



## wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 08:16 AM UTC

PDB ID : 8UX4 / pdb\_00008ux4  
EMDB ID : EMD-42687  
Title : Mitochondrial ribosome of saccharomyces cerevisiae class II from YEP with Dextrose culture  
Authors : Yu, Z.; Zheng, F.; Zhou, C.  
Deposited on : 2023-11-08  
Resolution : 3.30 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

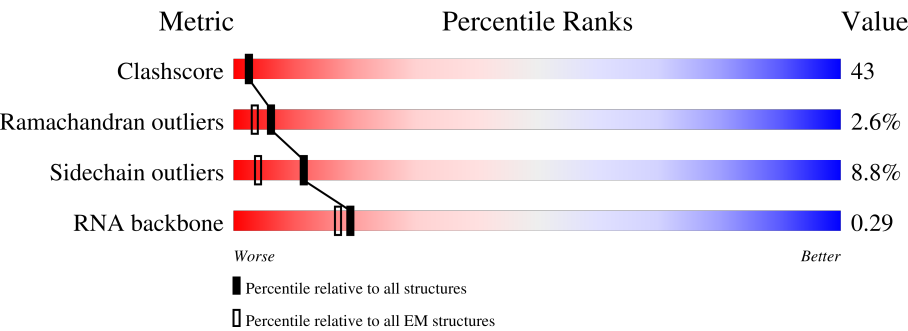
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins)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

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 3.30 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)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102
RNA backbone	8273	3508

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	AA	34	<div><div>71%</div><div>21%71%9%</div></div>
2	AB	95	<div><div>92%</div><div>20%57%22%</div><div>.</div></div>
3	AC	259	<div><div>95%</div><div>30%56%13%</div><div>.</div></div>
4	AD	301	<div><div>100%</div><div>32%54%14%</div></div>
5	AE	298	<div><div>99%</div><div>18%56%22%</div><div>.</div></div>
6	AF	320	<div><div>75%</div><div>23%40%14%</div><div>.</div><div>21%</div></div>
7	AG	236	<div><div>97%</div><div>34%56%10%</div></div>

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Mol	Chain	Length	Quality of chain
8	AH	234	100% 30% 57% 12% .
9	AI	405	96% 30% 57% 11% .
10	AJ	96	90% 27% 49% 20% .
11	AK	264	92% 33% 57% 9%
12	AL	1498	95% 17% 48% 35%
13	AM	76	96% 17% 32% 51%
14	AN	13	92% 15% 77% 8%
15	Z	91	95% 30% 48% 18% .
16	g	298	65% 23% 36% 8% 34%
17	h	267	93% 39% 51% 9% .
18	i	320	84% 25% 49% 17% . 8%
19	j	485	57% 26% 29% . . 41%
20	k	293	89% 40% 48% 9% .
21	l	131	98% 13% 73% 15%
22	m	161	99% 35% 47% 17% .
23	n	155	90% 62% 37% .
24	o	244	88% 52% 33% 7% . 7%
25	p	134	90% 27% 57% 15% .
26	q	152	99% 17% 70% 12%
27	r	125	84% 22% 66% 12% .
28	s	120	97% 24% 62% 12% .
29	t	113	85% 35% 51% 13% .
30	u	253	96% 23% 67% 10%
31	v	106	86% 25% 70% 5% .
32	w	204	100% 20% 62% 17% .

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Mol	Chain	Length	Quality of chain
33	x	99	
34	y	80	
35	z	92	
36	0	38	
37	1	348	
38	2	113	
39	3	130	
40	4	138	
41	5	324	
42	6	259	
43	7	106	
44	8	199	
45	9	215	
46	A	2876	
47	B	328	
48	C	249	
49	D	252	
50	E	274	
51	F	196	
52	G	74	
53	H	160	
54	I	138	
55	J	220	
56	K	195	
57	L	237	

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Mol	Chain	Length	Quality of chain
58	M	151	
59	N	118	
60	O	225	
61	P	207	
62	Q	296	
63	R	337	
64	S	185	
65	T	225	
66	U	82	
67	V	76	
68	W	112	
69	X	64	
70	Y	46	
71	a	177	
72	b	155	
73	c	119	
74	d	215	
75	e	165	
76	f	138	

## 2 Entry composition [i](#)

There are 76 unique types of molecules in this entry. The entry contains 201676 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 Small ribosomal subunit protein mS38.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	34	Total	C	N	O	S	0	0
			304	183	75	44	2		

- Molecule 2 is a protein called Small ribosomal subunit protein mS41.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AB	95	Total	C	N	O	S	0	0
			808	512	153	142	1		

- Molecule 3 is a protein called Small ribosomal subunit protein mS42.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AC	259	Total	C	N	O	S	0	0
			2079	1335	352	387	5		

- Molecule 4 is a protein called Small ribosomal subunit protein mS43.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AD	301	Total	C	N	O	S	0	0
			2422	1530	418	464	10		

- Molecule 5 is a protein called Small ribosomal subunit protein mS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AE	298	Total	C	N	O	S	0	0
			2432	1569	421	438	4		

- Molecule 6 is a protein called Small ribosomal subunit protein mS45.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AF	252	Total	C	N	O	S	0	0
			2079	1327	377	369	6		

- Molecule 7 is a protein called Small ribosomal subunit protein mS23.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AG	236	Total	C	N	O	S	0	0
			1931	1224	337	363	7		

- Molecule 8 is a protein called Small ribosomal subunit protein mS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AH	234	Total	C	N	O	S	0	0
			1887	1197	339	347	4		

- Molecule 9 is a protein called Small ribosomal subunit protein mS29.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AI	405	Total	C	N	O	S	0	0
			3243	2087	545	603	8		

- Molecule 10 is a protein called Small ribosomal subunit protein mS33.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AJ	96	Total	C	N	O	S	0	0
			774	496	140	135	3		

- Molecule 11 is a protein called Small ribosomal subunit protein mS35.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AK	264	Total	C	N	O	S	0	0
			2212	1397	399	412	4		

- Molecule 12 is a RNA chain called Small ribosomal subunit rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AL	1498	Total	C	N	O	P	0	0
			31820	14309	5622	10391	1498		

- Molecule 13 is a RNA chain called Small ribosomal subunit tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AM	76	Total	C	N	O	P	0	0
			1615	723	289	528	75		

- Molecule 14 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AN	13	Total	C	N	O	P	0	0
			270	123	49	86	12		

- Molecule 15 is a protein called Small ribosomal subunit protein mS37.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Z	87	Total	C	N	O	S	0	0
			687	435	128	118	6		

- Molecule 16 is a protein called Small ribosomal subunit protein bS1m.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	g	198	Total	C	N	O	S	0	0
			1577	1014	278	280	5		

- Molecule 17 is a protein called Small ribosomal subunit protein uS2m.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	h	267	Total	C	N	O	S	0	0
			2095	1319	368	406	2		

- Molecule 18 is a protein called Small ribosomal subunit protein uS3m.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	i	293	Total	C	N	O	S	0	0
			2461	1554	432	452	23		

- Molecule 19 is a protein called Small ribosomal subunit protein uS4m.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	j	287	Total	C	N	O	S	0	0
			2370	1542	420	404	4		

- Molecule 20 is a protein called Small ribosomal subunit protein uS5m.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	k	287	Total	C	N	O	S	0	0
			2297	1468	407	414	8		

- Molecule 21 is a protein called 37S ribosomal protein MRP17, mitochondrial.



Mol	Chain	Residues	Atoms					AltConf	Trace
21	l	131	Total	C	N	O	S	0	0
			1055	671	189	191	4		

- Molecule 22 is a protein called Small ribosomal subunit protein uS7m.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	m	161	Total	C	N	O	S	0	0
			1282	811	238	228	5		

- Molecule 23 is a protein called 37S ribosomal protein S8, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	n	155	Total	C	N	O	S	0	0
			1221	772	218	221	10		

- Molecule 24 is a protein called Small ribosomal subunit protein uS9m.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	o	226	Total	C	N	O	S	0	0
			1820	1167	332	316	5		

- Molecule 25 is a protein called Small ribosomal subunit protein uS10m.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	p	134	Total	C	N	O	S	0	0
			1108	719	192	193	4		

- Molecule 26 is a protein called Small ribosomal subunit protein uS11m.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	q	152	Total	C	N	O	S	0	0
			1208	775	211	216	6		

- Molecule 27 is a protein called Small ribosomal subunit protein uS12m.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	r	124	Total	C	N	O	S	0	0
			949	585	194	166	4		

- Molecule 28 is a protein called Small ribosomal subunit protein uS13m.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	s	119	Total	C	N	O	S	0	0
			930	587	178	159	6		

- Molecule 29 is a protein called Small ribosomal subunit protein uS14m.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	t	113	Total	C	N	O	S	0	0
			942	605	180	153	4		

- Molecule 30 is a protein called Small ribosomal subunit protein uS15m.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	u	253	Total	C	N	O	S	0	0
			2070	1292	387	383	8		

- Molecule 31 is a protein called Small ribosomal subunit protein bS16m.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	v	106	Total	C	N	O	S	0	0
			830	529	155	144	2		

- Molecule 32 is a protein called MRPL38 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	w	204	Total	C	N	O	S	0	0
			1683	1055	315	308	5		

- Molecule 33 is a protein called Small ribosomal subunit protein bS18m.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	x	91	Total	C	N	O	S	0	0
			738	463	143	128	4		

- Molecule 34 is a protein called Small ribosomal subunit protein uS19m.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	y	80	Total	C	N	O	S	0	0
			636	408	115	111	2		

- Molecule 35 is a protein called Small ribosomal subunit protein bS21m.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	z	92	Total	C	N	O	S	0	0
			760	475	150	130	5		

- Molecule 36 is a protein called Large ribosomal subunit protein bL36m.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	0	38	Total	C	N	O	S	0	0
			324	205	66	50	3		

- Molecule 37 is a protein called Large ribosomal subunit protein mL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	1	348	Total	C	N	O	S	0	0
			2875	1847	499	523	6		

- Molecule 38 is a protein called Large ribosomal subunit protein mL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	2	113	Total	C	N	O	S	0	0
			944	597	174	168	5		

- Molecule 39 is a protein called Large ribosomal subunit protein mL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	3	130	Total	C	N	O	S	0	0
			1046	671	189	183	3		

- Molecule 40 is a protein called Large ribosomal subunit protein mL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	4	138	Total	C	N	O	S	0	0
			1117	700	219	193	5		

- Molecule 41 is a protein called Large ribosomal subunit protein mL44.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	5	324	Total	C	N	O	S	0	0
			2552	1630	431	480	11		

- Molecule 42 is a protein called Large ribosomal subunit protein mL46.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	6	234	Total	C	N	O	S	0	0
			1932	1250	327	353	2		

- Molecule 43 is a protein called Large ribosomal subunit protein mL49.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	7	106	Total	C	N	O	S	0	0
			858	553	151	152	2		

- Molecule 44 is a protein called Large ribosomal subunit protein uL30m.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	8	199	Total	C	N	O	S	0	0
			1629	1032	278	315	4		

- Molecule 45 is a protein called Large ribosomal subunit protein mL57.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	9	202	Total	C	N	O	S	0	0
			1587	1014	279	289	5		

- Molecule 46 is a RNA chain called Large ribosomal subunit rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	A	2876	Total	C	N	O	P	0	0
			61141	27507	10875	19889	2870		

- Molecule 47 is a protein called Large ribosomal subunit protein uL2m.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	B	321	Total	C	N	O	S	0	0
			2527	1575	507	436	9		

- Molecule 48 is a protein called Large ribosomal subunit protein uL3m.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	C	249	Total	C	N	O	S	0	0
			1932	1218	360	344	10		

- Molecule 49 is a protein called Large ribosomal subunit protein uL4m.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	D	252	Total	C	N	O	S	0	0
			1991	1264	355	369	3		

- Molecule 50 is a protein called Large ribosomal subunit protein uL5m.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	E	274	Total	C	N	O	S	0	0
			2187	1396	391	394	6		

- Molecule 51 is a protein called Large ribosomal subunit protein uL6m.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	F	196	Total	C	N	O	S	0	0
			1524	967	273	280	4		

- Molecule 52 is a protein called Large ribosomal subunit protein bL9m.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	G	74	Total	C	N	O	S	0	0
			617	393	110	113	1		

- Molecule 53 is a protein called Large ribosomal subunit protein uL13m.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	H	160	Total	C	N	O	S	0	0
			1275	807	240	224	4		

- Molecule 54 is a protein called Large ribosomal subunit protein uL14m.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	I	127	Total	C	N	O	S	0	0
			956	595	180	170	11		

- Molecule 55 is a protein called Large ribosomal subunit protein uL15m.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	J	220	Total	C	N	O	S	0	0
			1746	1119	326	298	3		

- Molecule 56 is a protein called Large ribosomal subunit protein uL16m.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	K	195	Total	C	N	O	S	0	0
			1573	1001	297	270	5		

- Molecule 57 is a protein called Large ribosomal subunit protein bL17m.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	L	229	Total	C	N	O	S	0	0
			1817	1140	333	336	8		

- Molecule 58 is a protein called Large ribosomal subunit protein bL19m.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	M	151	Total	C	N	O	S	0	0
			1206	766	220	217	3		

- Molecule 59 is a protein called Large ribosomal subunit protein bL21m.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	N	118	Total	C	N	O	S	0	0
			948	598	177	171	2		

- Molecule 60 is a protein called Large ribosomal subunit protein uL22m.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	O	225	Total	C	N	O	S	0	0
			1826	1169	332	320	5		

- Molecule 61 is a protein called Large ribosomal subunit protein uL23m.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	P	207	Total	C	N	O	S	0	0
			1729	1104	310	309	6		

- Molecule 62 is a protein called Large ribosomal subunit protein uL24m.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	Q	284	Total	C	N	O	S	0	0
			2272	1451	396	417	8		

- Molecule 63 is a protein called Large ribosomal subunit protein bL27m.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	R	331	Total	C	N	O	S	0	0
			2738	1728	497	509	4		

- Molecule 64 is a protein called MRPS9 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	S	185	Total	C	N	O	S	0	0
			1543	994	281	265	3		

- Molecule 65 is a protein called Large ribosomal subunit protein uL29m.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	T	216	Total	C	N	O	S	0	0
			1792	1139	324	325	4		

- Molecule 66 is a protein called Large ribosomal subunit protein uL30m.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	U	82	Total	C	N	O	S	0	0
			639	410	116	113			

- Molecule 67 is a protein called Large ribosomal subunit protein bL31m.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	V	66	Total	C	N	O	S	0	0
			543	340	110	92	1		

- Molecule 68 is a protein called Large ribosomal subunit protein bL32m.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	W	112	Total	C	N	O	S	0	0
			937	587	181	163	6		

- Molecule 69 is a protein called Large ribosomal subunit protein bL33m.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	X	64	Total	C	N	O	S	0	0
			512	330	96	86			

- Molecule 70 is a protein called Large ribosomal subunit protein bL34m.

Mol	Chain	Residues	Atoms				AltConf	Trace
70	Y	46	Total	C	N	O	0	0
			385	245	82	58		

- Molecule 71 is a protein called Large ribosomal subunit protein mL58.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	a	177	Total	C	N	O	S	0	0
			1440	907	267	260	6		

- Molecule 72 is a protein called Large ribosomal subunit protein mL59.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	b	155	Total	C	N	O	S	0	0
			1299	850	225	221	3		

- Molecule 73 is a protein called Large ribosomal subunit protein mL60.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	c	119	Total	C	N	O	S	0	0
			1004	645	191	164	4		

- Molecule 74 is a protein called Large ribosomal subunit protein mL67.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	d	206	Total	C	N	O	S	0	0
			1746	1117	318	304	7		

- Molecule 75 is a protein called Large ribosomal subunit protein uL10m.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	e	165	Total	C	N	O	S	0	0
			1340	862	234	238	6		

- Molecule 76 is a protein called Large ribosomal subunit protein uL11m.

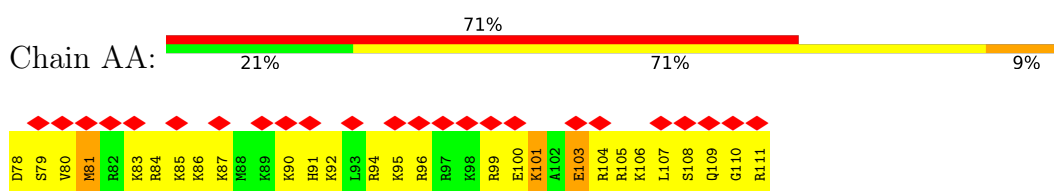
Mol	Chain	Residues	Atoms					AltConf	Trace
76	f	138	Total	C	N	O	S	0	0
			1032	668	176	183	5		



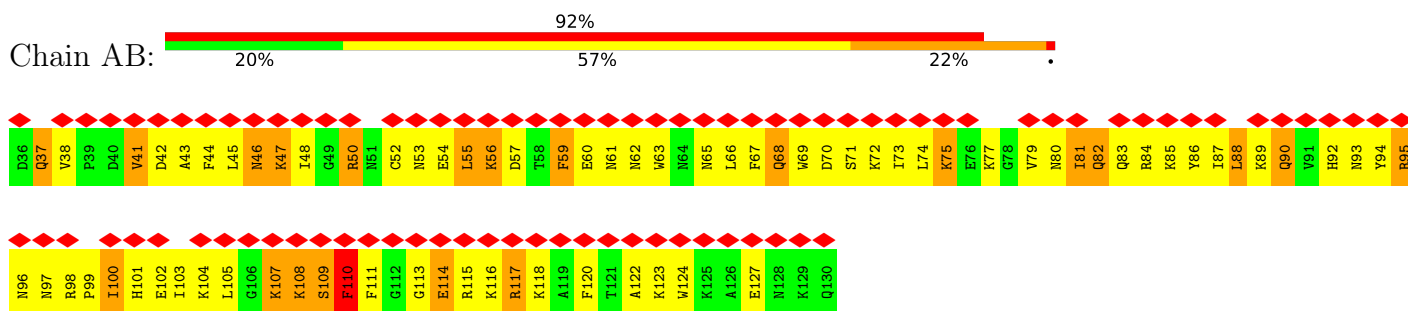
### 3 Residue-property plots [i](#)

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.

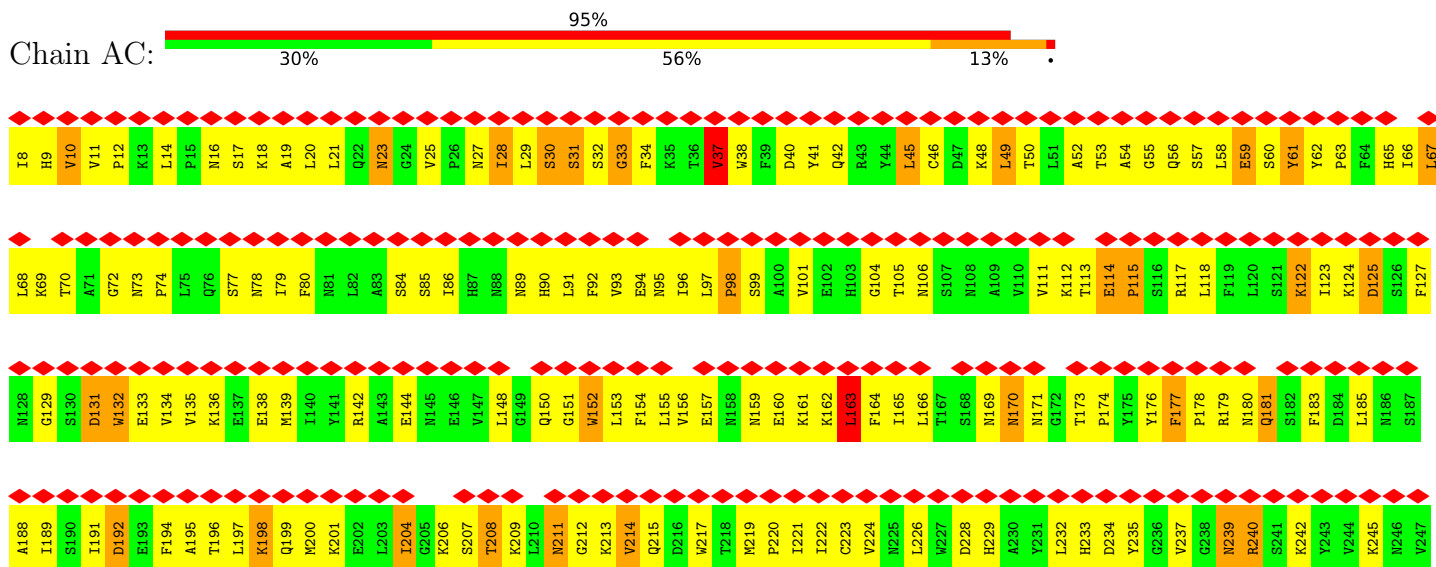
- Molecule 1: Small ribosomal subunit protein mS38

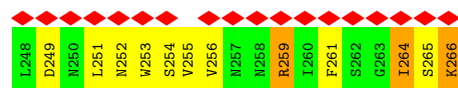


- Molecule 2: Small ribosomal subunit protein mS41

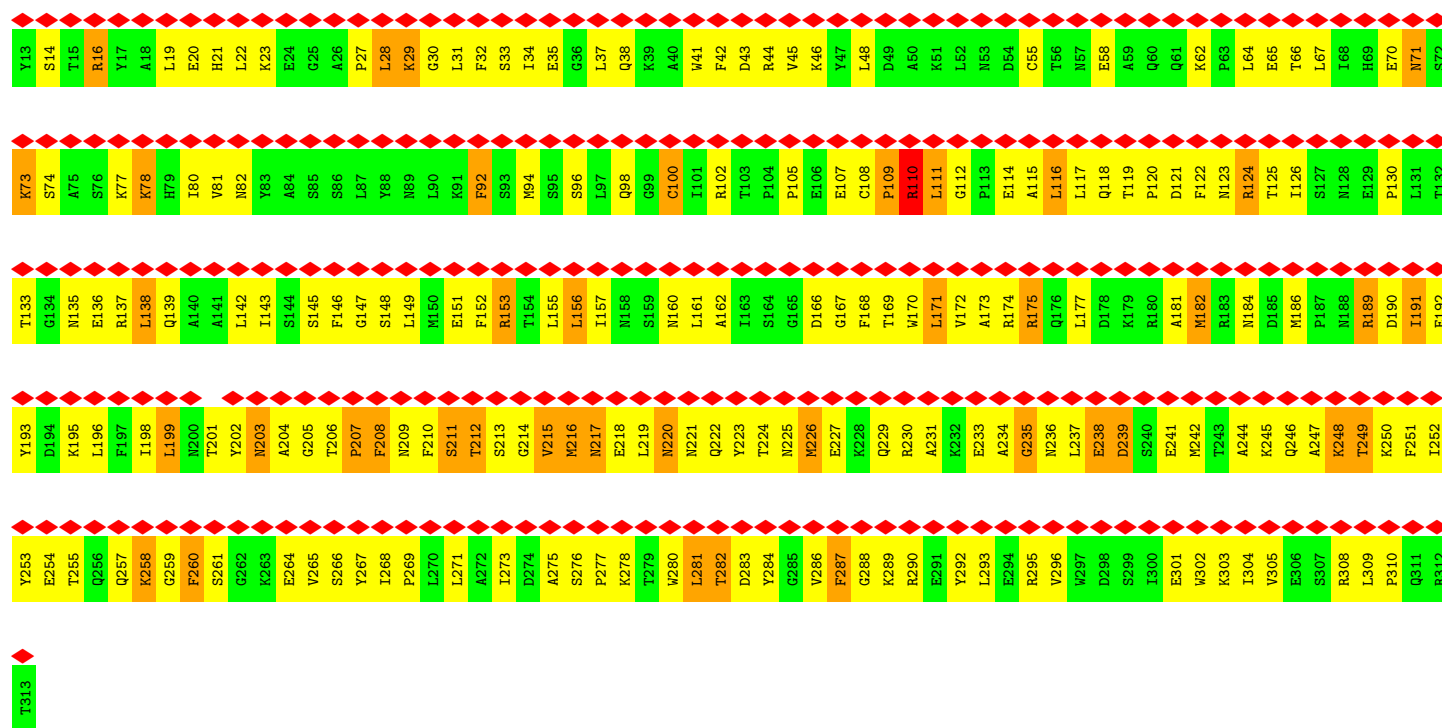


- Molecule 3: Small ribosomal subunit protein mS42

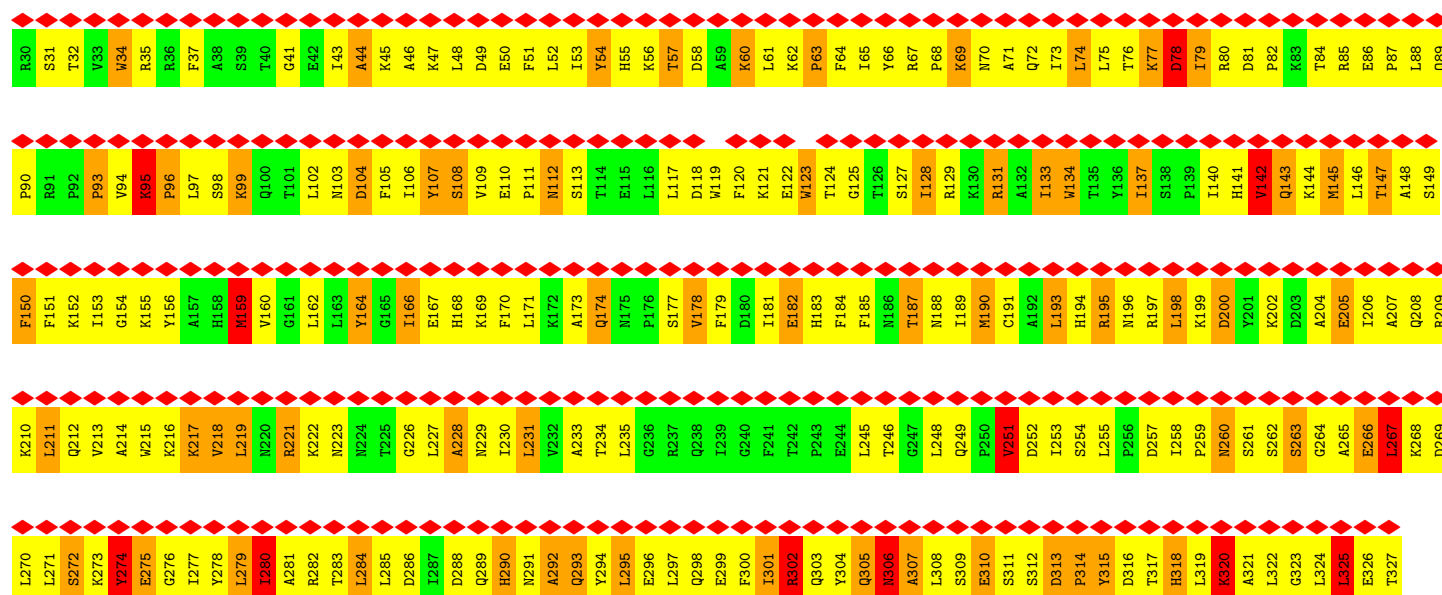




• Molecule 4: Small ribosomal subunit protein mS43



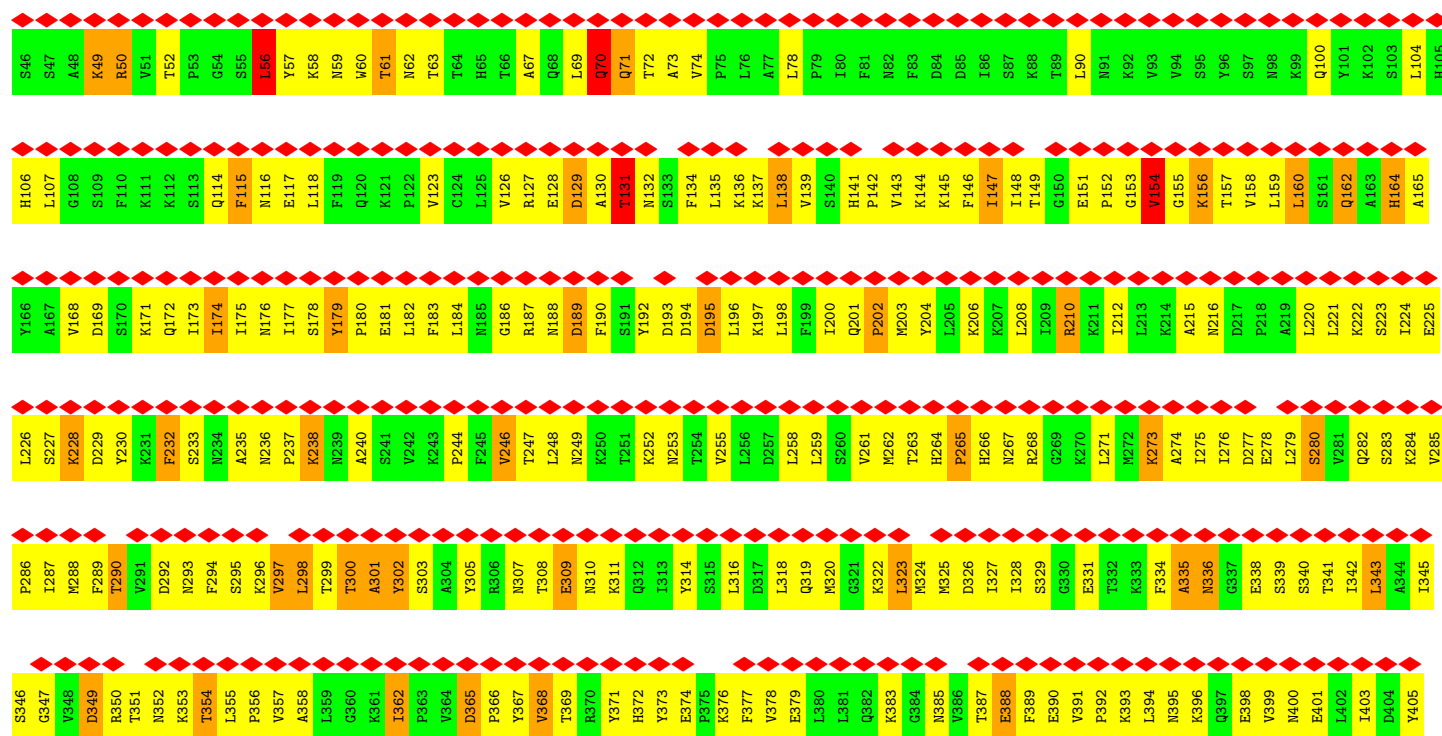
• Molecule 5: Small ribosomal subunit protein mS27



