



## wwPDB EM Validation Summary Report ⓘ

Nov 29, 2022 – 11:08 PM EST

PDB ID : 5T2C  
EMDB ID : EMD-8345  
Title : CryoEM structure of the human ribosome at 3.6 Angstrom resolution  
Authors : Zhang, X.; Lai, M.; Zhou, Z.H.  
Deposited on : 2016-08-23  
Resolution : 3.60 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

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

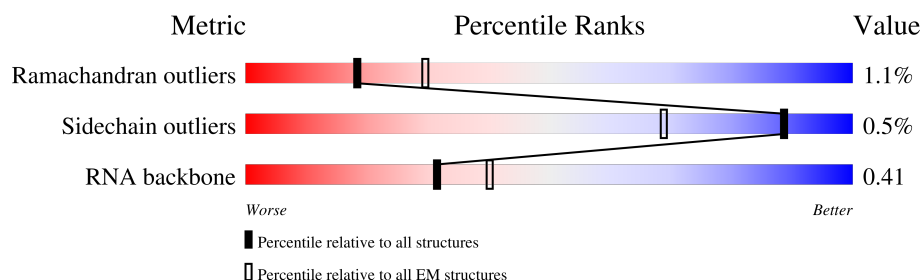
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.60 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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	B	121	
2	C	157	
3	D	257	
4	E	403	
5	F	427	
6	G	297	
7	I	203	
8	J	160	

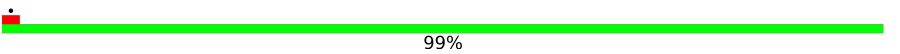

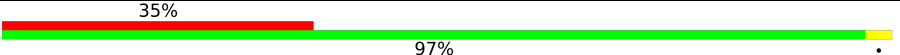
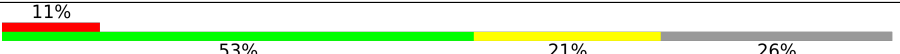
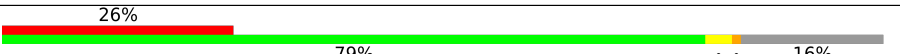
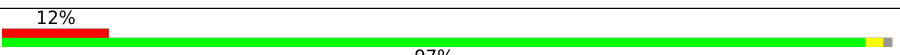
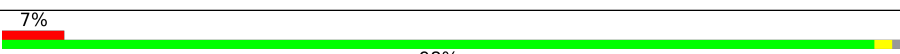
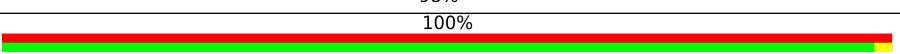
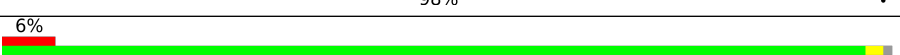
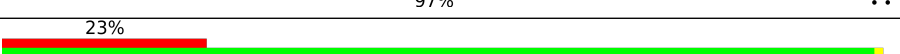
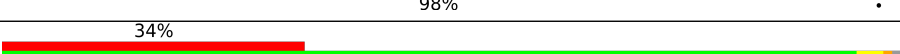
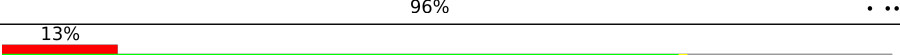
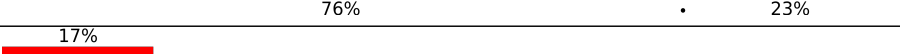
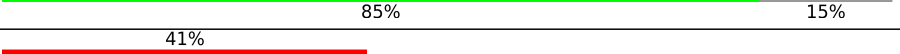

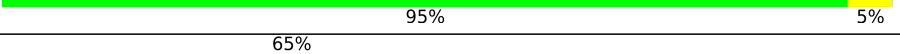
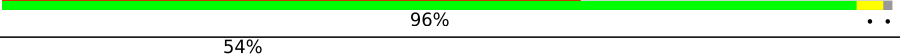



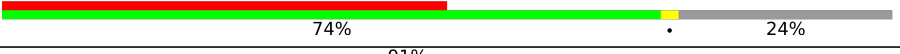
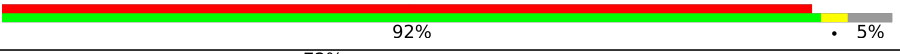
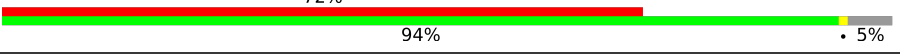
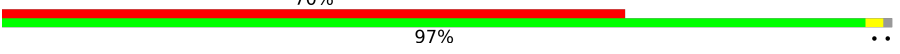
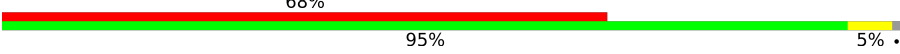
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Mol	Chain	Length	Quality of chain
9	L	196	
10	N	160	
11	O	128	
12	P	140	
13	Q	157	
14	S	145	
15	T	136	
16	U	148	
17	V	159	
18	X	125	
19	Y	135	
20	Z	110	
21	a	117	
22	b	123	
23	c	105	
24	d	97	
25	e	70	
26	f	51	
27	g	128	
28	j	92	
29	k	137	
30	m	248	
31	n	266	
32	o	192	
33	s	215	

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Mol	Chain	Length	Quality of chain
34	t	204	
35	h	25	
36	r	211	
37	A	5070	
38	H	288	
39	i	106	
40	K	188	
41	l	217	
42	M	176	
43	p	214	
44	q	178	
45	R	156	
46	W	115	
47	AA	1869	
48	AC	83	
49	AD	143	
50	AE	115	
51	AF	69	
52	AH	156	
53	AJ	293	
54	AK	249	
55	AL	194	
56	AN	151	
57	AP	130	
58	AQ	133	

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Mol	Chain	Length	Quality of chain
59	AR	125	
60	AT	59	
61	AV	84	
62	An	75	
63	Ap	264	
64	Aq	243	
65	Ar	263	
66	At	194	
67	Au	208	
68	Av	165	
69	Ay	146	
70	A0	152	
71	Ao	295	
72	As	204	
73	Aw	158	
74	Ax	145	
75	Az	135	
76	AB	119	
77	AG	56	
78	AI	317	
79	AM	132	
80	AO	151	
81	AU	145	

## 2 Entry composition

There are 81 unique types of molecules in this entry. The entry contains 217989 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 5S rRNA.

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

- Molecule 2 is a RNA chain called 5.8S rRNA.

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

- Molecule 3 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 4 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	402	Total	C	N	O	S	0	0
			3238	2060	608	556	14		

- Molecule 5 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	367	Total	C	N	O	S	0	0
			2919	1835	582	488	14		

- Molecule 6 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	293	Total	C	N	O	S	0	0
			2382	1507	434	427	14		

- Molecule 7 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	I	201	Total	C	N	O	S	0	0
			1650	1063	321	261	5		

- Molecule 8 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	J	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 9 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L	187	Total	C	N	O	S	0	0
			1566	971	336	250	9		

- Molecule 10 is a protein called 60S ribosomal protein L21.

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

- Molecule 11 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	O	101	Total	C	N	O	S	0	0
			825	529	144	150	2		

- Molecule 12 is a protein called 60S ribosomal protein L23.

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

- Molecule 13 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Q	64	Total	C	N	O	S	0	0
			534	340	104	87	3		

- Molecule 14 is a protein called 60S ribosomal protein L26.

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

- Molecule 15 is a protein called 60S ribosomal protein L27.

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

- Molecule 16 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	U	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 17 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	V	75	Total	C	N	O	S	0	0
			610	378	130	99	3		

- Molecule 18 is a protein called 60S ribosomal protein L31.

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

- Molecule 19 is a protein called 60S ribosomal protein L32.

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

- Molecule 20 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Z	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 21 is a protein called 60S ribosomal protein L34.



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

- Molecule 22 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	b	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		

- Molecule 23 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	c	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 24 is a protein called 60S ribosomal protein L37.

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

- Molecule 25 is a protein called 60S ribosomal protein L38.

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

- Molecule 26 is a protein called 60S ribosomal protein L39.

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

- Molecule 27 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 28 is a protein called 60S ribosomal protein L37a.

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

- Molecule 29 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	k	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		

- Molecule 30 is a protein called 60S ribosomal protein L7.

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

- Molecule 31 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	n	241	Total	C	N	O	S	0	0
			1927	1228	371	324	4		

- Molecule 32 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	o	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 33 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	s	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		

- Molecule 34 is a protein called 60S ribosomal protein L15.

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

- Molecule 35 is a protein called 60S Ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	h	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

- Molecule 36 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	r	210	Total	C	N	O	S	0	0
			1701	1064	352	281	4		

- Molecule 37 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	A	3776	Total	C	N	O	P	0	0
			80184	35672	14597	26140	3775		

- Molecule 38 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	H	242	Total	C	N	O	S	0	0
			1958	1257	372	325	4		

- Molecule 39 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	105	Total	C	N	O	S	0	0
			862	542	175	139	6		

- Molecule 40 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	K	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 41 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	l	217	Total	C	N	O	S	0	0
			1741	1113	312	307	9		

- Molecule 42 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	M	175	Total	C	N	O	S	0	0
			1453	925	283	235	10		

- Molecule 43 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	p	213	Total	C	N	O	S	0	0
			1711	1082	329	285	15		

- Molecule 44 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	q	176	Total	C	N	O	S	0	0
			1410	888	263	253	6		

- Molecule 45 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	R	120	Total	C	N	O	S	0	0
			985	630	185	169	1		

- Molecule 46 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	W	98	Total	C	N	O	S	0	0
			764	485	135	138	6		

- Molecule 47 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	AA	1742	Total	C	N	O	P	0	0
			36900	16458	6595	12106	1741		

- Molecule 48 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	AC	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
49	AD	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 50 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	AE	101	Total	C	N	O	S	0	0
			814	507	170	132	5		

- Molecule 51 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	AF	63	Total	C	N	O	S	0	0
			498	302	101	93	2		

- Molecule 52 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	AH	71	Total	C	N	O	S	0	0
			581	367	109	98	7		

- Molecule 53 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	AJ	222	Total	C	N	O	S	0	0
			1725	1115	298	302	10		

- Molecule 54 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	AK	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 55 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	AL	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 56 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	AN	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 57 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	AP	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 58 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	AQ	131	Total	C	N	O	S	0	0
			1065	673	209	178	5		

- Molecule 59 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	AR	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 60 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	AT	58	Total	C	N	O	S	0	0
			459	284	100	74	1		

- Molecule 61 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	AV	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 62 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	An	75	Total	C	N	O	P	0	0
			1604	717	298	515	74		

- Molecule 63 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Ap	214	Total	C	N	O	S	0	0
			1738	1103	310	311	14		

- Molecule 64 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Aq	227	Total	C	N	O	S	0	0
			1765	1125	317	315	8		

- Molecule 65 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Ar	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 66 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	At	189	Total	C	N	O	S	0	0
			1521	969	280	271	1		

- Molecule 67 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Au	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

- Molecule 68 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Av	98	Total	C	N	O	S	0	0
			827	539	148	134	6		

- Molecule 69 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Ay	146	Total	C	N	O	S	0	0
			1158	736	218	200	4		

- Molecule 70 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	A0	150	Total	C	N	O	S	0	0
			1235	776	250	208	1		

- Molecule 71 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Ao	222	Total	C	N	O	S	0	0
			1747	1109	306	324	8		

- Molecule 72 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	As	191	Total	C	N	O	S	0	0
			1509	943	286	273	7		

- Molecule 73 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Aw	153	Total	C	N	O	S	0	0
			1247	793	234	214	6		

- Molecule 74 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Ax	97	Total	C	N	O	S	0	0
			804	505	155	138	6		

- Molecule 75 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Az	132	Total	C	N	O	S	0	0
			1072	673	199	195	5		

- Molecule 76 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	AB	102	Total	C	N	O	S	0	0
			807	507	153	143	4		

- Molecule 77 is a protein called 40S ribosomal protein S29.



Mol	Chain	Residues	Atoms					AltConf	Trace
77	AG	53	Total	C	N	O	S	0	0
			445	278	90	72	5		

- Molecule 78 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	AI	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 79 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	AM	122	Total	C	N	O	S	0	0
			952	596	169	179	8		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AM	52	GLN	LEU	conflict	UNP P25398
AM	69	LEU	CYS	conflict	UNP P25398
AM	99	ASN	LYS	conflict	UNP P25398

- Molecule 80 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	AO	140	Total	C	N	O	S	0	0
			1049	642	204	197	6		

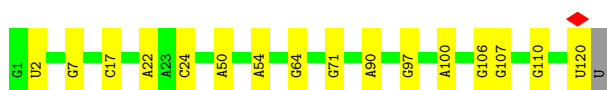
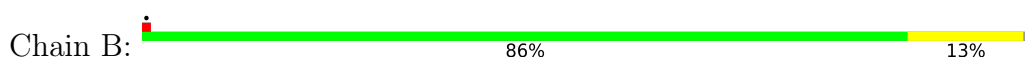
- Molecule 81 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	AU	143	Total	C	N	O	S	0	0
			1112	697	214	198	3		

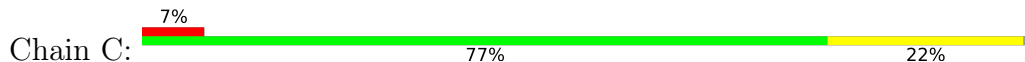
### 3 Residue-property plots [i](#)

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.

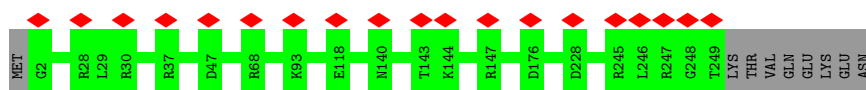
- Molecule 1: 5S rRNA



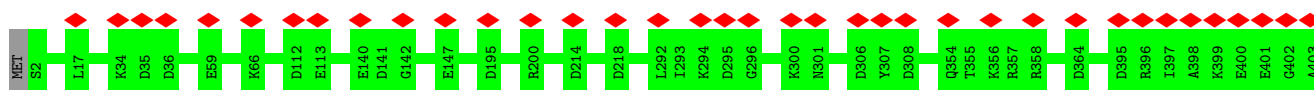
- Molecule 2: 5.8S rRNA



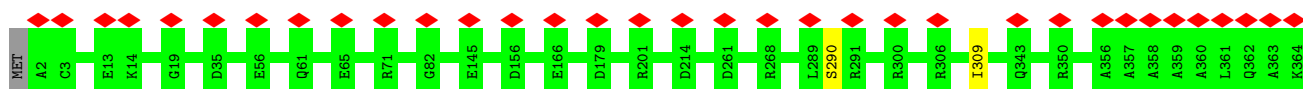
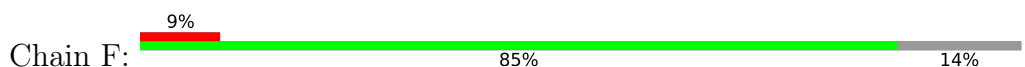
- Molecule 3: 60S ribosomal protein L8



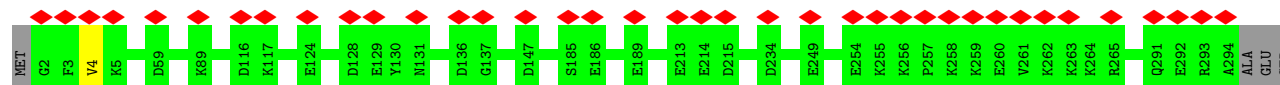
- Molecule 4: 60S ribosomal protein L3



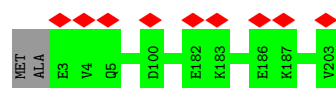
- Molecule 5: 60S ribosomal protein L4



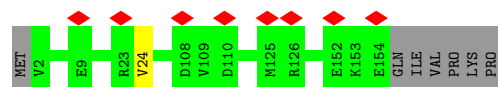
- Molecule 6: 60S ribosomal protein L5



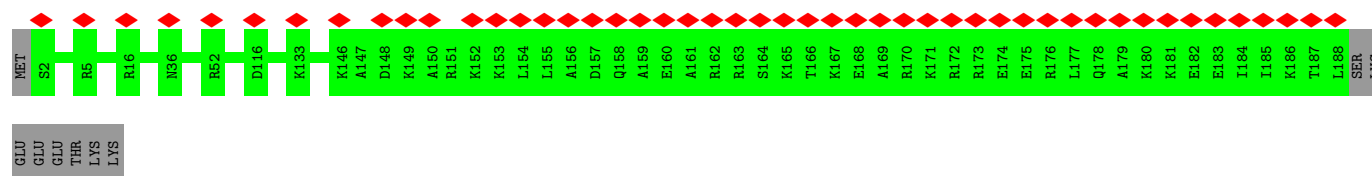
- Molecule 7: 60S ribosomal protein L13a



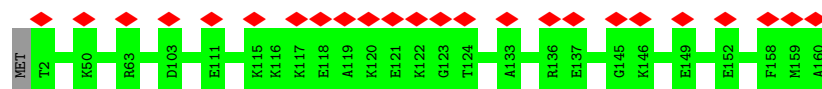
- Molecule 8: 60S ribosomal protein L17



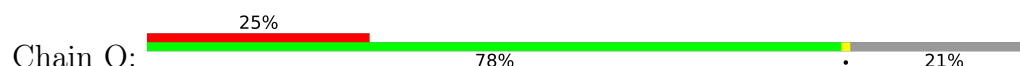
- Molecule 9: 60S ribosomal protein L19

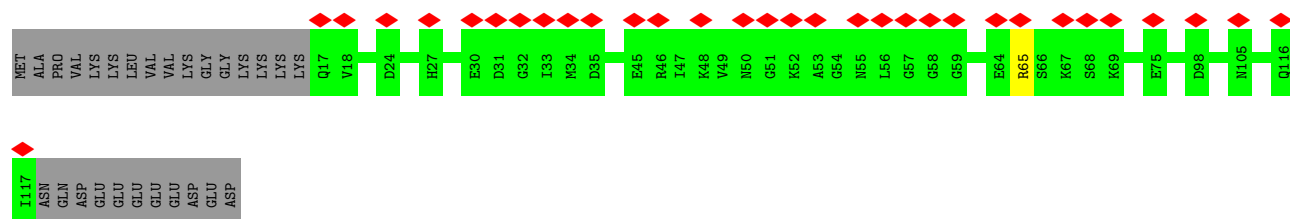


- Molecule 10: 60S ribosomal protein L21

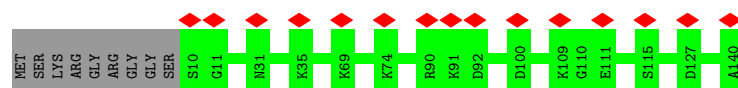


- Molecule 11: 60S ribosomal protein L22

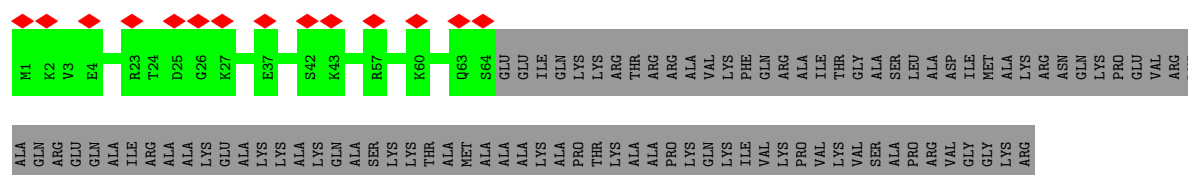




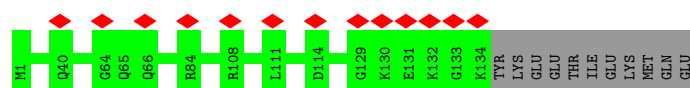
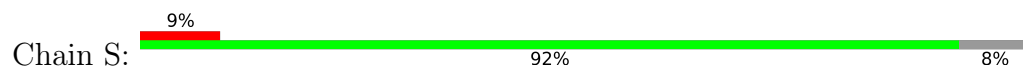
- Molecule 12: 60S ribosomal protein L23



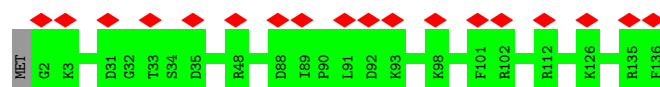
- Molecule 13: 60S ribosomal protein L24



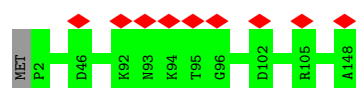
- Molecule 14: 60S ribosomal protein L26



