



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 08:39 PM UTC

PDB ID : 8Z71 / pdb_00008z71
EMDB ID : EMD-38657
Title : State 1a (S1a) of yeast 80S ribosome bound to open eEF3 and 2 tRNAs and eEF1A during mRNA decoding
Authors : Cheng, J.; Wu, C.L.; Li, J.X.; Zhang, X.Z.
Deposited on : 2024-04-19
Resolution : 3.60 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

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:

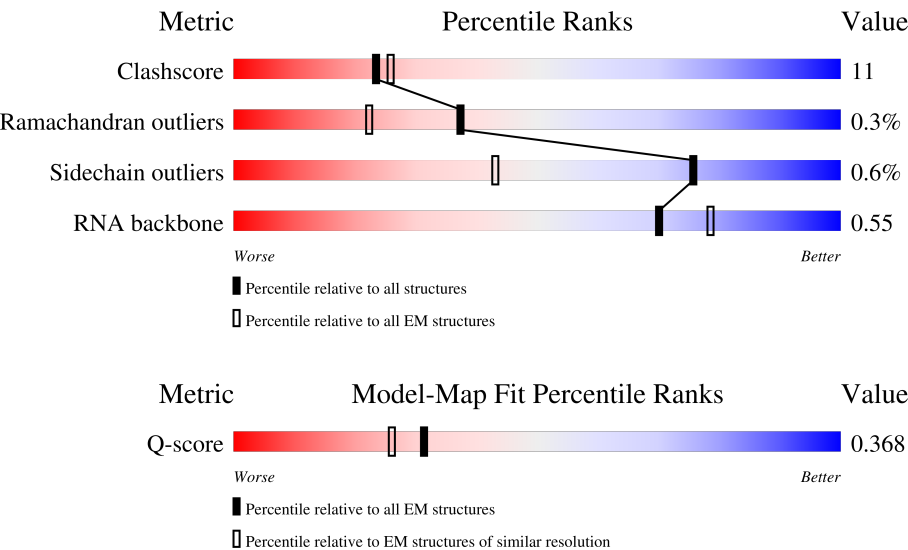
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.60 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	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	12797 (3.10 - 4.10)

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

Mol	Chain	Length	Quality of chain
1	2	1799	
2	SA	222	
3	SB	206	

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Mol	Chain	Length	Quality of chain
4	SC	92	
5	SD	121	
6	SE	117	
7	SF	141	
8	SG	121	
9	SH	145	
10	SI	143	
11	SJ	100	
12	SK	108	
13	SL	63	
14	SM	53	
15	SN	73	
16	SO	312	
17	SP	206	
18	SQ	232	
19	SR	216	
20	SS	258	
21	ST	228	
22	SU	184	
23	SV	200	
24	SW	184	
25	SX	142	
26	SY	150	
27	SZ	127	
28	Sa	87	

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Mol	Chain	Length	Quality of chain
29	Sb	129	
30	Sc	144	
31	Sd	134	
32	Se	94	
33	Sf	81	
34	Sg	60	
35	s	77	
36	t	75	
37	B	121	
38	C	158	
39	T	188	
40	Y	126	
41	A	3394	
42	D	251	
43	E	386	
44	F	361	
45	G	294	
46	H	175	
47	I	223	
48	J	233	
49	K	191	
50	L	218	
51	M	169	
52	N	193	
53	O	136	



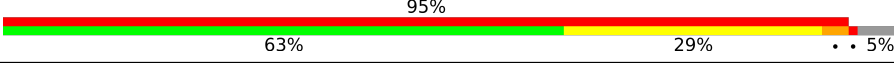

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Mol	Chain	Length	Quality of chain
54	P	203	<div>74%</div> <div>76%24%</div>
55	Q	197	<div>62%</div> <div>81%19%</div>
56	R	183	<div>55%</div> <div>81%19%</div>
57	S	185	<div>66%</div> <div>79%21%</div>
58	U	171	<div>66%</div> <div>77%23%</div>
59	V	159	<div>74%</div> <div>79%21%</div>
60	W	100	<div>91%</div> <div>69%31%</div>
61	X	136	<div>76%</div> <div>72%28%</div>
62	Z	121	<div>69%</div> <div>79%21%</div>
63	a	125	<div>66%</div> <div>78%22%</div>
64	b	135	<div>69%</div> <div>68%32%</div>
65	c	148	<div>67%</div> <div>84%16%</div>
66	d	58	<div>76%</div> <div>86%14%</div>
67	e	96	<div>74%</div> <div>73%27%</div>
68	f	109	<div>65%</div> <div>77%23%</div>
69	g	127	<div>65%</div> <div>83%17%</div>
70	h	106	<div>62%</div> <div>74%26%</div>
71	i	112	<div>74%</div> <div>74%25%</div>
72	j	119	<div>71%</div> <div>76%24%</div>
73	k	99	<div>76%</div> <div>82%18%</div>
74	l	81	<div>51%</div> <div>72%26%</div>
75	m	77	<div>90%</div> <div>79%21%</div>
76	n	50	<div>84%</div> <div>84%16%</div>
77	o	52	<div>77%</div> <div>83%17%</div>
78	p	25	<div>92%</div> <div>60%40%</div>

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Mol	Chain	Length	Quality of chain
79	q	103	
80	r	91	
81	x	462	
82	v	1044	

2 Entry composition

There are 82 unique types of molecules in this entry. The entry contains 213525 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	1771	Total	C	N	O	P	0	0
			37739	16872	6683	12413	1771		

- Molecule 2 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	SA	222	Total	C	N	O	S	0	0
			1729	1098	312	313	6		

- Molecule 3 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	SB	206	Total	C	N	O	S	0	0
			1605	1005	299	298	3		

- Molecule 4 is a protein called Small ribosomal subunit protein eS10A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	SC	92	Total	C	N	O	S	0	0
			752	487	122	141	2		

- Molecule 5 is a protein called Small ribosomal subunit protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	SD	121	Total	C	N	O	S	0	0
			875	551	153	169	2		

- Molecule 6 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	SE	117	Total	C	N	O	S	0	0
			916	583	171	155	7		

- Molecule 7 is a protein called Small ribosomal subunit protein uS9A.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	SF	141	Total	C	N	O	0	0
			1105	708	203	194		

- Molecule 8 is a protein called Small ribosomal subunit protein eS17A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SG	121	Total	C	N	O	S	0	0
			961	599	182	178	2		

- Molecule 9 is a protein called Small ribosomal subunit protein uS13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SH	145	Total	C	N	O	S	0	0
			1188	741	237	208	2		

- Molecule 10 is a protein called Small ribosomal subunit protein eS19A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	SI	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 11 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	SJ	100	Total	C	N	O	S	0	0
			797	506	144	146	1		

- Molecule 12 is a protein called Small ribosomal subunit protein eS25A.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	SK	82	Total	C	N	O	0	0
			651	416	123	112		

- Molecule 13 is a protein called Small ribosomal subunit protein eS28A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	SL	63	Total	C	N	O	S	0	0
			491	303	96	91	1		

- Molecule 14 is a protein called Small ribosomal subunit protein uS14A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	SM	53	Total	C	N	O	S	0	0
			442	274	92	72	4		

- Molecule 15 is a protein called Small ribosomal subunit protein eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	SN	73	Total	C	N	O	S	0	0
			556	352	105	95	4		

- Molecule 16 is a protein called Small ribosomal subunit protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SO	312	Total	C	N	O	S	0	0
			2383	1514	409	452	8		

- Molecule 17 is a protein called Small ribosomal subunit protein uS2A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	SP	206	Total	C	N	O	S	0	0
			1603	1030	284	287	2		

- Molecule 18 is a protein called Small ribosomal subunit protein eS1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SQ	226	Total	C	N	O	S	0	0
			1798	1139	330	325	4		

- Molecule 19 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	SR	216	Total	C	N	O	S	0	0
			1626	1042	287	295	2		

- Molecule 20 is a protein called Small ribosomal subunit protein eS4A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	SS	258	Total	C	N	O	S	0	0
			2056	1308	387	358	3		

- Molecule 21 is a protein called Small ribosomal subunit protein eS6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	ST	228	Total	C	N	O	S	0	0
			1815	1138	351	323	3		

- Molecule 22 is a protein called Small ribosomal subunit protein eS7A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	SU	184	Total	C	N	O		0	0
			1473	946	263	264			

- Molecule 23 is a protein called Small ribosomal subunit protein eS8A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	SV	187	Total	C	N	O	S	0	0
			1476	916	295	263	2		

- Molecule 24 is a protein called Small ribosomal subunit protein uS4A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	SW	184	Total	C	N	O	S	0	0
			1479	935	285	258	1		

- Molecule 25 is a protein called Small ribosomal subunit protein uS17A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	SX	142	Total	C	N	O	S	0	0
			1142	733	217	189	3		

- Molecule 26 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	SY	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 27 is a protein called Small ribosomal subunit protein uS11B.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	SZ	127	Total	C	N	O	S	0	0
			891	545	182	163	1		

- Molecule 28 is a protein called Small ribosomal subunit protein eS21A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Sa	87	Total	C	N	O	S	0	0
			673	415	125	131	2		

- Molecule 29 is a protein called Small ribosomal subunit protein uS8A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Sb	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 30 is a protein called Small ribosomal subunit protein uS12A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Sc	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 31 is a protein called Small ribosomal subunit protein eS24A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Sd	134	Total	C	N	O	S	0	0
			1073	676	208	189			

- Molecule 32 is a protein called Small ribosomal subunit protein eS26A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Se	94	Total	C	N	O	S	0	0
			750	462	157	126	5		

- Molecule 33 is a protein called Small ribosomal subunit protein eS27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Sf	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 34 is a protein called Small ribosomal subunit protein eS30A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Sg	60	Total	C	N	O	S	0	0
			472	298	97	76	1		

- Molecule 35 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	s	76	Total	C	N	O	P	0	0
			1616	723	291	527	75		

- Molecule 36 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	t	75	Total	C	N	O	P	0	0
			1606	716	297	518	75		

- Molecule 37 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	B	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 38 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	C	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 39 is a protein called Large ribosomal subunit protein eL19A.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	T	188	Total	C	N	O	0	0
			1515	932	323	260		

- Molecule 40 is a protein called Large ribosomal subunit protein eL24A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Y	126	Total	C	N	O	S	0	0
			836	525	165	145	1		

- Molecule 41 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	A	3187	Total	C	N	O	P	0	0
			68170	30449	12289	22245	3187		

- Molecule 42 is a protein called Large ribosomal subunit protein uL2A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	D	251	Total	C	N	O	S	0	0
			1899	1182	385	331	1		

- Molecule 43 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	E	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 44 is a protein called Large ribosomal subunit protein uL4A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	F	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 45 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	G	294	Total	C	N	O	S	0	0
			2351	1484	410	455	2		

- Molecule 46 is a protein called Large ribosomal subunit protein eL6B.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	H	167	Total	C	N	O	0	0
			1307	843	234	230		

- Molecule 47 is a protein called Large ribosomal subunit protein uL30A.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	I	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	22	ILE	THR	conflict	UNP P05737

- Molecule 48 is a protein called Large ribosomal subunit protein eL8A.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	J	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 49 is a protein called Large ribosomal subunit protein uL6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	K	191	Total	C	N	O	S	0	0
			1508	957	274	273	4		

- Molecule 50 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	L	218	Total	C	N	O	S	0	0
			1764	1117	334	306	7		

- Molecule 51 is a protein called Large ribosomal subunit protein uL5B.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	M	169	Total	C	N	O	S	0	0
			1346	843	252	247	4		

- Molecule 52 is a protein called Large ribosomal subunit protein eL13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	N	193	Total	C	N	O		0	0
			1543	962	315	266			

- Molecule 53 is a protein called Large ribosomal subunit protein eL14A.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	O	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 54 is a protein called Large ribosomal subunit protein eL15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	P	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 55 is a protein called Large ribosomal subunit protein uL13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Q	197	Total	C	N	O	S	197	0
			1555	1003	289	262	1		

- Molecule 56 is a protein called Large ribosomal subunit protein uL22A.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	R	183	Total	C	N	O		0	0
			1416	879	284	253			

- Molecule 57 is a protein called Large ribosomal subunit protein eL18A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	S	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 58 is a protein called Large ribosomal subunit protein eL20A.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	U	171	Total	C	N	O	S	0	0
			1437	925	266	243	3		

- Molecule 59 is a protein called Large ribosomal subunit protein eL21A.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	V	159	Total	C	N	O	S	0	0
			1272	802	245	221	4		

- Molecule 60 is a protein called Large ribosomal subunit protein eL22A.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	W	100	Total	C	N	O		0	0
			796	516	131	149			

- Molecule 61 is a protein called Large ribosomal subunit protein uL14A.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	X	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 62 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	Z	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

- Molecule 63 is a protein called Large ribosomal subunit protein uL24A.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	a	125	Total	C	N	O		0	0
			984	620	191	173			

- Molecule 64 is a protein called Large ribosomal subunit protein eL27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	b	135	Total	C	N	O		0	0
			1080	701	199	180			

- Molecule 65 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	c	148	Total	C	N	O	S	0	0
			1169	747	231	188	3		

- Molecule 66 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	d	58	Total	C	N	O		0	0
			462	289	100	73			

- Molecule 67 is a protein called Large ribosomal subunit protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	e	96	Total	C	N	O	S	0	0
			737	476	123	137	1		

- Molecule 68 is a protein called Large ribosomal subunit protein eL31A.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	f	109	Total	C	N	O	S	0	0
			876	556	167	152	1		

- Molecule 69 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	g	127	Total	C	N	O	S	0	0
			1013	642	205	165	1		

- Molecule 70 is a protein called Large ribosomal subunit protein eL33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	h	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 71 is a protein called Large ribosomal subunit protein eL34A.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	i	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 72 is a protein called Large ribosomal subunit protein uL29A.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	j	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 73 is a protein called Large ribosomal subunit protein eL36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	k	99	Total	C	N	O	S	0	0
			766	478	154	132	2		

- Molecule 74 is a protein called Large ribosomal subunit protein eL37A.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	l	81	Total	C	N	O	S	0	0
			645	393	141	106	5		

- Molecule 75 is a protein called Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms				AltConf	Trace
75	m	77	Total	C	N	O	0	0
			612	391	115	106		

- Molecule 76 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	n	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 77 is a protein called Large ribosomal subunit protein eL40A.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	o	52	Total	C	N	O	S	0	0
			410	254	86	65	5		

- Molecule 78 is a protein called Large ribosomal subunit protein eL41A.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	p	25	Total	C	N	O	S	0	0
			229	139	62	27	1		

- Molecule 79 is a protein called Large ribosomal subunit protein eL42A.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	q	103	Total	C	N	O	S	0	0
			824	517	167	135	5		

- Molecule 80 is a protein called Large ribosomal subunit protein eL43A.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	r	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 81 is a protein called Elongation factor 1-alpha 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	x	441	Total	C	N	O	S	0	0
			3379	2148	581	633	17		

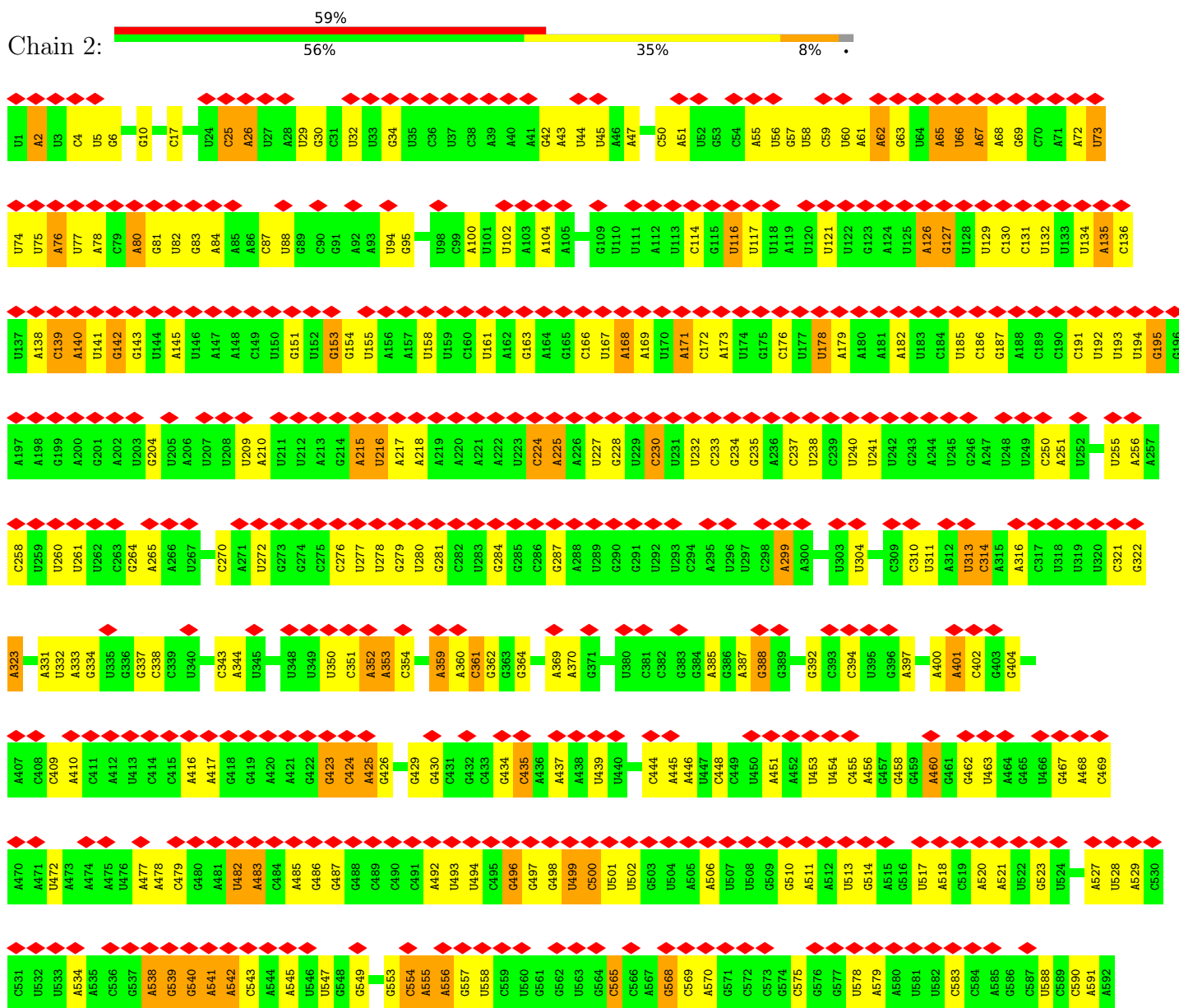
- Molecule 82 is a protein called Elongation factor 3A.