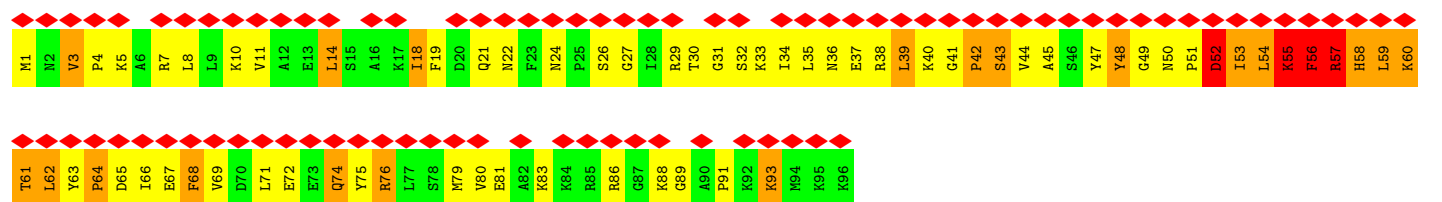




• Molecule 9: Small ribosomal subunit protein mS29

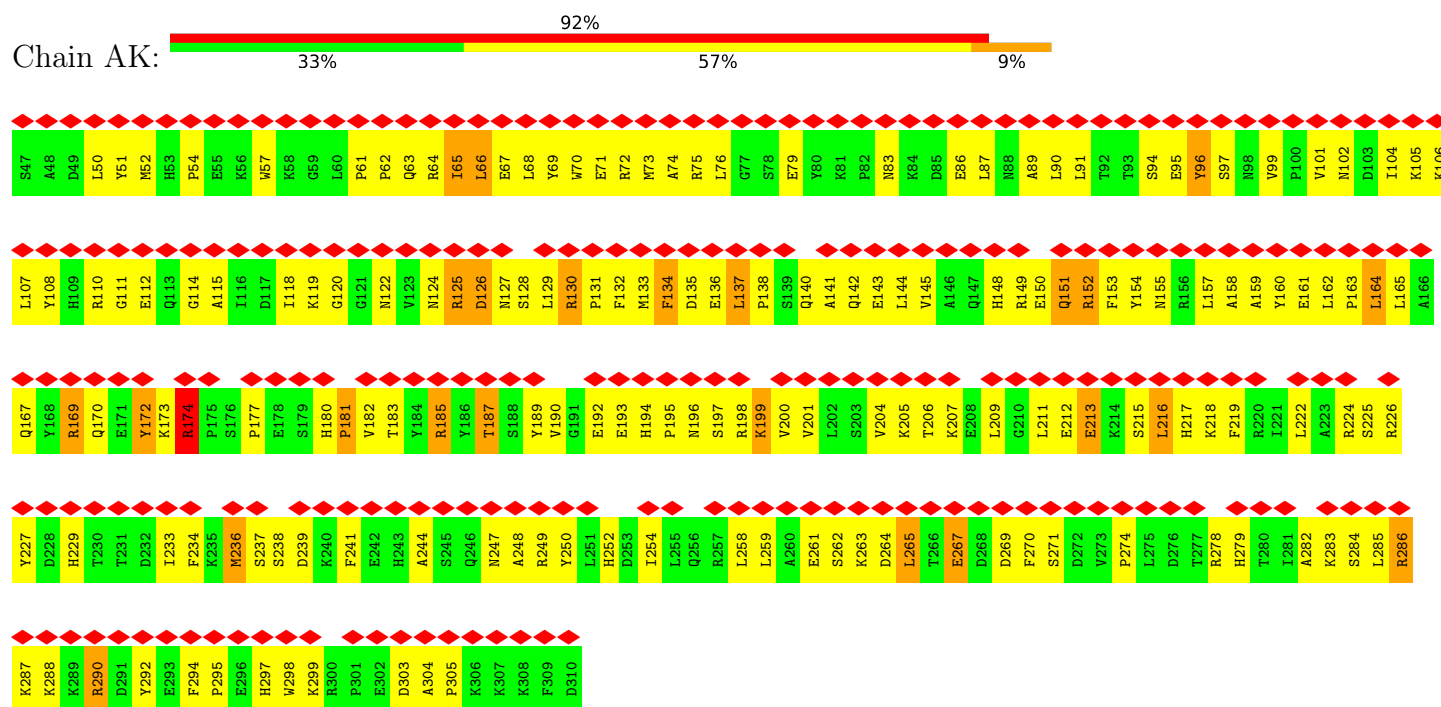


• Molecule 10: Small ribosomal subunit protein mS33



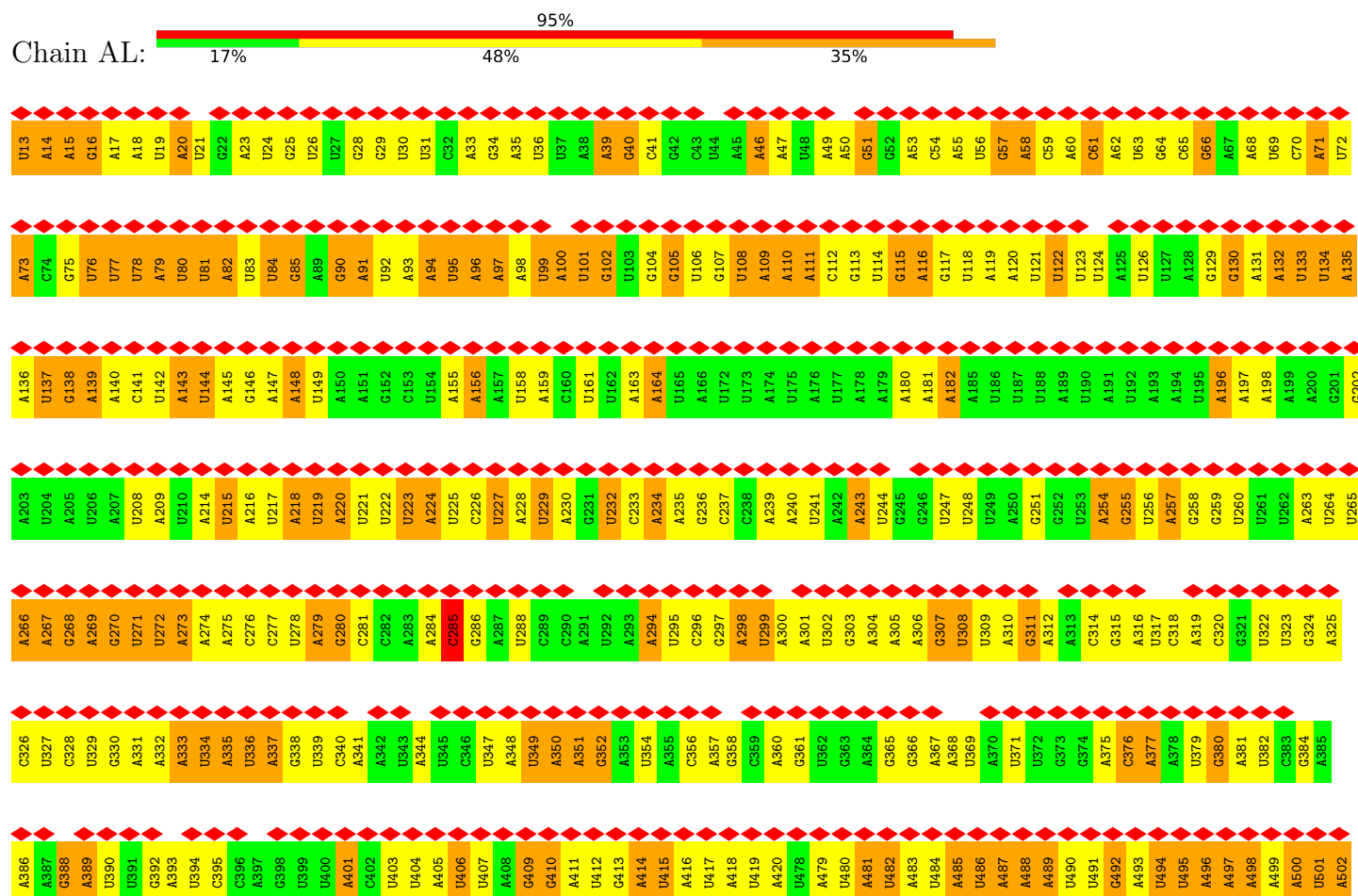
## ● Molecule 11: Small ribosomal subunit protein mS35

Chain AK:

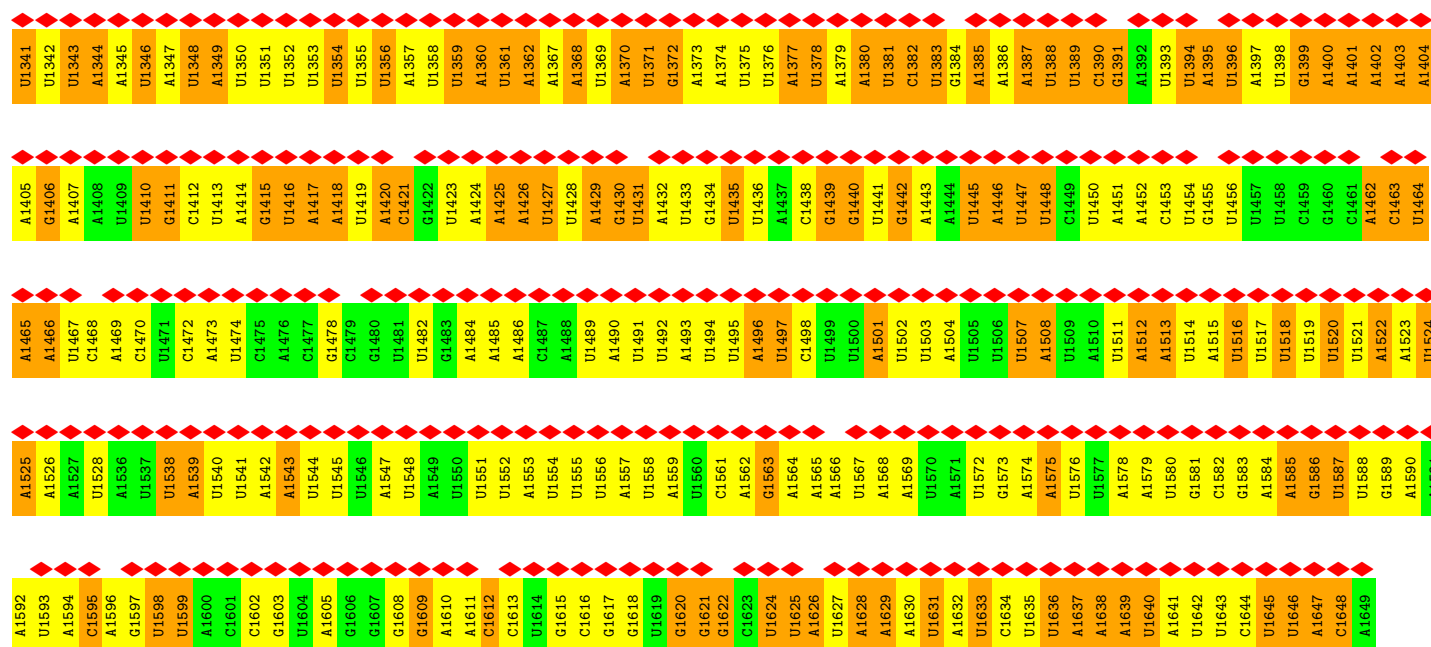


## ● Molecule 12: Small ribosomal subunit rRNA

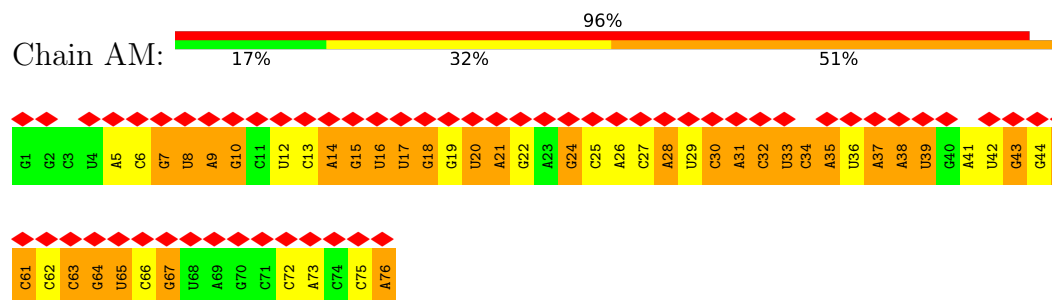
Chain AL:



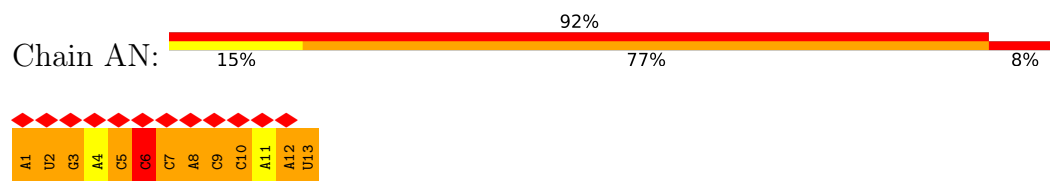
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U1221	U1222	A1223	A1224	G1225	A1226	C1227	A1228	A1229	A1230	U1231	C1232	A1233	U1234	A1235	A1236	U1237	G1238	A1239	U1240	C1241	C1242	U1243	U1244	A1245	A1246	A1247	A1248	U1249	A1250	U1251	U1252	G1253	G1254	U1255	A1256	A1257	U1258	A1259	G1260	A1261	C1262	G1263	U1264	G1265	C1266	U1267	A1268	U1269	A1270	A1271	U1272	A1273	A1274	A1275	A1276	U1277	G1278	A1279	U1280		
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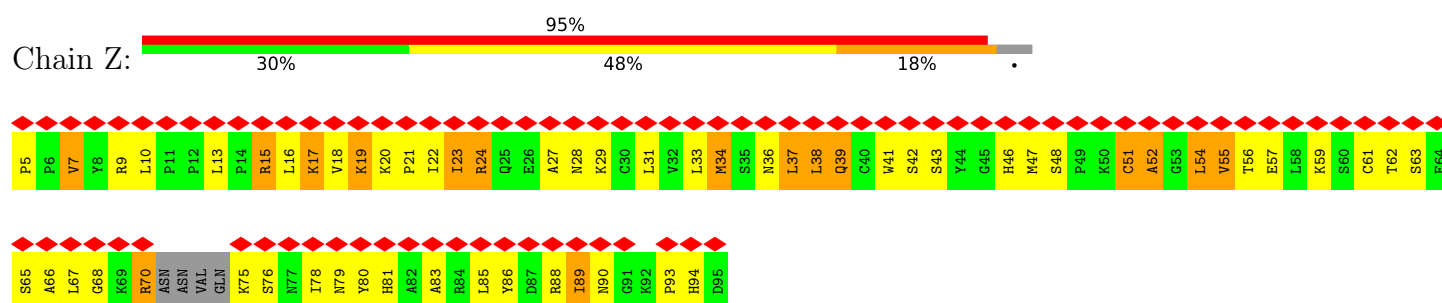
• Molecule 13: Small ribosomal subunit tRNA



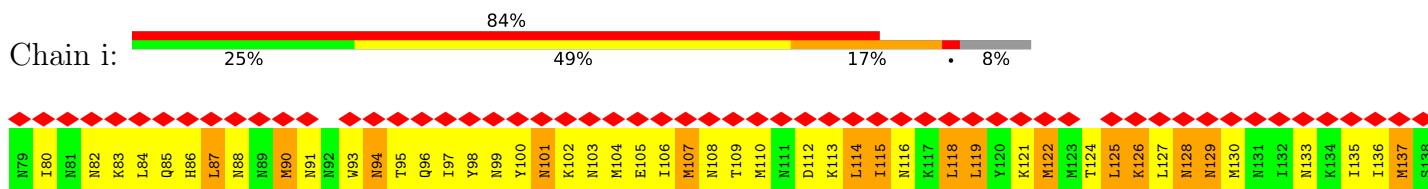
• Molecule 14: mRNA



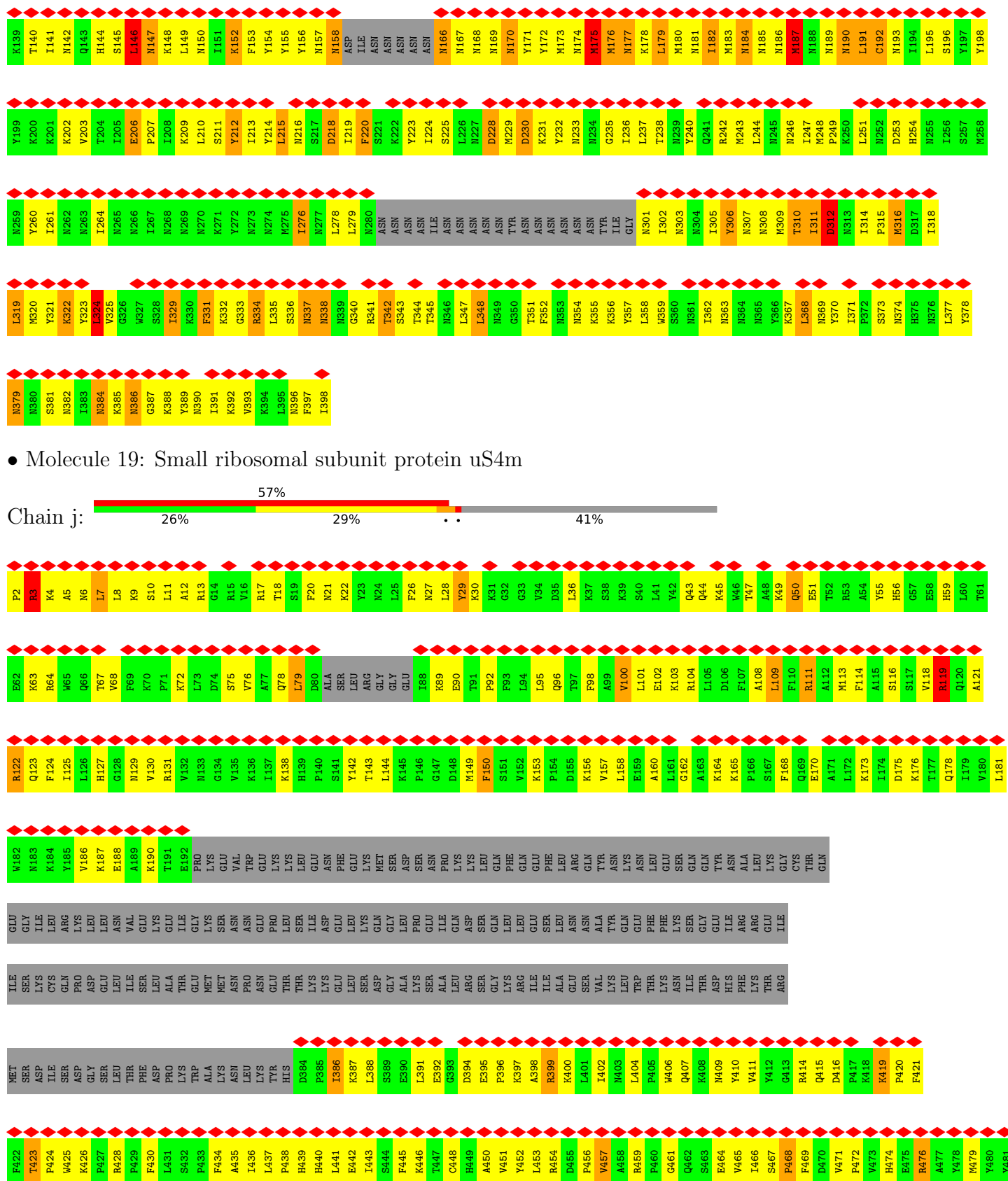
• Molecule 15: Small ribosomal subunit protein mS37



• Molecule 16: Small ribosomal subunit protein bS1m



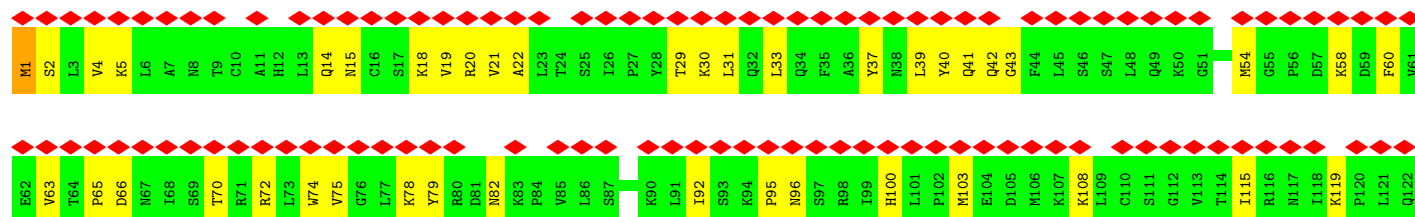




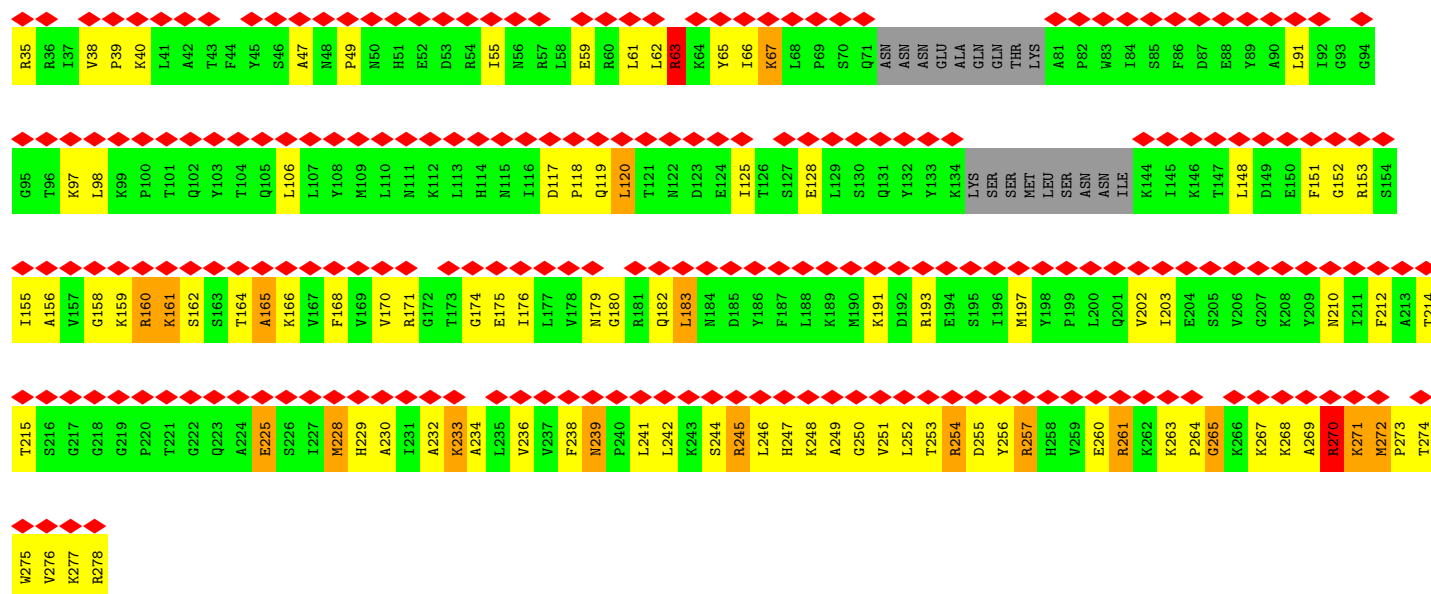
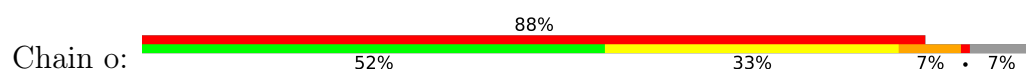




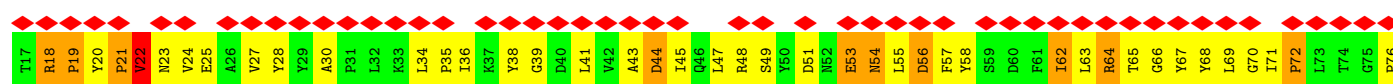
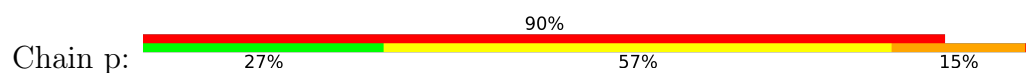
- Molecule 23: 37S ribosomal protein S8, mitochondrial