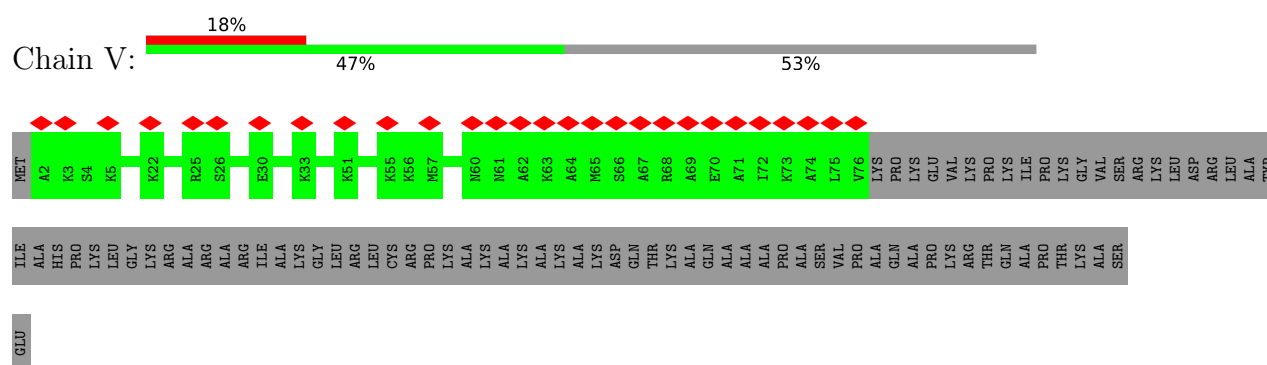
- Molecule 15: 60S ribosomal protein L27



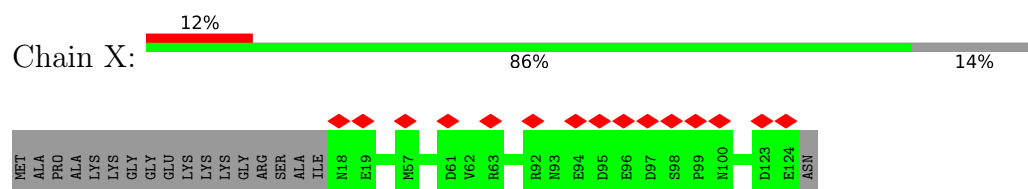
- Molecule 16: 60S ribosomal protein L27a



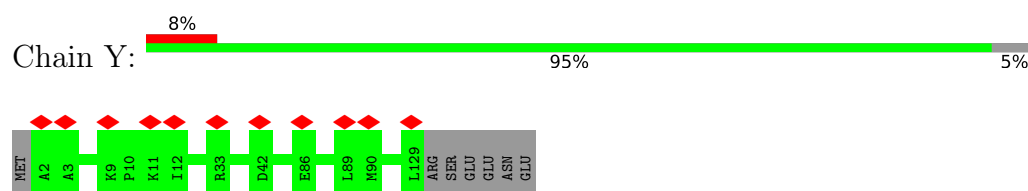
- Molecule 17: 60S ribosomal protein L29



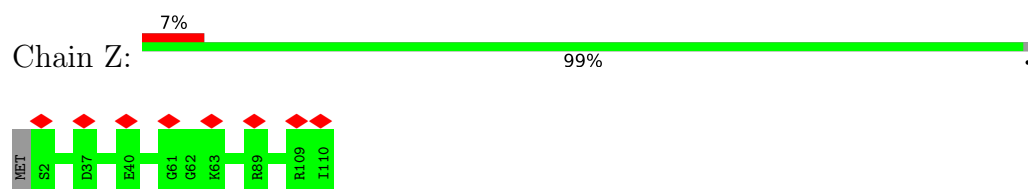
- Molecule 18: 60S ribosomal protein L31



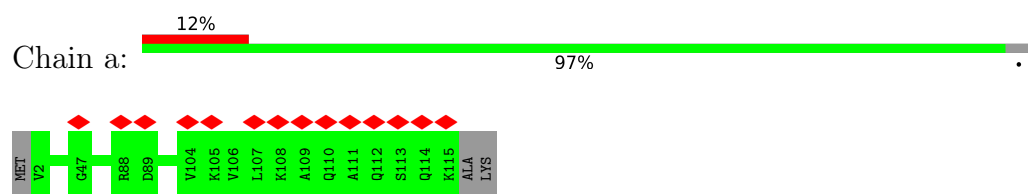
- Molecule 19: 60S ribosomal protein L32



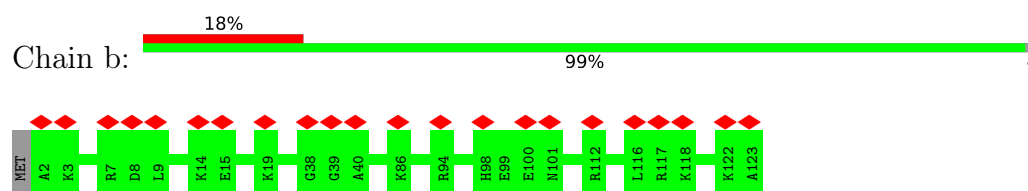
- Molecule 20: 60S ribosomal protein L35a



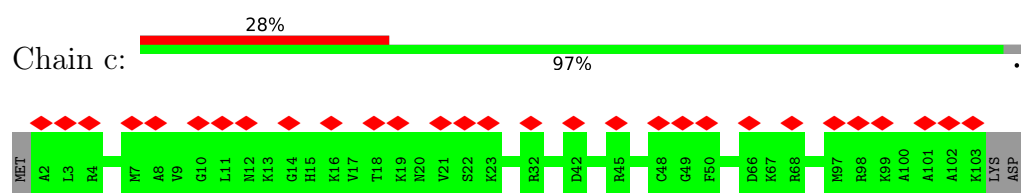
- Molecule 21: 60S ribosomal protein L34



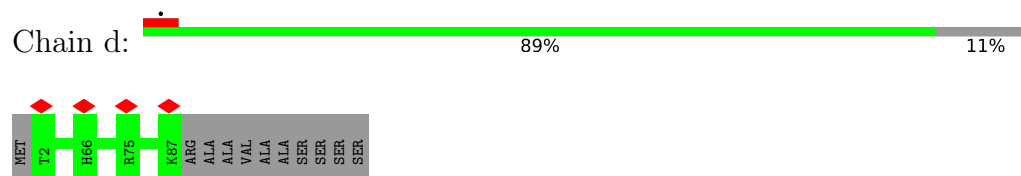
- Molecule 22: 60S ribosomal protein L35



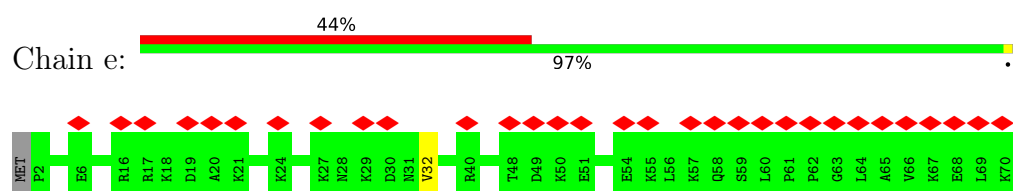
- Molecule 23: 60S ribosomal protein L36



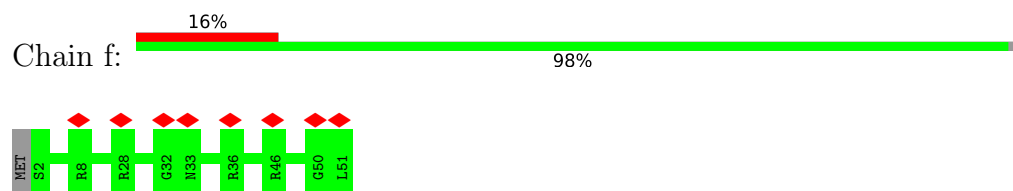
- Molecule 24: 60S ribosomal protein L37



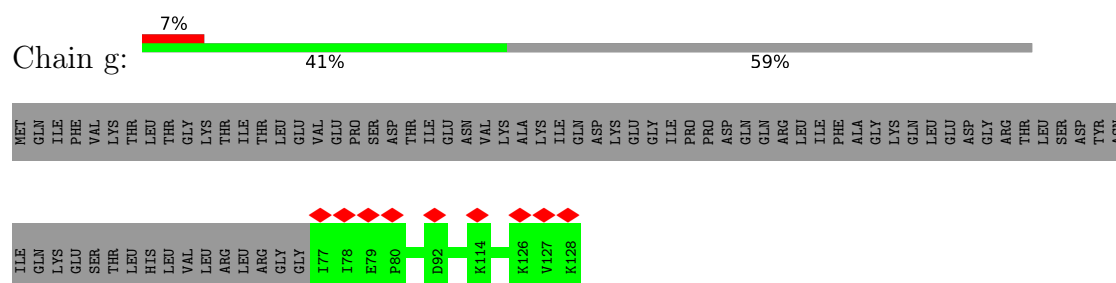
- Molecule 25: 60S ribosomal protein L38



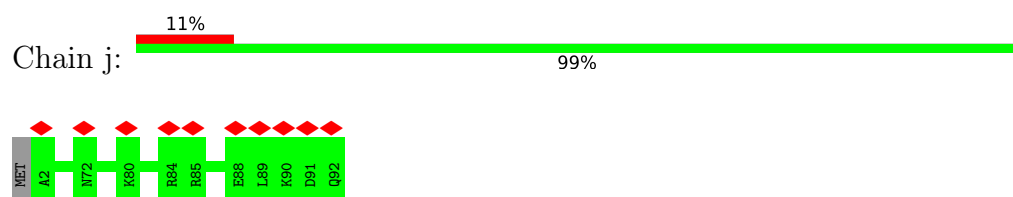
- Molecule 26: 60S ribosomal protein L39



- Molecule 27: Ubiquitin-60S ribosomal protein L40



- Molecule 28: 60S ribosomal protein L37a

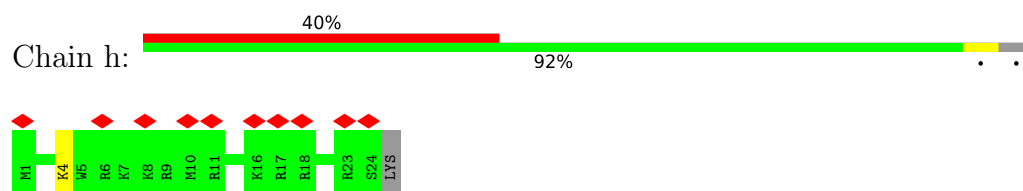


- Molecule 29: 60S ribosomal protein L28

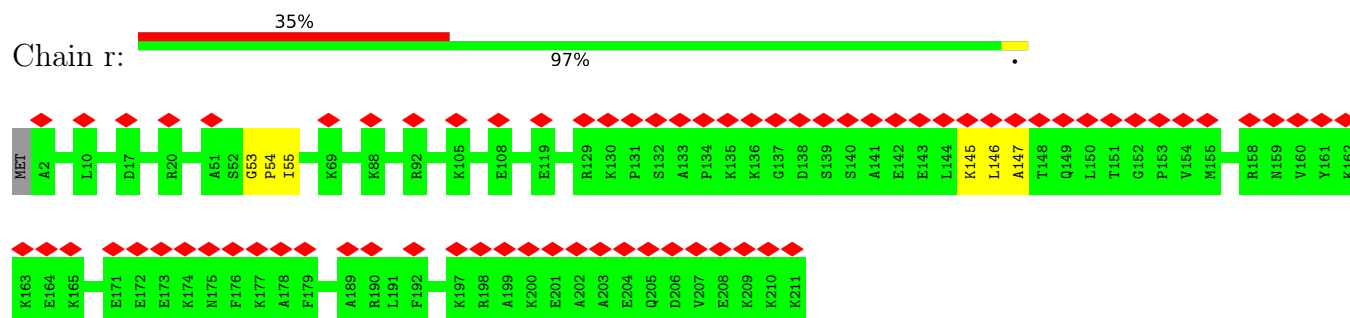




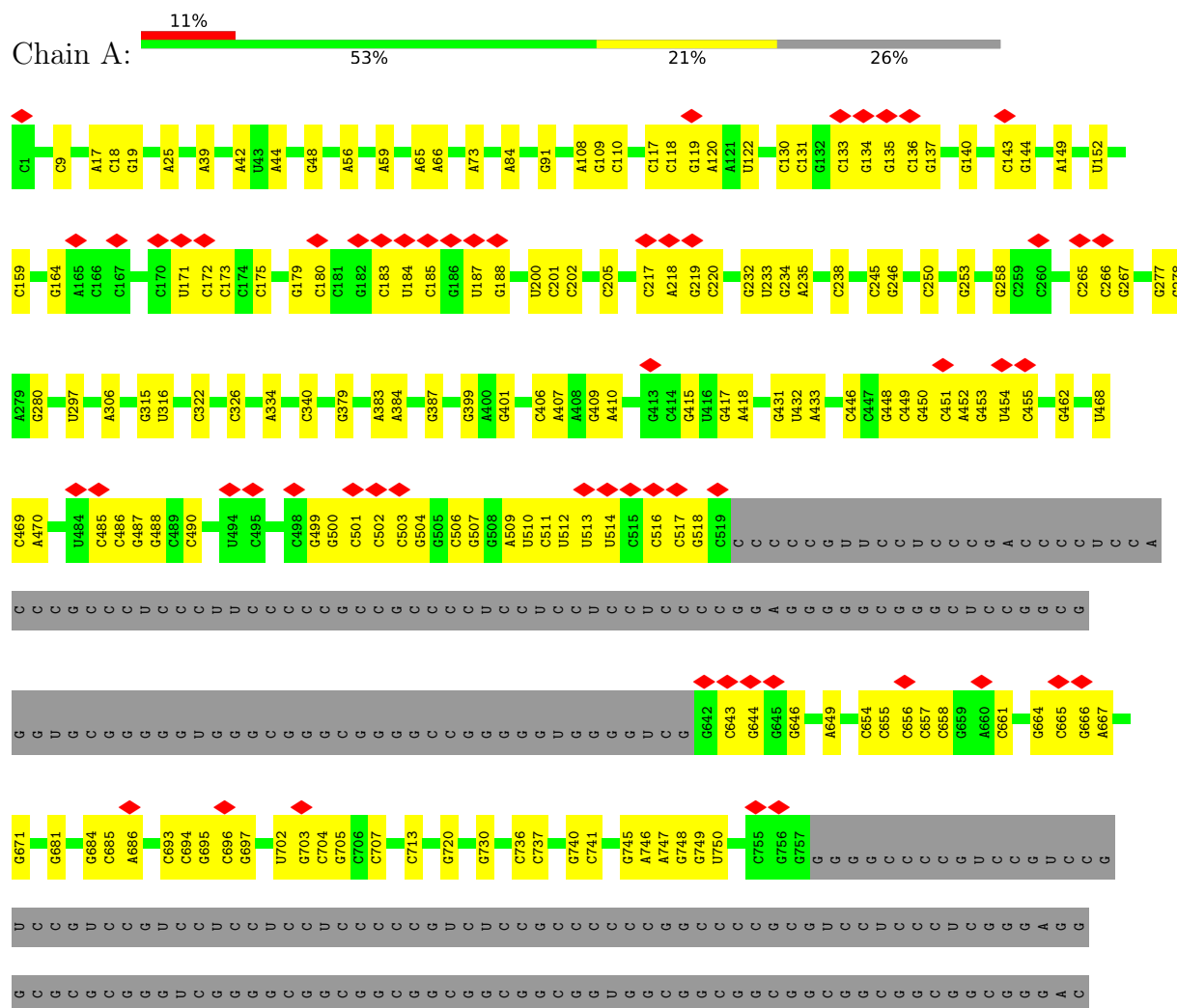
- Molecule 35: 60S Ribosomal protein L41



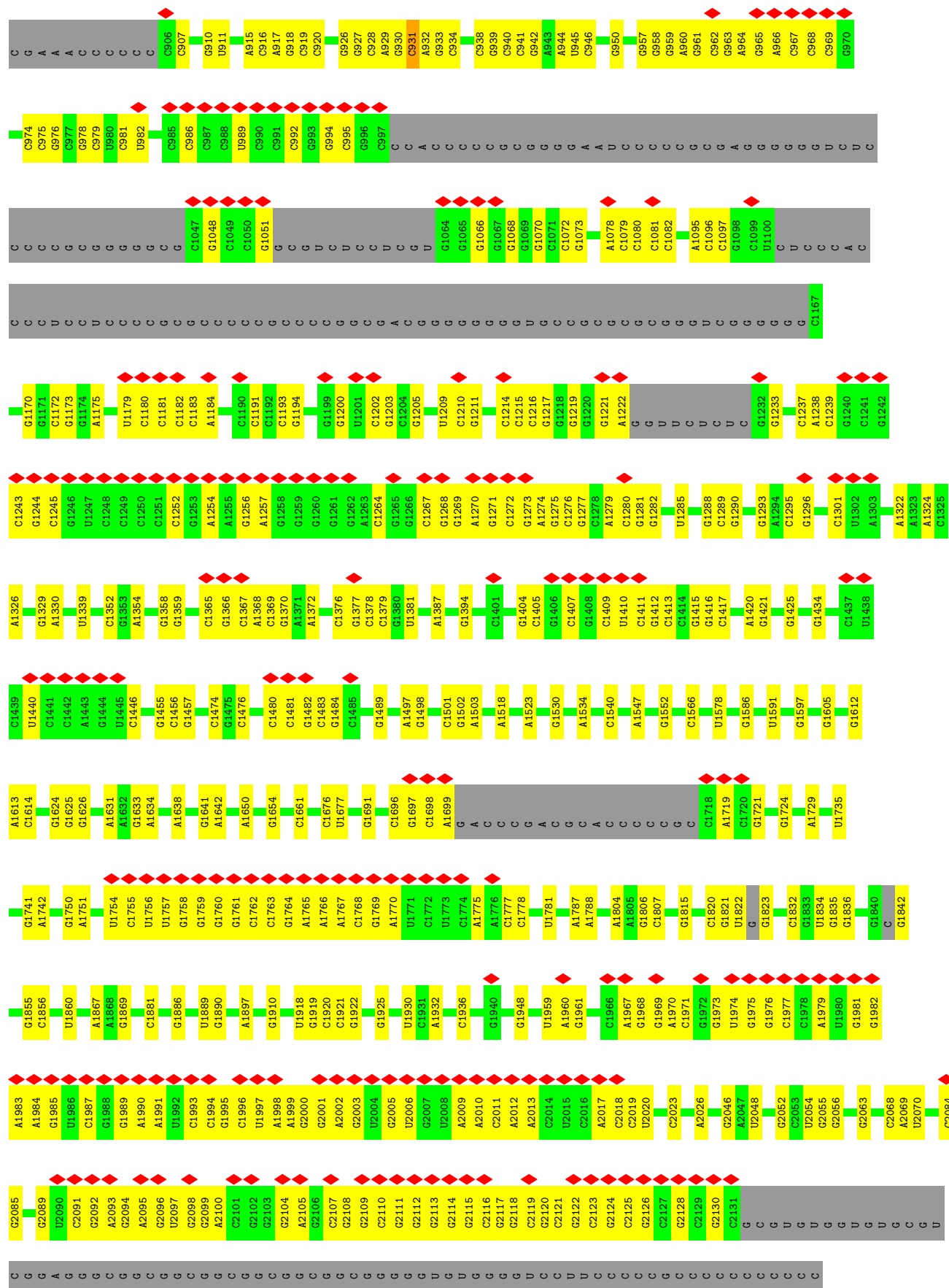
- Molecule 36: 60S ribosomal protein L13

