
Chain e:





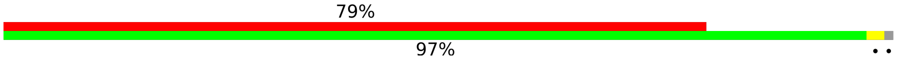
- Molecule 12: 60S ribosomal protein L6

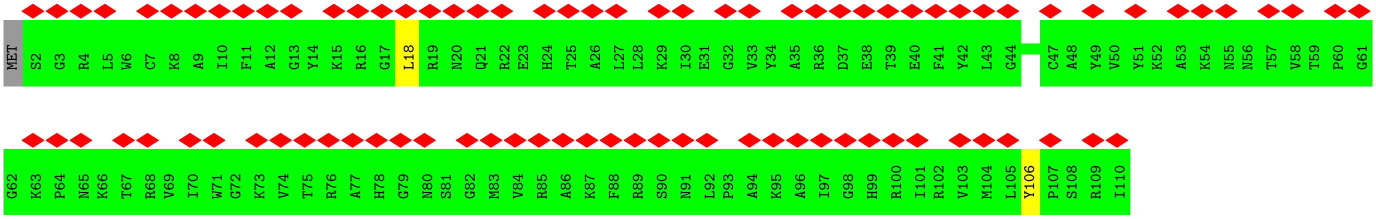
Chain E:



- Molecule 13: 60S ribosomal protein L35a

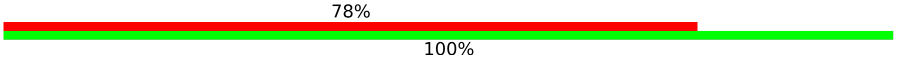
Chain f:

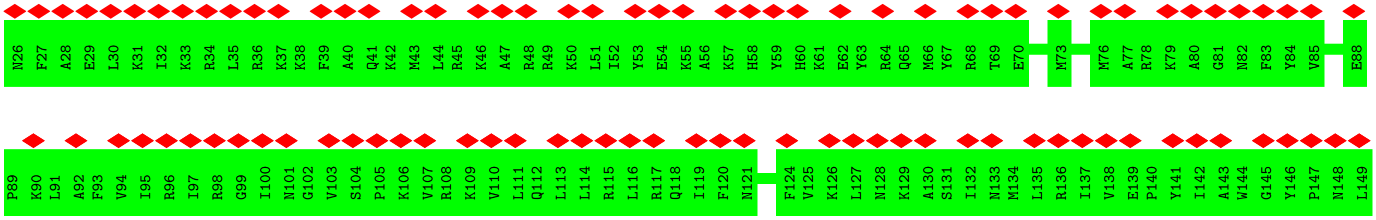


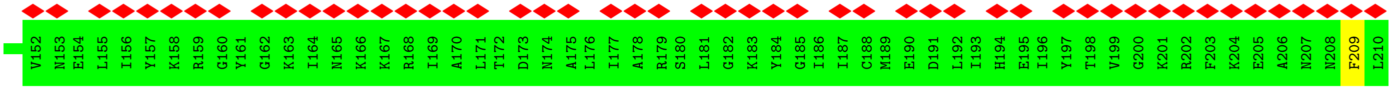


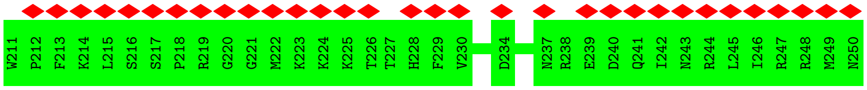
- Molecule 14: uL30

Chain F:



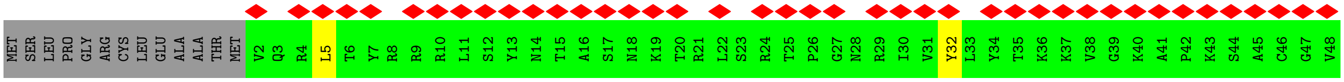


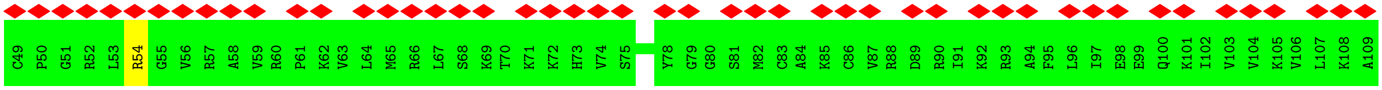


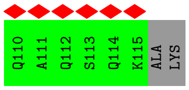


- Molecule 15: 60S ribosomal protein L34

Chain g:

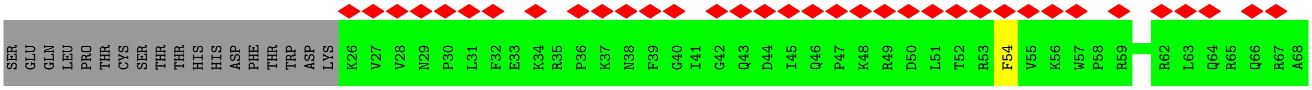


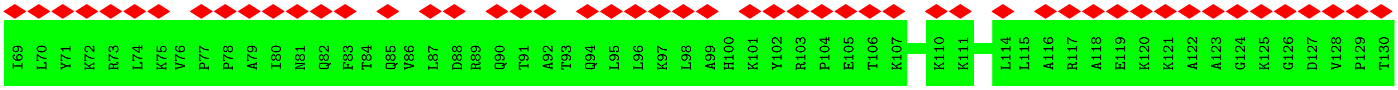


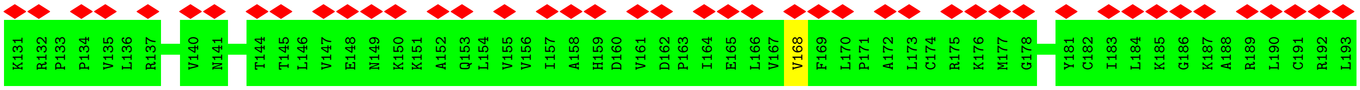


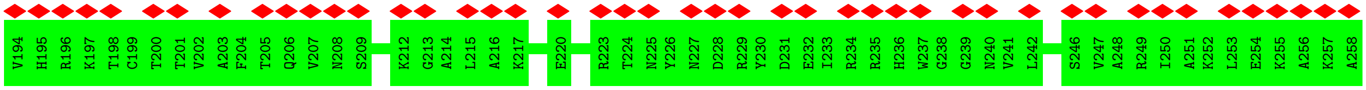
- Molecule 16: 60S ribosomal protein L7a

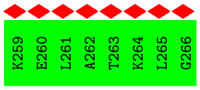
Chain G:





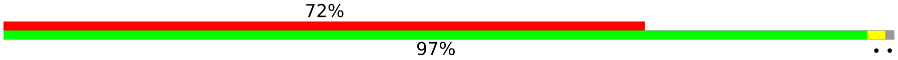


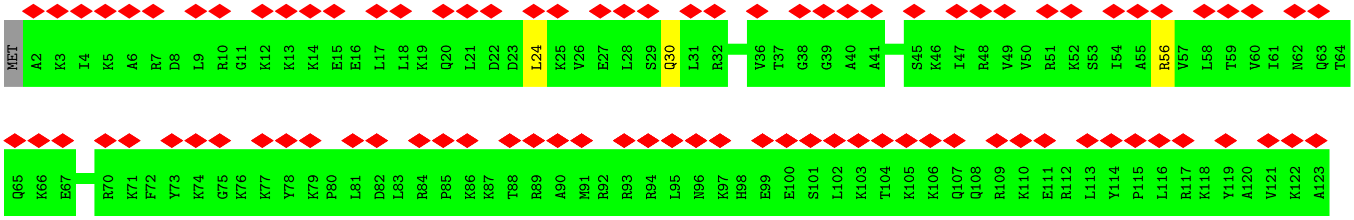




- Molecule 17: 60S ribosomal protein L35

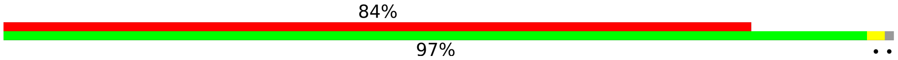
Chain h:

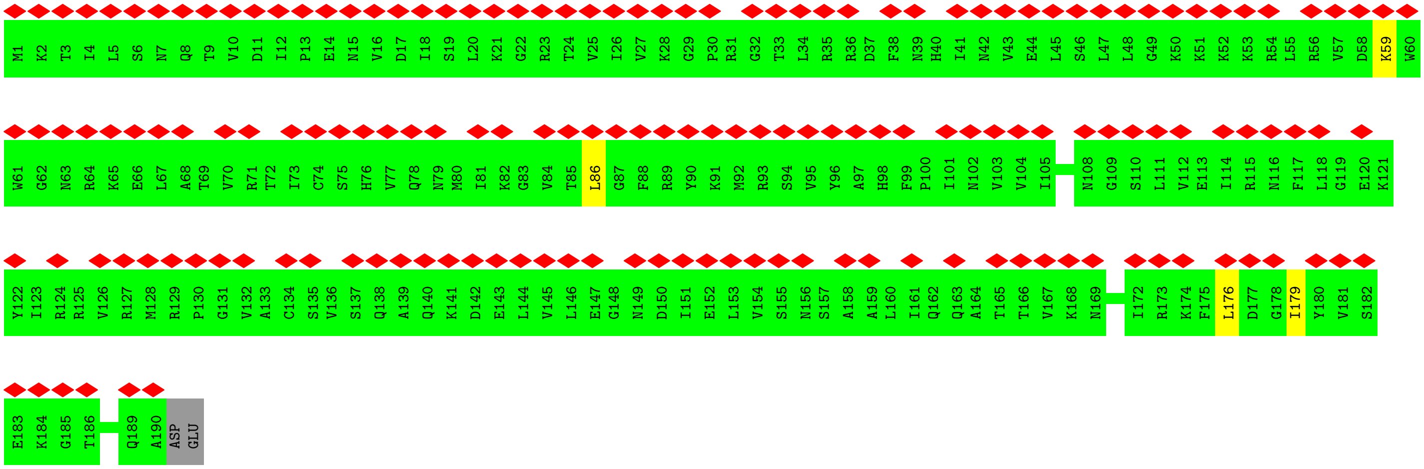




- Molecule 18: 60S ribosomal protein L9

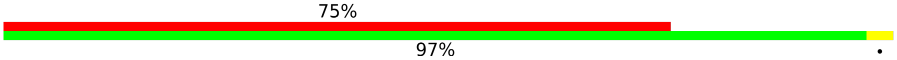
Chain H:

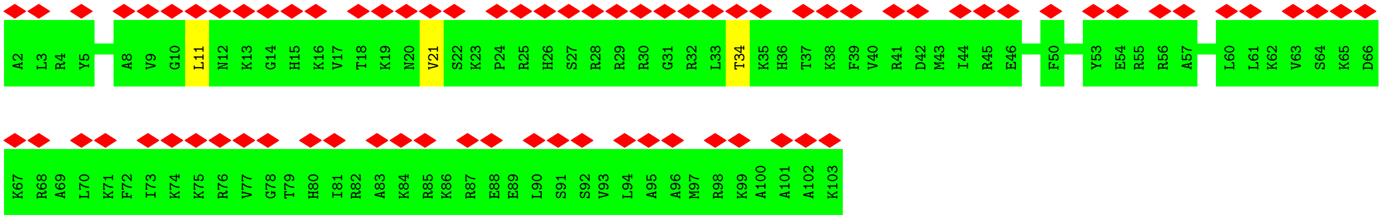




- Molecule 19: 60S ribosomal protein L36

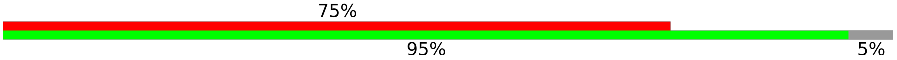
Chain i:

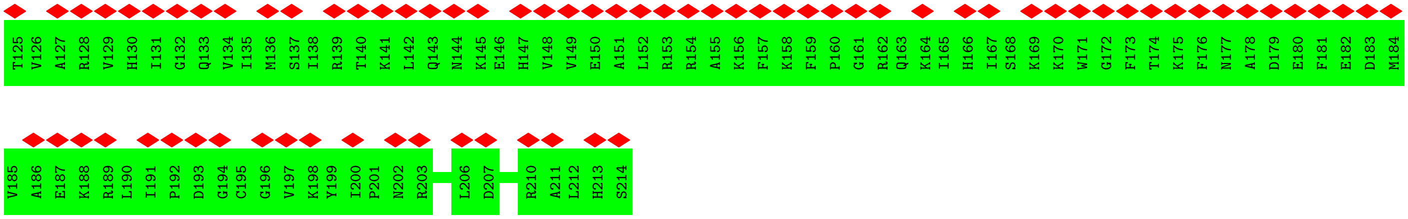




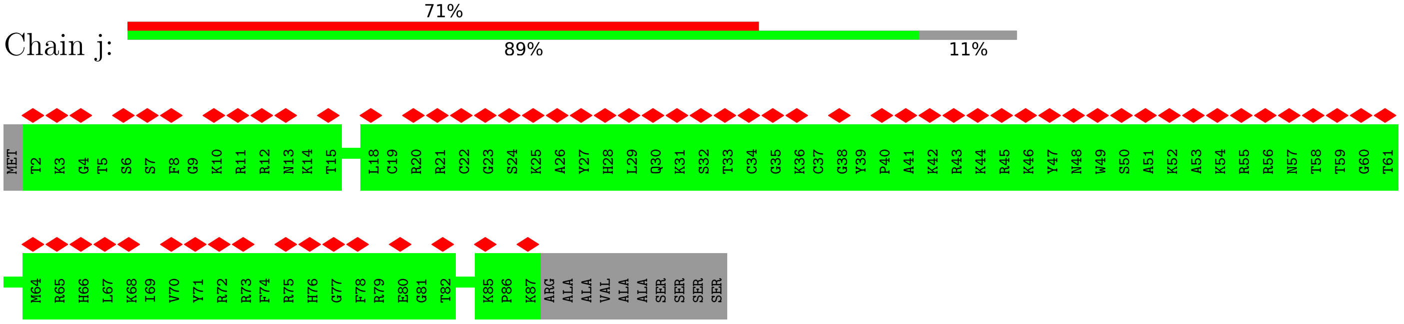
- Molecule 20: 60S ribosomal protein L10

Chain I:

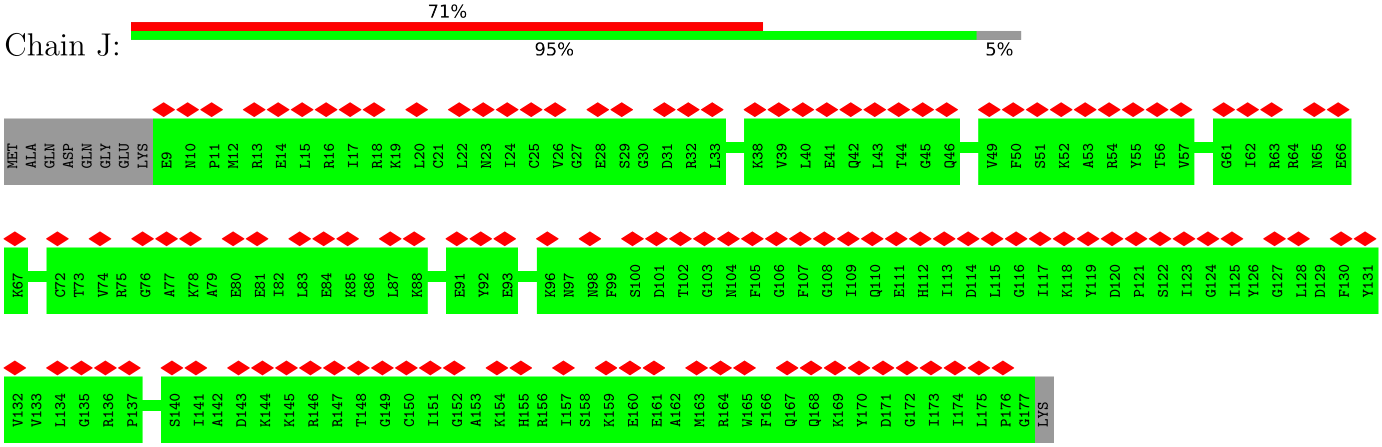




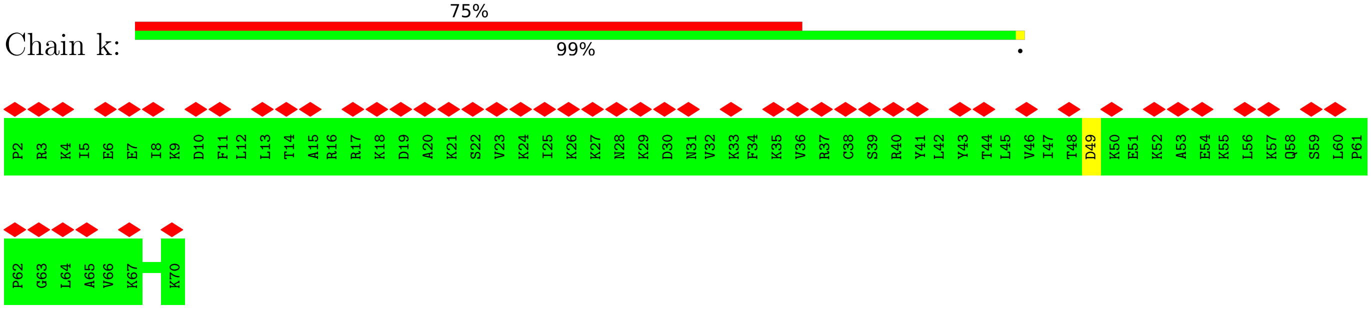
- Molecule 21: Ribosomal protein L37



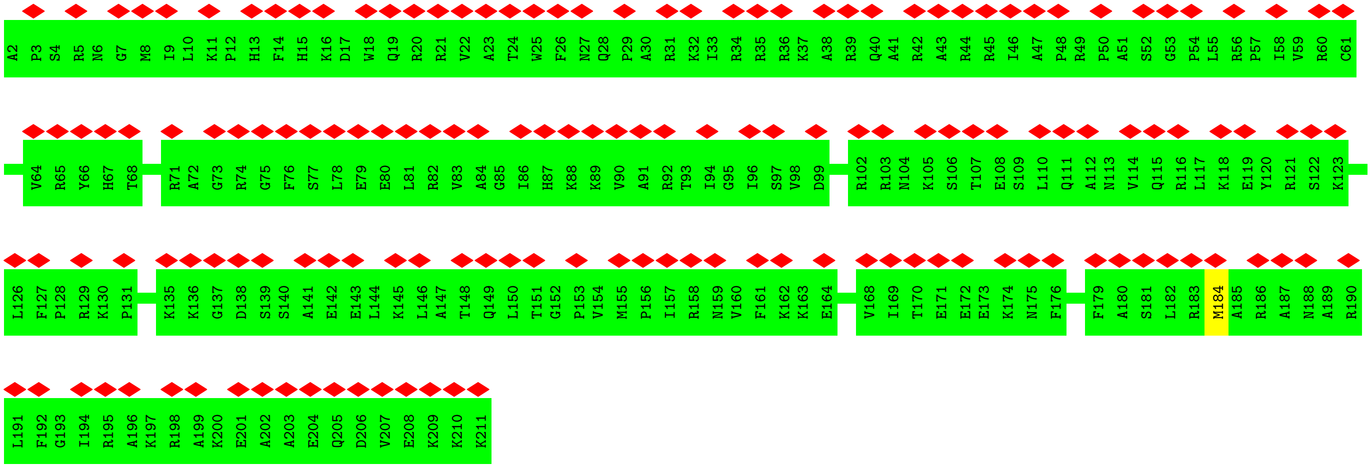
- Molecule 22: Ribosomal protein L11



- Molecule 23: Ribosomal protein L38

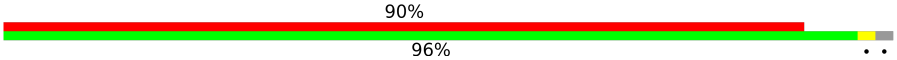


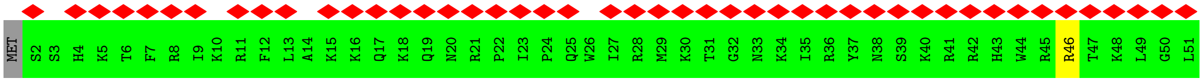
- Molecule 24: Ribosomal protein L13



- Molecule 25: Ribosomal protein L39

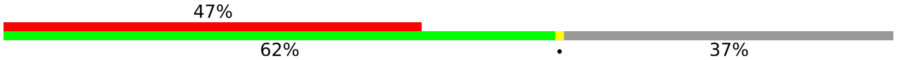
Chain l:

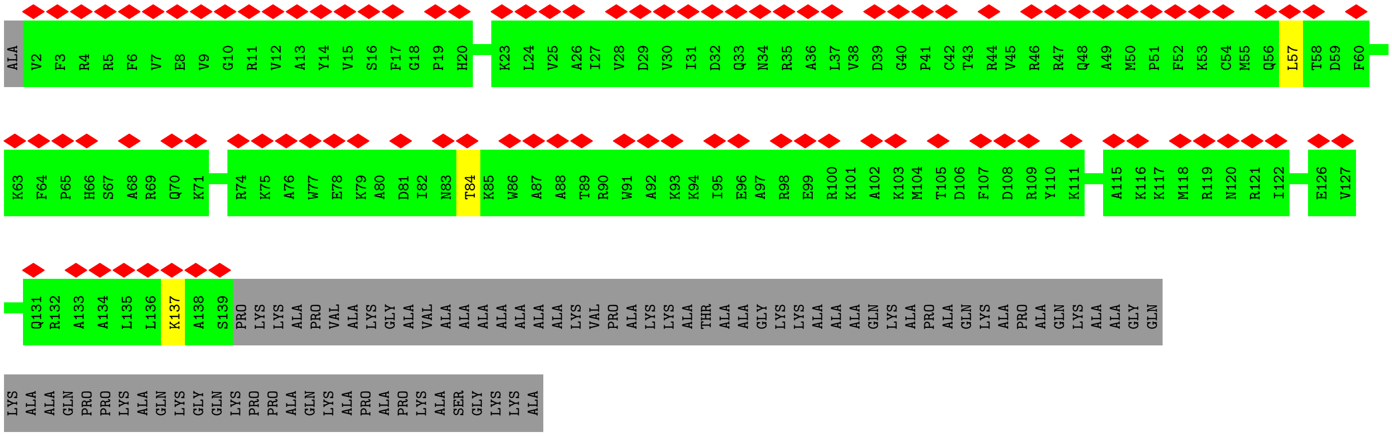




- Molecule 26: 60S ribosomal protein L14

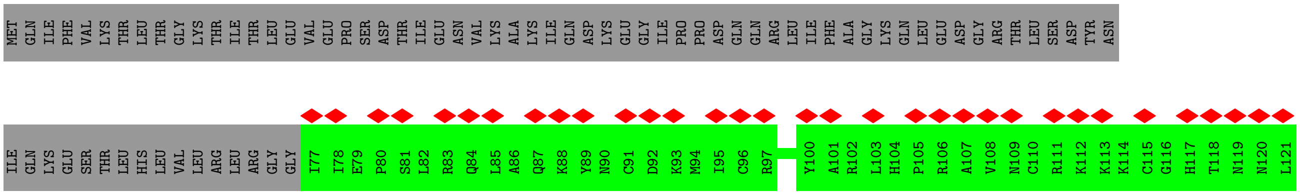
Chain M:

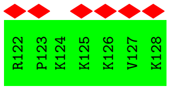




- Molecule 27: Ribosomal protein L40

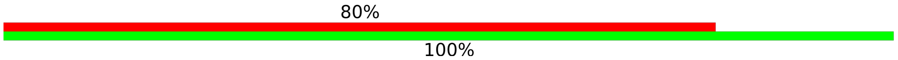
Chain m:





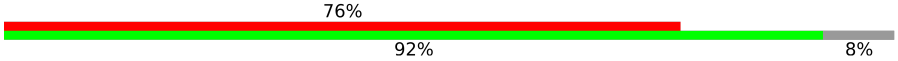
- Molecule 28: Ribosomal protein L15

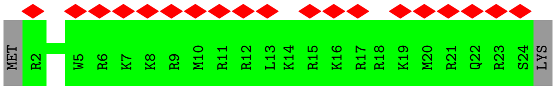
Chain N:



- Molecule 29: 60s ribosomal protein l41

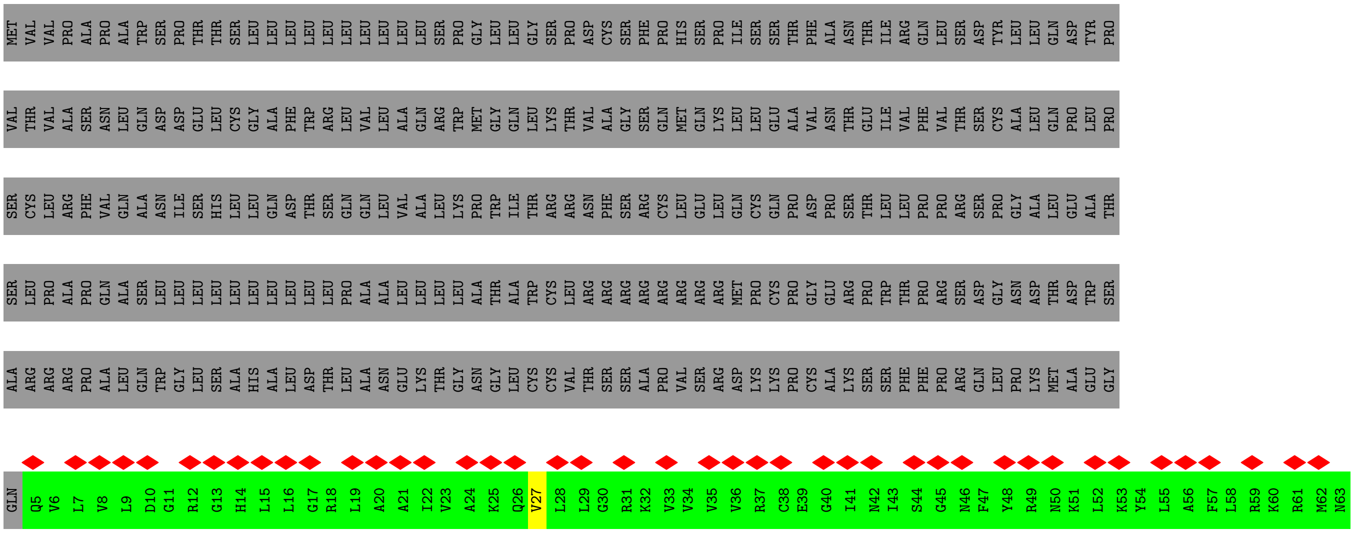
Chain n:

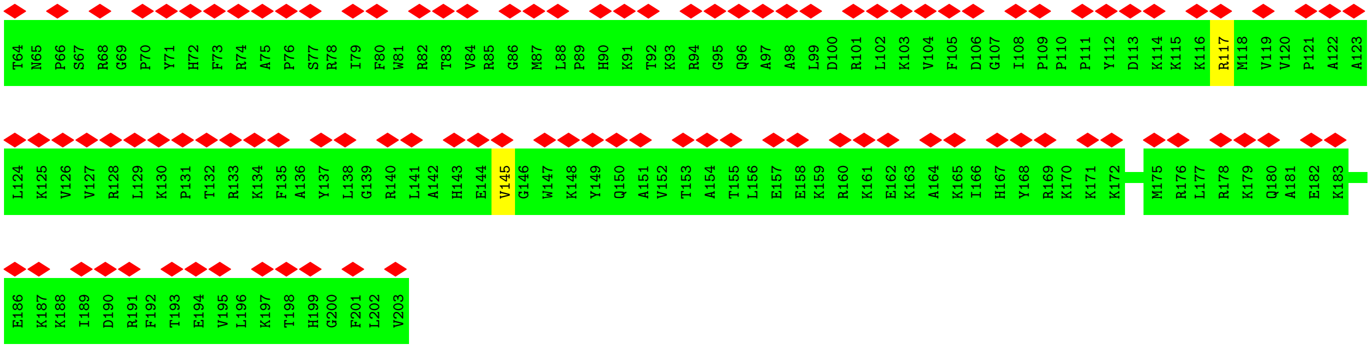




- Molecule 30: Ribosomal protein L13a

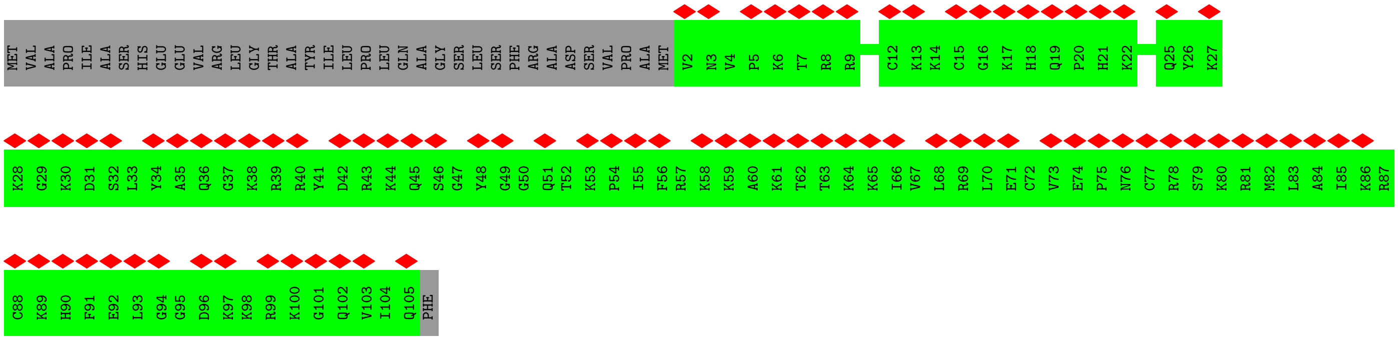
Chain O:





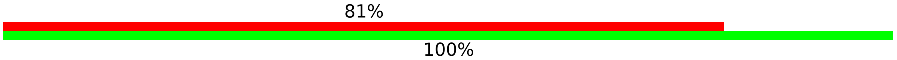
- Molecule 31: eL42

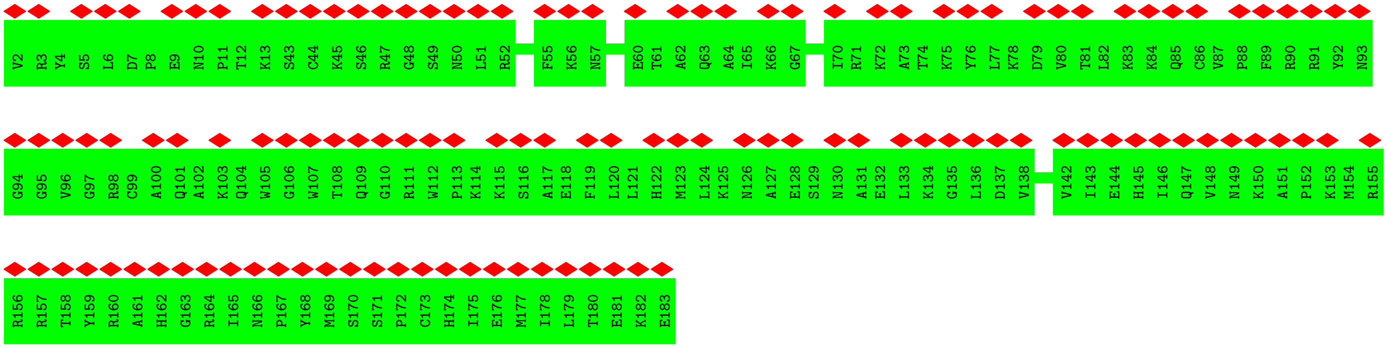
Chain o:



- Molecule 32: 60S ribosomal protein L17

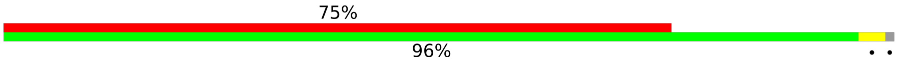
Chain P:

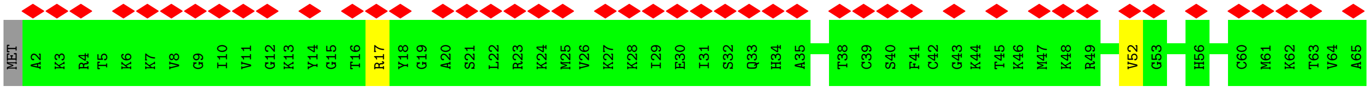


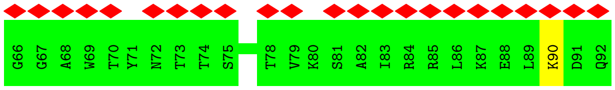


- Molecule 33: eL43

Chain p:







- Molecule 34: Ribosomal protein L18

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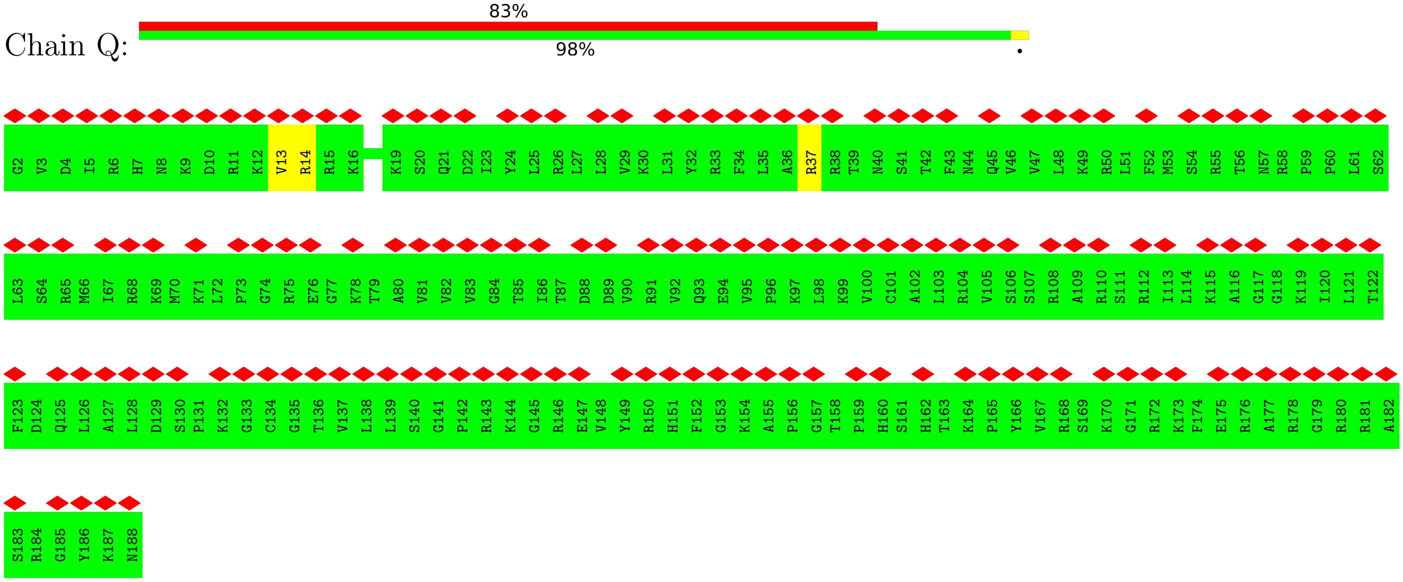