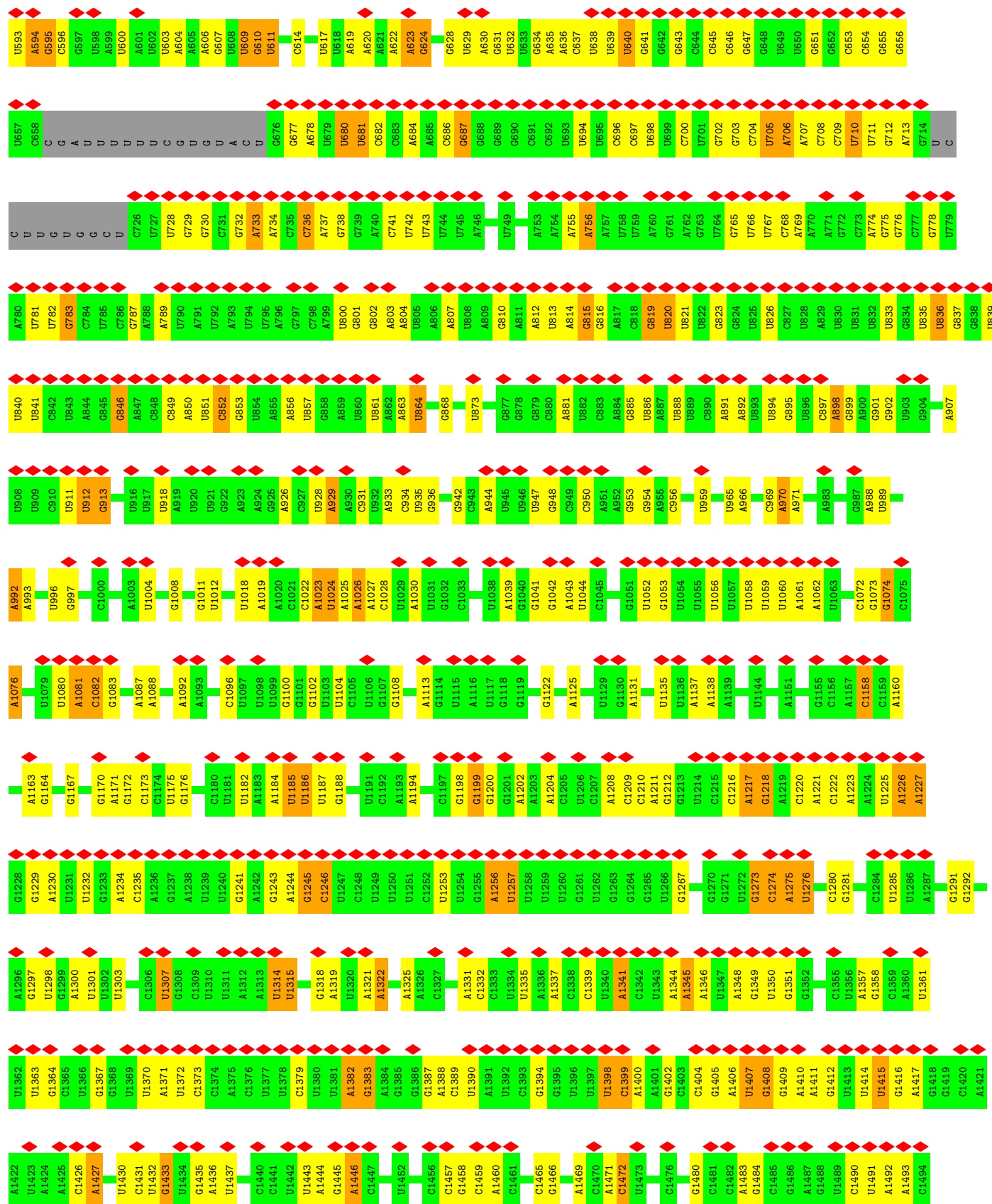
Mol	Chain	Residues	Atoms					AltConf	Trace
82	v	977	Total	C	N	O	S	0	0
			7476	4726	1295	1418	37		

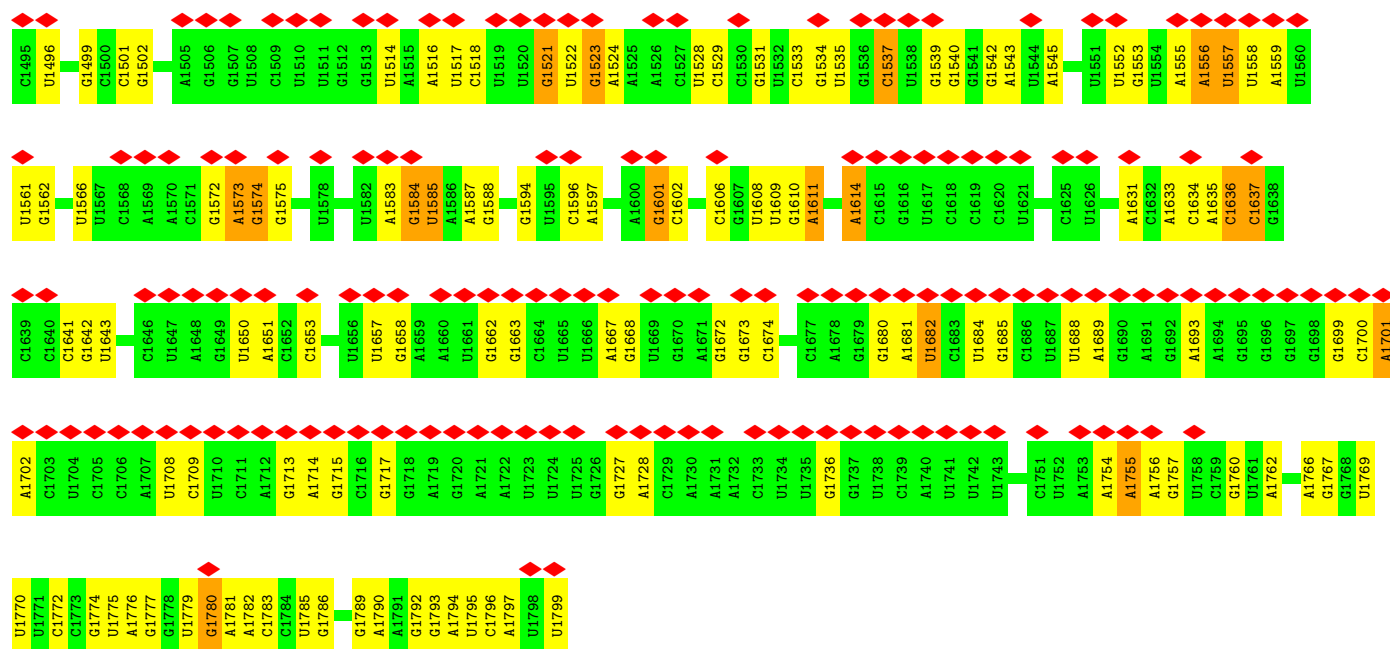
3 Residue-property plots

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

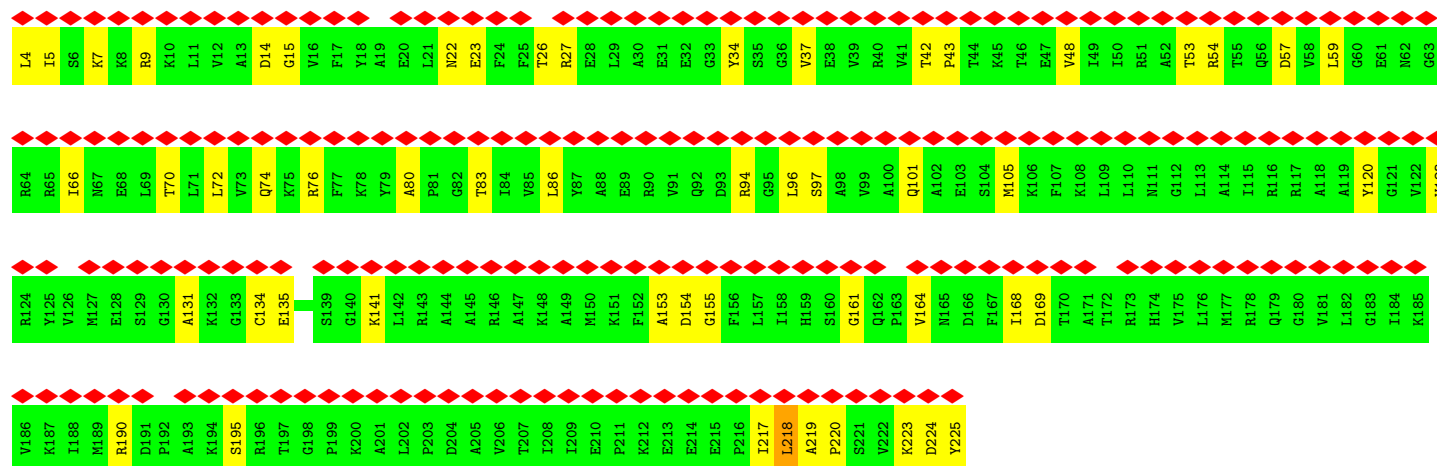
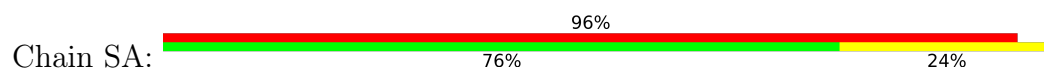
• Molecule 1: 18S rRNA





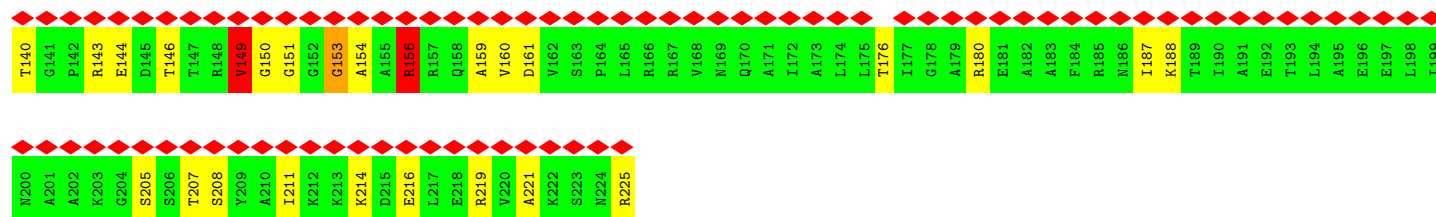


• Molecule 2: Small ribosomal subunit protein uS3

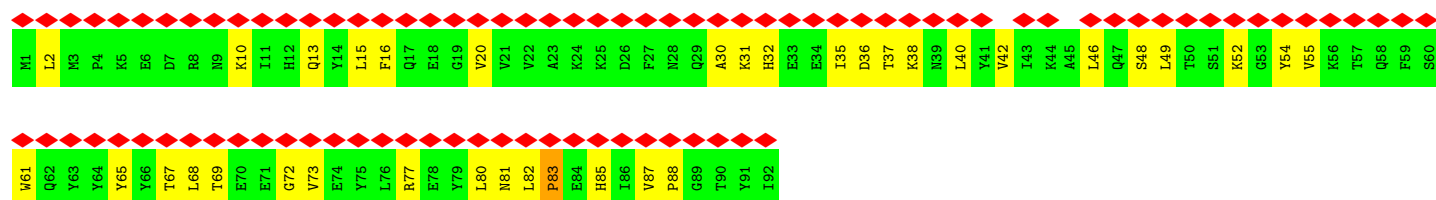


• Molecule 3: Small ribosomal subunit protein uS7

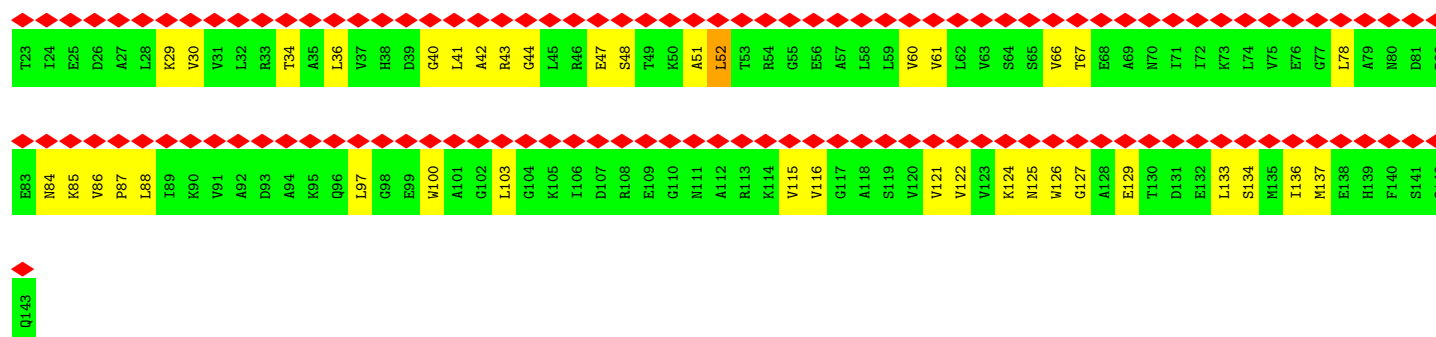




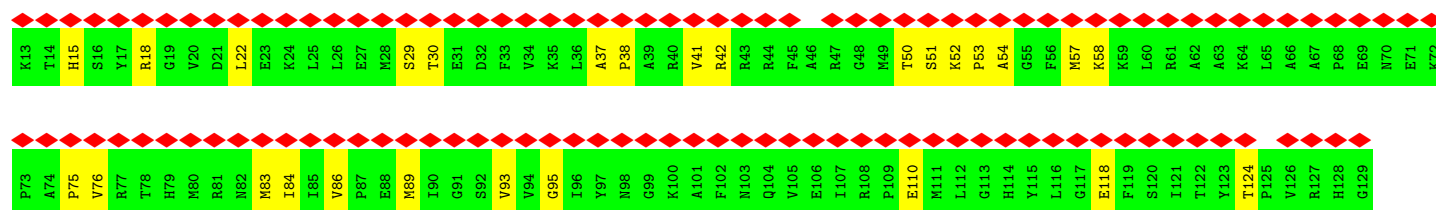
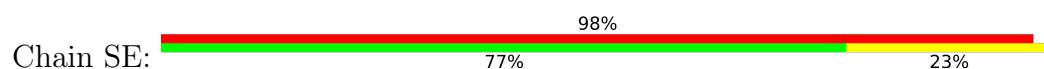
• Molecule 4: Small ribosomal subunit protein eS10A



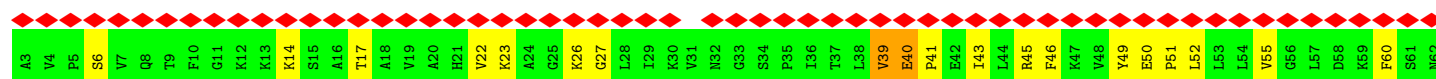
• Molecule 5: Small ribosomal subunit protein eS12

