wwPDB EM Validation Summary Report

Mar 25, 2026 – 10:09 PM UTC

PDB ID	:	9MR4 / pdb_00009mr4
EMDB ID	:	EMD-48552
Title	:	NAC: Ribosome nascent chain complex(Oxa1L)
Authors	:	Maldosevic, E.; Jomaa, A.
Deposited on	:	2025-01-06
Resolution	:	2.65 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

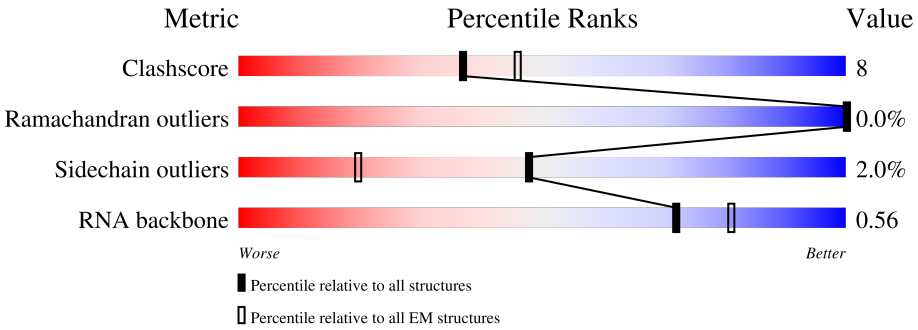
EMDB validation analysis	:	0.0.1.dev132
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

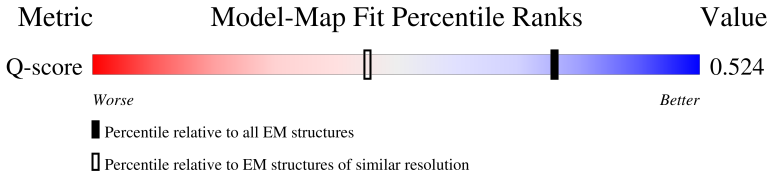
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.65 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.





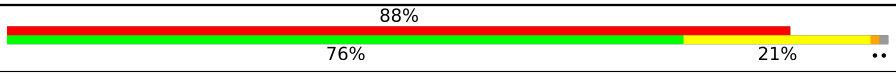
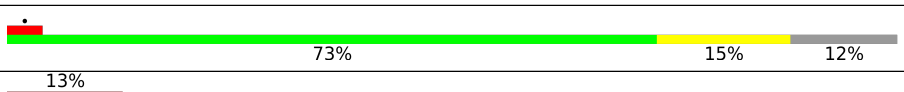
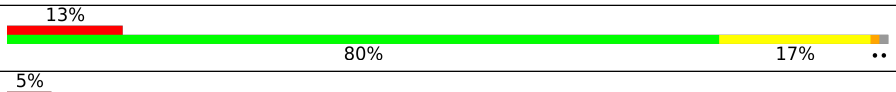
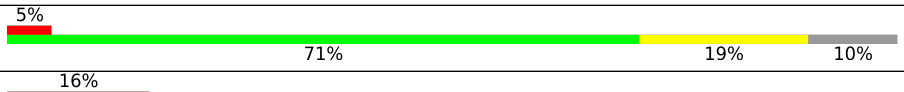
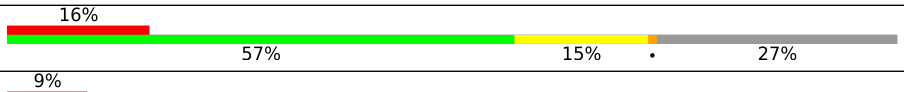
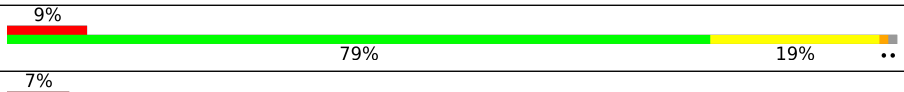
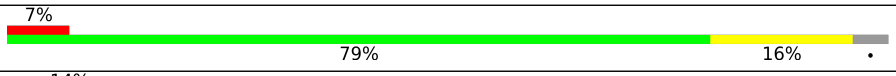
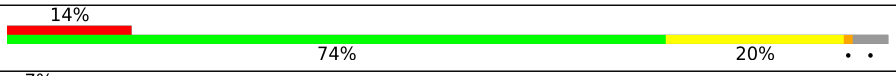
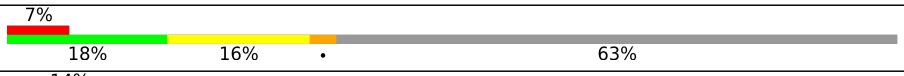
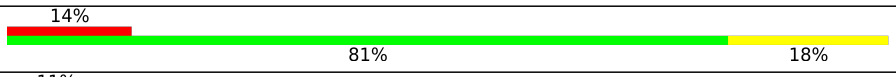
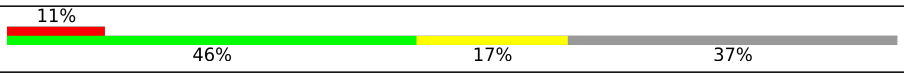
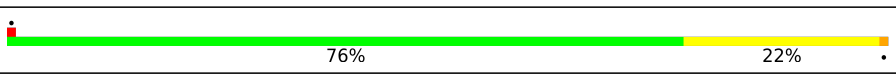
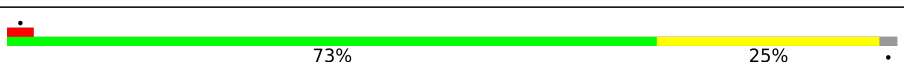
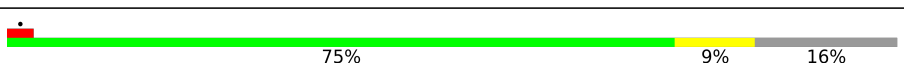
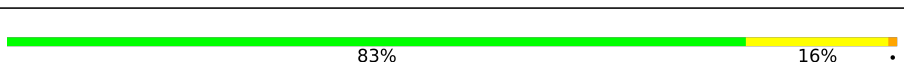
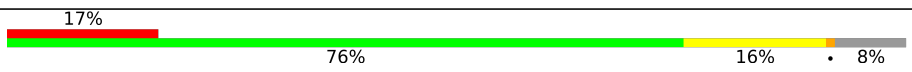
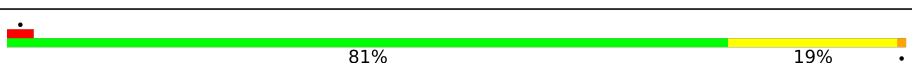
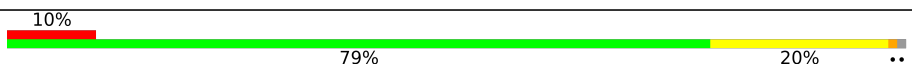
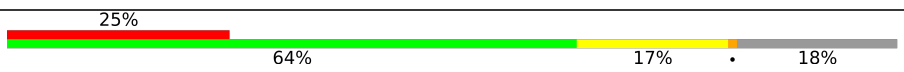
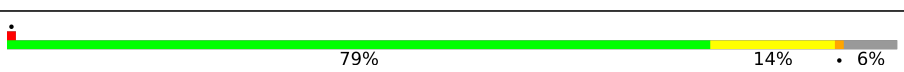
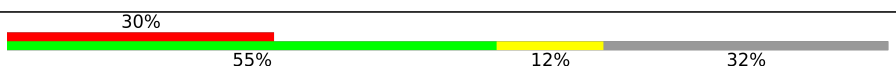
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	9050 (2.15 - 3.15)

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	m	128	6% 33% 6% • 60%
2	0	156	39% 32% 7% 61%
3	4	6	67% 100%

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Mol	Chain	Length	Quality of chain
4	6	317	
5	7	120	
6	9	56	
7	A	257	
8	B	403	
9	C	413	
10	D	297	
11	F	249	
12	G	319	
13	H	192	
14	I	214	
15	J	178	
16	K	4592	
17	L	211	
18	M	218	
19	N	204	
20	O	203	
21	P	183	
22	Q	187	
23	R	196	
24	S	176	
25	T	160	
26	U	128	
27	V	140	
28	W	157	

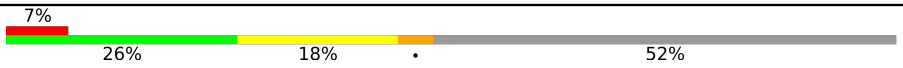
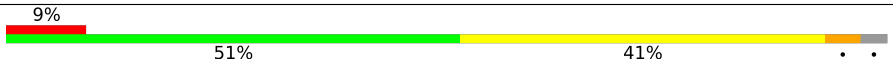
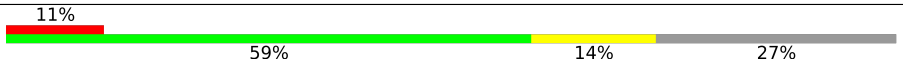
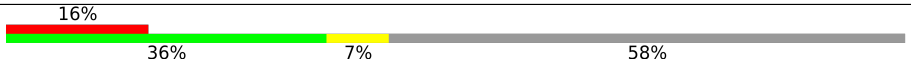
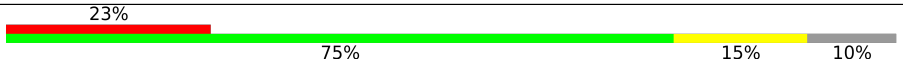
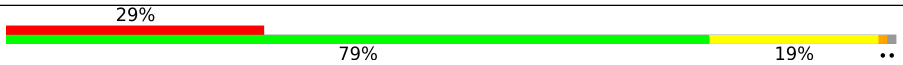
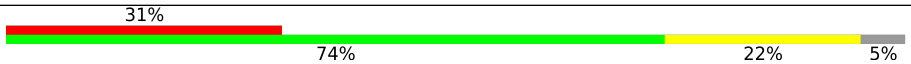
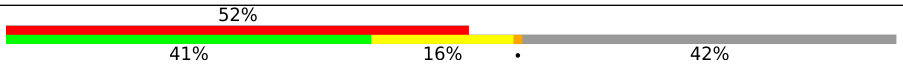
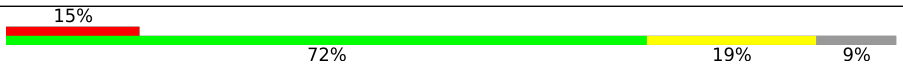
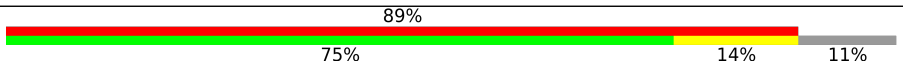
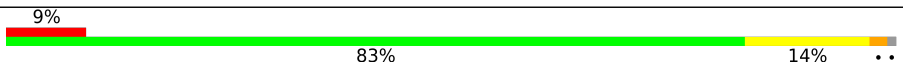
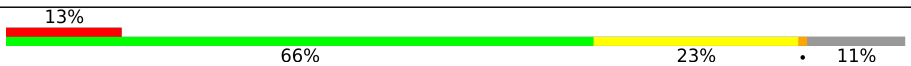
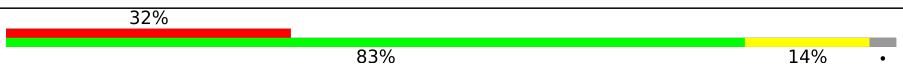
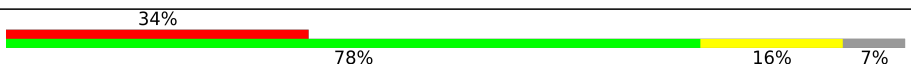
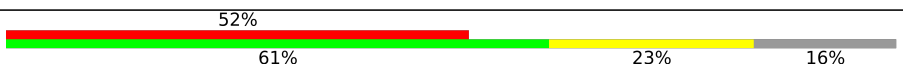
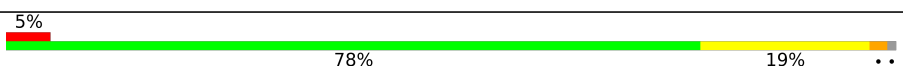
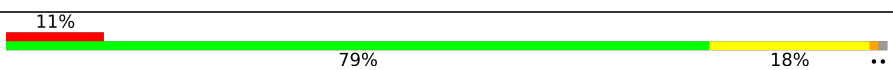
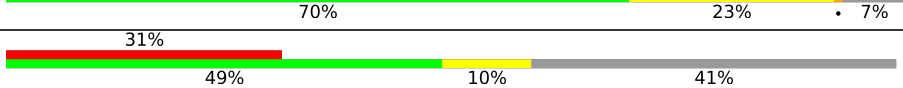
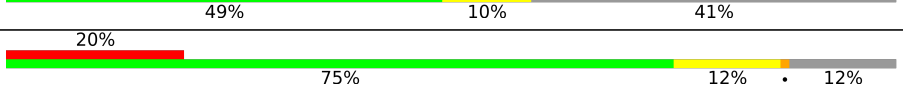
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Mol	Chain	Length	Quality of chain
29	X	156	63% 13% 24%
30	Y	145	6% 75% 17% 8%
31	Z	136	14% 81% 18%
32	a	148	82% 17%
33	c	115	9% 77% 8% 15%
34	d	125	7% 75% 10% 14%
35	e	135	79% 14% 5%
36	f	110	75% 22%
37	g	117	10% 88% 9%
38	h	123	85% 15%
39	i	105	15% 90% 8%
40	j	97	70% 18% 11%
41	k	70	37% 83% 16%
42	l	51	10% 78% 20%
43	n	25	84% 16%
44	o	111	8% 73% 21% 6%
45	p	92	5% 82% 17%
46	q	295	15% 57% 15% 26%
47	r	137	74% 15% 9%
48	u	264	20% 63% 18% 19%
49	v	293	12% 60% 15% 25%
50	w	243	51% 74% 19% 7%
51	x	263	29% 78% 20%
52	z	249	71% 75% 20% 5%
53	2	76	21% 45% 45% 9%

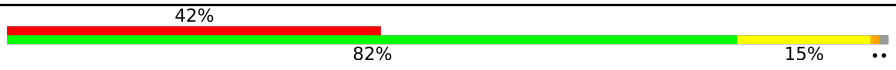
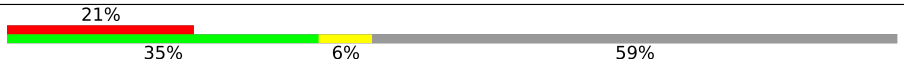
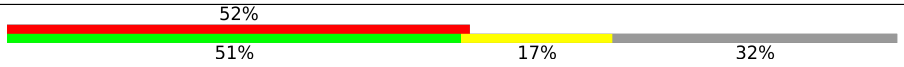
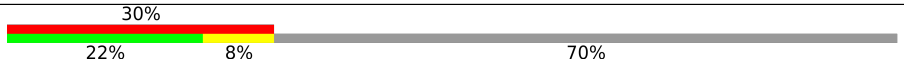
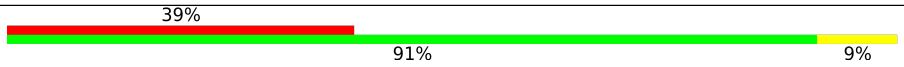
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Mol	Chain	Length	Quality of chain
54	5	7224	
55	8	156	
56	E	291	
57	b	245	
58	y	204	
59	BB	194	
60	CC	208	
61	DD	194	
62	SS	165	
63	EE	158	
64	RR	132	
65	QQ	151	
66	MM	151	
67	WW	145	
68	UU	146	
69	KK	135	
70	II	152	
71	PP	145	
72	GG	119	
73	HH	83	
74	TT	130	
75	VV	143	
76	NN	133	
77	OO	124	
78	LL	115	

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Mol	Chain	Length	Quality of chain
79	JJ	84	
80	FF	69	
81	AA	133	
82	EF	162	
83	EG	215	
84	EH	33	

2 Entry composition (i)

There are 86 unique types of molecules in this entry. The entry contains 211175 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 Ubiquitin-ribosomal protein eL40 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	m	51	419	260	88	65	6	0	0

- Molecule 2 is a protein called Ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	0	61	498	314	94	83	7	0	0

- Molecule 3 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	4	6	128	57	22	43	6	0	0

- Molecule 4 is a protein called RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	6	313	2436	1535	424	465	12	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
5	7	120	2558	1141	456	842	119	0	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
7	2	U	N	conflict	GB X06789.1
7	36	C	N	conflict	GB X06789.1
7	102	U	N	conflict	GB X06789.1

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Chain	Residue	Modelled	Actual	Comment	Reference
7	112	U	N	conflict	GB X06789.1
7	114	U	N	conflict	GB X06789.1
7	119	U	C	conflict	GB X06789.1
7	120	U	N	conflict	GB X06789.1

- Molecule 6 is a protein called eS29.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	9	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 7 is a protein called Ribosomal protein L8.

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

- Molecule 8 is a protein called Ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	394	Total	C	N	O	S	0	0
			3172	2020	597	542	13		

- Molecule 9 is a protein called 60S ribosomal protein L4.

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

- Molecule 10 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	293	Total	C	N	O	S	0	0
			2391	1512	438	427	14		

- Molecule 11 is a protein called uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	F	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		

- Molecule 12 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	G	233	Total	C	N	O	S	0	0
			1879	1199	361	315	4		

- Molecule 13 is a protein called 60S ribosomal protein L9.

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

- Molecule 14 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	I	205	Total	C	N	O	S	0	0
			1664	1056	321	274	13		

- Molecule 15 is a protein called Ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 16 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	1691	Total	C	N	O	P	0	0
			36101	16114	6482	11815	1690		

- Molecule 17 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L	210	Total	C	N	O	S	0	0
			1700	1065	352	279	4		

- Molecule 18 is a protein called 60S ribosomal protein L14.

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

- Molecule 19 is a protein called Ribosomal protein L15.

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

- Molecule 20 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	O	199	Total	C	N	O	S	0	0
			1630	1051	319	255	5		

- Molecule 21 is a protein called Large ribosomal subunit protein uL22.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	?	-	VAL	deletion	UNP G1SCJ6

- Molecule 22 is a protein called Large ribosomal subunit protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Q	187	Total	C	N	O	S	0	0
			1515	946	315	250	4		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	4	ASP	ASN	conflict	UNP G1TFE0
Q	14	ARG	TRP	conflict	UNP G1TFE0
Q	53	MET	LEU	conflict	UNP G1TFE0
Q	58	ARG	TRP	conflict	UNP G1TFE0
Q	75	ARG	GLN	conflict	UNP G1TFE0
Q	80	ALA	PRO	conflict	UNP G1TFE0
Q	86	VAL	ILE	conflict	UNP G1TFE0
Q	104	ARG	HIS	conflict	UNP G1TFE0
Q	110	ARG	CYS	conflict	UNP G1TFE0
Q	137	VAL	GLY	conflict	UNP G1TFE0
Q	157	GLY	ARG	conflict	UNP G1TFE0
Q	181	ARG	TRP	conflict	UNP G1TFE0

- Molecule 23 is a protein called Large ribosomal subunit protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	R	180	Total	C	N	O	S	0	0
			1507	933	327	238	9		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	38	ARG	HIS	conflict	UNP G1TYL6

- Molecule 24 is a protein called Large ribosomal subunit protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	S	176	Total	C	N	O	S	0	0
			1457	924	288	234	11		

- Molecule 25 is a protein called eL21.

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

- Molecule 26 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	U	105	Total	C	N	O	S	0	0
			874	555	155	162	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U	39	PHE	SER	conflict	UNP G1TSG1

- Molecule 27 is a protein called Ribosomal protein L23.

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

- Molecule 28 is a protein called eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	W	106	Total	C	N	O	S	0	0
			860	538	174	144	4		

- Molecule 29 is a protein called eL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	X	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 30 is a protein called uL24.

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

- Molecule 31 is a protein called 60S ribosomal protein L27.

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

- Molecule 32 is a protein called 60S ribosomal protein L27a.

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

- Molecule 33 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	c	98	Total	C	N	O	S	0	0
			761	481	134	140	6		

- Molecule 34 is a protein called eL31.

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

- Molecule 35 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	e	128	Total	C	N	O	S	0	0
			1058	675	214	164	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
e	108	ARG	CYS	conflict	UNP G1TUN8

- Molecule 36 is a protein called eL33.

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

- Molecule 37 is a protein called 60S ribosomal protein L34.

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

- Molecule 38 is a protein called eL35.

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

- Molecule 39 is a protein called Large ribosomal subunit protein eL36.

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

- Molecule 40 is a protein called Ribosomal protein L37.

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

- Molecule 41 is a protein called Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	k	69	Total	C	N	O	S	0	0
			568	364	103	100	1		

- Molecule 42 is a protein called eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	l	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 43 is a protein called eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	n	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 44 is a protein called Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	o	104	Total	C	N	O	S	0	0
			858	541	173	137	7		

- Molecule 45 is a protein called eL43.

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

- Molecule 46 is a protein called uS2 (SA).

Mol	Chain	Residues	Atoms					AltConf	Trace
46	q	217	Total	C	N	O	S	0	0
			1710	1086	300	316	8		

- Molecule 47 is a protein called eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	r	124	Total	C	N	O	S	0	0
			994	616	205	167	6		

- Molecule 48 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	u	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 49 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	v	221	Total	C	N	O	S	0	0
			1718	1114	296	299	9		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
v	97	PHE	CYS	conflict	UNP G1SWM1
v	191	VAL	-	insertion	UNP G1SWM1

- Molecule 50 is a protein called Ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	w	226	Total	C	N	O	S	0	0
			1755	1118	316	314	7		

- Molecule 51 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	x	261	Total	C	N	O	S	0	0
			2070	1322	383	356	9		

- Molecule 52 is a protein called 40S ribosomal protein S6.

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

- Molecule 53 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	2	76	Total	C	N	O	P	0	0
			1614	722	287	530	75		

- Molecule 54 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	5	3469	Total	C	N	O	P	0	0
			74394	33129	13626	24170	3469		

- Molecule 55 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	8	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 56 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	E	211	Total	C	N	O	S	0	0
			1697	1095	322	277	3		

- Molecule 57 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	b	104	Total	C	N	O	S	0	0
			848	527	189	129	3		

- Molecule 58 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	y	184	Total	C	N	O	S	0	0
			1464	917	276	264	7		

- Molecule 59 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	BB	183	Total	C	N	O	S	0	0
			1471	941	268	261	1		

- Molecule 60 is a protein called 40S ribosomal protein S8.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CC	47	ARG	GLY	conflict	UNP G1TJW1

- Molecule 61 is a protein called Ribosomal protein S9 (Predicted).

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

- Molecule 62 is a protein called S10_plectin domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SS	95	Total	C	N	O	S	0	0
			802	525	142	130	5		

- Molecule 63 is a protein called Ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	EE	143	Total	C	N	O	S	0	0
			1175	749	222	198	6		

- Molecule 64 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	RR	117	Total	C	N	O	S	0	0
			908	570	161	169	8		

- Molecule 65 is a protein called Ribosomal protein S13.

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

- Molecule 66 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	MM	135	Total	C	N	O	S	0	0
			1004	614	196	188	6		

- Molecule 67 is a protein called uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	WW	122	Total	C	N	O	S	0	0
			1009	643	189	170	7		

- Molecule 68 is a protein called uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	UU	141	Total	C	N	O	S	0	0
			1124	715	212	194	3		

- Molecule 69 is a protein called eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	KK	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 70 is a protein called uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	II	142	Total	C	N	O	S	0	0
			1172	736	236	199	1		

- Molecule 71 is a protein called eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	PP	141	Total	C	N	O	S	0	0
			1097	688	211	195	3		

- Molecule 72 is a protein called uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	GG	100	Total	C	N	O	S	0	0
			795	498	152	141	4		

- Molecule 73 is a protein called Small ribosomal subunit protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	HH	83	Total	C	N	O	S	0	0
			637	392	117	123	5		

- Molecule 74 is a protein called Ribosomal protein S15a.

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

- Molecule 75 is a protein called uS12.

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

- Molecule 76 is a protein called Small ribosomal subunit protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	NN	124	Total	C	N	O	S	0	0
			1011	640	198	168	5		

- Molecule 77 is a protein called eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	OO	73	Total	C	N	O	S	0	0
			585	374	108	102	1		

- Molecule 78 is a protein called eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	LL	101	Total	C	N	O	S	0	0
			816	509	170	132	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LL	28	ARG	CYS	conflict	UNP G1TFE8

- Molecule 79 is a protein called 40S ribosomal protein S27.

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

- Molecule 80 is a protein called Ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	FF	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 81 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	AA	55	Total	C	N	O	S	0	0
			443	274	97	71	1		

- Molecule 82 is a protein called Transcription factor BTF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	EF	110	Total	C	N	O	S	0	0
			854	534	158	158	4		

- Molecule 83 is a protein called Nascent polypeptide-associated complex subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	EG	65	Total	C	N	O	S	0	0
			513	324	93	95	1		

- Molecule 84 is a protein called Nascent Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	EH	33	Total	C	N	O	S	0	0
			245	161	44	37	3		

- Molecule 85 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

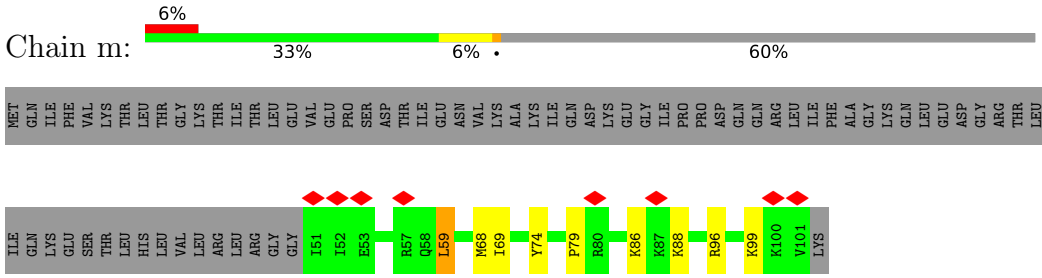
- Molecule 86 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
86	7	6	Total Mg 6 6	0
86	A	1	Total Mg 1 1	0
86	B	1	Total Mg 1 1	0
86	I	1	Total Mg 1 1	0
86	K	76	Total Mg 76 76	0
86	P	2	Total Mg 2 2	0
86	V	1	Total Mg 1 1	0
86	a	1	Total Mg 1 1	0
86	g	1	Total Mg 1 1	0
86	j	2	Total Mg 2 2	0
86	5	186	Total Mg 186 186	0
86	8	6	Total Mg 6 6	0
86	PP	1	Total Mg 1 1	0

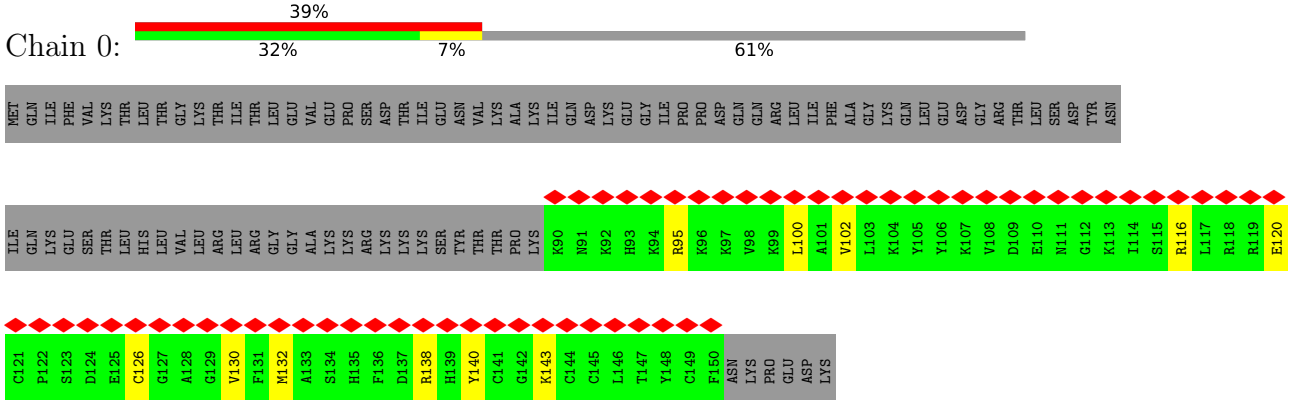
3 Residue-property plots (i)

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.