- Molecule 35: 60S ribosomal protein L28

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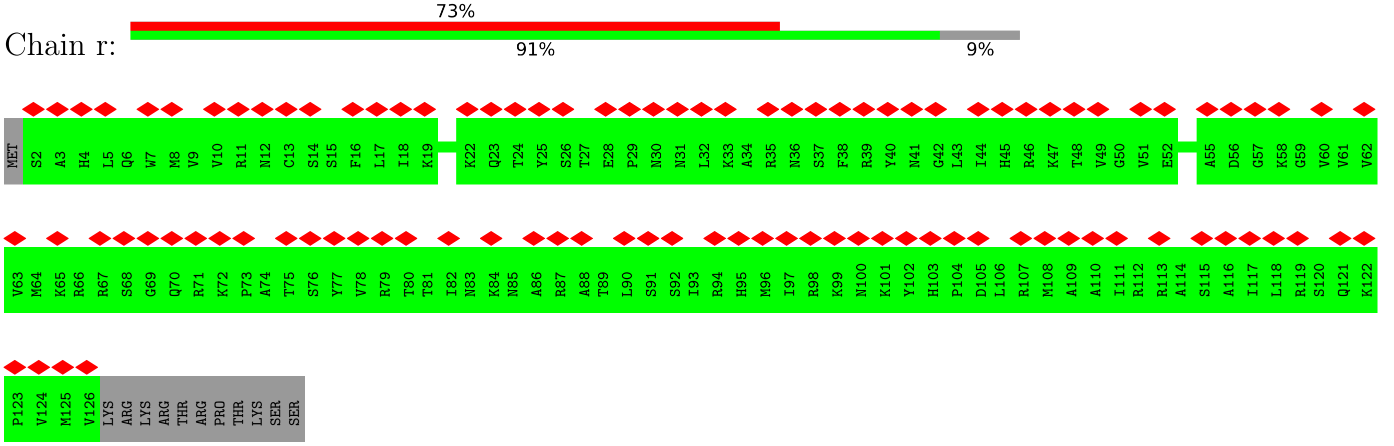

- Molecule 36: 60S ribosomal protein L19

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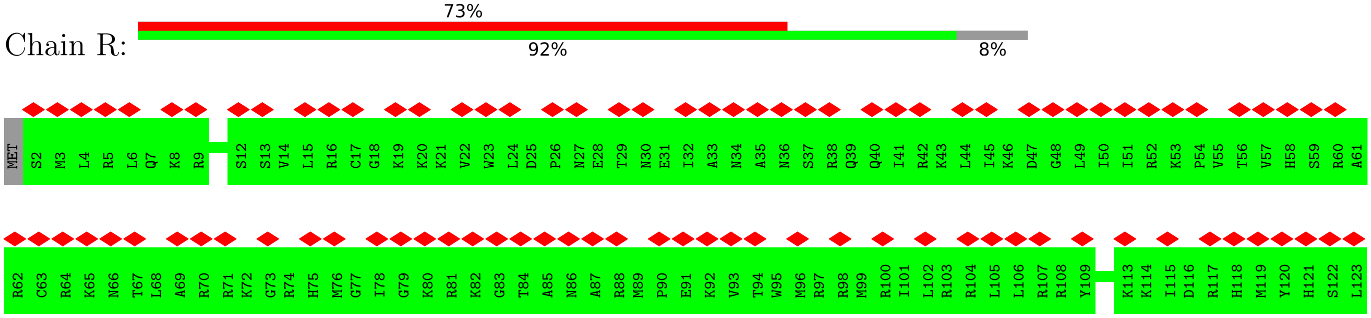

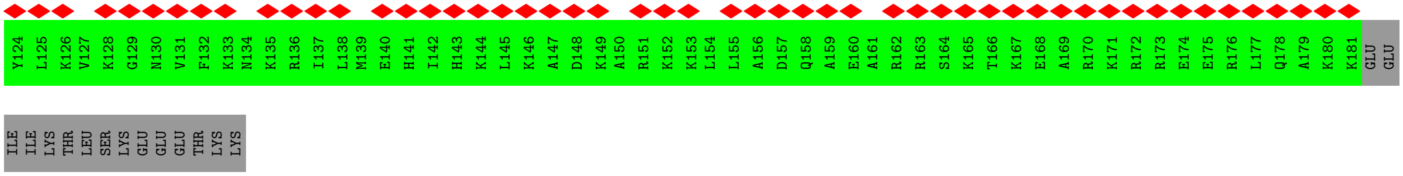

- Molecule 37: Ribosomal protein L18a

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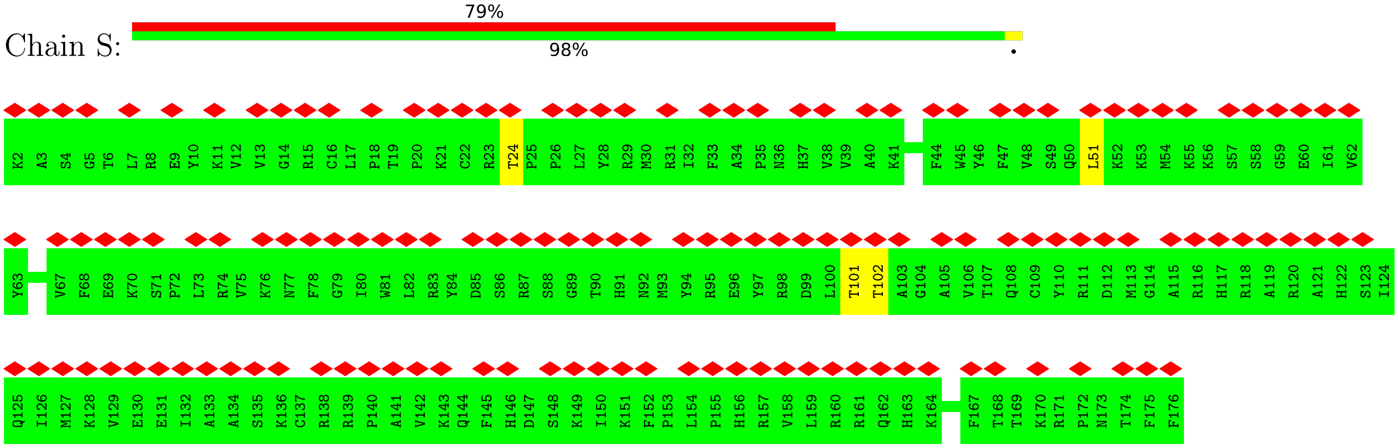

- Molecule 38: 60S ribosomal protein L21

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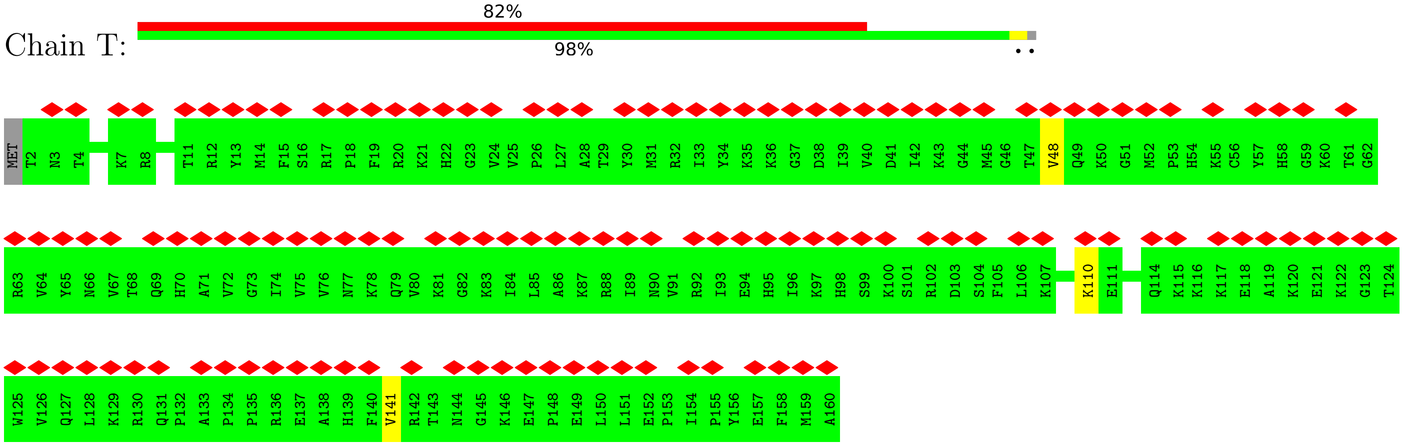

- Molecule 39: Ribosomal protein L22

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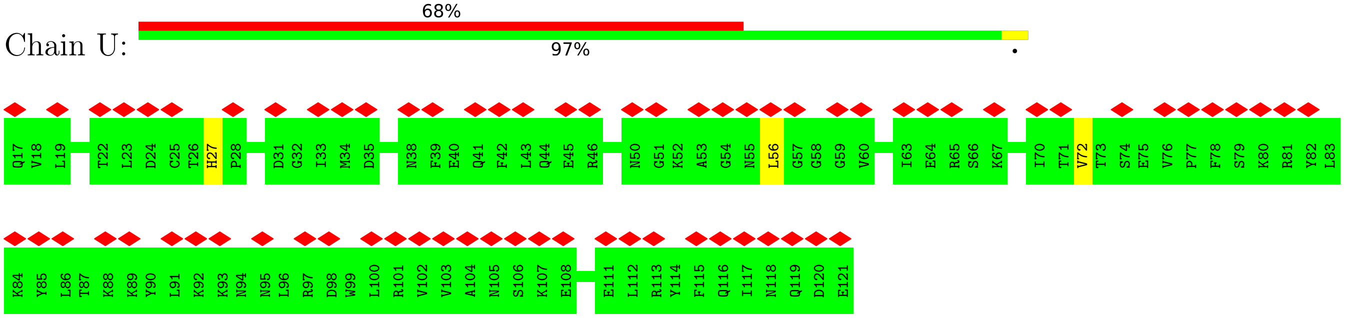

- Molecule 40: Ribosomal protein L23

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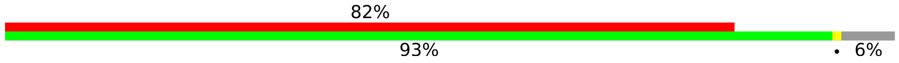

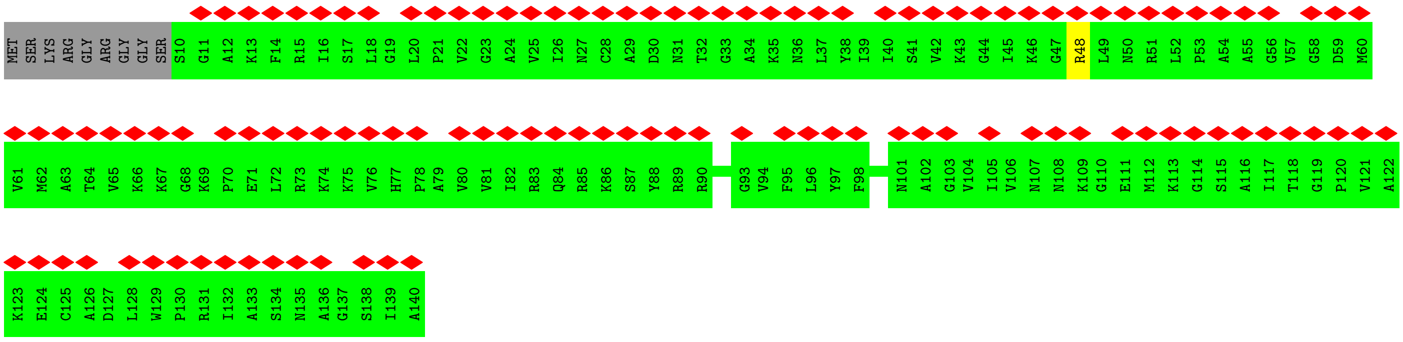

- Molecule 41: Ribosomal protein L24

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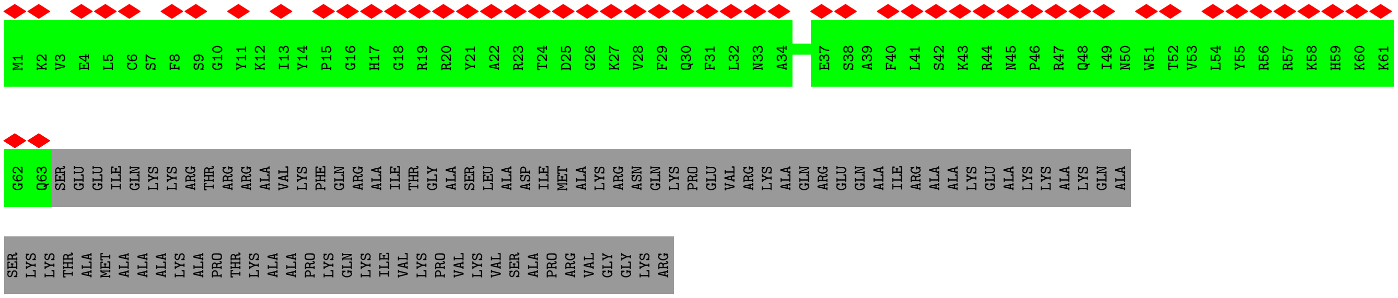

- Molecule 42: 28S rRNA

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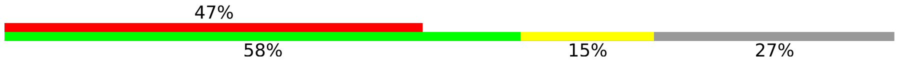