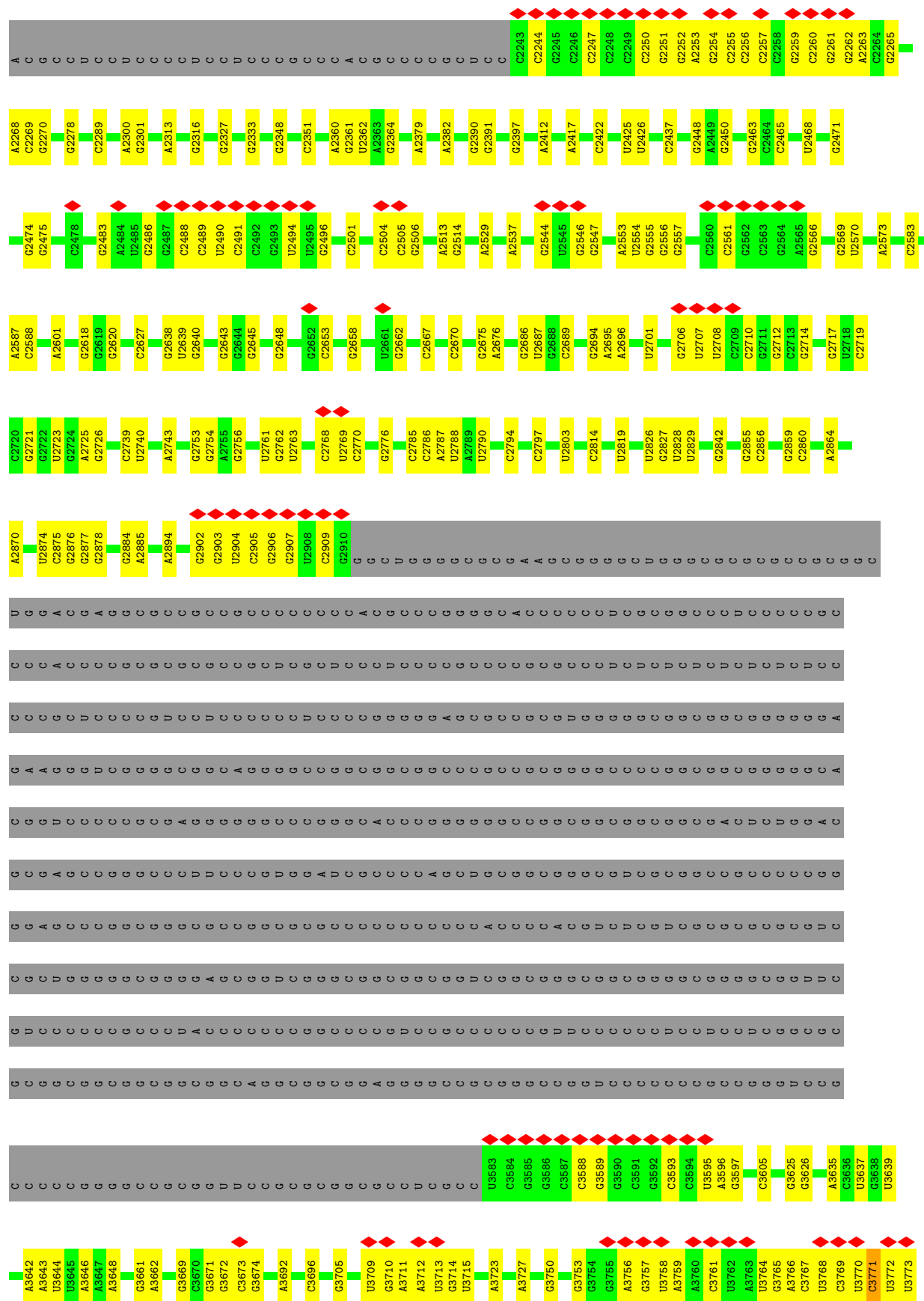


- Molecule 37: 28S rRNA

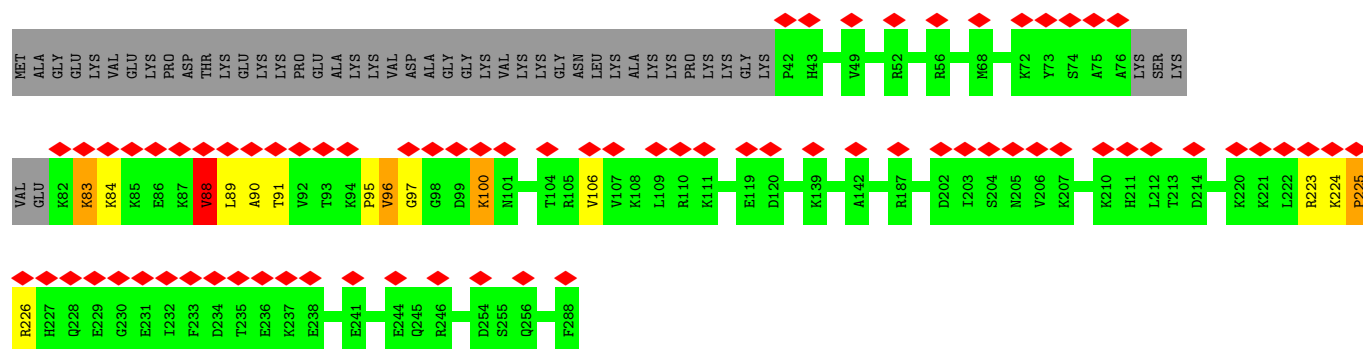




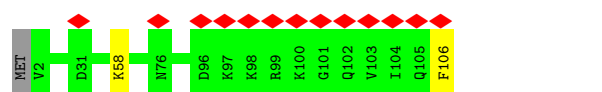




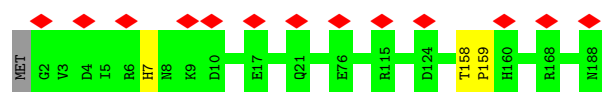




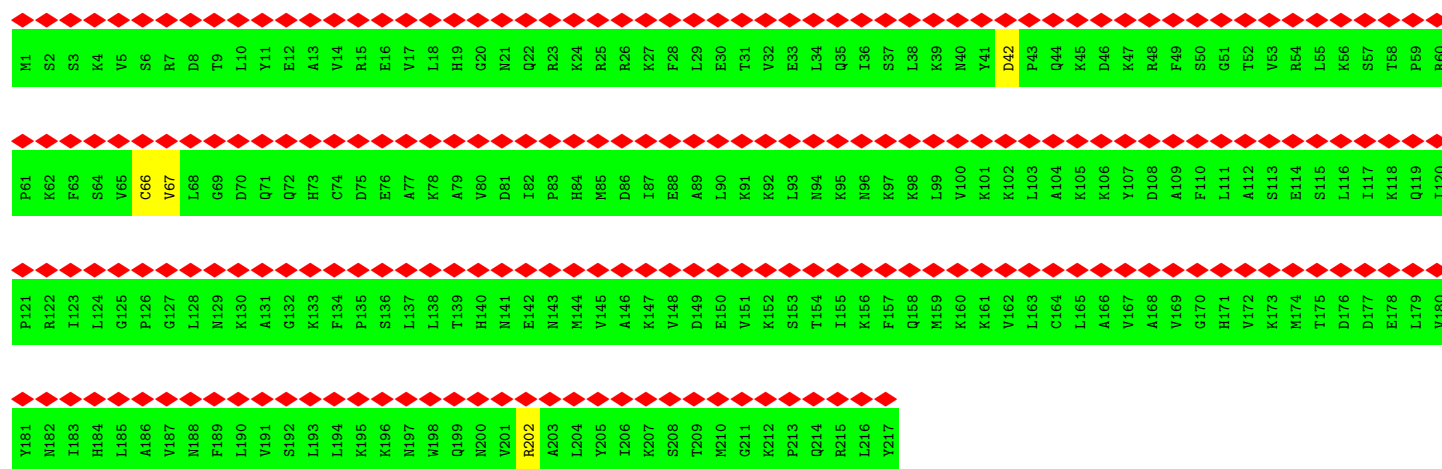
- Molecule 39: 60S ribosomal protein L36a



- Molecule 40: 60S ribosomal protein L18

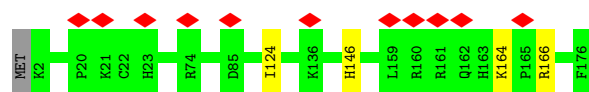


- Molecule 41: 60S ribosomal protein L10a

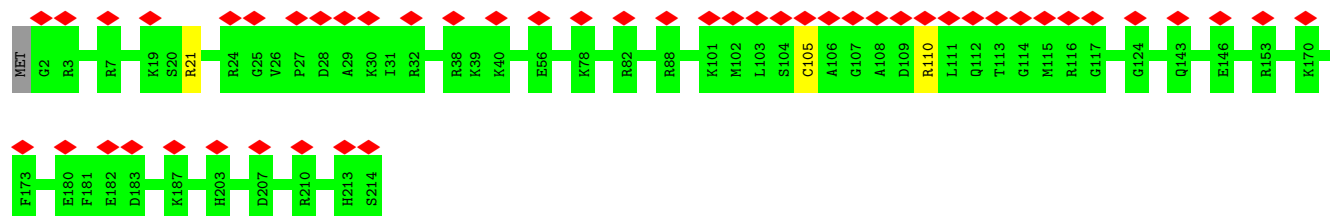


- Molecule 42: 60S ribosomal protein L18a

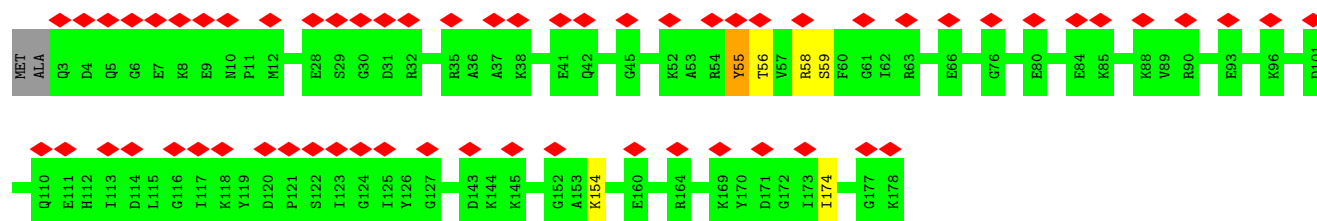
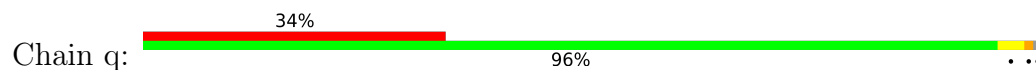




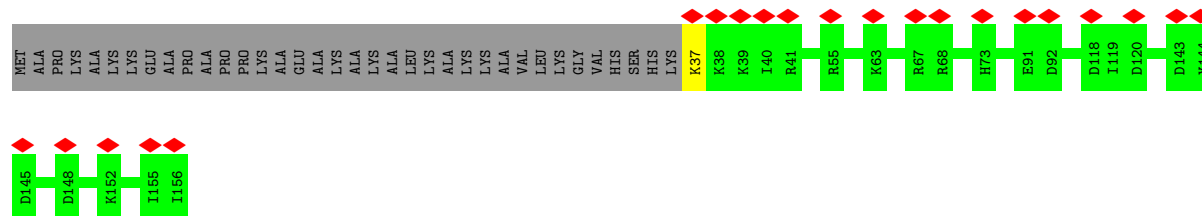
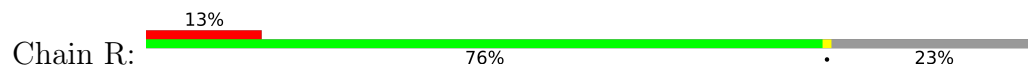
- Molecule 43: 60S ribosomal protein L10-like



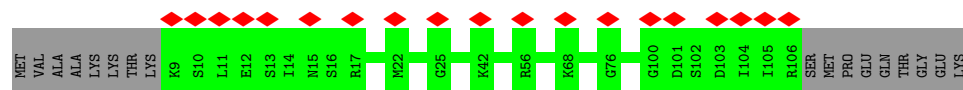
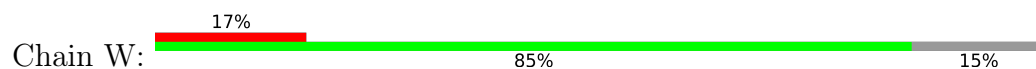
- Molecule 44: 60S ribosomal protein L11



- Molecule 45: 60S ribosomal protein L23a

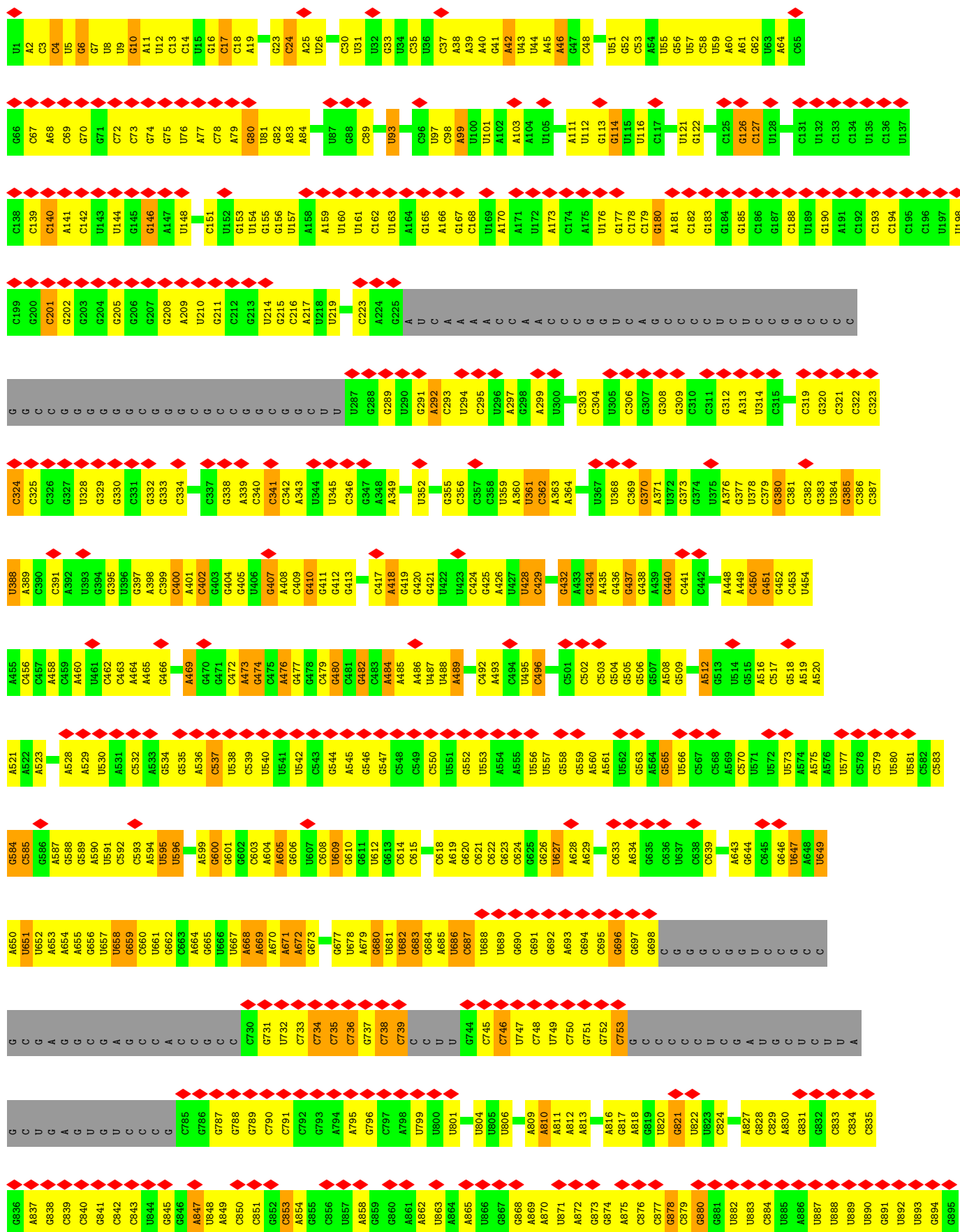


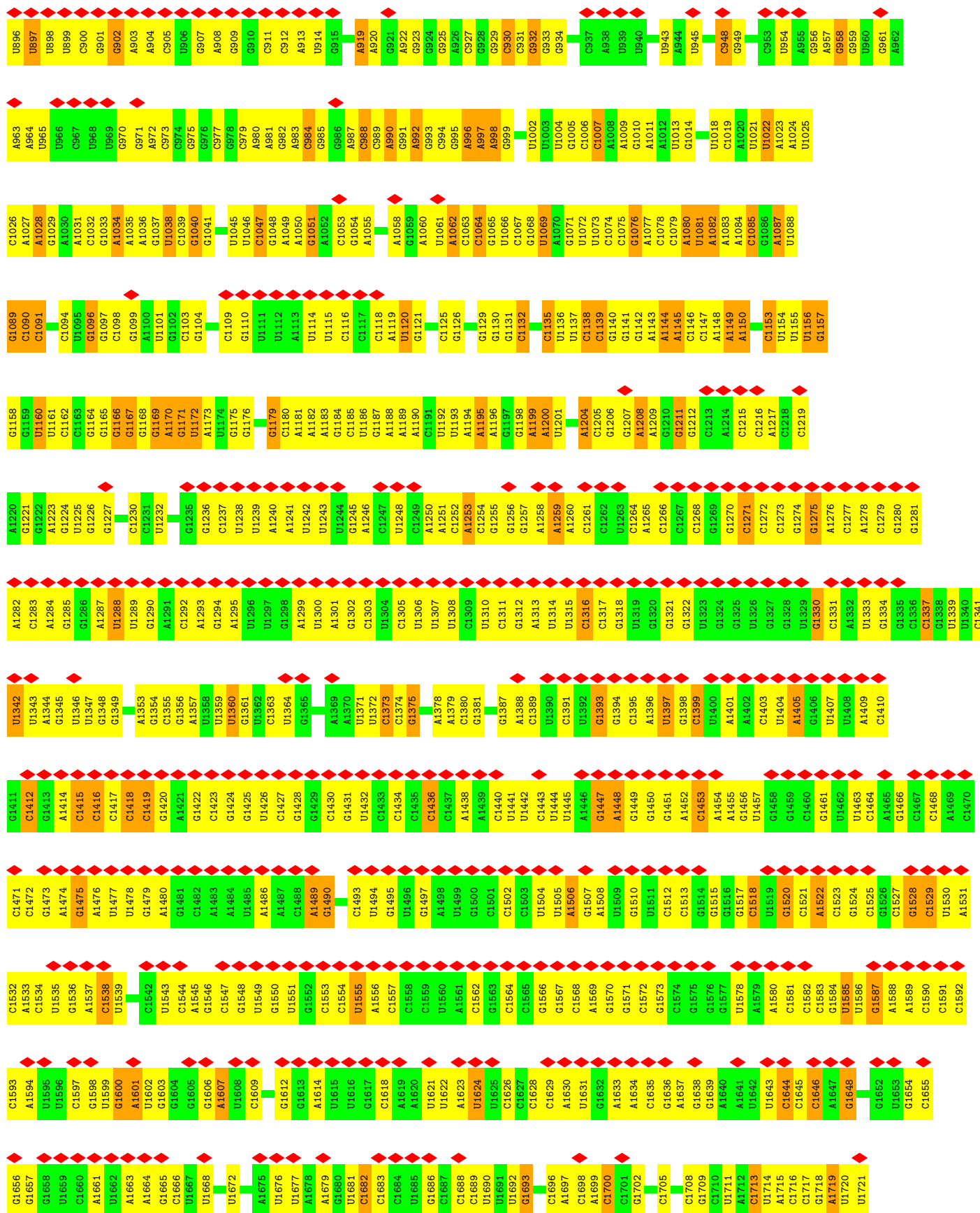
- Molecule 46: 60S ribosomal protein L30

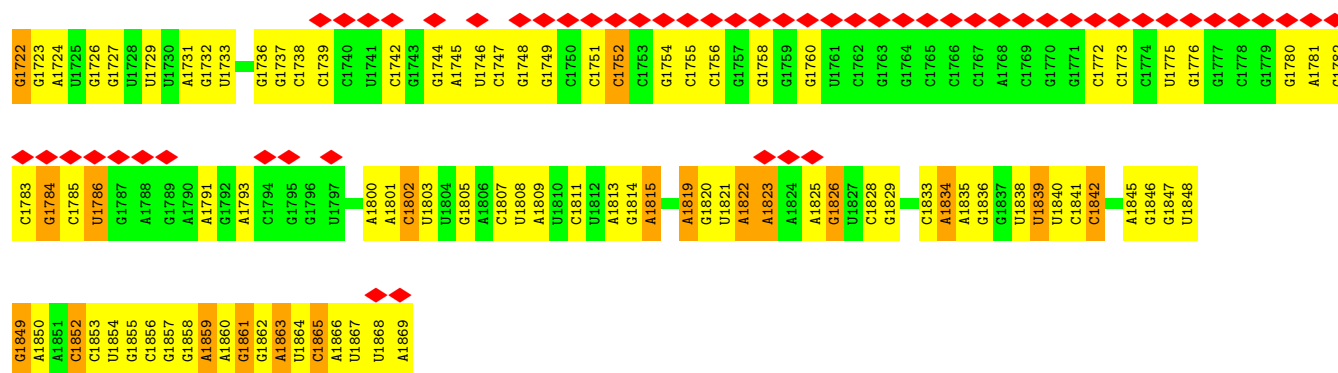


- Molecule 47: 18S rRNA

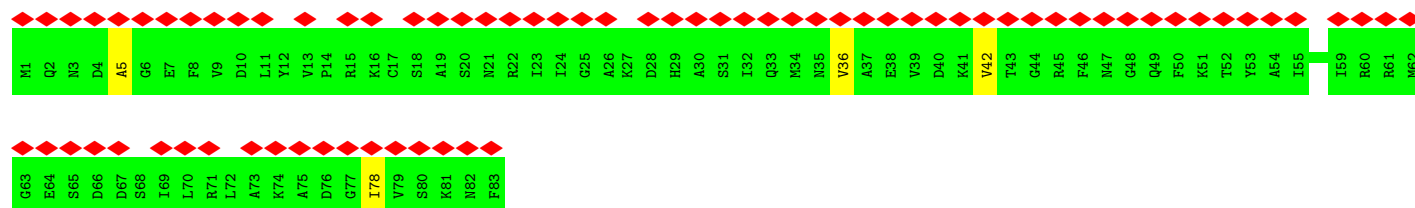
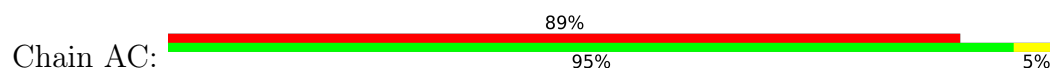