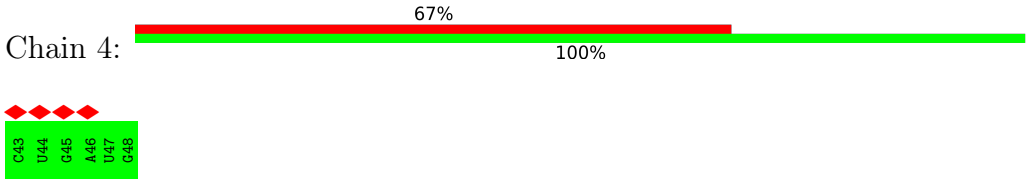
• Molecule 1: Ubiquitin-ribosomal protein eL40 fusion protein



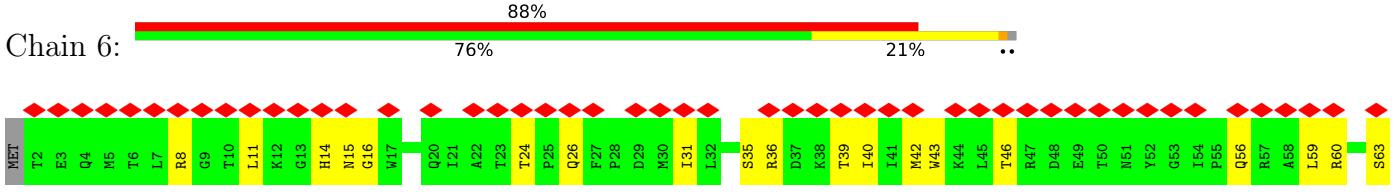
• Molecule 2: Ribosomal protein S27a

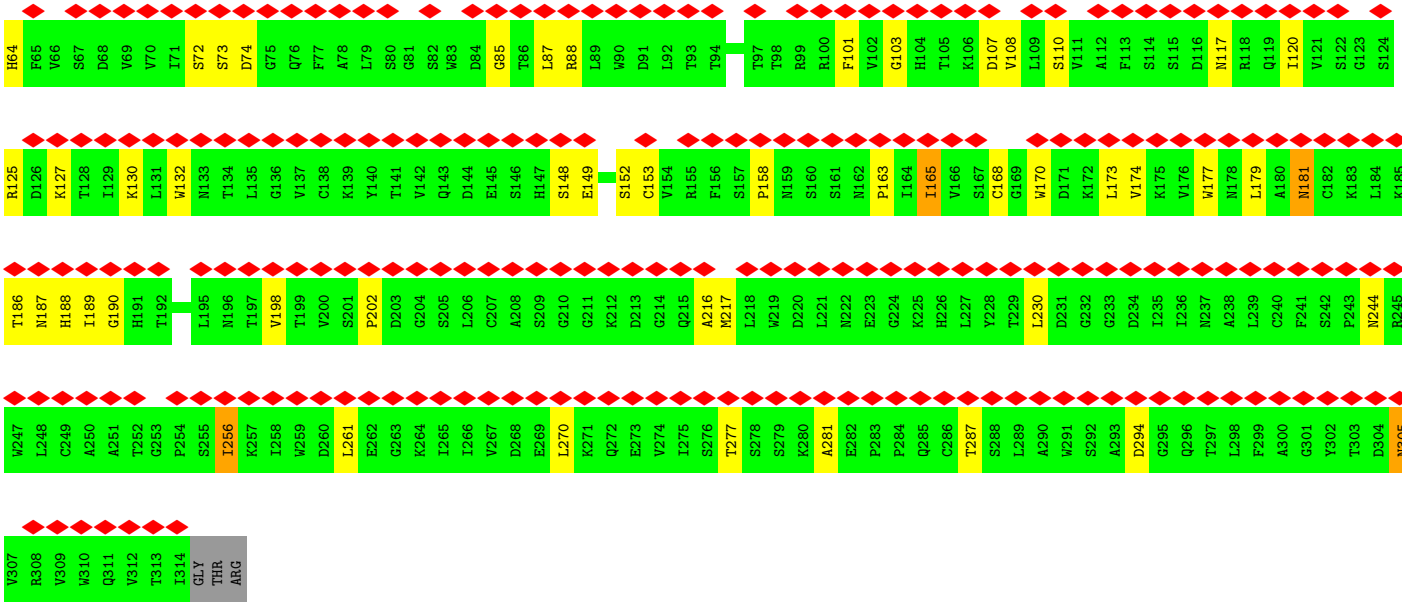


• Molecule 3: mRNA



• Molecule 4: RACK1

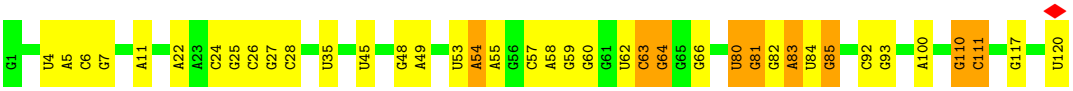




- Molecule 5: 5S rRNA

Chain 7:

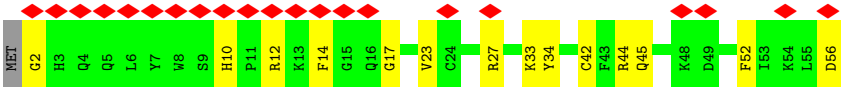




- Molecule 6: eS29

Chain 9:

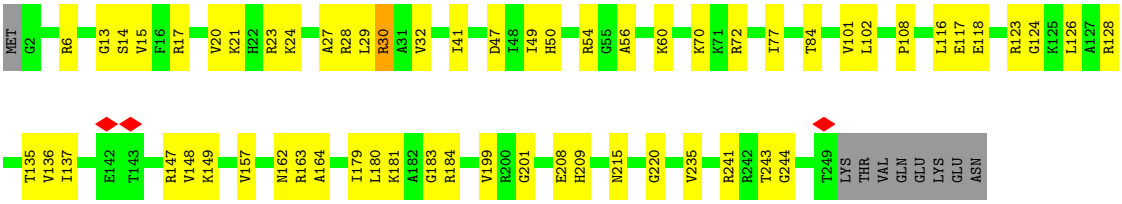




- Molecule 7: Ribosomal protein L8

Chain A:



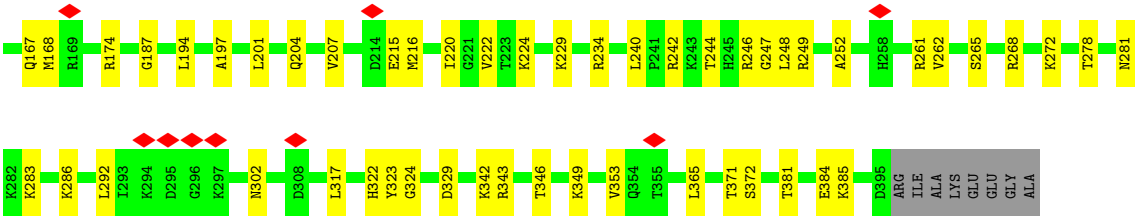


- Molecule 8: Ribosomal protein L3

Chain B:



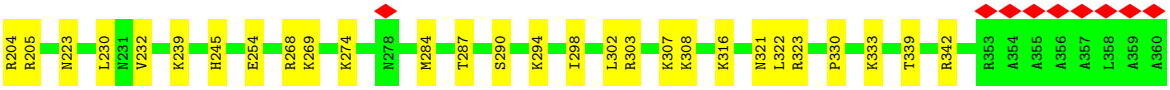


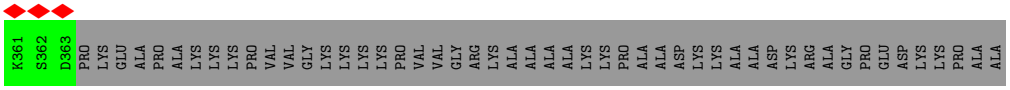


• Molecule 9: 60S ribosomal protein L4

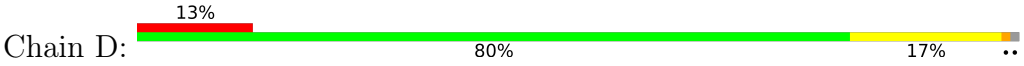


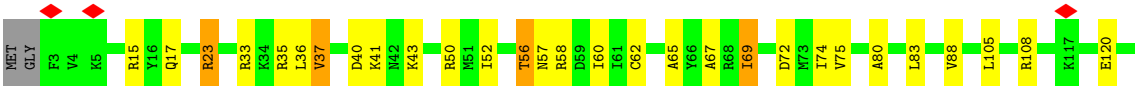


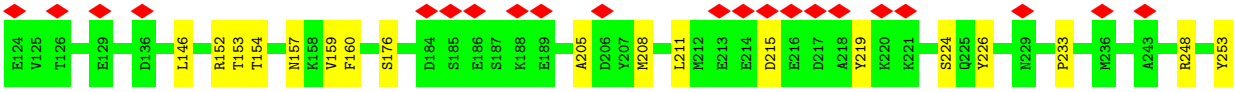


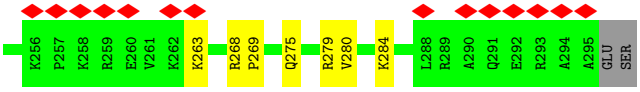


• Molecule 10: Large ribosomal subunit protein uL18



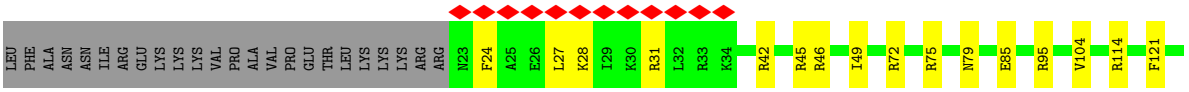


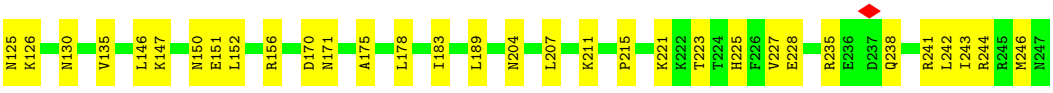




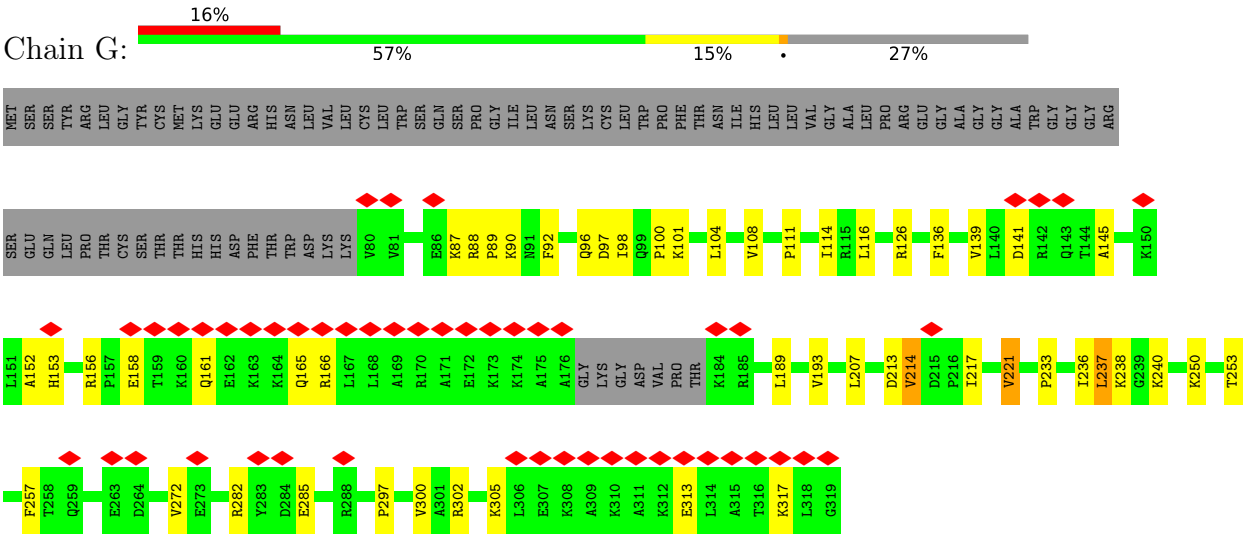
• Molecule 11: uL30



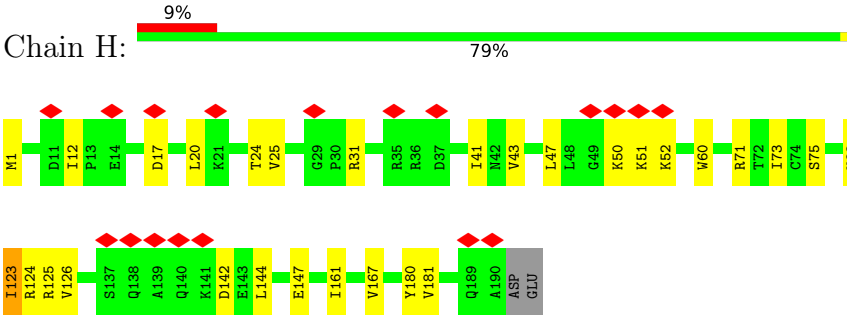




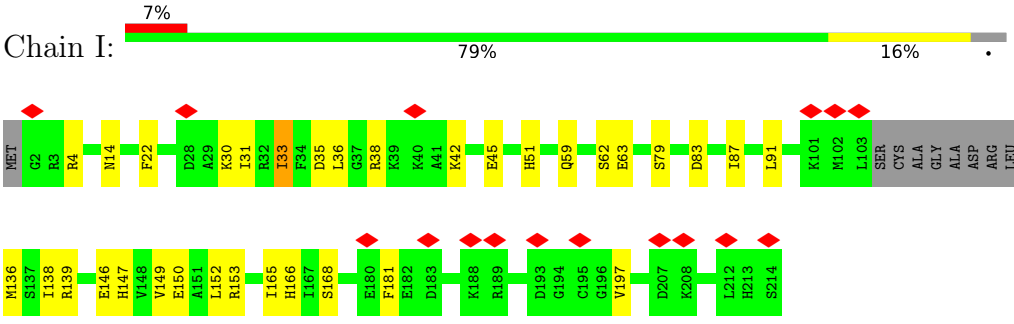
• Molecule 12: 60S ribosomal protein L7a



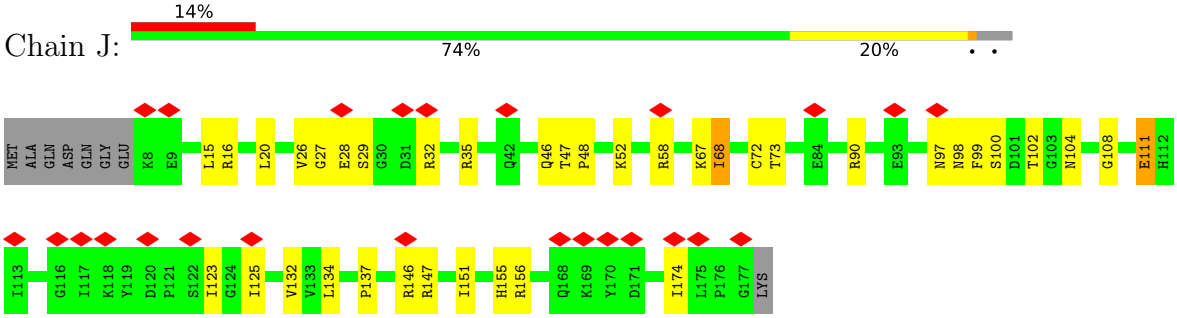
• Molecule 13: 60S ribosomal protein L9



• Molecule 14: 60S ribosomal protein L10



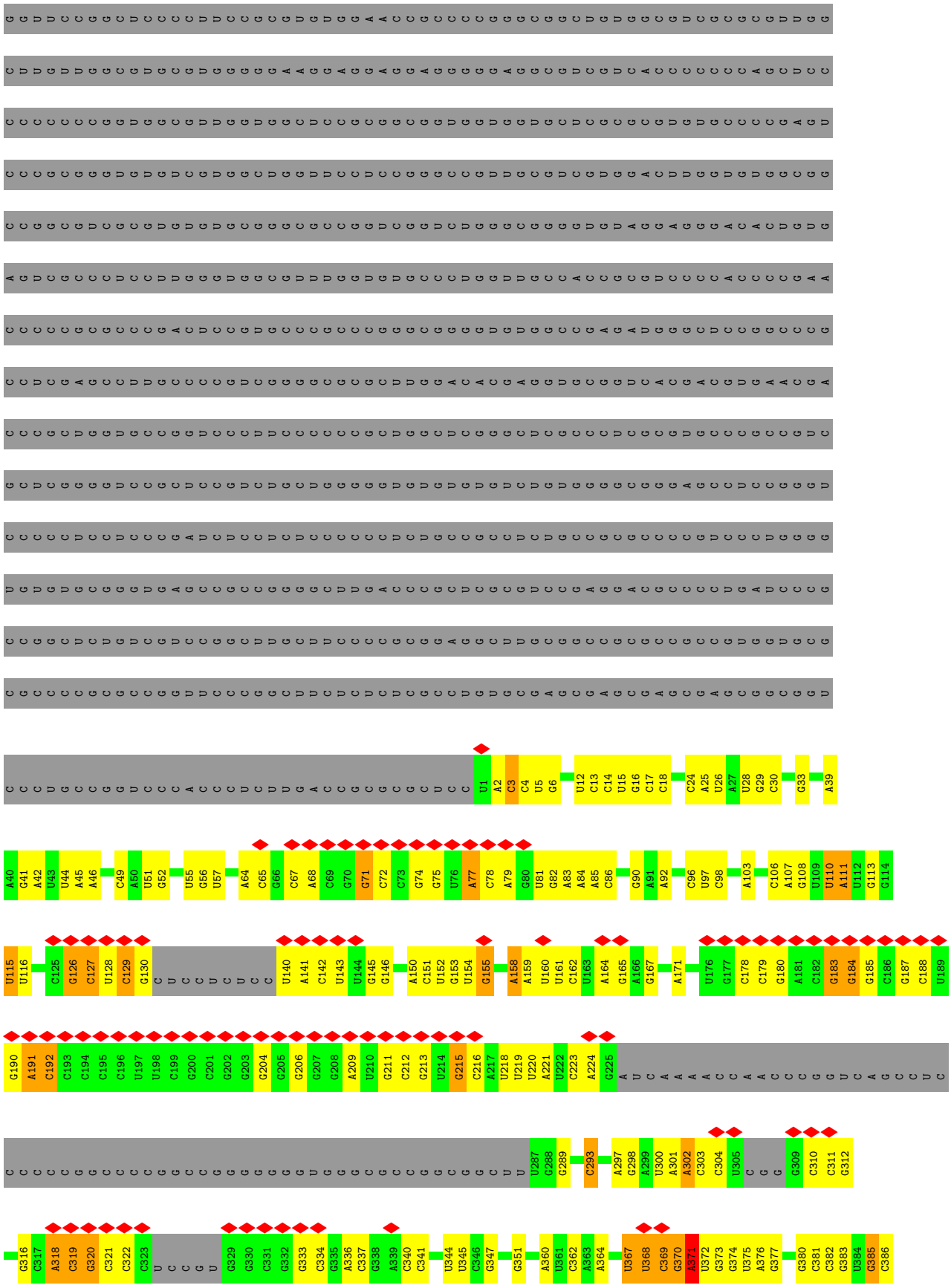
• Molecule 15: Ribosomal protein L11

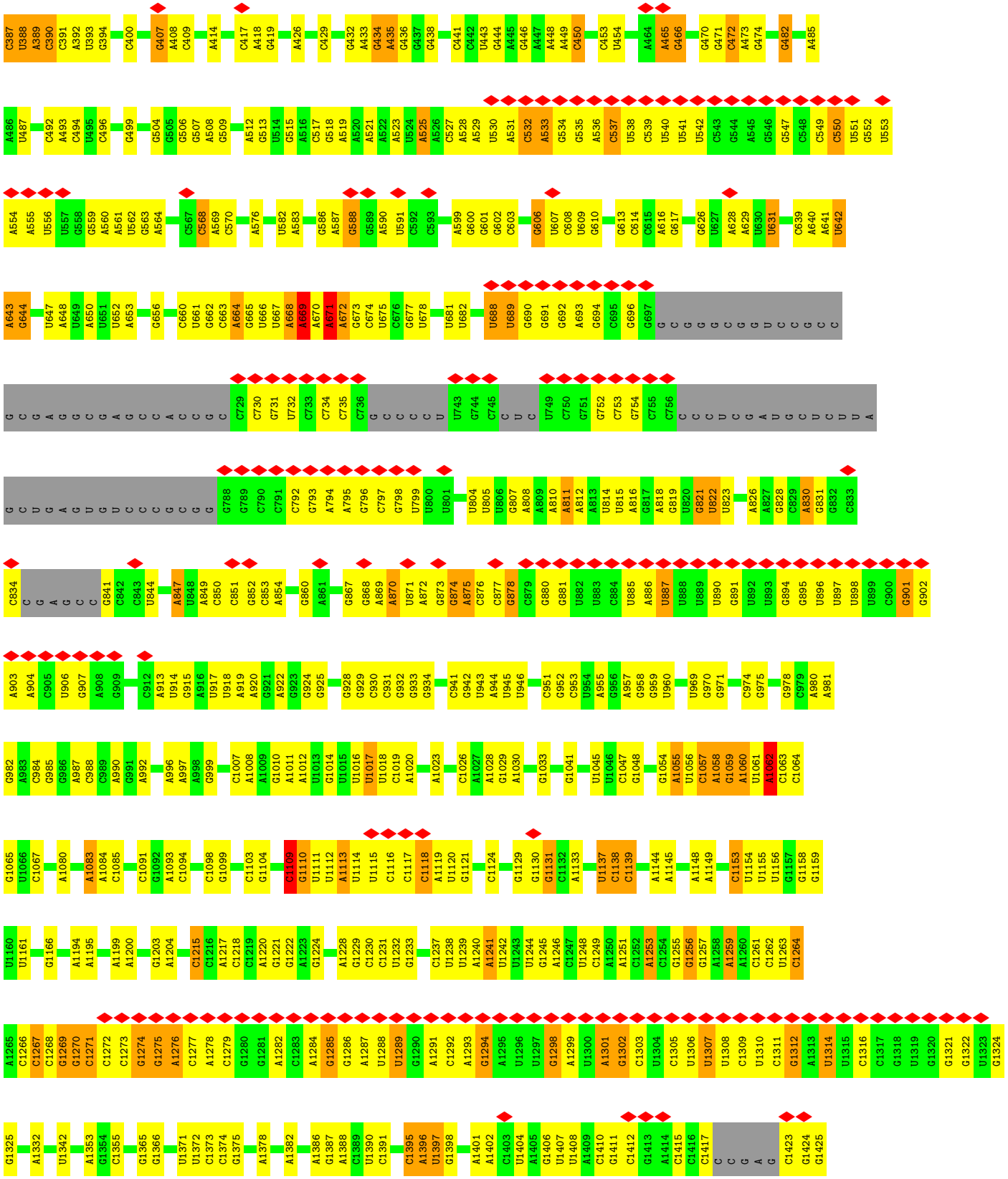


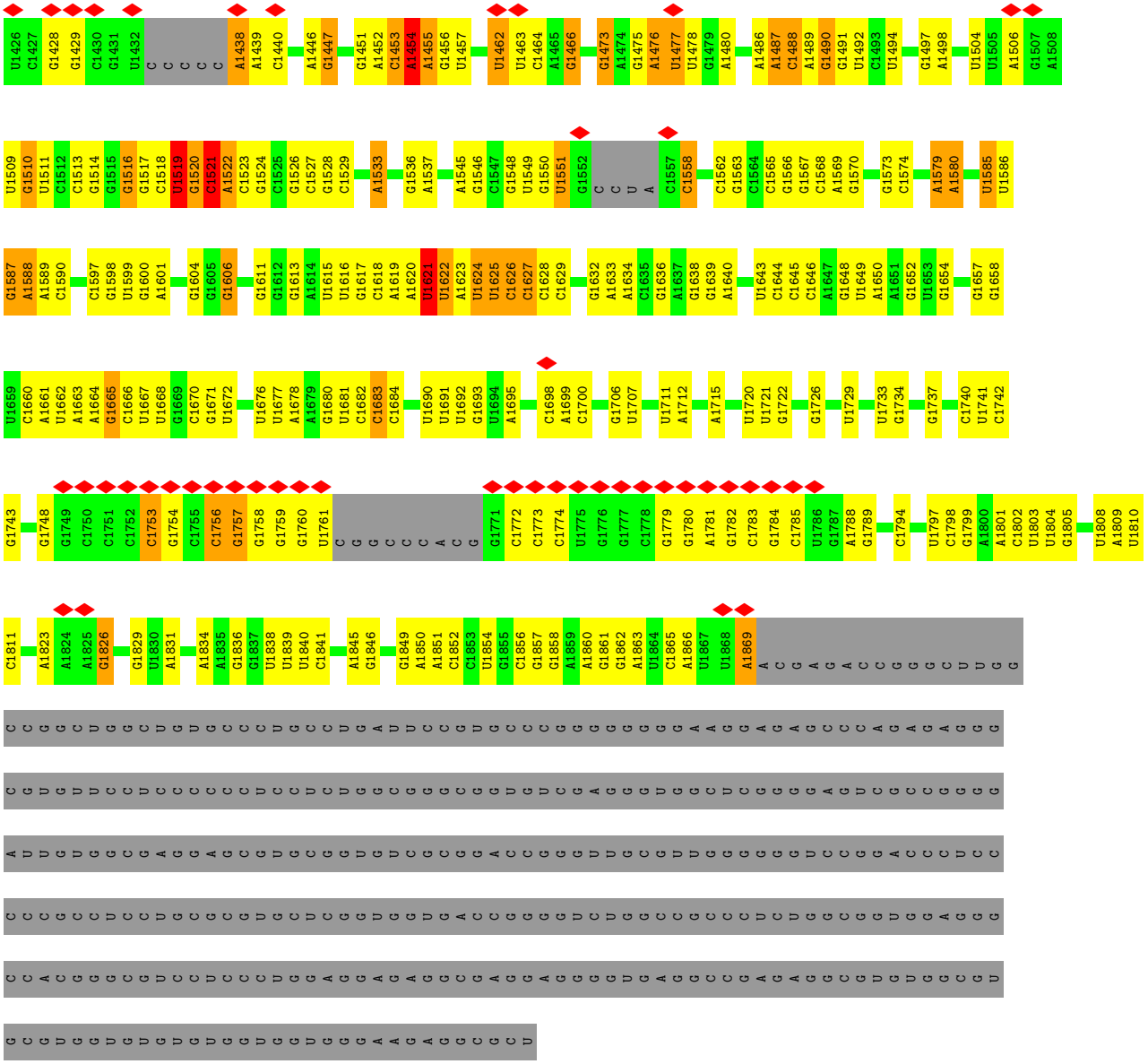
• Molecule 16: 18S rRNA

Chain K:





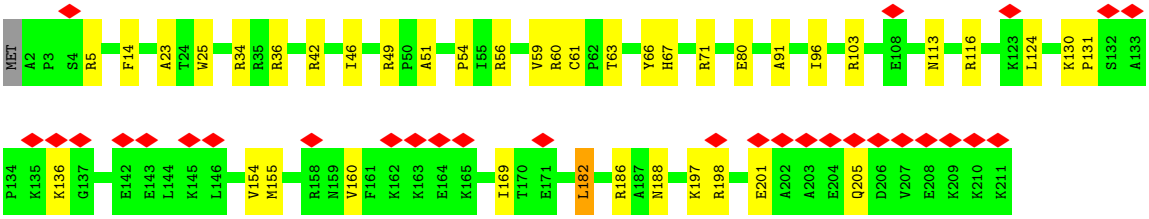




• Molecule 17: Large ribosomal subunit protein eL13

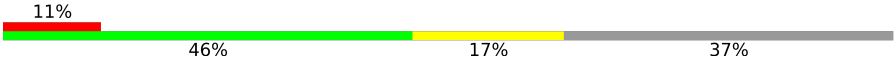
Chain L:

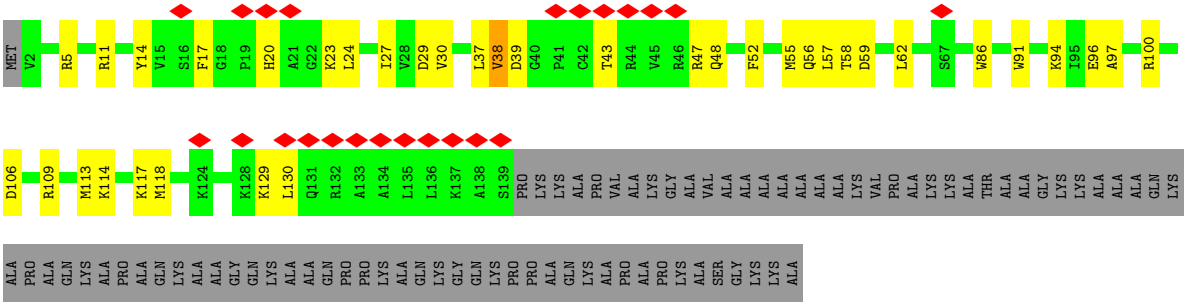




• Molecule 18: 60S ribosomal protein L14

Chain M:

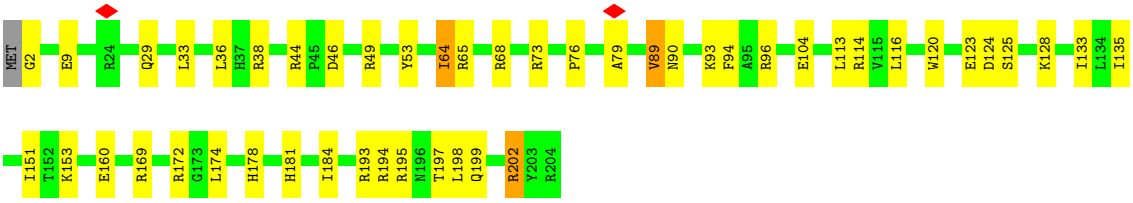




• Molecule 19: Ribosomal protein L15

Chain N:

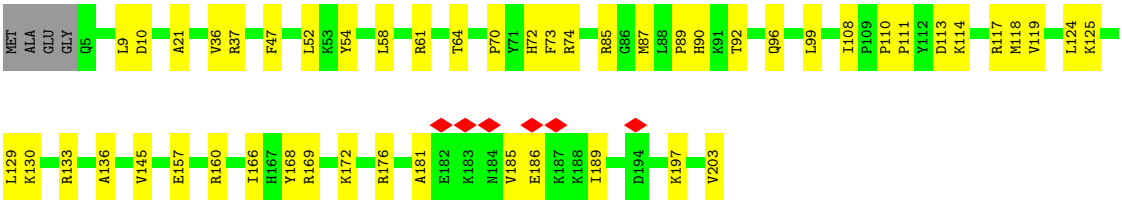




• Molecule 20: Large ribosomal subunit protein uL13

Chain O:

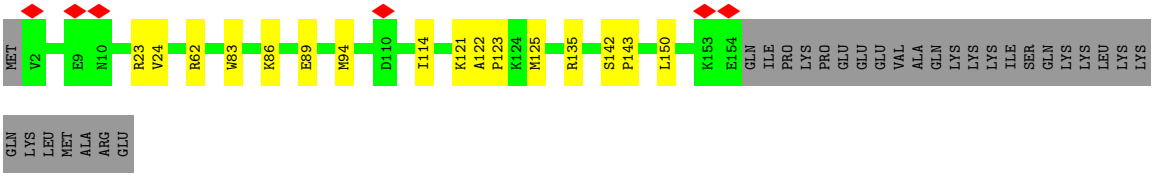




• Molecule 21: Large ribosomal subunit protein uL22

Chain P:

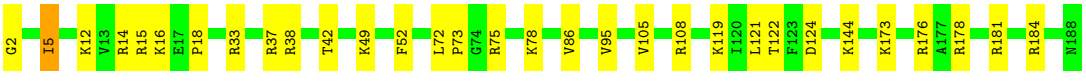




• Molecule 22: Large ribosomal subunit protein eL18

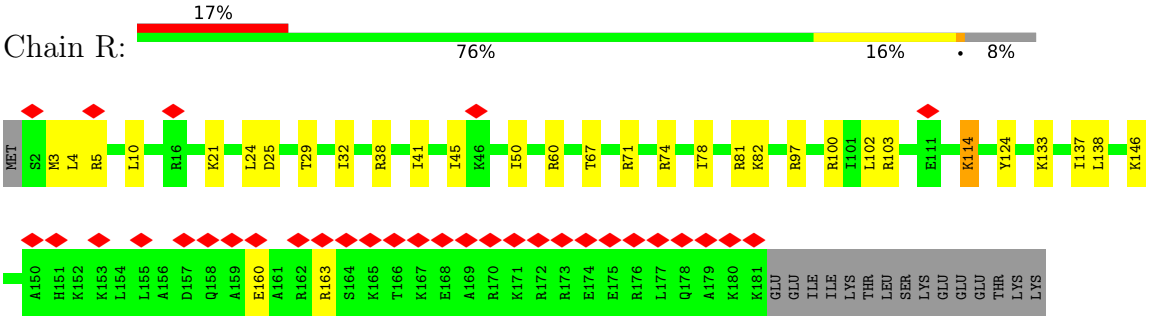
Chain Q:





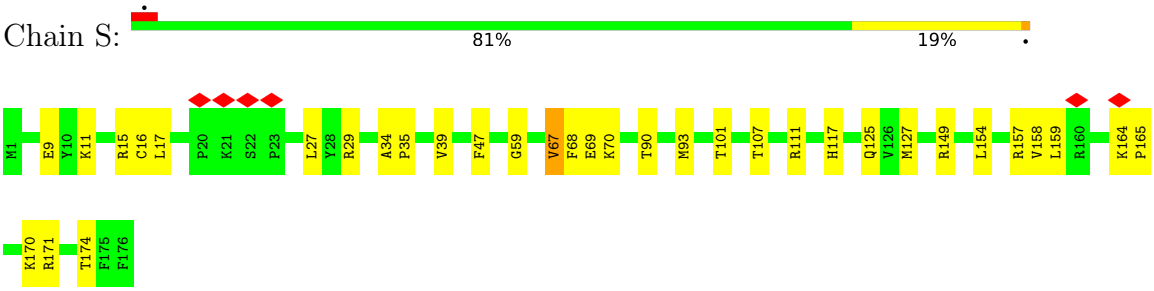
• Molecule 23: Large ribosomal subunit protein eL19

Chain R:



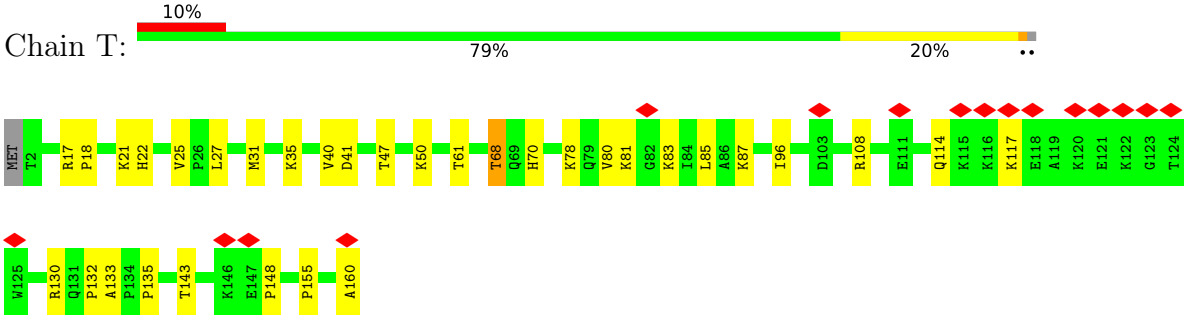
• Molecule 24: Large ribosomal subunit protein eL20

Chain S:



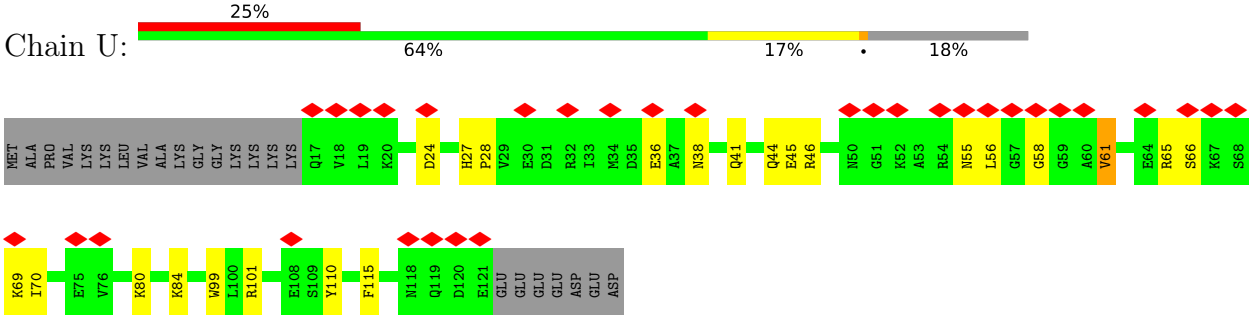
• Molecule 25: eL21

Chain T:



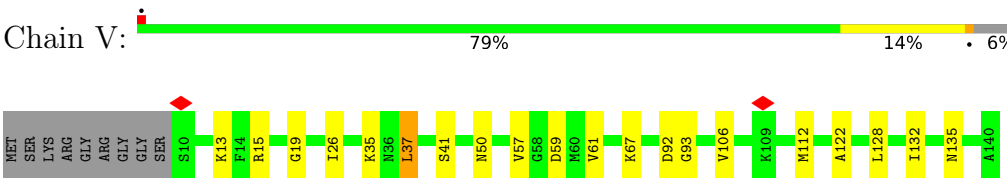
• Molecule 26: Large ribosomal subunit protein eL22

Chain U:



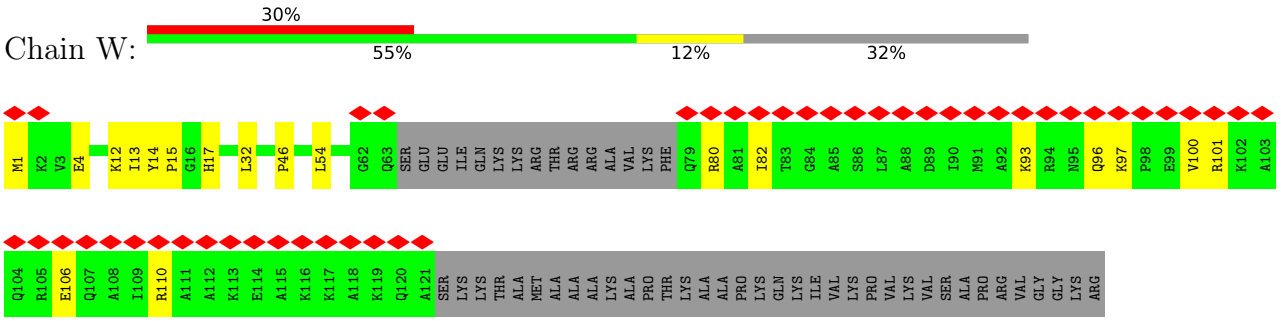
• Molecule 27: Ribosomal protein L23

Chain V:



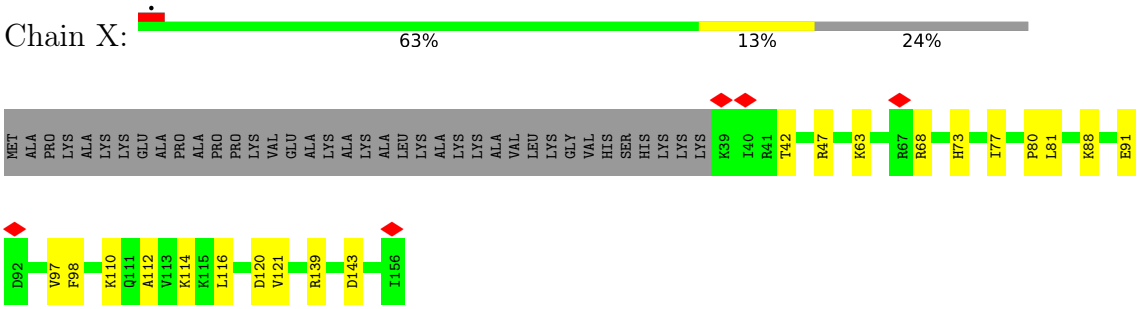
• Molecule 28: eL24

Chain W:



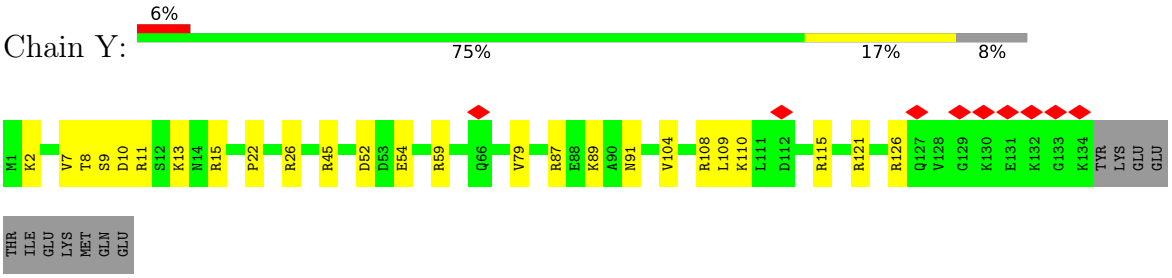
• Molecule 29: eL23

Chain X:



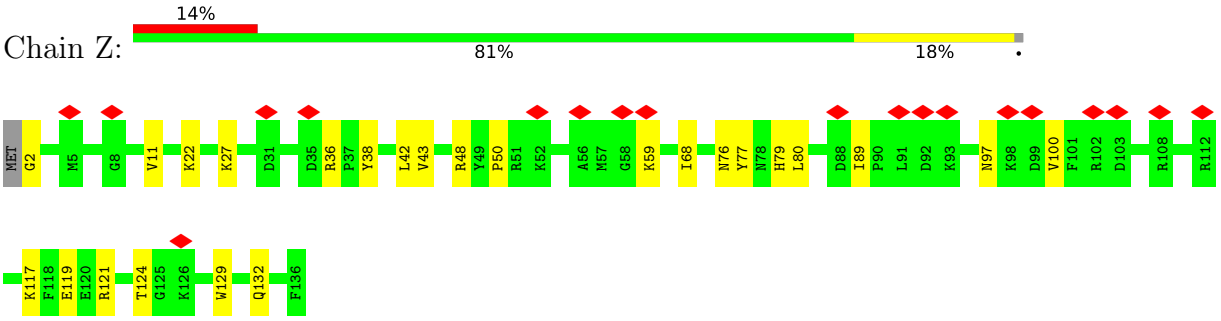
• Molecule 30: uL24

Chain Y:



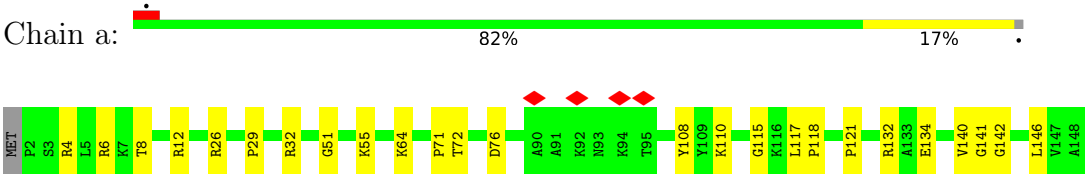
• Molecule 31: 60S ribosomal protein L27

Chain Z:



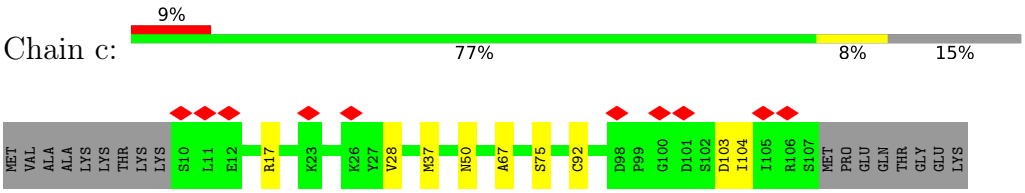
• Molecule 32: 60S ribosomal protein L27a

Chain a:



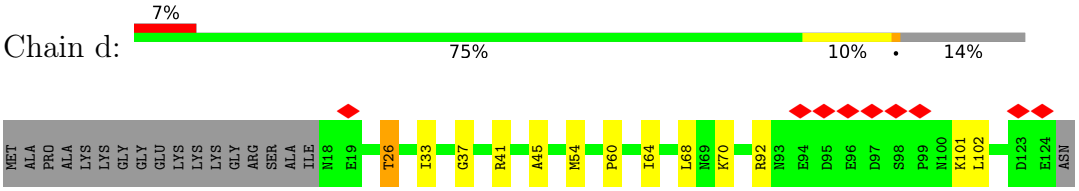
• Molecule 33: eL30

Chain c:



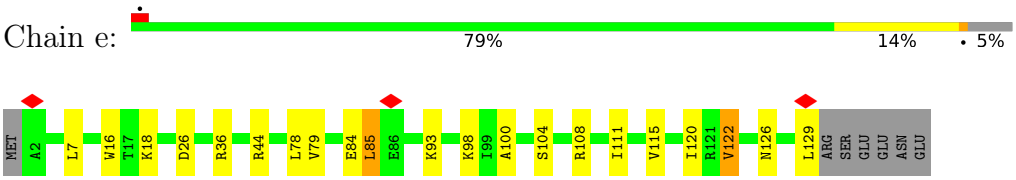
• Molecule 34: eL31

Chain d:



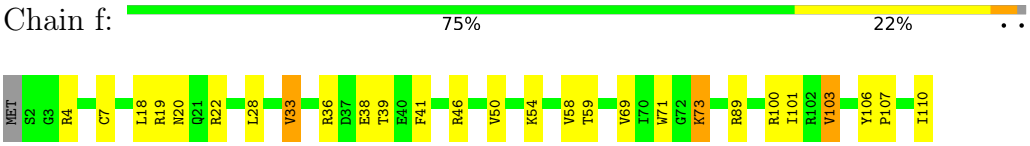
• Molecule 35: Large ribosomal subunit protein eL32

Chain e:



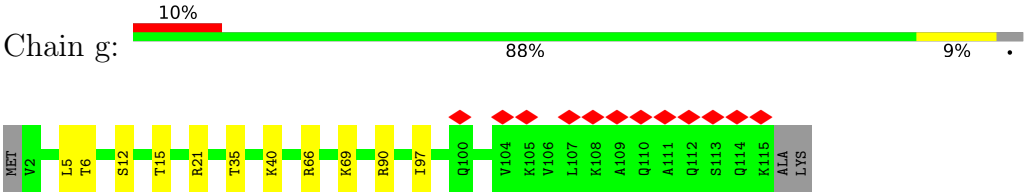
• Molecule 36: eL33

Chain f:



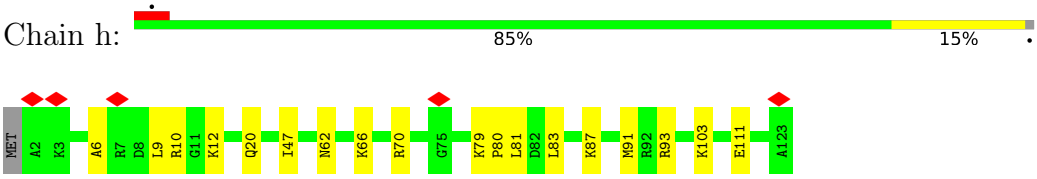
• Molecule 37: 60S ribosomal protein L34

Chain g:



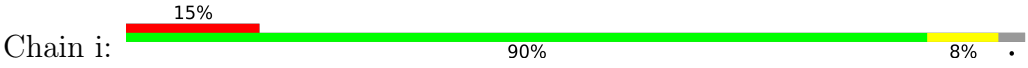
• Molecule 38: eL35

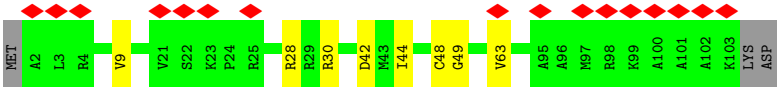
Chain h:



• Molecule 39: Large ribosomal subunit protein eL36

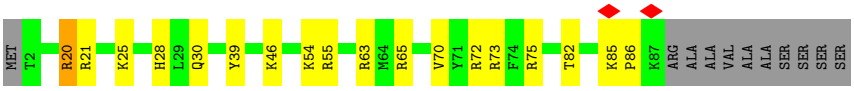
Chain i:



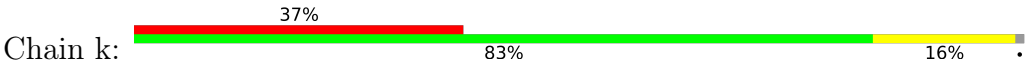


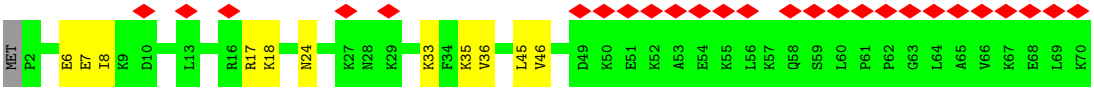
• Molecule 40: Ribosomal protein L37



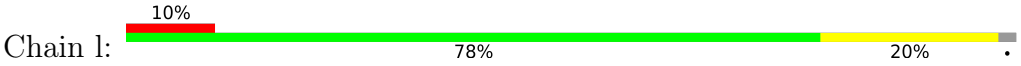


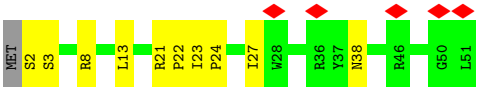
• Molecule 41: Large ribosomal subunit protein eL38



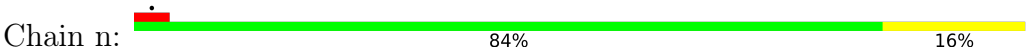


• Molecule 42: eL39





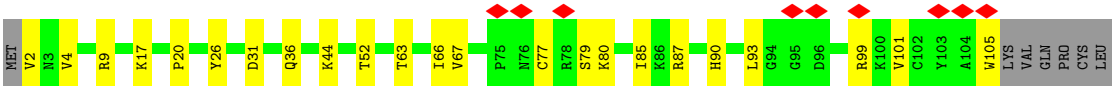
• Molecule 43: eL41



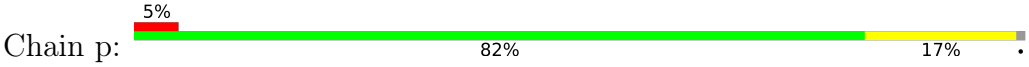


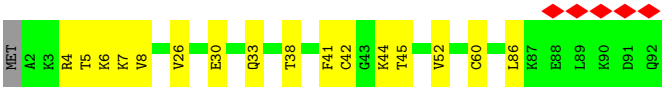
• Molecule 44: Large ribosomal subunit protein eL42





• Molecule 45: eL43

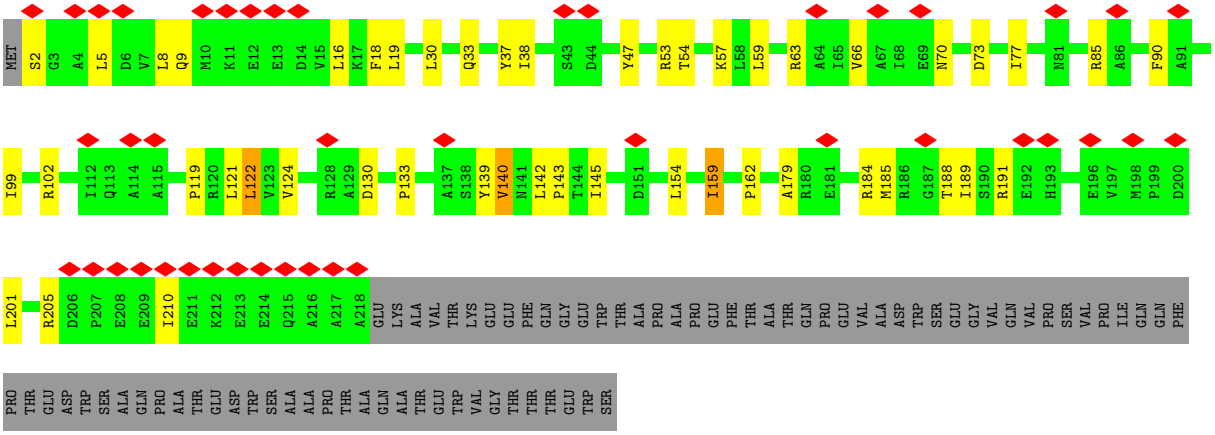




• Molecule 46: uS2 (SA)

Chain q:

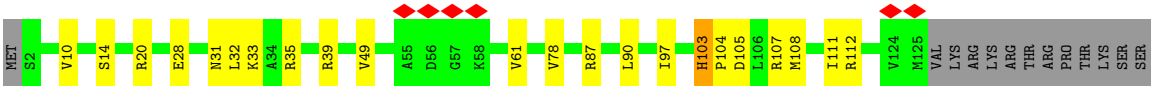




• Molecule 47: eL28

Chain r:

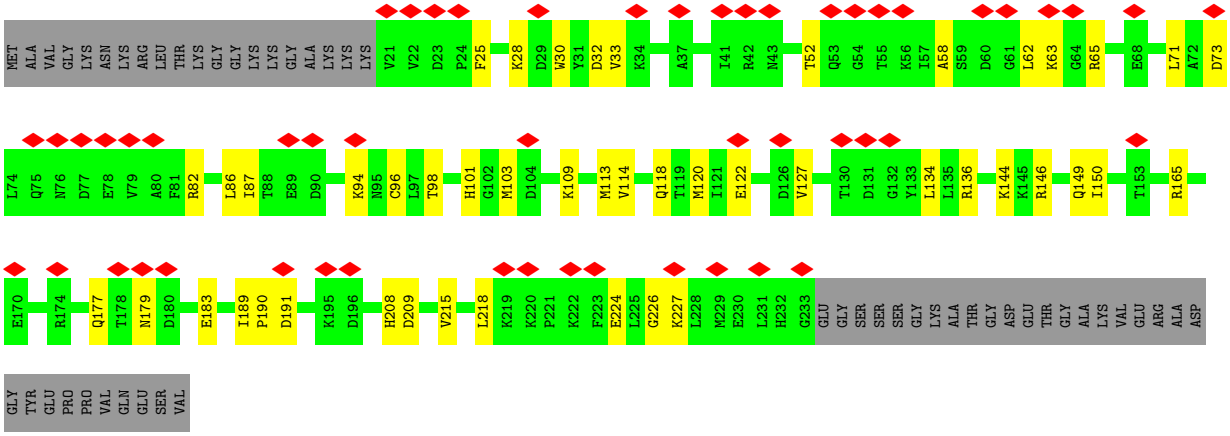




• Molecule 48: 40S ribosomal protein S3a

Chain u:

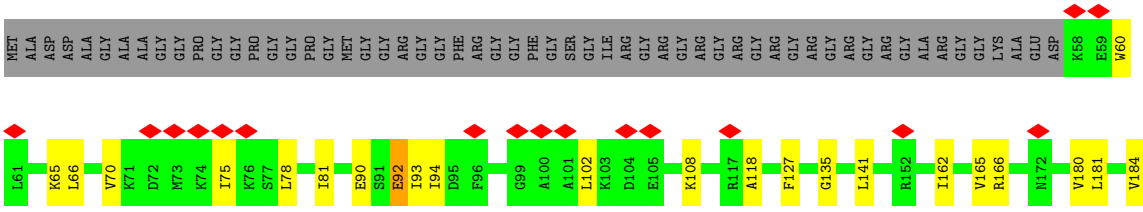


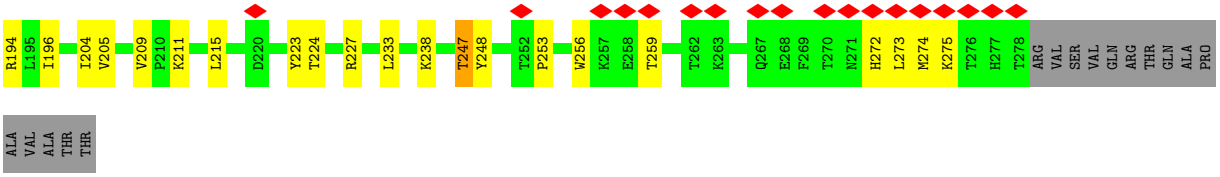


• Molecule 49: Small ribosomal subunit protein uS5

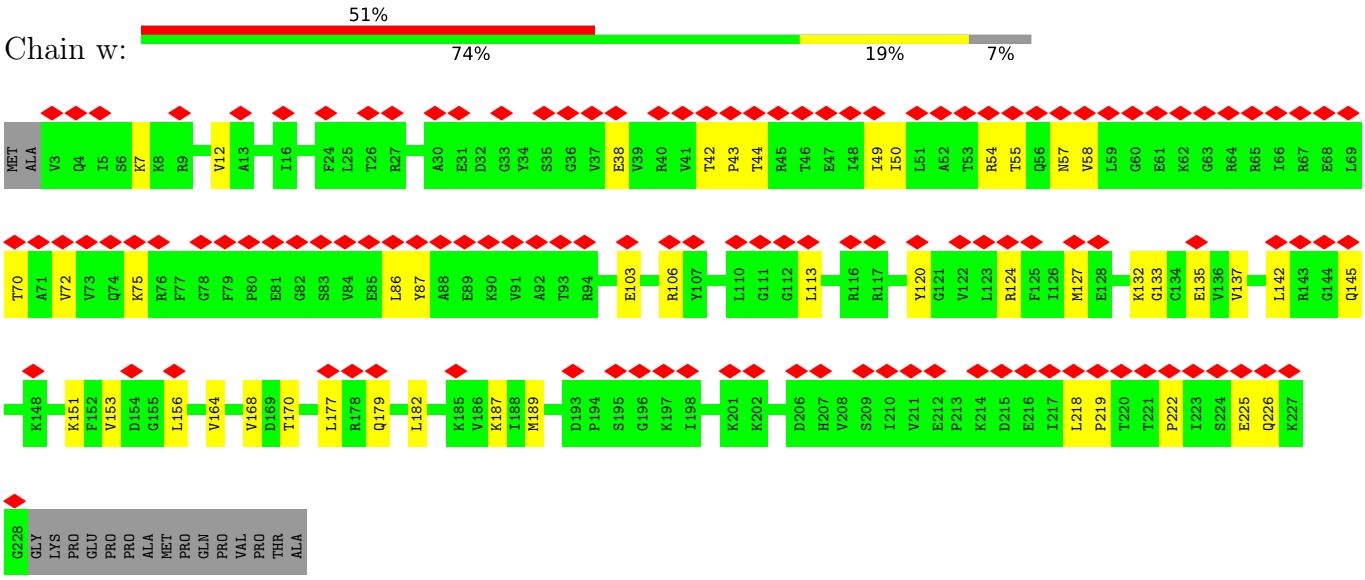
Chain v:



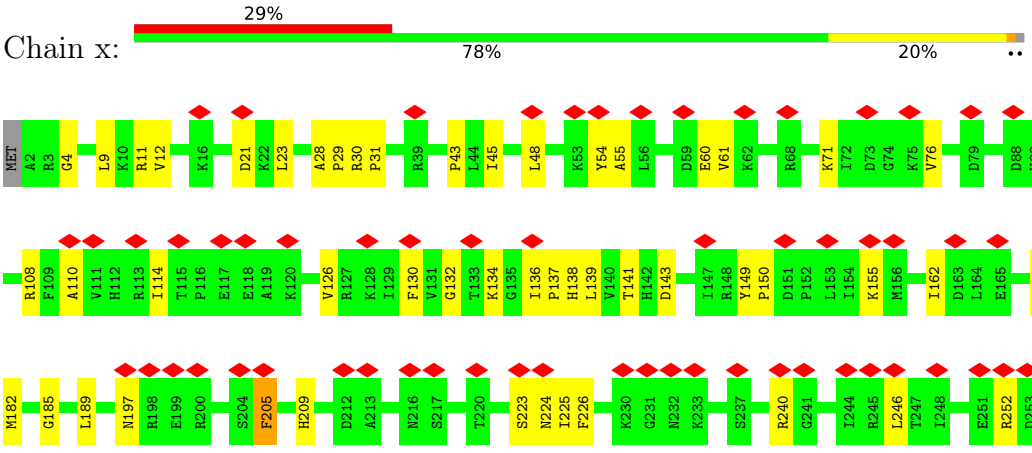




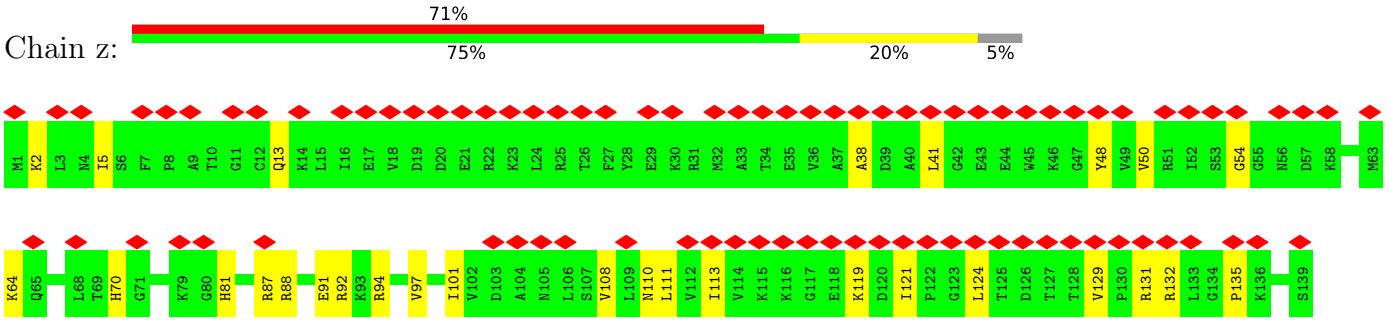
• Molecule 50: Ribosomal protein S3

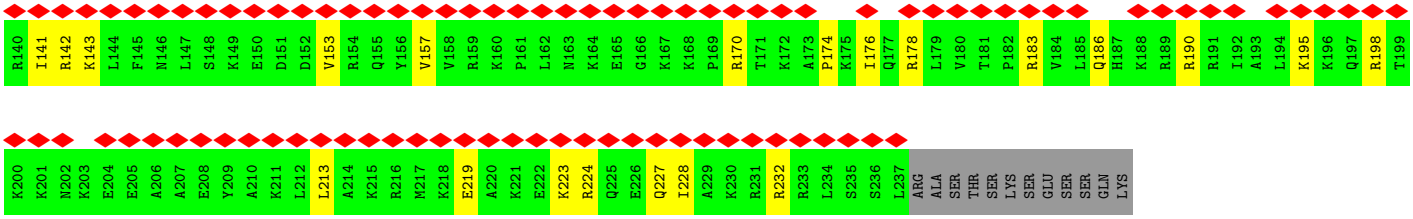


• Molecule 51: 40S ribosomal protein S4



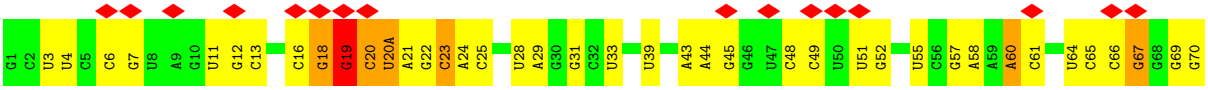
• Molecule 52: 40S ribosomal protein S6





- Molecule 53: tRNA

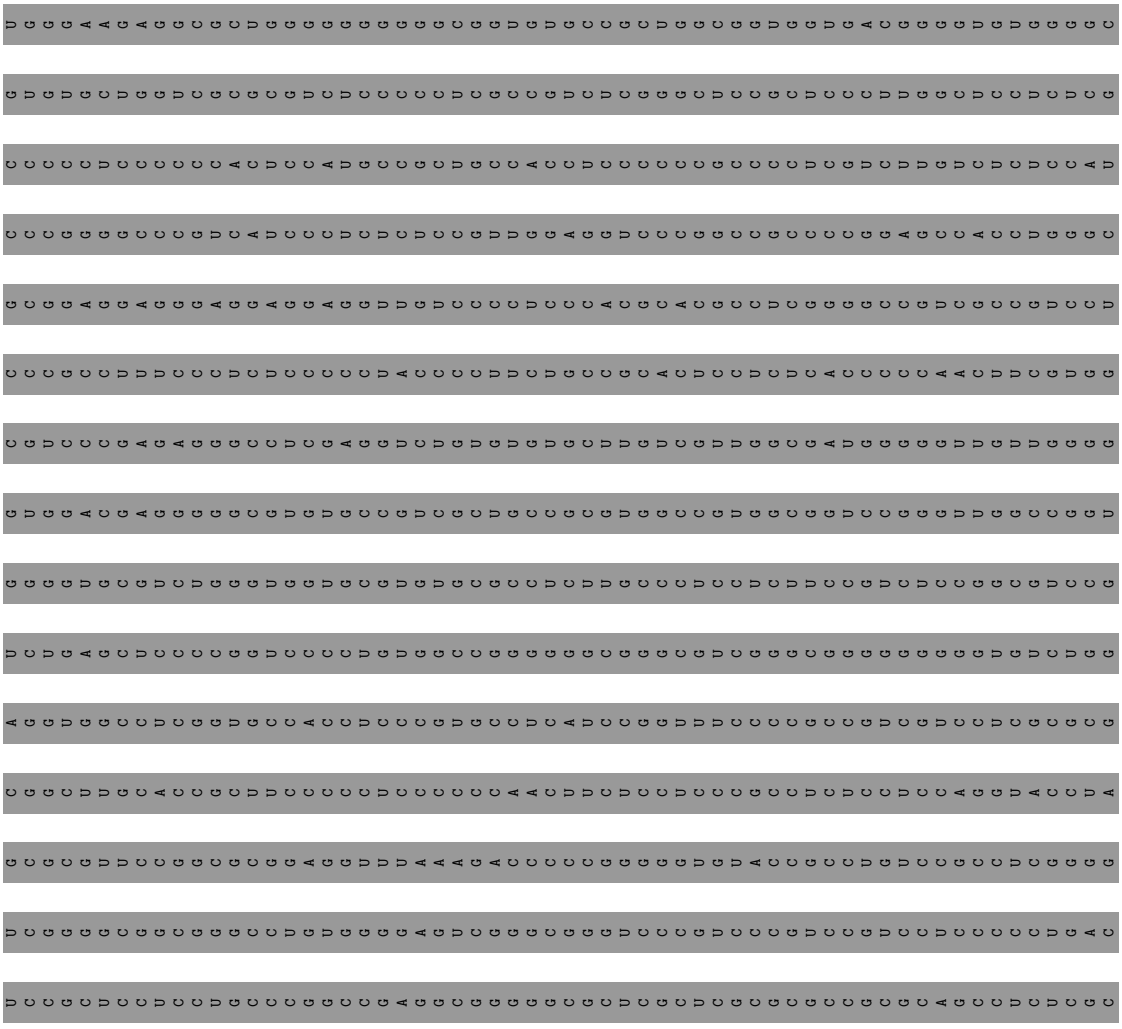


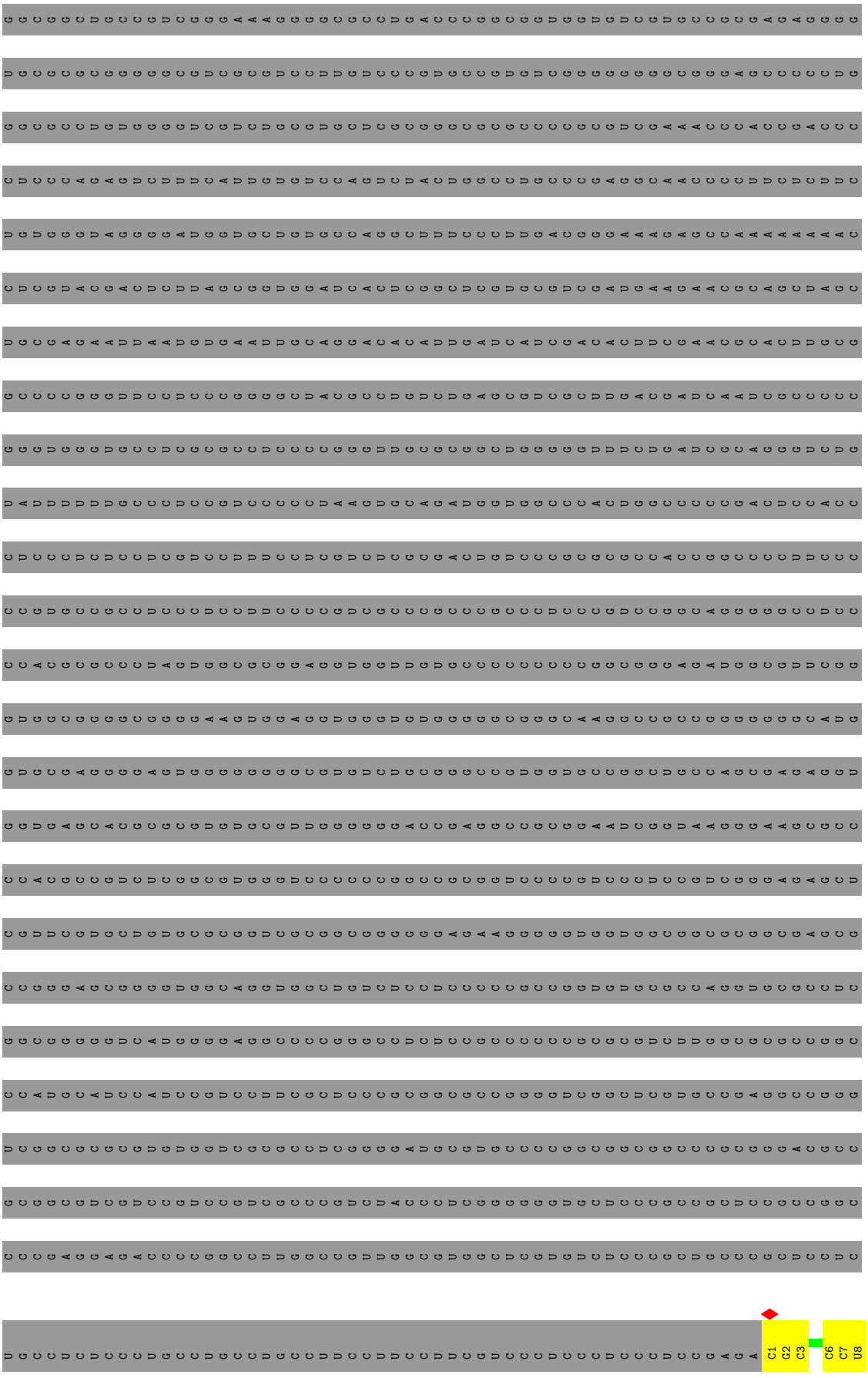


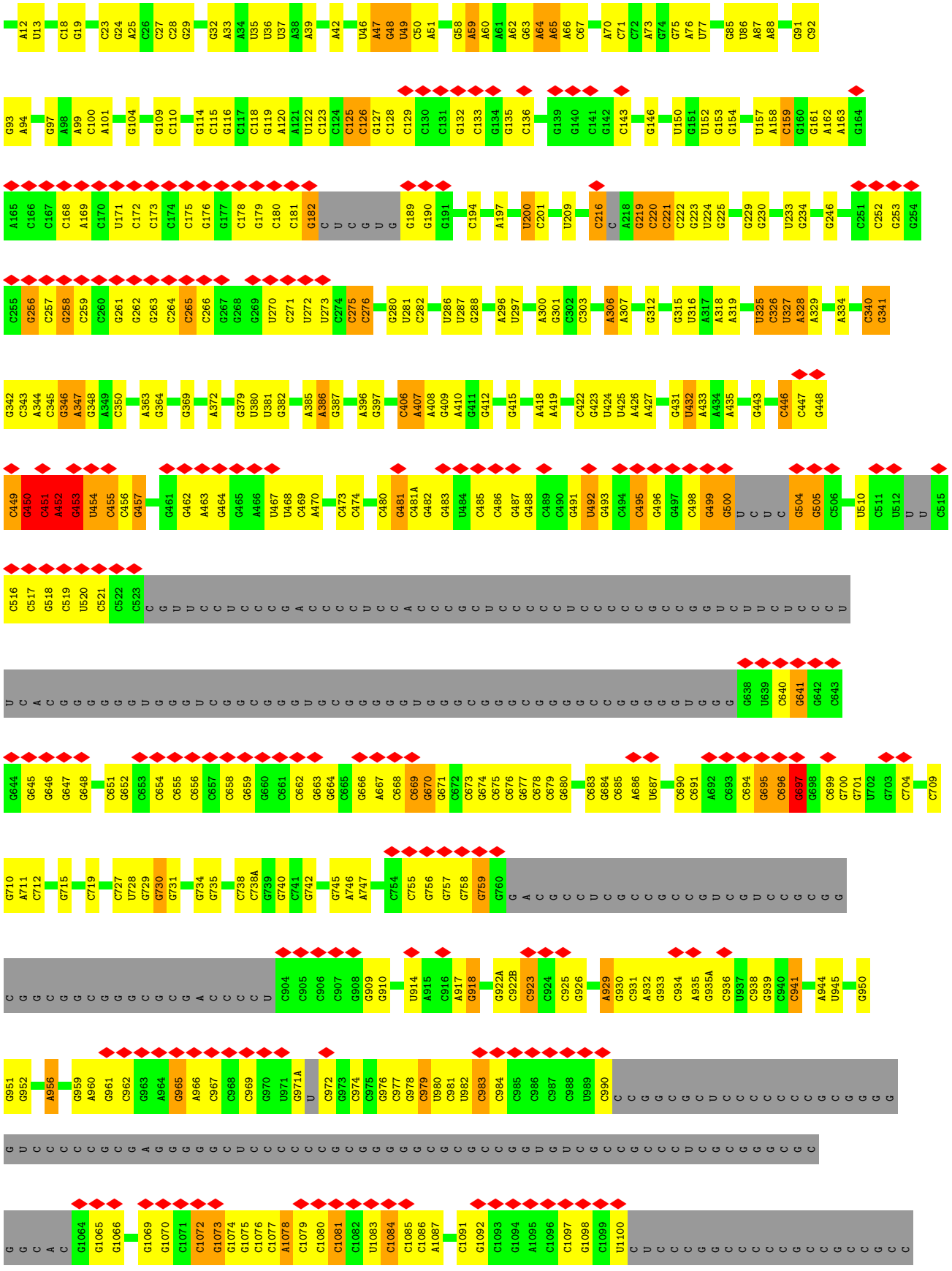


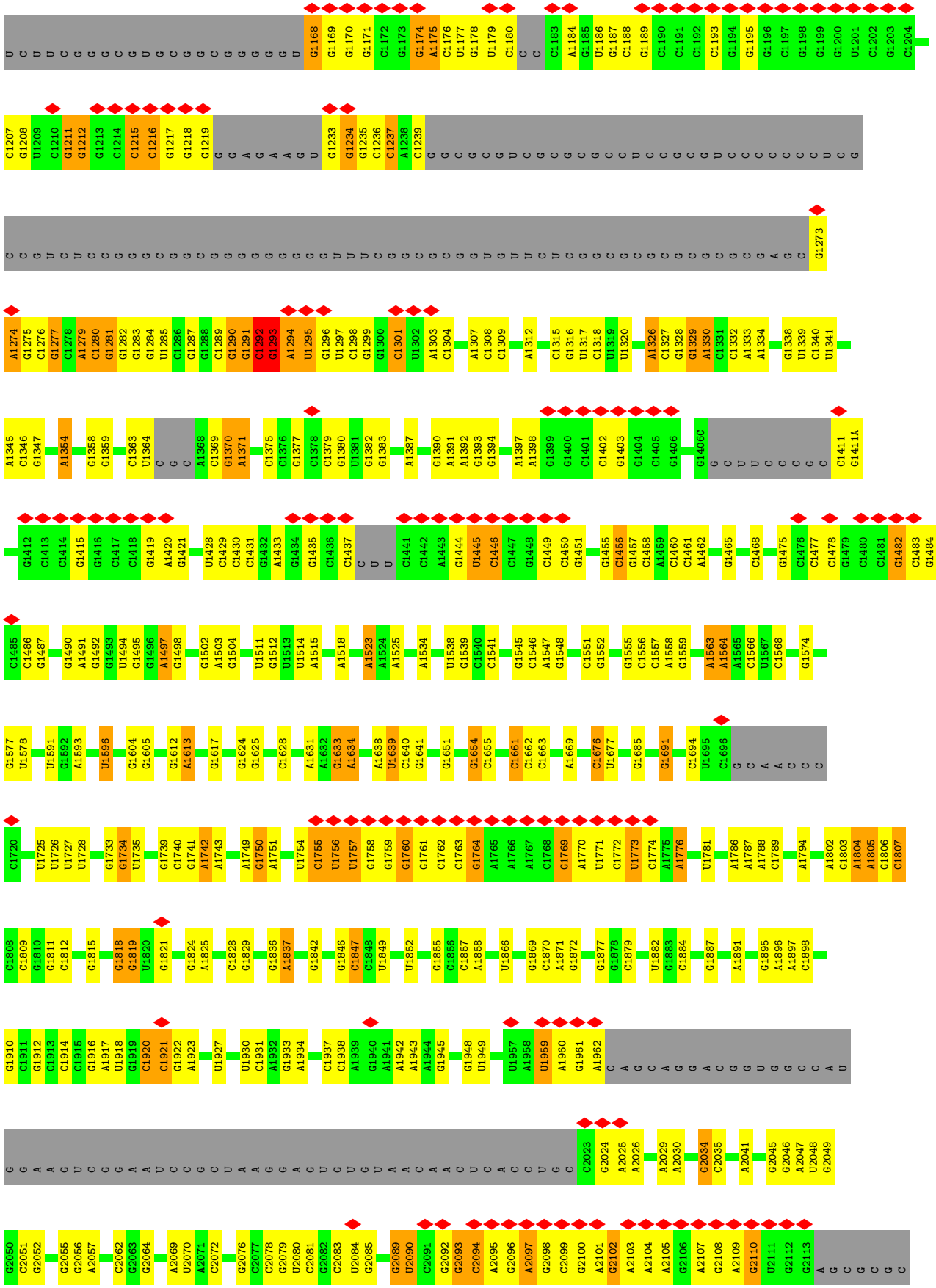
- Molecule 54: 28S rRNA

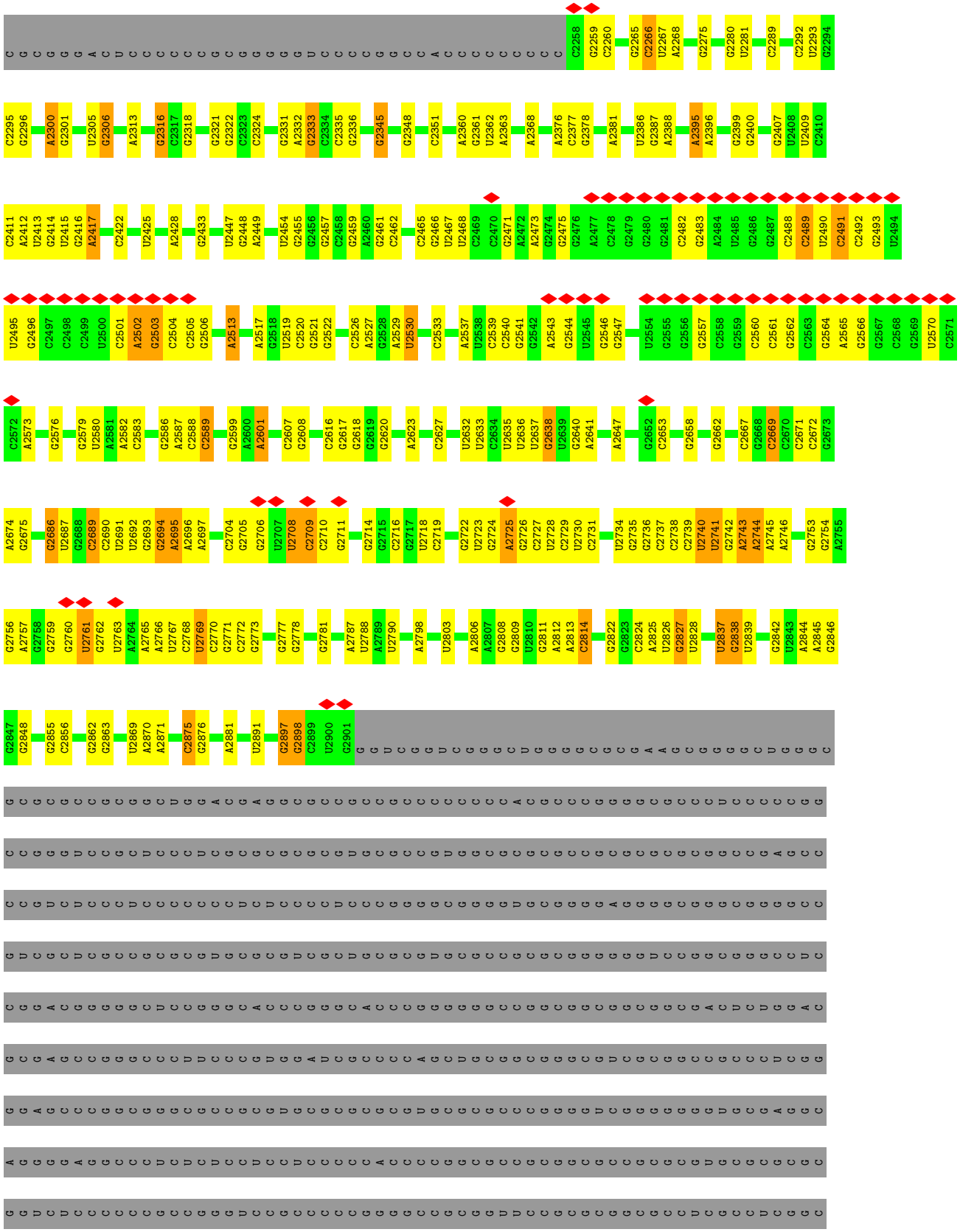


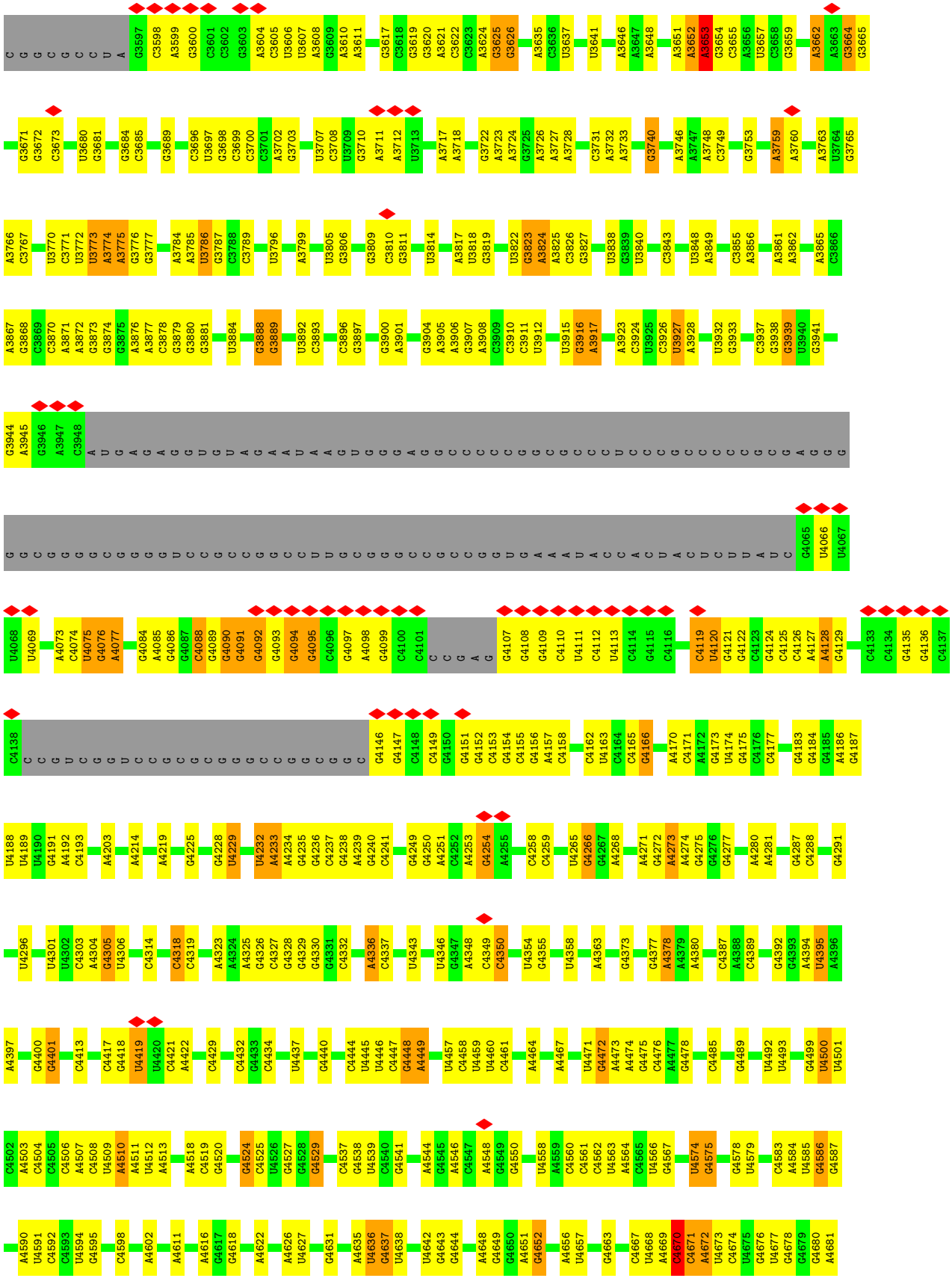


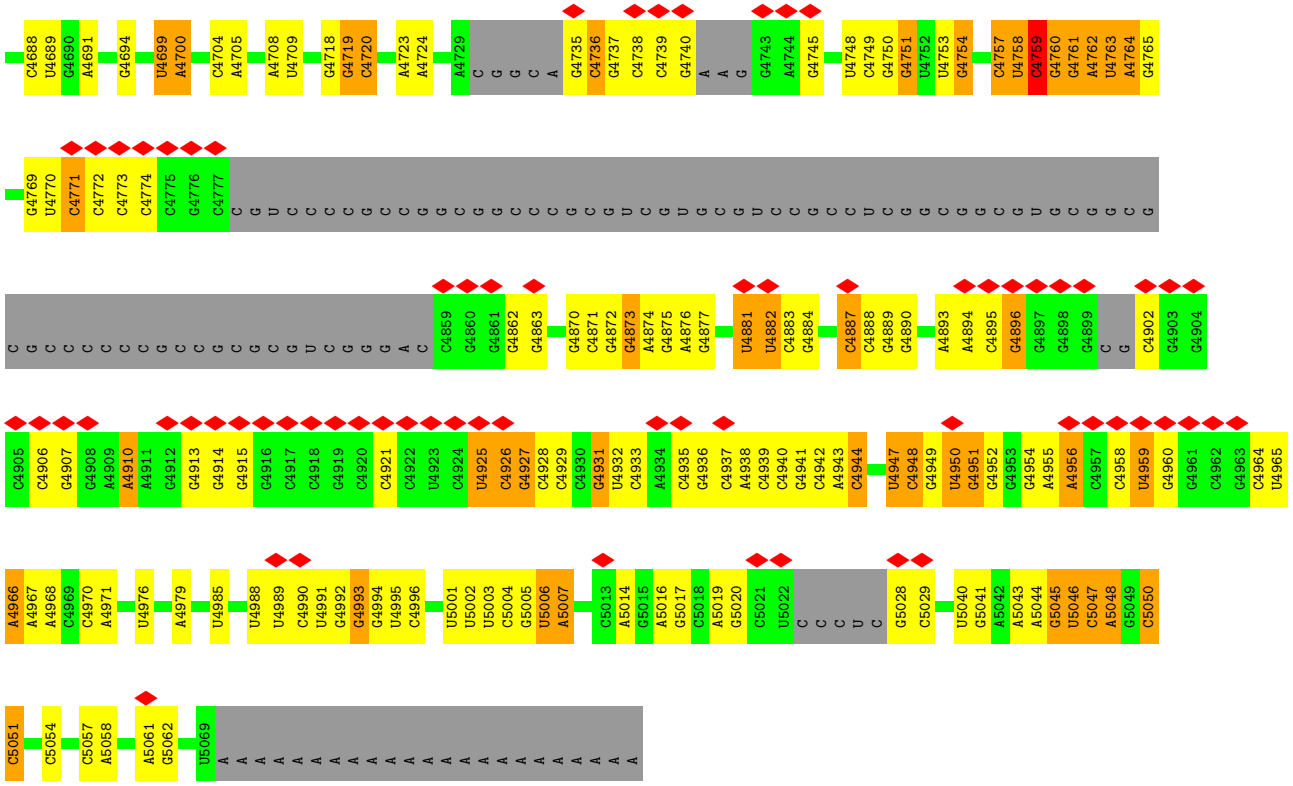

C1
G2
C3
C6
C7
U8







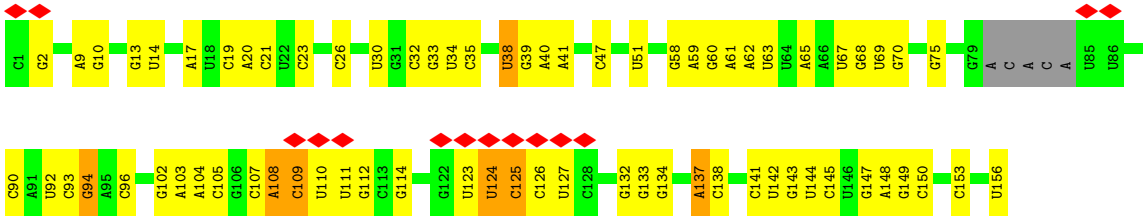




• Molecule 55: 5.8S rRNA

Chain 8:

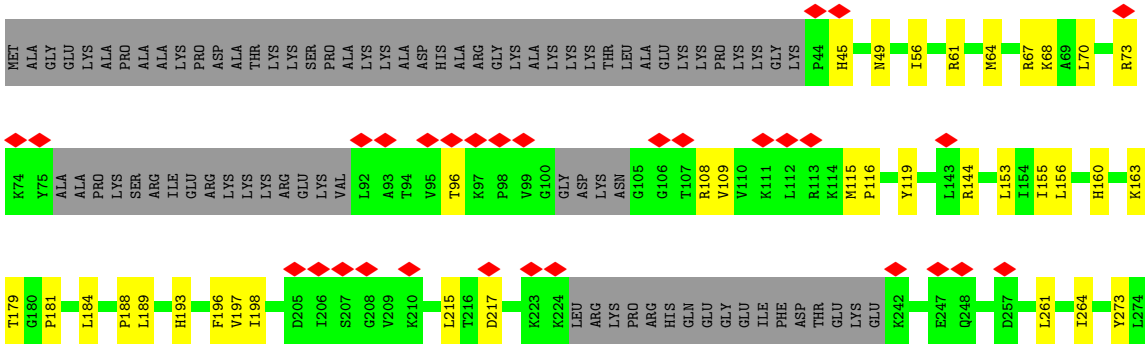


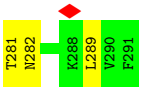


• Molecule 56: 60S ribosomal protein L6

Chain E:

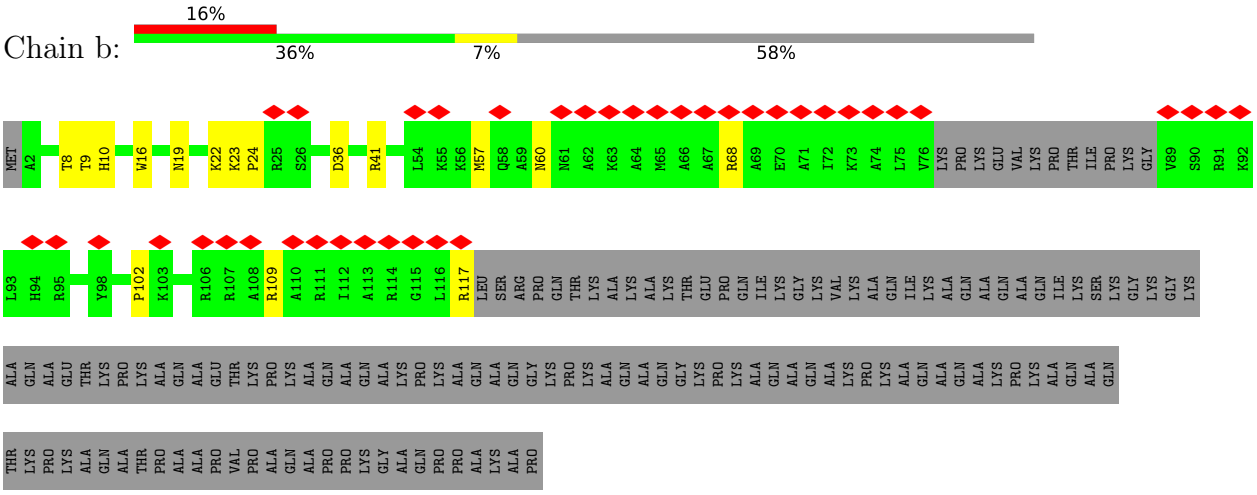






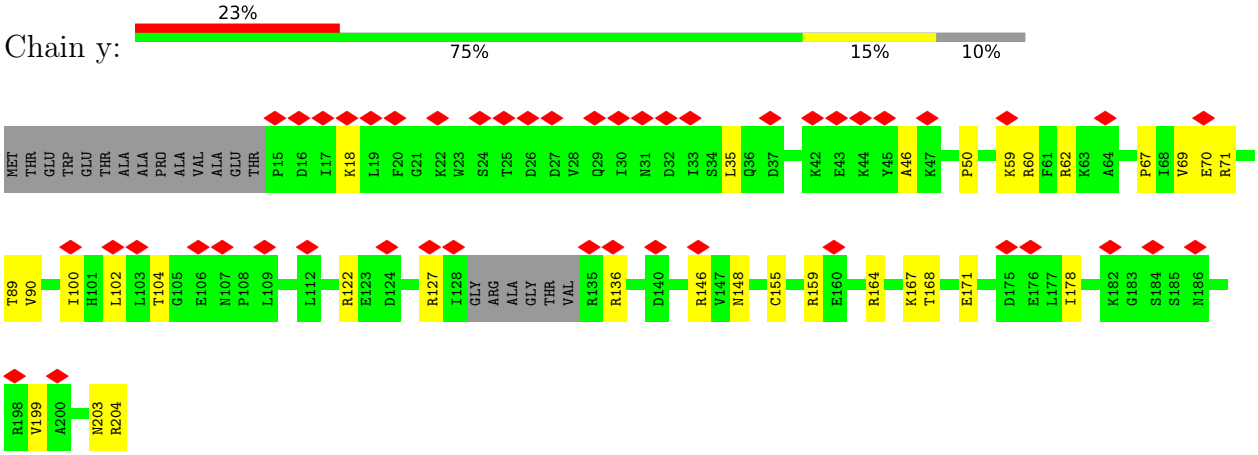
• Molecule 57: Large ribosomal subunit protein eL29

Chain b:



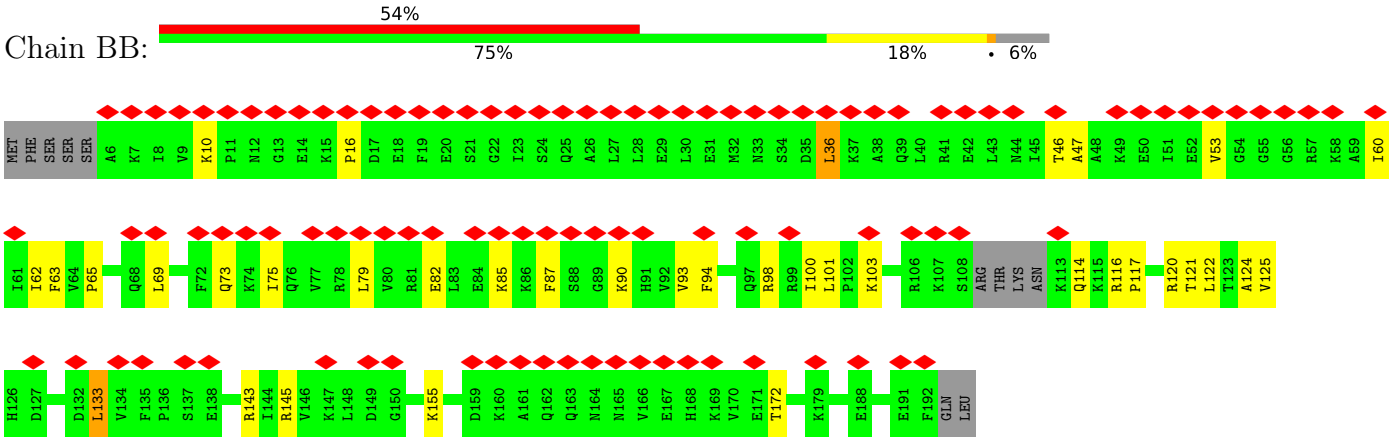
• Molecule 58: Ribosomal protein S5

Chain y:



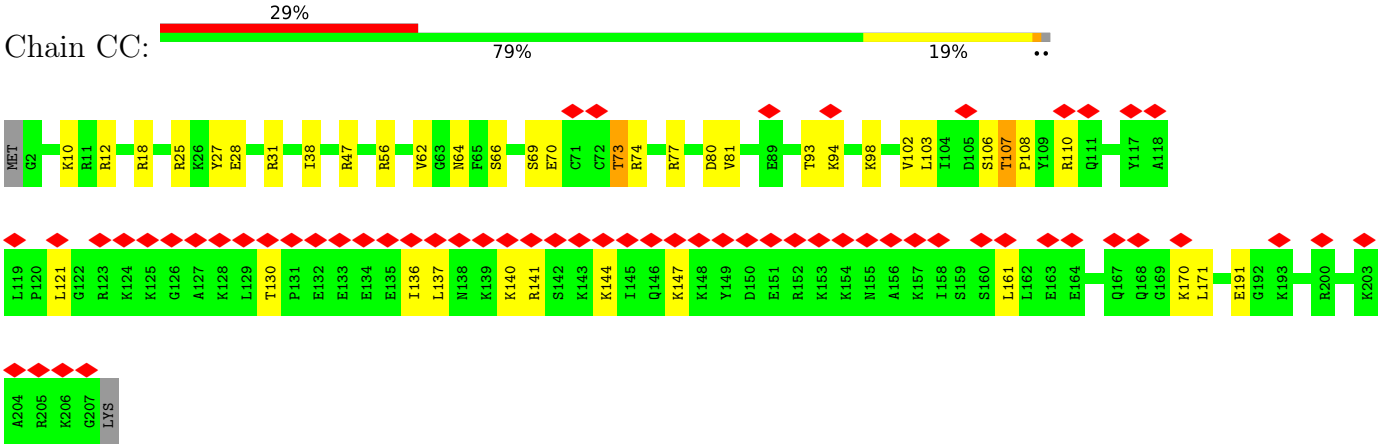
• Molecule 59: 40S ribosomal protein S7

Chain BB:



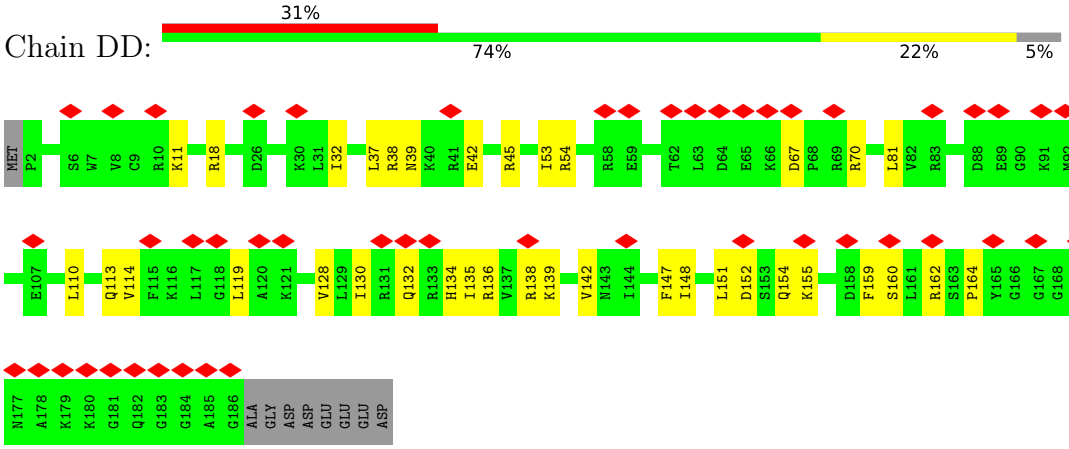
• Molecule 60: 40S ribosomal protein S8

Chain CC:



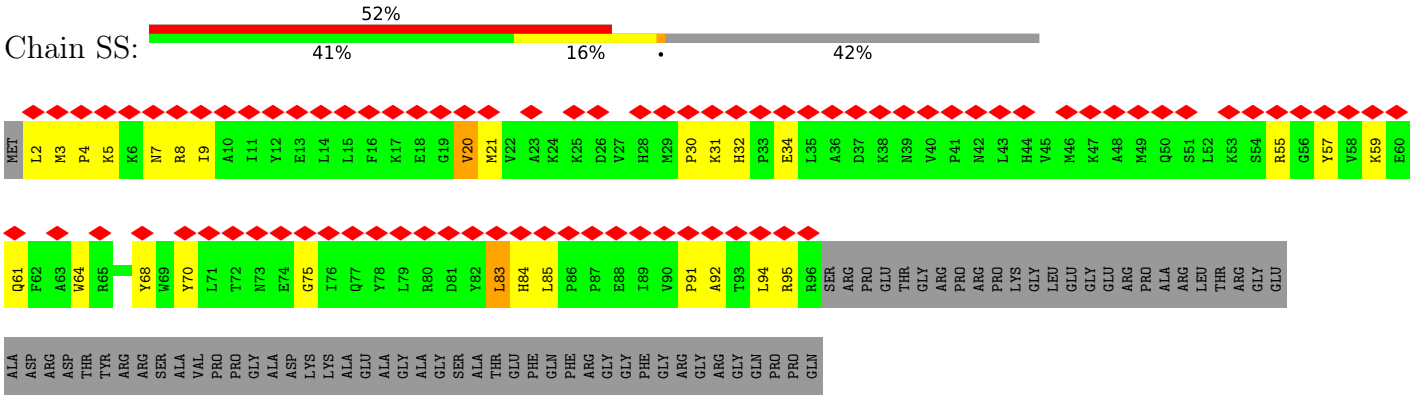
- Molecule 61: Ribosomal protein S9 (Predicted)

Chain DD:



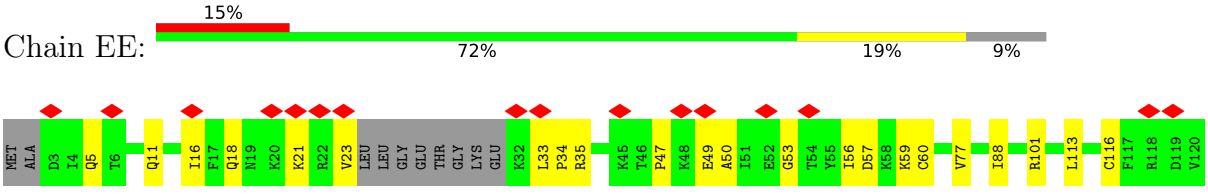
- Molecule 62: S10_plectin domain-containing protein

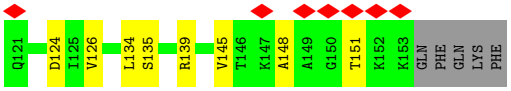
Chain SS:



- Molecule 63: Ribosomal protein S11

Chain EE:

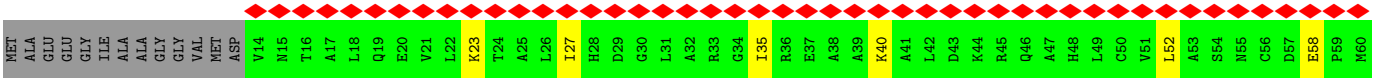


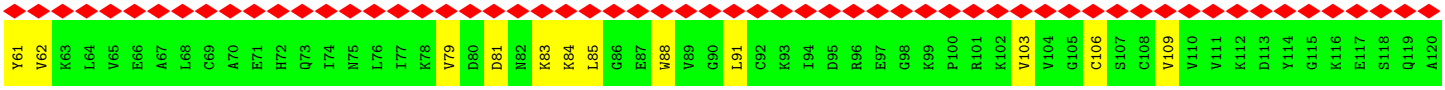


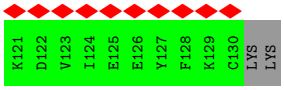
• Molecule 64: 40S ribosomal protein S12

Chain RR:





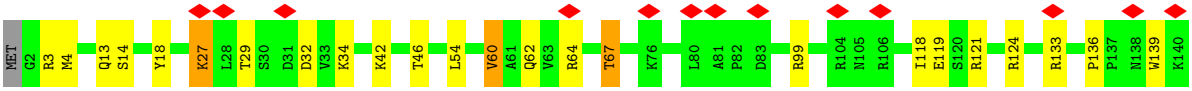


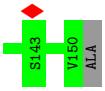


• Molecule 65: Ribosomal protein S13

Chain QQ:



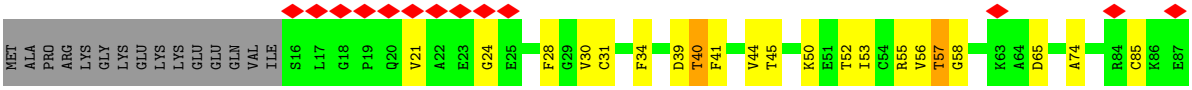


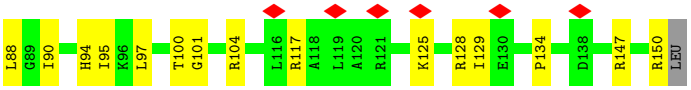


• Molecule 66: Small ribosomal subunit protein uS11

Chain MM:



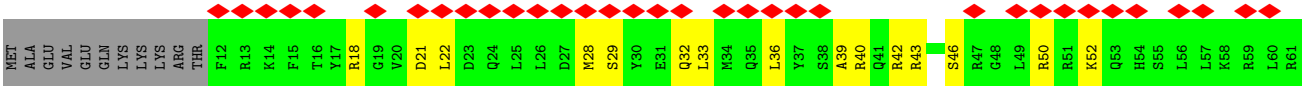


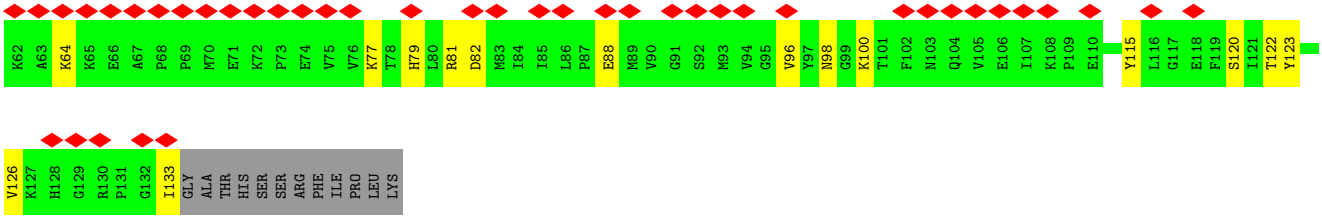


• Molecule 67: uS19

Chain WW:



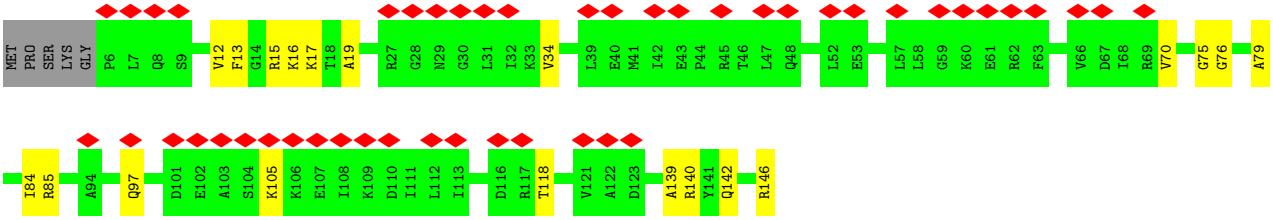




• Molecule 68: uS9

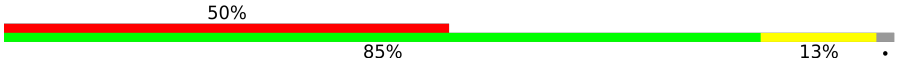
Chain UU:

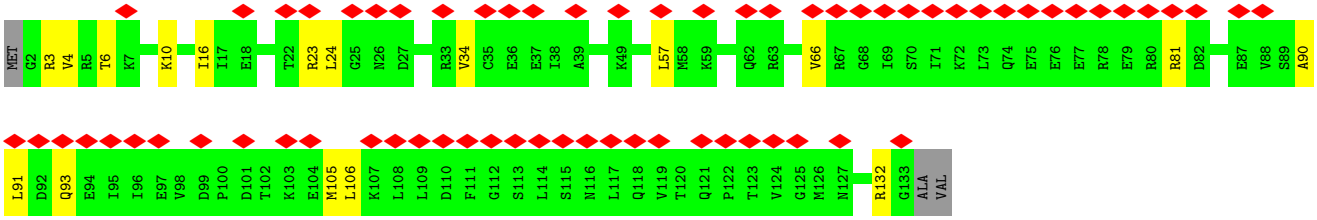




• Molecule 69: eS17

Chain KK:

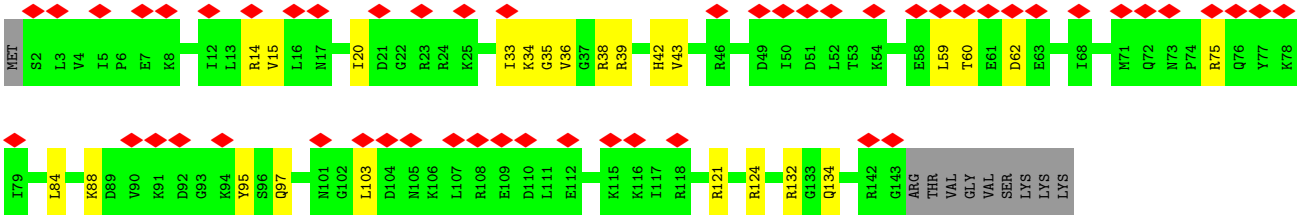




• Molecule 70: uS13

Chain II:

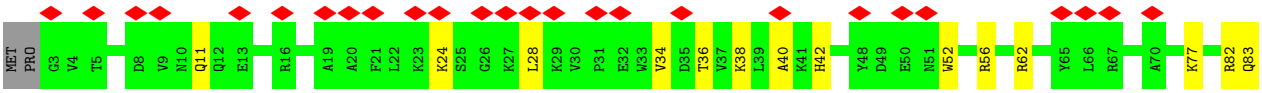


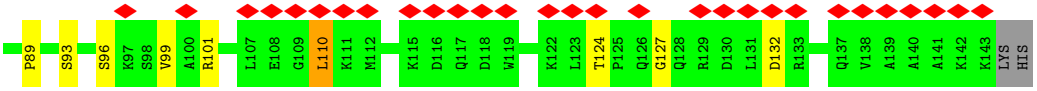


• Molecule 71: eS19

Chain PP:

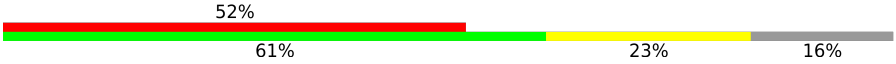


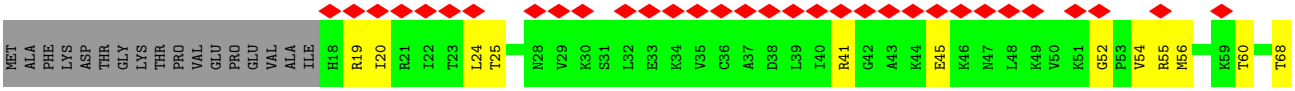


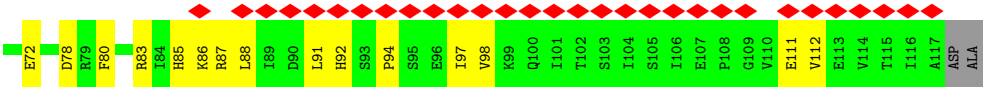


• Molecule 72: uS10

Chain GG:



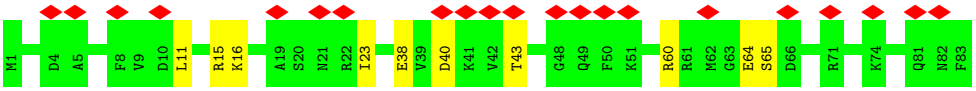




• Molecule 73: Small ribosomal subunit protein eS21

Chain HH:

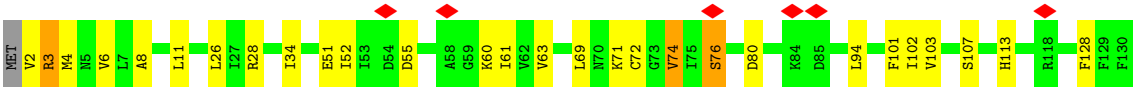




• Molecule 74: Ribosomal protein S15a

Chain TT:

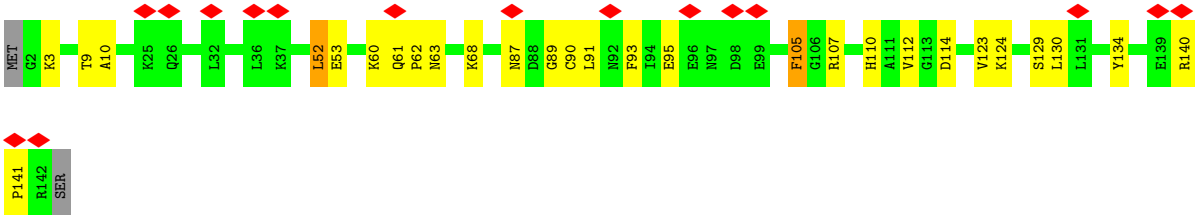




• Molecule 75: uS12

Chain VV:

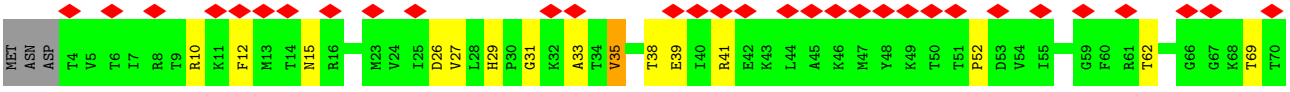


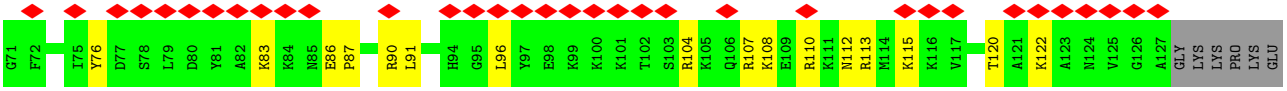


• Molecule 76: Small ribosomal subunit protein eS24

Chain NN:



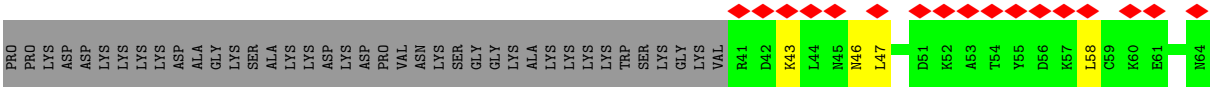


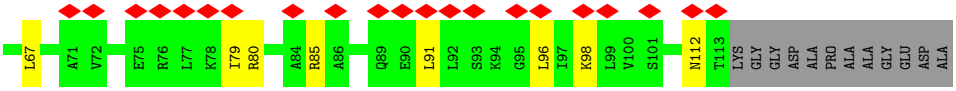


• Molecule 77: eS25

Chain OO:



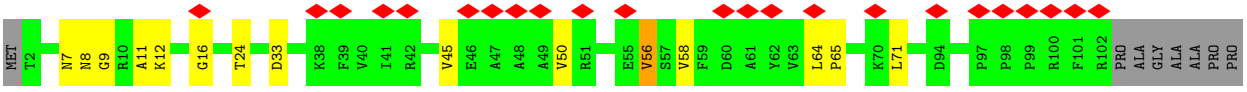




• Molecule 78: eS26

Chain LL:



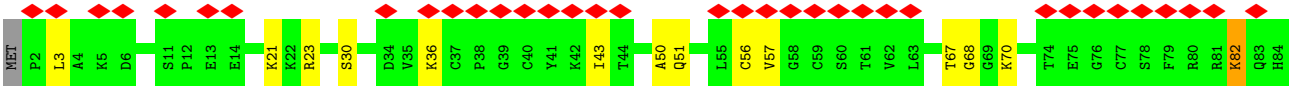




• Molecule 79: 40S ribosomal protein S27

Chain JJ:

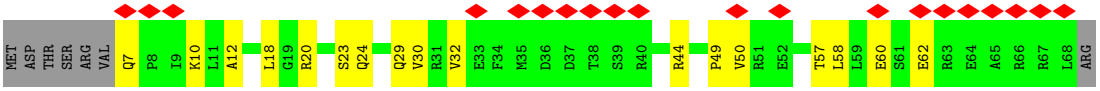




• Molecule 80: Ribosomal protein S28

Chain FF:



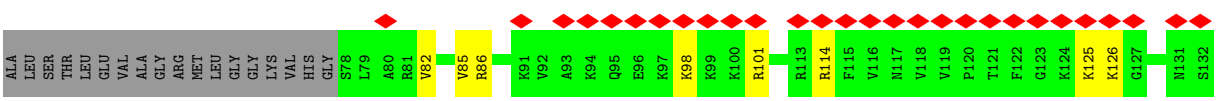


• Molecule 81: 40S ribosomal protein S30

Chain AA:

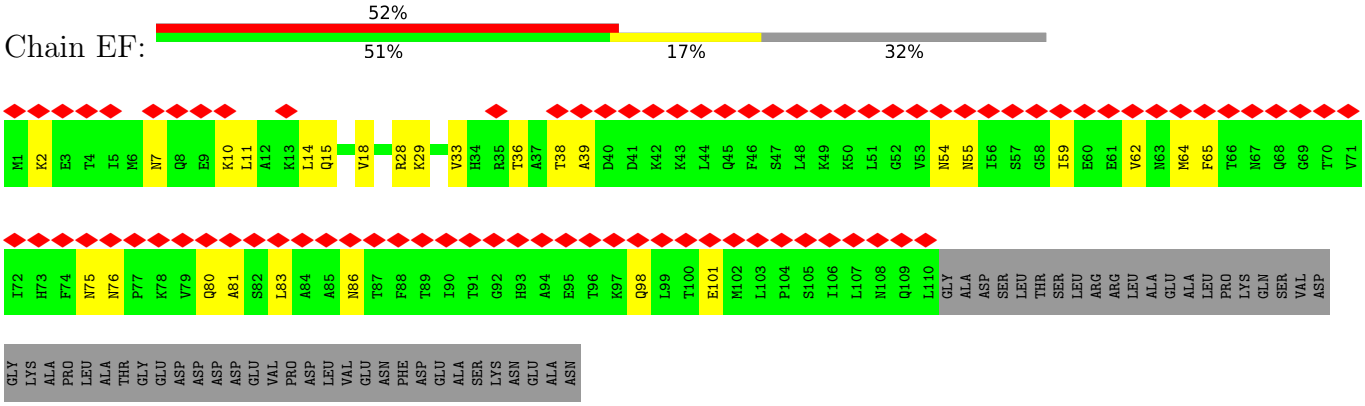






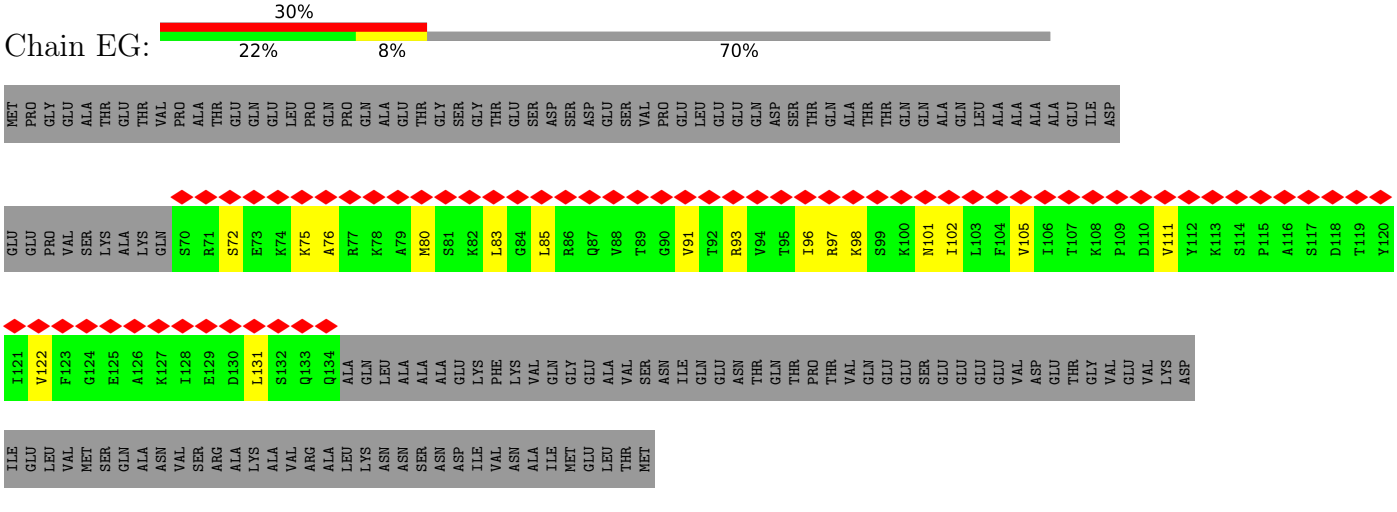
• Molecule 82: Transcription factor BTF3

Chain EF:



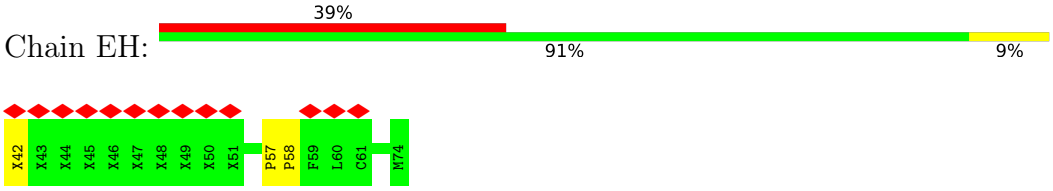
• Molecule 83: Nascent polypeptide-associated complex subunit alpha

Chain EG:



• Molecule 84: Nascent Chain

Chain EH:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	72007	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	32	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.160	Depositor
Minimum map value	-0.658	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.047	Depositor
Recommended contour level	0.11	Depositor
Map size (Å)	424.96, 424.96, 424.96	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	m	0.07	0/425	0.23	0/564
2	0	0.06	0/508	0.20	0/673
3	4	0.09	0/142	0.27	0/219
4	6	0.16	0/2493	0.24	0/3394
5	7	0.19	0/2858	0.40	6/4455 (0.1%)
6	9	0.07	0/470	0.19	0/623
7	A	0.08	0/1936	0.24	0/2596
8	B	0.07	0/3240	0.21	0/4339
9	C	0.08	0/2937	0.22	0/3946
10	D	0.13	0/2437	0.23	0/3264
11	F	0.09	0/1911	0.22	0/2549
12	G	0.08	0/1910	0.22	0/2569
13	H	0.07	0/1535	0.22	0/2063
14	I	0.08	0/1702	0.21	0/2272
15	J	0.07	0/1385	0.22	0/1852
16	K	0.17	0/40364	0.37	65/62897 (0.1%)
17	L	0.08	0/1733	0.21	0/2318
18	M	0.08	0/1158	0.22	0/1547
19	N	0.08	0/1746	0.22	0/2338
20	O	0.10	0/1662	0.23	0/2222
21	P	0.08	0/1268	0.24	0/1700
22	Q	0.08	0/1539	0.24	0/2054
23	R	0.08	0/1524	0.19	0/2014
24	S	0.09	0/1497	0.23	0/2008
25	T	0.08	0/1326	0.23	0/1770
26	U	0.08	0/889	0.25	0/1193
27	V	0.07	0/993	0.21	0/1332
28	W	0.07	0/873	0.20	0/1158
29	X	0.07	0/984	0.20	0/1323
30	Y	0.07	0/1132	0.21	0/1504
31	Z	0.07	0/1130	0.20	0/1507
32	a	0.08	0/1191	0.22	0/1590

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
33	c	0.07	0/771	0.20	0/1034
34	d	0.09	0/903	0.23	0/1216
35	e	0.07	0/1078	0.22	0/1439
36	f	0.08	0/895	0.25	0/1198
37	g	0.08	0/916	0.22	0/1220
38	h	0.07	0/1021	0.19	0/1348
39	i	0.08	0/841	0.19	0/1112
40	j	0.08	0/720	0.23	0/952
41	k	0.07	0/574	0.21	0/761
42	l	0.07	0/459	0.20	0/608
43	n	0.09	0/240	0.18	0/305
44	o	0.08	0/874	0.25	0/1156
45	p	0.07	0/718	0.19	0/953
46	q	0.08	0/1747	0.23	0/2374
47	r	0.08	0/1010	0.25	0/1354
48	u	0.08	0/1756	0.21	0/2350
49	v	0.08	0/1754	0.23	0/2369
50	w	0.07	0/1783	0.22	0/2400
51	x	0.07	0/2112	0.21	0/2841
52	z	0.08	0/1946	0.21	0/2590
53	2	0.25	0/1802	0.51	7/2804 (0.2%)
54	5	0.15	0/83213	0.32	68/129774 (0.1%)
55	8	0.08	0/3581	0.21	0/5577
56	E	0.08	0/1730	0.24	0/2320
57	b	0.07	0/861	0.20	0/1138
58	y	0.08	0/1485	0.24	0/1994
59	BB	0.08	0/1493	0.22	0/1999
60	CC	0.07	0/1715	0.22	0/2287
61	DD	0.07	0/1550	0.19	0/2069
62	SS	0.08	0/826	0.28	0/1115
63	EE	0.07	0/1195	0.21	0/1597
64	RR	0.07	0/918	0.22	0/1233
65	QQ	0.07	0/1226	0.21	0/1649
66	MM	0.07	0/1017	0.20	0/1365
67	WW	0.09	0/1029	0.25	0/1374
68	UU	0.08	0/1142	0.22	0/1528
69	KK	0.06	0/1082	0.17	0/1452
70	II	0.08	0/1190	0.22	0/1594
71	PP	0.08	0/1115	0.23	0/1493
72	GG	0.06	0/805	0.19	0/1081
73	HH	0.14	0/644	0.25	0/862
74	TT	0.08	0/1051	0.22	0/1406
75	VV	0.08	0/1116	0.21	0/1490

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
76	NN	0.06	0/1028	0.20	0/1366
77	OO	0.08	0/591	0.22	0/794
78	LL	0.08	0/830	0.22	0/1112
79	JJ	0.06	0/665	0.21	0/891
80	FF	0.06	0/490	0.17	0/656
81	AA	0.06	0/447	0.20	0/587
82	EF	0.41	0/862	0.54	0/1155
83	EG	0.11	0/518	0.26	0/692
84	EH	0.07	0/206	0.23	0/282
All	All	0.13	0/226439	0.30	146/332169 (0.0%)

There are no bond length outliers.

The worst 5 of 146 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
53	2	20	C	P-O3'-C3'	-9.58	108.20	119.70
5	7	82	G	P-O3'-C3'	-9.36	106.16	120.20
54	5	3655	C	P-O3'-C3'	-8.55	107.38	120.20
16	K	1270	G	P-O3'-C3'	-8.48	107.48	120.20
54	5	2737	C	P-O3'-C3'	-8.48	107.48	120.20

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	m	419	0	452	8	0
2	0	498	0	506	10	0
3	4	128	0	65	0	0
4	6	2436	0	2393	38	0
5	7	2558	0	1296	29	0
6	9	459	0	452	15	0
7	A	1898	0	1993	43	0
8	B	3172	0	3310	57	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	C	2883	0	3053	46	0
10	D	2391	0	2424	41	0
11	F	1875	0	1995	38	0
12	G	1879	0	2025	32	0
13	H	1516	0	1597	20	0
14	I	1664	0	1712	21	0
15	J	1362	0	1399	24	0
16	K	36101	0	18235	587	0
17	L	1700	0	1808	28	0
18	M	1137	0	1211	22	0
19	N	1701	0	1749	38	0
20	O	1630	0	1778	33	0
21	P	1242	0	1274	12	0
22	Q	1515	0	1634	24	0
23	R	1507	0	1658	22	0
24	S	1457	0	1492	21	0
25	T	1298	0	1366	27	0
26	U	874	0	885	19	0
27	V	979	0	1039	13	0
28	W	860	0	903	13	0
29	X	967	0	1040	14	0
30	Y	1115	0	1205	18	0
31	Z	1107	0	1182	15	0
32	a	1162	0	1209	20	0
33	c	761	0	794	5	0
34	d	888	0	930	8	0
35	e	1058	0	1156	15	0
36	f	876	0	912	22	0
37	g	906	0	998	8	0
38	h	1013	0	1147	14	0
39	i	830	0	914	4	0
40	j	705	0	737	13	0
41	k	568	0	630	6	0
42	l	447	0	480	8	0
43	n	239	0	289	3	0
44	o	858	0	919	13	0
45	p	708	0	757	12	0
46	q	1710	0	1711	28	0
47	r	994	0	1051	16	0
48	u	1729	0	1803	31	0
49	v	1718	0	1816	34	0
50	w	1755	0	1849	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
51	x	2070	0	2174	37	0
52	z	1923	0	2089	37	0
53	2	1614	0	822	30	0
54	5	74394	0	37589	1023	0
55	8	3208	0	1629	39	0
56	E	1697	0	1849	29	0
57	b	848	0	920	11	0
58	y	1464	0	1516	19	0
59	BB	1471	0	1563	18	0
60	CC	1686	0	1772	30	0
61	DD	1525	0	1640	33	0
62	SS	802	0	824	20	0
63	EE	1175	0	1249	16	0
64	RR	908	0	939	14	0
65	QQ	1202	0	1289	15	0
66	MM	1004	0	1023	24	0
67	WW	1009	0	1059	23	0
68	UU	1124	0	1193	13	0
69	KK	1068	0	1121	12	0
70	II	1172	0	1229	15	0
71	PP	1097	0	1130	18	0
72	GG	795	0	862	19	0
73	HH	637	0	632	7	0
74	TT	1034	0	1080	19	0
75	VV	1098	0	1167	23	0
76	NN	1011	0	1083	22	0
77	OO	585	0	640	8	0
78	LL	816	0	867	10	0
79	JJ	651	0	672	11	0
80	FF	488	0	514	11	0
81	AA	443	0	492	10	0
82	EF	854	0	905	15	0
83	EG	513	0	552	10	0
84	EH	245	0	201	2	0
85	LL	1	0	0	0	0
85	g	1	0	0	0	0
85	j	1	0	0	0	0
85	m	1	0	0	0	0
85	o	1	0	0	0	0
85	p	1	0	0	0	0
86	5	186	0	0	0	0
86	7	6	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
86	8	6	0	0	0	0
86	A	1	0	0	0	0
86	B	1	0	0	0	0
86	I	1	0	0	0	0
86	K	76	0	0	0	0
86	P	2	0	0	0	0
86	PP	1	0	0	0	0
86	V	1	0	0	0	0
86	a	1	0	0	0	0
86	g	1	0	0	0	0
86	j	2	0	0	0	0
All	All	211175	0	157519	2731	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

The worst 5 of 2731 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:5:4887:C:H42	54:5:4932:U:H3	1.11	0.96
54:5:1083:U:H3	54:5:1216:C:H42	1.16	0.94
26:U:99:TRP:HE1	82:EF:15:GLN:HB2	1.36	0.89
54:5:3710:G:H22	54:5:3740:G:H1	1.23	0.87
9:C:323:ARG:HG3	54:5:1280:C:H2'	1.57	0.85