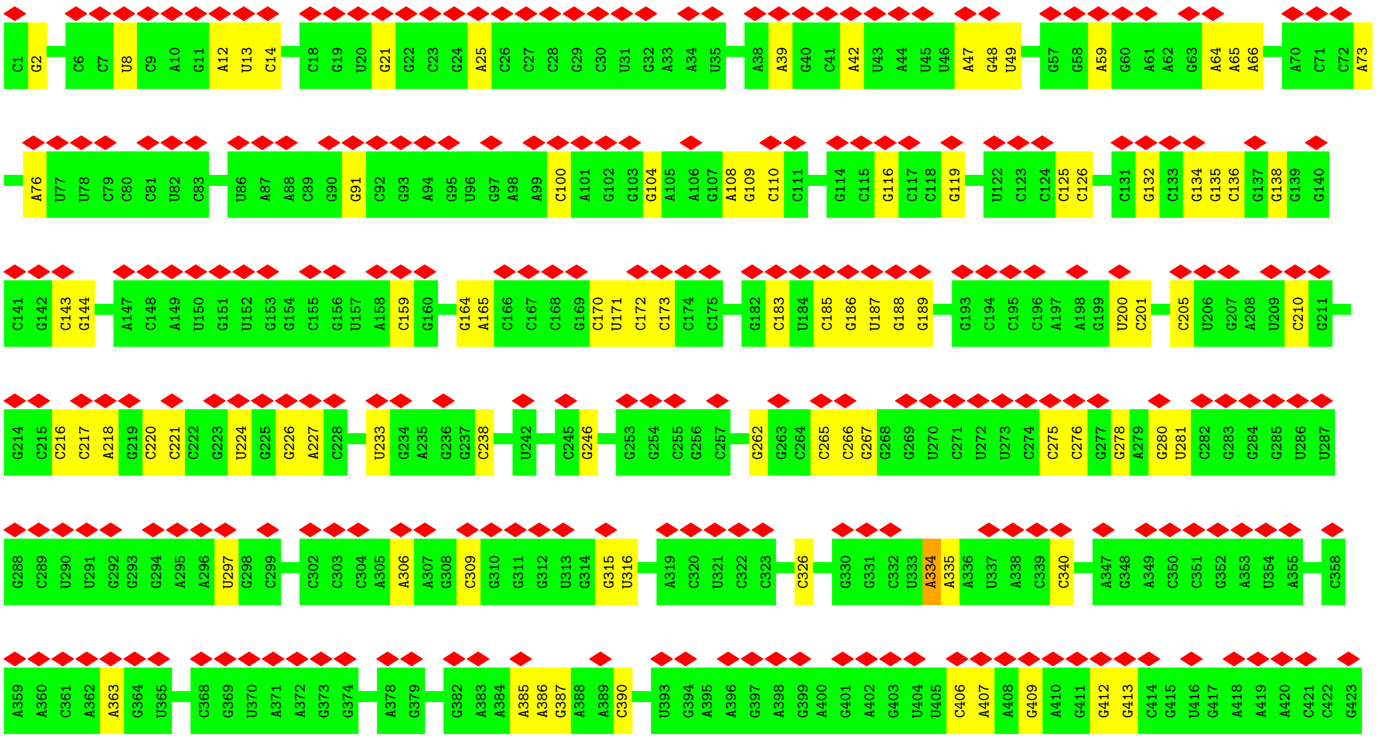

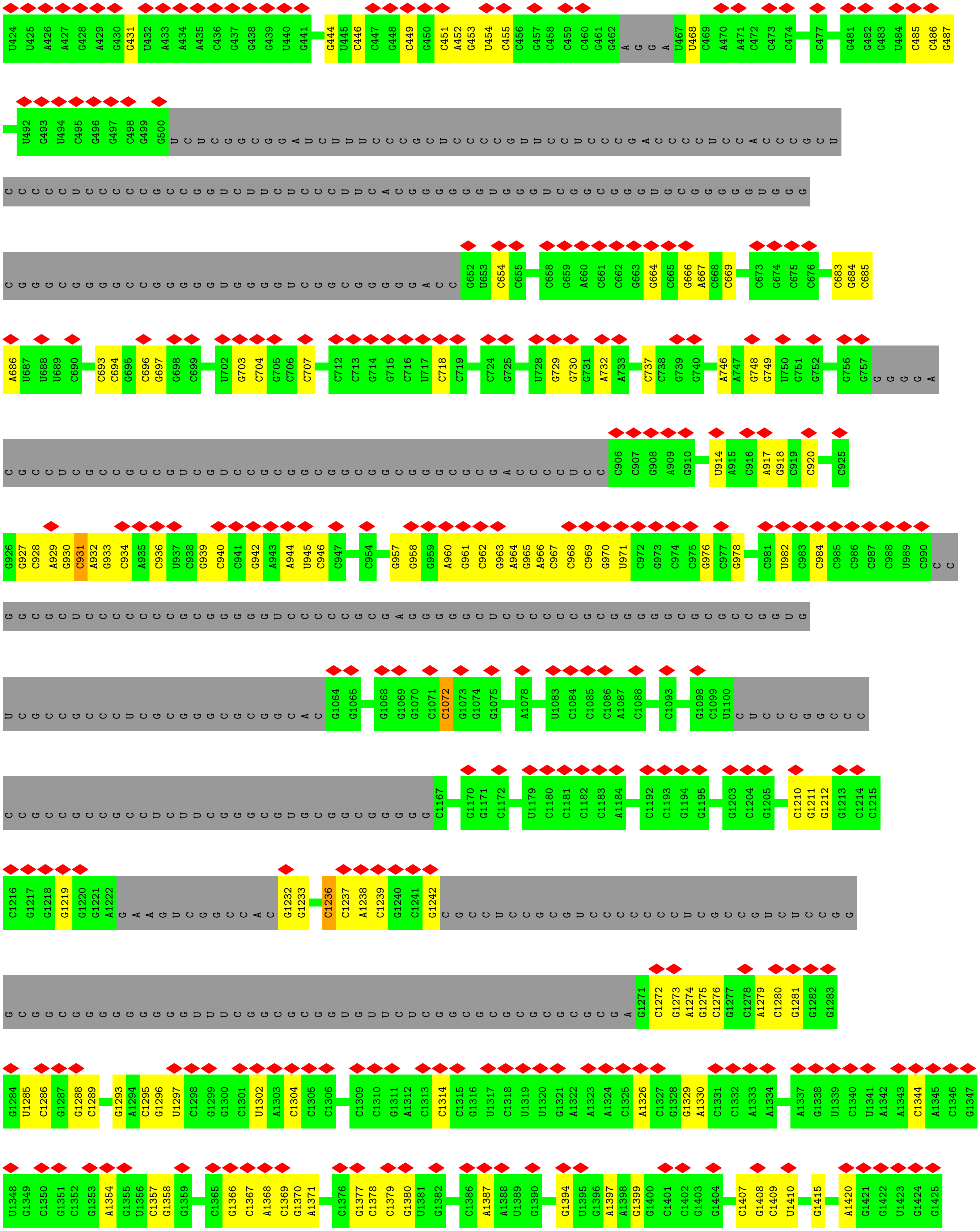
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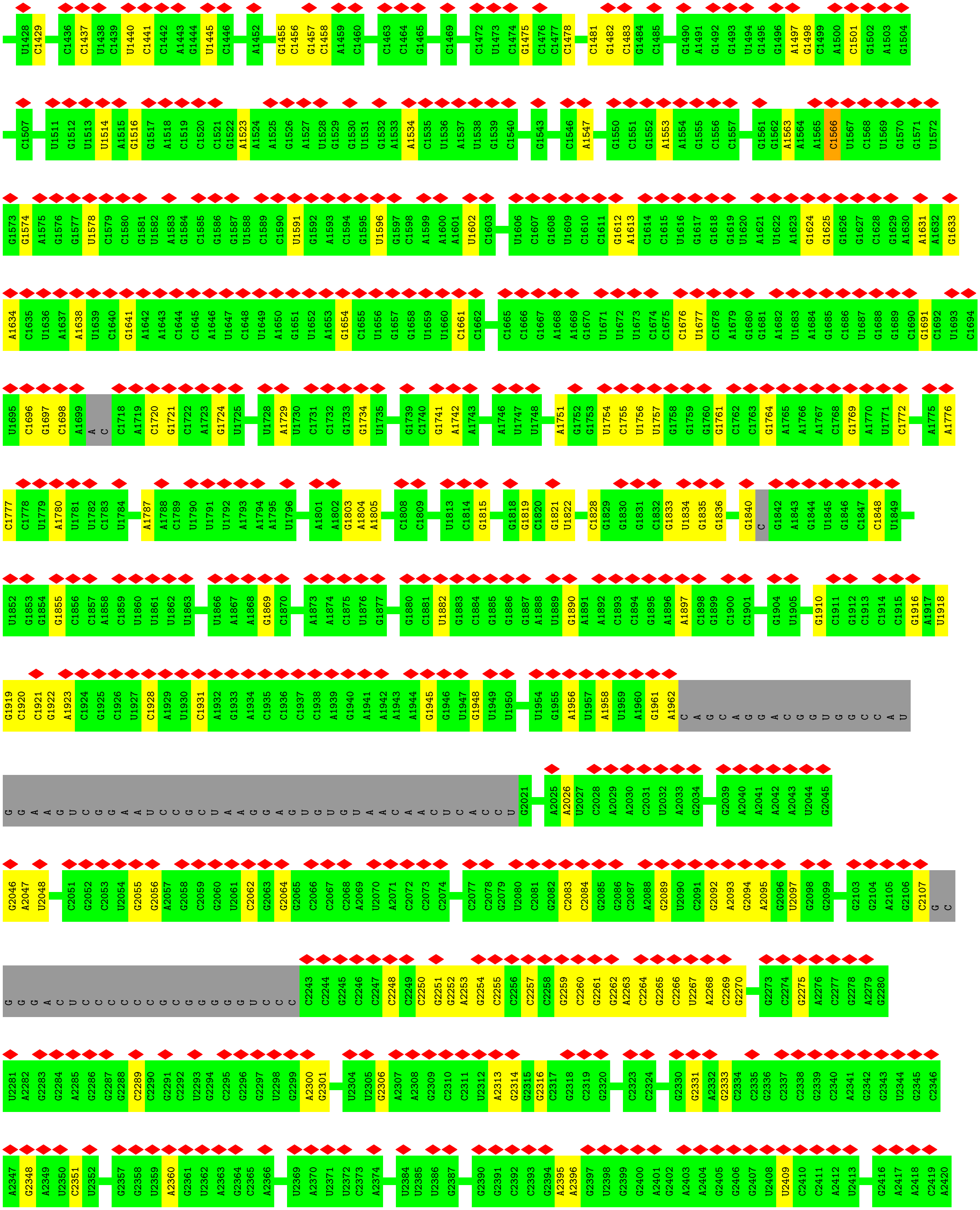
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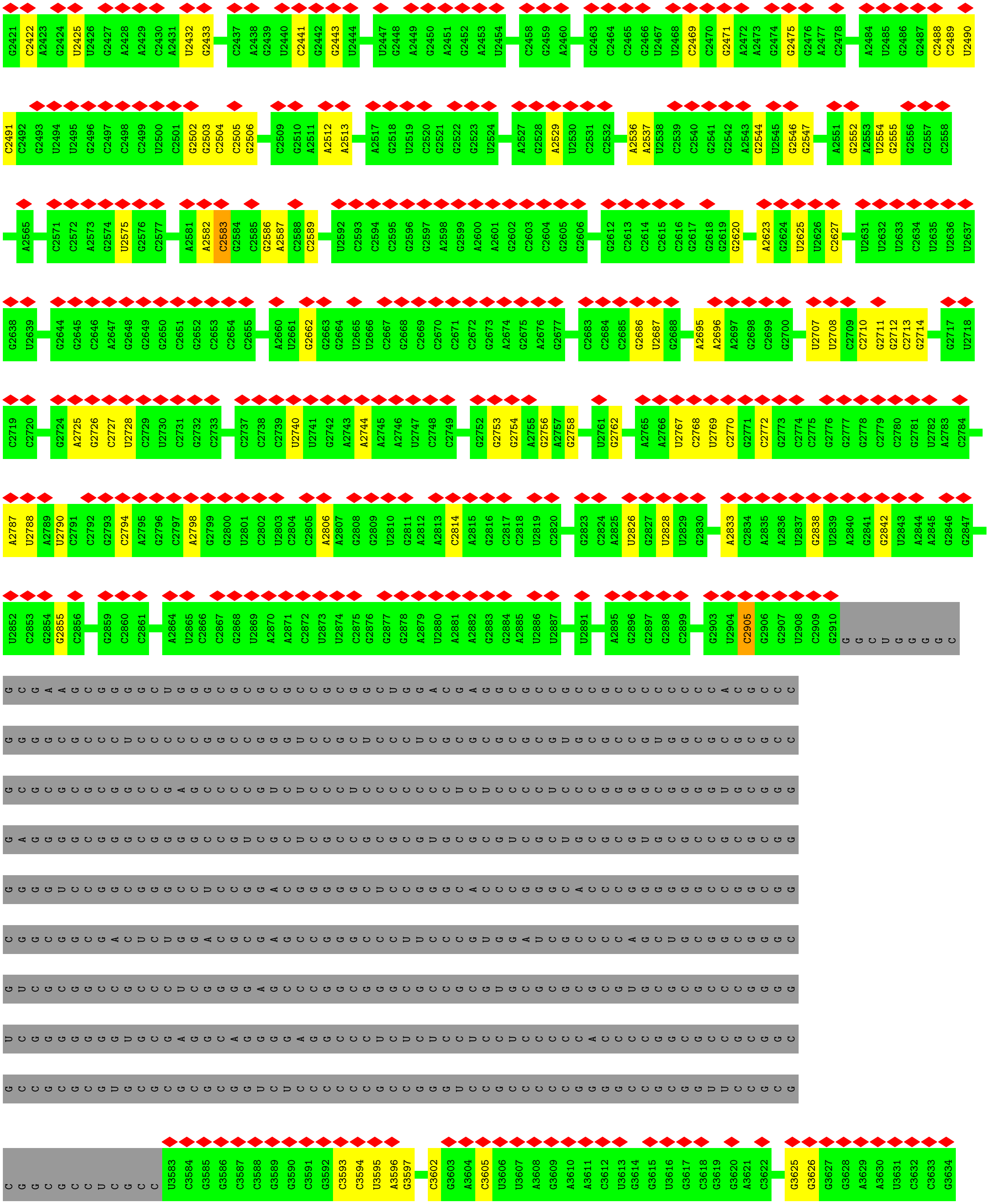
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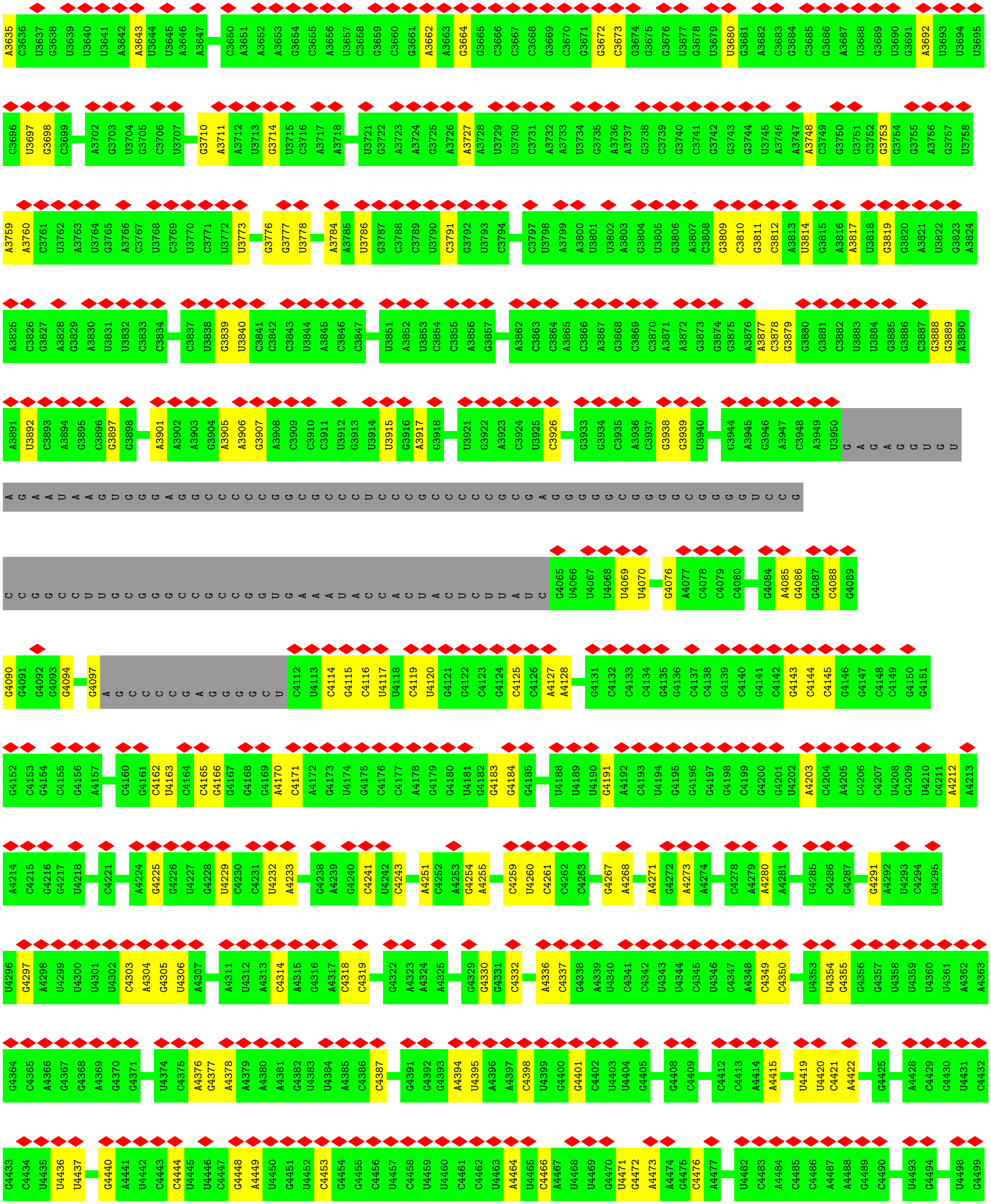
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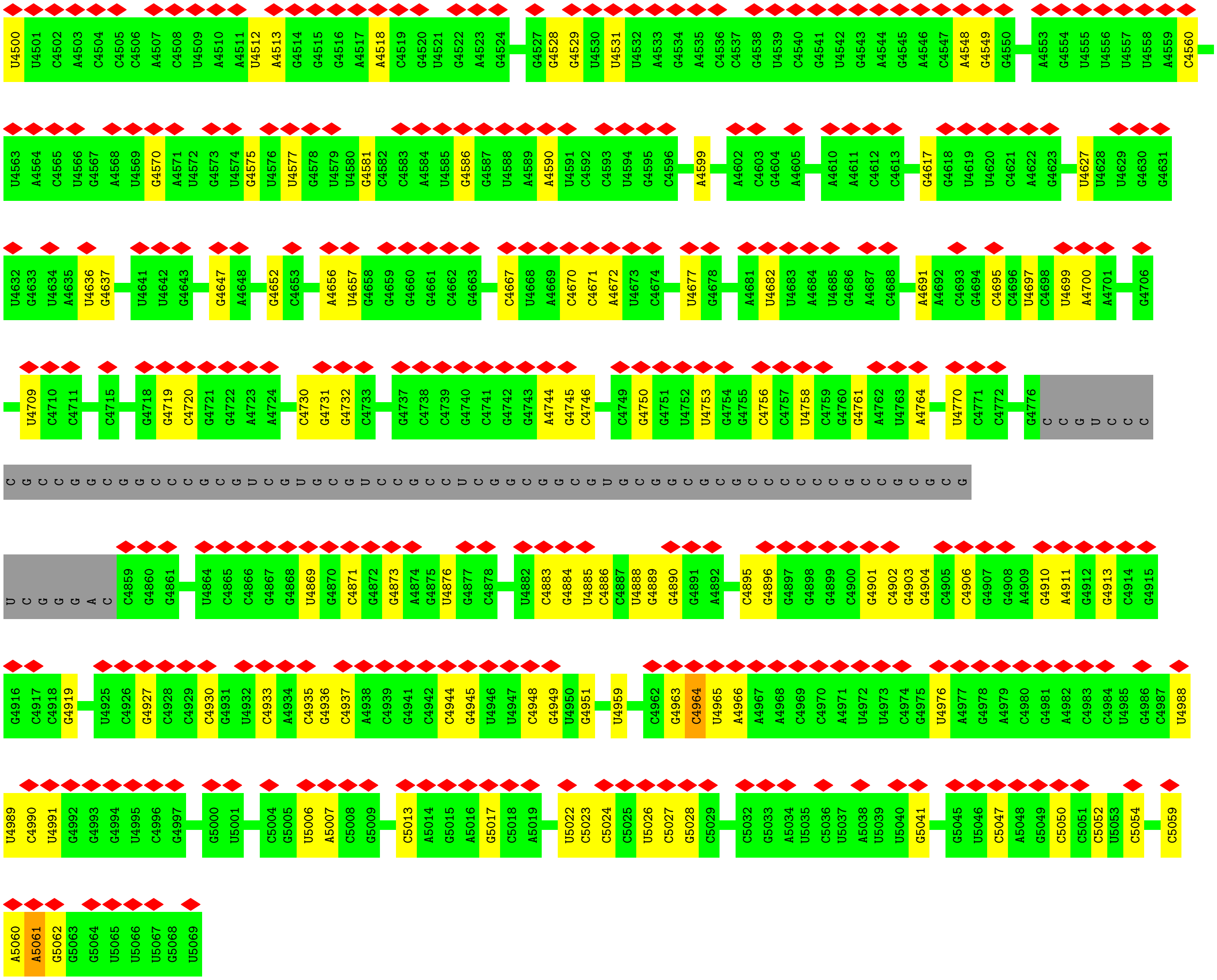
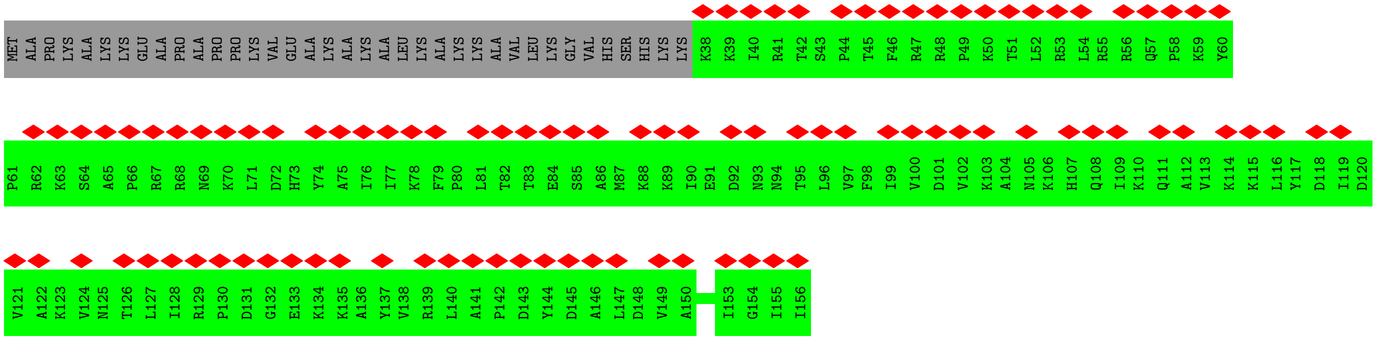
A3891 U3892 C3893 A3894 G3895 C3896 G3897 G3898 A3901 A3902 A3903 G3904 A3905 A3906 G3907 A3908 C3909 C3910 C3911 U3912 G3913 U3914 U3915 G3916 A3917 G3918 U3921 G3922 A3923 C3924 U3925 C3926 G3933 G3934 C3935 A3936 C3937 G3938 G3939 U3940 G3944 A3945 G3946 A3947 C3948 A3949 U3950 G A G A G G U G U
A G A A U A A G U G G G A G G C C C C C G G C G C C C U C C C G C C C C C G C G A G G G G G C G G G G C G G G G U C C G
C C G G C C U U G C G G G C C C G C C G G U G A A A U A C C A C U A C U C U U A U C G4065 U4066 U4067 U4068 U4069 U4070 G4076 A4077 C4078 C4079 C4080 G4084 A4085 G4086 G4087 C4088 G4089
G4090 G4091 G4092 G4093 G4094 G4097 A G C C C C G A G G G G C U C4112 U4113 C4114 G4115 C4116 U4117 U4118 C4119 U4120 G4121 C4122 G4123 C4124 C4125 C4126 A4127 A4128 G4131 C4132 C4133 C4134 G4135 G4136 C4137 C4138 G4139 C4140 G4141 C4142 G4143 C4144 C4145 G4146 G4147 C4148 C4149 G4150 G4151
G4152 C4153 G4154 C4155 G4156 A4157 C4160 G4161 C4162 U4163 C4164 C4165 G4166 G4167 G4168 G4169 A4170 C4171 A4172 G4173 U4174 G4175 C4176 C4177 A4178 G4179 G4180 U4181 G4182 G4183 G4184 G4185 U4188 U4189 U4190 G4191 A4192 C4193 U4194 G4195 G4196 G4197 G4198 C4199 G4200 G4201 U4202 A4203 C4204 A4205 C4206 C4207 U4208 G4209 U4210 C4211 A4212 A4213
A4214 C4215 G4216 G4217 U4218 C4221 A4224 G4225 G4226 U4227 G4228 U4229 C4230 C4231 U4232 A4233 G4238 A4239 G4240 C4241 U4242 C4243 A4251 C4252 A4253 G4254 A4255 C4259 U4260 C4261 C4262 C4263 G4267 A4268 A4271 G4272 A4273 A4274 C4278 A4279 A4280 A4281 U4285 C4286 G4287 G4291 A4292 U4293 C4294 U4295
U4296 G4297 A4298 U4299 U4300 U4301 U4302 C4303 A4304 G4305 U4306 A4307 A4311 U4312 A4313 C4314 A4315 G4316 A4317 C4318 C4319 U4322 A4323 A4324 A4325 G4329 G4330 G4331 C4332 A4336 C4337 G4338 A4339 U4340 C4341 C4342 U4343 U4344 C4345 G4346 G4347 A4348 C4349 C4350 U4353 U4354 G4355 G4356 G4357 U4358 U4359 U4360 U4361 A4362 A4363
G4364 C4365 A4366 G4367 G4368 A4369 G4370 G4371 U4374 C4375 A4376 G4377 A4378 A4379 A4380 A4381 G4382 U4383 U4384 A4385 C4386 C4387 G4391 G4392 G4393 A4394 U4395 A4396 A4397 C4398 U4399 G4400 G4401 C4402 U4403 U4404 G4405 G4408 C4409 C4412 C4413 A4414 A4415 U4419 U4420 C4421 A4422 G4425 A4428 C4429 G4430 U4431 C4432
G4433 C4434 U4435 U4436 U4437 G4440 A4441 U4442 C4443 C4444 U4445 U4446 C4447 G4448 A4449 U4450 G4451 U4452 C4453 G4454 G4455 C4456 U4457 C4458 U4459 U4460 C4461 C4462 C4463 A4464 U4465 C4466 A4467 U4468 U4469 G4470 U4471 G4472 A4473 A4474 G4475 C4476 A4477 U4482 C4483 A4484 C4485 C4486 A4487 A4488 G4489 C4490 U4493 G4494 U4498 G4499