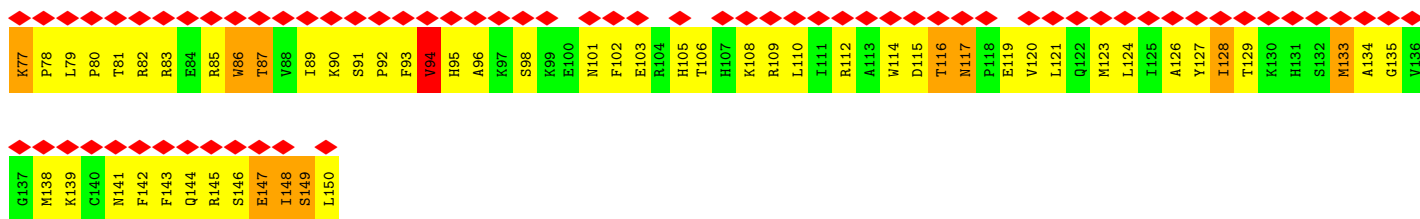


- Molecule 24: Small ribosomal subunit protein uS9m

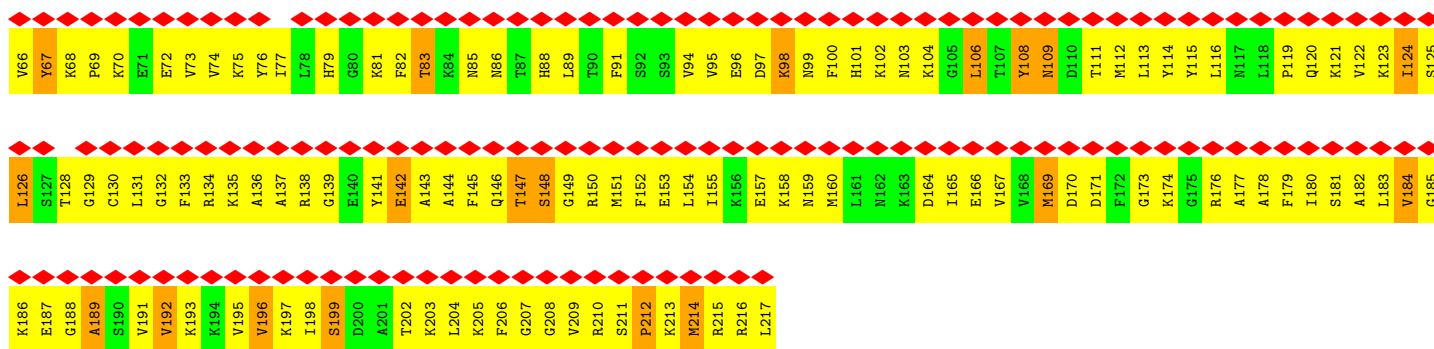


- Molecule 25: Small ribosomal subunit protein uS10m

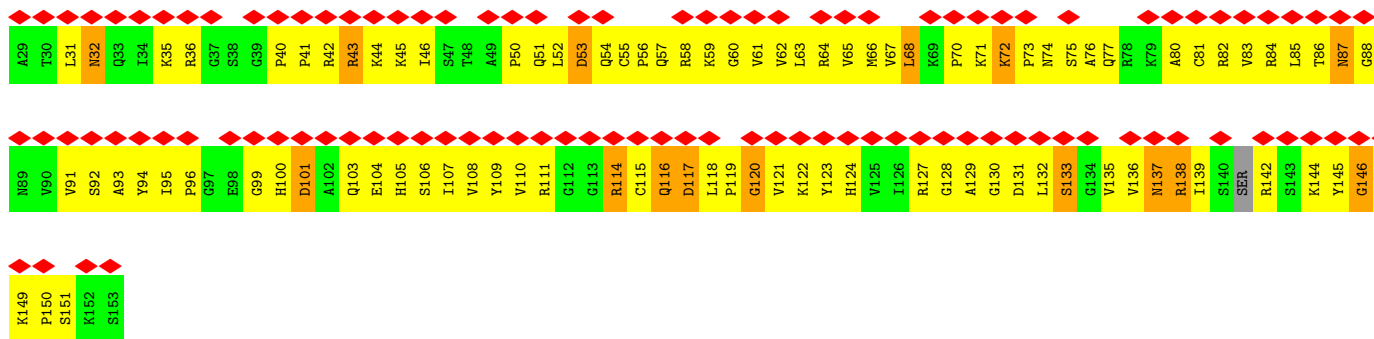
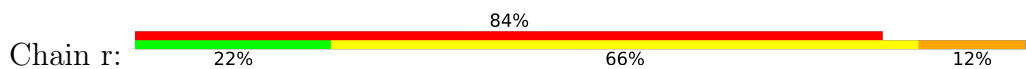




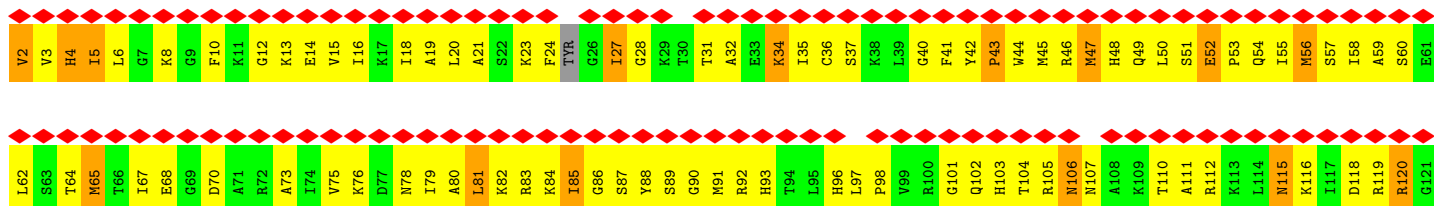
• Molecule 26: Small ribosomal subunit protein uS11m



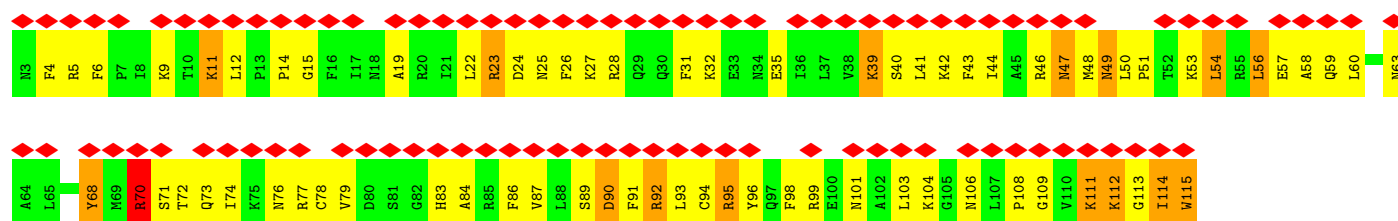
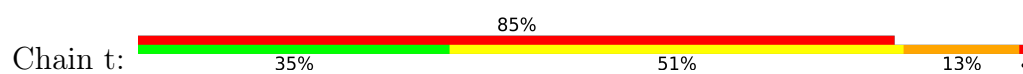
• Molecule 27: Small ribosomal subunit protein uS12m



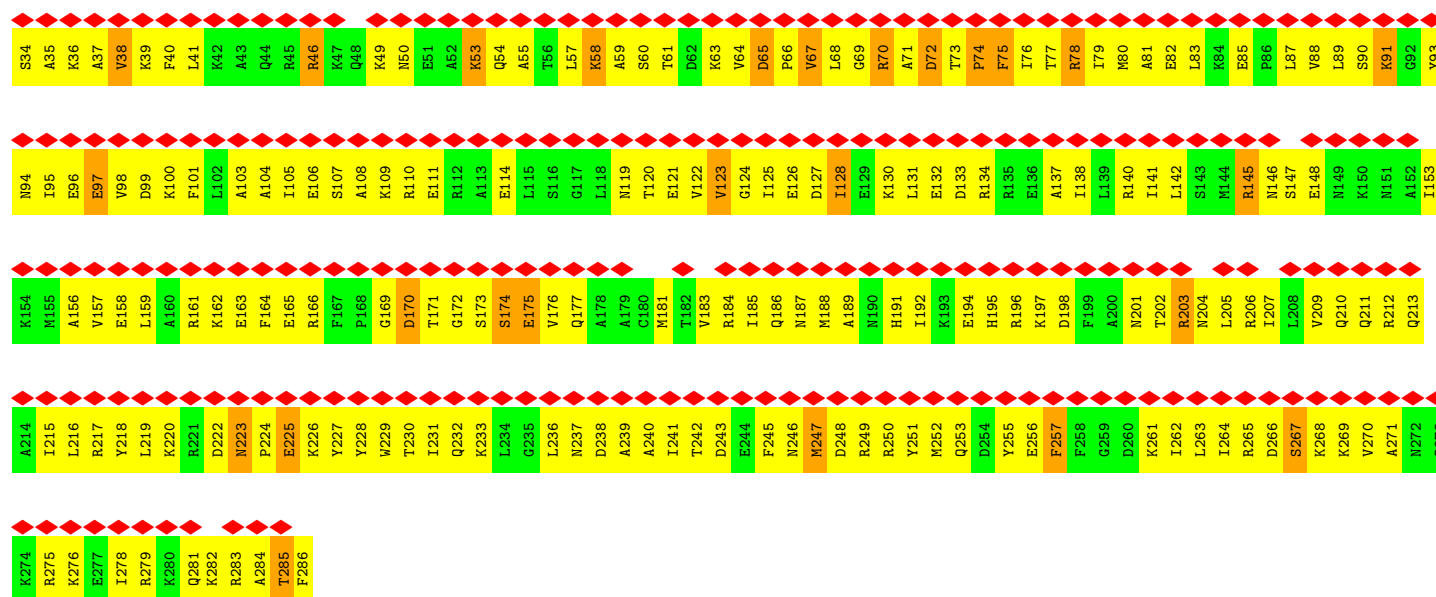
• Molecule 28: Small ribosomal subunit protein uS13m



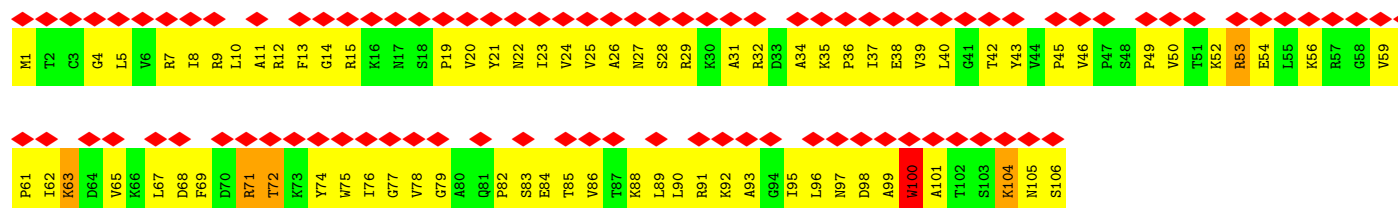
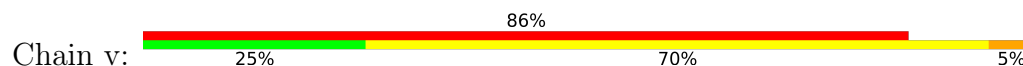
• Molecule 29: Small ribosomal subunit protein uS14m



• Molecule 30: Small ribosomal subunit protein uS15m

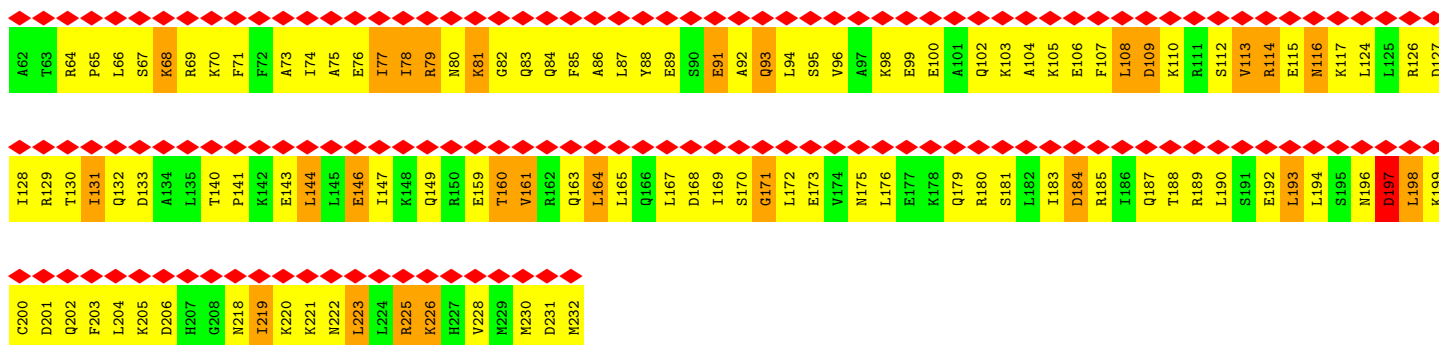


• Molecule 31: Small ribosomal subunit protein bS16m

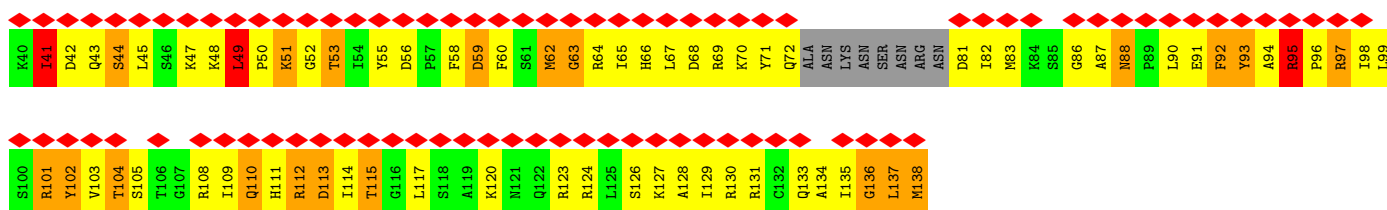
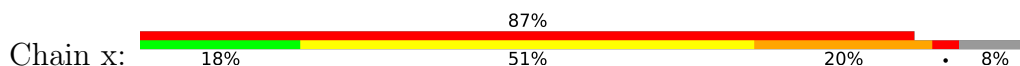


• Molecule 32: MRPL38 isoform 1

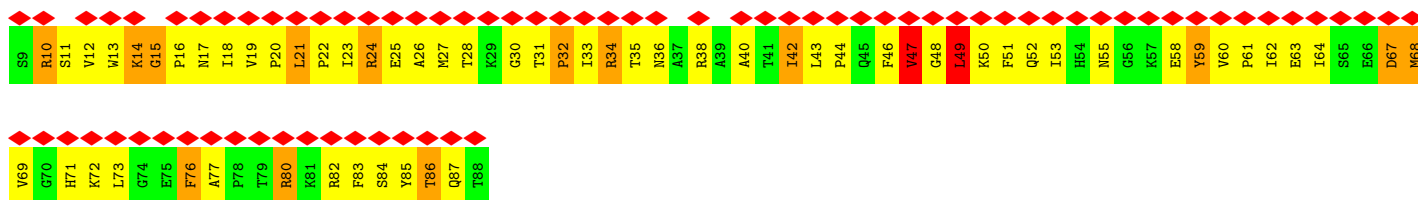




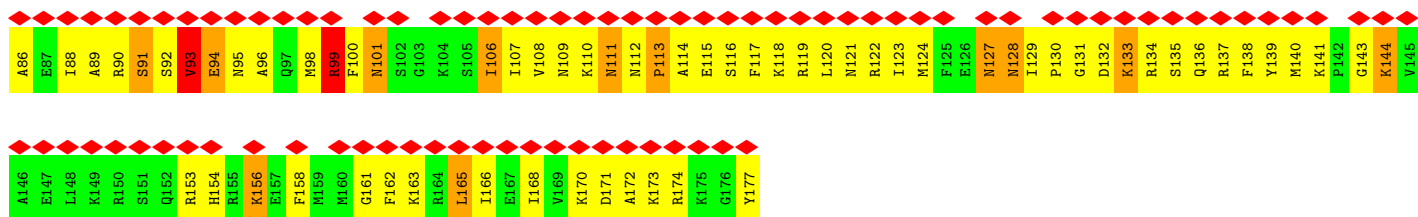
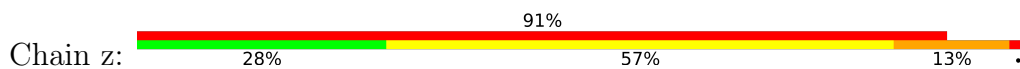
• Molecule 33: Small ribosomal subunit protein bS18m



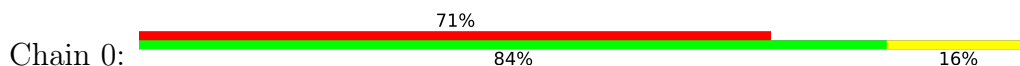
• Molecule 34: Small ribosomal subunit protein uS19m

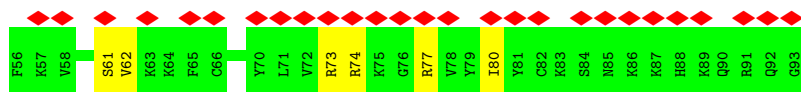


• Molecule 35: Small ribosomal subunit protein bS21m

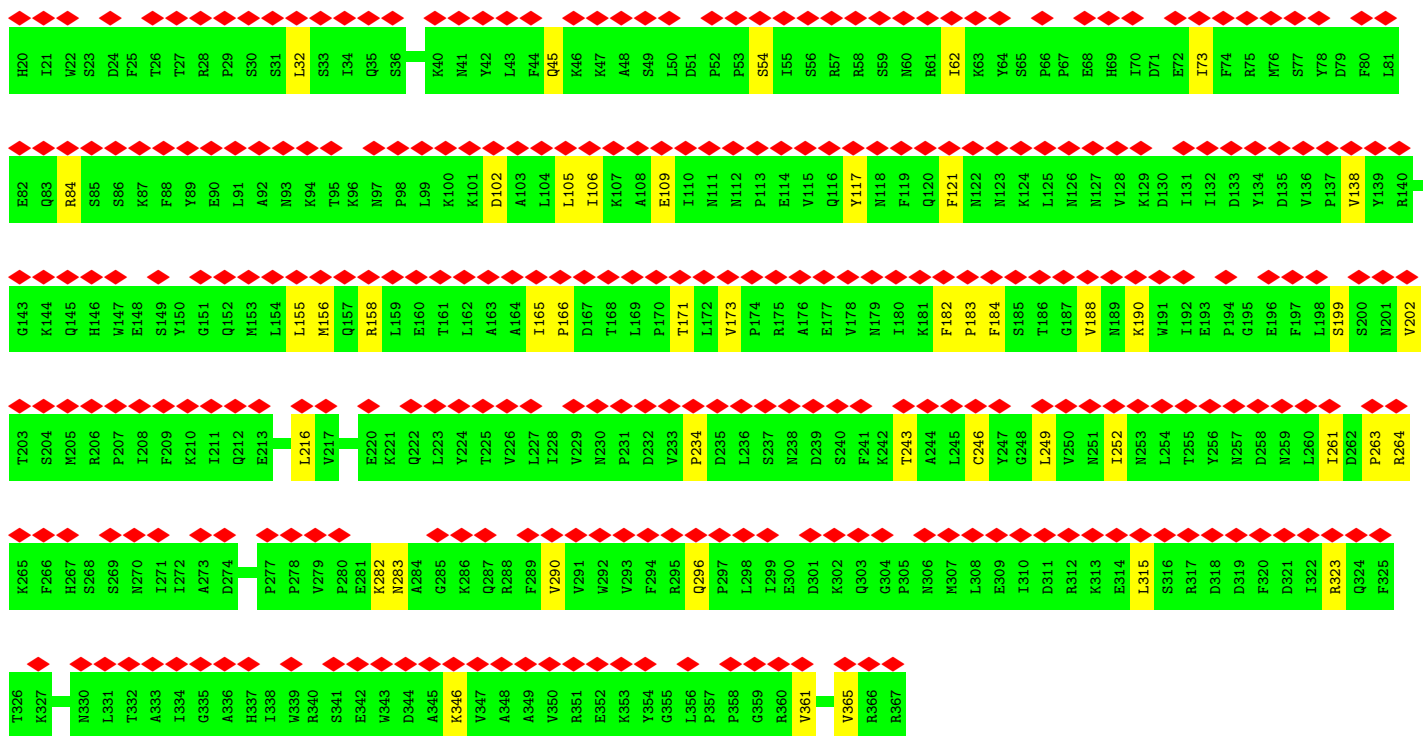
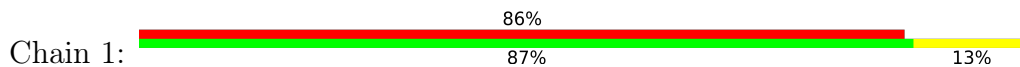


• Molecule 36: Large ribosomal subunit protein bL36m

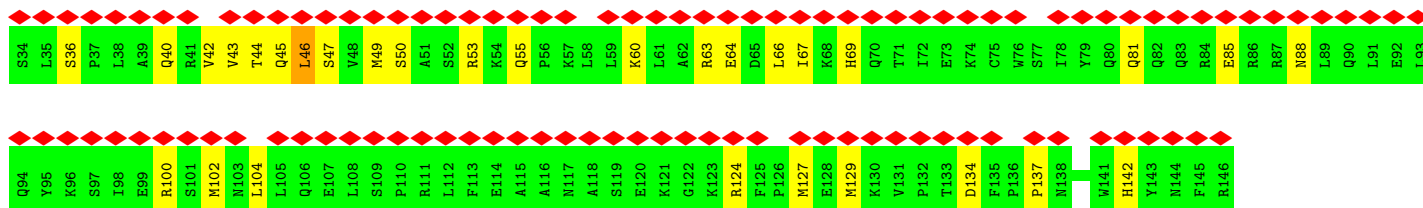
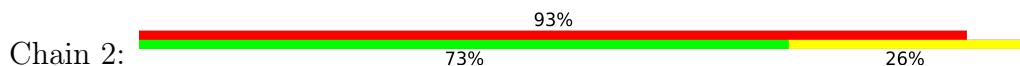




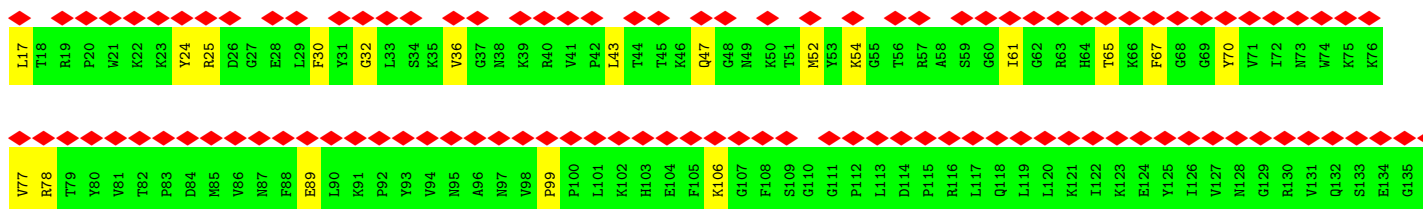
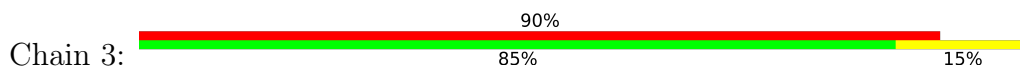
• Molecule 37: Large ribosomal subunit protein mL38

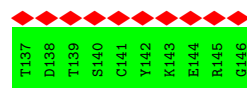


• Molecule 38: Large ribosomal subunit protein mL40

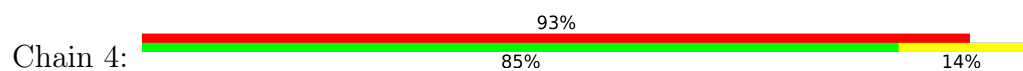


• Molecule 39: Large ribosomal subunit protein mL41

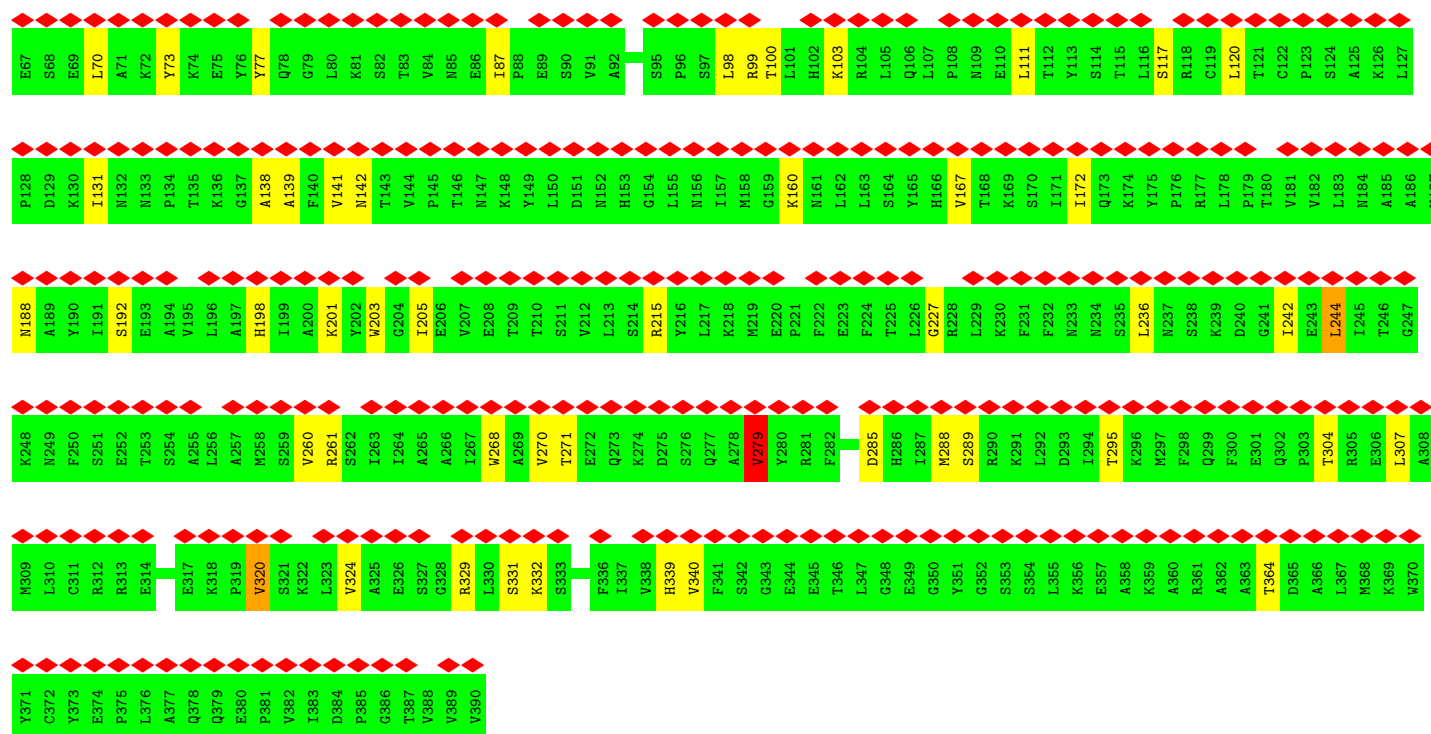
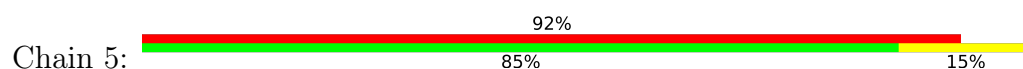




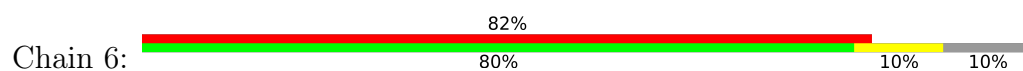
• Molecule 40: Large ribosomal subunit protein mL43