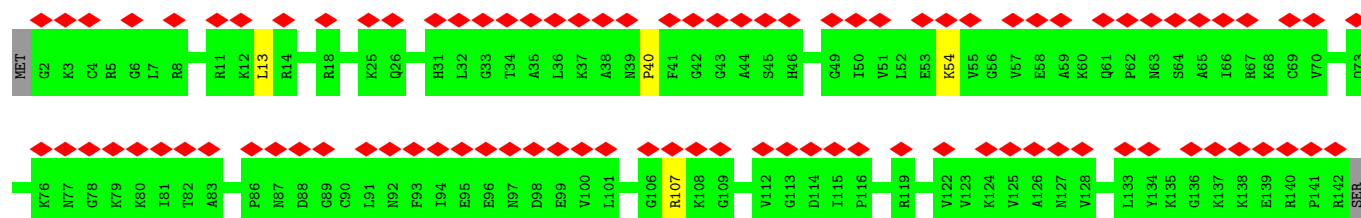




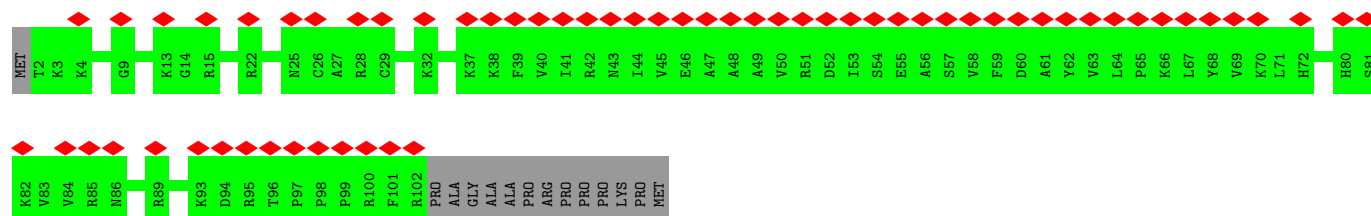
• Molecule 48: 40S ribosomal protein S21



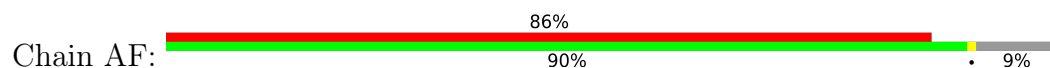
• Molecule 49: 40S ribosomal protein S23



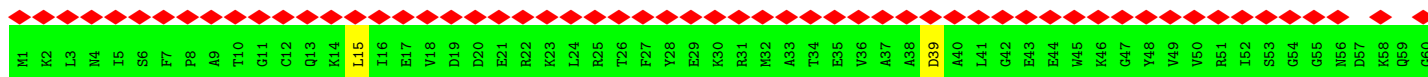
• Molecule 50: 40S ribosomal protein S26

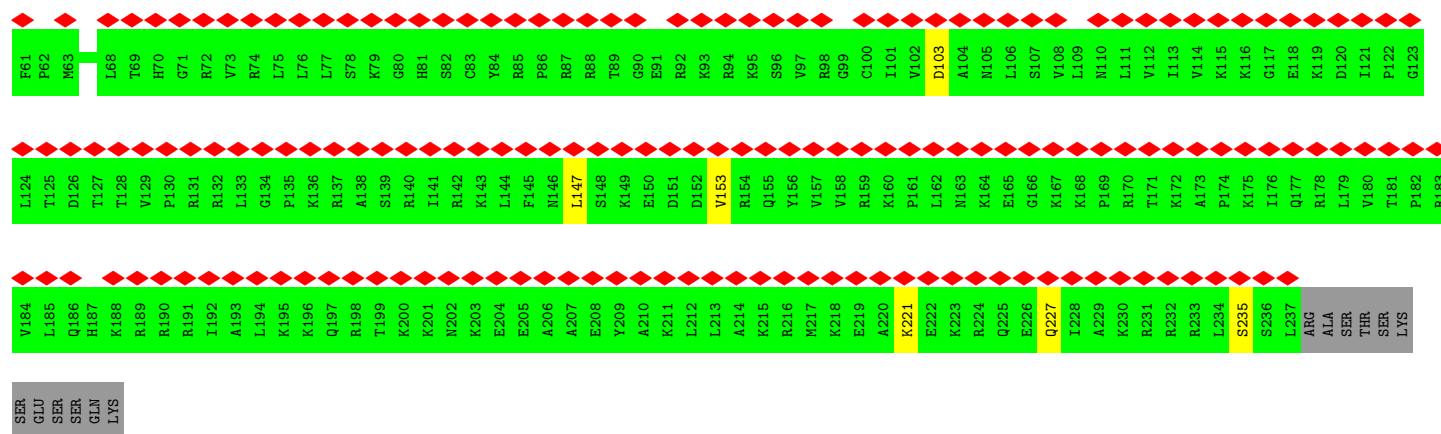


• Molecule 51: 40S ribosomal protein S28



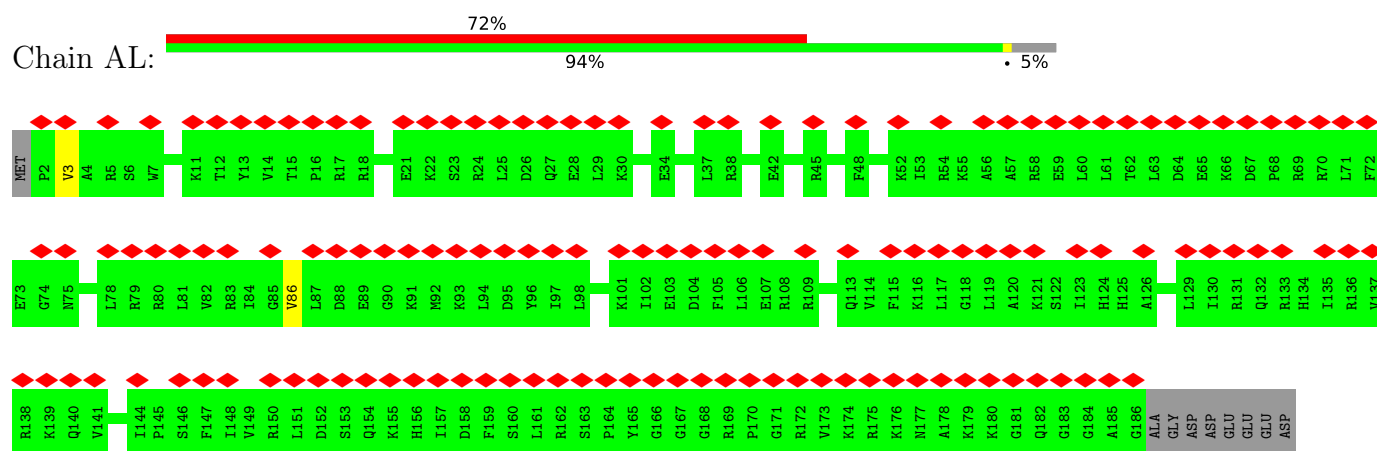






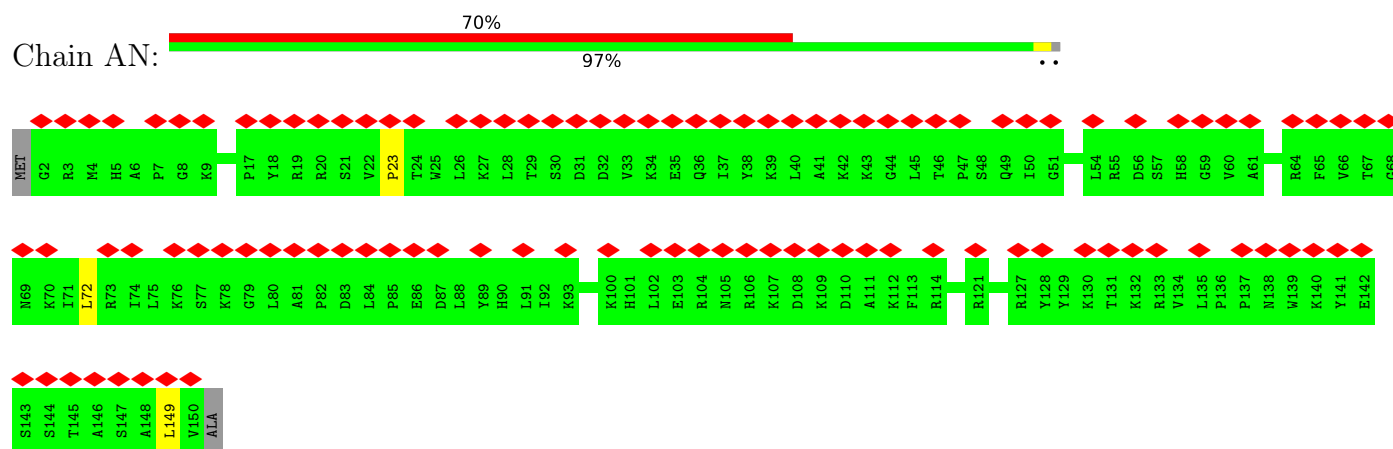
• Molecule 55: 40S ribosomal protein S9

Chain AL:



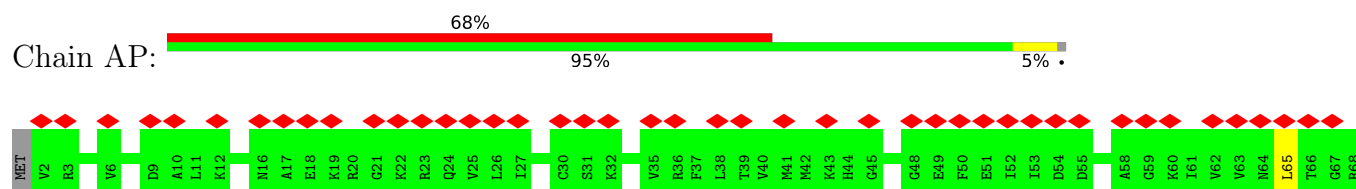
• Molecule 56: 40S ribosomal protein S13

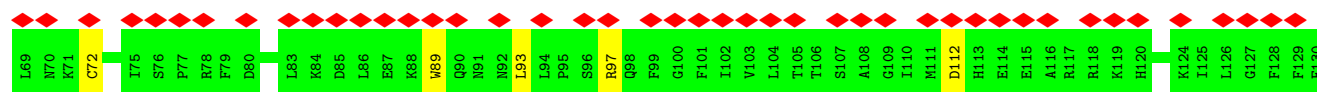
Chain AN:



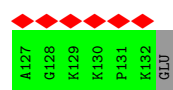
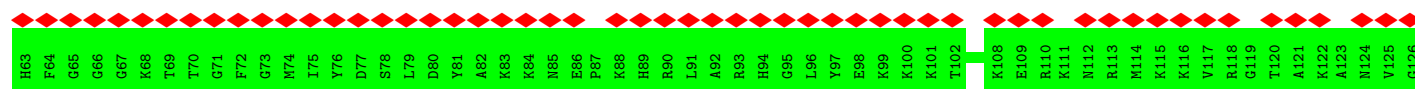
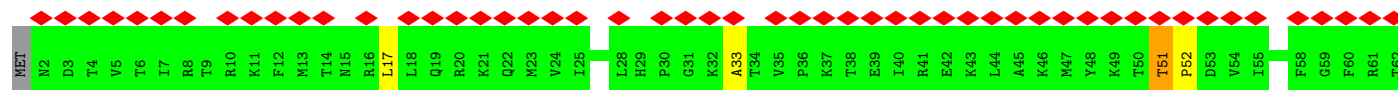
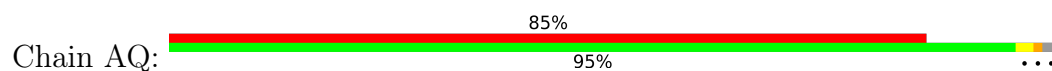
• Molecule 57: 40S ribosomal protein S15a

Chain AP:

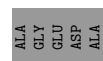
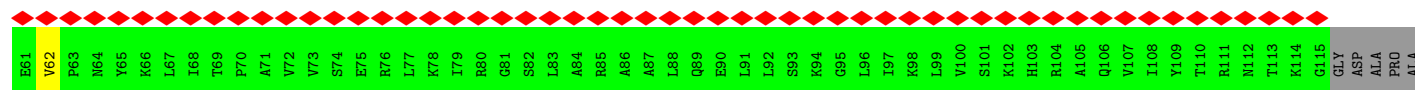
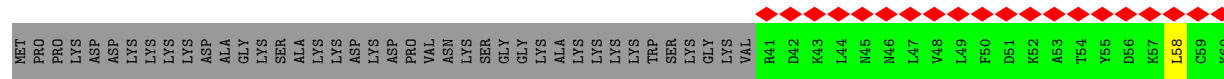




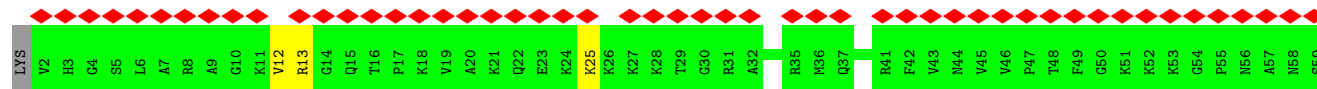
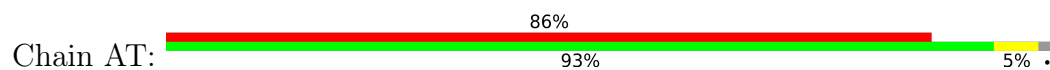
• Molecule 58: 40S ribosomal protein S24



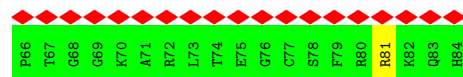
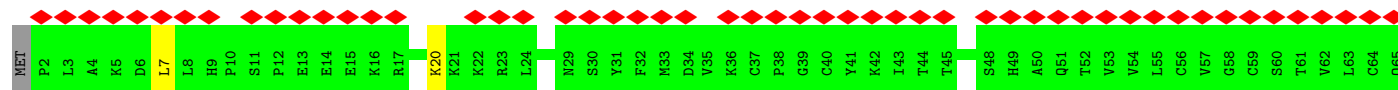
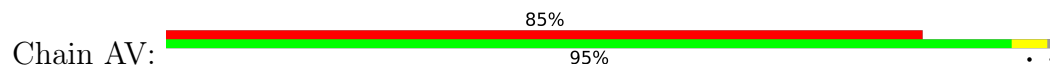
• Molecule 59: 40S ribosomal protein S25



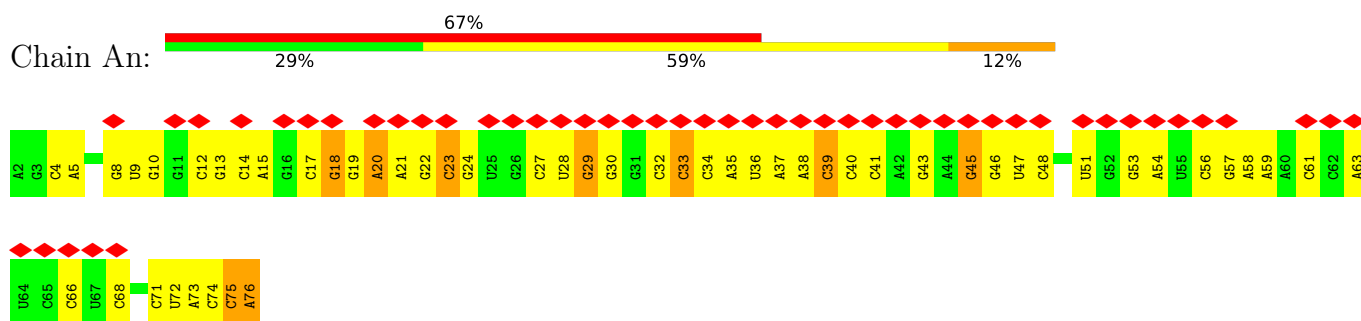
• Molecule 60: 40S ribosomal protein S30



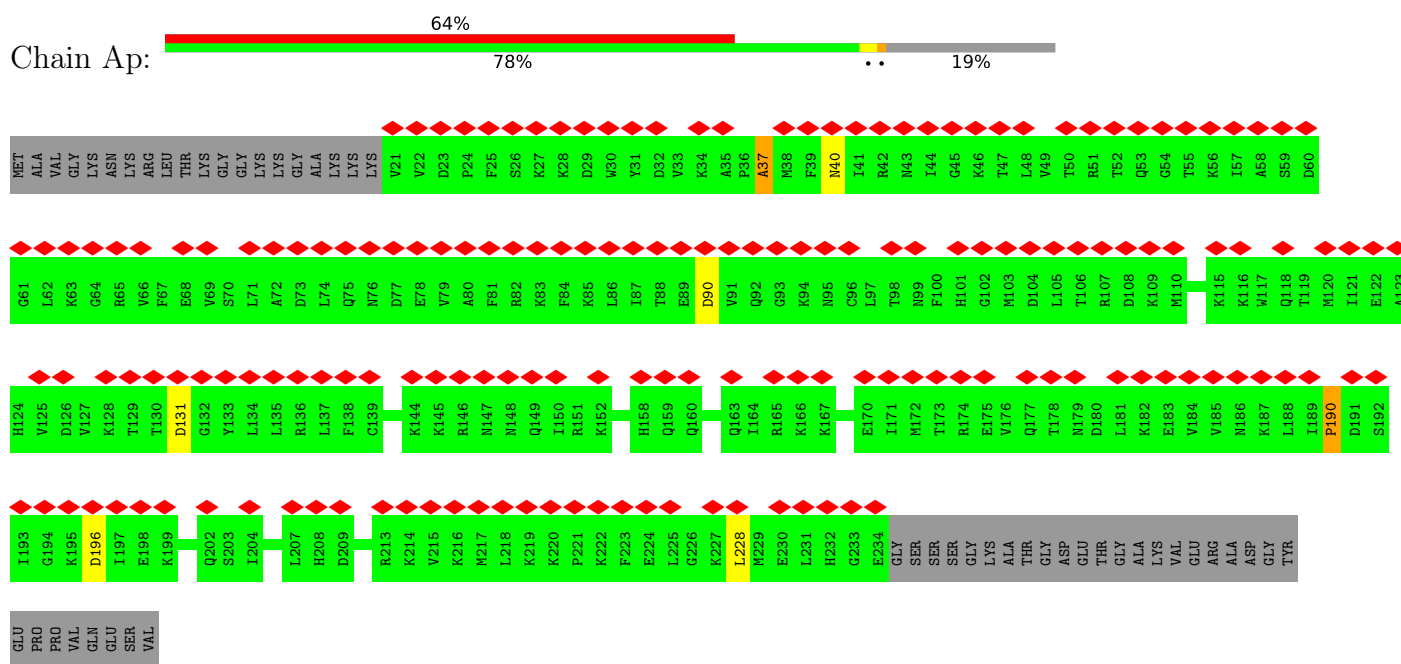
• Molecule 61: 40S ribosomal protein S27