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	m	49/128 (38%)	47 (96%)	2 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	0	59/156 (38%)	56 (95%)	3 (5%)	0	100	100
4	6	311/317 (98%)	297 (96%)	14 (4%)	0	100	100
6	9	53/56 (95%)	53 (100%)	0	0	100	100
7	A	246/257 (96%)	235 (96%)	11 (4%)	0	100	100
8	B	392/403 (97%)	383 (98%)	9 (2%)	0	100	100
9	C	360/413 (87%)	350 (97%)	10 (3%)	0	100	100
10	D	291/297 (98%)	285 (98%)	5 (2%)	1 (0%)	36	52
11	F	223/249 (90%)	219 (98%)	4 (2%)	0	100	100
12	G	229/319 (72%)	227 (99%)	2 (1%)	0	100	100
13	H	188/192 (98%)	186 (99%)	2 (1%)	0	100	100
14	I	201/214 (94%)	195 (97%)	6 (3%)	0	100	100
15	J	168/178 (94%)	164 (98%)	4 (2%)	0	100	100
17	L	208/211 (99%)	200 (96%)	8 (4%)	0	100	100
18	M	136/218 (62%)	130 (96%)	6 (4%)	0	100	100
19	N	201/204 (98%)	193 (96%)	8 (4%)	0	100	100
20	O	197/203 (97%)	193 (98%)	4 (2%)	0	100	100
21	P	151/183 (82%)	149 (99%)	2 (1%)	0	100	100
22	Q	185/187 (99%)	182 (98%)	3 (2%)	0	100	100
23	R	178/196 (91%)	174 (98%)	4 (2%)	0	100	100
24	S	174/176 (99%)	167 (96%)	7 (4%)	0	100	100
25	T	157/160 (98%)	151 (96%)	6 (4%)	0	100	100
26	U	103/128 (80%)	97 (94%)	6 (6%)	0	100	100
27	V	129/140 (92%)	129 (100%)	0	0	100	100
28	W	102/157 (65%)	100 (98%)	2 (2%)	0	100	100
29	X	116/156 (74%)	114 (98%)	2 (2%)	0	100	100
30	Y	132/145 (91%)	129 (98%)	3 (2%)	0	100	100
31	Z	133/136 (98%)	130 (98%)	3 (2%)	0	100	100
32	a	145/148 (98%)	141 (97%)	4 (3%)	0	100	100
33	c	96/115 (84%)	95 (99%)	1 (1%)	0	100	100
34	d	105/125 (84%)	103 (98%)	2 (2%)	0	100	100
35	e	126/135 (93%)	125 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	f	107/110 (97%)	106 (99%)	1 (1%)	0	100	100
37	g	112/117 (96%)	111 (99%)	1 (1%)	0	100	100
38	h	120/123 (98%)	119 (99%)	1 (1%)	0	100	100
39	i	100/105 (95%)	97 (97%)	3 (3%)	0	100	100
40	j	84/97 (87%)	83 (99%)	1 (1%)	0	100	100
41	k	67/70 (96%)	66 (98%)	1 (2%)	0	100	100
42	l	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
43	n	23/25 (92%)	23 (100%)	0	0	100	100
44	o	102/111 (92%)	96 (94%)	5 (5%)	1 (1%)	12	20
45	p	89/92 (97%)	88 (99%)	1 (1%)	0	100	100
46	q	215/295 (73%)	211 (98%)	4 (2%)	0	100	100
47	r	122/137 (89%)	119 (98%)	3 (2%)	0	100	100
48	u	211/264 (80%)	208 (99%)	3 (1%)	0	100	100
49	v	219/293 (75%)	214 (98%)	5 (2%)	0	100	100
50	w	224/243 (92%)	221 (99%)	3 (1%)	0	100	100
51	x	259/263 (98%)	252 (97%)	7 (3%)	0	100	100
52	z	235/249 (94%)	233 (99%)	2 (1%)	0	100	100
56	E	203/291 (70%)	198 (98%)	5 (2%)	0	100	100
57	b	100/245 (41%)	98 (98%)	2 (2%)	0	100	100
58	y	180/204 (88%)	174 (97%)	6 (3%)	0	100	100
59	BB	179/194 (92%)	177 (99%)	2 (1%)	0	100	100
60	CC	204/208 (98%)	197 (97%)	7 (3%)	0	100	100
61	DD	183/194 (94%)	182 (100%)	1 (0%)	0	100	100
62	SS	93/165 (56%)	86 (92%)	7 (8%)	0	100	100
63	EE	139/158 (88%)	133 (96%)	6 (4%)	0	100	100
64	RR	115/132 (87%)	110 (96%)	5 (4%)	0	100	100
65	QQ	147/151 (97%)	146 (99%)	1 (1%)	0	100	100
66	MM	133/151 (88%)	130 (98%)	3 (2%)	0	100	100
67	WW	120/145 (83%)	114 (95%)	6 (5%)	0	100	100
68	UU	139/146 (95%)	134 (96%)	5 (4%)	0	100	100
69	KK	130/135 (96%)	130 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
70	II	140/152 (92%)	137 (98%)	3 (2%)	0	100	100
71	PP	139/145 (96%)	134 (96%)	5 (4%)	0	100	100
72	GG	98/119 (82%)	95 (97%)	3 (3%)	0	100	100
73	HH	81/83 (98%)	80 (99%)	1 (1%)	0	100	100
74	TT	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
75	VV	139/143 (97%)	136 (98%)	3 (2%)	0	100	100
76	NN	122/133 (92%)	120 (98%)	2 (2%)	0	100	100
77	OO	71/124 (57%)	71 (100%)	0	0	100	100
78	LL	99/115 (86%)	94 (95%)	5 (5%)	0	100	100
79	JJ	81/84 (96%)	79 (98%)	2 (2%)	0	100	100
80	FF	60/69 (87%)	60 (100%)	0	0	100	100
81	AA	53/133 (40%)	53 (100%)	0	0	100	100
82	EF	108/162 (67%)	105 (97%)	3 (3%)	0	100	100
83	EG	63/215 (29%)	59 (94%)	4 (6%)	0	100	100
84	EH	22/33 (67%)	22 (100%)	0	0	100	100
All	All	11349/13306 (85%)	11069 (98%)	278 (2%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	D	263	LYS
44	o	101	VAL

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	m	47/116 (40%)	46 (98%)	1 (2%)	47	69
2	0	54/140 (39%)	54 (100%)	0	100	100
4	6	272/275 (99%)	261 (96%)	11 (4%)	28	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	9	48/49 (98%)	48 (100%)	0	100	100
7	A	190/199 (96%)	185 (97%)	5 (3%)	40	63
8	B	342/348 (98%)	334 (98%)	8 (2%)	44	66
9	C	302/337 (90%)	300 (99%)	2 (1%)	76	86
10	D	247/250 (99%)	241 (98%)	6 (2%)	43	65
11	F	196/218 (90%)	196 (100%)	0	100	100
12	G	200/273 (73%)	196 (98%)	4 (2%)	48	69
13	H	169/171 (99%)	162 (96%)	7 (4%)	27	46
14	I	175/181 (97%)	174 (99%)	1 (1%)	78	88
15	J	143/149 (96%)	140 (98%)	3 (2%)	47	69
17	L	175/176 (99%)	169 (97%)	6 (3%)	32	53
18	M	117/161 (73%)	111 (95%)	6 (5%)	21	36
19	N	171/172 (99%)	167 (98%)	4 (2%)	44	66
20	O	171/173 (99%)	167 (98%)	4 (2%)	44	66
21	P	134/162 (83%)	134 (100%)	0	100	100
22	Q	164/164 (100%)	161 (98%)	3 (2%)	51	72
23	R	159/175 (91%)	158 (99%)	1 (1%)	78	88
24	S	154/154 (100%)	149 (97%)	5 (3%)	34	55
25	T	139/140 (99%)	136 (98%)	3 (2%)	45	67
26	U	97/116 (84%)	96 (99%)	1 (1%)	68	81
27	V	101/107 (94%)	99 (98%)	2 (2%)	48	69
28	W	86/126 (68%)	84 (98%)	2 (2%)	44	66
29	X	106/134 (79%)	106 (100%)	0	100	100
30	Y	124/135 (92%)	122 (98%)	2 (2%)	55	74
31	Z	117/118 (99%)	115 (98%)	2 (2%)	53	73
32	a	119/120 (99%)	117 (98%)	2 (2%)	53	73
33	c	84/98 (86%)	83 (99%)	1 (1%)	63	79
34	d	98/110 (89%)	97 (99%)	1 (1%)	68	81
35	e	116/123 (94%)	114 (98%)	2 (2%)	53	73
36	f	88/89 (99%)	85 (97%)	3 (3%)	32	53
37	g	98/100 (98%)	95 (97%)	3 (3%)	35	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
38	h	109/110 (99%)	108 (99%)	1 (1%)	70 82
39	i	86/90 (96%)	83 (96%)	3 (4%)	32 52
40	j	73/80 (91%)	72 (99%)	1 (1%)	59 76
41	k	64/65 (98%)	63 (98%)	1 (2%)	55 74
42	l	47/48 (98%)	47 (100%)	0	100 100
43	n	24/24 (100%)	24 (100%)	0	100 100
44	o	92/99 (93%)	91 (99%)	1 (1%)	65 80
45	p	74/75 (99%)	73 (99%)	1 (1%)	59 76
46	q	180/244 (74%)	175 (97%)	5 (3%)	38 60
47	r	108/121 (89%)	105 (97%)	3 (3%)	38 60
48	u	194/231 (84%)	192 (99%)	2 (1%)	68 81
49	v	186/223 (83%)	182 (98%)	4 (2%)	45 67
50	w	189/202 (94%)	186 (98%)	3 (2%)	55 74
51	x	224/225 (100%)	221 (99%)	3 (1%)	61 77
52	z	207/218 (95%)	205 (99%)	2 (1%)	68 81
56	E	188/251 (75%)	186 (99%)	2 (1%)	65 80
57	b	84/184 (46%)	82 (98%)	2 (2%)	43 65
58	y	157/170 (92%)	156 (99%)	1 (1%)	78 88
59	BB	163/174 (94%)	157 (96%)	6 (4%)	30 50
60	CC	178/180 (99%)	174 (98%)	4 (2%)	45 67
61	DD	161/168 (96%)	160 (99%)	1 (1%)	78 88
62	SS	86/136 (63%)	84 (98%)	2 (2%)	44 66
63	EE	130/142 (92%)	127 (98%)	3 (2%)	44 66
64	RR	99/108 (92%)	99 (100%)	0	100 100
65	QQ	130/131 (99%)	125 (96%)	5 (4%)	29 49
66	MM	104/119 (87%)	99 (95%)	5 (5%)	23 39
67	WW	110/130 (85%)	108 (98%)	2 (2%)	51 72
68	UU	117/121 (97%)	117 (100%)	0	100 100
69	KK	119/121 (98%)	116 (98%)	3 (2%)	42 64
70	II	123/132 (93%)	121 (98%)	2 (2%)	55 74
71	PP	111/116 (96%)	110 (99%)	1 (1%)	70 82

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
72	GG	92/107 (86%)	91 (99%)	1 (1%)	65 80
73	HH	68/68 (100%)	68 (100%)	0	100 100
74	TT	112/113 (99%)	107 (96%)	5 (4%)	24 42
75	VV	113/115 (98%)	111 (98%)	2 (2%)	51 72
76	NN	107/115 (93%)	105 (98%)	2 (2%)	50 71
77	OO	65/102 (64%)	64 (98%)	1 (2%)	57 75
78	LL	89/99 (90%)	88 (99%)	1 (1%)	65 80
79	JJ	75/76 (99%)	74 (99%)	1 (1%)	61 77
80	FF	55/62 (89%)	53 (96%)	2 (4%)	31 51
81	AA	46/106 (43%)	46 (100%)	0	100 100
82	EF	94/136 (69%)	86 (92%)	8 (8%)	10 17
83	EG	58/183 (32%)	55 (95%)	3 (5%)	21 36
84	EH	21/21 (100%)	21 (100%)	0	100 100
All	All	9915/11300 (88%)	9719 (98%)	196 (2%)	48 69

5 of 196 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
47	r	78	VAL
60	CC	93	THR
49	v	92	GLU
52	z	213	LEU
63	EE	56	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 77 such sidechains are listed below:

Mol	Chain	Res	Type
58	y	203	ASN
76	NN	19	GLN
59	BB	73	GLN
66	MM	32	HIS
82	EF	34	HIS

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
16	K	1679/4592 (36%)	289 (17%)	16 (0%)
3	4	5/6 (83%)	0	0
5	7	119/120 (99%)	9 (7%)	0
53	2	74/76 (97%)	10 (13%)	0
54	5	3445/7224 (47%)	639 (18%)	47 (1%)
55	8	149/156 (95%)	29 (19%)	1 (0%)
All	All	5471/12174 (44%)	976 (17%)	64 (1%)

5 of 976 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	7	22	A
5	7	53	U
5	7	54	A
5	7	63	C
5	7	64	G

5 of 64 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
54	5	4448	G
54	5	4719	G
54	5	485	C
54	5	480	C
54	5	4925	U

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 291 ligands modelled in this entry, 291 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
53	2	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	2	16:C	O3'	18:G	P	5.37

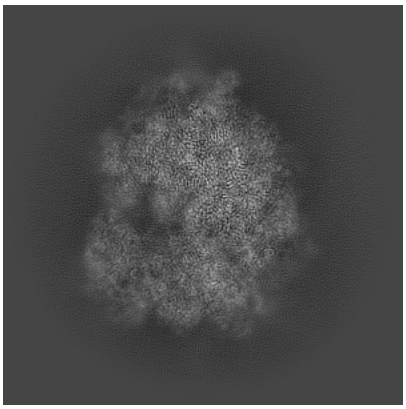
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-48552. These allow visual inspection of the internal detail of the map and identification of artifacts.

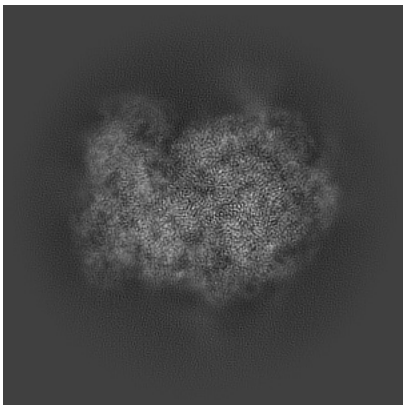
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

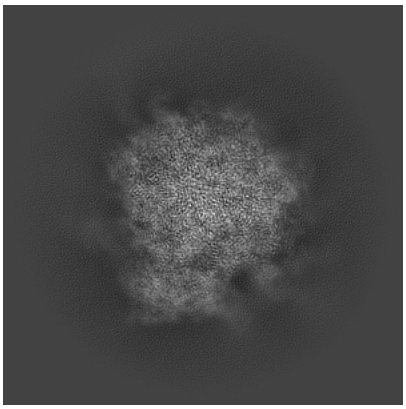
6.1.1 Primary map



X

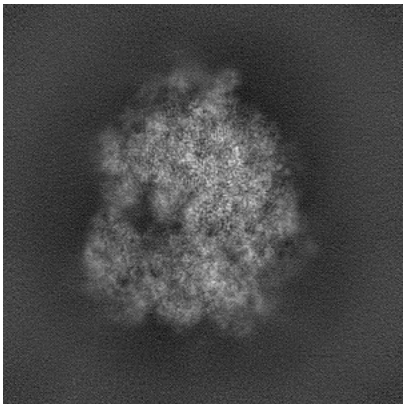


Y

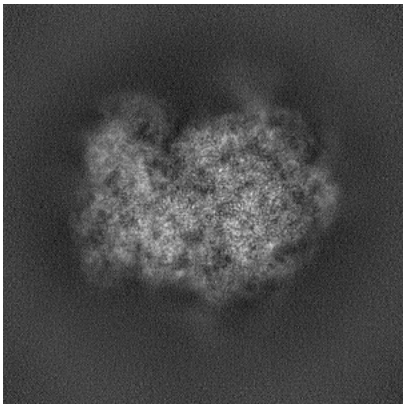


Z

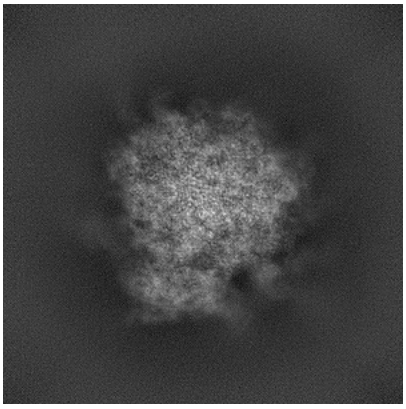
6.1.2 Raw map



X



Y

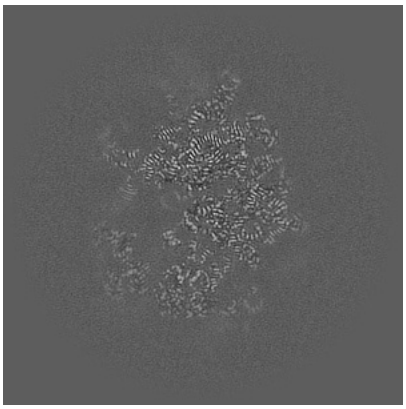


Z

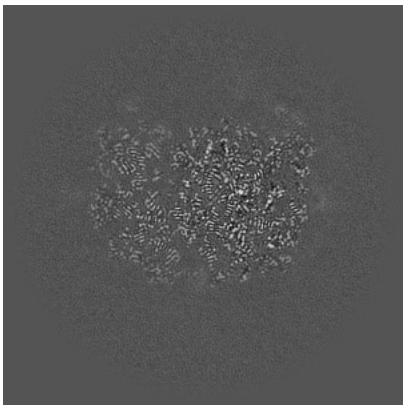
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

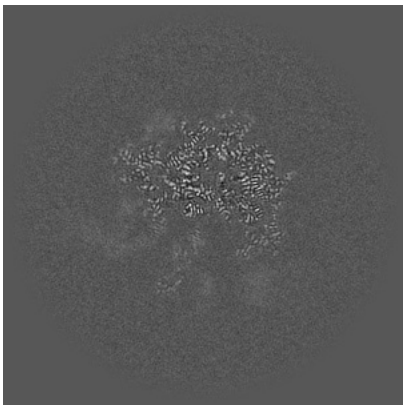
6.2.1 Primary map



X Index: 256

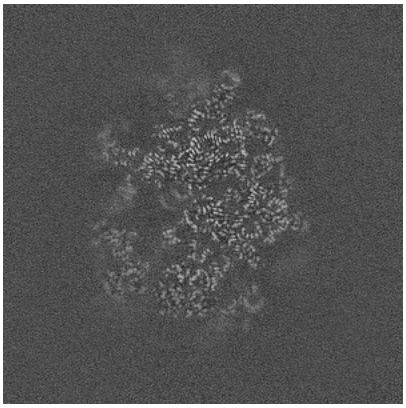


Y Index: 256

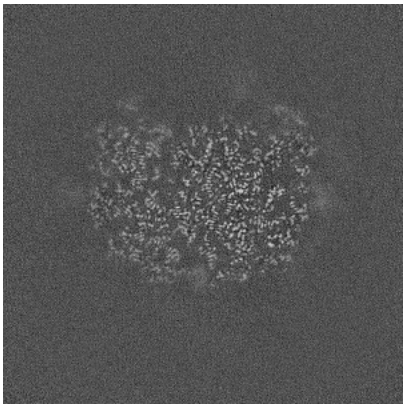


Z Index: 256

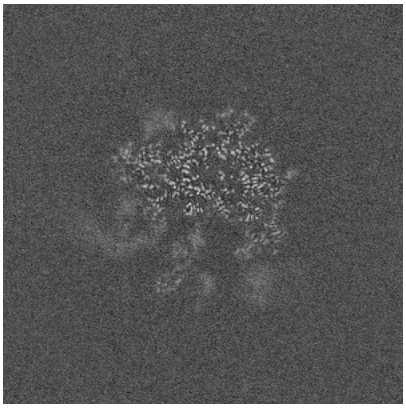
6.2.2 Raw map



X Index: 256



Y Index: 256

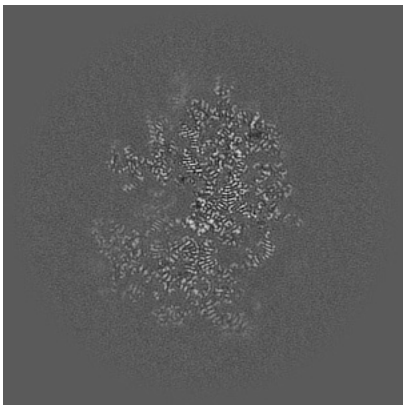


Z Index: 256

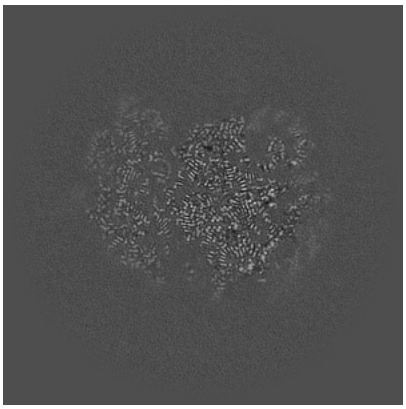
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

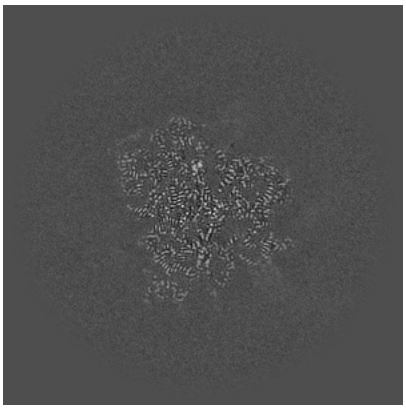
6.3.1 Primary map



X Index: 239

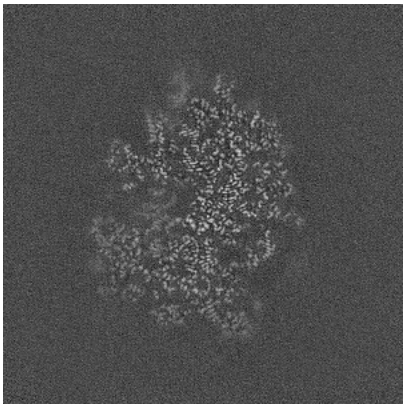


Y Index: 267

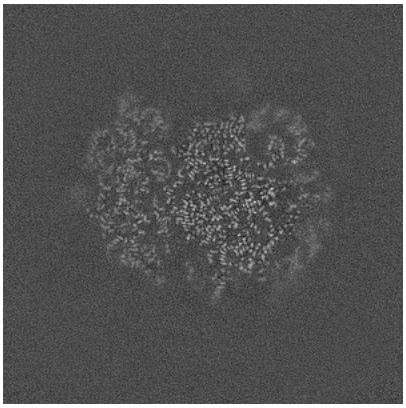


Z Index: 297

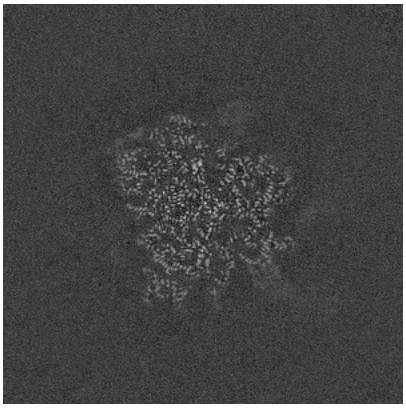
6.3.2 Raw map



X Index: 239



Y Index: 267

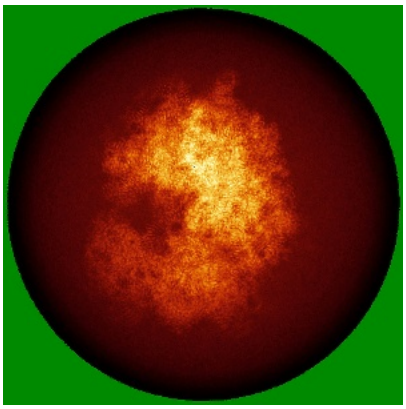


Z Index: 297

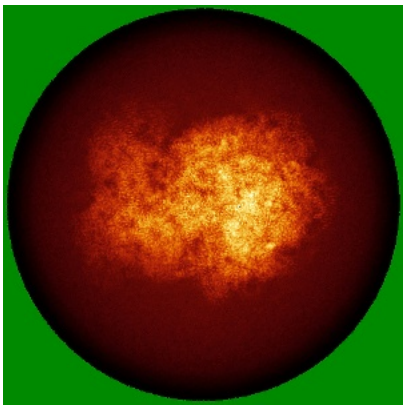
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

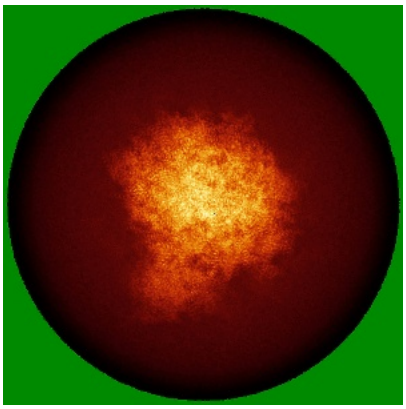
6.4.1 Primary map



X

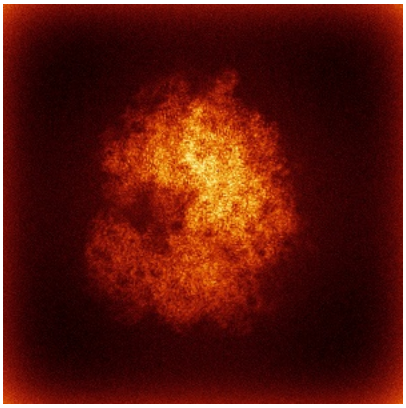


Y

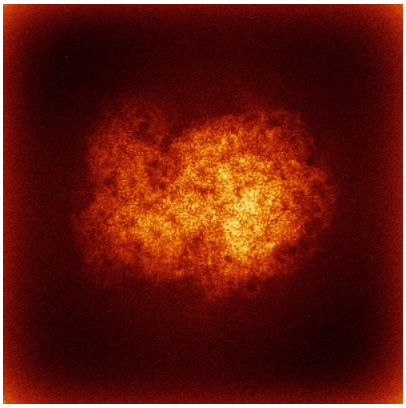


Z

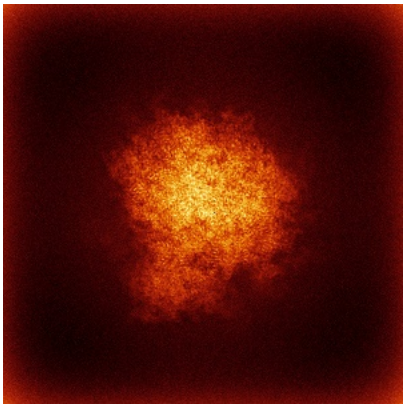
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.11. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

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

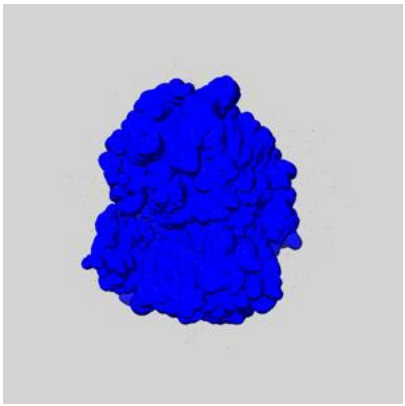
6.6 Mask visualisation (i)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

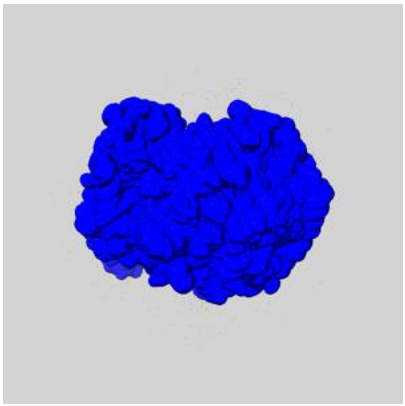
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

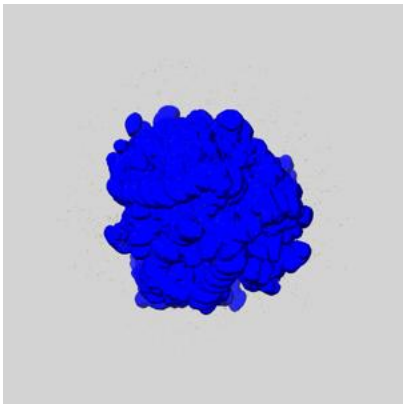
6.6.1 emd_48552_msk_1.map (i)