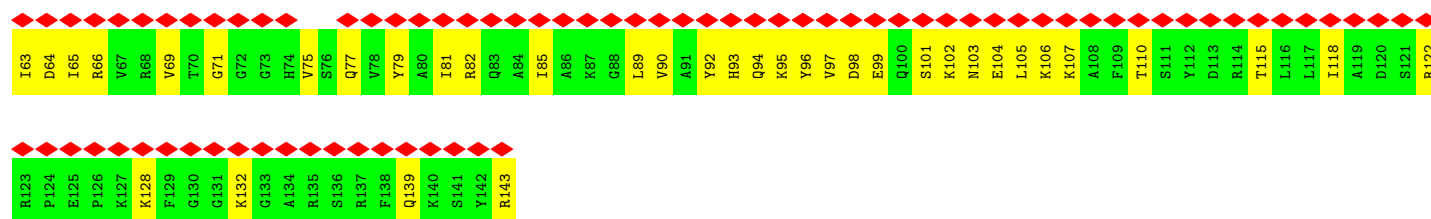


• Molecule 6: Small ribosomal subunit protein uS19

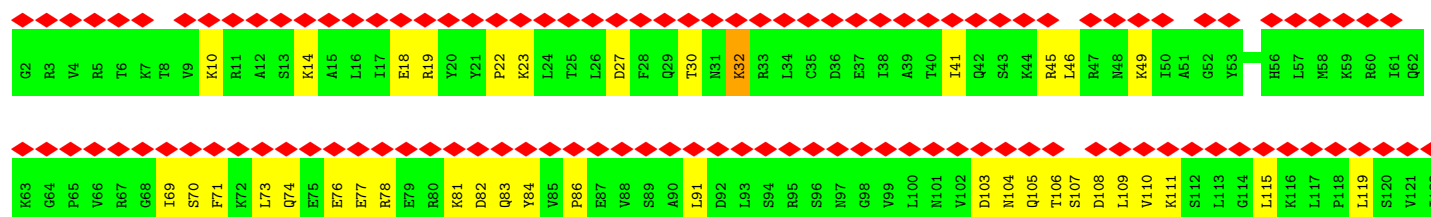


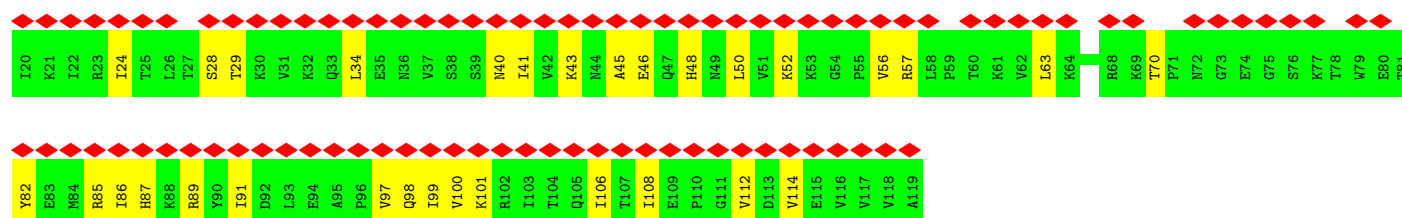
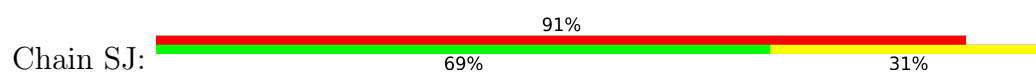
• Molecule 7: Small ribosomal subunit protein uS9A



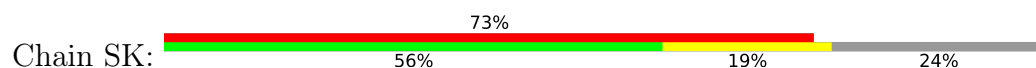


• Molecule 8: Small ribosomal subunit protein eS17A

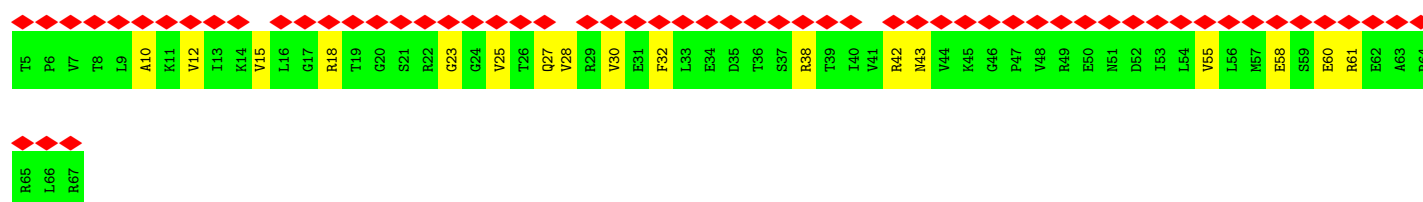
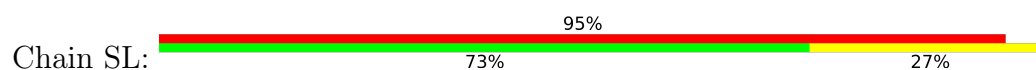




- Molecule 12: Small ribosomal subunit protein eS25A



- Molecule 13: Small ribosomal subunit protein eS28A



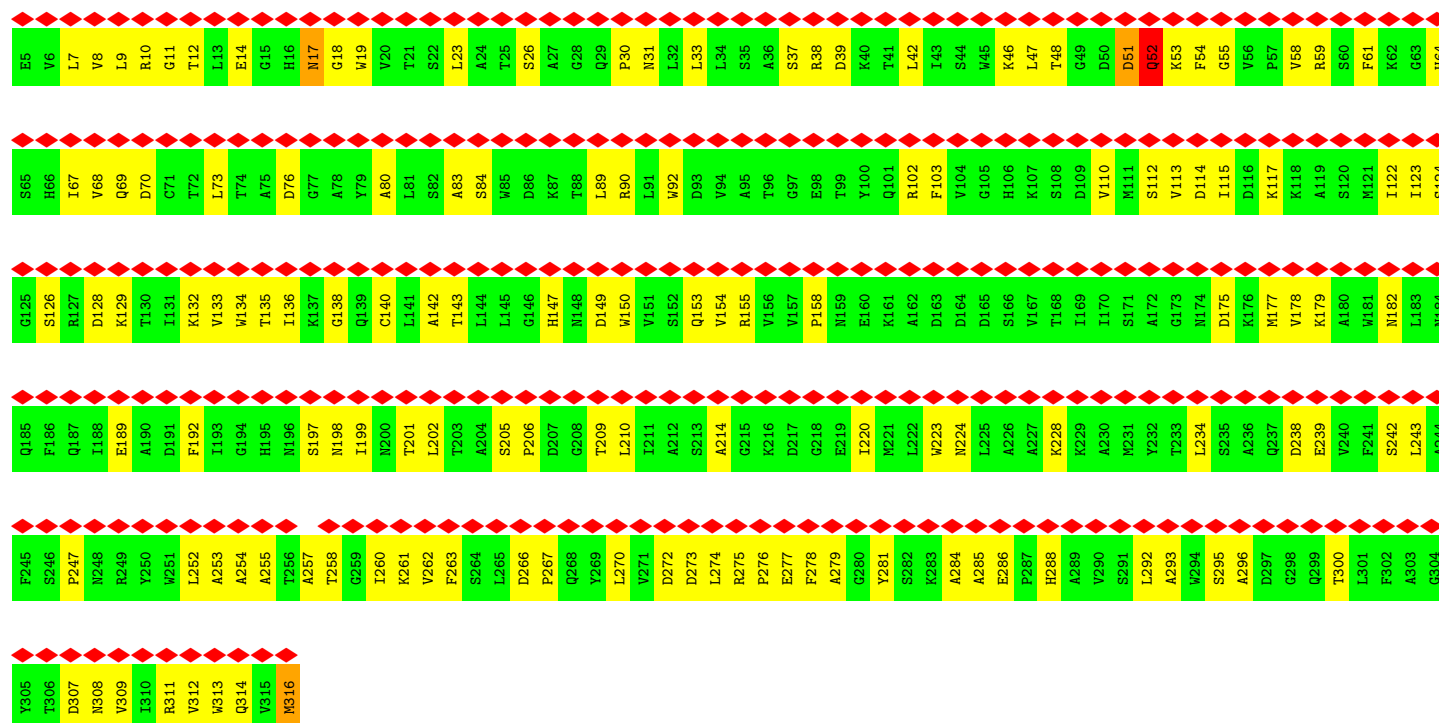
- Molecule 14: Small ribosomal subunit protein uS14A



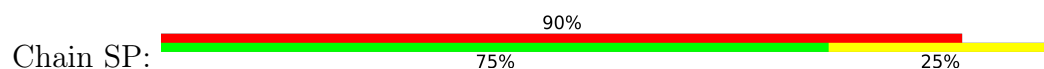
- Molecule 15: Small ribosomal subunit protein eS31



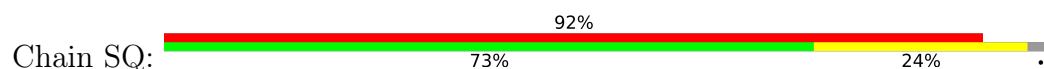
- Molecule 16: Small ribosomal subunit protein RACK1



• Molecule 17: Small ribosomal subunit protein uS2A

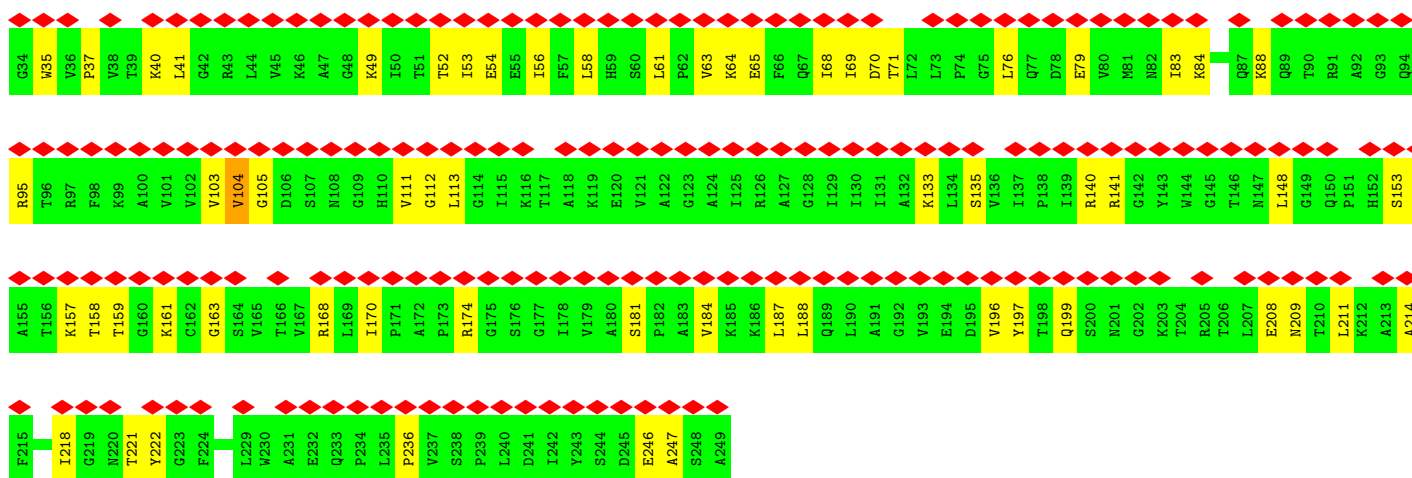
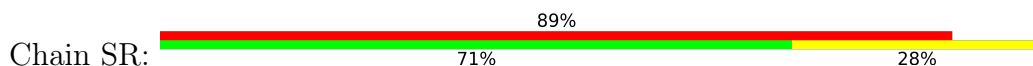


• Molecule 18: Small ribosomal subunit protein eS1A

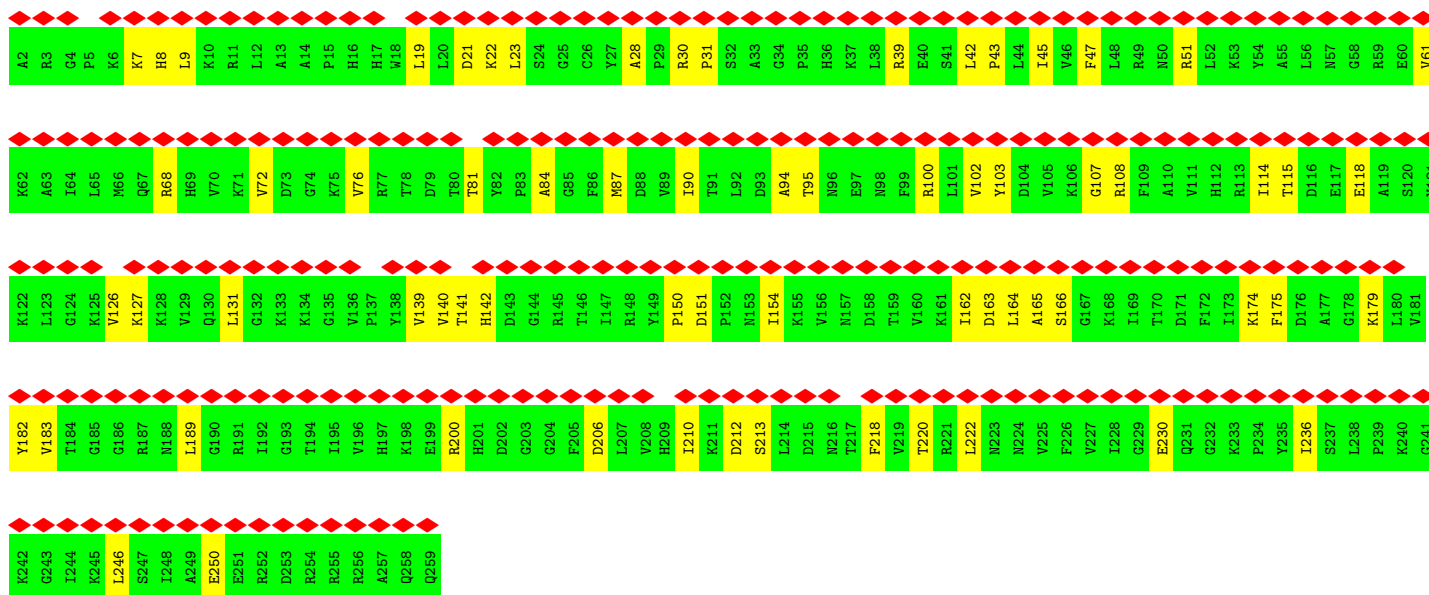
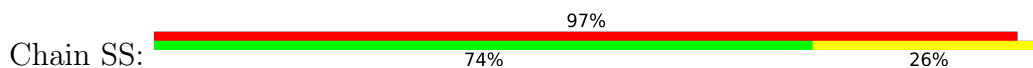




• Molecule 19: Small ribosomal subunit protein uS5



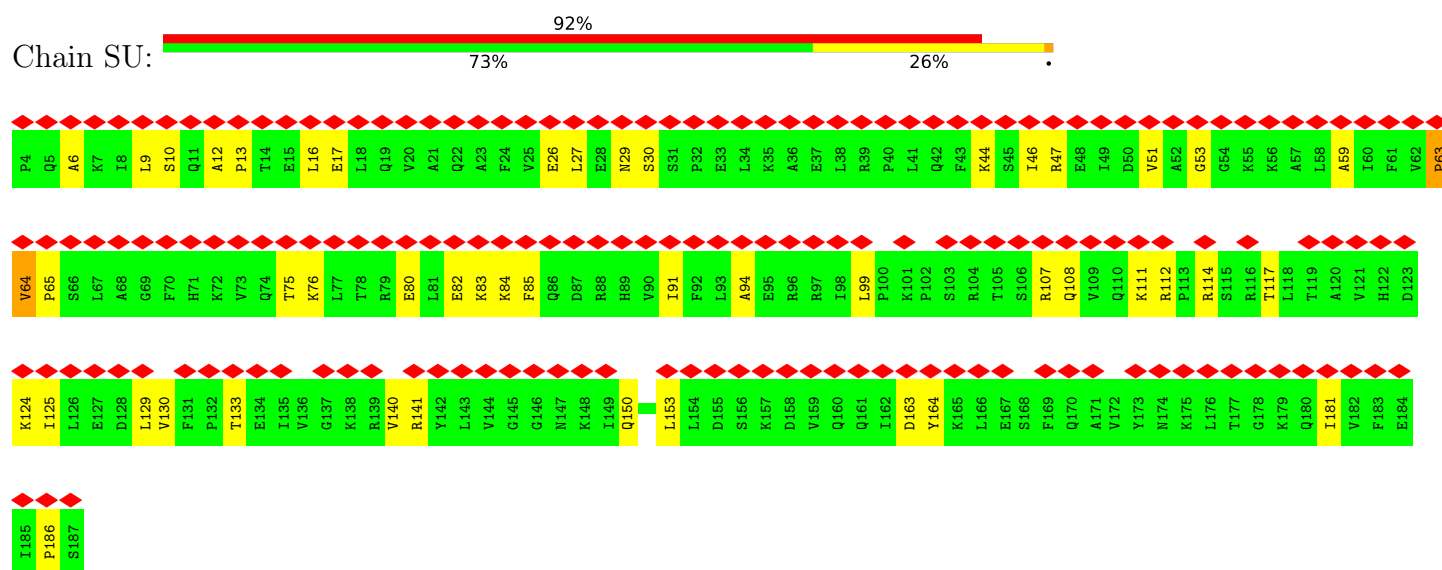
• Molecule 20: Small ribosomal subunit protein eS4A