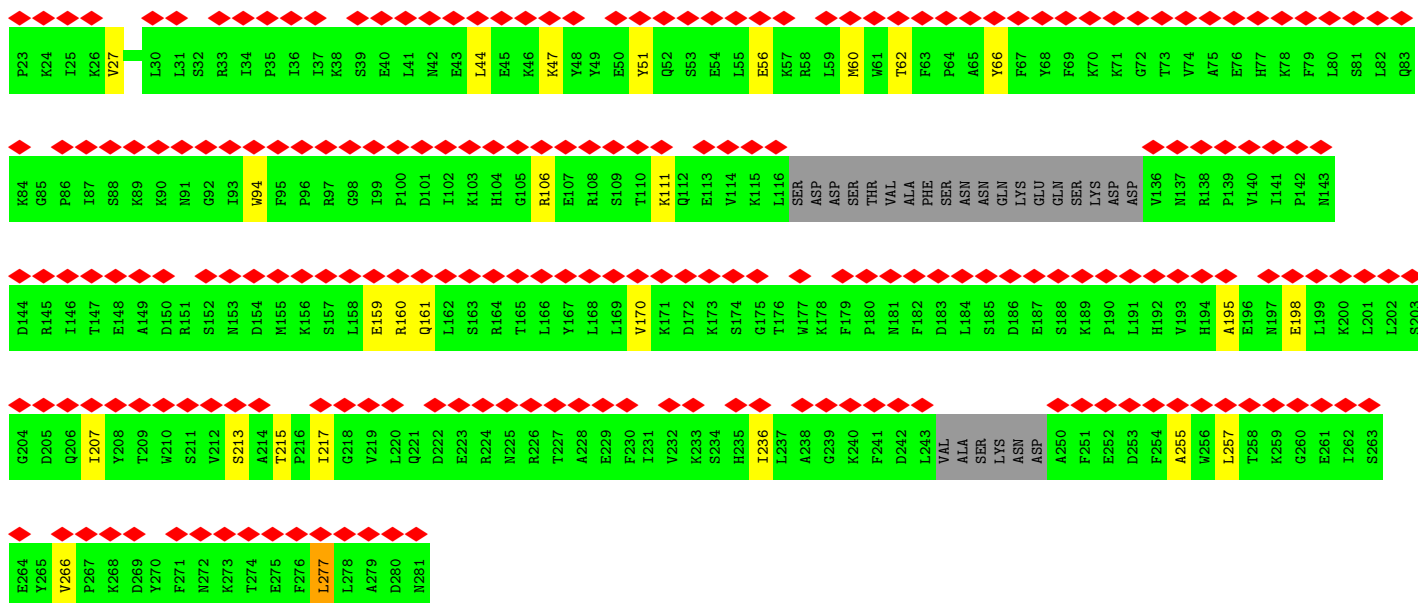
• Molecule 41: Large ribosomal subunit protein mL44



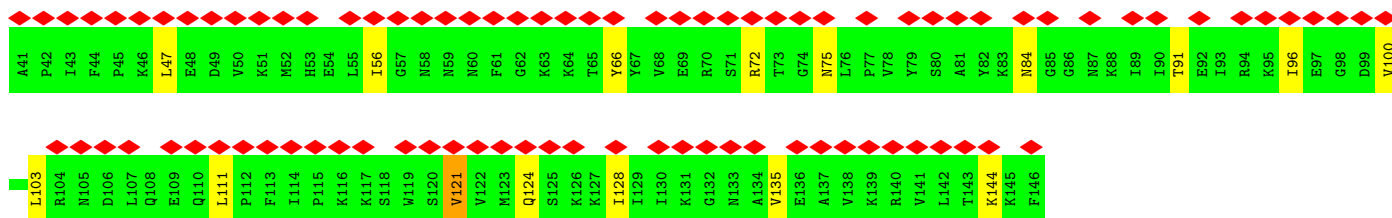
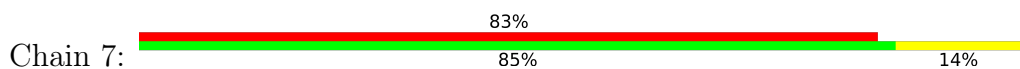
• Molecule 42: Large ribosomal subunit protein mL46



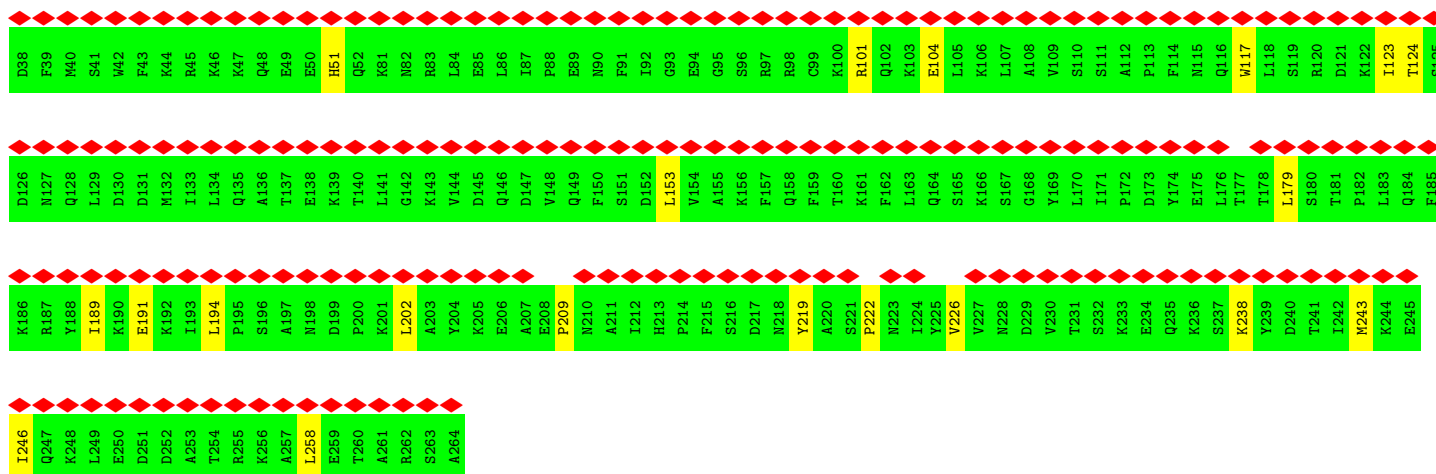
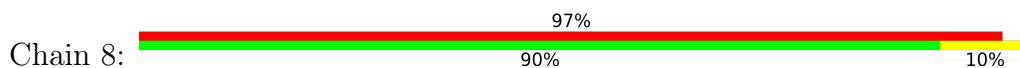




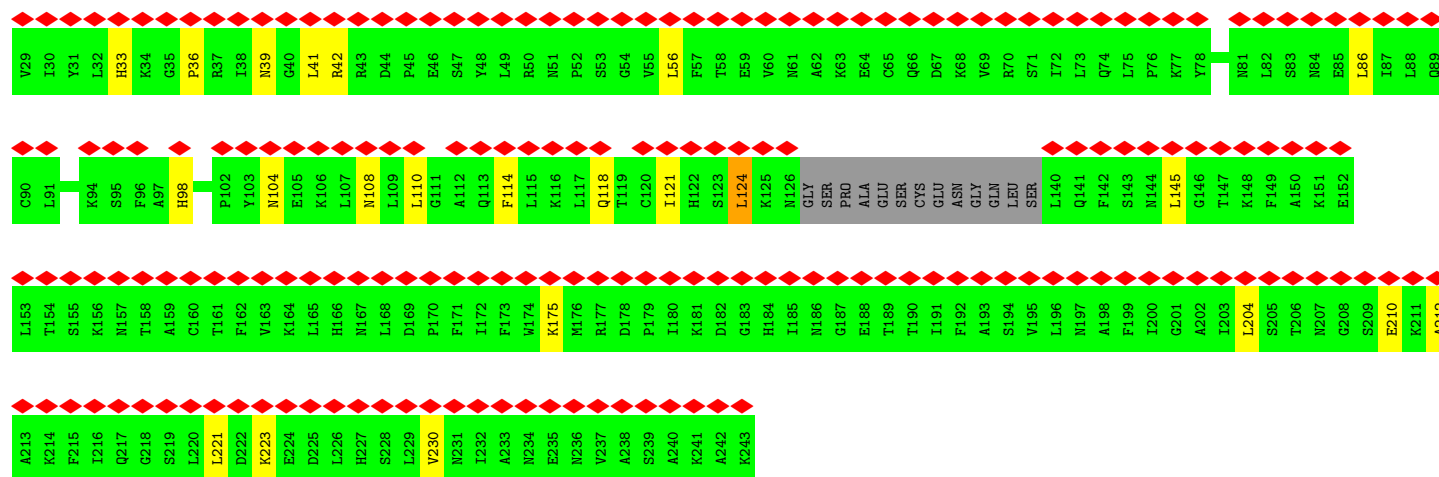
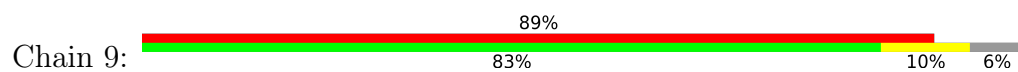
• Molecule 43: Large ribosomal subunit protein mL49



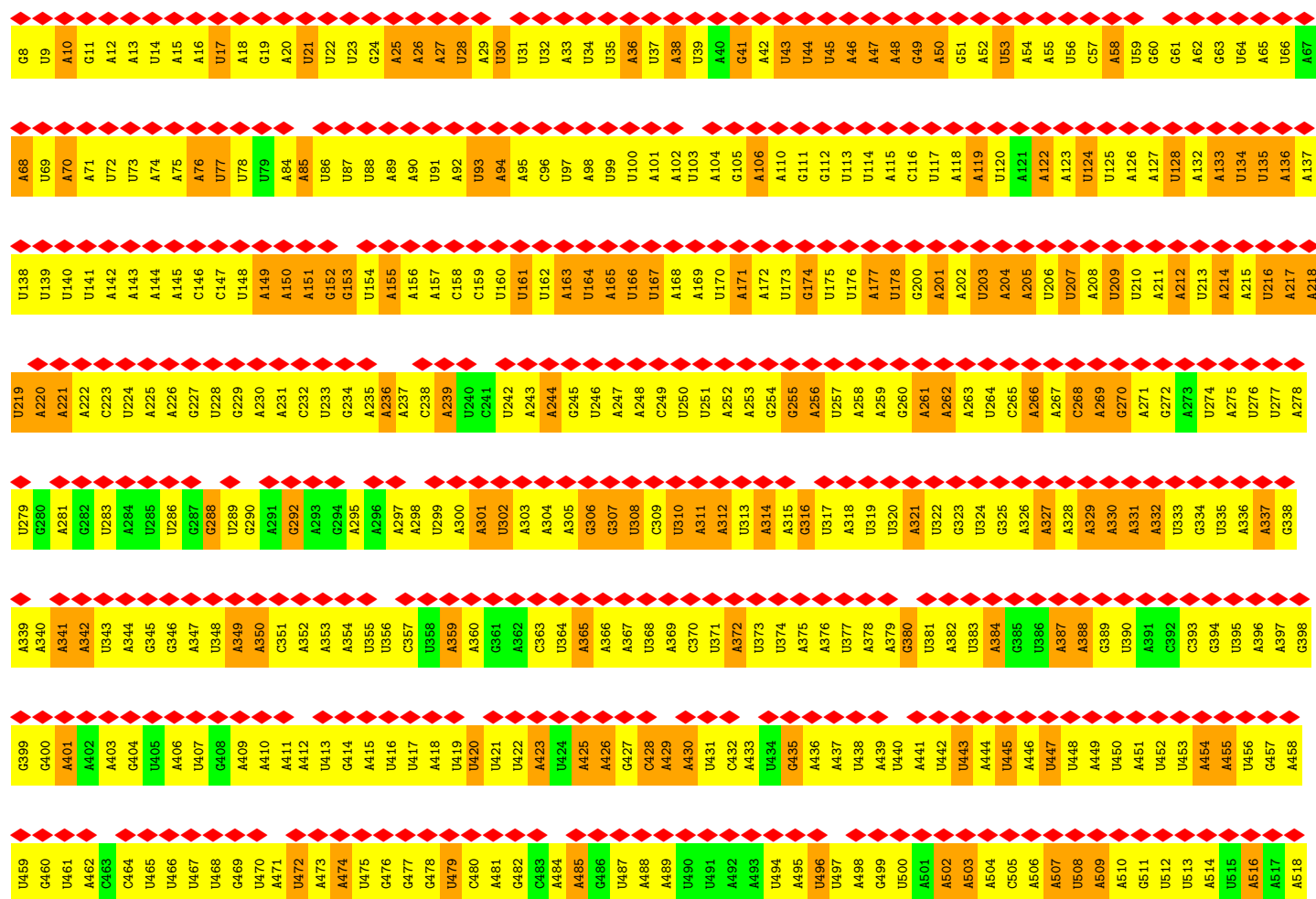
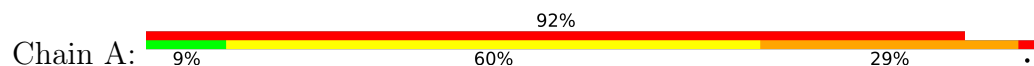
• Molecule 44: Large ribosomal subunit protein uL30m



• Molecule 45: Large ribosomal subunit protein mL57



• Molecule 46: Large ribosomal subunit rRNA



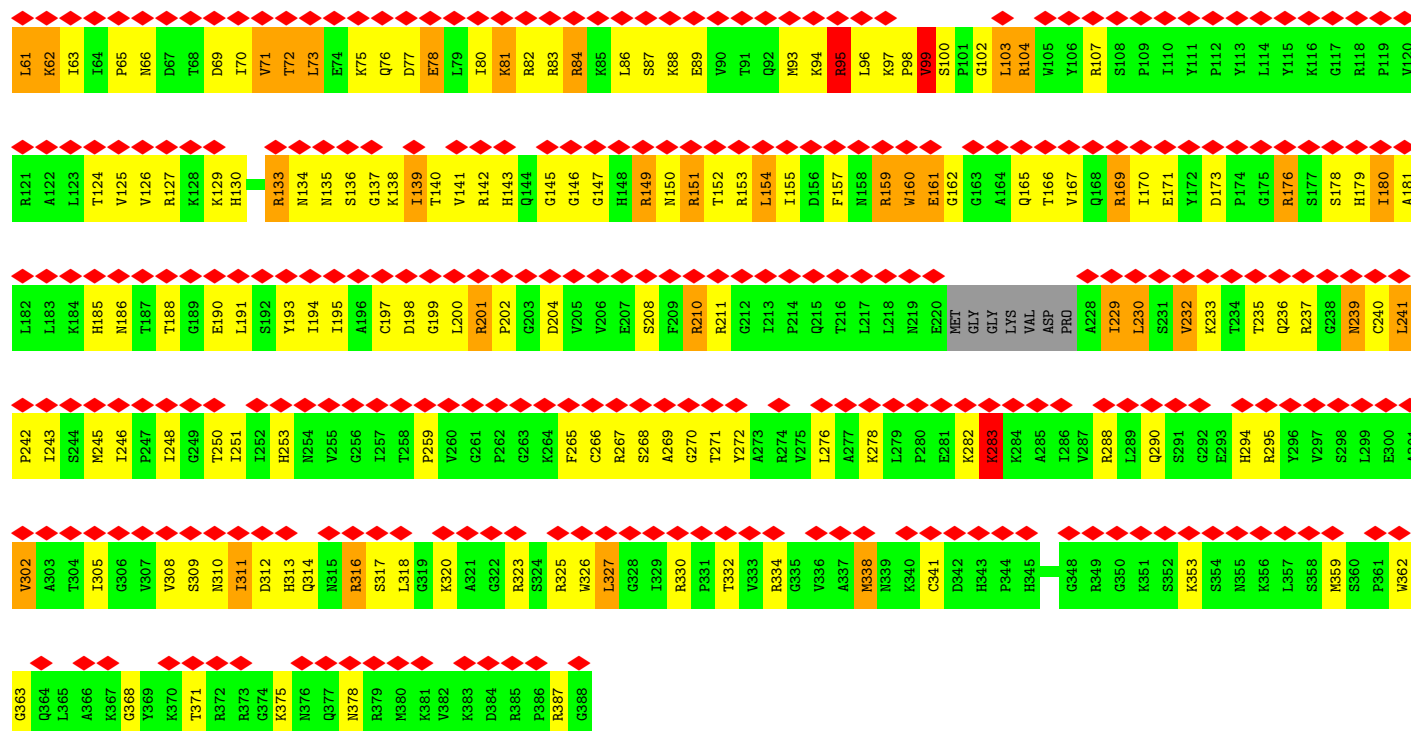
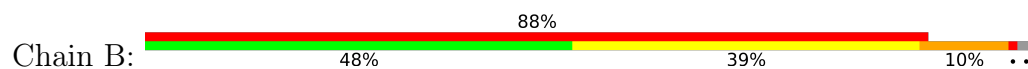
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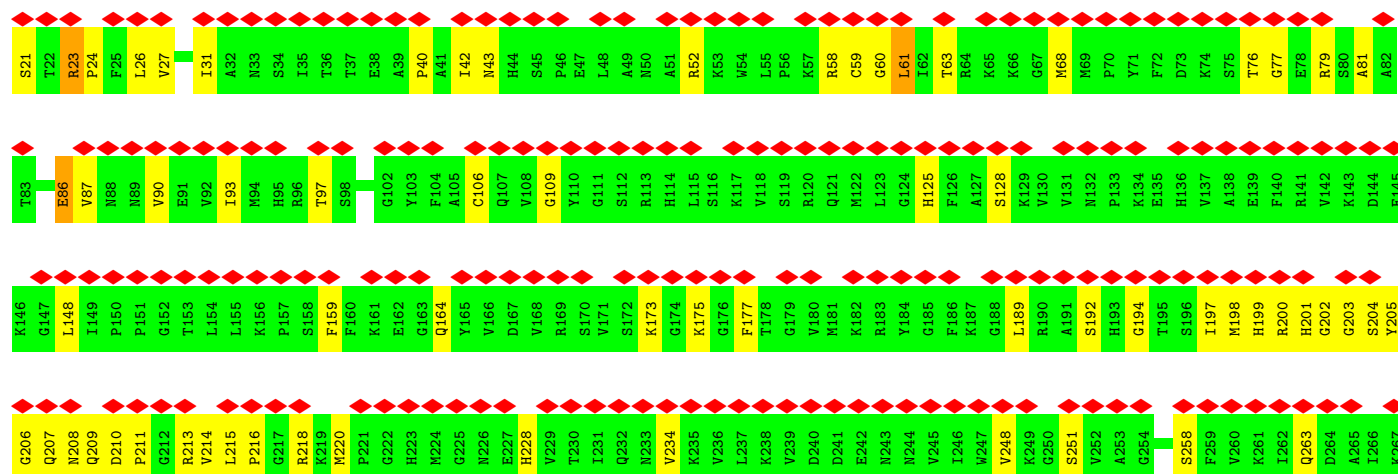
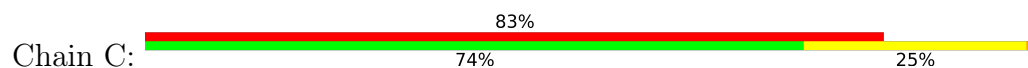
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U3169	U3048	A2968	A2908	G2848	U2788	U2728	G2607	G2453	A2378	A2313
A3170	A3049	U2969	U2909	G2849	U2789	A2729	C2608	U2454	A2379	U2314
U3171	U3050	A2970	A2910	G2850	U2790	G2730	G2609	A2455	U2380	A2315
A3172	G3050	U2971	U2911	U2851	U2791	C2731	A2610	A2456	U2381	A2316
U3173	U3051	U2972	C2912	U2852	G2792	G2732	U2611	G2457	A2382	A2317
A3174	A3052	A2973	U2913	A2853	G2793	A2733	A2612	G2458	A2383	U2318
U3175	U3053	U2974	C2914	G2854	U2794	A2734	A2613	A2459	A2384	A2319
A3176	A3054	A2975	U2915	A2855	U2795	A2735	U2614	A2460	U2385	A2320
U3177	U3055	A2976	U2916	U2856	G2796	G2736	U2615	A2461	A2386	A2321
A3178	A3056	U2977	U2917	U2857	U2797	A2737	G2616	A2462	U2387	U2322
U3179	G3057	U2978	A2918	A2858	A2798	G2738	U2617	C2463	G2388	A2323
A3180	U3058	U2979	U2919	C2859	U2799	U2739	A2618	U2464	U2389	U2324
U3181	U3059	U2980	U2920	A2860	A2800	A2740	A2619	A2465	U2390	A2325
U3182	A3060	U2981	A2921	U2861	G2801	G2741	C2620	A2466	U2391	U2326
A3183	A3061	U2982	G2922	U2862	A2802	A2742	A2621	A2467	A2392	A2327
U3184	A3062	U2983	U2923	G2863	C2803	U2743	C2622	U2468	A2408	A2328
U3185	G3063	U2984	A2924	U2864	U2804	A2744	A2623	U2469	U2409	A2329
A3186	U3064	A2985	C2925	A2865	A2805	U2745	A2624	A2470	U2410	A2330
U3187	U3065	A2986	G2926	A2866	A2806	U2746	U2625	A2471	G2411	U2331
A3188	G3066	U3002	G2927	A2867	A2807	G2747	G2626	C2472	U2473	U2332
U3189	A3067	A3003	A2928	C2868	A2808	U2748	A2628	U2474	A2413	A2333
U3190	U3068	A3004	A2928	C2868	A2808	U2748	A2628	U2474	A2413	A2333



• Molecule 47: Large ribosomal subunit protein uL2m

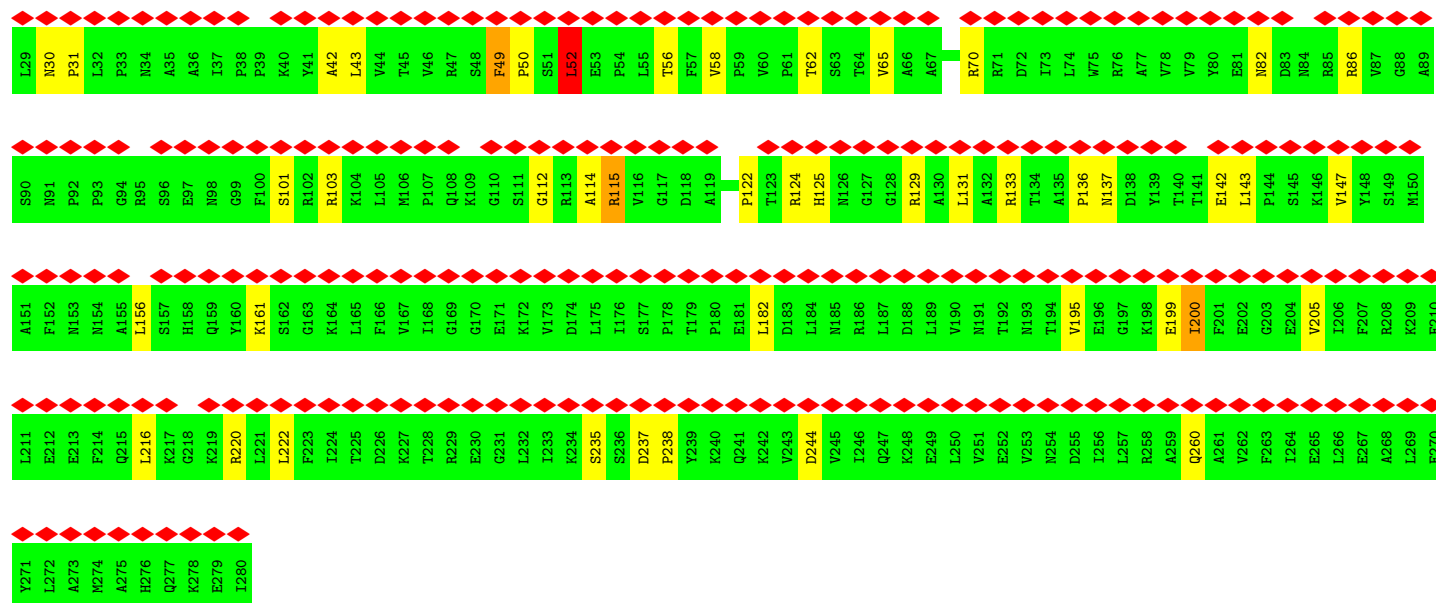
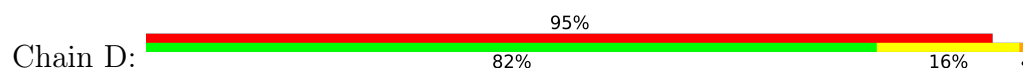


• Molecule 48: Large ribosomal subunit protein uL3m

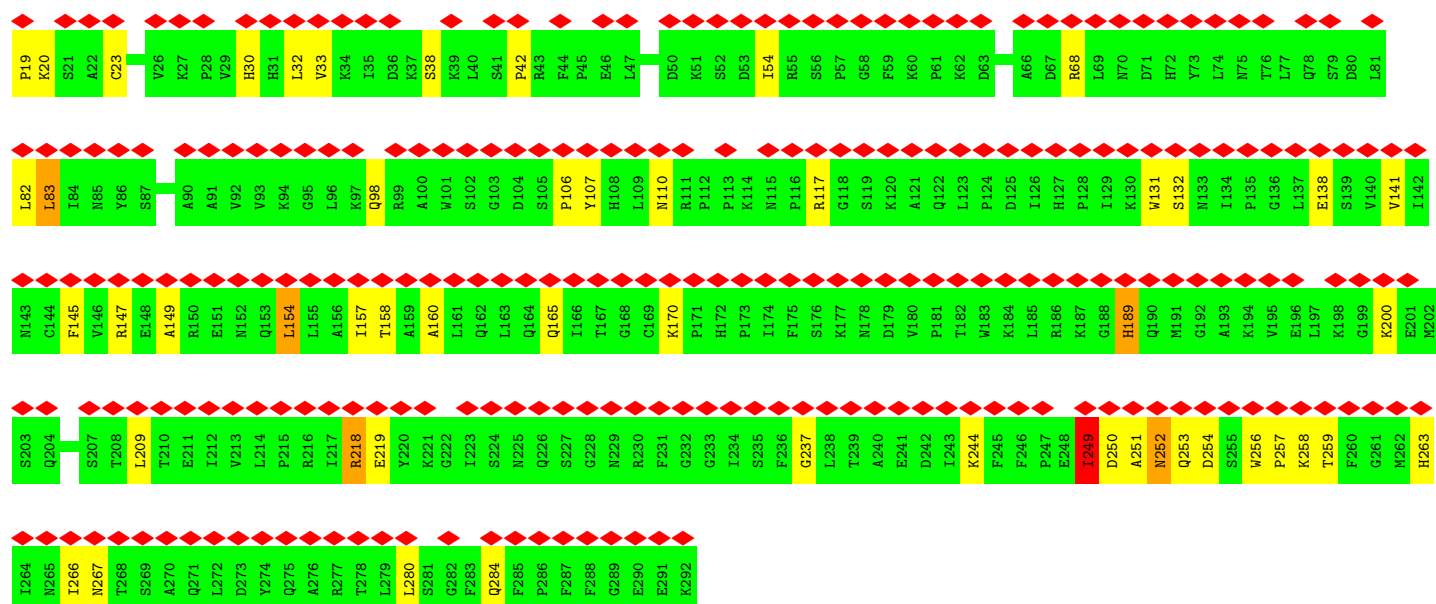
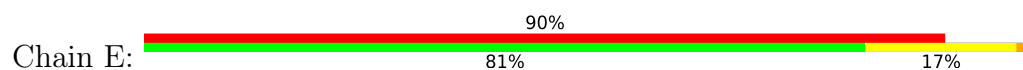




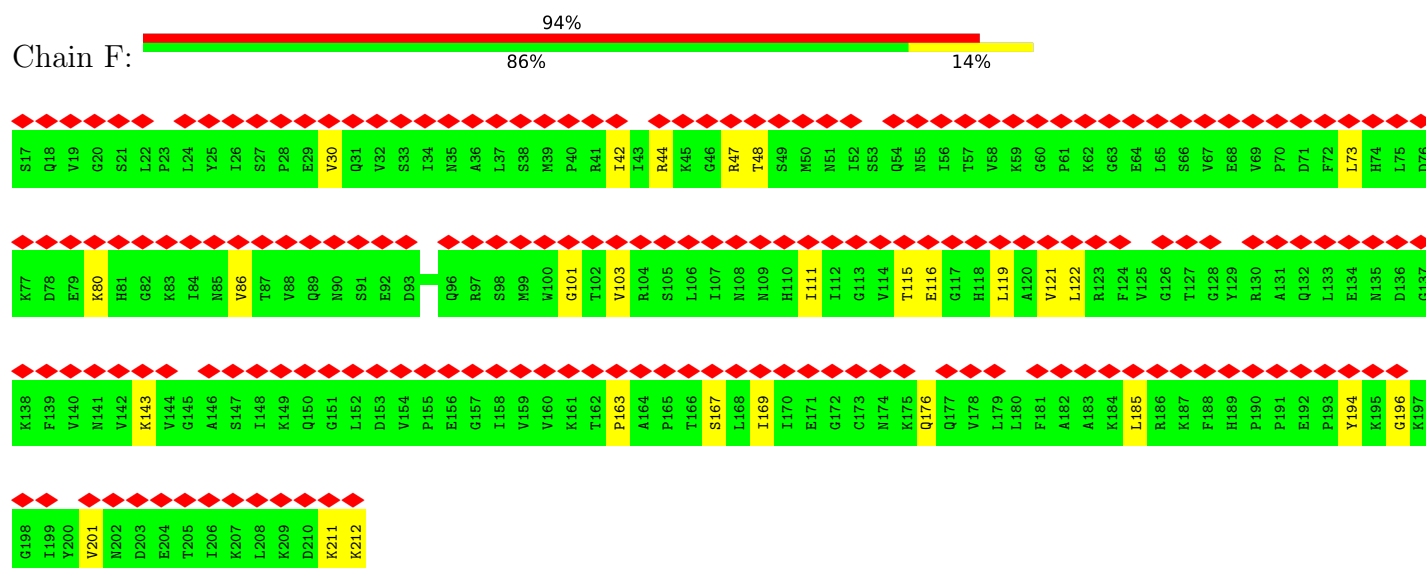
- Molecule 49: Large ribosomal subunit protein uL4m