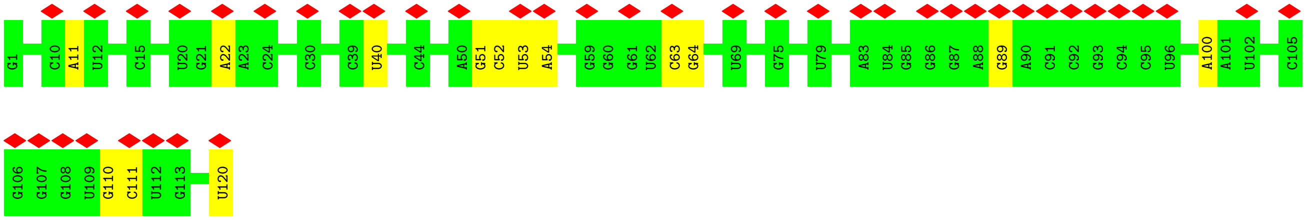
- Molecule 43: Ribosomal_L23eN domain-containing protein

Chain X:

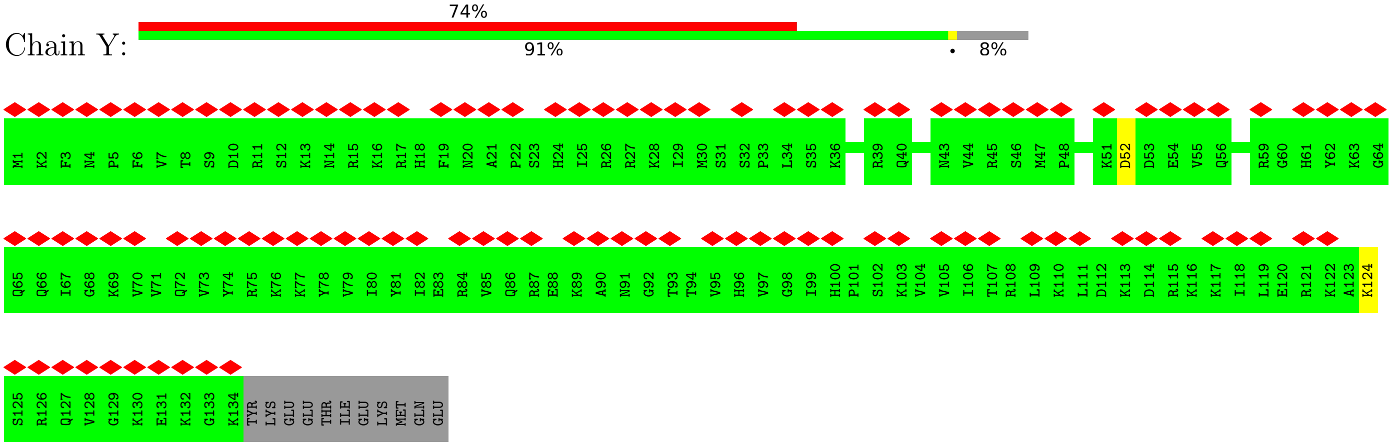


- Molecule 44: 5S rRNA

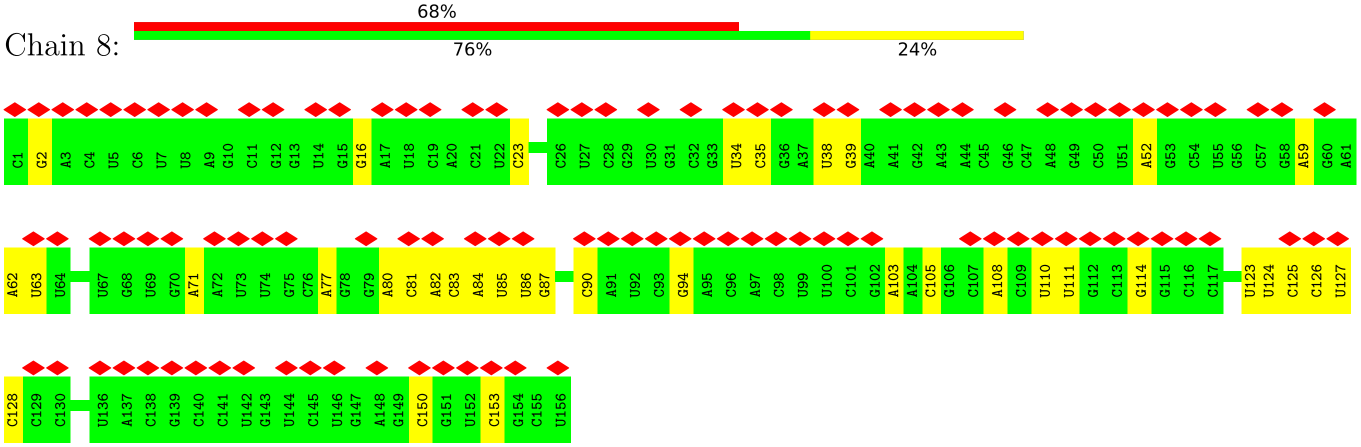
Chain 7:



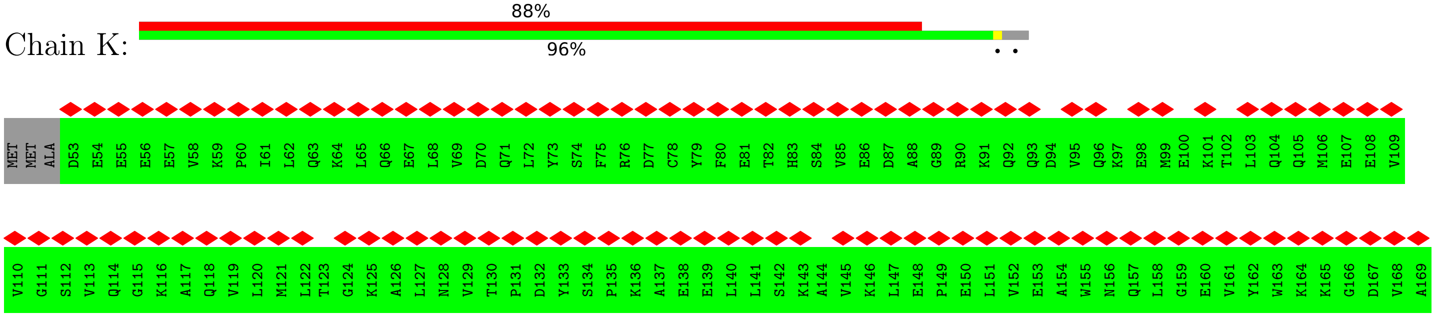
- Molecule 45: Ribosomal protein L26

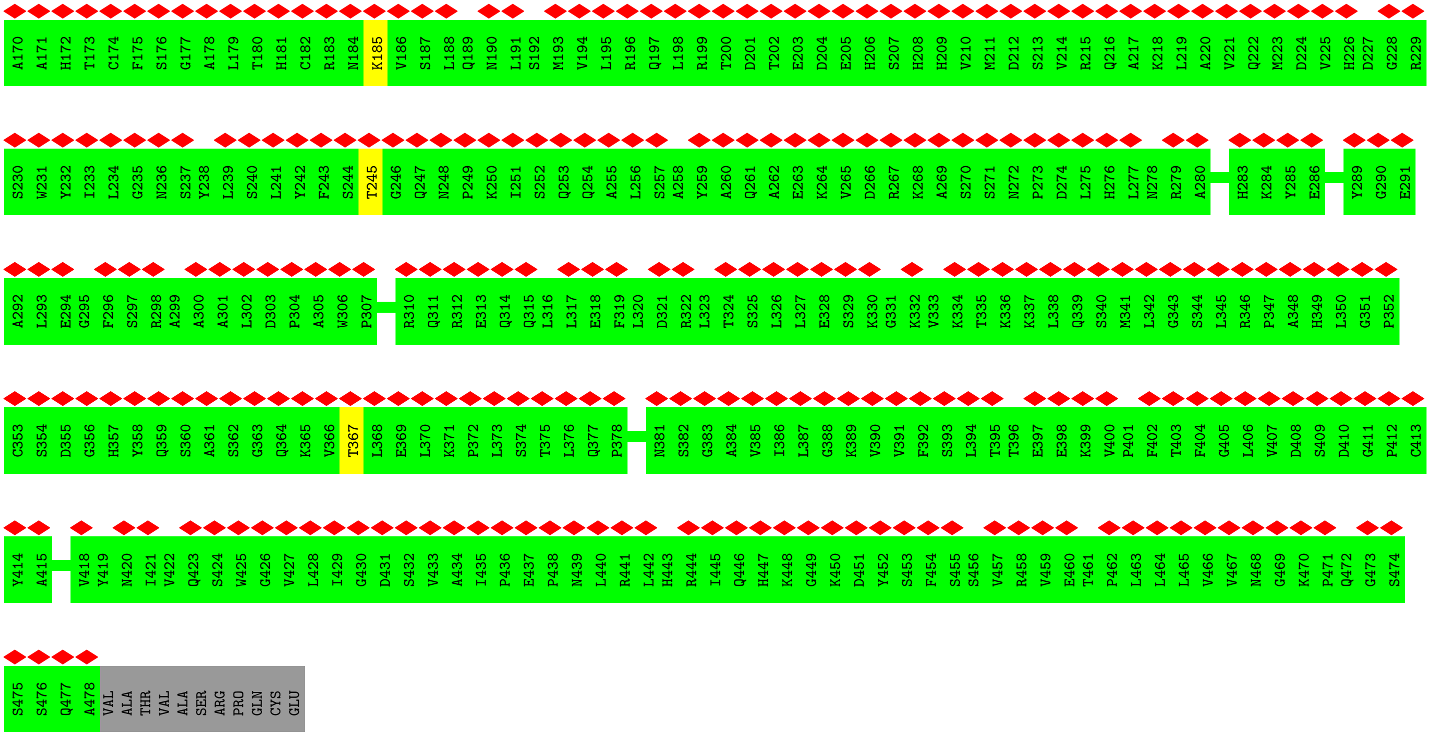


- Molecule 46: 5.8S rRNA



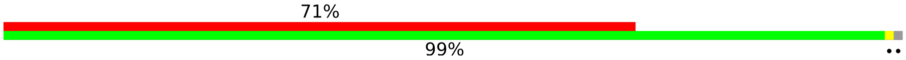
- Molecule 47: Tetratricopeptide repeat protein 5