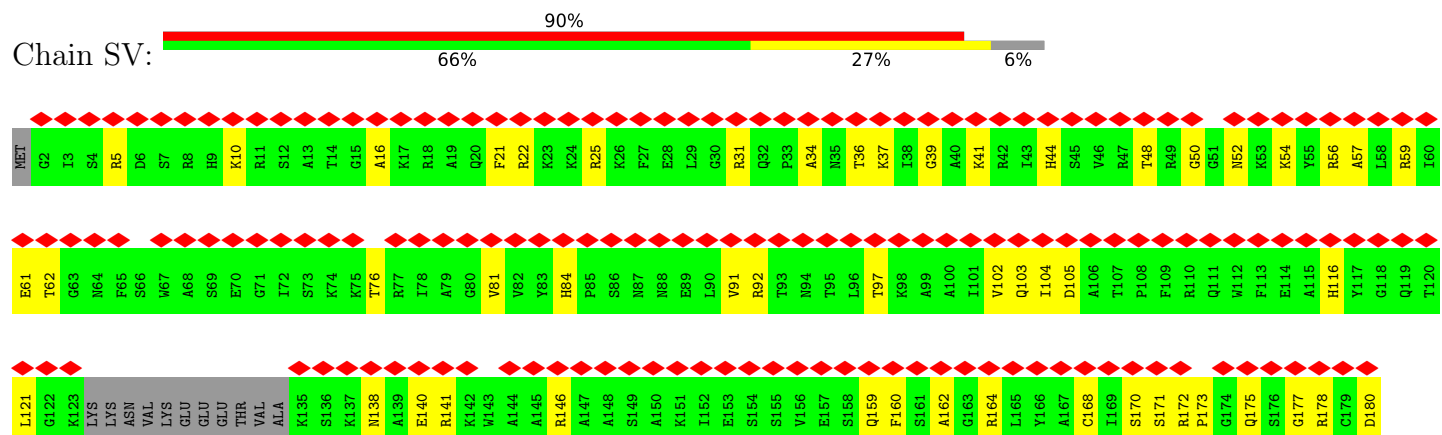
• Molecule 21: Small ribosomal subunit protein eS6A

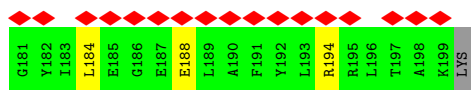


• Molecule 22: Small ribosomal subunit protein eS7A

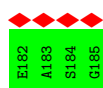
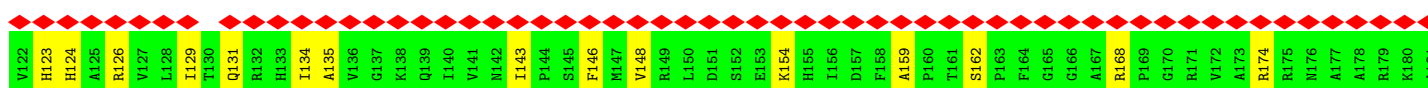
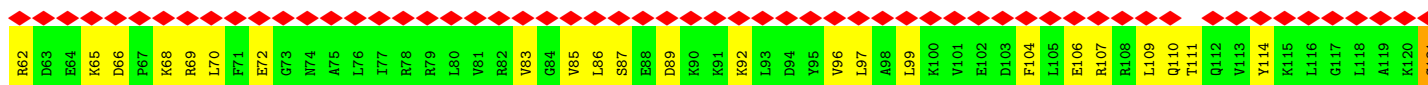
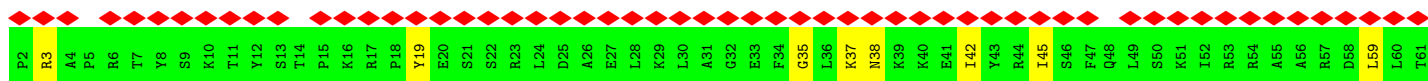
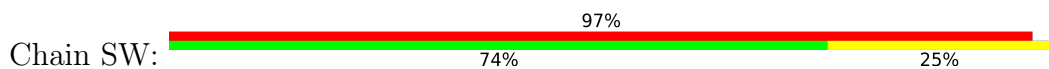


• Molecule 23: Small ribosomal subunit protein eS8A

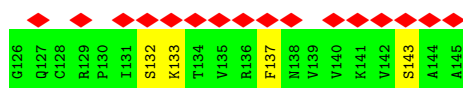
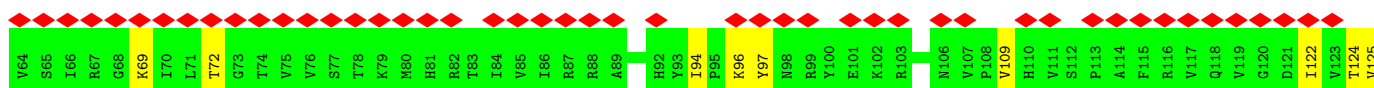
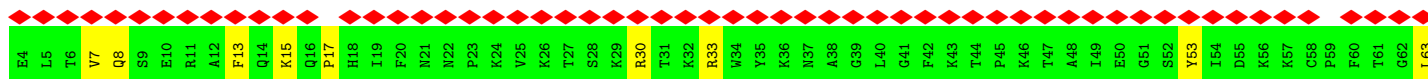
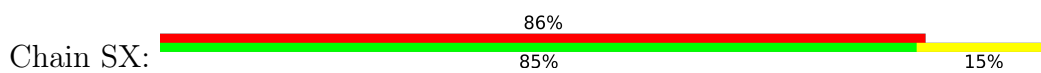




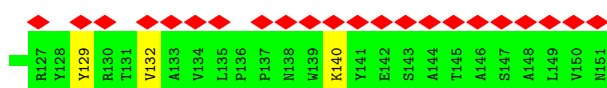
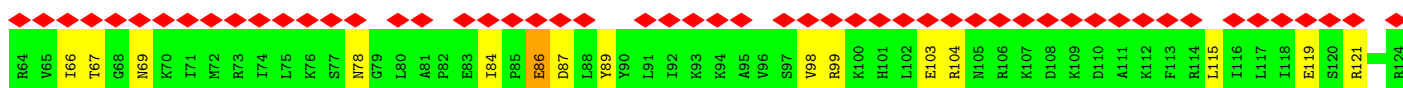
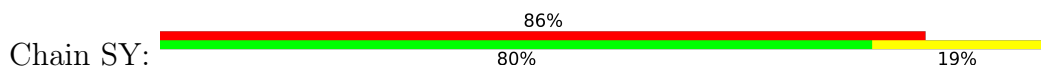
• Molecule 24: Small ribosomal subunit protein uS4A



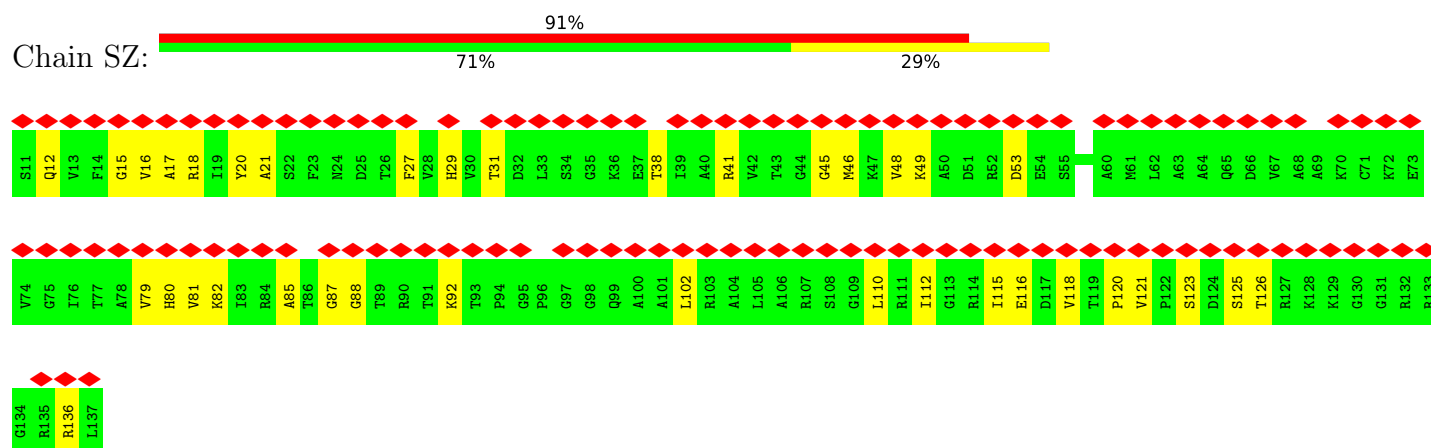
• Molecule 25: Small ribosomal subunit protein uS17A



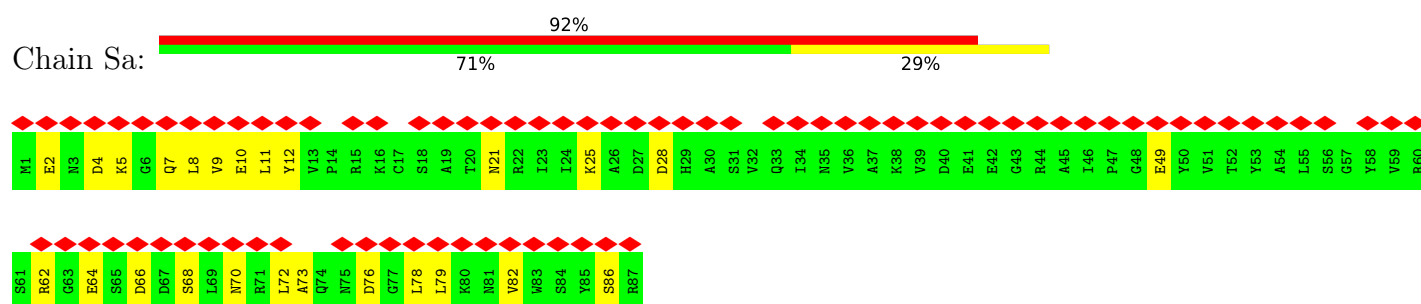
• Molecule 26: Small ribosomal subunit protein uS15



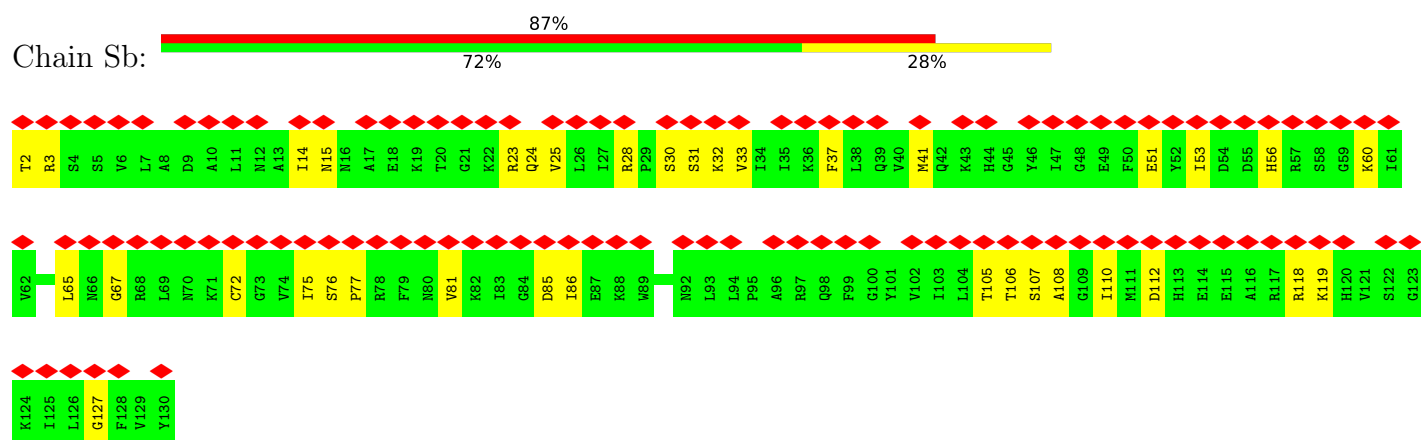
- Molecule 27: Small ribosomal subunit protein uS11B



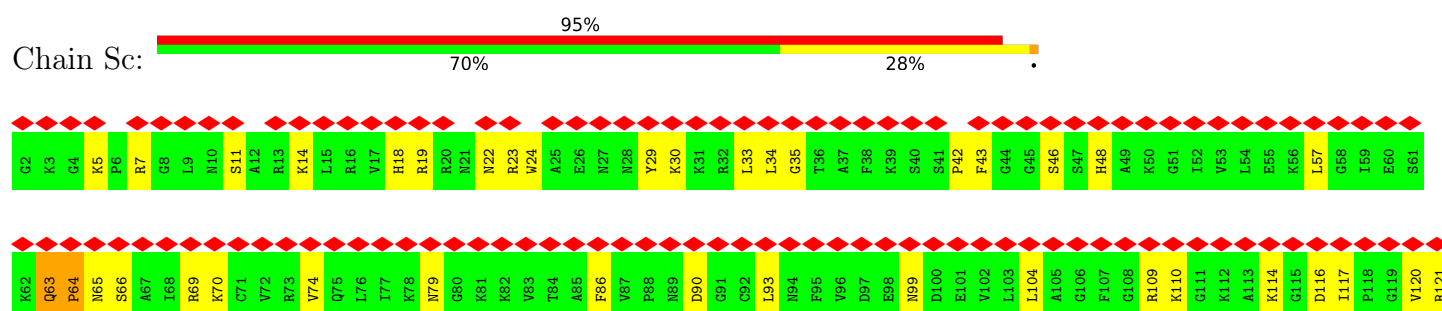
- Molecule 28: Small ribosomal subunit protein eS21A

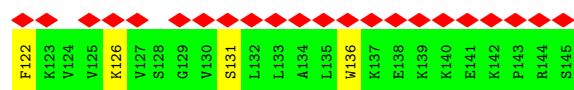


- Molecule 29: Small ribosomal subunit protein uS8A

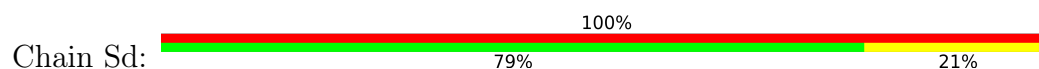


- Molecule 30: Small ribosomal subunit protein uS12A

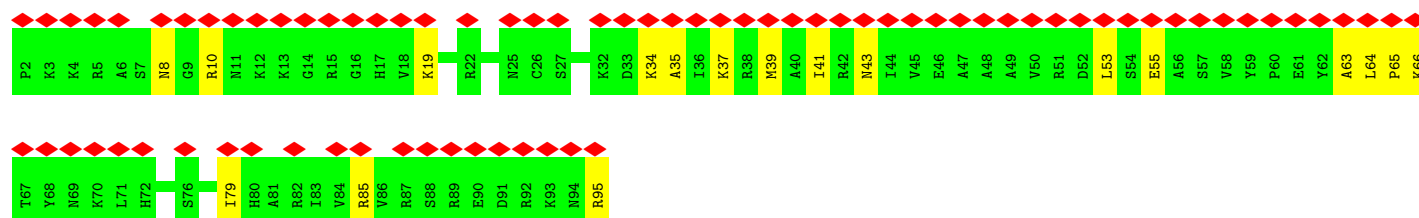
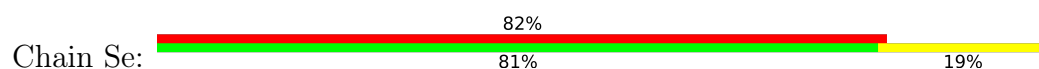




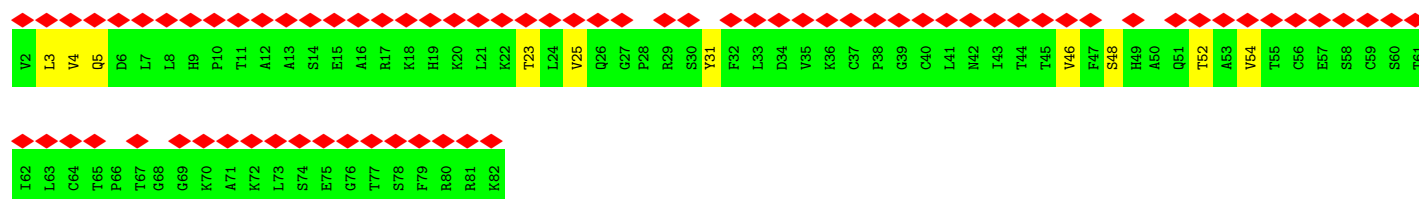
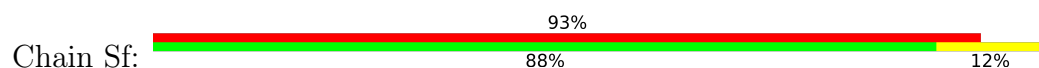
- Molecule 31: Small ribosomal subunit protein eS24A