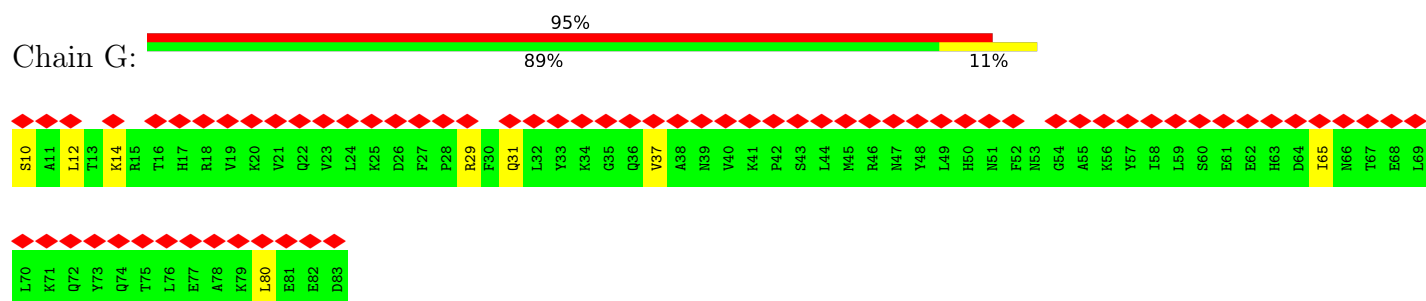
- Molecule 50: Large ribosomal subunit protein uL5m



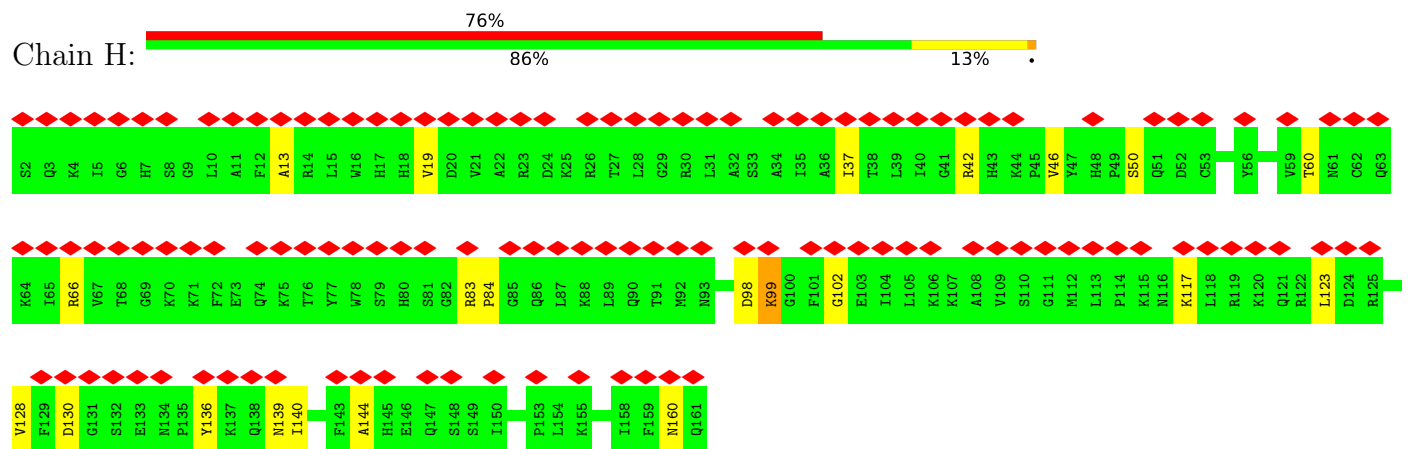
- Molecule 51: Large ribosomal subunit protein uL6m



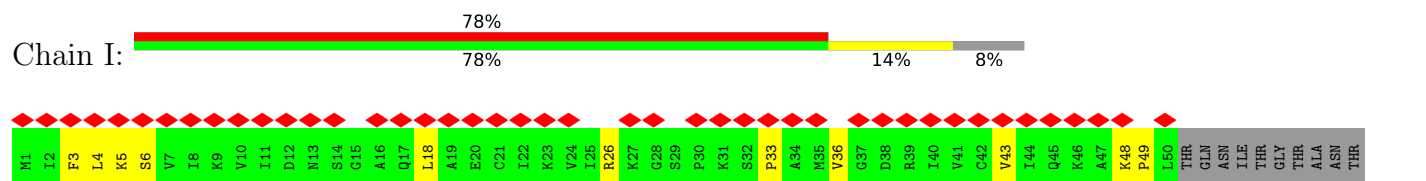
- Molecule 52: Large ribosomal subunit protein bL9m



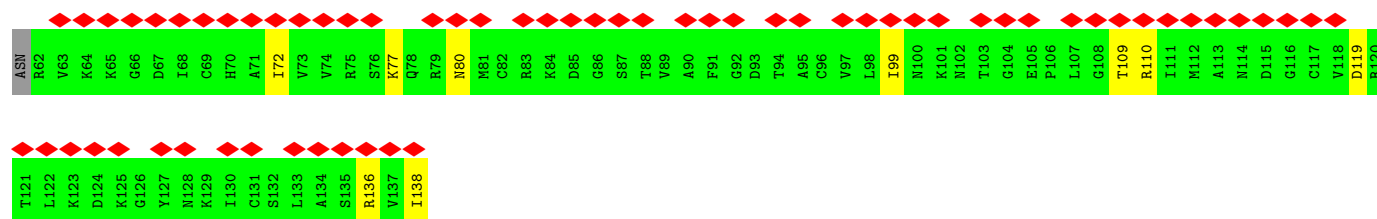
- Molecule 53: Large ribosomal subunit protein uL13m



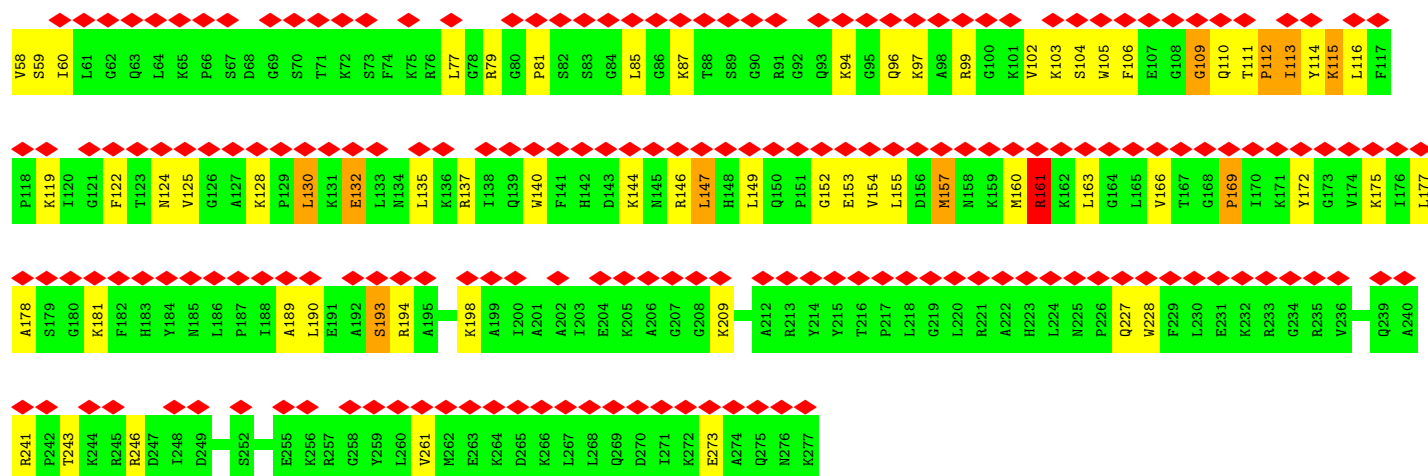
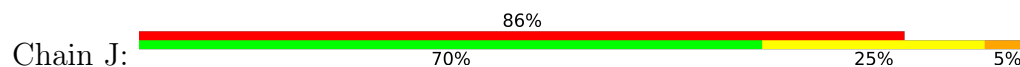
- Molecule 54: Large ribosomal subunit protein uL14m



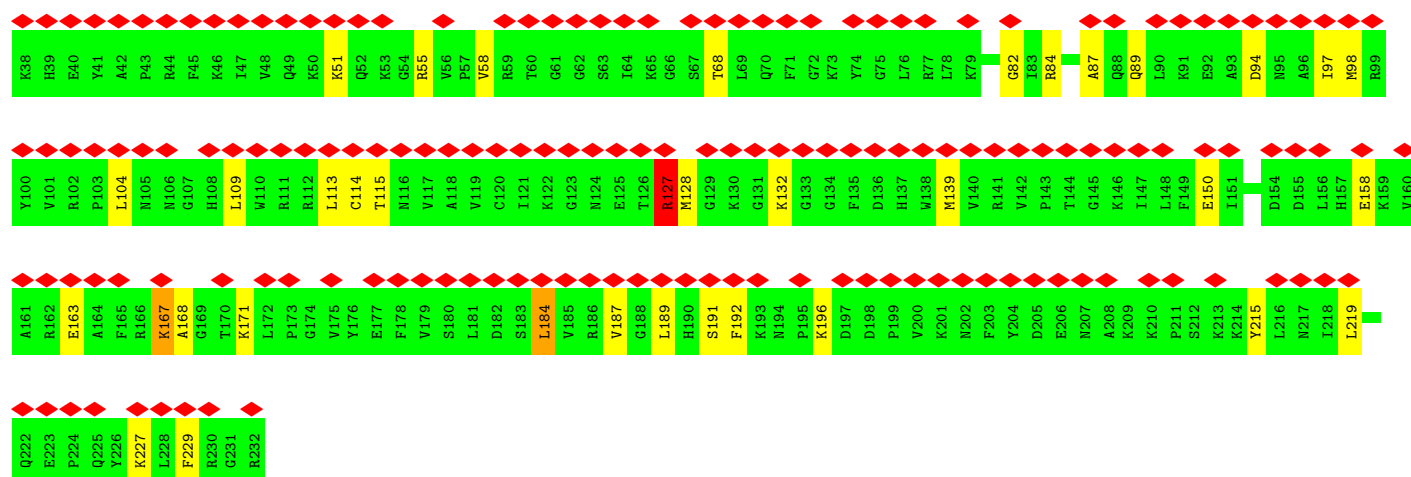
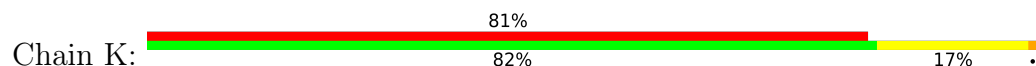




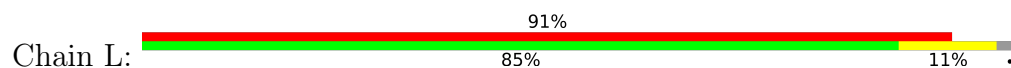
• Molecule 55: Large ribosomal subunit protein uL15m

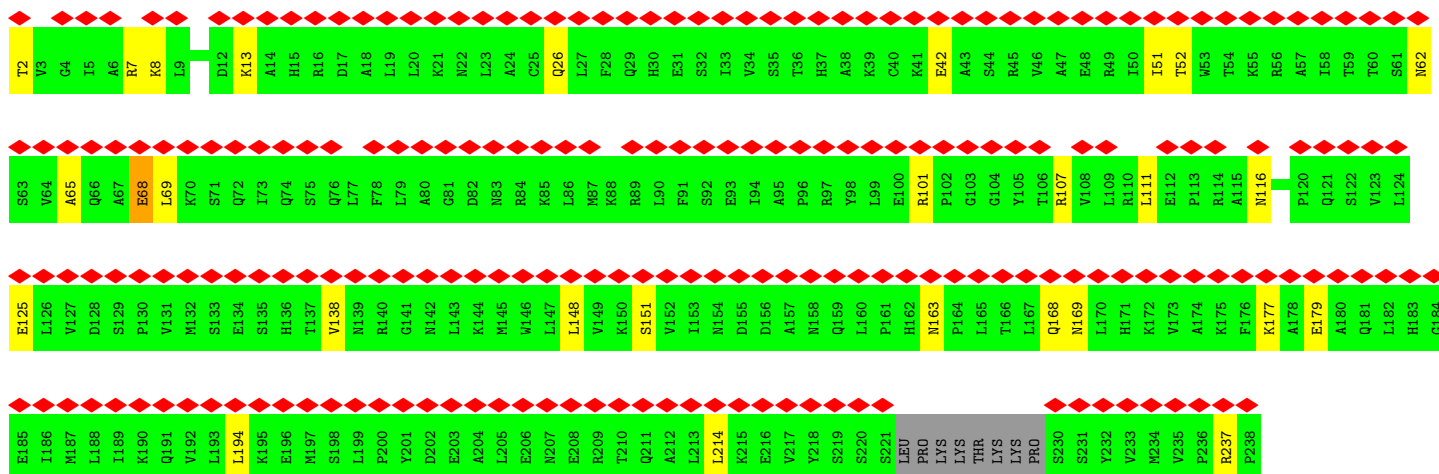


• Molecule 56: Large ribosomal subunit protein uL16m

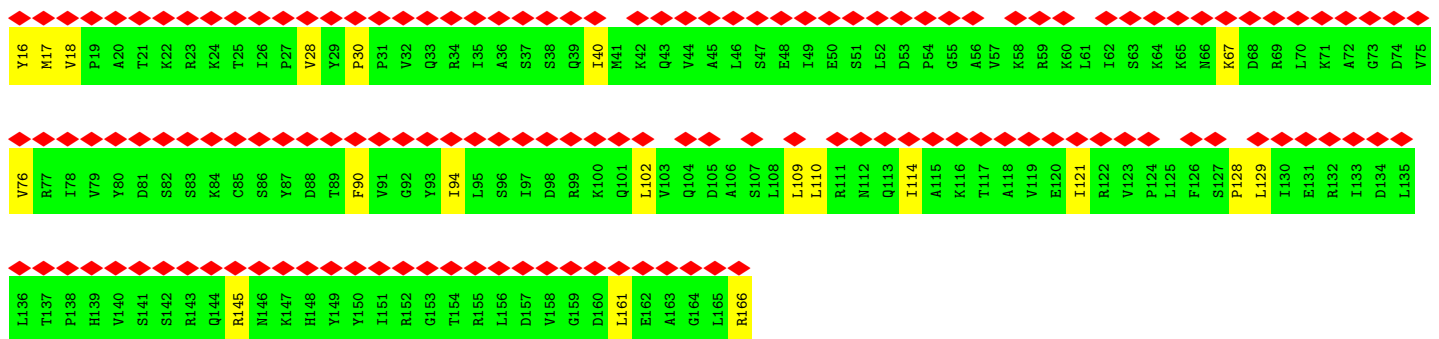
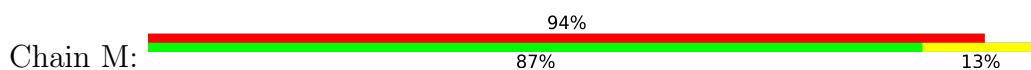


• Molecule 57: Large ribosomal subunit protein bL17m

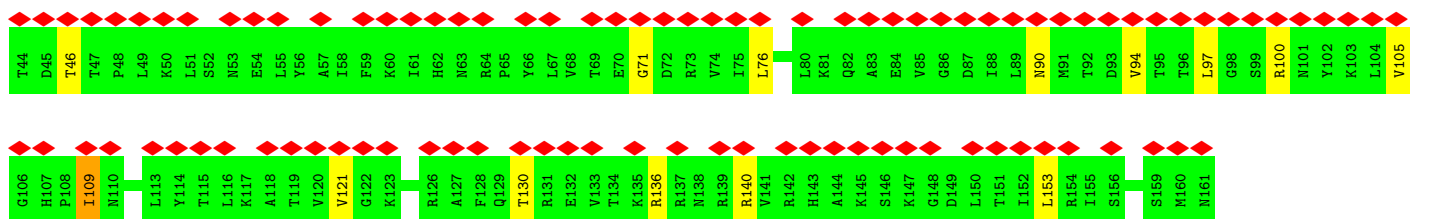
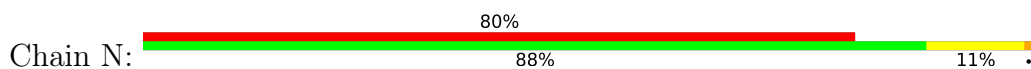




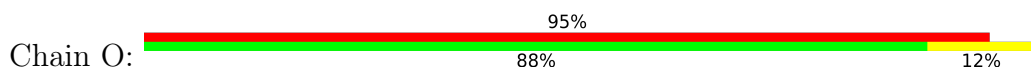
- Molecule 58: Large ribosomal subunit protein bL19m

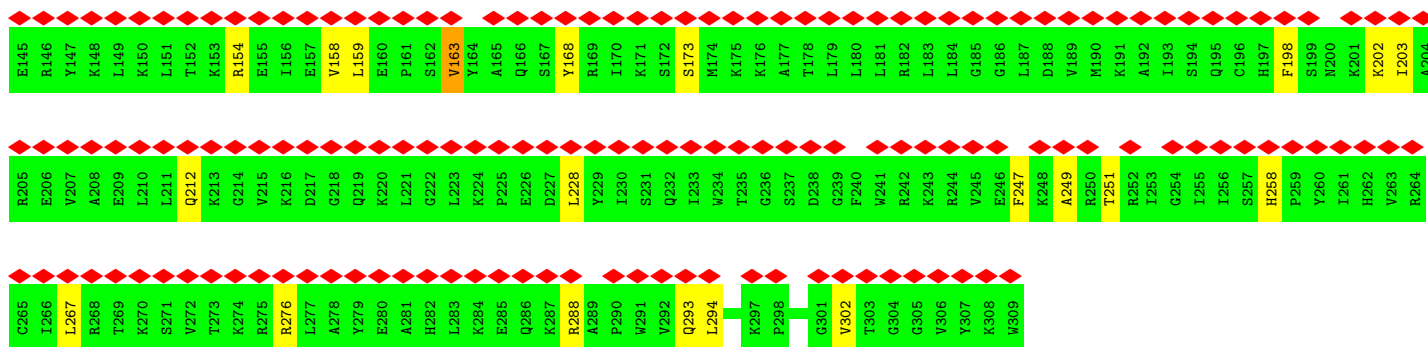


- Molecule 59: Large ribosomal subunit protein bL21m

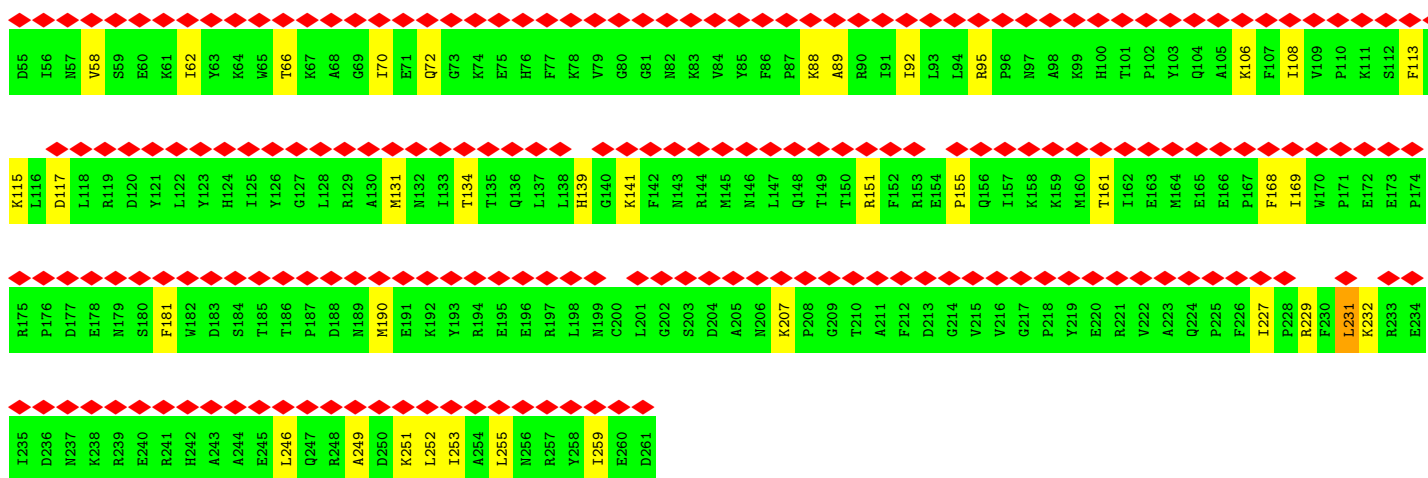
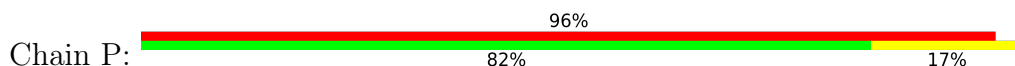


- Molecule 60: Large ribosomal subunit protein uL22m

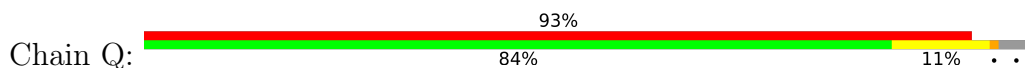




• Molecule 61: Large ribosomal subunit protein uL23m

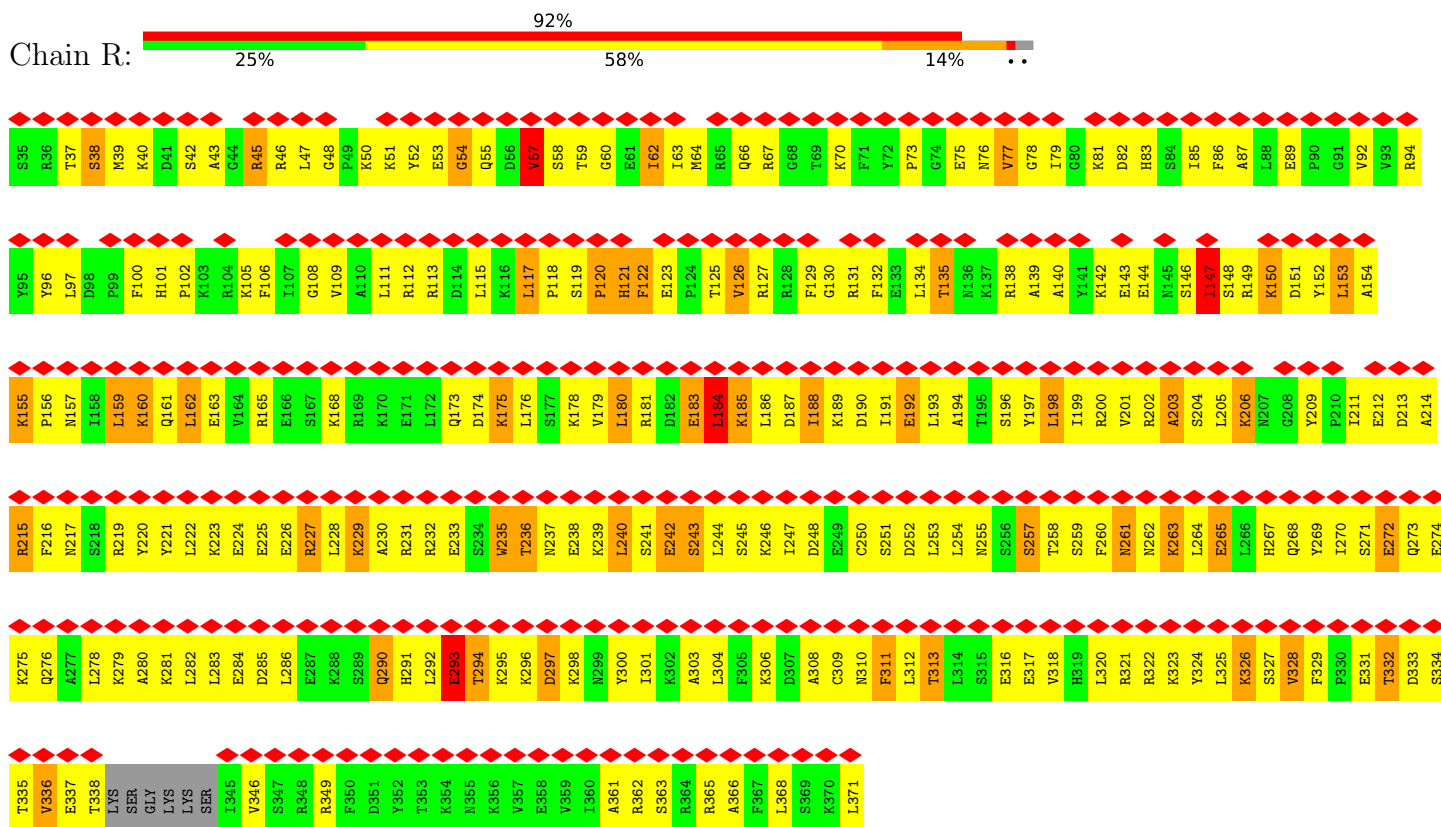


• Molecule 62: Large ribosomal subunit protein uL24m

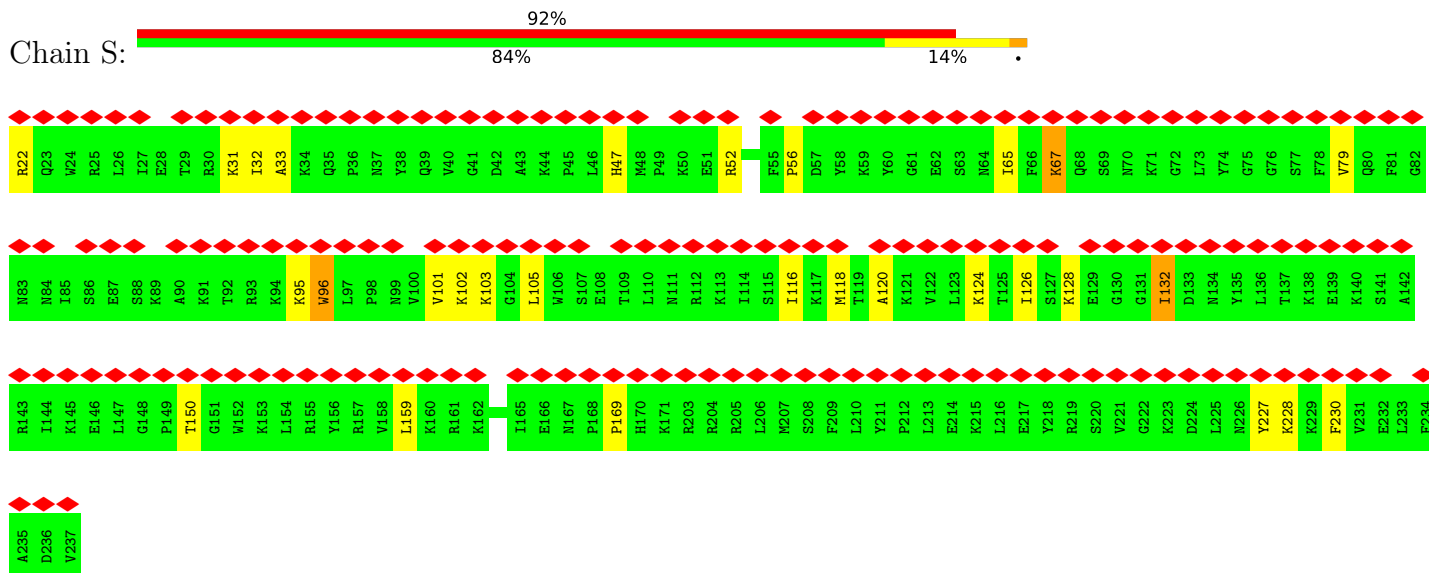




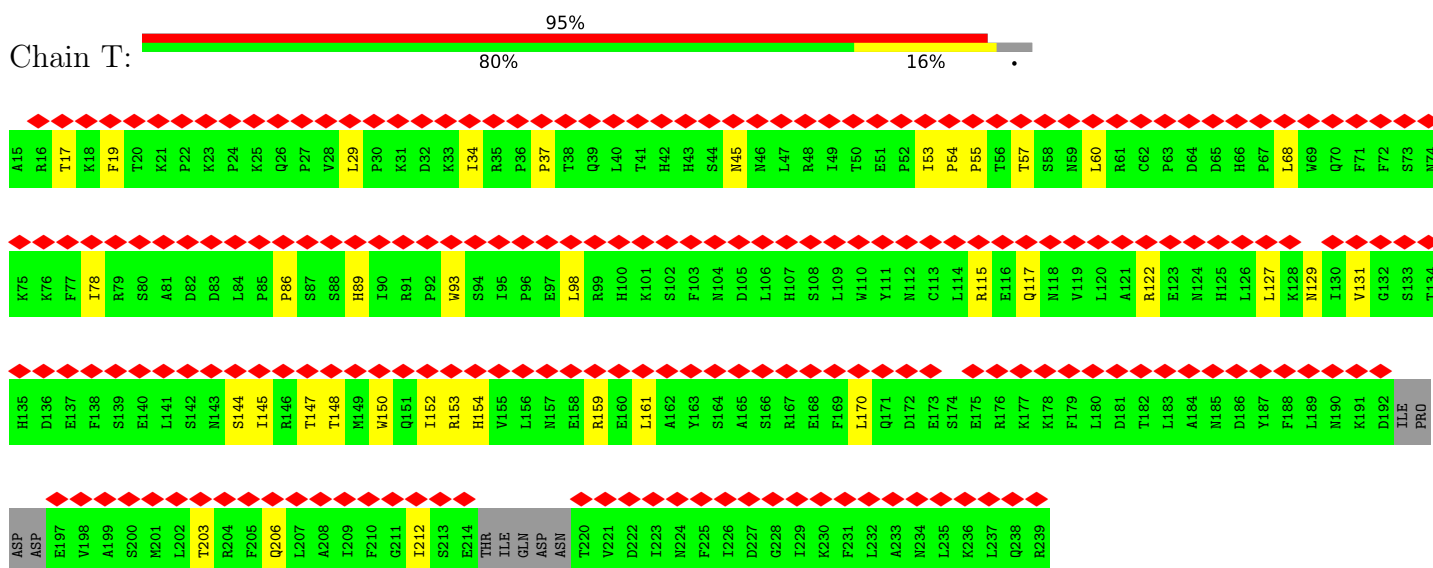
- Molecule 63: Large ribosomal subunit protein bL27m