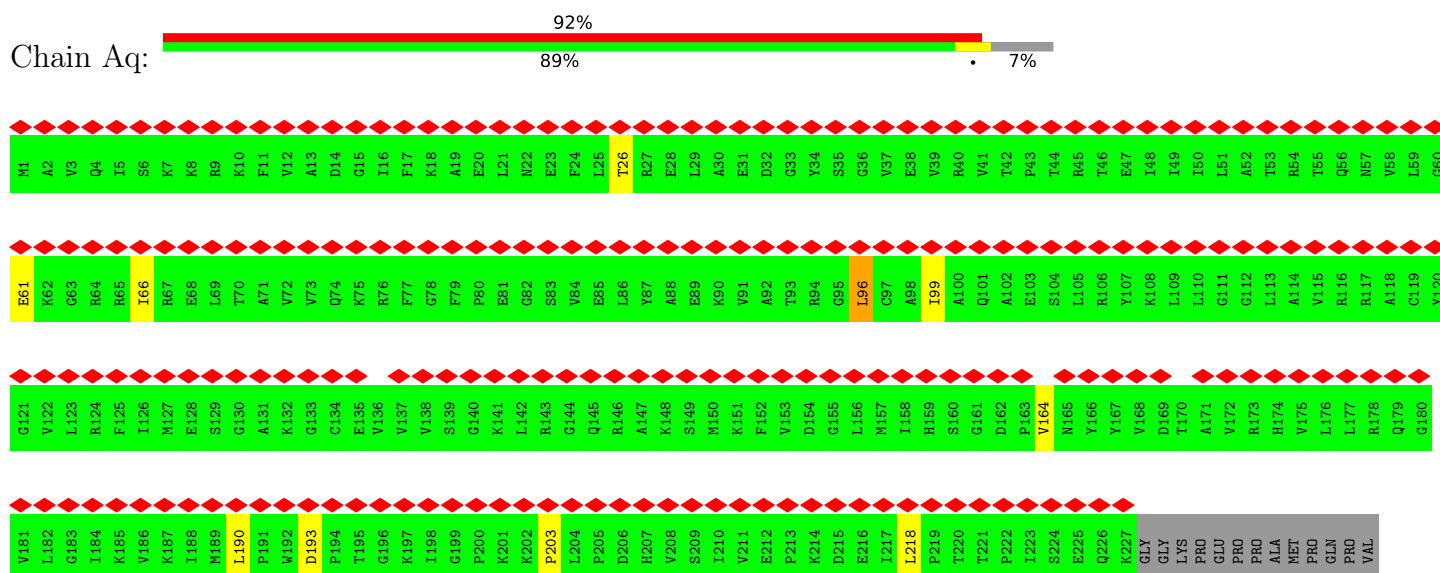
- Molecule 62: tRNA



- Molecule 63: 40S ribosomal protein S3a

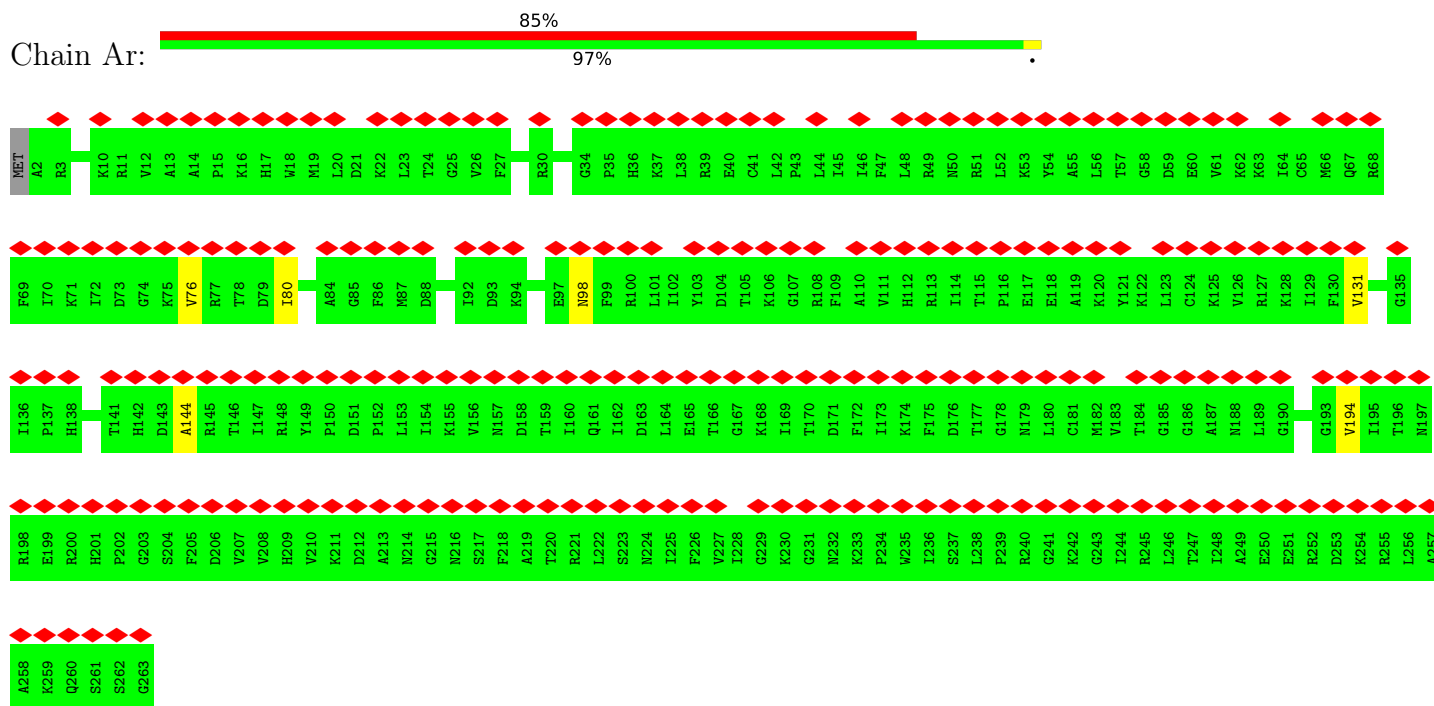


- Molecule 64: 40S ribosomal protein S3

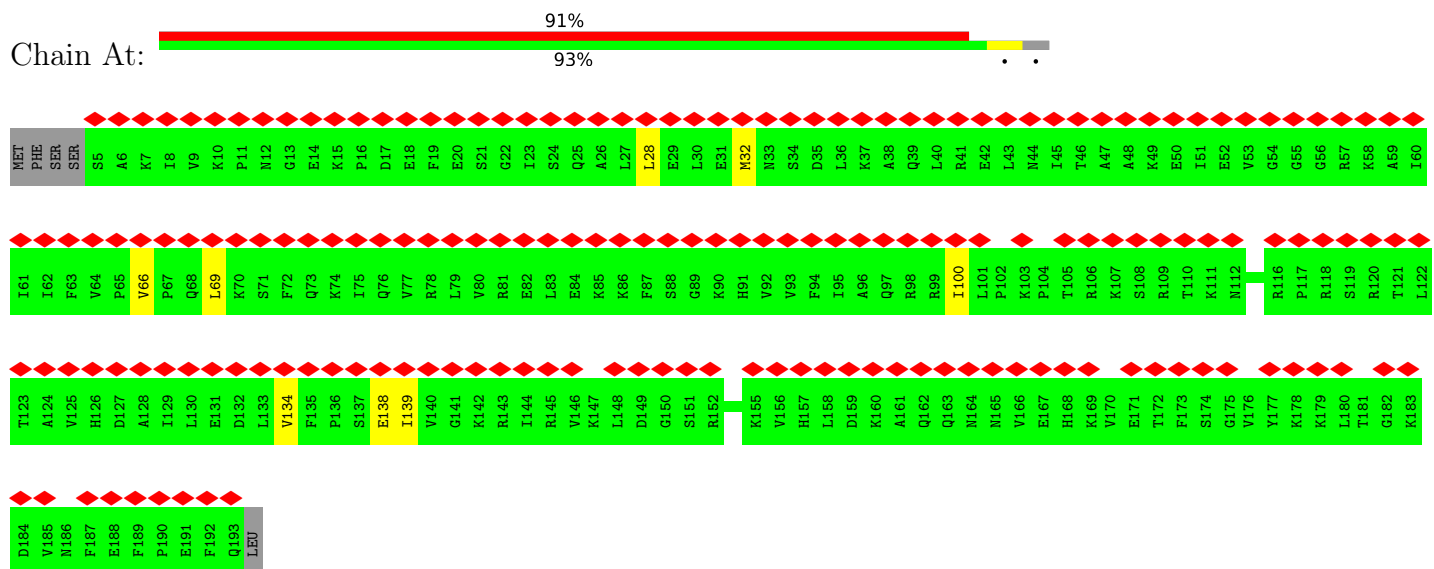


PRO  
THR  
ALA

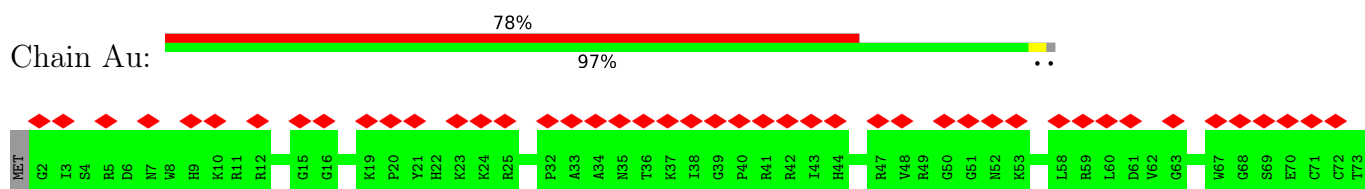
- Molecule 65: 40S ribosomal protein S4, X isoform

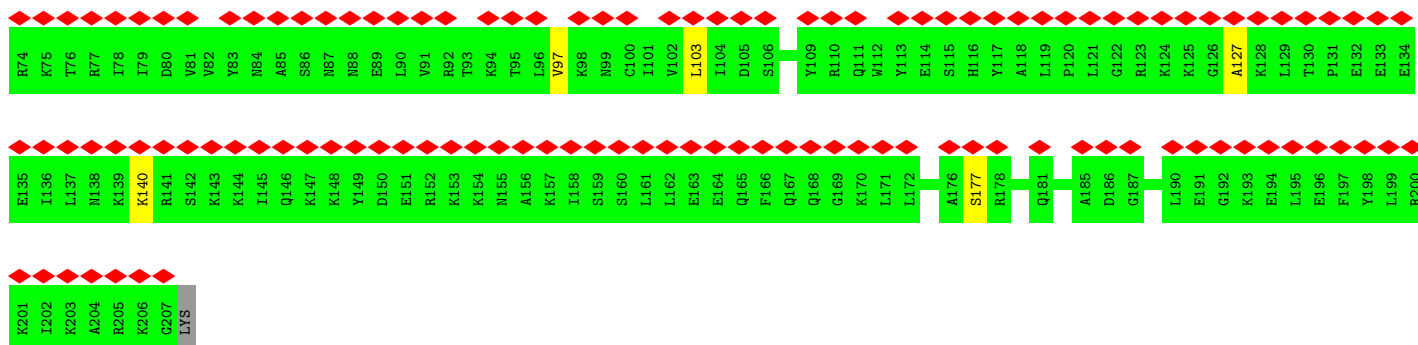


- Molecule 66: 40S ribosomal protein S7

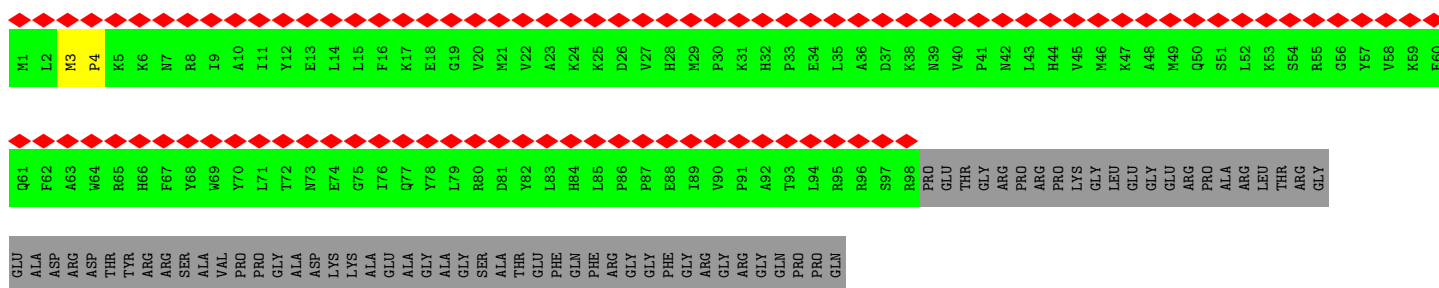


- Molecule 67: 40S ribosomal protein S8

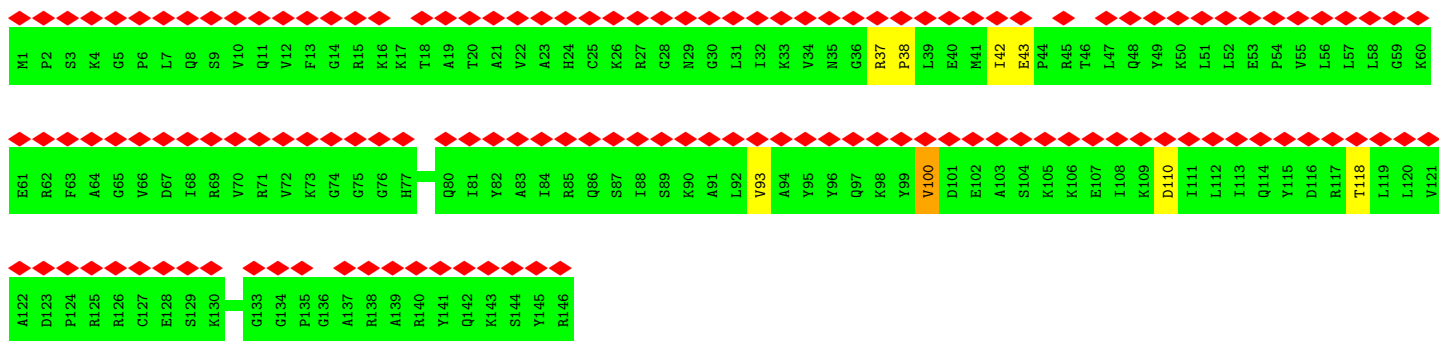




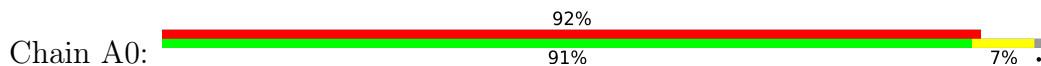
• Molecule 68: 40S ribosomal protein S10



• Molecule 69: 40S ribosomal protein S16

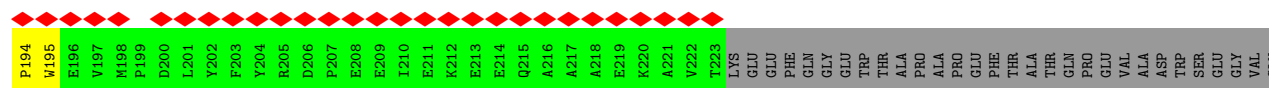
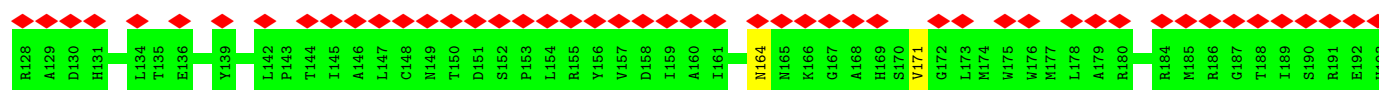
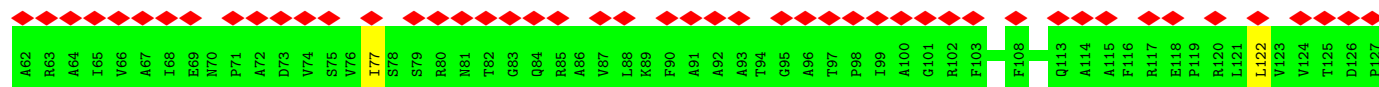
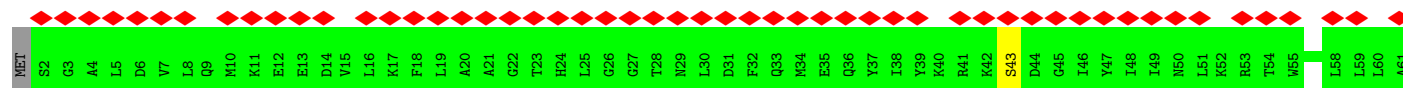
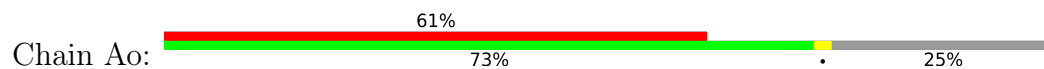


• Molecule 70: 40S ribosomal protein S18

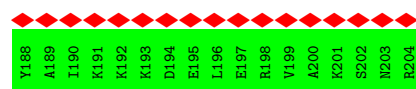
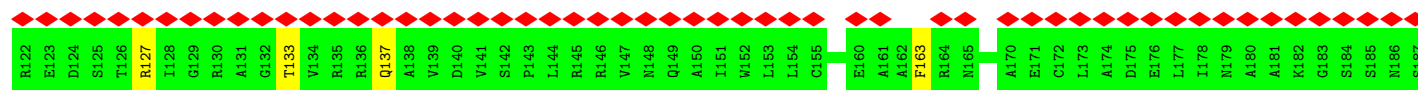
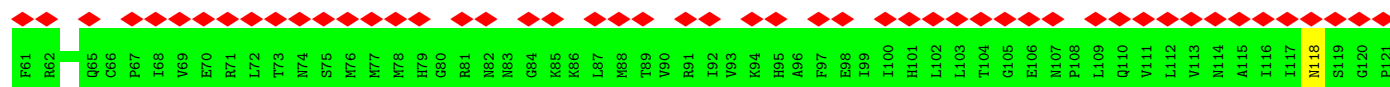
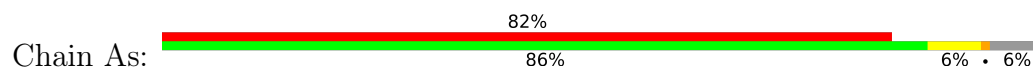




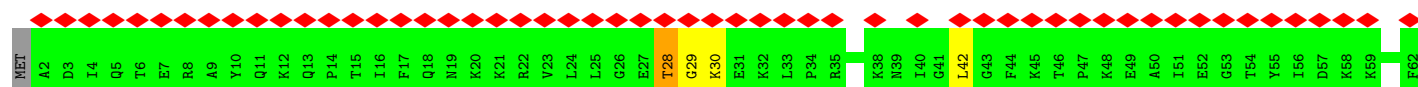
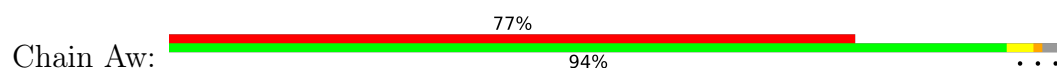
- Molecule 71: 40S ribosomal protein SA