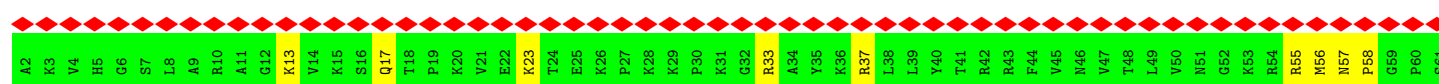
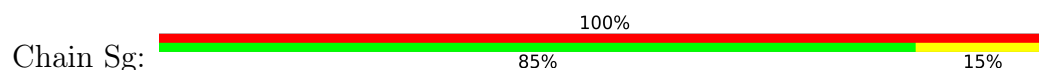
- Molecule 32: Small ribosomal subunit protein eS26A



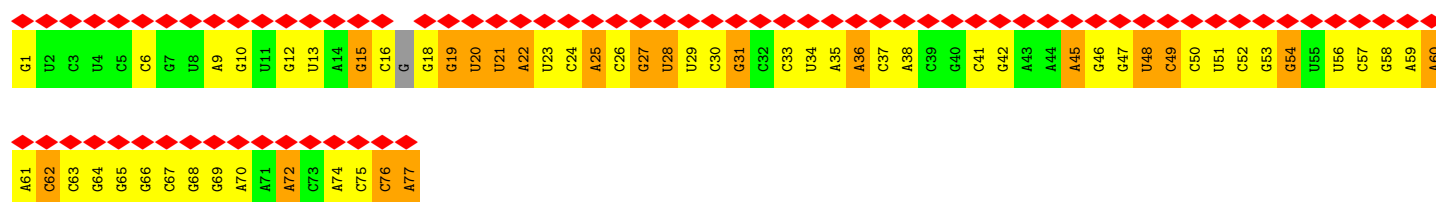
- Molecule 33: Small ribosomal subunit protein eS27A



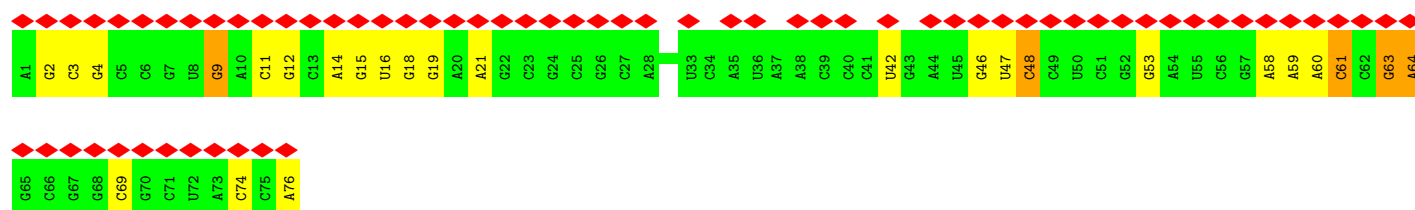
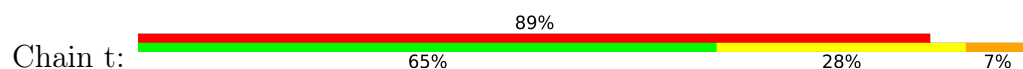
- Molecule 34: Small ribosomal subunit protein eS30A



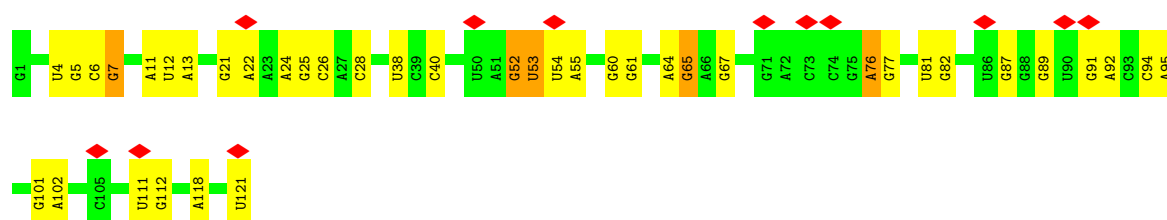
- Molecule 35: tRNA



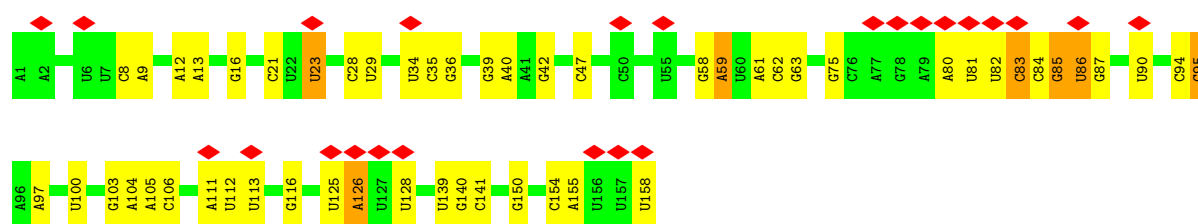
• Molecule 36: tRNA



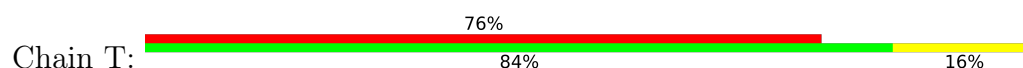
• Molecule 37: 5S rRNA

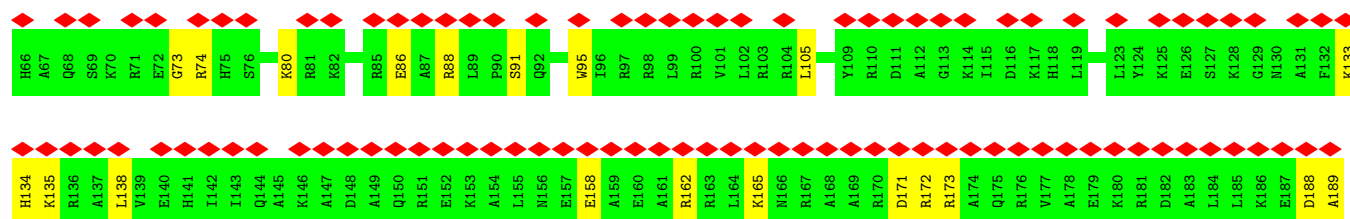


• Molecule 38: 5.8S rRNA

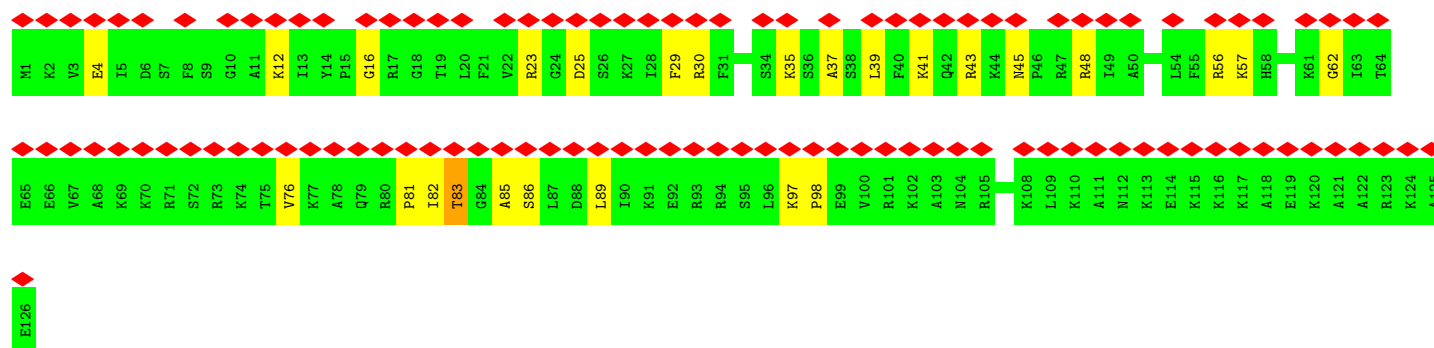
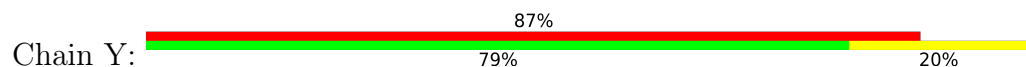