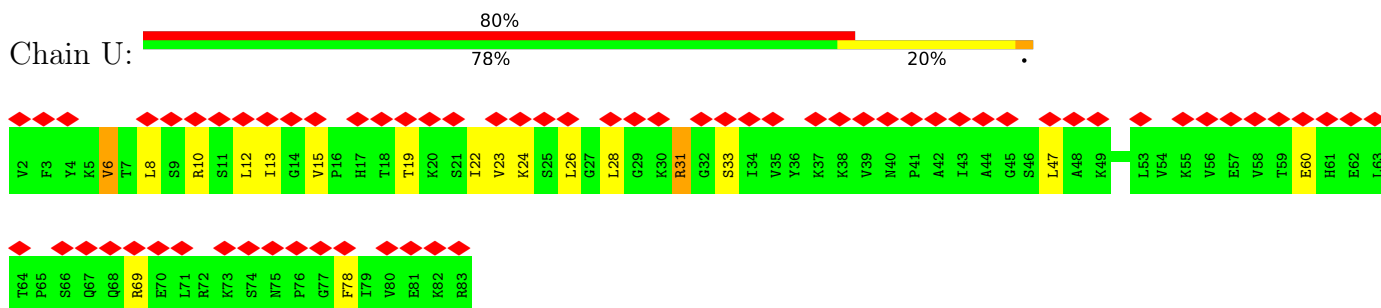
- Molecule 64: MRPS9 isoform 1



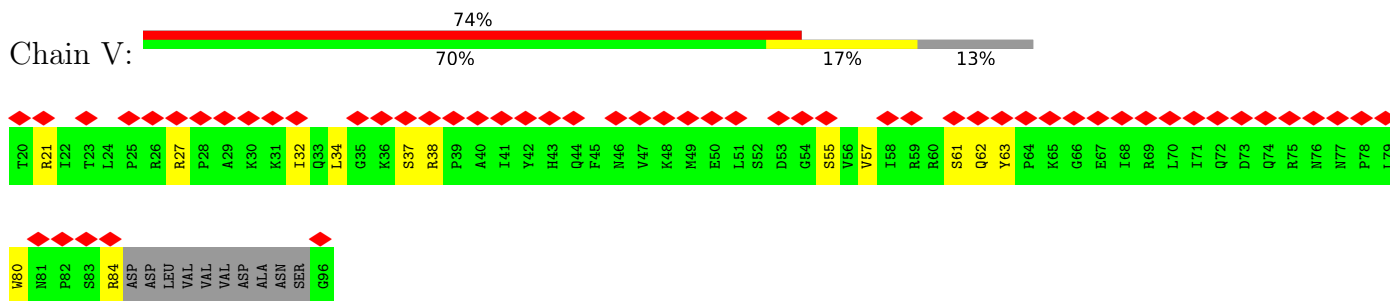
- Molecule 65: Large ribosomal subunit protein uL29m



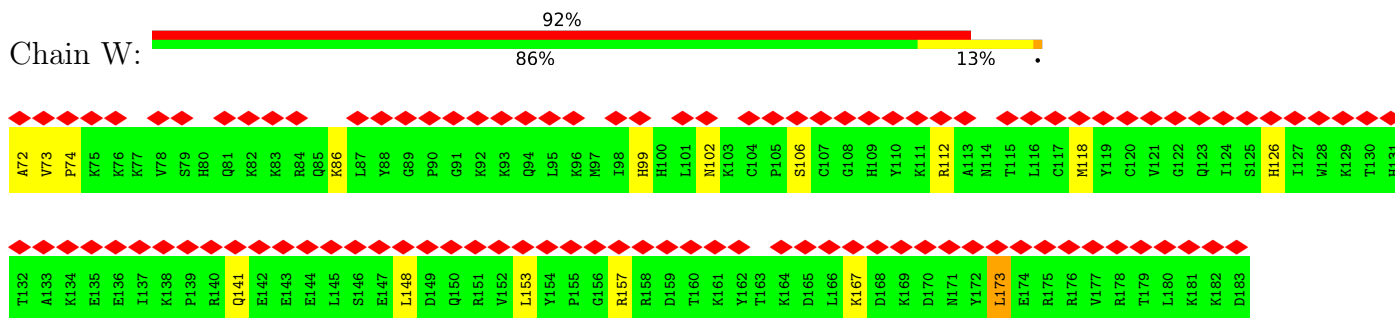
- Molecule 66: Large ribosomal subunit protein uL30m



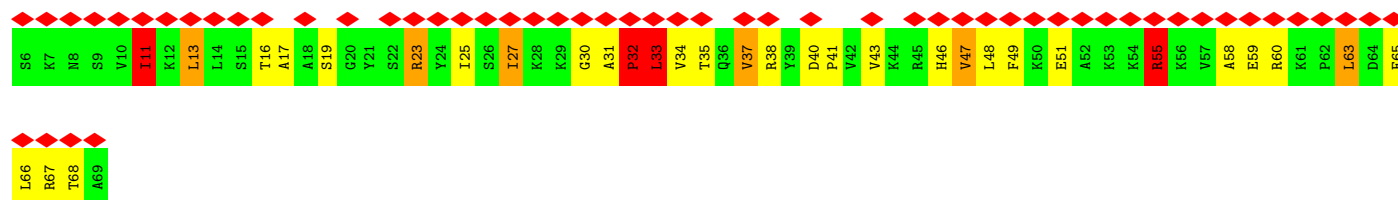
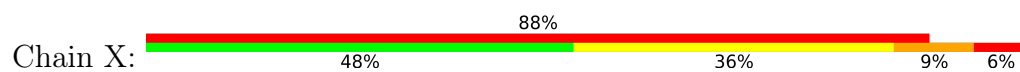
- Molecule 67: Large ribosomal subunit protein bL31m



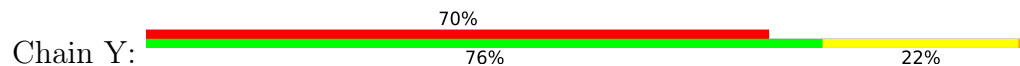
- Molecule 68: Large ribosomal subunit protein bL32m



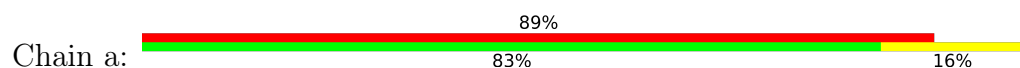
- Molecule 69: Large ribosomal subunit protein bL33m



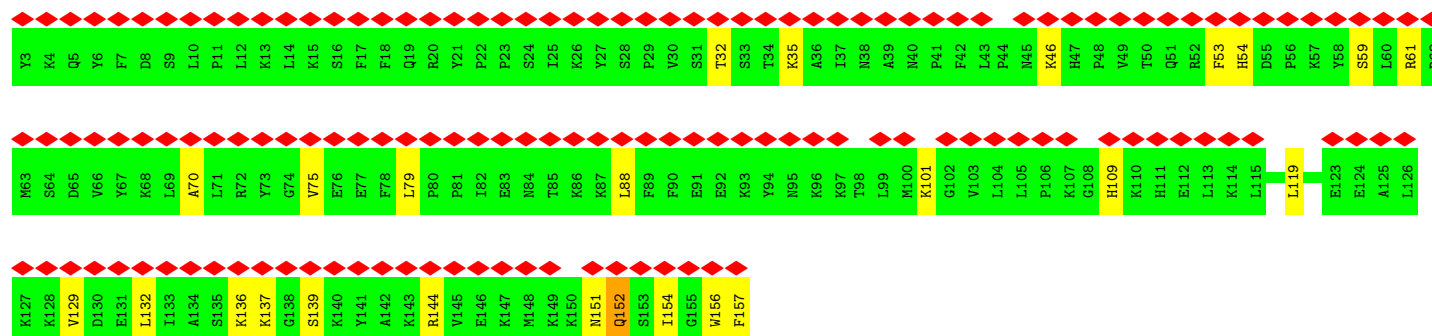
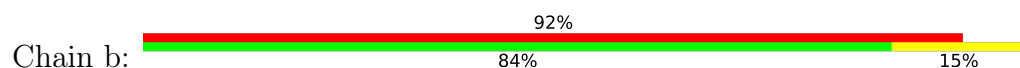
- Molecule 70: Large ribosomal subunit protein bL34m



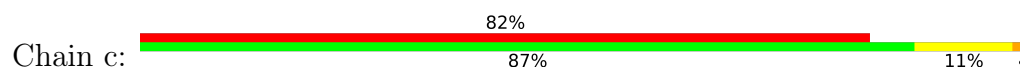
- Molecule 71: Large ribosomal subunit protein mL58

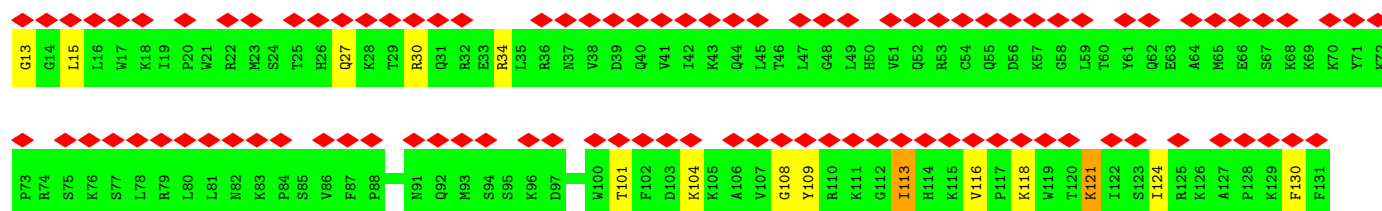


- Molecule 72: Large ribosomal subunit protein mL59

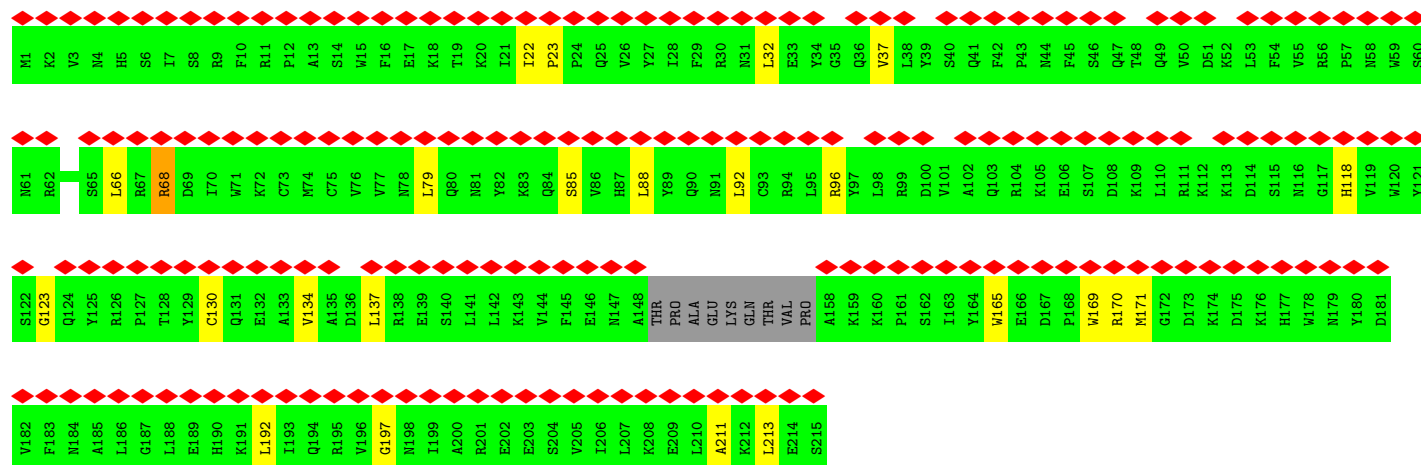
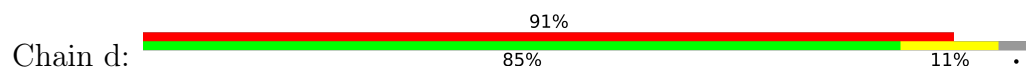


- Molecule 73: Large ribosomal subunit protein mL60

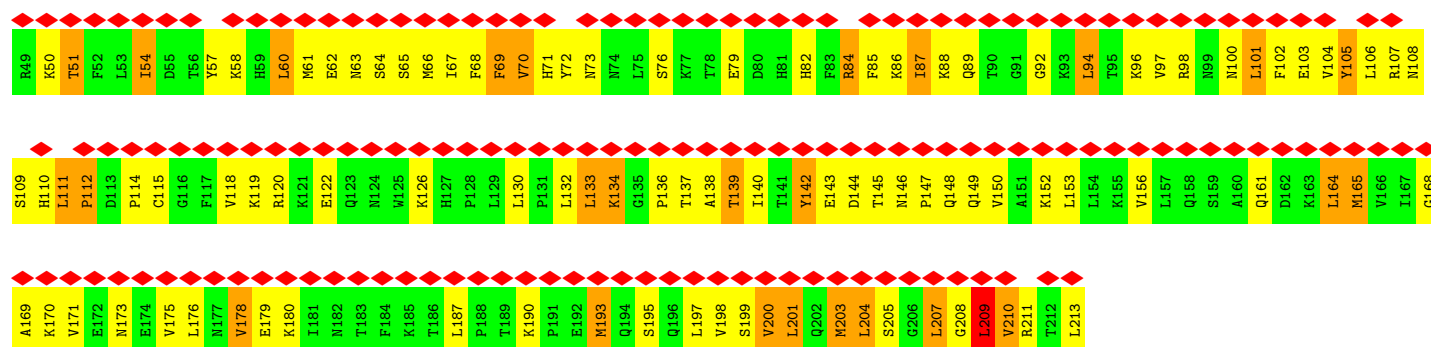




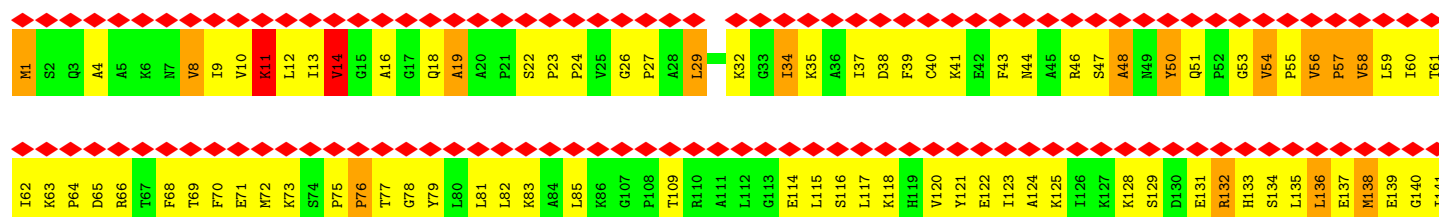
• Molecule 74: Large ribosomal subunit protein mL67



• Molecule 75: Large ribosomal subunit protein uL10m



• Molecule 76: Large ribosomal subunit protein uL11m



V142	K143	S144	I145	V146	G147	V148	A149	K150	S151	M152	G153	I154	K155	V156	V157	P158
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## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	14356	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	60	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	21.532	Depositor
Minimum map value	-14.432	Depositor
Average map value	0.067	Depositor
Map value standard deviation	1.665	Depositor
Recommended contour level	4.3	Depositor
Map size ( $\text{\AA}$ )	427.52, 427.52, 427.52	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	0.835, 0.835, 0.835	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z  > 5$	RMSZ	# $ Z  > 5$
1	AA	0.85	0/304	1.22	0/386
2	AB	0.78	0/825	1.03	3/1101 (0.3%)
3	AC	0.89	0/2130	1.21	1/2891 (0.0%)
4	AD	0.90	0/2472	1.23	3/3338 (0.1%)
5	AE	0.83	0/2490	1.23	31/3372 (0.9%)
6	AF	0.88	0/2130	1.18	4/2867 (0.1%)
7	AG	0.88	0/1974	1.19	1/2668 (0.0%)
8	AH	0.92	0/1915	1.21	1/2559 (0.0%)
9	AI	0.94	0/3309	1.13	19/4472 (0.4%)
10	AJ	0.79	0/788	1.10	2/1052 (0.2%)
11	AK	0.94	0/2268	1.13	2/3058 (0.1%)
12	AL	0.57	0/35625	0.81	13/55407 (0.0%)
13	AM	0.74	0/1805	0.94	0/2811
14	AN	0.72	0/301	1.12	1/466 (0.2%)
15	Z	0.89	0/702	1.23	5/945 (0.5%)
16	g	0.92	0/1610	1.15	2/2168 (0.1%)
17	h	0.89	0/2138	1.27	2/2903 (0.1%)
18	i	0.88	0/2503	1.14	0/3375
19	j	0.91	0/2435	1.16	1/3281 (0.0%)
20	k	0.88	0/2350	1.20	6/3165 (0.2%)
21	l	0.98	0/1068	1.15	2/1430 (0.1%)
22	m	1.01	0/1305	1.21	10/1763 (0.6%)
23	n	0.73	0/1240	1.19	1/1670 (0.1%)
24	o	0.67	0/1855	1.00	0/2492
25	p	0.89	0/1140	1.16	0/1547
26	q	1.04	2/1228 (0.2%)	1.10	5/1638 (0.3%)
27	r	0.91	0/963	1.17	6/1289 (0.5%)
28	s	0.91	0/943	1.27	0/1256
29	t	0.94	1/961 (0.1%)	1.18	3/1285 (0.2%)
30	u	1.00	0/2094	1.10	7/2796 (0.3%)
31	v	0.88	0/845	1.11	1/1143 (0.1%)
32	w	0.91	0/1694	1.17	10/2252 (0.4%)
33	x	0.90	0/749	1.26	8/998 (0.8%)
34	y	0.92	0/652	1.16	1/882 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
35	z	0.87	0/771	1.19	5/1019 (0.5%)
36	0	0.42	0/329	0.56	0/432
37	1	0.47	0/2949	0.84	0/3998
38	2	0.44	0/963	0.94	0/1295
39	3	0.48	0/1072	0.79	0/1442
40	4	0.46	0/1138	0.88	0/1526
41	5	0.45	0/2604	0.92	1/3526 (0.0%)
42	6	0.48	0/1978	0.83	0/2664
43	7	0.51	0/873	0.84	0/1170
44	8	0.46	0/1659	0.95	0/2230
45	9	0.48	0/1616	0.95	0/2177
46	A	0.45	0/68487	0.75	117/106545 (0.1%)
47	B	0.80	0/2573	1.18	3/3456 (0.1%)
48	C	0.49	0/1975	0.79	0/2657
49	D	0.51	0/2031	0.91	0/2751
50	E	0.48	0/2244	0.82	1/3033 (0.0%)
51	F	0.50	0/1551	0.82	0/2093
52	G	0.44	0/628	0.88	0/844
53	H	0.48	0/1302	0.90	0/1749
54	I	0.46	0/962	0.80	0/1285
55	J	0.62	0/1783	1.03	1/2384 (0.0%)
56	K	0.51	0/1606	0.91	0/2148
57	L	0.45	0/1845	0.95	0/2489
58	M	0.51	0/1224	0.83	0/1651
59	N	0.46	0/961	0.75	0/1295
60	O	0.45	0/1859	0.89	0/2495
61	P	0.44	0/1773	0.88	0/2390
62	Q	0.50	0/2323	0.83	0/3135
63	R	0.96	1/2783 (0.0%)	1.12	20/3723 (0.5%)
64	S	0.48	0/1576	0.88	0/2104
65	T	0.49	0/1837	0.96	0/2486
66	U	0.60	0/648	0.89	2/870 (0.2%)
67	V	0.48	0/553	0.68	0/742
68	W	0.44	0/955	0.83	0/1273
69	X	0.93	0/520	1.25	0/696
70	Y	0.43	0/392	0.98	0/515
71	a	0.48	0/1471	0.97	0/1976
72	b	0.45	0/1333	0.92	0/1783
73	c	0.46	0/1028	0.91	0/1372
74	d	0.44	0/1791	0.90	0/2415
75	e	0.96	0/1367	1.13	0/1844
76	f	0.97	0/1051	1.21	1/1416 (0.1%)
All	All	0.63	4/215195 (0.0%)	0.91	302/311820 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	AB	0	2
3	AC	0	3
4	AD	0	5
5	AE	0	2
6	AF	0	4
7	AG	0	6
8	AH	0	5
9	AI	0	2
10	AJ	0	2
11	AK	0	7
16	g	0	3
17	h	0	5
19	j	0	8
20	k	0	1
21	l	0	1
22	m	0	1
24	o	0	6
25	p	0	1
27	r	0	2
28	s	0	2
29	t	0	2
30	u	0	2
31	v	0	1
33	x	0	1
34	y	0	3
47	B	0	15
48	C	0	1
55	J	0	1
56	K	0	1
63	R	0	1
69	X	0	3
75	e	0	1
76	f	0	1
All	All	0	101

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
63	R	148	SER	CA-C	-6.41	1.49	1.52

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	q	147	THR	CA-C	-5.11	1.46	1.52
26	q	142	GLU	CA-C	-5.09	1.46	1.52
29	t	47	ASN	CA-C	5.07	1.59	1.53

The worst 5 of 302 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	A	2067	A	P-O3'-C3'	-15.91	96.34	120.20
46	A	2072	U	P-O3'-C3'	-15.35	97.17	120.20
46	A	2018	C	P-O3'-C3'	-13.27	100.30	120.20
46	A	2023	U	P-O3'-C3'	-12.84	100.95	120.20
46	A	2064	G	P-O3'-C3'	-12.74	101.08	120.20

There are no chirality outliers.

5 of 101 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	AB	117	ARG	Sidechain
2	AB	50	ARG	Sidechain
3	AC	142	ARG	Sidechain
3	AC	240	ARG	Sidechain
3	AC	259	ARG	Sidechain

## 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	304	0	357	72	0
2	AB	808	0	809	170	0
3	AC	2079	0	2056	493	0
4	AD	2422	0	2393	387	0
5	AE	2432	0	2479	462	0
6	AF	2079	0	2101	514	0
7	AG	1931	0	1922	631	0
8	AH	1887	0	1996	534	0
9	AI	3243	0	3339	493	0
10	AJ	774	0	818	216	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	AK	2212	0	2173	581	0
12	AL	31820	0	15952	3213	0
13	AM	1615	0	821	117	0
14	AN	270	0	143	34	0
15	Z	687	0	719	217	0
16	g	1577	0	1608	525	0
17	h	2095	0	2101	464	0
18	i	2461	0	2449	602	0
19	j	2370	0	2428	362	0
20	k	2297	0	2317	427	0
21	l	1055	0	1127	338	0
22	m	1282	0	1337	314	0
23	n	1221	0	1289	150	0
24	o	1820	0	1902	381	0
25	p	1108	0	1112	358	0
26	q	1208	0	1262	297	0
27	r	949	0	1003	143	0
28	s	930	0	984	208	0
29	t	942	0	991	256	0
30	u	2070	0	2138	382	0
31	v	830	0	890	252	0
32	w	1683	0	1769	359	0
33	x	738	0	771	279	0
34	y	636	0	654	162	0
35	z	760	0	789	189	0
36	0	324	0	347	14	0
37	1	2875	0	2881	58	0
38	2	944	0	969	45	0
39	3	1046	0	1071	34	0
40	4	1117	0	1142	21	0
41	5	2552	0	2600	46	0
42	6	1932	0	1950	22	0
43	7	858	0	908	9	0
44	8	1629	0	1633	11	0
45	9	1587	0	1628	17	0
46	A	61141	0	30663	4502	0
47	B	2527	0	2649	249	0
48	C	1932	0	1969	108	0
49	D	1991	0	2032	31	0
50	E	2187	0	2203	82	0
51	F	1524	0	1587	41	0
52	G	617	0	626	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
53	H	1275	0	1310	19	0
54	I	956	0	1037	19	0
55	J	1746	0	1840	88	0
56	K	1573	0	1629	56	0
57	L	1817	0	1878	23	0
58	M	1206	0	1283	29	0
59	N	948	0	1006	8	0
60	O	1826	0	1933	18	0
61	P	1729	0	1724	50	0
62	Q	2272	0	2334	31	0
63	R	2738	0	2811	388	0
64	S	1543	0	1621	36	0
65	T	1792	0	1782	28	0
66	U	639	0	699	12	0
67	V	543	0	568	35	0
68	W	937	0	978	19	0
69	X	512	0	563	65	0
70	Y	385	0	423	15	0
71	a	1440	0	1473	34	0
72	b	1299	0	1367	34	0
73	c	1004	0	1065	20	0
74	d	1746	0	1743	19	0
75	e	1340	0	1396	174	0
76	f	1032	0	1115	155	0
All	All	201676	0	157435	15269	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 43.