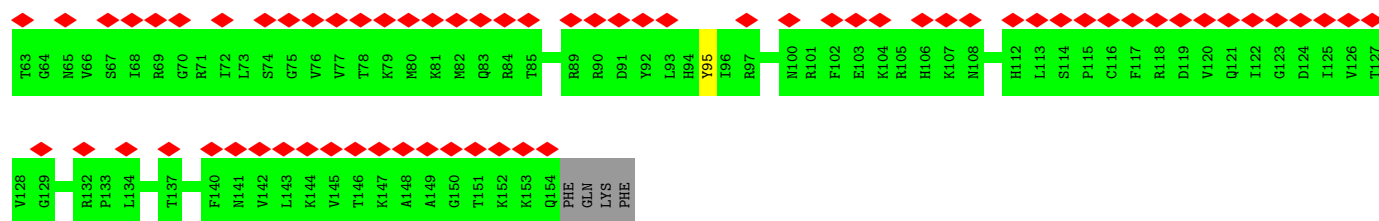


- Molecule 72: 40S ribosomal protein S5

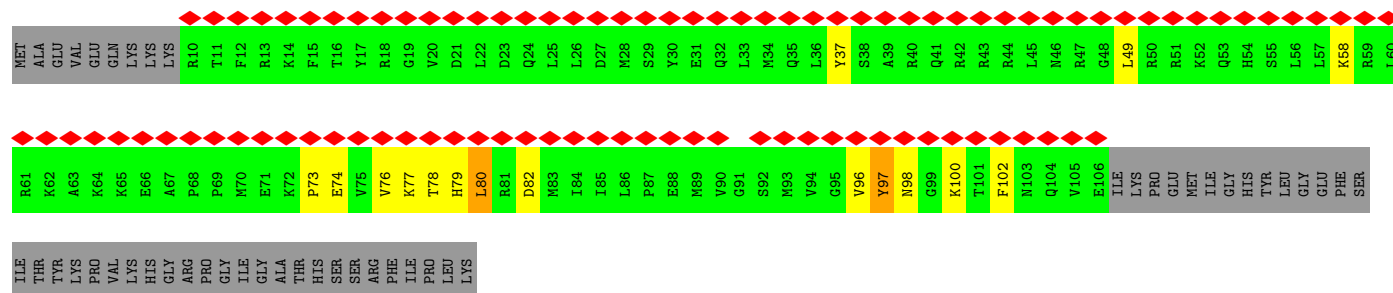


- Molecule 73: 40S ribosomal protein S11

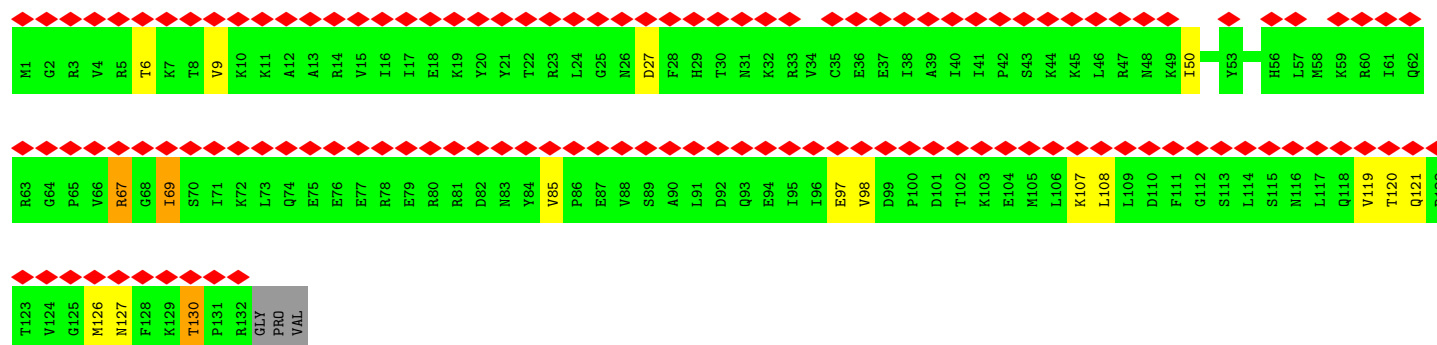
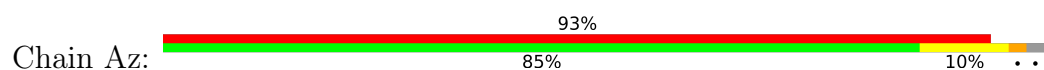




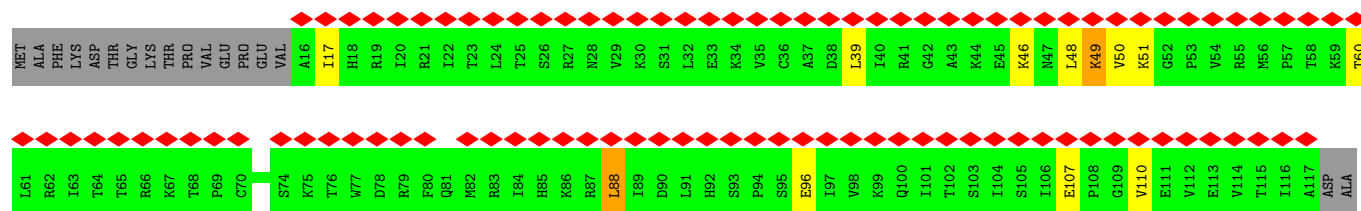
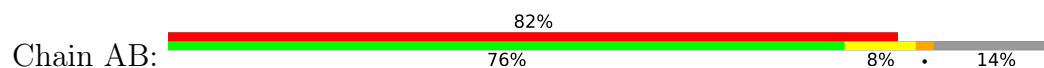
• Molecule 74: 40S ribosomal protein S15



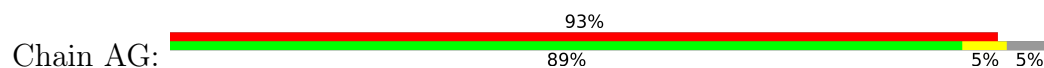
• Molecule 75: 40S ribosomal protein S17



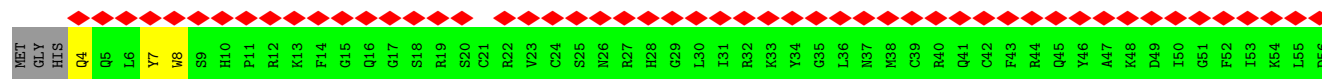
• Molecule 76: 40S ribosomal protein S20



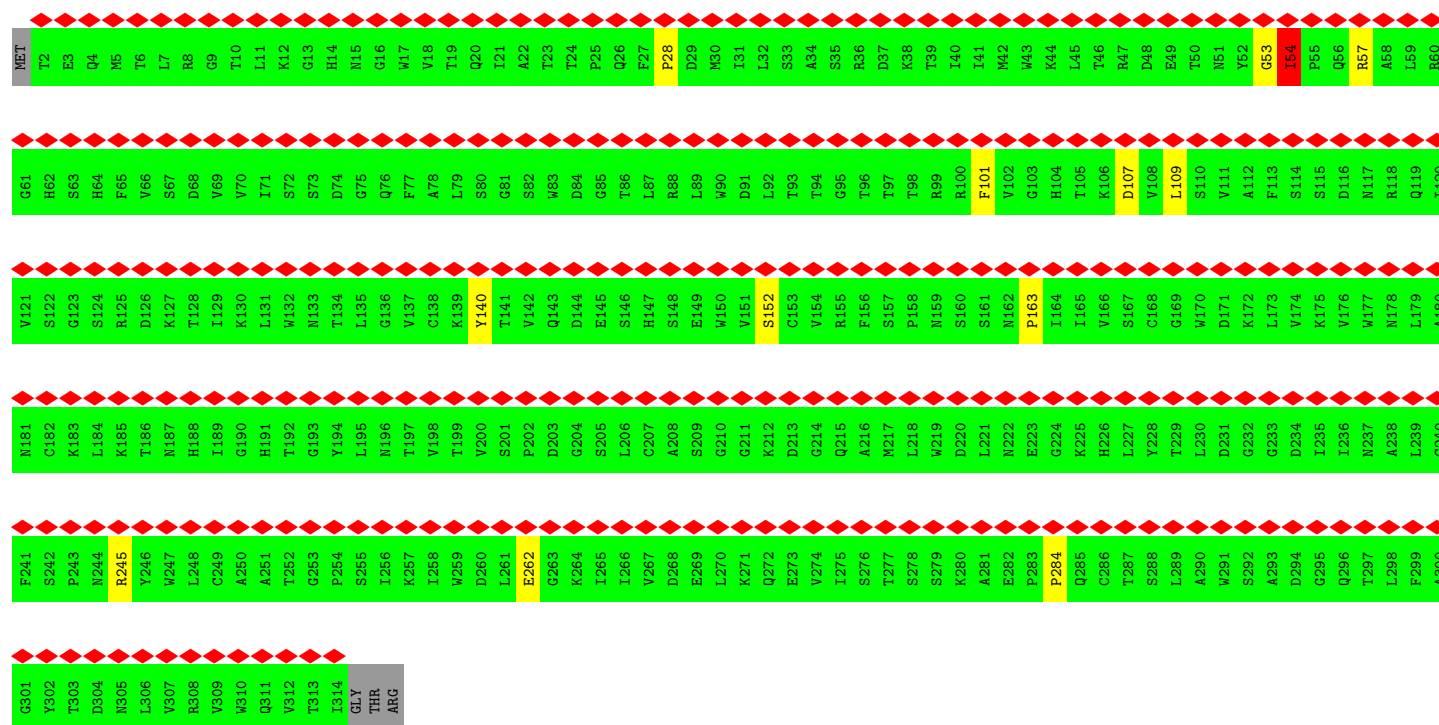
• Molecule 77: 40S ribosomal protein S29



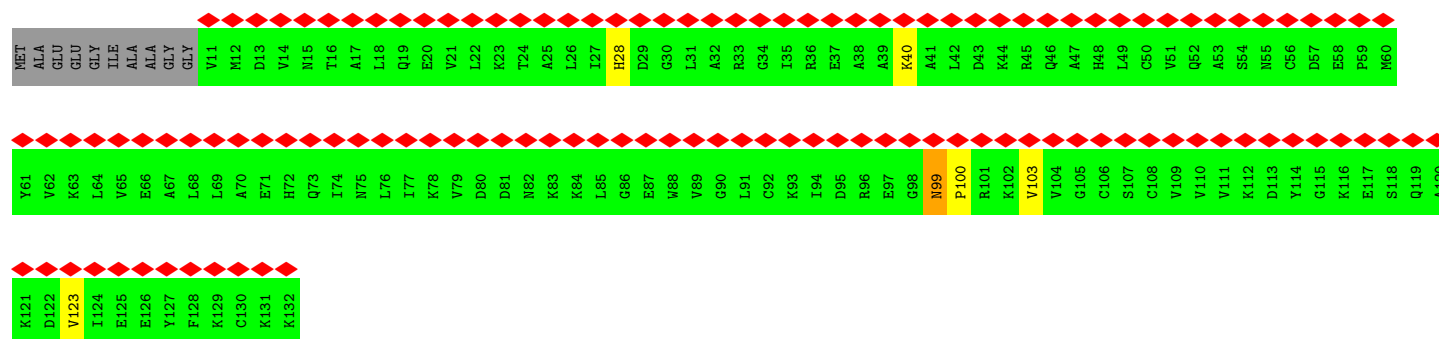




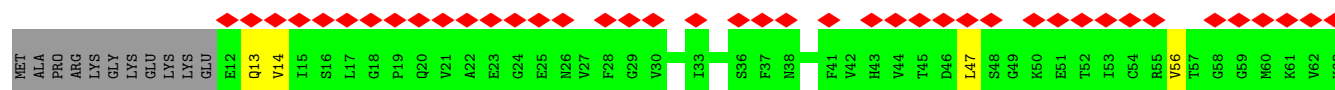
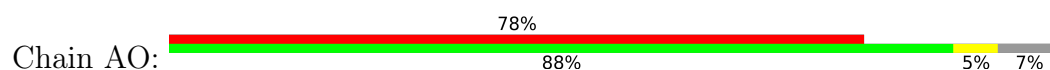
- Molecule 78: Receptor of activated protein C kinase 1

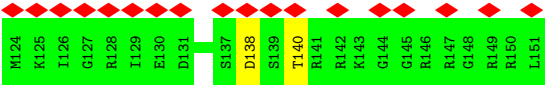
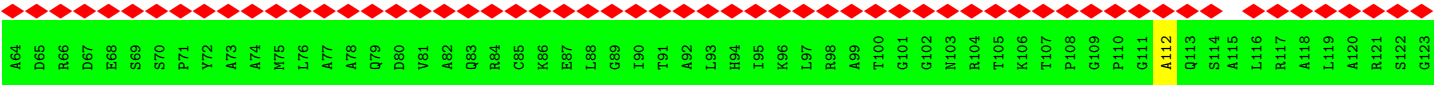


- Molecule 79: 40S ribosomal protein S12

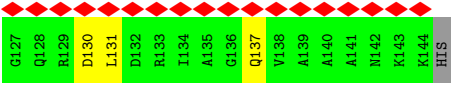
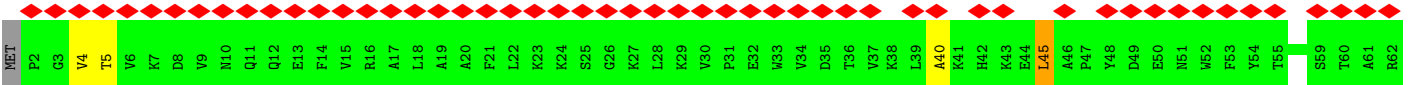
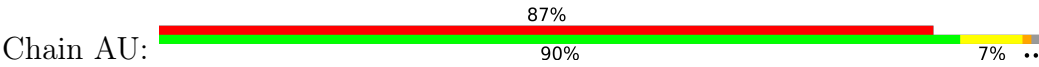


- Molecule 80: 40S ribosomal protein S14





• Molecule 81: 40S ribosomal protein S19



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	175708	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	25	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.127	Depositor
Minimum map value	-0.052	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.03	Depositor
Map size ( $\text{\AA}$ )	374.50003, 374.50003, 374.50003	wwPDB
Map dimensions	350, 350, 350	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.07, 1.07, 1.07	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	B	0.22	0/2858	0.68	0/4455
2	C	0.23	0/3701	0.71	3/5766 (0.1%)
3	D	0.28	0/1936	0.50	0/2596
4	E	0.26	0/3306	0.49	0/4424
5	F	0.25	0/2973	0.47	0/3992
6	G	0.26	0/2428	0.45	0/3252
7	I	0.26	0/1682	0.45	0/2250
8	J	0.26	0/1268	0.45	0/1701
9	L	0.24	0/1582	0.45	0/2091
10	N	0.26	0/1326	0.44	0/1770
11	O	0.27	0/839	0.46	0/1126
12	P	0.27	0/993	0.47	0/1332
13	Q	0.26	0/547	0.44	0/728
14	S	0.25	0/1132	0.46	0/1504
15	T	0.27	0/1130	0.47	0/1507
16	U	0.28	0/1191	0.51	0/1591
17	V	0.24	0/620	0.41	0/819
18	X	0.25	0/903	0.44	0/1216
19	Y	0.26	0/1071	0.46	0/1429
20	Z	0.27	0/895	0.50	0/1198
21	a	0.25	0/916	0.46	0/1220
22	b	0.24	0/1023	0.43	0/1351
23	c	0.25	0/843	0.44	0/1115
24	d	0.25	0/720	0.48	0/952
25	e	0.26	0/575	0.51	0/761
26	f	0.24	0/454	0.41	0/599
27	g	0.23	0/435	0.44	0/575
28	j	0.29	0/718	0.45	0/953
29	k	0.26	0/1017	0.49	0/1364
30	m	0.26	0/1905	0.42	0/2539
31	n	0.25	0/1960	0.45	0/2637
32	o	0.25	0/1537	0.49	0/2066
33	s	0.28	0/1161	0.45	0/1554
34	t	0.26	0/1746	0.48	1/2338 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
35	h	0.21	0/231	0.36	0/294
36	r	0.29	0/1732	0.51	2/2315 (0.1%)
37	A	0.24	0/89645	0.73	17/139764 (0.0%)
38	H	0.34	0/1996	0.86	9/2673 (0.3%)
39	i	0.26	0/876	0.47	0/1156
40	K	0.27	0/1537	0.70	1/2052 (0.0%)
41	l	0.29	0/1769	0.52	1/2371 (0.0%)
42	M	0.32	0/1493	0.50	0/2003
43	p	0.26	0/1751	0.48	0/2340
44	q	0.25	0/1432	0.46	0/1912
45	R	0.25	0/1002	0.44	0/1345
46	W	0.26	0/774	0.46	0/1038
47	AA	1.45	406/41243 (1.0%)	1.53	695/64257 (1.1%)
48	AC	0.64	0/643	0.79	0/860
49	AD	0.83	0/1116	0.85	1/1490 (0.1%)
50	AE	0.75	0/828	0.78	0/1109
51	AF	0.50	0/500	0.83	1/669 (0.1%)
52	AH	0.51	0/593	0.80	1/786 (0.1%)
53	AJ	0.75	0/1762	0.83	3/2381 (0.1%)
54	AK	0.48	0/1946	0.75	1/2590 (0.0%)
55	AL	0.61	0/1550	0.77	0/2069
56	AN	0.67	0/1226	0.79	2/1649 (0.1%)
57	AP	0.74	0/1051	0.93	4/1406 (0.3%)
58	AQ	0.59	1/1083 (0.1%)	0.79	1/1438 (0.1%)
59	AR	0.42	0/604	0.80	1/810 (0.1%)
60	AT	0.54	0/465	0.73	0/612
61	AV	0.58	0/665	0.75	1/891 (0.1%)
62	An	1.24	10/1795 (0.6%)	1.64	46/2798 (1.6%)
63	Ap	0.66	0/1765	0.78	1/2362 (0.0%)
64	Aq	0.54	2/1793 (0.1%)	0.77	2/2414 (0.1%)
65	Ar	0.60	0/2118	0.72	0/2849
66	At	0.53	0/1544	0.79	3/2068 (0.1%)
67	Au	0.69	0/1715	0.76	1/2287 (0.0%)
68	Av	0.45	0/851	0.79	0/1147
69	Ay	0.49	0/1177	0.74	0/1575
70	A0	0.50	0/1253	0.84	1/1676 (0.1%)
71	Ao	0.68	0/1784	0.76	1/2424 (0.0%)
72	As	0.48	0/1531	0.76	1/2059 (0.0%)
73	Aw	0.79	1/1268 (0.1%)	0.83	1/1696 (0.1%)
74	Ax	0.44	0/815	0.78	1/1087 (0.1%)
75	Az	0.55	0/1086	0.84	0/1457
76	AB	0.47	0/817	0.84	2/1097 (0.2%)
77	AG	0.52	0/455	0.68	0/603

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
78	AI	0.46	0/2493	0.75	3/3394 (0.1%)
79	AM	0.41	0/962	0.80	1/1290 (0.1%)
80	AO	0.61	0/1062	0.83	0/1425
81	AU	0.52	0/1131	0.82	2/1515 (0.1%)
All	All	0.69	420/234319 (0.2%)	0.92	811/344274 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
5	F	0	1
11	O	0	1
33	s	0	1
38	H	0	1
39	i	0	1
40	K	0	1
48	AC	0	1
49	AD	0	3
52	AH	0	2
53	AJ	0	1
54	AK	0	5
55	AL	0	1
56	AN	0	1
59	AR	0	1
60	AT	0	3
61	AV	0	1
63	Ap	0	3
64	Aq	0	3
65	Ar	0	2
66	At	0	3
67	Au	0	1
68	Av	0	1
69	Ay	0	5
70	A0	0	4
71	Ao	0	4
72	As	0	6
75	Az	0	4
76	AB	0	4
78	AI	0	5
79	AM	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
80	AO	0	2
81	AU	0	4
All	All	0	78

The worst 5 of 420 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
47	AA	1031	A	N9-C4	-10.37	1.31	1.37
47	AA	1170	A	N9-C4	-9.35	1.32	1.37
47	AA	1815	A	N9-C4	-9.17	1.32	1.37
47	AA	1815	A	N3-C4	-8.95	1.29	1.34
47	AA	1173	A	N9-C4	-8.77	1.32	1.37

The worst 5 of 811 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
40	K	158	THR	C-N-CD	-21.62	73.03	120.60
38	H	96	VAL	N-CA-C	-18.95	59.84	111.00
38	H	89	LEU	N-CA-C	-15.05	70.37	111.00
47	AA	1130	G	N3-C4-C5	12.10	134.65	128.60
47	AA	1861	G	N3-C4-C5	-11.49	122.85	128.60

There are no chirality outliers.