• Molecule 39: Large ribosomal subunit protein eL19A

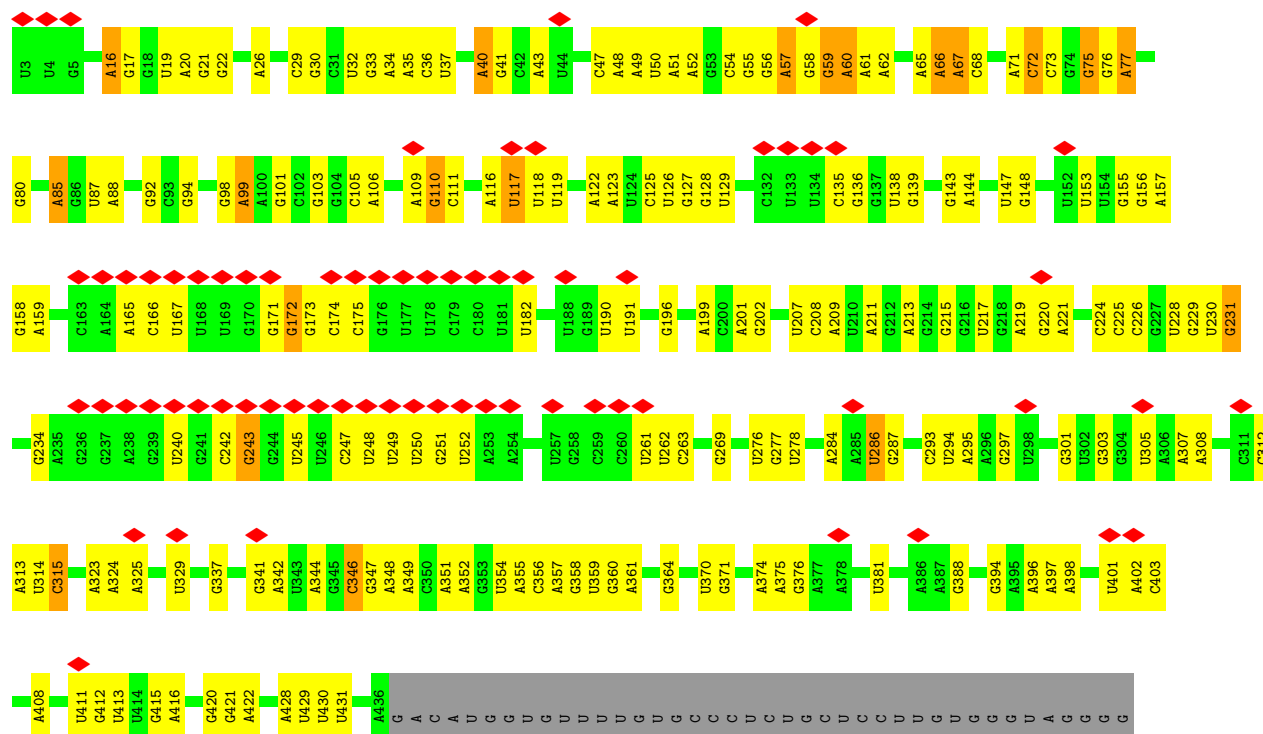


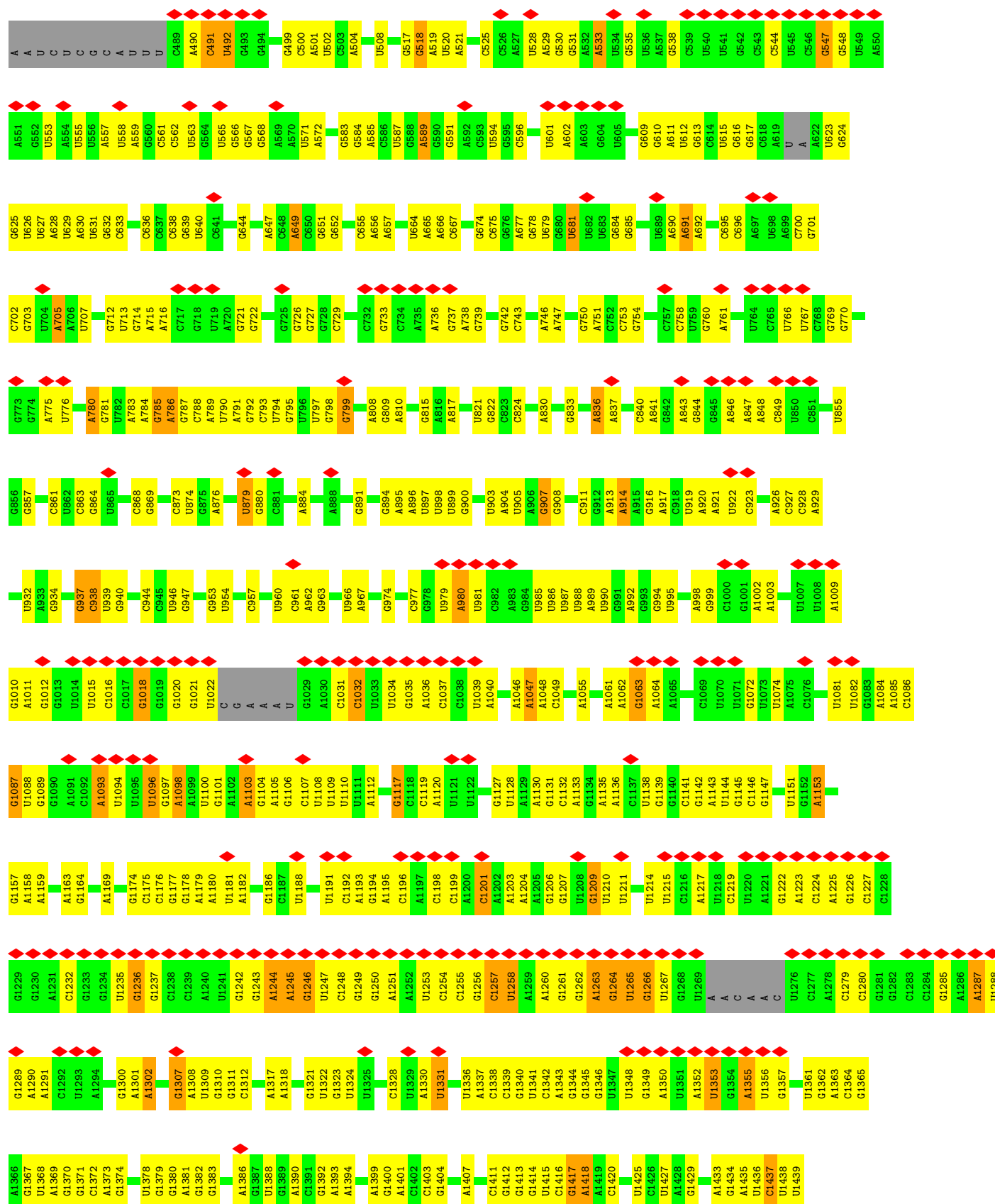


• Molecule 40: Large ribosomal subunit protein eL24A

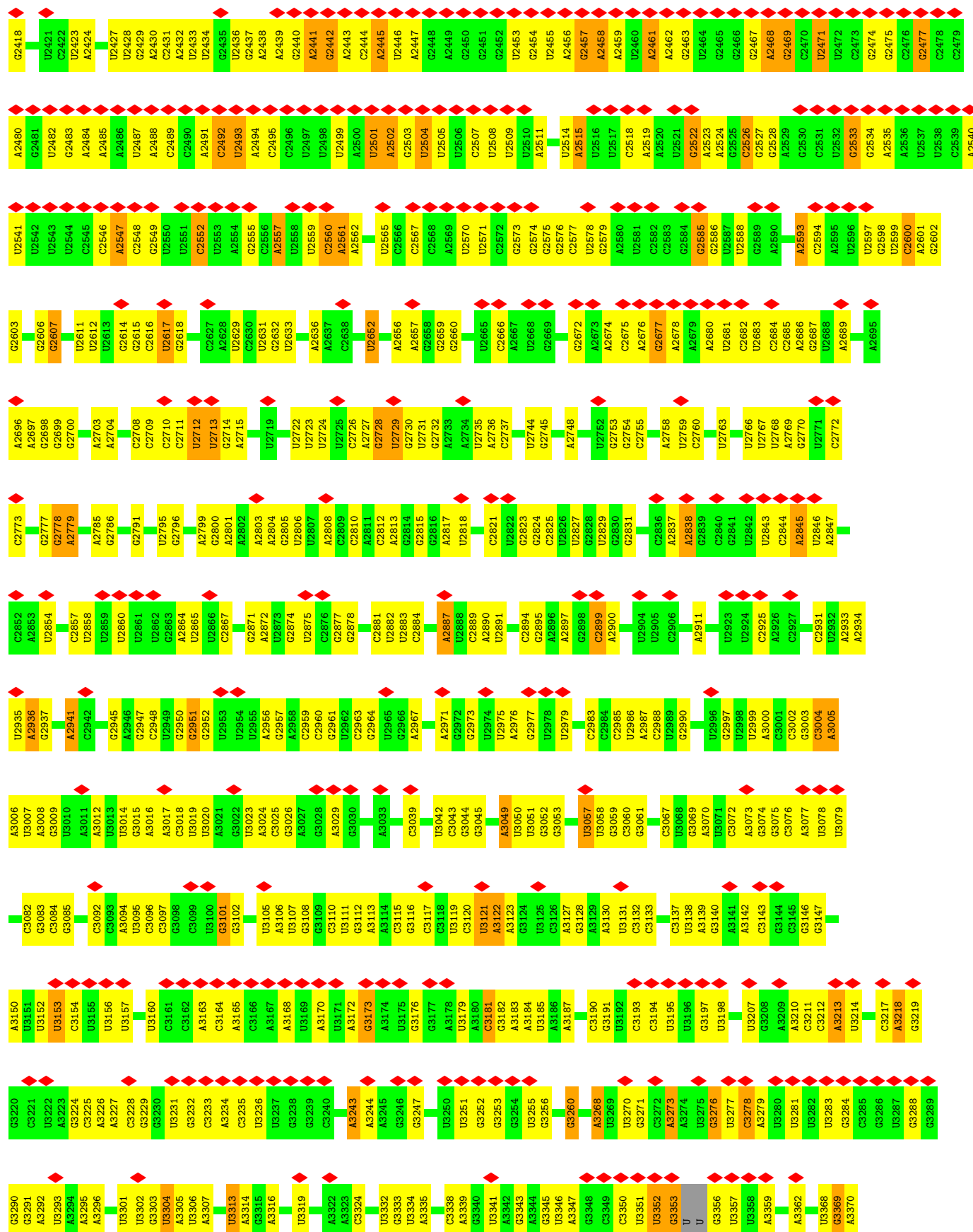


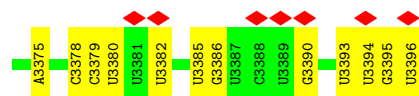
• Molecule 41: 25S rRNA



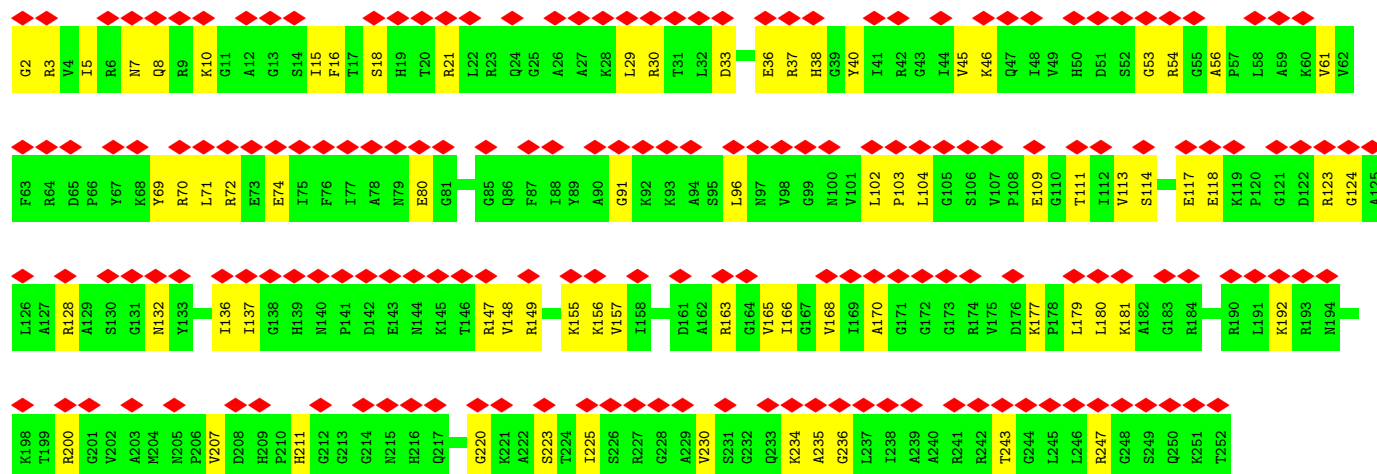




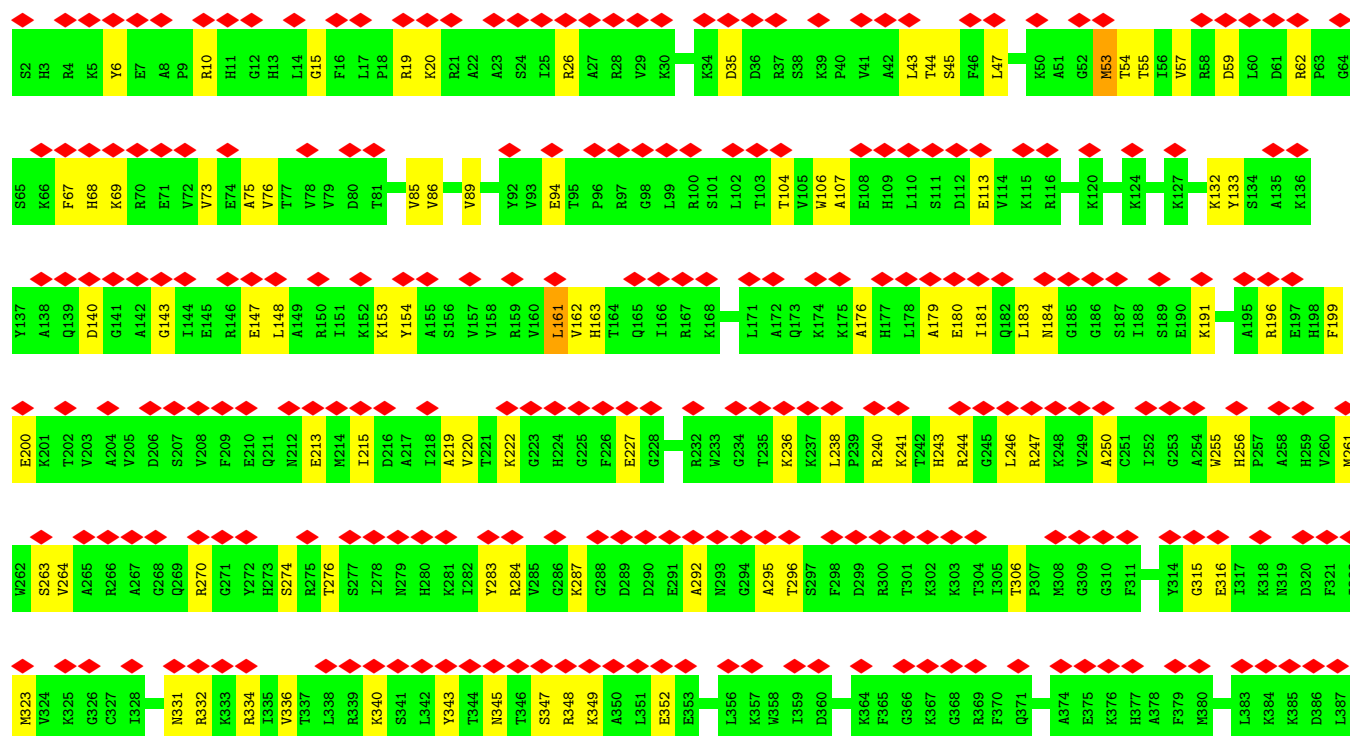
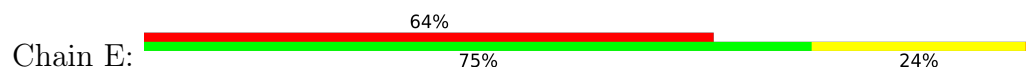





• Molecule 42: Large ribosomal subunit protein uL2A

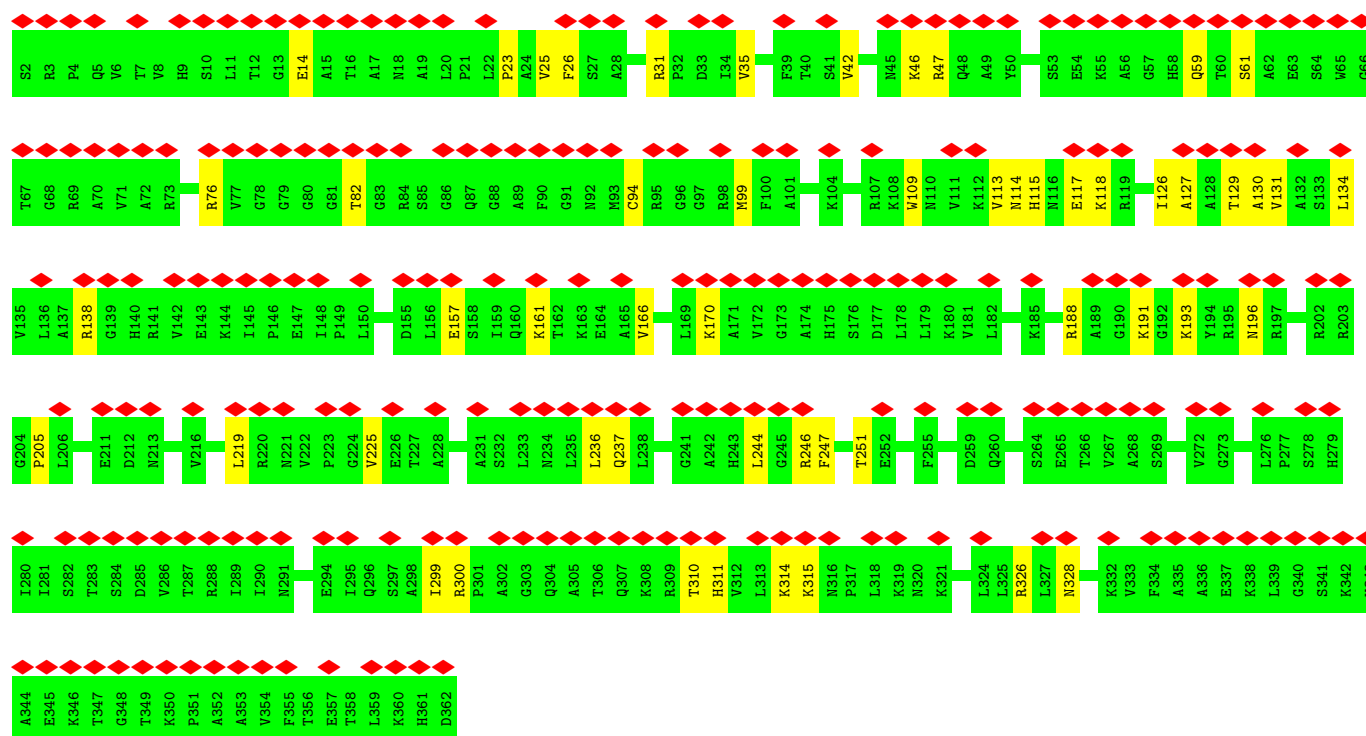


• Molecule 43: Large ribosomal subunit protein uL3




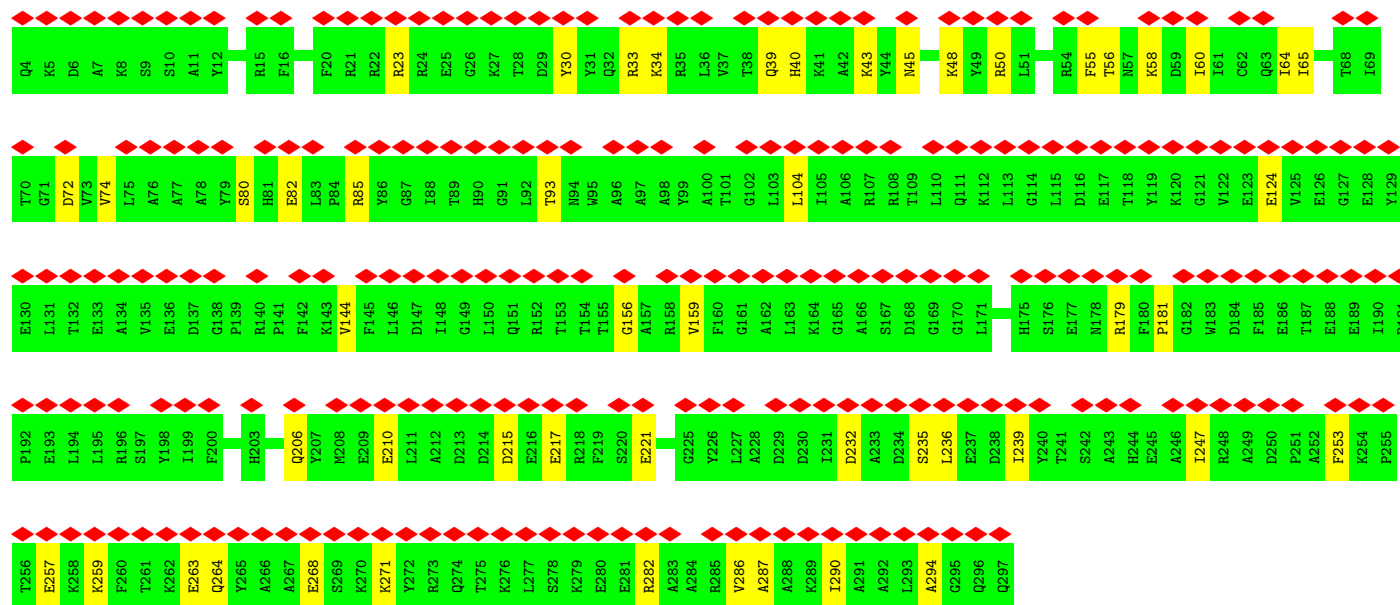
• Molecule 44: Large ribosomal subunit protein uL4A

Chain F: 




• Molecule 45: Large ribosomal subunit protein uL18

Chain G: 

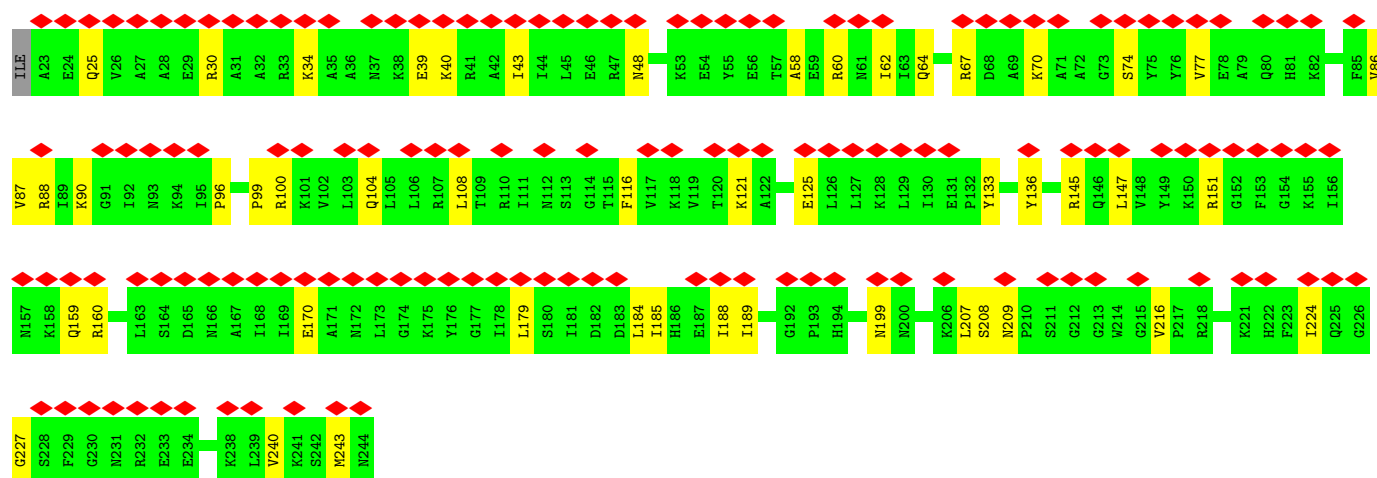
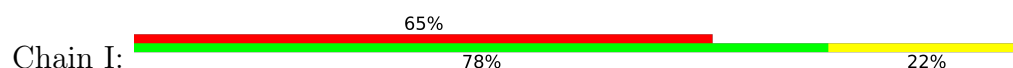