The worst 5 of 15269 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)
16:g:7:LEU:CD1	17:h:189:MET:HE1	1.25	1.65
8:AH:104:ARG:CD	12:AL:143:A:H4'	1.27	1.65
4:AD:208:PHE:CE2	16:g:214:LEU:HB3	1.28	1.64
16:g:7:LEU:HD12	17:h:189:MET:CE	1.28	1.64
3:AC:9:HIS:CE1	17:h:164:ILE:CD1	1.81	1.64

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AA	32/34 (94%)	31 (97%)	1 (3%)	0	100	100
2	AB	93/95 (98%)	71 (76%)	14 (15%)	8 (9%)	0	4
3	AC	257/259 (99%)	208 (81%)	34 (13%)	15 (6%)	1	9
4	AD	299/301 (99%)	219 (73%)	62 (21%)	18 (6%)	1	9
5	AE	296/298 (99%)	215 (73%)	64 (22%)	17 (6%)	1	9
6	AF	248/320 (78%)	182 (73%)	46 (18%)	20 (8%)	1	5
7	AG	234/236 (99%)	197 (84%)	30 (13%)	7 (3%)	3	20
8	AH	232/234 (99%)	192 (83%)	33 (14%)	7 (3%)	3	20
9	AI	403/405 (100%)	319 (79%)	60 (15%)	24 (6%)	1	9
10	AJ	94/96 (98%)	70 (74%)	13 (14%)	11 (12%)	0	1
11	AK	262/264 (99%)	235 (90%)	24 (9%)	3 (1%)	11	39
15	Z	83/91 (91%)	63 (76%)	17 (20%)	3 (4%)	2	17
16	g	190/298 (64%)	158 (83%)	29 (15%)	3 (2%)	7	31
17	h	265/267 (99%)	214 (81%)	39 (15%)	12 (4%)	2	13
18	i	287/320 (90%)	233 (81%)	38 (13%)	16 (6%)	1	9
19	j	281/485 (58%)	255 (91%)	23 (8%)	3 (1%)	11	39
20	k	281/293 (96%)	219 (78%)	52 (18%)	10 (4%)	2	17
21	l	129/131 (98%)	103 (80%)	17 (13%)	9 (7%)	1	7
22	m	159/161 (99%)	136 (86%)	16 (10%)	7 (4%)	2	13
23	n	153/155 (99%)	150 (98%)	3 (2%)	0	100	100
24	o	220/244 (90%)	196 (89%)	17 (8%)	7 (3%)	3	19
25	p	132/134 (98%)	100 (76%)	24 (18%)	8 (6%)	1	9
26	q	150/152 (99%)	115 (77%)	25 (17%)	10 (7%)	1	7
27	r	120/125 (96%)	87 (72%)	25 (21%)	8 (7%)	1	7
28	s	115/120 (96%)	92 (80%)	17 (15%)	6 (5%)	1	11

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	t	111/113 (98%)	99 (89%)	10 (9%)	2 (2%)	6	29
30	u	251/253 (99%)	205 (82%)	35 (14%)	11 (4%)	2	13
31	v	104/106 (98%)	93 (89%)	10 (10%)	1 (1%)	12	40
32	w	194/204 (95%)	156 (80%)	28 (14%)	10 (5%)	1	11
33	x	87/99 (88%)	66 (76%)	13 (15%)	8 (9%)	0	3
34	y	78/80 (98%)	51 (65%)	17 (22%)	10 (13%)	0	1
35	z	90/92 (98%)	72 (80%)	12 (13%)	6 (7%)	1	7
36	0	36/38 (95%)	33 (92%)	3 (8%)	0	100	100
37	1	346/348 (99%)	329 (95%)	17 (5%)	0	100	100
38	2	111/113 (98%)	106 (96%)	5 (4%)	0	100	100
39	3	128/130 (98%)	122 (95%)	6 (5%)	0	100	100
40	4	136/138 (99%)	130 (96%)	6 (4%)	0	100	100
41	5	322/324 (99%)	306 (95%)	16 (5%)	0	100	100
42	6	228/259 (88%)	221 (97%)	7 (3%)	0	100	100
43	7	104/106 (98%)	97 (93%)	7 (7%)	0	100	100
44	8	195/199 (98%)	192 (98%)	3 (2%)	0	100	100
45	9	198/215 (92%)	186 (94%)	12 (6%)	0	100	100
47	B	317/328 (97%)	267 (84%)	41 (13%)	9 (3%)	4	21
48	C	247/249 (99%)	232 (94%)	14 (6%)	1 (0%)	30	60
49	D	250/252 (99%)	236 (94%)	10 (4%)	4 (2%)	7	31
50	E	272/274 (99%)	254 (93%)	15 (6%)	3 (1%)	11	39
51	F	194/196 (99%)	183 (94%)	10 (5%)	1 (0%)	24	55
52	G	72/74 (97%)	70 (97%)	2 (3%)	0	100	100
53	H	158/160 (99%)	152 (96%)	6 (4%)	0	100	100
54	I	123/138 (89%)	114 (93%)	9 (7%)	0	100	100
55	J	218/220 (99%)	193 (88%)	19 (9%)	6 (3%)	4	21
56	K	193/195 (99%)	185 (96%)	8 (4%)	0	100	100
57	L	225/237 (95%)	217 (96%)	8 (4%)	0	100	100
58	M	149/151 (99%)	139 (93%)	10 (7%)	0	100	100
59	N	116/118 (98%)	106 (91%)	10 (9%)	0	100	100
60	O	223/225 (99%)	211 (95%)	12 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
61	P	205/207 (99%)	196 (96%)	9 (4%)	0	100	100
62	Q	280/296 (95%)	268 (96%)	12 (4%)	0	100	100
63	R	327/337 (97%)	269 (82%)	44 (14%)	14 (4%)	2	14
64	S	181/185 (98%)	171 (94%)	10 (6%)	0	100	100
65	T	210/225 (93%)	199 (95%)	11 (5%)	0	100	100
66	U	80/82 (98%)	78 (98%)	2 (2%)	0	100	100
67	V	63/76 (83%)	61 (97%)	2 (3%)	0	100	100
68	W	110/112 (98%)	105 (96%)	5 (4%)	0	100	100
69	X	62/64 (97%)	50 (81%)	8 (13%)	4 (6%)	1	8
70	Y	44/46 (96%)	41 (93%)	3 (7%)	0	100	100
71	a	175/177 (99%)	163 (93%)	12 (7%)	0	100	100
72	b	153/155 (99%)	146 (95%)	7 (5%)	0	100	100
73	c	117/119 (98%)	112 (96%)	4 (3%)	1 (1%)	14	43
74	d	202/215 (94%)	189 (94%)	13 (6%)	0	100	100
75	e	163/165 (99%)	131 (80%)	26 (16%)	6 (4%)	2	17
76	f	134/138 (97%)	104 (78%)	20 (15%)	10 (8%)	1	6
All	All	12997/13751 (94%)	11366 (88%)	1292 (10%)	339 (3%)	6	23

5 of 339 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AB	82	GLN
2	AB	95	ARG
3	AC	33	GLY
3	AC	59	GLU
3	AC	170	ASN

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AA	32/32 (100%)	29 (91%)	3 (9%)	8	30
2	AB	86/86 (100%)	73 (85%)	13 (15%)	3	13
3	AC	234/234 (100%)	205 (88%)	29 (12%)	4	19
4	AD	265/265 (100%)	235 (89%)	30 (11%)	5	21
5	AE	266/266 (100%)	213 (80%)	53 (20%)	1	6
6	AF	230/290 (79%)	193 (84%)	37 (16%)	2	12
7	AG	211/211 (100%)	191 (90%)	20 (10%)	8	29
8	AH	211/211 (100%)	173 (82%)	38 (18%)	2	8
9	AI	371/371 (100%)	349 (94%)	22 (6%)	18	46
10	AJ	84/84 (100%)	66 (79%)	18 (21%)	1	5
11	AK	241/241 (100%)	219 (91%)	22 (9%)	9	31
15	Z	78/82 (95%)	65 (83%)	13 (17%)	2	11
16	g	173/267 (65%)	143 (83%)	30 (17%)	2	9
17	h	234/234 (100%)	209 (89%)	25 (11%)	6	24
18	i	287/313 (92%)	231 (80%)	56 (20%)	1	6
19	j	256/436 (59%)	236 (92%)	20 (8%)	11	36
20	k	248/252 (98%)	221 (89%)	27 (11%)	6	23
21	l	120/120 (100%)	110 (92%)	10 (8%)	10	34
22	m	138/138 (100%)	123 (89%)	15 (11%)	6	23
23	n	142/142 (100%)	137 (96%)	5 (4%)	32	58
24	o	196/215 (91%)	178 (91%)	18 (9%)	8	30
25	p	121/121 (100%)	103 (85%)	18 (15%)	3	13
26	q	131/131 (100%)	122 (93%)	9 (7%)	14	41
27	r	103/104 (99%)	94 (91%)	9 (9%)	9	32
28	s	99/100 (99%)	80 (81%)	19 (19%)	1	7
29	t	102/102 (100%)	90 (88%)	12 (12%)	5	20
30	u	220/220 (100%)	207 (94%)	13 (6%)	18	46
31	v	91/91 (100%)	87 (96%)	4 (4%)	25	54
32	w	187/187 (100%)	162 (87%)	25 (13%)	4	16
33	x	80/87 (92%)	64 (80%)	16 (20%)	1	6
34	y	69/69 (100%)	56 (81%)	13 (19%)	1	7
35	z	81/81 (100%)	70 (86%)	11 (14%)	3	16

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	0	36/36 (100%)	36 (100%)	0	100	100
37	1	323/323 (100%)	308 (95%)	15 (5%)	24	53
38	2	106/106 (100%)	100 (94%)	6 (6%)	18	47
39	3	112/112 (100%)	110 (98%)	2 (2%)	51	70
40	4	121/121 (100%)	116 (96%)	5 (4%)	27	55
41	5	284/284 (100%)	278 (98%)	6 (2%)	47	67
42	6	213/236 (90%)	203 (95%)	10 (5%)	23	52
43	7	95/95 (100%)	90 (95%)	5 (5%)	20	49
44	8	182/182 (100%)	174 (96%)	8 (4%)	25	54
45	9	176/186 (95%)	168 (96%)	8 (4%)	24	53
47	B	272/277 (98%)	236 (87%)	36 (13%)	4	17
48	C	210/210 (100%)	197 (94%)	13 (6%)	16	45
49	D	218/218 (100%)	196 (90%)	22 (10%)	7	26
50	E	242/242 (100%)	227 (94%)	15 (6%)	16	45
51	F	172/172 (100%)	167 (97%)	5 (3%)	37	62
52	G	68/68 (100%)	65 (96%)	3 (4%)	25	54
53	H	138/138 (100%)	131 (95%)	7 (5%)	21	50
54	I	108/117 (92%)	104 (96%)	4 (4%)	30	58
55	J	181/181 (100%)	167 (92%)	14 (8%)	12	37
56	K	167/167 (100%)	151 (90%)	16 (10%)	8	29
57	L	203/211 (96%)	195 (96%)	8 (4%)	28	56
58	M	136/136 (100%)	131 (96%)	5 (4%)	30	58
59	N	107/107 (100%)	102 (95%)	5 (5%)	23	52
60	O	200/200 (100%)	187 (94%)	13 (6%)	15	43
61	P	185/185 (100%)	180 (97%)	5 (3%)	39	63
62	Q	256/267 (96%)	244 (95%)	12 (5%)	23	52
63	R	303/308 (98%)	270 (89%)	33 (11%)	6	23
64	S	167/167 (100%)	157 (94%)	10 (6%)	17	46
65	T	204/213 (96%)	197 (97%)	7 (3%)	32	59
66	U	73/73 (100%)	68 (93%)	5 (7%)	14	42
67	V	60/69 (87%)	58 (97%)	2 (3%)	33	59

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
68	W	104/104 (100%)	102 (98%)	2 (2%)	50	68
69	X	56/56 (100%)	45 (80%)	11 (20%)	1	6
70	Y	40/40 (100%)	39 (98%)	1 (2%)	42	64
71	a	158/158 (100%)	150 (95%)	8 (5%)	21	50
72	b	144/144 (100%)	138 (96%)	6 (4%)	26	55
73	c	110/110 (100%)	108 (98%)	2 (2%)	51	70
74	d	191/199 (96%)	186 (97%)	5 (3%)	40	64
75	e	154/154 (100%)	127 (82%)	27 (18%)	2	9
76	f	113/113 (100%)	96 (85%)	17 (15%)	3	13
All	All	11775/12268 (96%)	10738 (91%)	1037 (9%)	11	32

5 of 1037 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
63	R	278	LEU
66	U	24	LYS
63	R	272	GLU
18	i	244	LEU
18	i	187	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 301 such sidechains are listed below:

Mol	Chain	Res	Type
47	B	179	HIS
71	a	96	GLN
48	C	209	GLN
56	K	39	HIS
75	e	196	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
12	AL	1487/1498 (99%)	622 (41%)	140 (9%)
13	AM	75/76 (98%)	46 (61%)	8 (10%)
14	AN	13/13 (100%)	10 (76%)	6 (46%)
46	A	2849/2876 (99%)	978 (34%)	184 (6%)
All	All	4424/4463 (99%)	1656 (37%)	338 (7%)

5 of 1656 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
12	AL	14	A
12	AL	15	A
12	AL	16	G
12	AL	20	A
12	AL	39	A

5 of 338 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
46	A	1331	A
46	A	2204	A
46	A	1489	U
46	A	1818	G
46	A	2437	U

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

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

## 5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

There are no ligands in this entry.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
46	A	22

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Mol	Chain	Number of breaks
12	AL	17
32	w	4
44	8	1
76	f	1
64	S	1

The worst 5 of 46 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	1418:U	O3'	1423:A	P	30.32
1	8	52:GLN	C	81:LYS	N	26.49
1	A	2100:U	O3'	2183:A	P	21.91
1	AL	563:U	O3'	600:A	P	20.02
1	AL	210:U	O3'	214:A	P	18.58

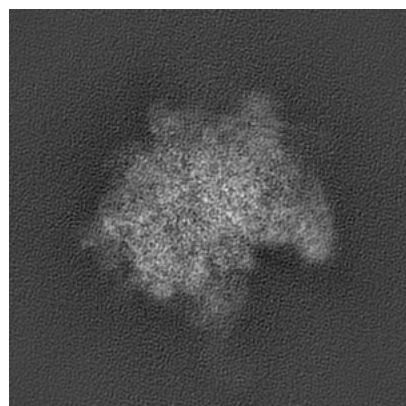
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42687. These allow visual inspection of the internal detail of the map and identification of artifacts.

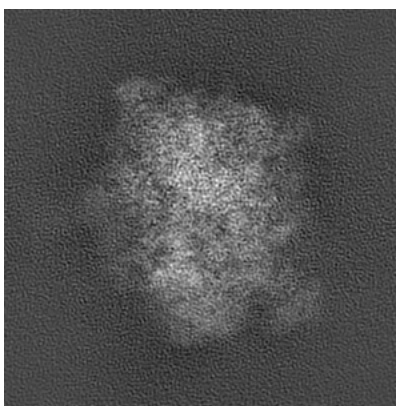
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

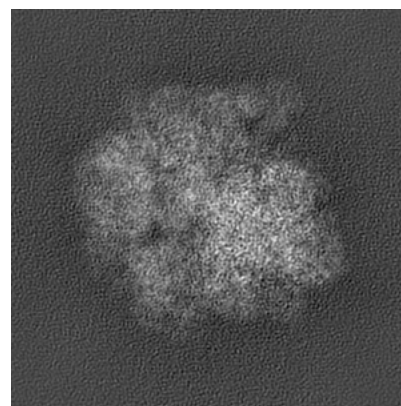
#### 6.1.1 Primary map



X

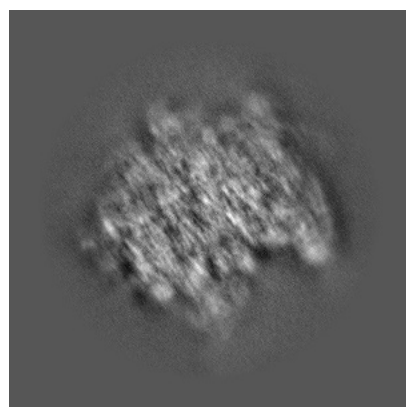


Y

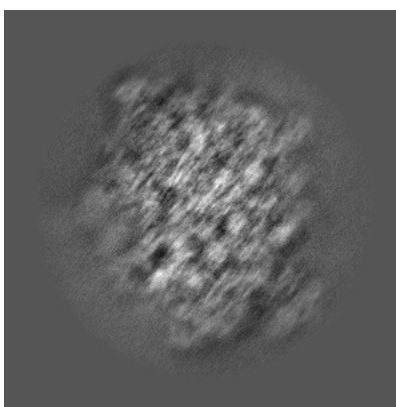


Z

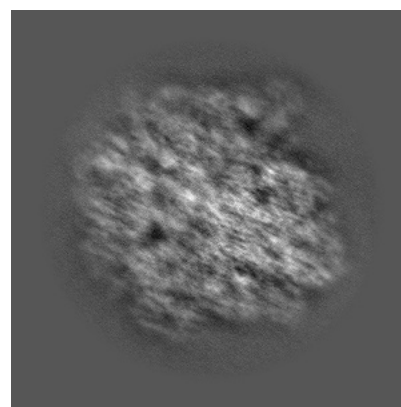
#### 6.1.2 Raw map



X



Y



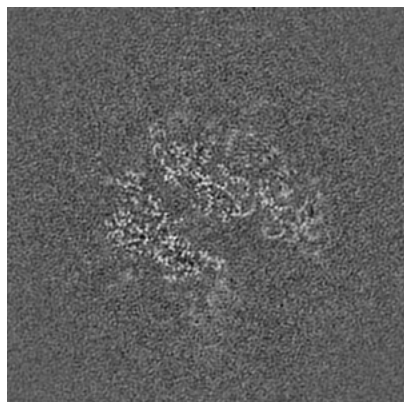
Z

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

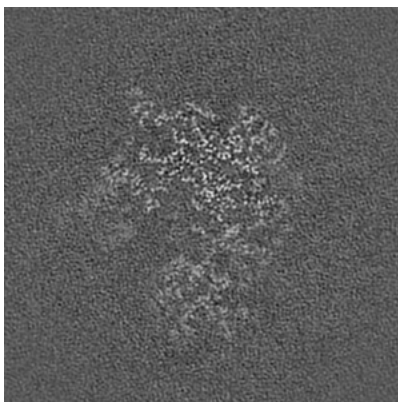


## 6.2 Central slices [i](#)

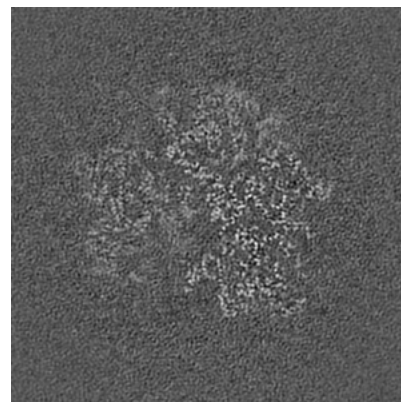
### 6.2.1 Primary map



X Index: 256

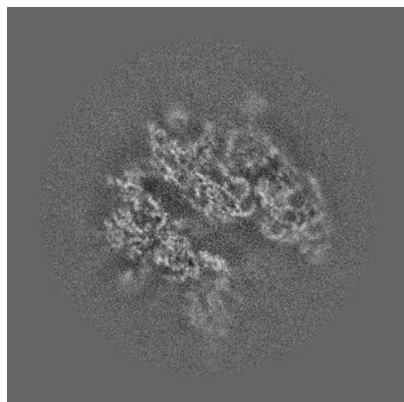


Y Index: 256

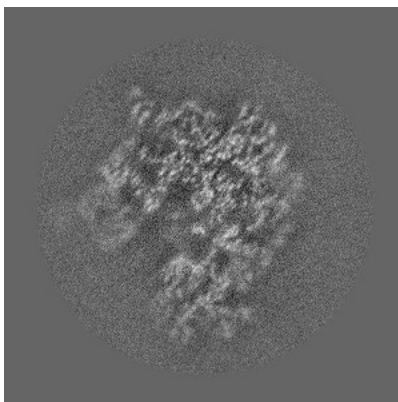


Z Index: 256

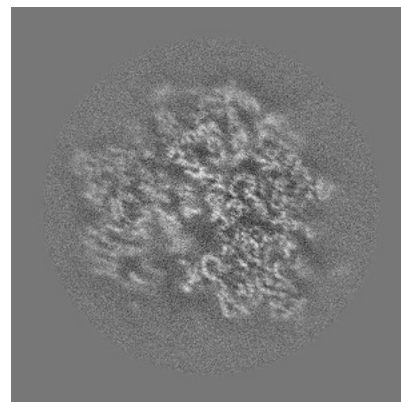
### 6.2.2 Raw map



X Index: 256



Y Index: 256

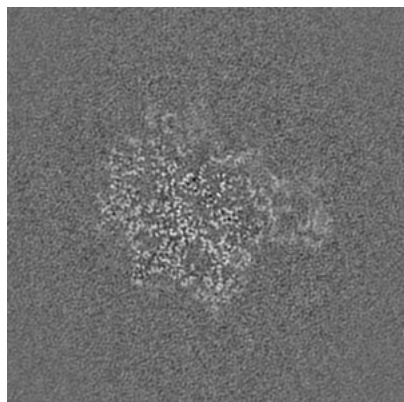


Z Index: 256

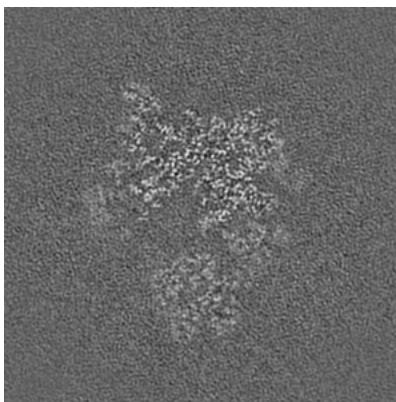
The images above show central slices of the map in three orthogonal directions.

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

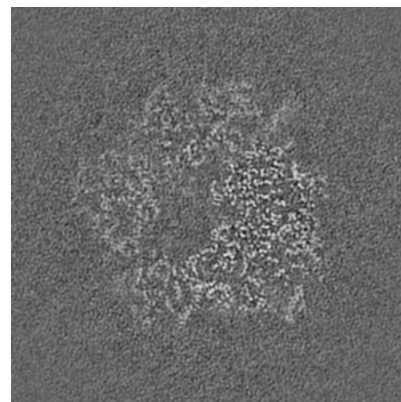
### 6.3.1 Primary map



X Index: 296

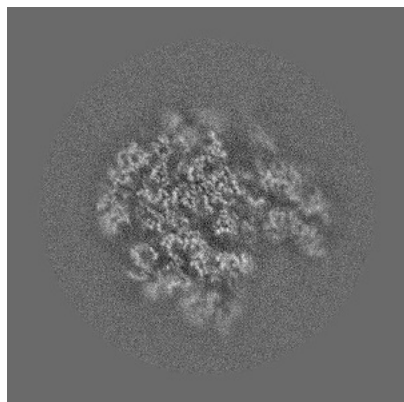


Y Index: 249

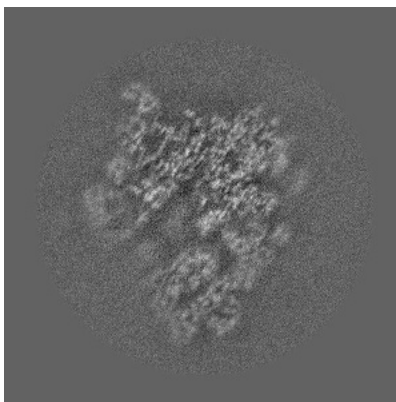


Z Index: 238

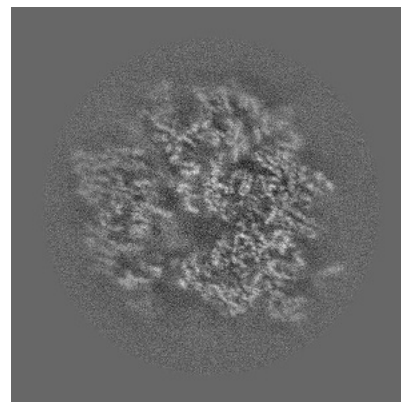
### 6.3.2 Raw map



X Index: 276



Y Index: 249

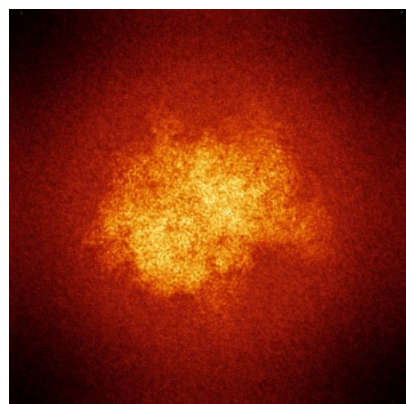


Z Index: 250

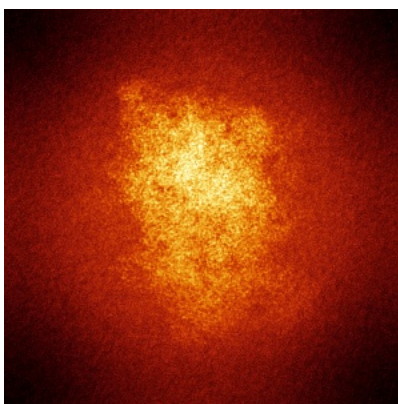
The images above show the largest variance slices of the map in three orthogonal directions.