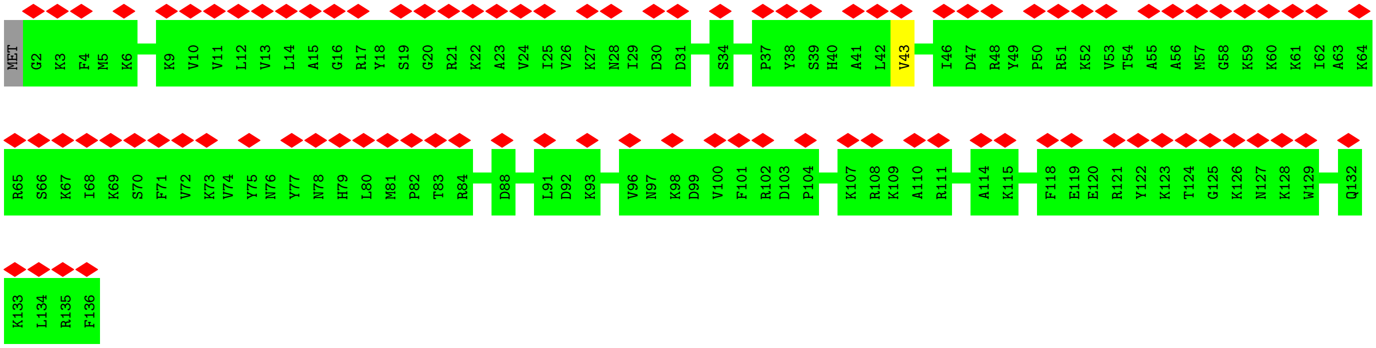




- Molecule 48: 60S ribosomal protein L27

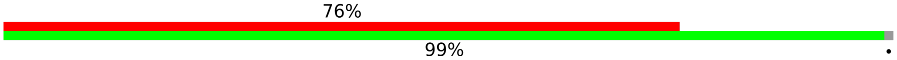
Chain Z:

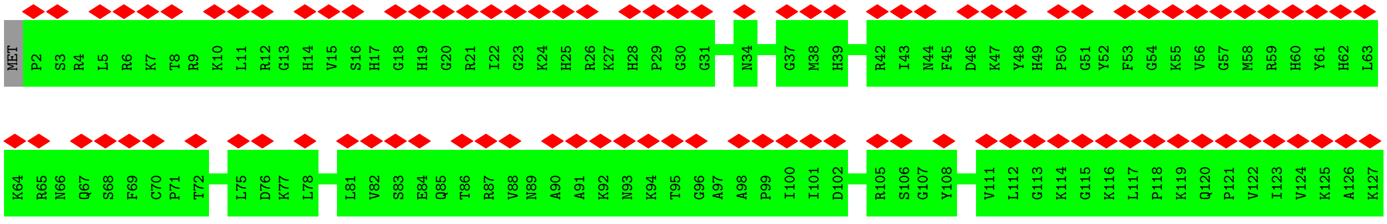


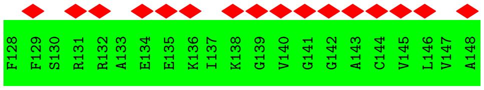


- Molecule 49: 60S ribosomal protein L27a

Chain a:






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 $(e^-/\text{Å}^2)$	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 (Å)	535.6, 535.6, 535.6	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.339, 1.339, 1.339	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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.

All (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
42	5	1072	C	C2-N1-C1’	8.13	127.74	118.80
42	5	2727	C	N1-C2-O2	8.09	123.75	118.90
42	5	931	C	N3-C2-O2	-7.42	116.70	121.90
42	5	1236	C	N3-C2-O2	-7.30	116.79	121.90
42	5	5061	A	P-O3’-C3’	7.04	128.15	119.70
42	5	4261	C	N3-C2-O2	-7.01	117.00	121.90
42	5	334	A	O4’-C1’-N9	6.80	113.64	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
42	5	1072	C	N3-C2-O2	-6.62	117.27	121.90
42	5	931	C	C6-N1-C2	-6.57	117.67	120.30
42	5	5061	A	OP2-P-O3’	6.25	118.95	105.20
42	5	1566	C	N3-C4-C5	6.07	124.33	121.90
42	5	449	C	C2-N1-C1’	6.02	125.42	118.80
42	5	4259	C	C6-N1-C2	-5.99	117.90	120.30
42	5	2583	C	N3-C2-O2	-5.97	117.72	121.90
42	5	449	C	N1-C2-O2	5.96	122.48	118.90
42	5	100	C	C2-N1-C1’	5.86	125.25	118.80
42	5	4259	C	N1-C2-O2	5.83	122.40	118.90
42	5	2728	U	C5-C6-N1	-5.81	119.80	122.70
42	5	931	C	C6-N1-C1’	-5.75	113.90	120.80
42	5	4420	U	C2-N1-C1’	5.73	124.58	117.70
42	5	1072	C	C6-N1-C1’	-5.71	113.95	120.80
44	7	52	C	N3-C2-O2	-5.70	117.91	121.90
42	5	2728	U	C4-C5-C6	5.69	123.12	119.70
42	5	4964	C	N3-C2-O2	-5.61	117.97	121.90
42	5	1236	C	N1-C2-O2	5.57	122.24	118.90
42	5	4420	U	N1-C2-O2	5.52	126.66	122.80
42	5	4260	U	C5-C6-N1	-5.50	119.95	122.70
42	5	2905	C	N3-C2-O2	-5.48	118.07	121.90
42	5	1566	C	N1-C2-N3	-5.29	115.50	119.20
42	5	4261	C	N1-C2-O2	5.12	121.97	118.90
42	5	931	C	C5-C6-N1	5.08	123.54	121.00
42	5	138	G	N1-C6-O6	-5.06	116.86	119.90
42	5	1458	C	N1-C2-O2	5.05	121.93	118.90
42	5	1072	C	C6-N1-C2	-5.03	118.29	120.30

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 ⓘ

5.3.1 Protein backbone ⓘ

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
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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 ⓘ

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
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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

All (80) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	u	49	LYS
4	A	30	ARG
4	A	73	THR
4	A	193	ARG
5	b	40	LEU
6	B	205	VAL
6	B	258	HIS
6	B	309	LEU
6	B	344	VAL
6	B	370	THR
7	c	93	THR
8	C	79	VAL
8	C	174	LEU
8	C	188	ARG
8	C	230	LEU
8	C	266	THR
8	C	326	LEU
9	d	20	VAL
9	d	46	LEU

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Mol	Chain	Res	Type
9	d	57	MET
9	d	102	LEU
10	D	55	VAL
10	D	60	ILE
10	D	105	LEU
10	D	117	LYS
10	D	177	THR
12	E	58	MET
12	E	100	THR
12	E	147	ILE
12	E	162	LYS
12	E	218	LEU
12	E	260	VAL
13	f	18	LEU
14	F	209	PHE
15	g	5	LEU
15	g	32	TYR
15	g	54	ARG
16	G	54	PHE
16	G	168	VAL
17	h	24	LEU
17	h	30	GLN
17	h	56	ARG
18	H	59	LYS
18	H	86	LEU
18	H	176	LEU
18	H	179	ILE
19	i	21	VAL
19	i	34	THR
23	k	49	ASP
24	L	184	MET
25	l	46	ARG
26	M	57	LEU
26	M	84	THR
26	M	137	LYS
30	O	27	VAL
30	O	117	ARG
30	O	145	VAL
33	p	17	ARG
33	p	52	VAL
33	p	90	LYS
34	Q	13	VAL

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Mol	Chain	Res	Type
34	Q	14	ARG
34	Q	37	ARG
37	S	24	THR
37	S	51	LEU
37	S	101	THR
37	S	102	THR
38	T	48	VAL
38	T	110	LYS
38	T	141	VAL
39	U	27	HIS
39	U	56	LEU
39	U	72	VAL
40	V	48	ARG
45	Y	52	ASP
45	Y	124	LYS
47	K	185	LYS
47	K	245	THR
47	K	367	THR
48	Z	43	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (114) such sidechains are listed below:

Mol	Chain	Res	Type
3	u	15	GLN
3	u	45	GLN
3	u	76	ASN
3	u	80	GLN
4	A	95	GLN
4	A	162	ASN
5	b	7	HIS
5	b	17	HIS
5	b	49	HIS
5	b	50	ASN
5	b	58	GLN
6	B	68	ASN
6	B	121	ASN
6	B	179	HIS
6	B	186	ASN
6	B	271	GLN
6	B	315	ASN
6	B	380	GLN
7	c	19	GLN

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Mol	Chain	Res	Type
8	C	38	ASN
8	C	41	HIS
8	C	50	GLN
8	C	231	ASN
8	C	299	GLN
8	C	329	ASN
8	C	346	ASN
8	C	347	HIS
9	d	18	ASN
9	d	118	GLN
10	D	39	GLN
10	D	63	GLN
10	D	111	ASN
10	D	138	GLN
10	D	267	ASN
10	D	282	GLN
11	e	52	GLN
11	e	124	ASN
12	E	132	HIS
12	E	186	HIS
12	E	217	GLN
12	E	280	HIS
15	g	28	ASN
15	g	100	GLN
16	G	64	GLN
16	G	82	GLN
16	G	100	HIS
16	G	141	ASN
16	G	149	ASN
16	G	153	GLN
16	G	159	HIS
16	G	227	ASN
17	h	30	GLN
17	h	63	GLN
18	H	76	HIS
20	I	86	HIS
20	I	92	HIS
20	I	202	ASN
22	J	42	GLN
22	J	71	HIS
22	J	98	ASN
23	k	58	GLN

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Mol	Chain	Res	Type
24	L	28	GLN
24	L	87	HIS
24	L	104	ASN
24	L	149	GLN
25	l	33	ASN
25	l	38	ASN
26	M	33	GLN
26	M	125	ASN
27	m	119	ASN
28	N	87	HIS
28	N	109	HIS
30	O	26	GLN
30	O	96	GLN
31	o	36	GLN
31	o	51	GLN
31	o	102	GLN
32	P	50	ASN
32	P	54	HIS
32	P	63	GLN
32	P	101	GLN
32	P	109	GLN
32	P	130	ASN
32	P	145	HIS
32	P	166	ASN
32	P	174	HIS
34	Q	21	GLN
35	r	12	ASN
35	r	31	ASN
35	r	121	GLN
36	R	27	ASN
36	R	130	ASN
37	S	125	GLN
37	S	162	GLN
38	T	54	HIS
38	T	58	HIS
39	U	38	ASN
40	V	31	ASN
40	V	101	ASN
41	W	59	HIS
43	X	73	HIS
45	Y	14	ASN
45	Y	24	HIS

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Mol	Chain	Res	Type
45	Y	65	GLN
45	Y	72	GLN
47	K	93	GLN
47	K	189	GLN
47	K	248	ASN
47	K	276	HIS
47	K	443	HIS
47	K	468	ASN
49	a	17	HIS
49	a	66	ASN
49	a	120	GLN

5.3.3 RNA ⓘ

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%)

All (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
42	5	21	G
42	5	25	A
42	5	39	A
42	5	42	A
42	5	48	G
42	5	49	U
42	5	59	A
42	5	64	A
42	5	65	A
42	5	66	A
42	5	73	A
42	5	76	A
42	5	91	G

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Mol	Chain	Res	Type
42	5	104	G
42	5	108	A
42	5	109	G
42	5	110	C
42	5	116	G
42	5	119	G
42	5	126	C
42	5	132	G
42	5	134	G
42	5	135	G
42	5	136	C
42	5	143	C
42	5	144	G
42	5	159	C
42	5	164	G
42	5	165	A
42	5	171	U
42	5	172	C
42	5	173	C
42	5	183	C
42	5	185	C
42	5	186	G
42	5	188	G
42	5	189	G
42	5	200	U
42	5	201	C
42	5	205	C
42	5	210	C
42	5	216	C
42	5	217	C
42	5	218	A
42	5	220	C
42	5	221	C
42	5	224	U
42	5	226	G
42	5	227	A
42	5	233	U
42	5	238	C
42	5	246	G
42	5	262	G
42	5	265	C
42	5	266	C

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Mol	Chain	Res	Type
42	5	267	G
42	5	276	C
42	5	278	G
42	5	280	G
42	5	281	U
42	5	297	U
42	5	306	A
42	5	309	C
42	5	315	G
42	5	316	U
42	5	326	C
42	5	334	A
42	5	335	A
42	5	340	C
42	5	363	A
42	5	386	A
42	5	387	G
42	5	390	C
42	5	407	A
42	5	409	G
42	5	412	G
42	5	413	G
42	5	431	G
42	5	444	G
42	5	446	C
42	5	451	C
42	5	452	A
42	5	453	G
42	5	454	U
42	5	455	C
42	5	468	U
42	5	485	C
42	5	486	C
42	5	487	G
42	5	654	C
42	5	664	G
42	5	666	G
42	5	667	A
42	5	669	C
42	5	683	C
42	5	684	G
42	5	685	C

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Mol	Chain	Res	Type
42	5	686	A
42	5	694	C
42	5	696	C
42	5	697	G
42	5	703	G
42	5	704	C
42	5	707	C
42	5	718	C
42	5	729	G
42	5	730	G
42	5	732	A
42	5	737	C
42	5	746	A
42	5	748	G
42	5	749	G
42	5	914	U
42	5	918	G
42	5	920	C
42	5	927	G
42	5	928	C
42	5	929	A
42	5	930	G
42	5	931	C
42	5	932	A
42	5	933	G
42	5	934	C
42	5	936	C
42	5	939	G
42	5	940	C
42	5	942	G
42	5	944	A
42	5	945	U
42	5	946	C
42	5	957	G
42	5	958	G
42	5	960	A
42	5	961	G
42	5	962	C
42	5	963	G
42	5	964	A
42	5	965	G
42	5	966	A

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Mol	Chain	Res	Type
42	5	967	C
42	5	968	C
42	5	969	C
42	5	970	G
42	5	971	U
42	5	976	G
42	5	978	G
42	5	982	U
42	5	984	C
42	5	1072	C
42	5	1210	C
42	5	1211	G
42	5	1212	G
42	5	1219	G
42	5	1233	G
42	5	1236	C
42	5	1237	C
42	5	1238	A
42	5	1239	C
42	5	1242	G
42	5	1272	C
42	5	1273	G
42	5	1274	A
42	5	1275	G
42	5	1276	C
42	5	1279	A
42	5	1280	C
42	5	1281	G
42	5	1285	U
42	5	1286	C
42	5	1288	G
42	5	1289	C
42	5	1293	G
42	5	1295	C
42	5	1296	G
42	5	1297	U
42	5	1302	U
42	5	1304	C
42	5	1314	C
42	5	1326	A
42	5	1330	A
42	5	1344	C

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Mol	Chain	Res	Type
42	5	1354	A
42	5	1358	G
42	5	1366	G
42	5	1367	C
42	5	1369	C
42	5	1370	G
42	5	1371	A
42	5	1377	G
42	5	1378	C
42	5	1379	C
42	5	1380	G
42	5	1387	A
42	5	1394	G
42	5	1397	A
42	5	1399	G
42	5	1407	C
42	5	1408	G
42	5	1409	C
42	5	1410	U
42	5	1415	G
42	5	1420	A
42	5	1429	C
42	5	1437	C
42	5	1440	U
42	5	1441	C
42	5	1445	U
42	5	1456	C
42	5	1457	G
42	5	1475	G
42	5	1478	C
42	5	1481	C
42	5	1482	G
42	5	1483	C
42	5	1497	A
42	5	1498	G
42	5	1501	C
42	5	1514	U
42	5	1516	G
42	5	1523	A
42	5	1534	A
42	5	1547	A
42	5	1553	A

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Mol	Chain	Res	Type
42	5	1563	A
42	5	1566	C
42	5	1574	G
42	5	1578	U
42	5	1591	U
42	5	1596	U
42	5	1602	U
42	5	1612	G
42	5	1613	A
42	5	1624	G
42	5	1625	G
42	5	1631	A
42	5	1633	G
42	5	1634	A
42	5	1638	A
42	5	1641	G
42	5	1654	G
42	5	1661	C
42	5	1676	C
42	5	1677	U
42	5	1691	G
42	5	1696	C
42	5	1697	G
42	5	1698	C
42	5	1720	C
42	5	1721	G
42	5	1724	G
42	5	1729	A
42	5	1734	G
42	5	1741	G
42	5	1742	A
42	5	1751	A
42	5	1754	U
42	5	1755	C
42	5	1756	U
42	5	1757	U
42	5	1761	G
42	5	1764	G
42	5	1769	G
42	5	1772	C
42	5	1776	A
42	5	1777	C

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Mol	Chain	Res	Type
42	5	1780	A
42	5	1787	A
42	5	1803	G
42	5	1804	A
42	5	1805	A
42	5	1815	G
42	5	1819	G
42	5	1821	G
42	5	1822	U
42	5	1828	C
42	5	1833	G
42	5	1834	U
42	5	1835	G
42	5	1836	G
42	5	1840	G
42	5	1848	C
42	5	1855	G
42	5	1869	G
42	5	1882	U
42	5	1890	G
42	5	1897	A
42	5	1910	G
42	5	1916	G
42	5	1918	U
42	5	1919	G
42	5	1920	C
42	5	1921	C
42	5	1922	G
42	5	1923	A
42	5	1928	C
42	5	1931	C
42	5	1945	G
42	5	1948	G
42	5	1956	A
42	5	1958	A
42	5	1961	G
42	5	1962	A
42	5	2026	A
42	5	2047	A
42	5	2048	U
42	5	2055	G
42	5	2056	G