5 of 78 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	F	290	SER	Peptide
38	H	88	VAL	Mainchain
11	O	65	ARG	Peptide
39	i	58	LYS	Peptide
33	s	40	GLY	Peptide

## 5.2 Too-close contacts ⓘ

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	
3	D	246/257 (96%)	227 (92%)	19 (8%)	0	100	100
4	E	400/403 (99%)	378 (94%)	22 (6%)	0	100	100
5	F	365/427 (86%)	331 (91%)	33 (9%)	1 (0%)	41	75
6	G	291/297 (98%)	270 (93%)	20 (7%)	1 (0%)	41	75
7	I	199/203 (98%)	195 (98%)	4 (2%)	0	100	100
8	J	151/160 (94%)	145 (96%)	5 (3%)	1 (1%)	22	61
9	L	185/196 (94%)	177 (96%)	8 (4%)	0	100	100
10	N	157/160 (98%)	149 (95%)	8 (5%)	0	100	100
11	O	99/128 (77%)	94 (95%)	5 (5%)	0	100	100
12	P	129/140 (92%)	122 (95%)	7 (5%)	0	100	100
13	Q	62/157 (40%)	58 (94%)	4 (6%)	0	100	100
14	S	132/145 (91%)	121 (92%)	11 (8%)	0	100	100
15	T	133/136 (98%)	128 (96%)	5 (4%)	0	100	100
16	U	145/148 (98%)	134 (92%)	11 (8%)	0	100	100
17	V	73/159 (46%)	65 (89%)	8 (11%)	0	100	100
18	X	105/125 (84%)	99 (94%)	6 (6%)	0	100	100
19	Y	126/135 (93%)	123 (98%)	3 (2%)	0	100	100
20	Z	107/110 (97%)	100 (94%)	7 (6%)	0	100	100
21	a	112/117 (96%)	109 (97%)	3 (3%)	0	100	100
22	b	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
23	c	100/105 (95%)	96 (96%)	4 (4%)	0	100	100
24	d	84/97 (87%)	79 (94%)	5 (6%)	0	100	100
25	e	67/70 (96%)	62 (92%)	4 (6%)	1 (2%)	10	47
26	f	48/51 (94%)	42 (88%)	6 (12%)	0	100	100
27	g	50/128 (39%)	45 (90%)	5 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	j	89/92 (97%)	81 (91%)	8 (9%)	0	100	100
29	k	123/137 (90%)	110 (89%)	13 (11%)	0	100	100
30	m	223/248 (90%)	212 (95%)	11 (5%)	0	100	100
31	n	239/266 (90%)	228 (95%)	11 (5%)	0	100	100
32	o	188/192 (98%)	172 (92%)	16 (8%)	0	100	100
33	s	137/215 (64%)	124 (90%)	13 (10%)	0	100	100
34	t	201/204 (98%)	191 (95%)	10 (5%)	0	100	100
35	h	22/25 (88%)	19 (86%)	2 (9%)	1 (4%)	2	23
36	r	208/211 (99%)	189 (91%)	17 (8%)	2 (1%)	15	55
38	H	238/288 (83%)	203 (85%)	30 (13%)	5 (2%)	7	40
39	i	103/106 (97%)	99 (96%)	4 (4%)	0	100	100
40	K	185/188 (98%)	177 (96%)	7 (4%)	1 (0%)	29	68
41	l	215/217 (99%)	188 (87%)	25 (12%)	2 (1%)	17	57
42	M	173/176 (98%)	158 (91%)	13 (8%)	2 (1%)	13	51
43	p	211/214 (99%)	196 (93%)	14 (7%)	1 (0%)	29	68
44	q	172/178 (97%)	163 (95%)	6 (4%)	3 (2%)	9	45
45	R	118/156 (76%)	112 (95%)	6 (5%)	0	100	100
46	W	96/115 (84%)	90 (94%)	6 (6%)	0	100	100
48	AC	81/83 (98%)	70 (86%)	8 (10%)	3 (4%)	3	28
49	AD	139/143 (97%)	117 (84%)	22 (16%)	0	100	100
50	AE	99/115 (86%)	93 (94%)	6 (6%)	0	100	100
51	AF	61/69 (88%)	55 (90%)	6 (10%)	0	100	100
52	AH	69/156 (44%)	54 (78%)	13 (19%)	2 (3%)	4	33
53	AJ	220/293 (75%)	195 (89%)	25 (11%)	0	100	100
54	AK	235/249 (94%)	206 (88%)	27 (12%)	2 (1%)	17	57
55	AL	183/194 (94%)	161 (88%)	21 (12%)	1 (0%)	29	68
56	AN	147/151 (97%)	125 (85%)	22 (15%)	0	100	100
57	AP	127/130 (98%)	112 (88%)	15 (12%)	0	100	100
58	AQ	129/133 (97%)	118 (92%)	8 (6%)	3 (2%)	6	38
59	AR	73/125 (58%)	61 (84%)	12 (16%)	0	100	100
60	AT	56/59 (95%)	51 (91%)	5 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
61	AV	81/84 (96%)	73 (90%)	7 (9%)	1 (1%)	13	51
63	Ap	212/264 (80%)	184 (87%)	25 (12%)	3 (1%)	11	48
64	Aq	225/243 (93%)	195 (87%)	26 (12%)	4 (2%)	8	43
65	Ar	260/263 (99%)	226 (87%)	31 (12%)	3 (1%)	13	51
66	At	187/194 (96%)	155 (83%)	30 (16%)	2 (1%)	14	53
67	Au	204/208 (98%)	179 (88%)	22 (11%)	3 (2%)	10	47
68	Av	96/165 (58%)	77 (80%)	18 (19%)	1 (1%)	15	55
69	Ay	144/146 (99%)	123 (85%)	18 (12%)	3 (2%)	7	40
70	A0	148/152 (97%)	121 (82%)	21 (14%)	6 (4%)	3	26
71	Ao	220/295 (75%)	190 (86%)	28 (13%)	2 (1%)	17	57
72	As	189/204 (93%)	158 (84%)	23 (12%)	8 (4%)	3	25
73	Aw	151/158 (96%)	130 (86%)	18 (12%)	3 (2%)	7	41
74	Ax	95/145 (66%)	60 (63%)	21 (22%)	14 (15%)	0	3
75	Az	130/135 (96%)	93 (72%)	26 (20%)	11 (8%)	1	10
76	AB	100/119 (84%)	82 (82%)	14 (14%)	4 (4%)	3	26
77	AG	51/56 (91%)	43 (84%)	6 (12%)	2 (4%)	3	27
78	AI	311/317 (98%)	261 (84%)	44 (14%)	6 (2%)	8	42
79	AM	120/132 (91%)	91 (76%)	26 (22%)	3 (2%)	5	36
80	AO	138/151 (91%)	112 (81%)	21 (15%)	5 (4%)	3	29
81	AU	141/145 (97%)	116 (82%)	18 (13%)	7 (5%)	2	21
All	All	11449/12881 (89%)	10266 (90%)	1060 (9%)	123 (1%)	18	53

5 of 123 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
38	H	100	LYS
38	H	225	PRO
40	K	159	PRO
44	q	55	TYR
44	q	59	SER

### 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	
3	D	190/199 (96%)	190 (100%)	0	100	100
4	E	348/349 (100%)	348 (100%)	0	100	100
5	F	305/348 (88%)	305 (100%)	0	100	100
6	G	246/250 (98%)	246 (100%)	0	100	100
7	I	173/174 (99%)	173 (100%)	0	100	100
8	J	134/141 (95%)	134 (100%)	0	100	100
9	L	166/175 (95%)	166 (100%)	0	100	100
10	N	139/140 (99%)	139 (100%)	0	100	100
11	O	91/115 (79%)	91 (100%)	0	100	100
12	P	101/107 (94%)	101 (100%)	0	100	100
13	Q	56/126 (44%)	56 (100%)	0	100	100
14	S	124/135 (92%)	124 (100%)	0	100	100
15	T	117/118 (99%)	117 (100%)	0	100	100
16	U	120/121 (99%)	120 (100%)	0	100	100
17	V	63/126 (50%)	63 (100%)	0	100	100
18	X	98/110 (89%)	98 (100%)	0	100	100
19	Y	114/121 (94%)	114 (100%)	0	100	100
20	Z	88/89 (99%)	88 (100%)	0	100	100
21	a	98/100 (98%)	98 (100%)	0	100	100
22	b	109/110 (99%)	109 (100%)	0	100	100
23	c	86/89 (97%)	86 (100%)	0	100	100
24	d	73/80 (91%)	73 (100%)	0	100	100
25	e	64/65 (98%)	64 (100%)	0	100	100
26	f	47/48 (98%)	47 (100%)	0	100	100
27	g	48/116 (41%)	48 (100%)	0	100	100
28	j	74/75 (99%)	74 (100%)	0	100	100
29	k	109/121 (90%)	109 (100%)	0	100	100
30	m	194/215 (90%)	194 (100%)	0	100	100
31	n	203/223 (91%)	203 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	o	169/171 (99%)	169 (100%)	0	100	100
33	s	118/161 (73%)	118 (100%)	0	100	100
34	t	171/172 (99%)	171 (100%)	0	100	100
35	h	23/24 (96%)	23 (100%)	0	100	100
36	r	176/177 (99%)	174 (99%)	2 (1%)	73	88
38	H	215/252 (85%)	209 (97%)	6 (3%)	43	72
39	i	93/94 (99%)	92 (99%)	1 (1%)	73	88
40	K	164/165 (99%)	164 (100%)	0	100	100
41	l	195/196 (100%)	194 (100%)	1 (0%)	88	95
42	M	156/157 (99%)	154 (99%)	2 (1%)	69	86
43	p	180/181 (99%)	178 (99%)	2 (1%)	73	88
44	q	148/149 (99%)	144 (97%)	4 (3%)	44	73
45	R	108/133 (81%)	107 (99%)	1 (1%)	78	90
46	W	83/97 (86%)	83 (100%)	0	100	100
48	AC	67/67 (100%)	67 (100%)	0	100	100
49	AD	113/115 (98%)	113 (100%)	0	100	100
50	AE	88/98 (90%)	88 (100%)	0	100	100
51	AF	56/62 (90%)	56 (100%)	0	100	100
52	AH	64/140 (46%)	64 (100%)	0	100	100
53	AJ	188/225 (84%)	186 (99%)	2 (1%)	73	88
54	AK	207/218 (95%)	207 (100%)	0	100	100
55	AL	161/168 (96%)	161 (100%)	0	100	100
56	AN	130/131 (99%)	130 (100%)	0	100	100
57	AP	112/113 (99%)	110 (98%)	2 (2%)	59	81
58	AQ	113/115 (98%)	113 (100%)	0	100	100
59	AR	66/103 (64%)	66 (100%)	0	100	100
60	AT	47/48 (98%)	47 (100%)	0	100	100
61	AV	75/76 (99%)	75 (100%)	0	100	100
63	Ap	195/231 (84%)	193 (99%)	2 (1%)	76	88
64	Aq	190/202 (94%)	190 (100%)	0	100	100
65	Ar	224/225 (100%)	223 (100%)	1 (0%)	91	97

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
66	At	169/174 (97%)	169 (100%)	0	100	100
67	Au	178/180 (99%)	178 (100%)	0	100	100
68	Av	89/136 (65%)	89 (100%)	0	100	100
69	Ay	121/121 (100%)	120 (99%)	1 (1%)	81	91
70	A0	130/132 (98%)	130 (100%)	0	100	100
71	Ao	184/243 (76%)	184 (100%)	0	100	100
72	As	161/170 (95%)	159 (99%)	2 (1%)	71	87
73	Aw	137/142 (96%)	136 (99%)	1 (1%)	84	93
74	Ax	87/130 (67%)	84 (97%)	3 (3%)	37	69
75	Az	120/122 (98%)	115 (96%)	5 (4%)	30	63
76	AB	93/107 (87%)	89 (96%)	4 (4%)	29	63
77	AG	47/49 (96%)	46 (98%)	1 (2%)	53	78
78	AI	272/275 (99%)	270 (99%)	2 (1%)	84	93
79	AM	104/108 (96%)	103 (99%)	1 (1%)	76	88
80	AO	110/119 (92%)	110 (100%)	0	100	100
81	AU	113/115 (98%)	112 (99%)	1 (1%)	78	90
All	All	9988/10975 (91%)	9941 (100%)	47 (0%)	89	95

5 of 47 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
72	As	45	TYR
75	Az	120	THR
73	Aw	28	THR
74	Ax	97	TYR
75	Az	130	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 95 such sidechains are listed below:

Mol	Chain	Res	Type
56	AN	105	ASN
70	A0	125	HIS
61	AV	19	HIS
66	At	44	ASN
73	Aw	13	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	B	119/121 (98%)	16 (13%)	0
2	C	155/157 (98%)	34 (21%)	1 (0%)
37	A	3707/5070 (73%)	1071 (28%)	50 (1%)
47	AA	1716/1869 (91%)	906 (52%)	48 (2%)
62	An	74/75 (98%)	37 (50%)	0
All	All	5771/7292 (79%)	2064 (35%)	99 (1%)

5 of 2064 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	B	2	U
1	B	7	G
1	B	17	C
1	B	22	A
1	B	24	C

5 of 99 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
47	AA	428	U
47	AA	912	C
47	AA	465	A
47	AA	681	U
47	AA	991	G

## 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 ⓘ

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
44	q	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	q	151:ILE	C	152:GLY	N	2.01

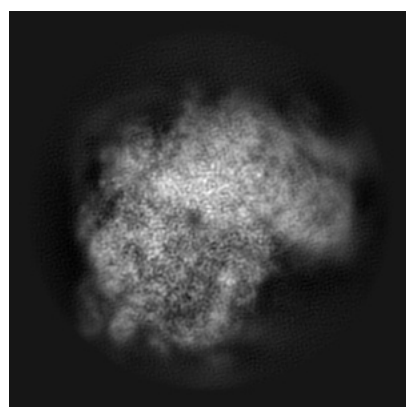
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8345. These allow visual inspection of the internal detail of the map and identification of artifacts.

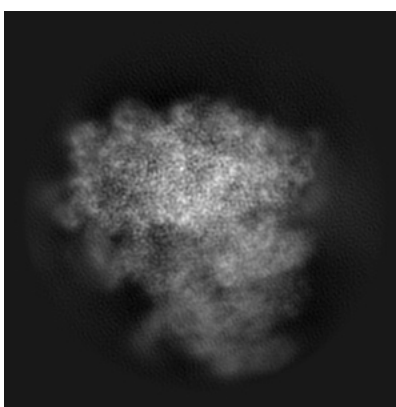
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

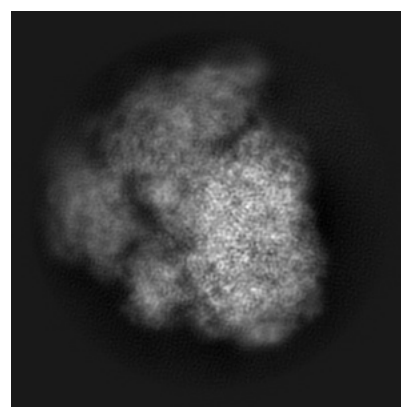
#### 6.1.1 Primary map



X



Y

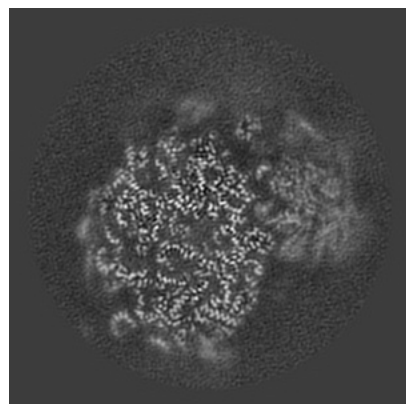


Z

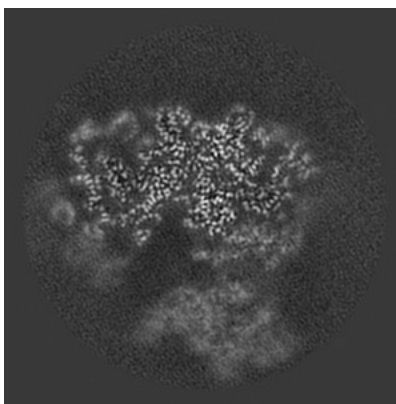
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

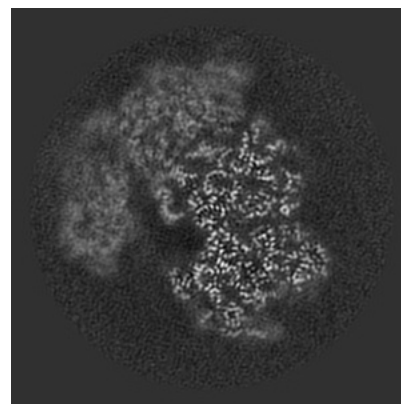
#### 6.2.1 Primary map



X Index: 175



Y Index: 175



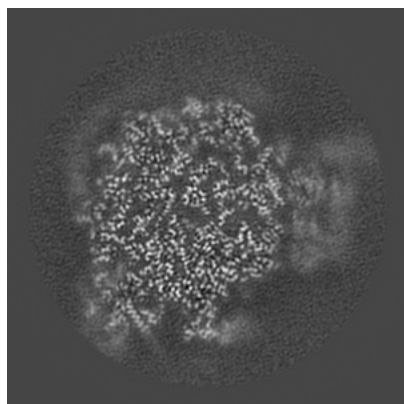
Z Index: 175



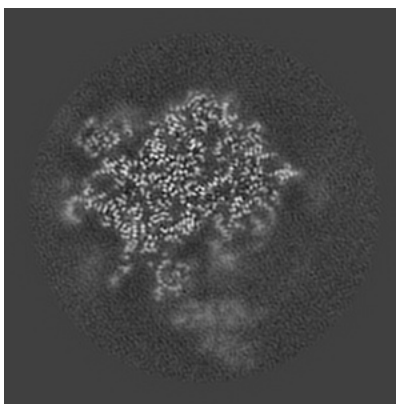
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

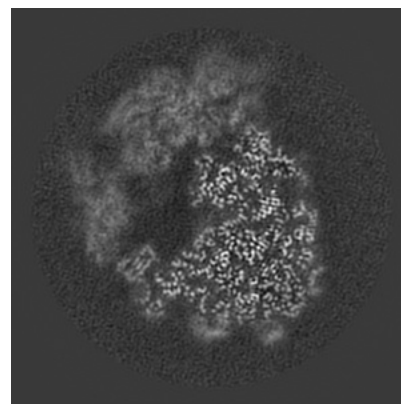
### 6.3.1 Primary map



X Index: 202



Y Index: 132



Z Index: 156

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

## 6.4 Orthogonal surface views [i](#)

### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

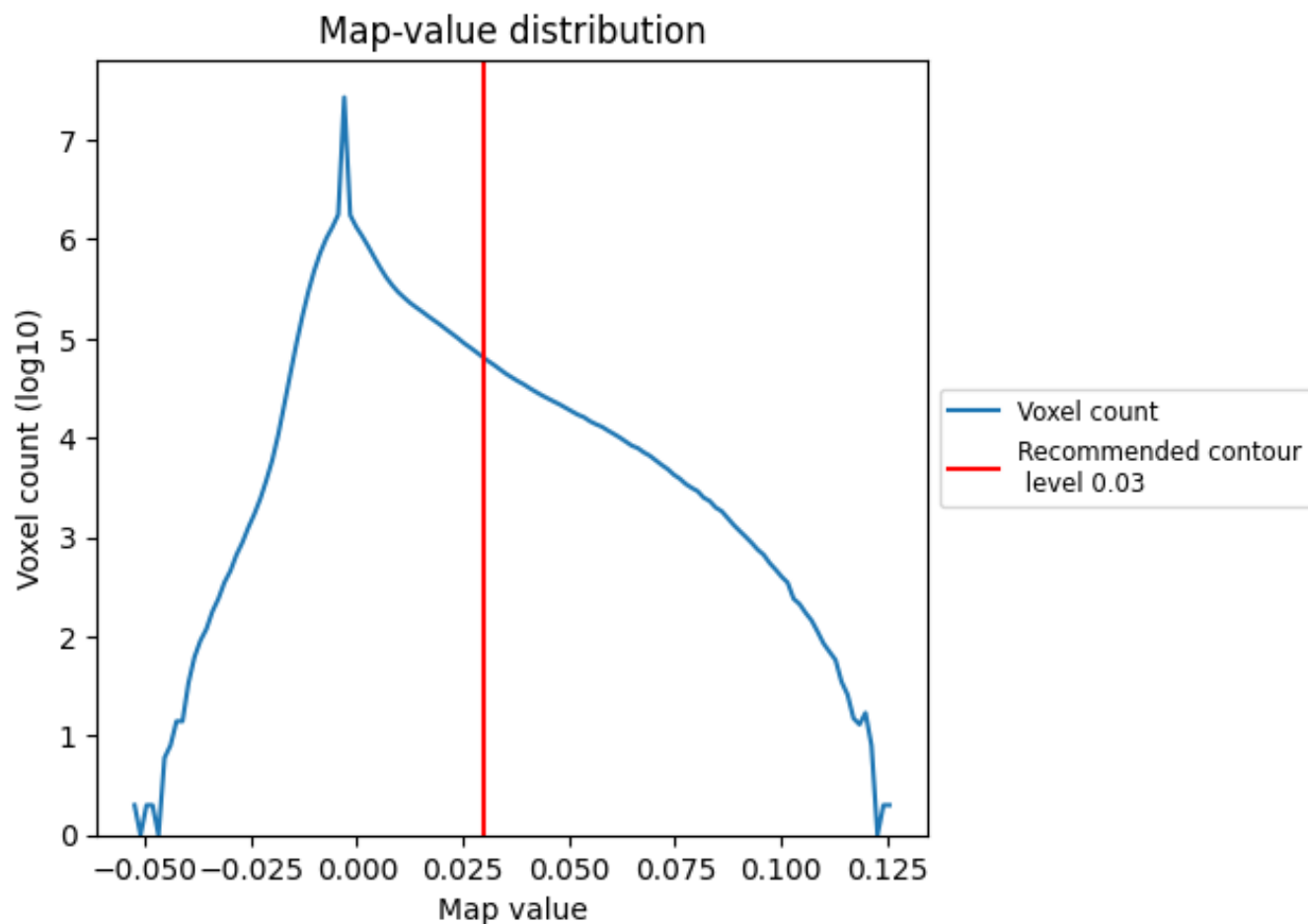
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