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

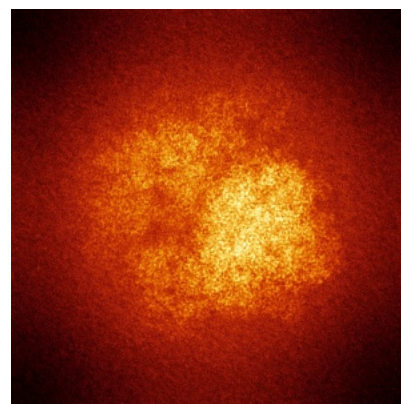
### 6.4.1 Primary map



X

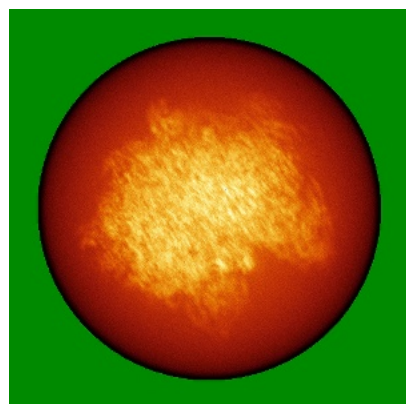


Y

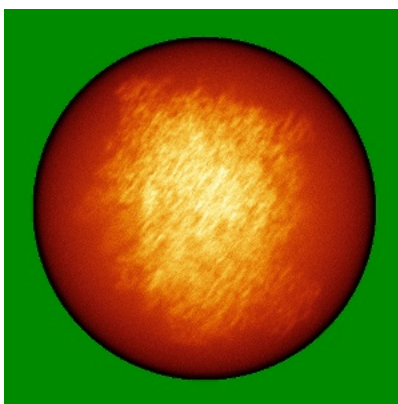


Z

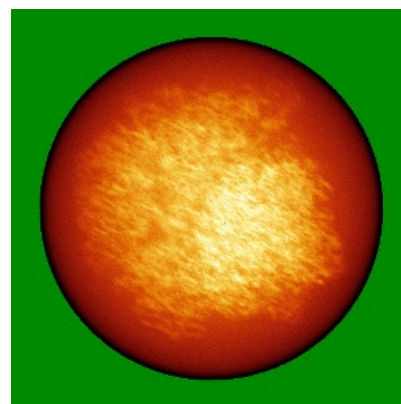
### 6.4.2 Raw map



X



Y



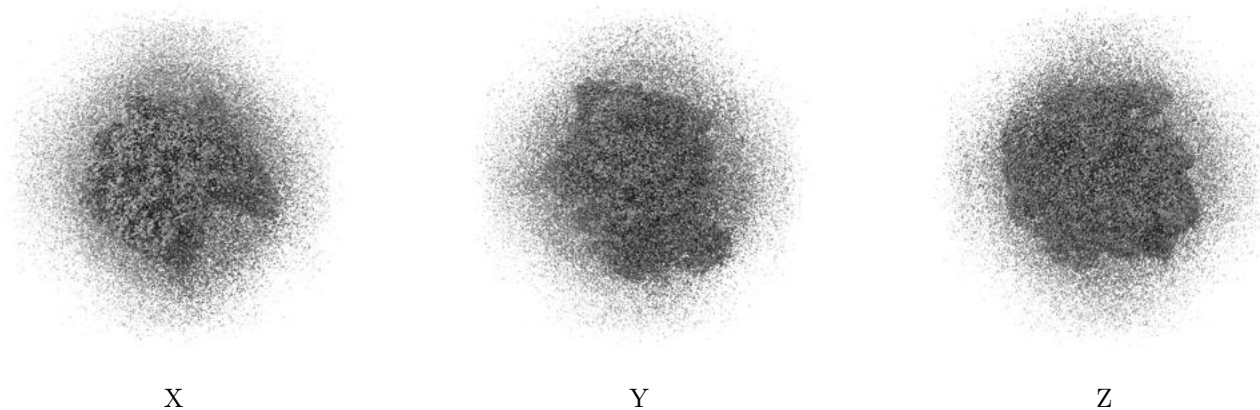
Z

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



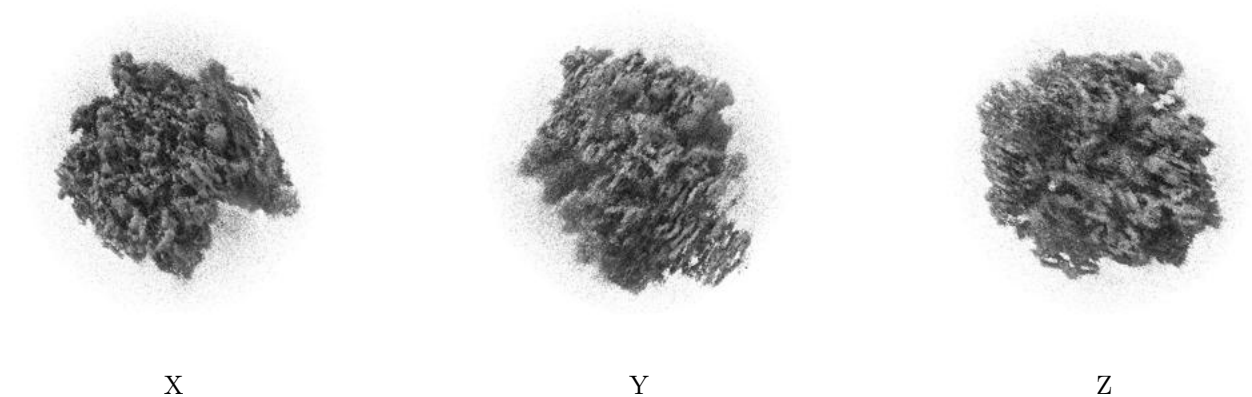
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 4.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



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

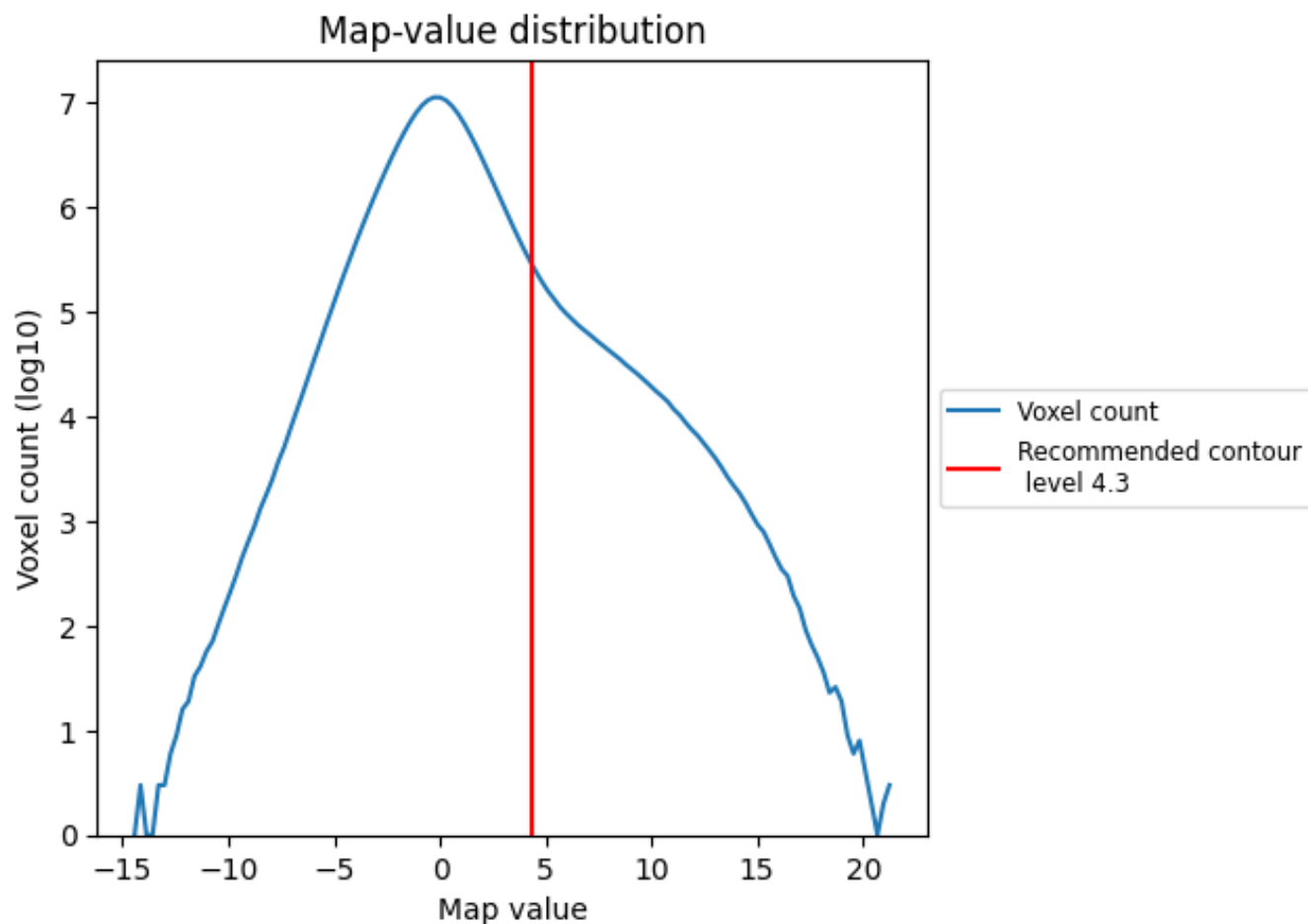
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

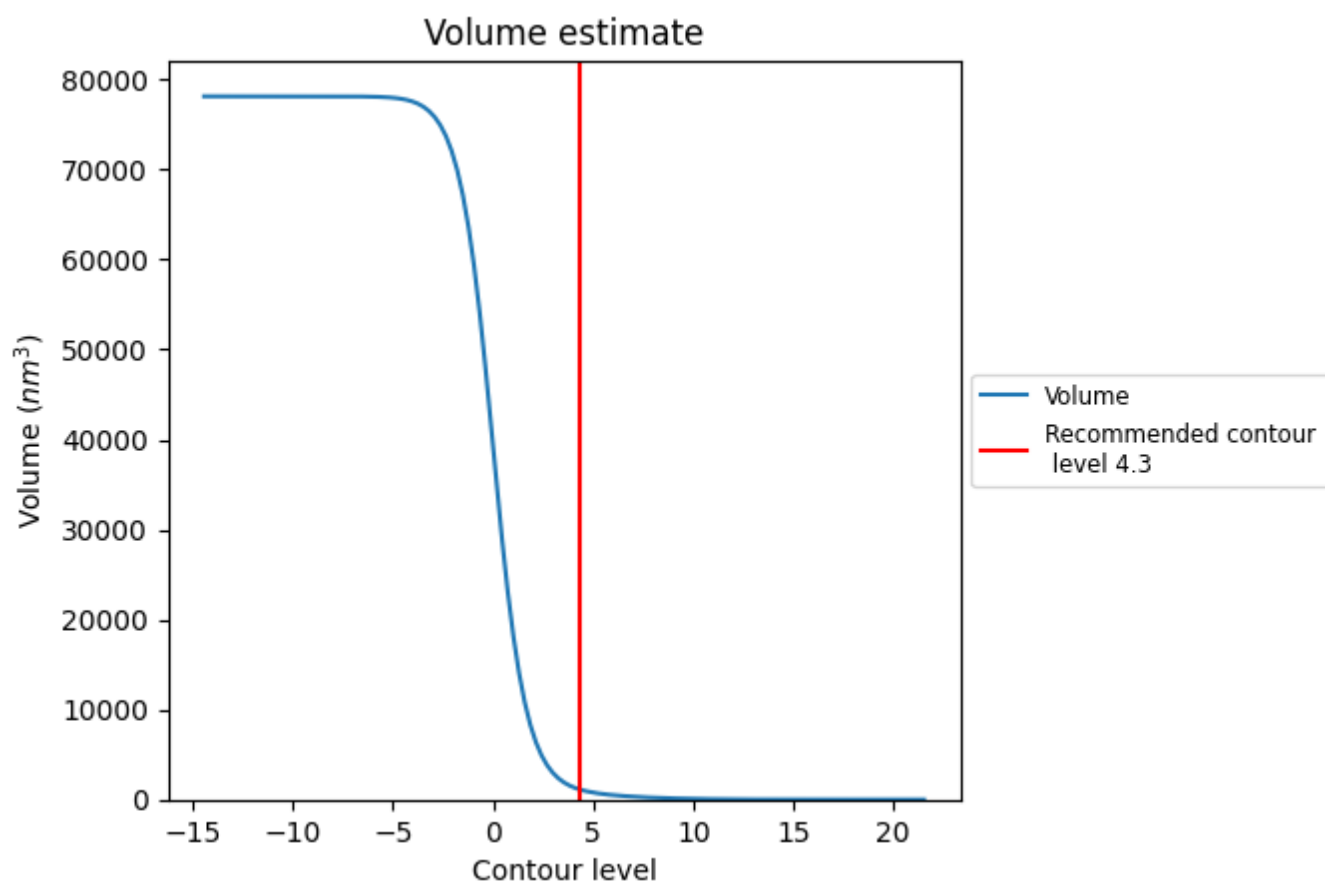
This section contains the results of statistical analysis of the map.

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



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

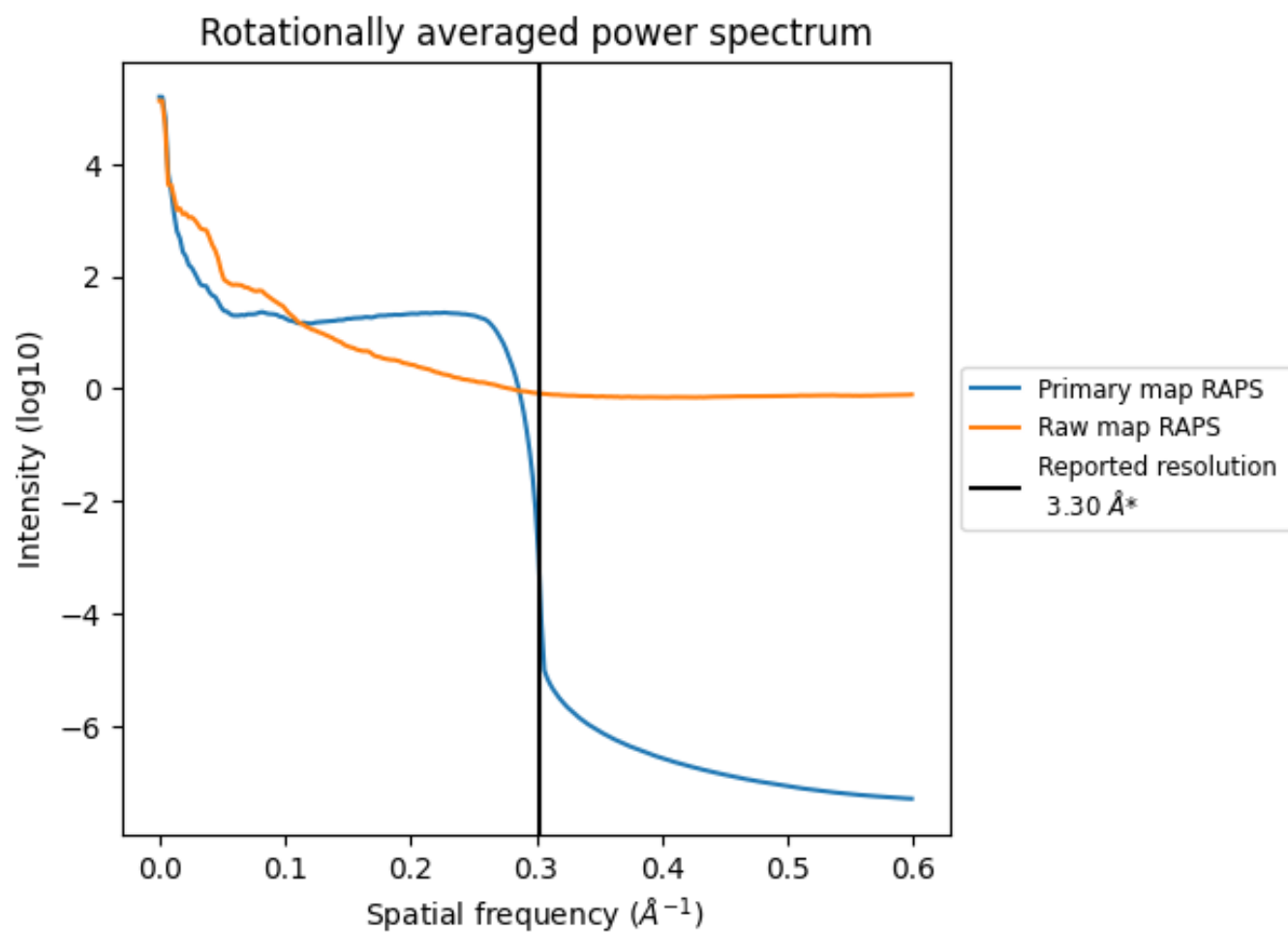
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1149 nm<sup>3</sup>; this corresponds to an approximate mass of 1038 kDa.

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

### 7.3 Rotationally averaged power spectrum ⓘ

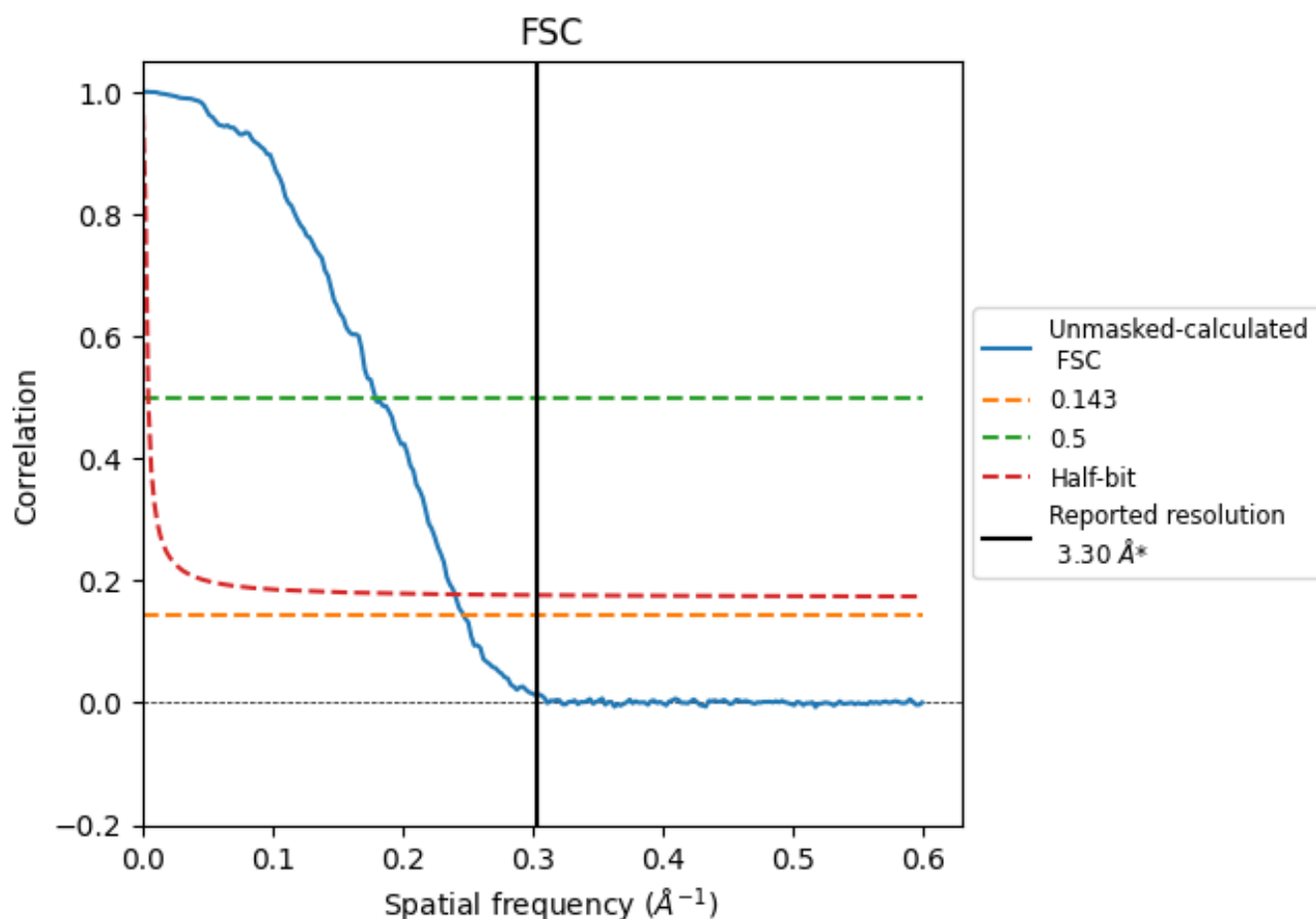


\*Reported resolution corresponds to spatial frequency of 0.303  $\text{\AA}^{-1}$

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.303 Å<sup>-1</sup>



## 8.2 Resolution estimates [i](#)

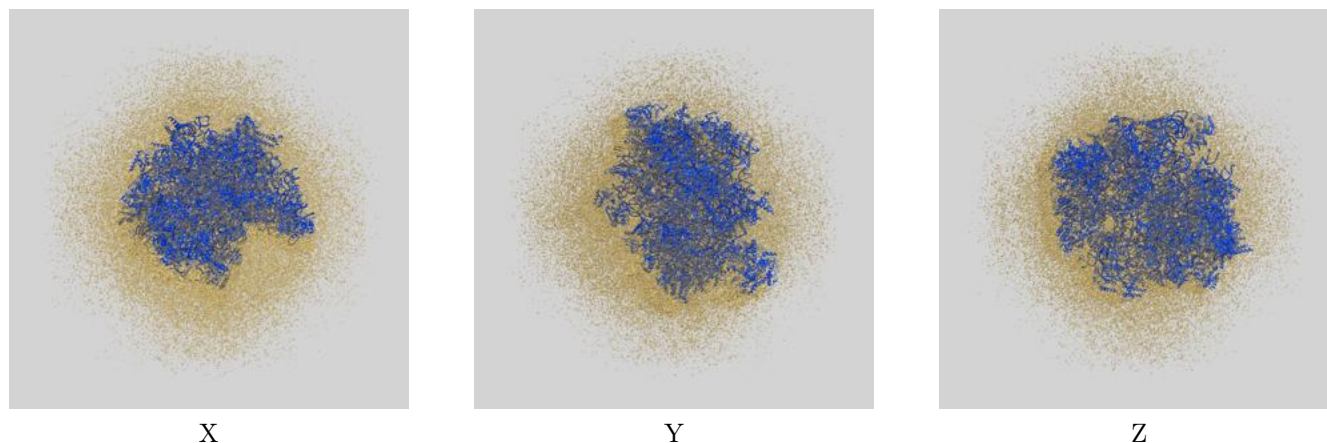
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.05	5.59	4.17

\*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 4.05 differs from the reported value 3.3 by more than 10 %

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

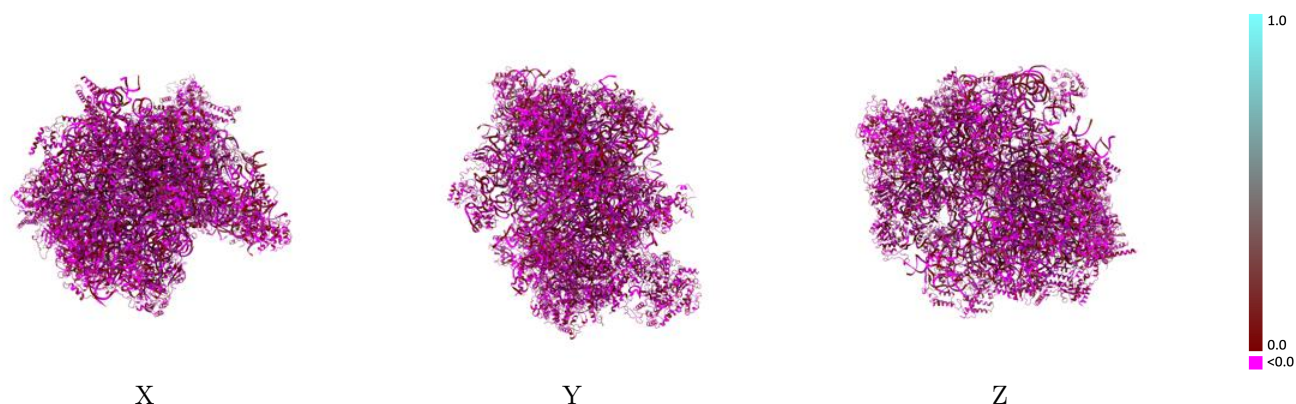
This section contains information regarding the fit between EMDB map EMD-42687 and PDB model 8UX4. Per-residue inclusion information can be found in [section 3](#) on [page 17](#).

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



The images above show the 3D surface view of the map at the recommended contour level 4.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

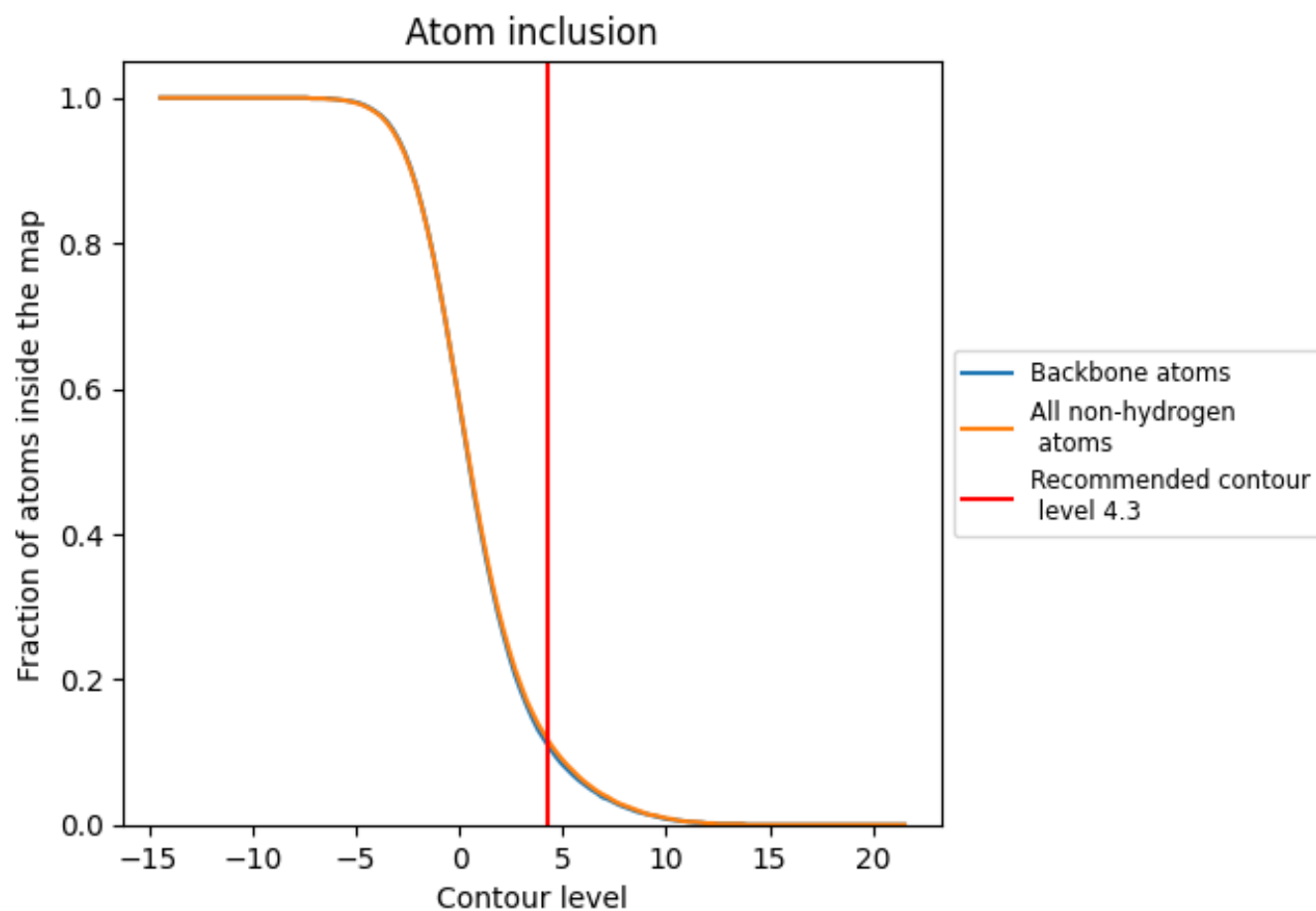


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

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

This section was not generated.







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 11% of all backbone atoms, 12% 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 (4.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.1160	 -0.0060
0	 0.2770	 0.0530
1	 0.1680	 -0.0120
2	 0.1040	 -0.0210
3	 0.0890	 -0.0140
4	 0.0940	 -0.0020
5	 0.0930	 -0.0010
6	 0.1130	 -0.0240
7	 0.1680	 0.0050
8	 0.0450	 -0.0130
9	 0.0690	 0.0040
A	 0.1500	 -0.0120
AA	 0.2520	 0.0100
AB	 0.1110	 0.0130
AC	 0.0800	 0.0130
AD	 0.0180	 0.0060
AE	 0.0470	 -0.0140
AF	 0.0760	 -0.0060
AG	 0.0600	 0.0020
AH	 0.0180	 -0.0010
AI	 0.0610	 -0.0040
AJ	 0.1270	 -0.0180
AK	 0.1140	 -0.0030
AL	 0.1190	 -0.0030
AM	 0.1130	 0.0110
AN	 0.1630	 -0.0530
B	 0.1110	 -0.0140
C	 0.1810	 -0.0070
D	 0.0820	 0.0030
E	 0.1340	 -0.0060
F	 0.0700	 -0.0090
G	 0.0960	 0.0200
H	 0.1950	 0.0050
I	 0.1650	 -0.0220
J	 0.1320	 -0.0210



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Chain	Atom inclusion	Q-score
K	0.1850	-0.0060
L	0.0690	0.0030
M	0.0820	-0.0310
N	0.2130	-0.0010
O	0.0590	-0.0090
P	0.0640	0.0100
Q	0.0520	0.0050
R	0.0760	0.0090
S	0.1160	-0.0010
T	0.0220	0.0040
U	0.2060	-0.0340
V	0.1690	0.0190
W	0.0880	-0.0060
X	0.1090	-0.0150
Y	0.2630	0.0130
Z	0.0660	-0.0120
a	0.0920	-0.0120
b	0.0910	0.0280
c	0.2150	-0.0240
d	0.0740	-0.0050
e	0.0860	-0.0020
f	0.0420	-0.0060
g	0.0370	-0.0020
h	0.1160	-0.0030
i	0.1330	-0.0030
j	0.0740	0.0060
k	0.1200	-0.0160
l	0.0290	0.0080
m	0.0680	0.0030
n	0.1230	0.0120
o	0.0870	-0.0080
p	0.1310	-0.0100
q	0.0600	0.0080
r	0.1600	-0.0100
s	0.0450	0.0080
t	0.1930	-0.0160
u	0.0540	-0.0000
v	0.1290	-0.0010
w	0.0130	0.0050
x	0.0880	0.0190
y	0.0790	-0.0220
z	0.0990	0.0170