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Mol	Chain	Res	Type
42	5	2062	C
42	5	2064	G
42	5	2084	C
42	5	2089	G
42	5	2092	G
42	5	2093	A
42	5	2094	G
42	5	2095	A
42	5	2097	U
42	5	2107	C
42	5	2248	C
42	5	2250	C
42	5	2251	G
42	5	2252	G
42	5	2253	A
42	5	2254	G
42	5	2255	C
42	5	2257	C
42	5	2259	G
42	5	2260	C
42	5	2261	G
42	5	2263	A
42	5	2264	C
42	5	2265	G
42	5	2266	C
42	5	2267	U
42	5	2268	A
42	5	2269	C
42	5	2270	G
42	5	2275	G
42	5	2289	C
42	5	2300	A
42	5	2301	G
42	5	2306	G
42	5	2313	A
42	5	2314	G
42	5	2316	G
42	5	2331	G
42	5	2333	G
42	5	2348	G
42	5	2351	C
42	5	2360	A

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Mol	Chain	Res	Type
42	5	2395	A
42	5	2396	A
42	5	2409	U
42	5	2422	C
42	5	2425	U
42	5	2432	U
42	5	2433	G
42	5	2441	C
42	5	2443	G
42	5	2469	C
42	5	2471	G
42	5	2475	G
42	5	2488	C
42	5	2489	C
42	5	2490	U
42	5	2491	C
42	5	2503	G
42	5	2504	C
42	5	2505	C
42	5	2506	G
42	5	2512	A
42	5	2513	A
42	5	2529	A
42	5	2536	A
42	5	2537	A
42	5	2544	G
42	5	2546	G
42	5	2547	G
42	5	2552	G
42	5	2554	U
42	5	2555	G
42	5	2575	U
42	5	2582	A
42	5	2583	C
42	5	2586	G
42	5	2587	A
42	5	2589	C
42	5	2620	G
42	5	2623	A
42	5	2625	U
42	5	2627	C
42	5	2662	G

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Mol	Chain	Res	Type
42	5	2686	G
42	5	2687	U
42	5	2695	A
42	5	2696	A
42	5	2707	U
42	5	2708	U
42	5	2710	C
42	5	2711	G
42	5	2713	C
42	5	2714	G
42	5	2725	A
42	5	2726	G
42	5	2740	U
42	5	2744	A
42	5	2753	G
42	5	2754	G
42	5	2756	G
42	5	2758	G
42	5	2762	G
42	5	2767	U
42	5	2768	C
42	5	2769	U
42	5	2770	C
42	5	2772	C
42	5	2787	A
42	5	2788	U
42	5	2790	U
42	5	2794	C
42	5	2798	A
42	5	2806	A
42	5	2814	C
42	5	2826	U
42	5	2828	U
42	5	2833	A
42	5	2838	G
42	5	2842	G
42	5	2855	G
42	5	2905	C
42	5	3593	C
42	5	3594	C
42	5	3595	U
42	5	3596	A

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Mol	Chain	Res	Type
42	5	3597	G
42	5	3602	C
42	5	3605	C
42	5	3625	G
42	5	3626	G
42	5	3635	A
42	5	3643	A
42	5	3662	A
42	5	3664	G
42	5	3672	G
42	5	3673	C
42	5	3680	U
42	5	3692	A
42	5	3698	G
42	5	3710	G
42	5	3711	A
42	5	3714	G
42	5	3727	A
42	5	3748	A
42	5	3753	G
42	5	3759	A
42	5	3760	A
42	5	3773	U
42	5	3776	G
42	5	3777	G
42	5	3778	U
42	5	3784	A
42	5	3786	U
42	5	3791	C
42	5	3809	G
42	5	3810	C
42	5	3811	G
42	5	3812	C
42	5	3814	U
42	5	3817	A
42	5	3819	G
42	5	3839	G
42	5	3840	U
42	5	3877	A
42	5	3878	C
42	5	3879	G
42	5	3889	G

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Mol	Chain	Res	Type
42	5	3892	U
42	5	3897	G
42	5	3901	A
42	5	3905	A
42	5	3906	A
42	5	3907	G
42	5	3915	U
42	5	3917	A
42	5	3926	C
42	5	3938	G
42	5	3939	G
42	5	4069	U
42	5	4070	U
42	5	4076	G
42	5	4085	A
42	5	4086	G
42	5	4088	C
42	5	4090	G
42	5	4094	G
42	5	4097	G
42	5	4114	C
42	5	4115	G
42	5	4116	C
42	5	4117	U
42	5	4120	U
42	5	4125	C
42	5	4127	A
42	5	4128	A
42	5	4143	G
42	5	4144	C
42	5	4145	C
42	5	4162	C
42	5	4163	U
42	5	4165	C
42	5	4166	G
42	5	4171	C
42	5	4183	G
42	5	4184	G
42	5	4191	G
42	5	4203	A
42	5	4212	A
42	5	4225	G

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Mol	Chain	Res	Type
42	5	4229	U
42	5	4233	A
42	5	4241	C
42	5	4243	C
42	5	4251	A
42	5	4254	G
42	5	4255	A
42	5	4267	G
42	5	4268	A
42	5	4271	A
42	5	4273	A
42	5	4280	A
42	5	4291	G
42	5	4297	G
42	5	4303	C
42	5	4304	A
42	5	4305	G
42	5	4306	U
42	5	4314	C
42	5	4318	C
42	5	4319	C
42	5	4330	G
42	5	4332	C
42	5	4336	A
42	5	4337	C
42	5	4349	C
42	5	4350	C
42	5	4354	U
42	5	4355	G
42	5	4376	A
42	5	4377	G
42	5	4378	A
42	5	4387	C
42	5	4394	A
42	5	4395	U
42	5	4398	C
42	5	4401	G
42	5	4415	A
42	5	4419	U
42	5	4421	C
42	5	4422	A
42	5	4436	U

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Mol	Chain	Res	Type
42	5	4437	U
42	5	4440	G
42	5	4444	C
42	5	4448	G
42	5	4449	A
42	5	4453	C
42	5	4464	A
42	5	4466	C
42	5	4471	U
42	5	4472	G
42	5	4473	A
42	5	4476	C
42	5	4500	U
42	5	4512	U
42	5	4513	A
42	5	4518	A
42	5	4528	G
42	5	4529	G
42	5	4531	U
42	5	4548	A
42	5	4549	G
42	5	4560	C
42	5	4570	G
42	5	4575	G
42	5	4577	U
42	5	4581	G
42	5	4586	G
42	5	4590	A
42	5	4599	A
42	5	4617	G
42	5	4627	U
42	5	4636	U
42	5	4637	G
42	5	4647	G
42	5	4652	G
42	5	4656	A
42	5	4657	U
42	5	4667	C
42	5	4670	C
42	5	4671	C
42	5	4672	A
42	5	4677	U

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Mol	Chain	Res	Type
42	5	4682	U
42	5	4691	A
42	5	4695	C
42	5	4697	U
42	5	4700	A
42	5	4709	U
42	5	4719	G
42	5	4720	C
42	5	4730	C
42	5	4731	G
42	5	4732	G
42	5	4744	A
42	5	4745	G
42	5	4746	C
42	5	4750	G
42	5	4753	U
42	5	4756	C
42	5	4758	U
42	5	4761	G
42	5	4764	A
42	5	4770	U
42	5	4869	U
42	5	4871	C
42	5	4873	G
42	5	4876	U
42	5	4883	C
42	5	4884	G
42	5	4886	C
42	5	4889	G
42	5	4890	G
42	5	4895	C
42	5	4896	G
42	5	4901	G
42	5	4902	C
42	5	4903	G
42	5	4904	G
42	5	4906	C
42	5	4910	G
42	5	4911	A
42	5	4913	G
42	5	4919	G
42	5	4927	G

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Mol	Chain	Res	Type
42	5	4930	C
42	5	4933	C
42	5	4936	G
42	5	4937	C
42	5	4944	C
42	5	4945	G
42	5	4948	C
42	5	4949	G
42	5	4951	G
42	5	4959	U
42	5	4963	G
42	5	4964	C
42	5	4965	U
42	5	4966	A
42	5	4976	U
42	5	4988	U
42	5	4989	U
42	5	4990	C
42	5	4991	U
42	5	5006	U
42	5	5007	A
42	5	5013	C
42	5	5017	G
42	5	5023	C
42	5	5024	C
42	5	5026	U
42	5	5027	C
42	5	5028	G
42	5	5041	G
42	5	5047	C
42	5	5050	C
42	5	5052	C
42	5	5054	C
42	5	5060	A
42	5	5061	A
42	5	5062	G
44	7	11	A
44	7	22	A
44	7	40	U
44	7	51	G
44	7	53	U
44	7	54	A

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Mol	Chain	Res	Type
44	7	63	C
44	7	64	G
44	7	89	G
44	7	100	A
44	7	110	G
44	7	111	C
44	7	120	U
46	8	2	G
46	8	16	G
46	8	23	C
46	8	34	U
46	8	35	C
46	8	38	U
46	8	39	G
46	8	52	A
46	8	59	A
46	8	62	A
46	8	63	U
46	8	71	A
46	8	77	A
46	8	80	A
46	8	81	C
46	8	82	A
46	8	83	C
46	8	84	A
46	8	85	U
46	8	86	U
46	8	87	G
46	8	90	C
46	8	94	G
46	8	103	A
46	8	105	C
46	8	108	A
46	8	110	U
46	8	111	U
46	8	114	G
46	8	123	U
46	8	125	C
46	8	126	C
46	8	127	U
46	8	128	C
46	8	150	C

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Mol	Chain	Res	Type
46	8	153	C

All (66) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
42	5	12	A
42	5	47	A
42	5	48	G
42	5	125	C
42	5	134	G
42	5	170	C
42	5	187	U
42	5	216	C
42	5	226	G
42	5	265	C
42	5	275	C
42	5	385	A
42	5	406	C
42	5	451	C
42	5	454	U
42	5	684	G
42	5	693	C
42	5	917	A
42	5	930	G
42	5	932	A
42	5	957	G
42	5	965	G
42	5	1211	G
42	5	1232	G
42	5	1236	C
42	5	1238	A
42	5	1296	G
42	5	1329	G
42	5	1357	C
42	5	1368	A
42	5	1407	C
42	5	1440	U
42	5	1455	G
42	5	1633	G
42	5	1804	A
42	5	2046	G
42	5	2083	C

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Mol	Chain	Res	Type
42	5	2093	A
42	5	2260	C
42	5	2262	G
42	5	2502	G
42	5	2695	A
42	5	2712	G
42	5	3625	G
42	5	3697	U
42	5	3888	G
42	5	4069	U
42	5	4119	C
42	5	4170	A
42	5	4232	U
42	5	4448	G
42	5	4528	G
42	5	4656	A
42	5	4699	U
42	5	4719	G
42	5	4885	U
42	5	4888	U
42	5	4889	G
42	5	4935	C
42	5	4948	C
42	5	5022	U
42	5	5027	C
42	5	5059	C
42	5	5060	A
42	5	5061	A
46	8	124	U

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

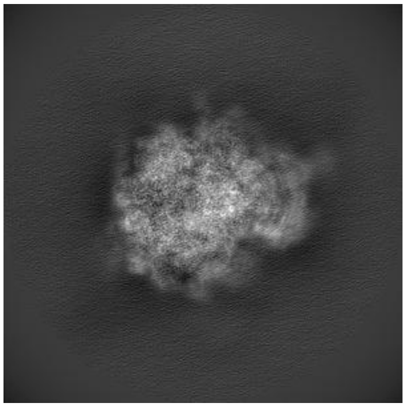
6 Map visualisation

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.

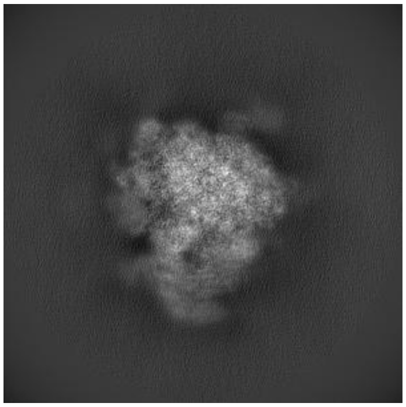
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

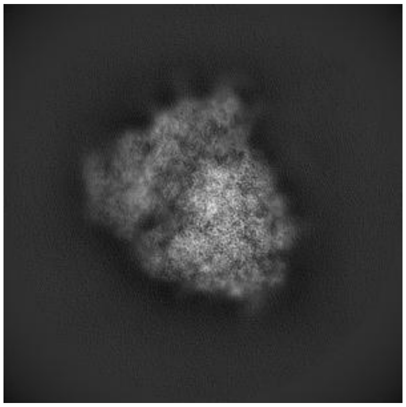
6.1.1 Primary map



X



Y

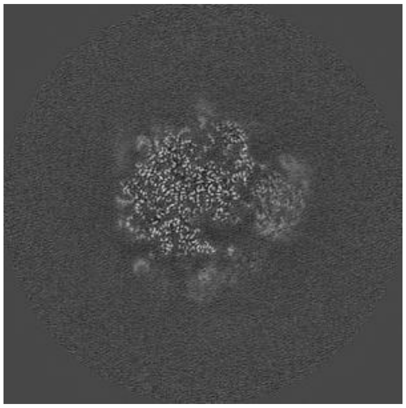


Z

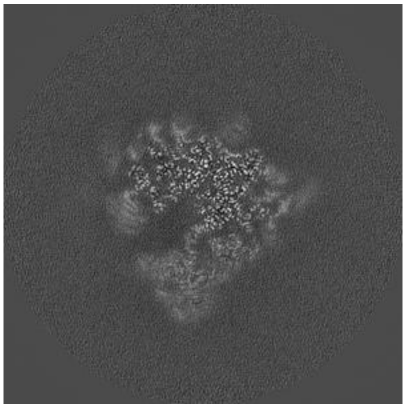
The images above show the map projected in three orthogonal directions.