• Molecule 46: Large ribosomal subunit protein eL6B

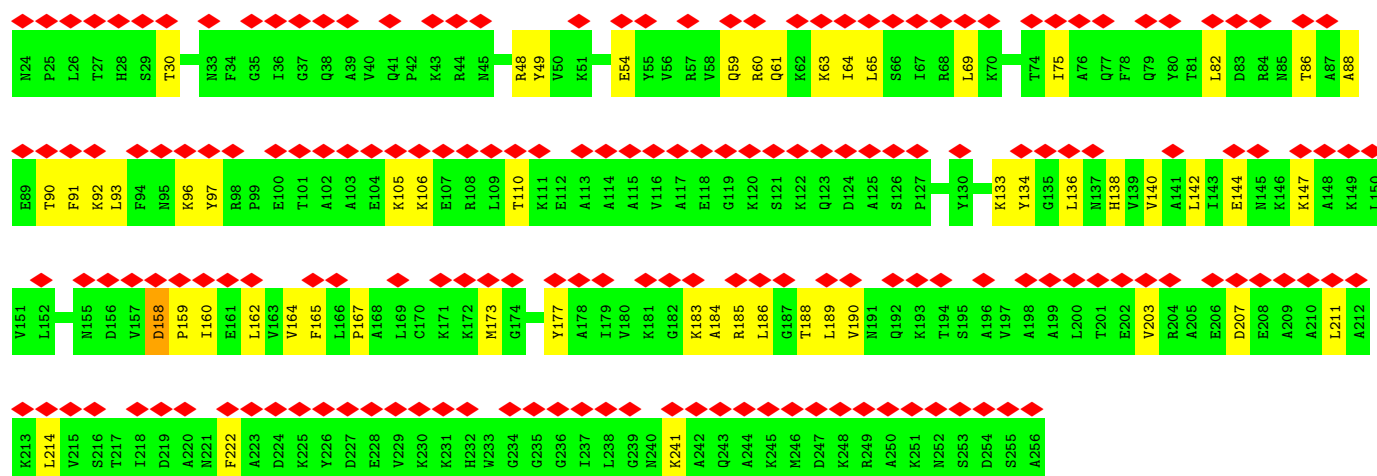
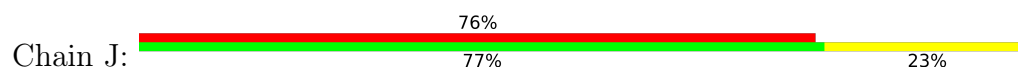
Chain H: 



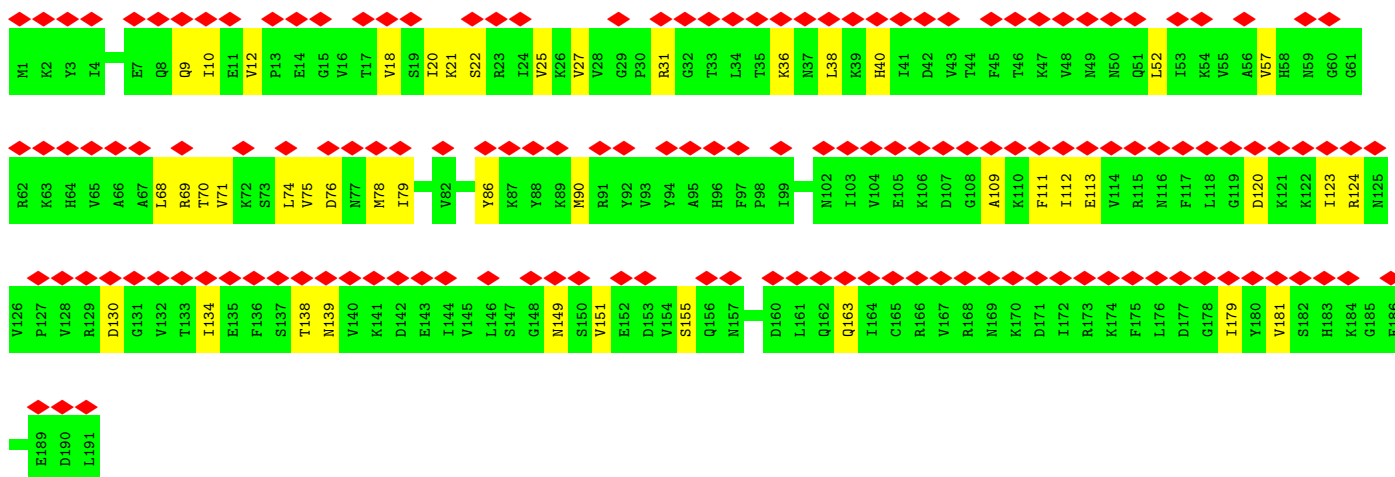
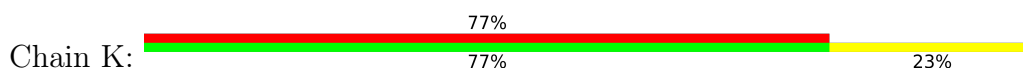
• Molecule 47: Large ribosomal subunit protein uL30A



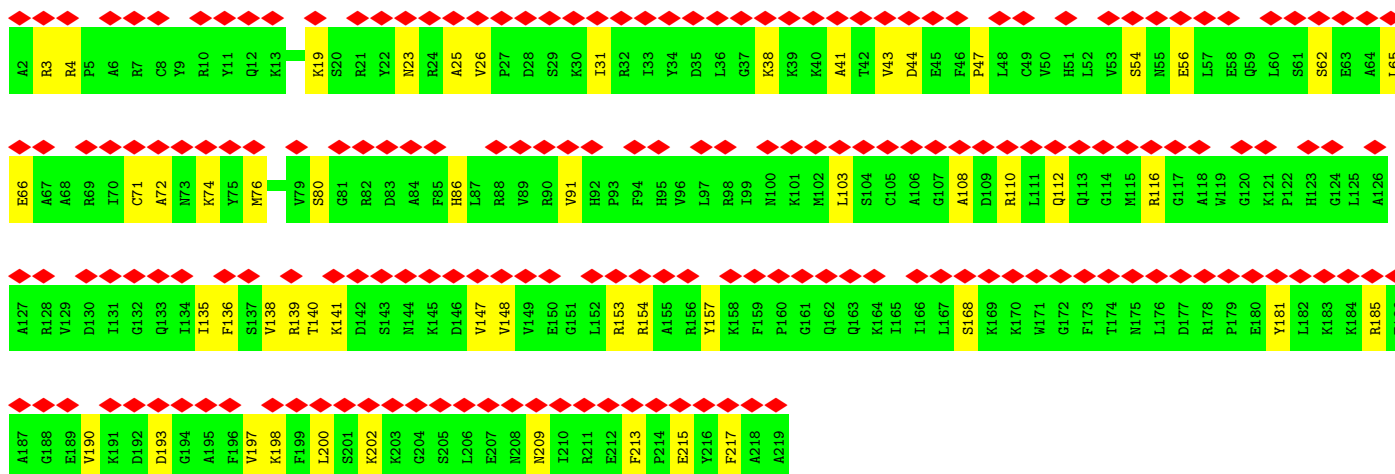
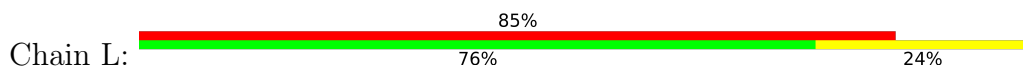
• Molecule 48: Large ribosomal subunit protein eL8A



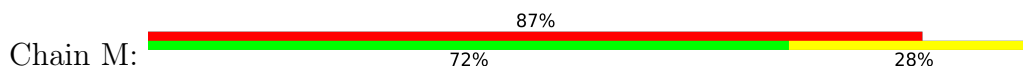
• Molecule 49: Large ribosomal subunit protein uL6A



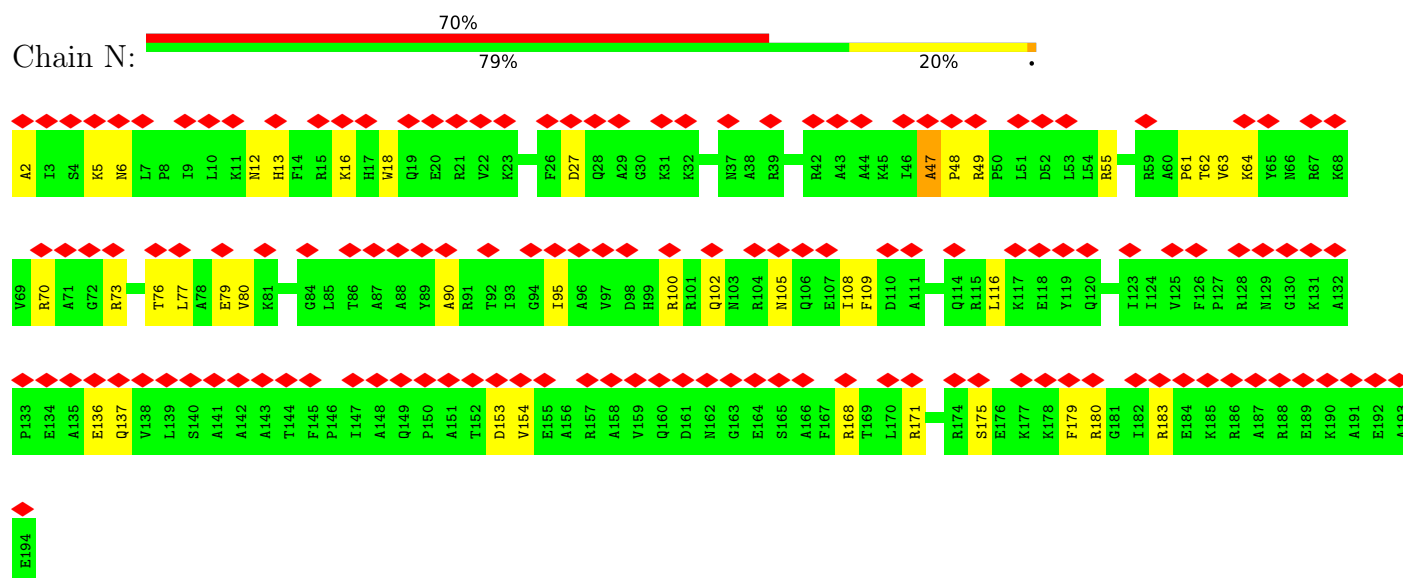
- Molecule 50: Large ribosomal subunit protein uL16



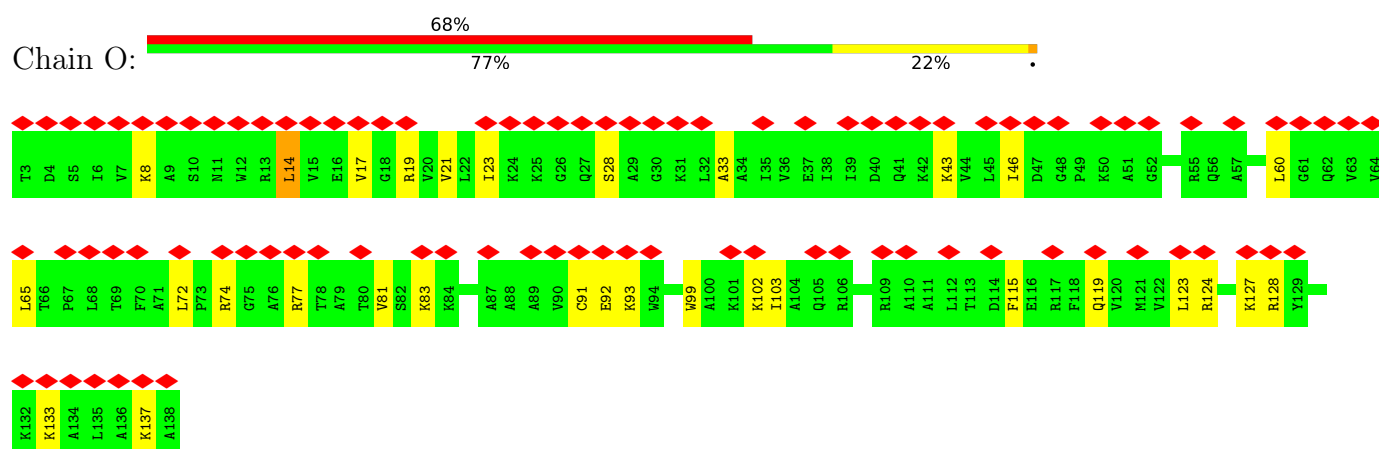
- Molecule 51: Large ribosomal subunit protein uL5B



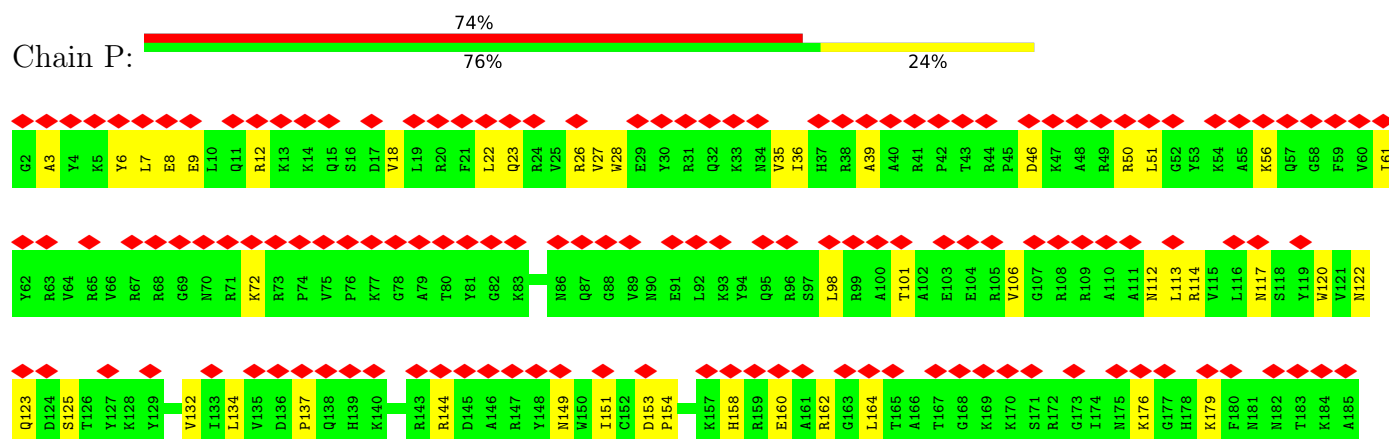
- Molecule 52: Large ribosomal subunit protein eL13A

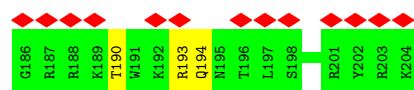


- Molecule 53: Large ribosomal subunit protein eL14A

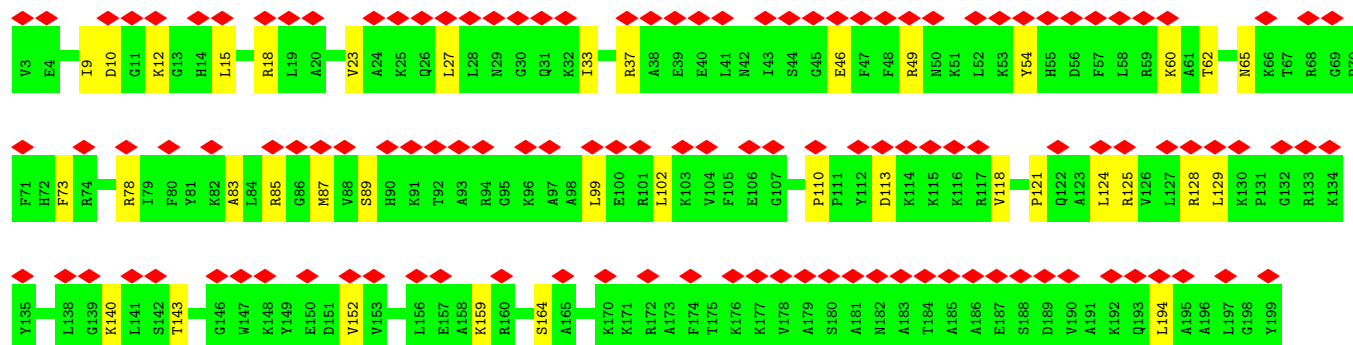
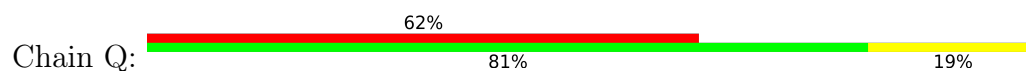