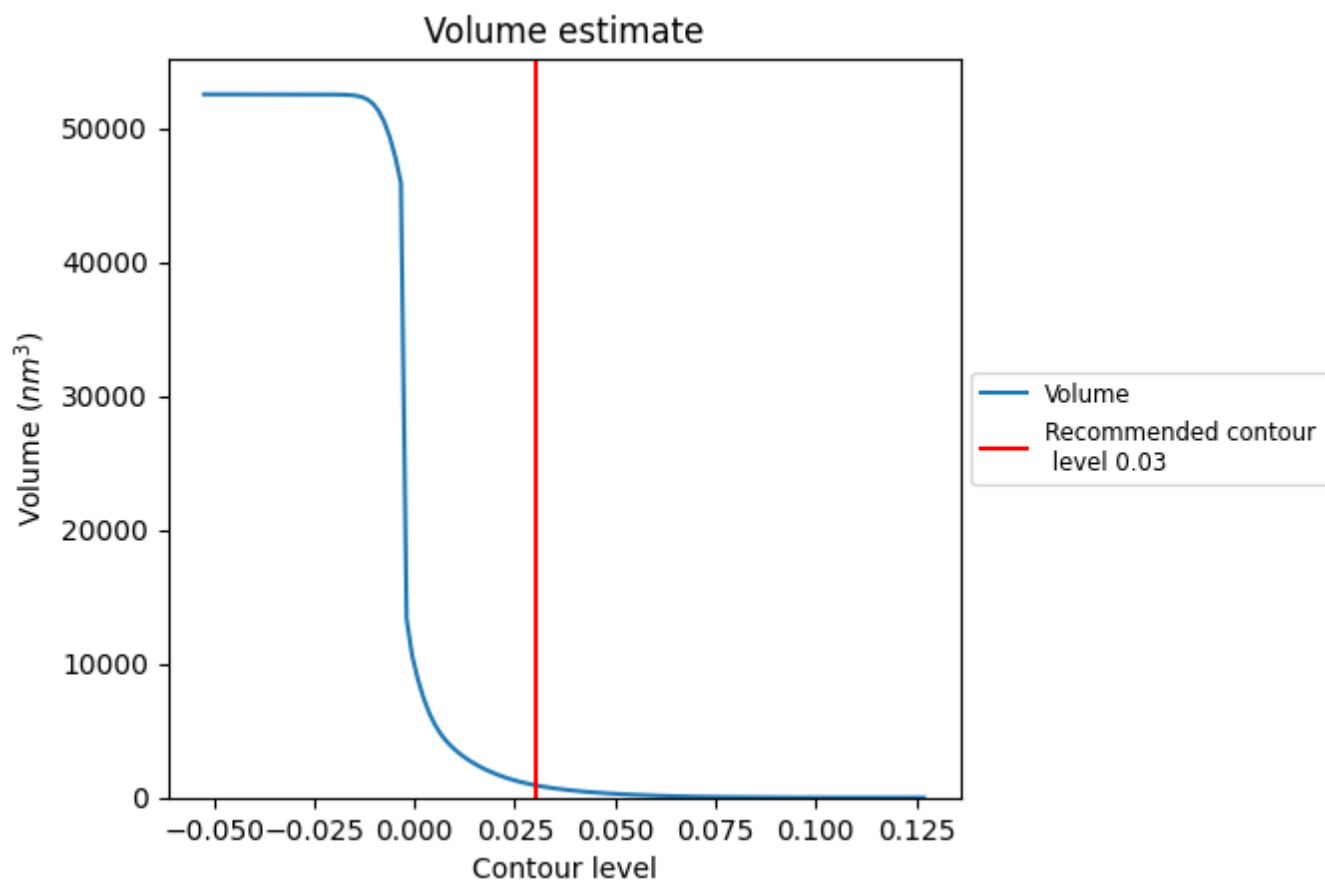
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



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

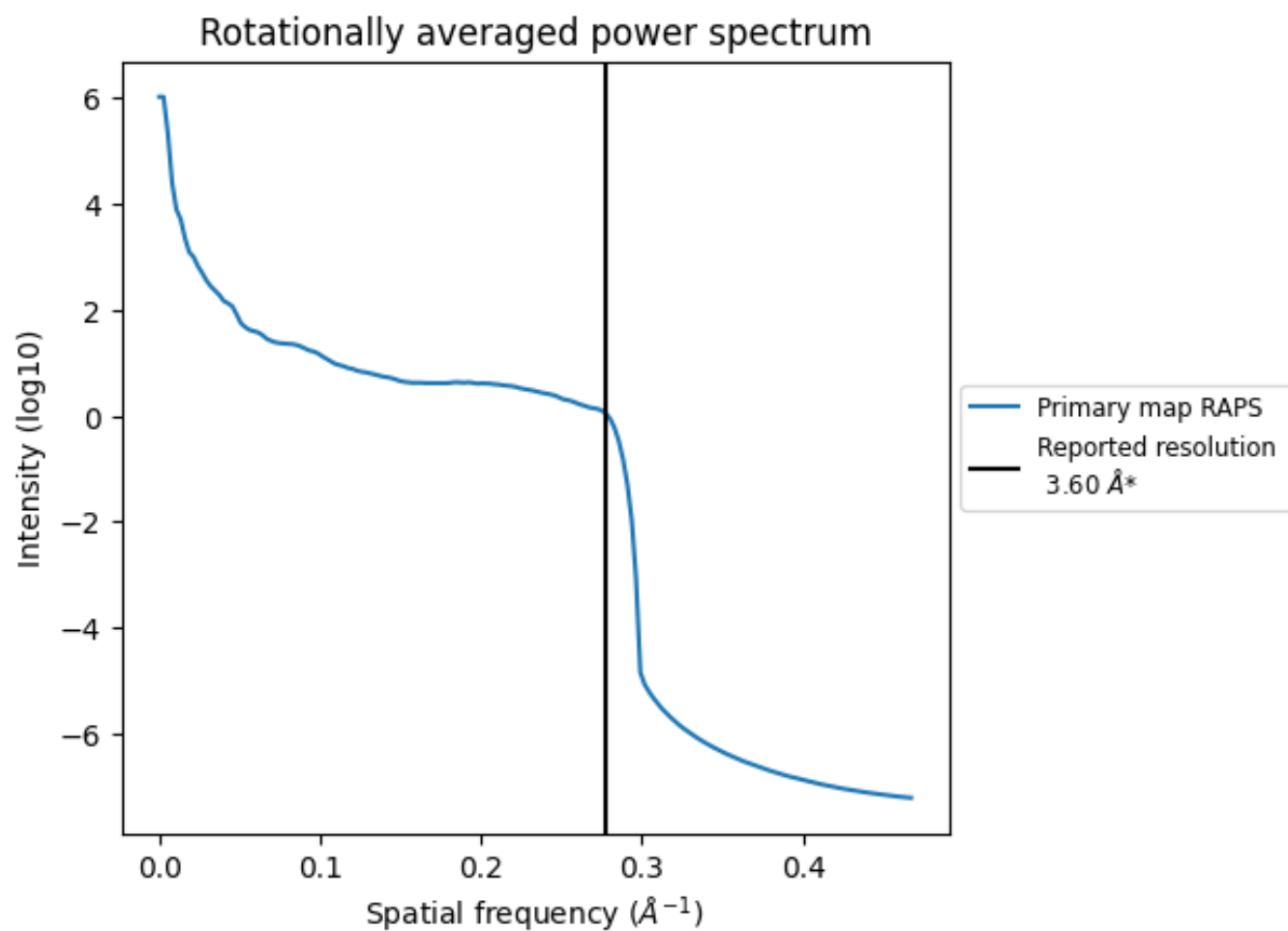
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 928 nm<sup>3</sup>; this corresponds to an approximate mass of 838 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 0.278 Å<sup>-1</sup>

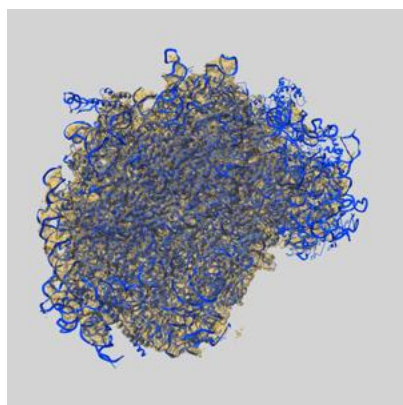
## 8 Fourier-Shell correlation

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

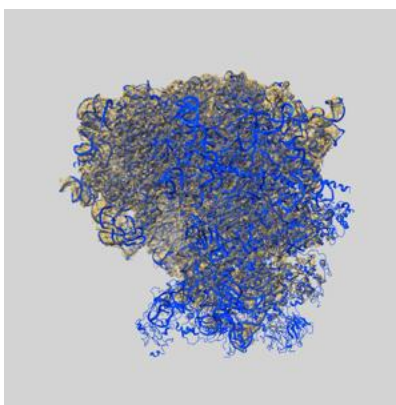
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-8345 and PDB model 5T2C. Per-residue inclusion information can be found in [section 3](#) on [page 18](#).

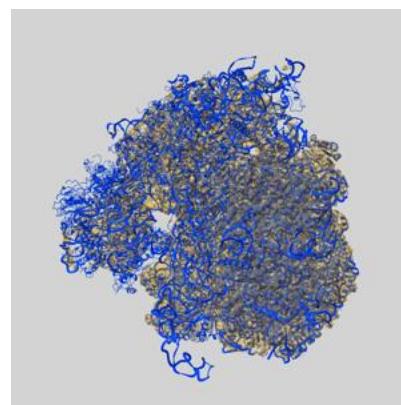
### 9.1 Map-model overlay [i](#)



X



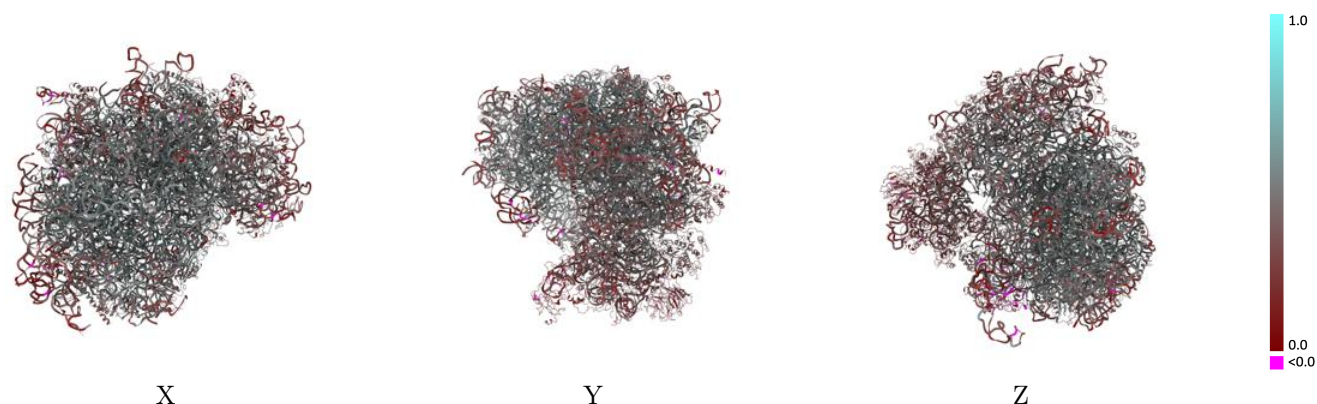
Y



Z

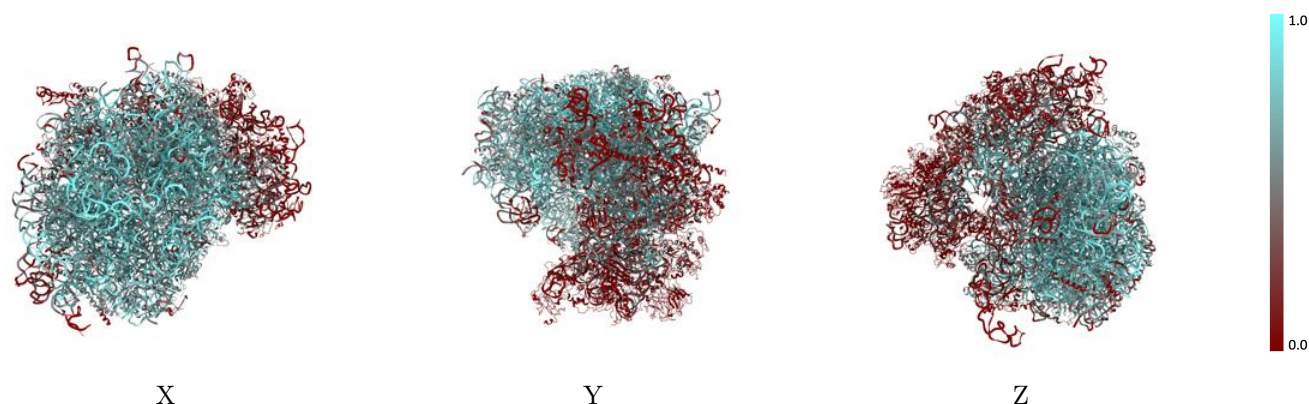
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 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.

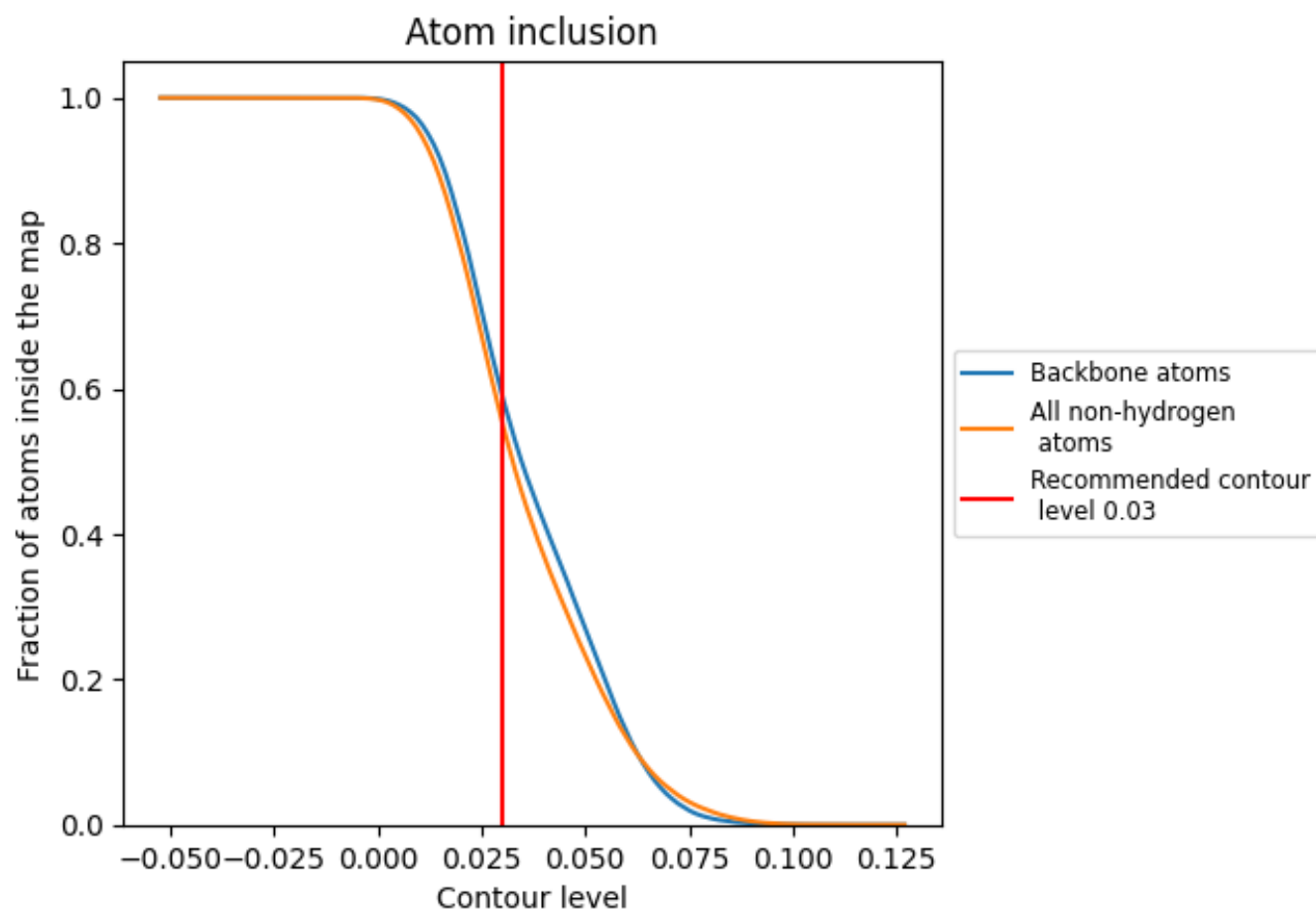
## 9.3 Atom inclusion mapped to coordinate model [i](#)



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 (0.03).









































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 59% of all backbone atoms, 55% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5532	 0.4190
A	 0.7526	 0.4420
A0	 0.0815	 0.2900
AA	 0.4671	 0.3940
AB	 0.0483	 0.3020
AC	 0.1672	 0.3780
AD	 0.3240	 0.4300
AE	 0.3227	 0.4420
AF	 0.0711	 0.3370
AG	 0.0609	 0.3260
AH	 0.0035	 0.2180
AI	 0.0054	 0.2700
AJ	 0.2980	 0.4100
AK	 0.0652	 0.3290
AL	 0.2457	 0.3850
AM	 0.0000	 0.2500
AN	 0.2864	 0.4450
AO	 0.1833	 0.4010
AP	 0.3010	 0.4190
AQ	 0.1449	 0.3330
AR	 0.0069	 0.2640
AT	 0.1396	 0.3800
AU	 0.1386	 0.2840
AV	 0.1455	 0.4080
An	 0.3198	 0.3210
Ao	 0.2081	 0.3830
Ap	 0.1909	 0.4150
Aq	 0.0238	 0.3290
Ar	 0.1872	 0.4020
As	 0.1185	 0.3070
At	 0.0804	 0.3510
Au	 0.2034	 0.4180
Av	 0.0087	 0.2770
Aw	 0.1955	 0.4350
Ax	 0.0388	 0.2670













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Chain	Atom inclusion	Q-score
Ay	 0.0651	 0.3010
Az	 0.0633	 0.3070
B	 0.8984	 0.4870
C	 0.8286	 0.4720
D	 0.6561	 0.4920
E	 0.6322	 0.4730
F	 0.6400	 0.4710
G	 0.6207	 0.4260
H	 0.4895	 0.3930
I	 0.6479	 0.4870
J	 0.6750	 0.4910
K	 0.6526	 0.4830
L	 0.5470	 0.4320
M	 0.6809	 0.4810
N	 0.6223	 0.4670
O	 0.5006	 0.4070
P	 0.6102	 0.4860
Q	 0.5087	 0.4620
R	 0.5971	 0.4380
S	 0.6382	 0.4550
T	 0.5983	 0.4590
U	 0.6929	 0.4890
V	 0.4966	 0.4210
W	 0.5288	 0.4210
X	 0.6219	 0.4610
Y	 0.6618	 0.4880
Z	 0.6722	 0.4970
a	 0.5857	 0.4600
b	 0.5800	 0.4290
c	 0.5276	 0.4330
d	 0.7202	 0.5010
e	 0.4327	 0.3730
f	 0.6288	 0.4800
g	 0.6193	 0.4610
h	 0.4833	 0.4250
i	 0.5909	 0.4570
j	 0.5916	 0.4690
k	 0.6490	 0.4770
l	 0.0006	 0.1070
m	 0.6569	 0.4770
n	 0.3946	 0.3930
o	 0.6101	 0.4550

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Chain	Atom inclusion	Q-score
p	 0.5473	 0.4470
q	 0.4982	 0.3960
r	 0.4963	 0.4350
s	 0.6206	 0.4520
t	 0.7204	 0.5050