X



Y

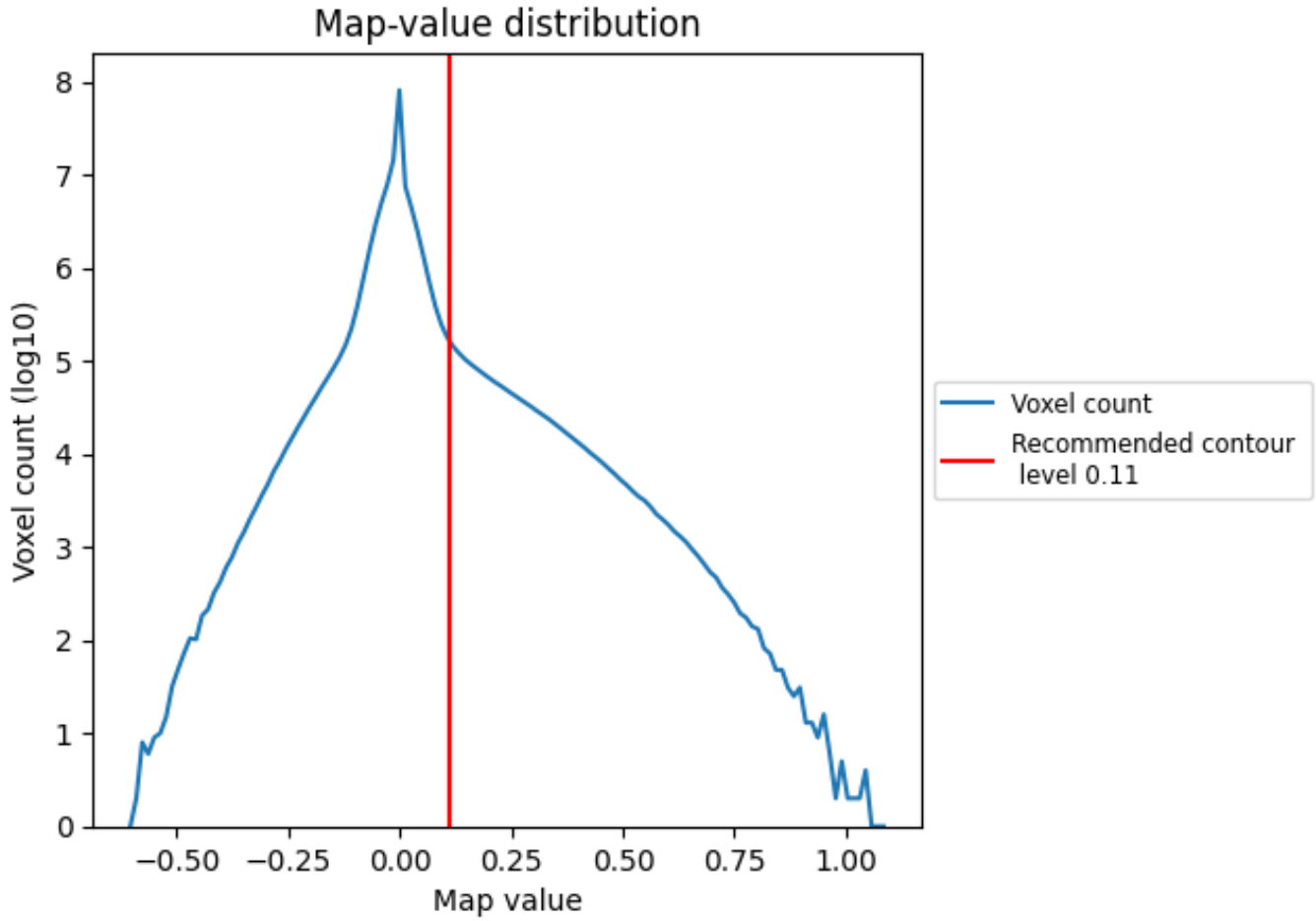


Z

7 Map analysis

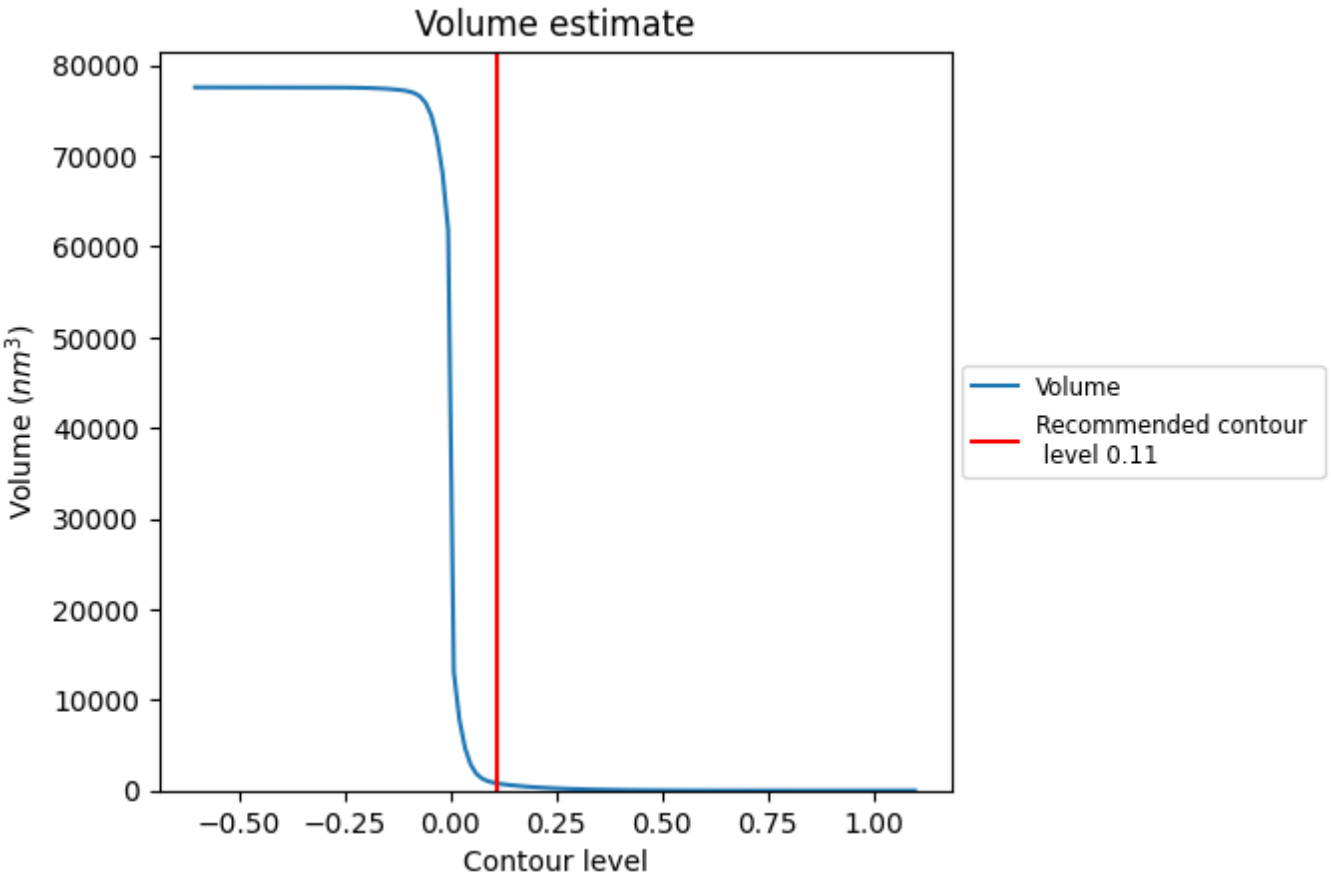
This section contains the results of statistical analysis of the map.

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.

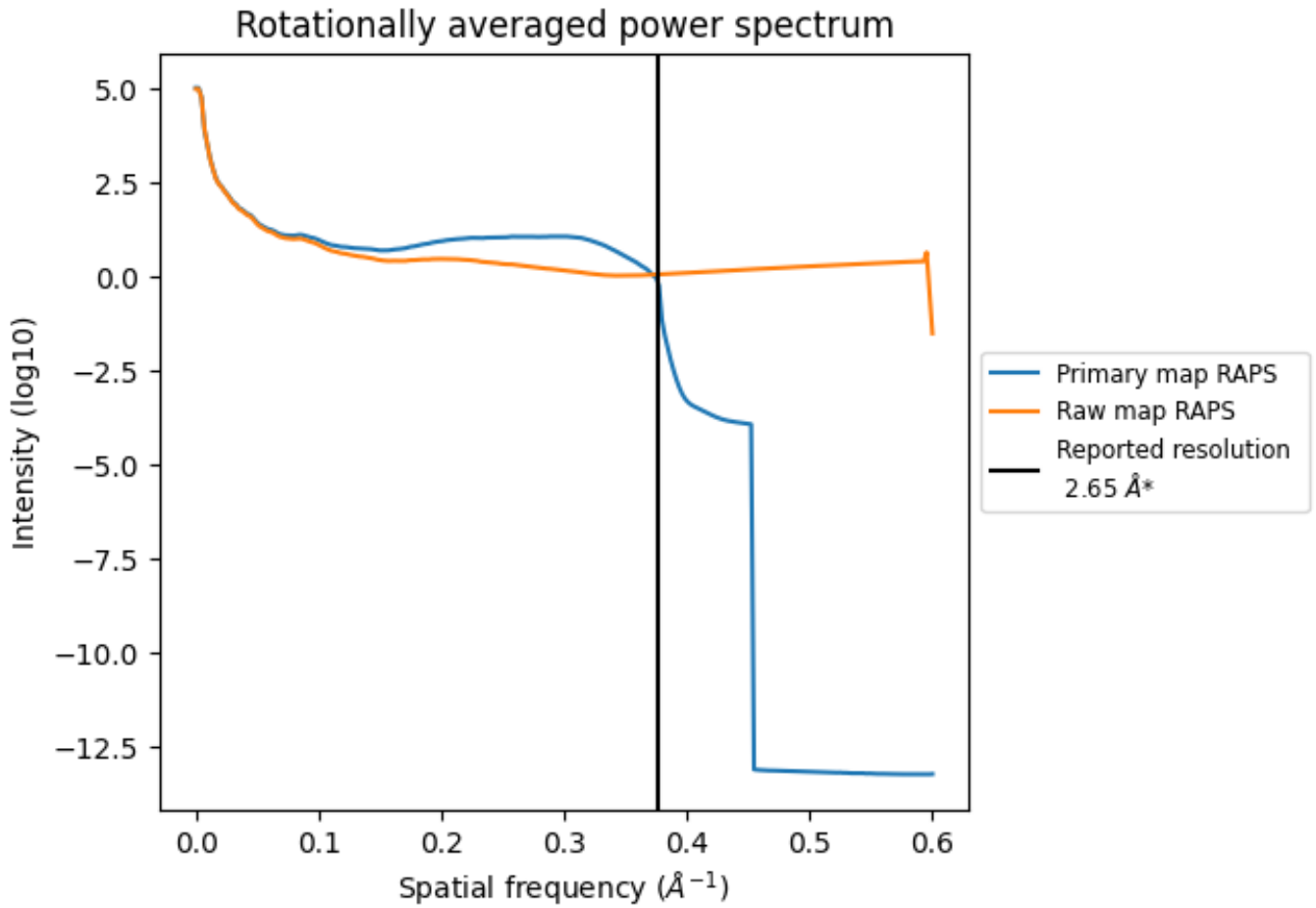
7.2 Volume estimate (i)



The volume at the recommended contour level is 802 nm^3; this corresponds to an approximate mass of 725 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)

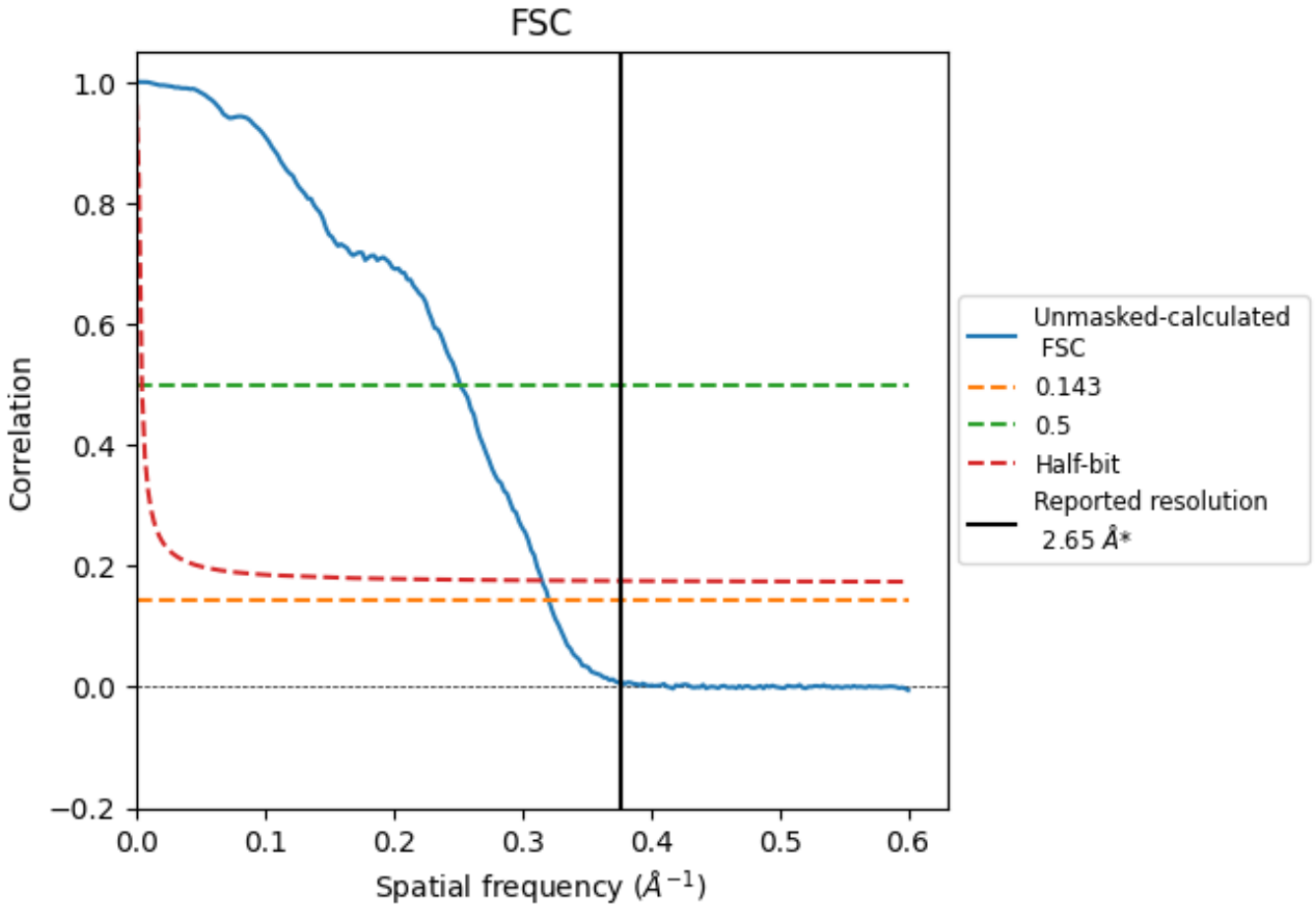


*Reported resolution corresponds to spatial frequency of 0.377 $Å^{-1}$

8 Fourier-Shell correlation

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.377 Å^{-1}

8.2 Resolution estimates (i)

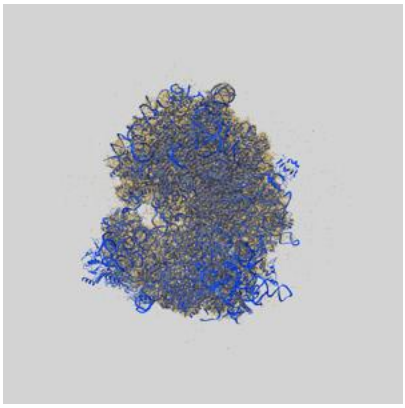
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.65	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.12	3.97	3.17

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.12 differs from the reported value 2.65 by more than 10 %

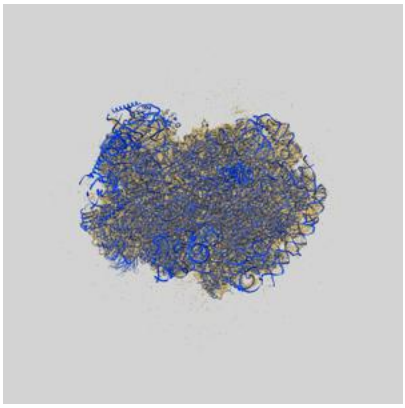
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-48552 and PDB model 9MR4. Per-residue inclusion information can be found in section 3 on page 22.

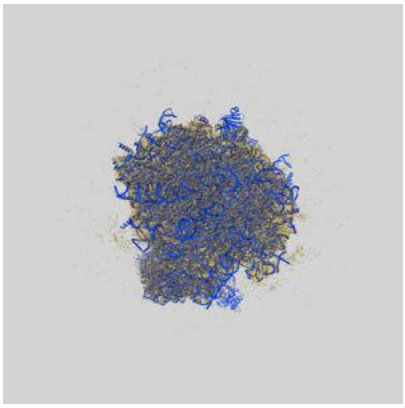
9.1 Map-model overlay



X



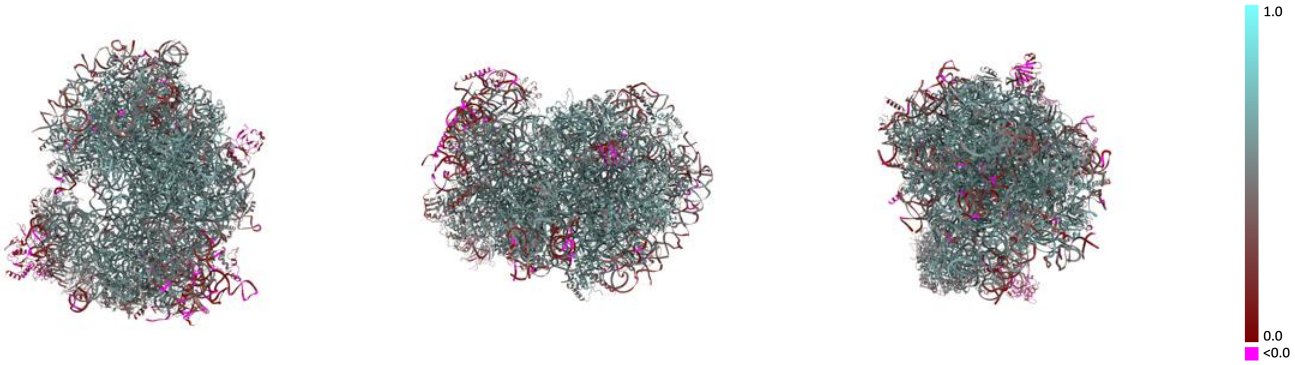
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.11 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.

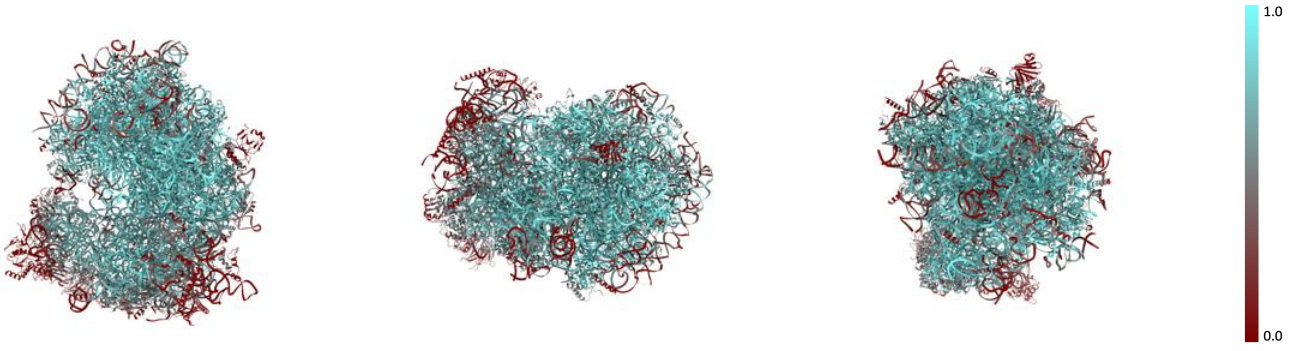
9.2 Q-score mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according 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.

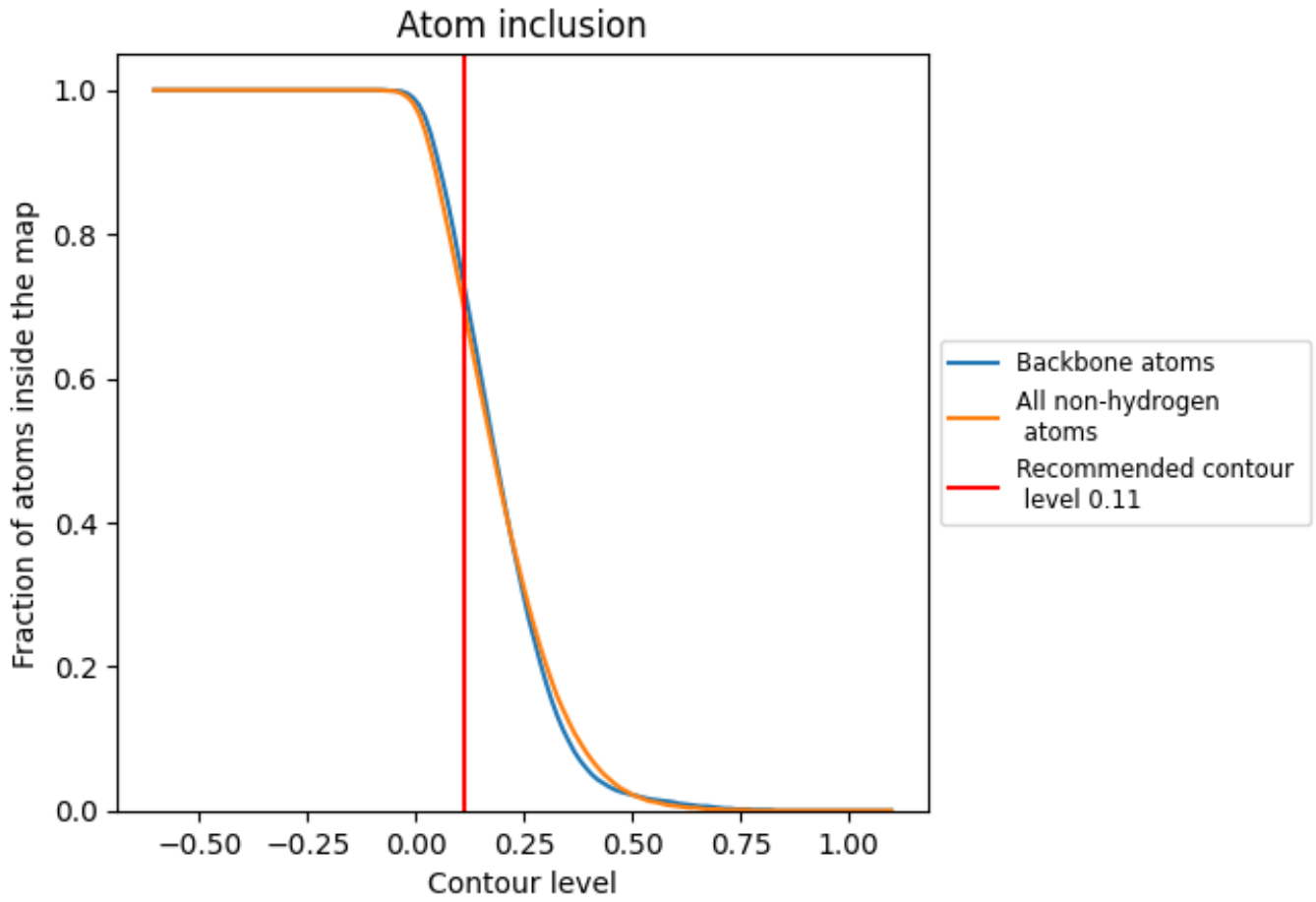
9.3 Atom inclusion mapped to coordinate model



X Y Z

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 (0.11).

9.4 Atom inclusion (i)



At the recommended contour level, 73% of all backbone atoms, 70% 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 (0.11) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7010	0.5240
0	0.0020	0.0720
2	0.5580	0.4850
4	0.2580	0.4050
5	0.7830	0.5480
6	0.1740	0.3420
7	0.9150	0.6140
8	0.8380	0.5710
9	0.4900	0.4120
A	0.8810	0.6150
AA	0.3870	0.3960
B	0.8500	0.6050
BB	0.3660	0.4030
C	0.8440	0.5920
CC	0.5430	0.4750
D	0.7190	0.5400
DD	0.5350	0.4860
E	0.6820	0.5220
EE	0.6660	0.5300
EF	0.2000	0.2490
EG	0.0060	0.0700
EH	0.5830	0.4940
F	0.8270	0.5840
FF	0.4910	0.4770
G	0.6290	0.5150
GG	0.3440	0.3880
H	0.7140	0.5520
HH	0.5710	0.5060
I	0.7780	0.5730
II	0.4900	0.4690
J	0.6160	0.4960
JJ	0.4850	0.4360
K	0.6810	0.5040
KK	0.4280	0.4540
L	0.7170	0.5340



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Chain	Atom inclusion	Q-score
LL	0.6430	0.5030
M	0.7180	0.5290
MM	0.6450	0.5120
N	0.8930	0.6170
NN	0.3860	0.4300
O	0.8520	0.6020
OO	0.4170	0.4700
P	0.8560	0.6160
PP	0.4580	0.4700
Q	0.8750	0.6060
QQ	0.6830	0.5400
R	0.6980	0.5280
RR	0.0020	0.0550
S	0.8560	0.6000
SS	0.1930	0.3220
T	0.7780	0.5680
TT	0.7390	0.5520
U	0.5600	0.4840
UU	0.5140	0.5010
V	0.8470	0.6150
VV	0.7090	0.5550
W	0.4900	0.4190
WW	0.3370	0.3940
X	0.7710	0.5630
Y	0.7780	0.5750
Z	0.6940	0.5400
a	0.8730	0.6110
b	0.5780	0.4740
c	0.7410	0.5600
d	0.7680	0.5700
e	0.8540	0.6000
f	0.8940	0.6130
g	0.7630	0.5640
h	0.7370	0.5440
i	0.6650	0.5310
j	0.8700	0.6010
k	0.5360	0.4910
l	0.7870	0.5860
m	0.6630	0.5590
n	0.7980	0.5940
o	0.7530	0.5650
p	0.8140	0.5820

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Chain	Atom inclusion	Q-score
q	0.5960	0.5080
r	0.8280	0.5910
u	0.5800	0.4970
v	0.6350	0.5260
w	0.3660	0.4210
x	0.5200	0.4930
y	0.5330	0.4870
z	0.2700	0.3360