6.2 Central slices

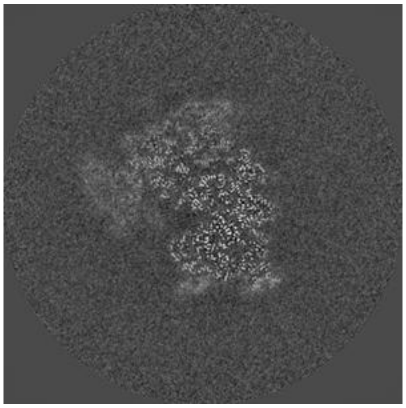
6.2.1 Primary map



X Index: 200



Y Index: 200

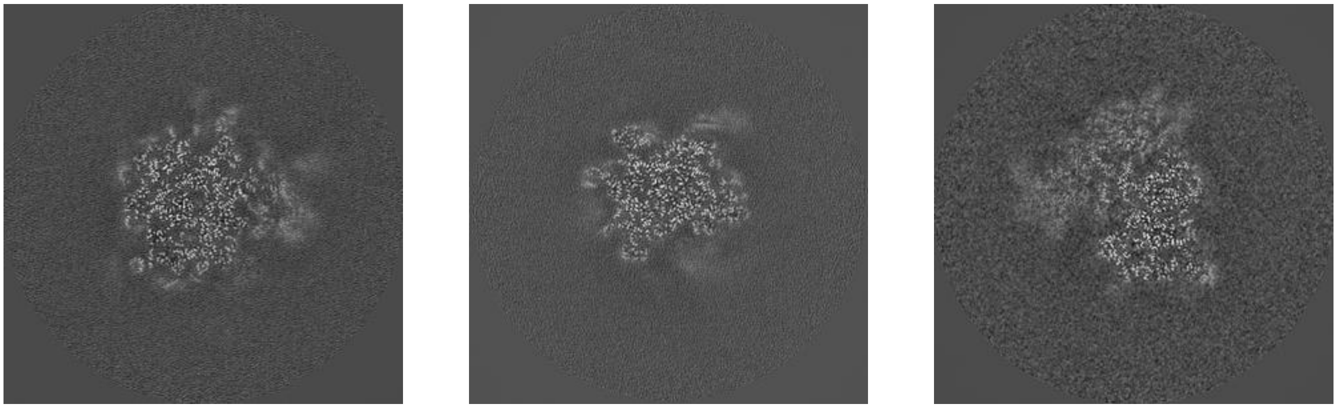


Z Index: 200

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

6.3 Largest variance slices

6.3.1 Primary map

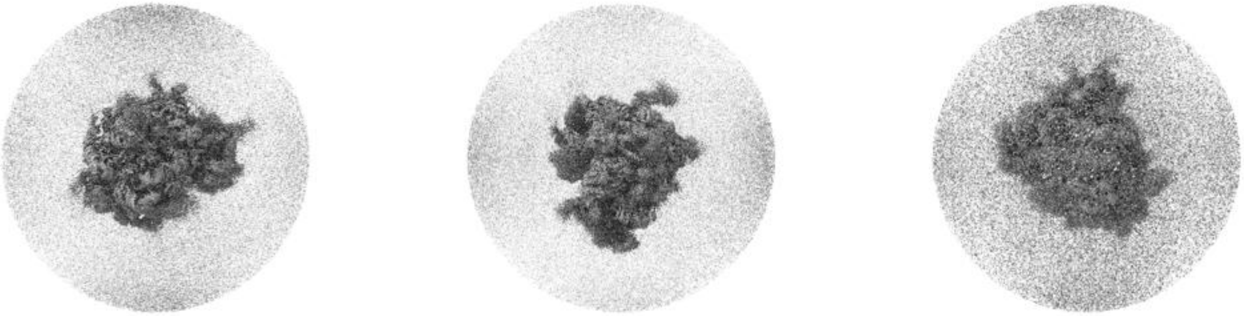


X Index: 216 Y Index: 160 Z Index: 191

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

6.4 Orthogonal surface views

6.4.1 Primary map



X Y Z

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

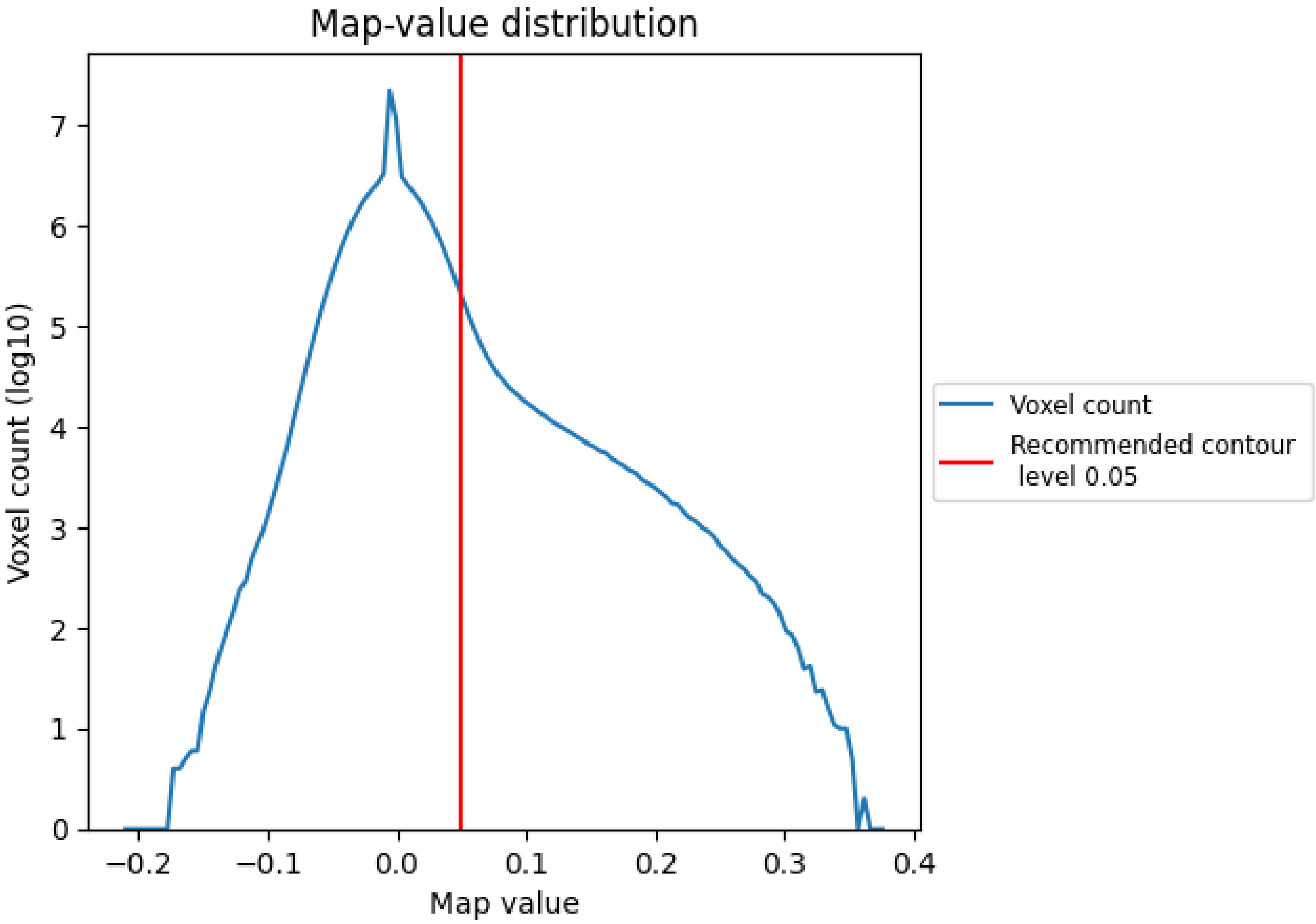
6.5 Mask visualisation ⓘ

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

7 Map analysis ⓘ

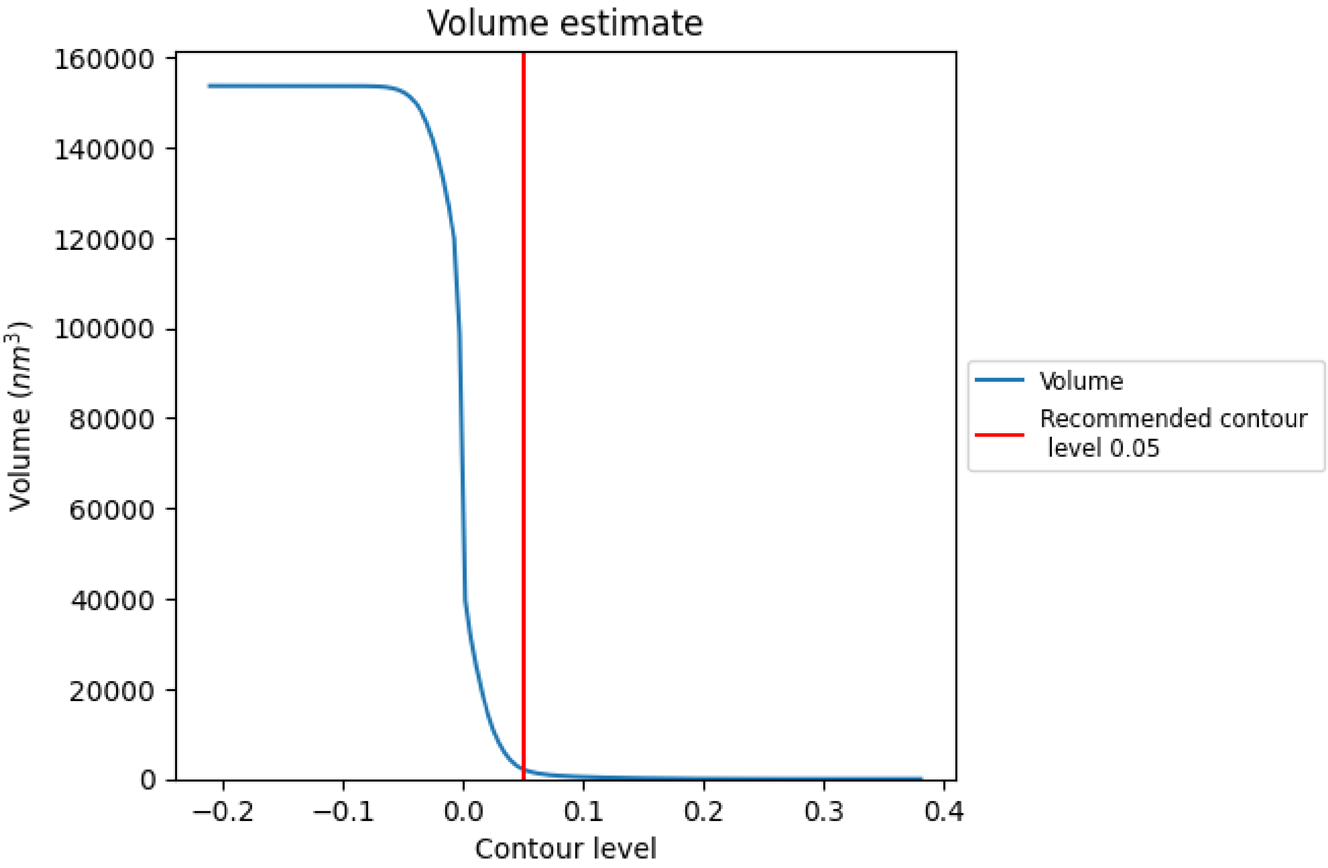
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ



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.

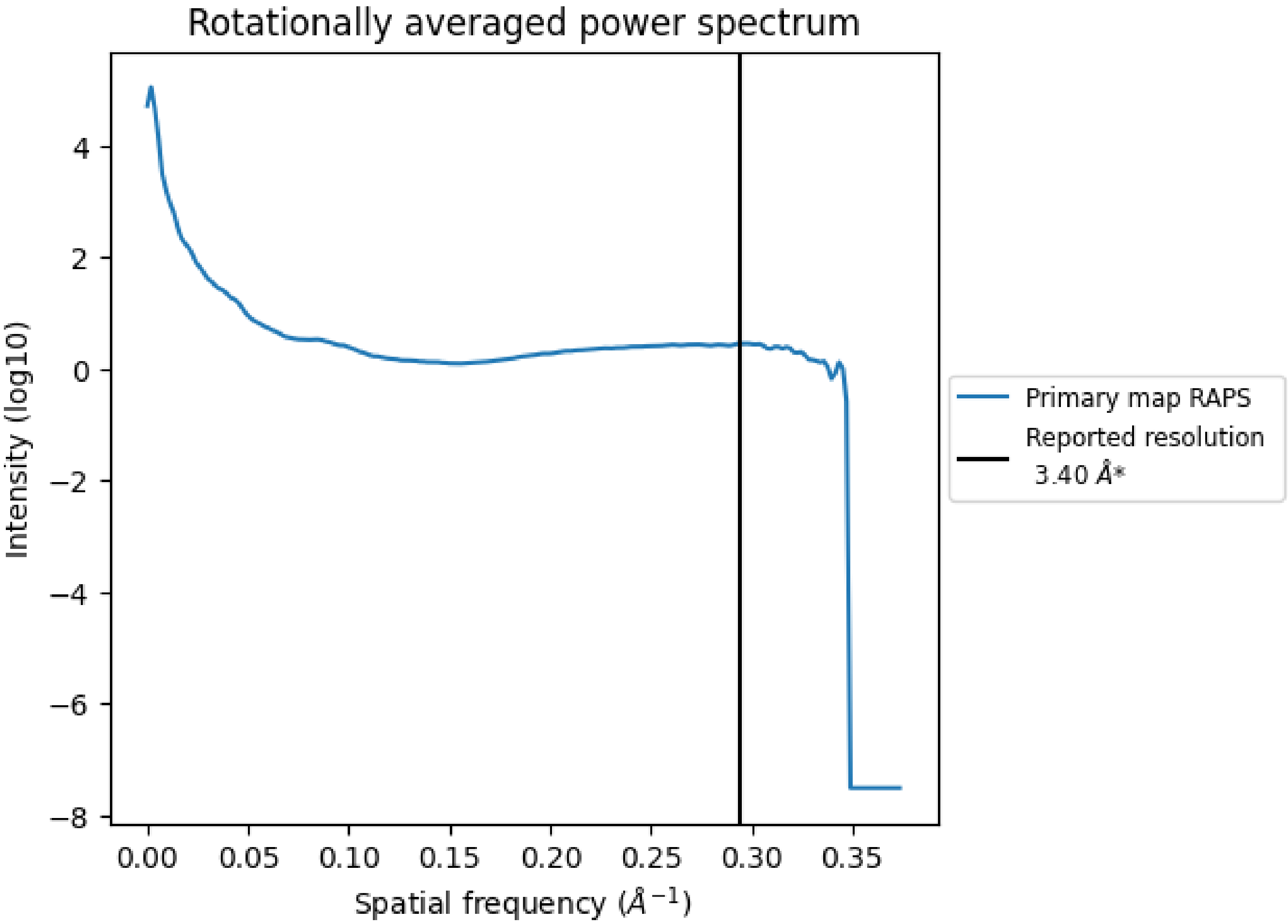
7.2 Volume estimate ⓘ



The volume at the recommended contour level is 2230 nm^3; 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 ⓘ



*Reported resolution corresponds to spatial frequency of 0.294 Å^{-1}

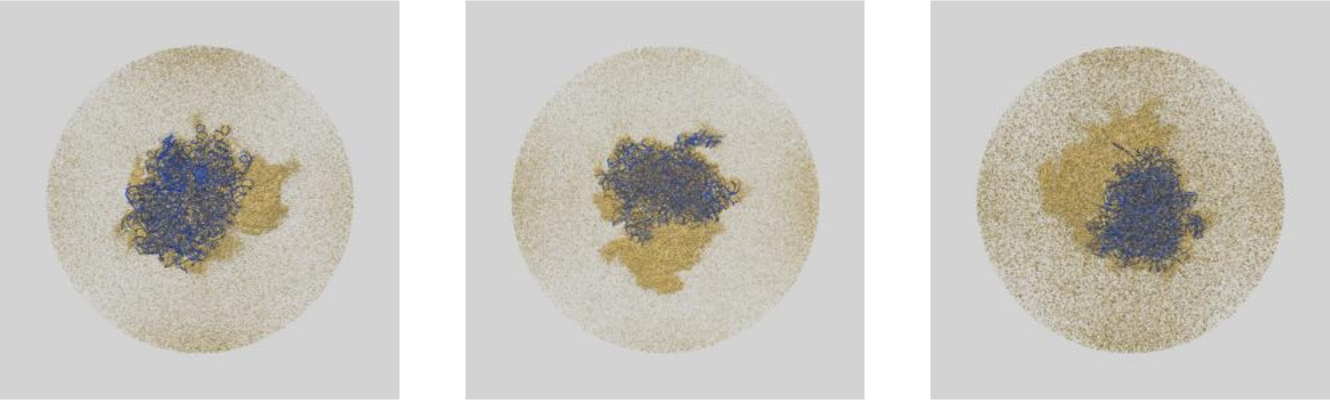
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit

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.

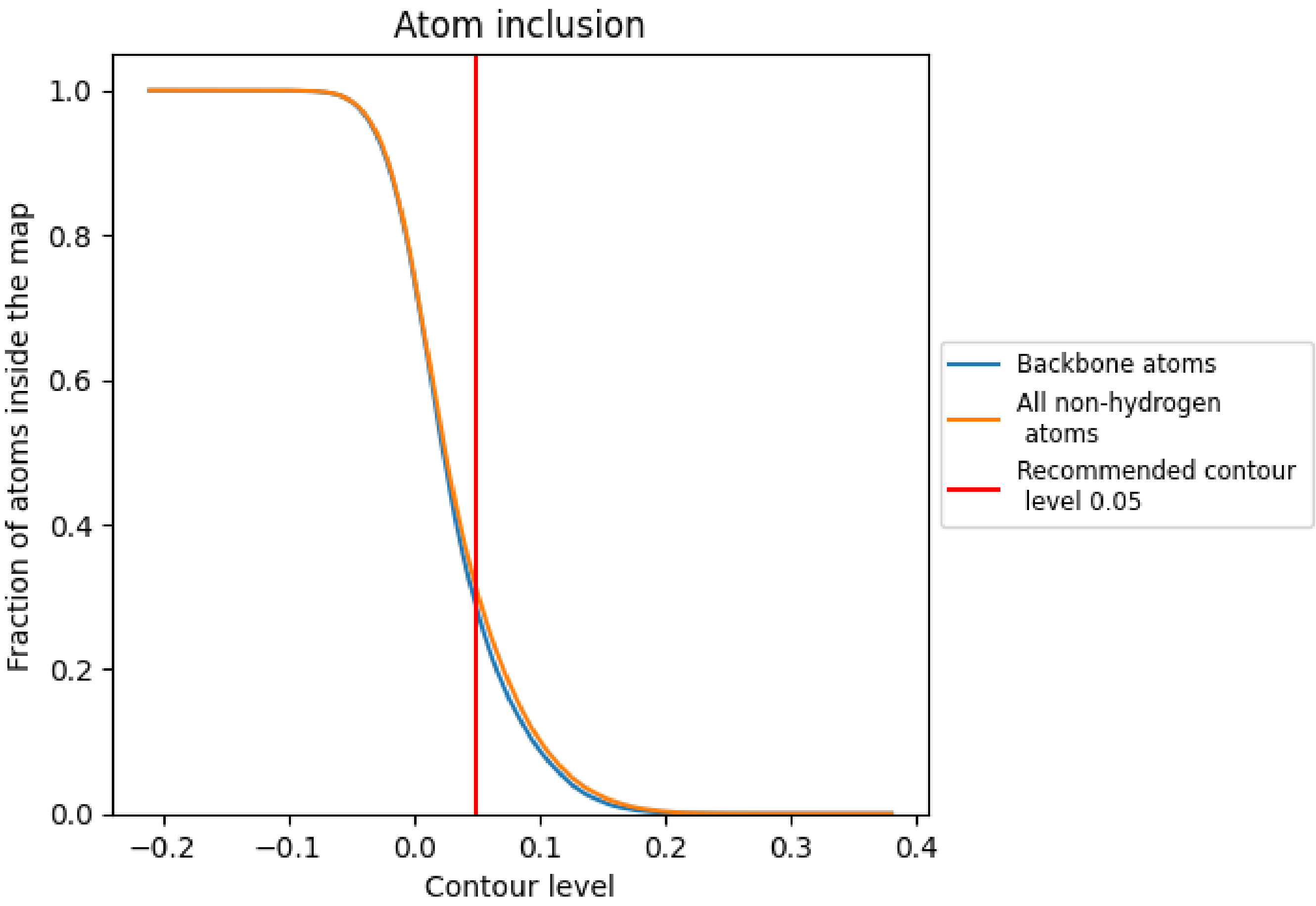
9.1 Map-model overlay



X Y Z

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 Atom inclusion ⓘ



At the recommended contour level, 29% of all backbone atoms, 31% of all non-hydrogen atoms, are inside the map.