- Molecule 54: Large ribosomal subunit protein eL15A

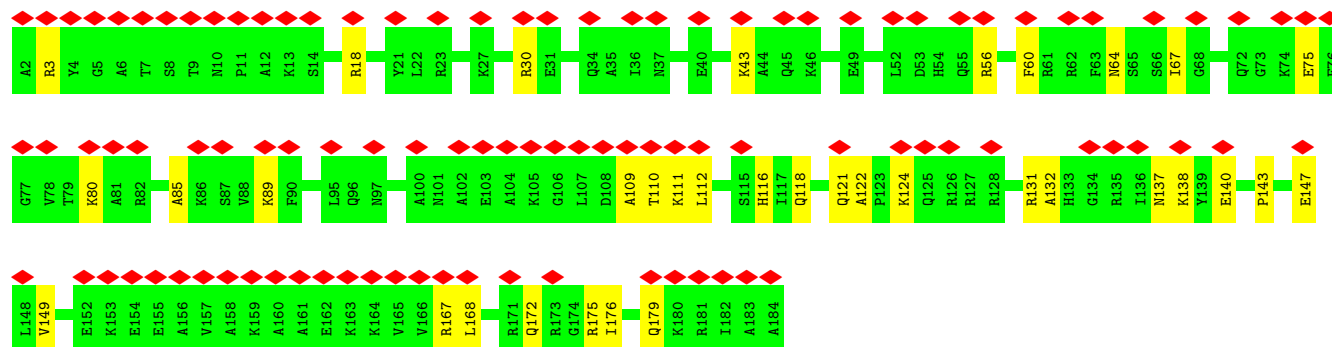
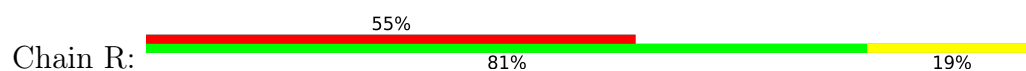




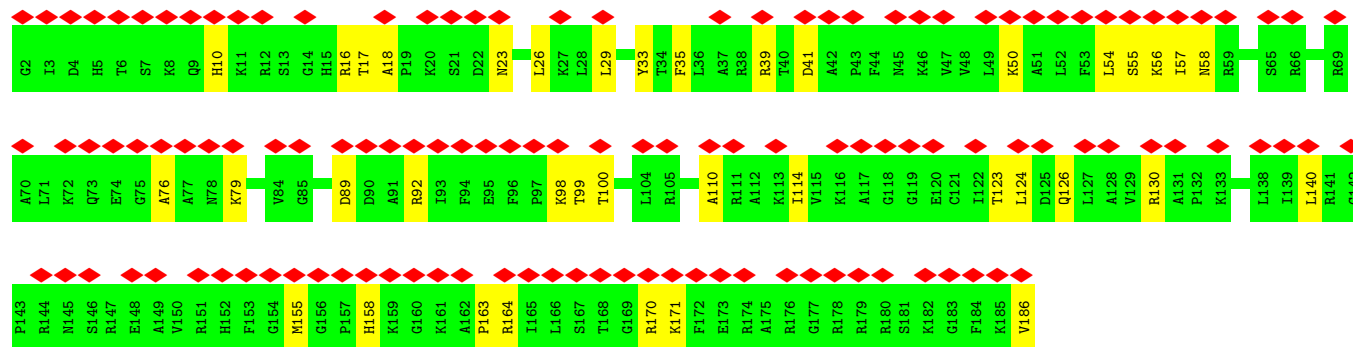
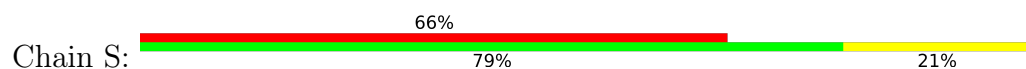
- Molecule 55: Large ribosomal subunit protein uL13A



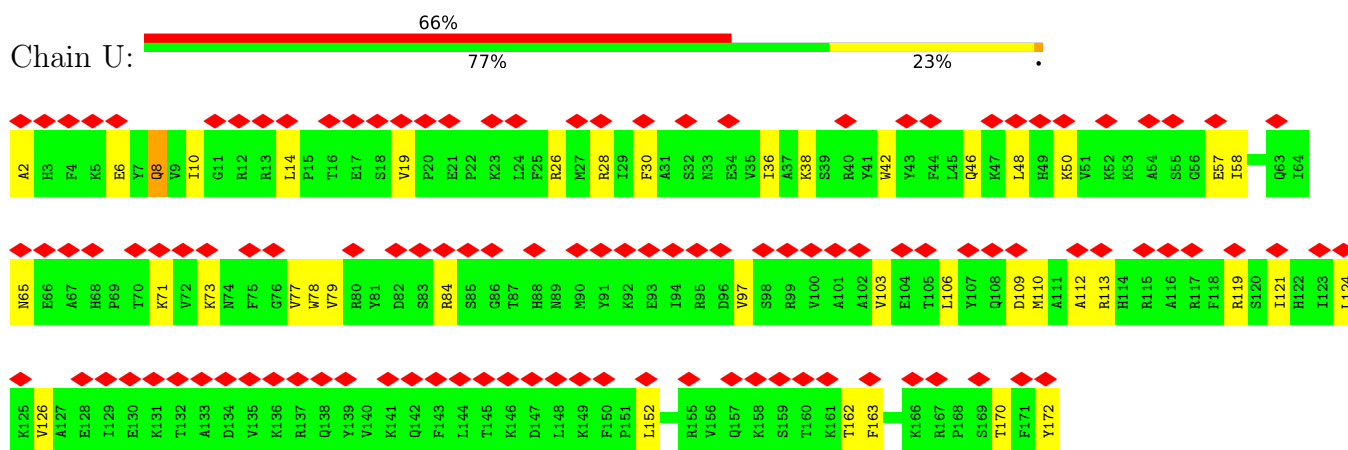
- Molecule 56: Large ribosomal subunit protein uL22A



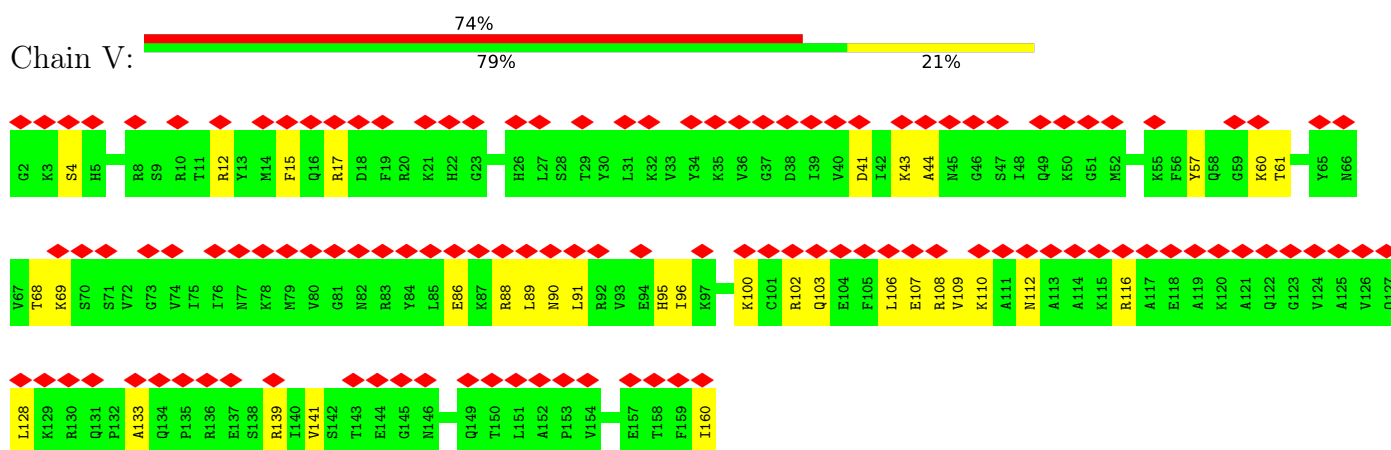
- Molecule 57: Large ribosomal subunit protein eL18A



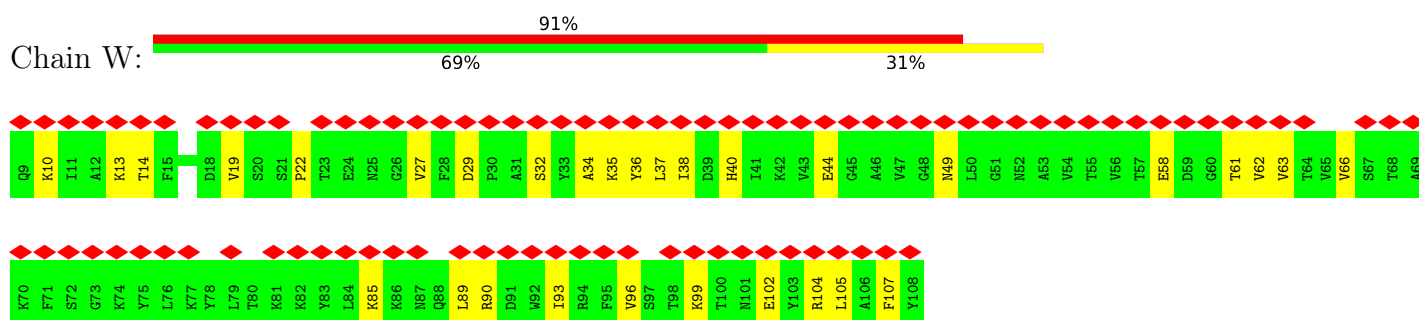
- Molecule 58: Large ribosomal subunit protein eL20A



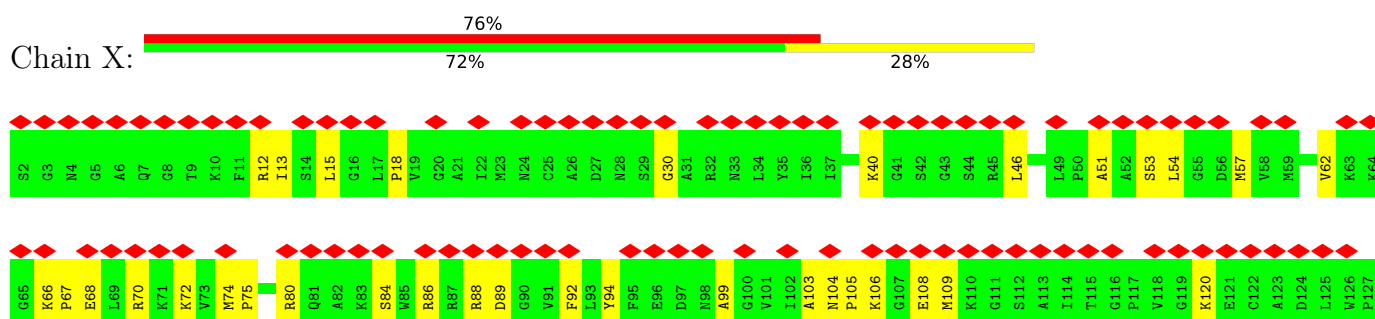
• Molecule 59: Large ribosomal subunit protein eL21A



• Molecule 60: Large ribosomal subunit protein eL22A

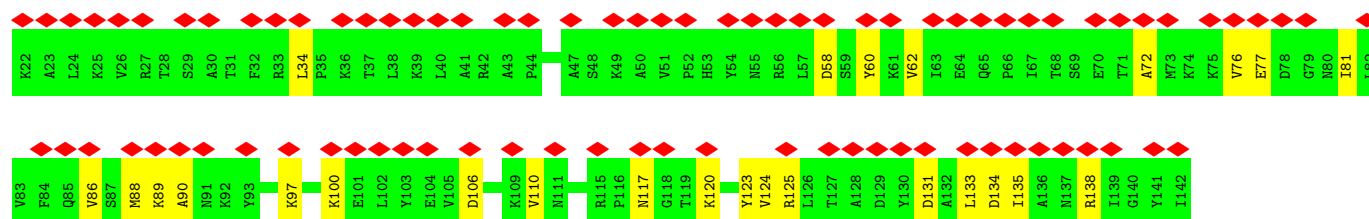
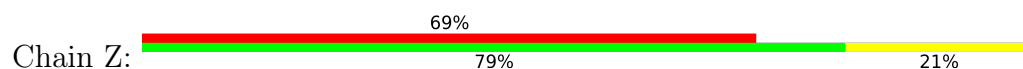


• Molecule 61: Large ribosomal subunit protein uL14A

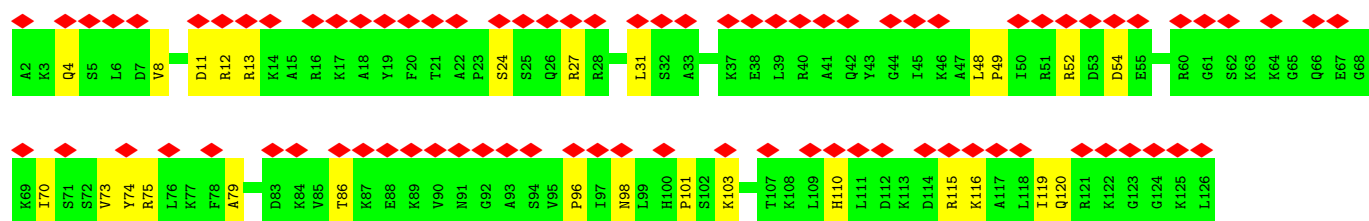
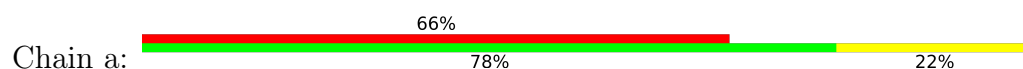




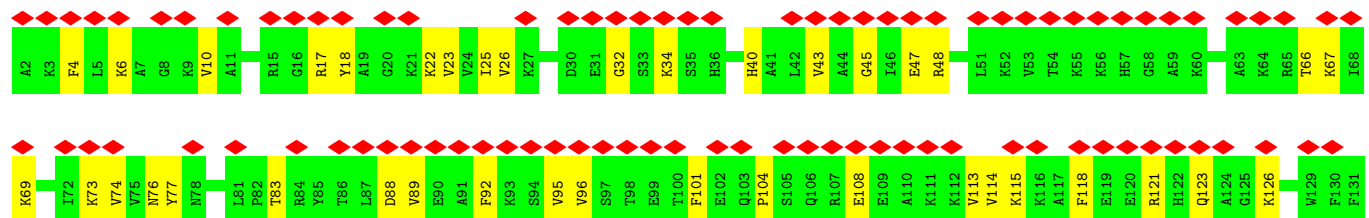
- Molecule 62: Large ribosomal subunit protein uL23



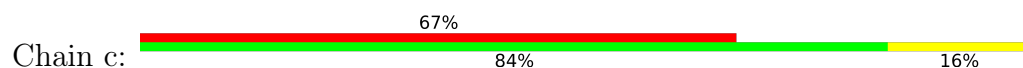
- Molecule 63: Large ribosomal subunit protein uL24A

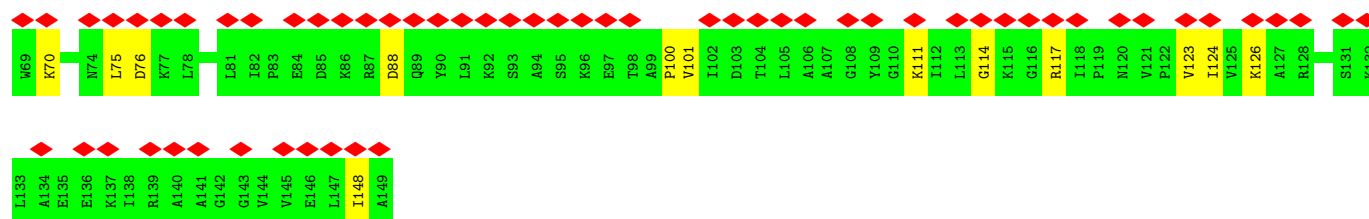


- Molecule 64: Large ribosomal subunit protein eL27A

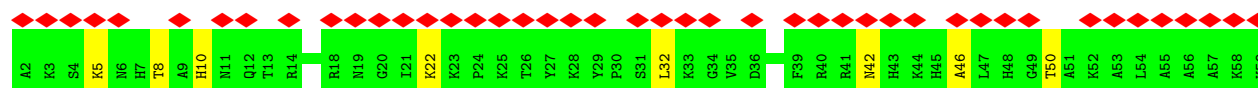
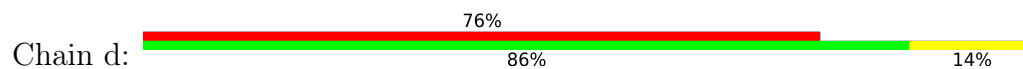


- Molecule 65: Large ribosomal subunit protein uL15

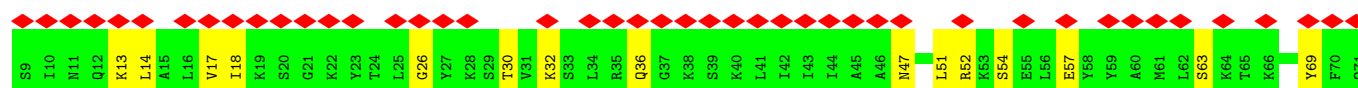
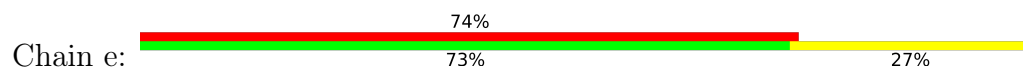




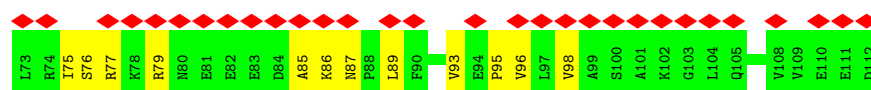
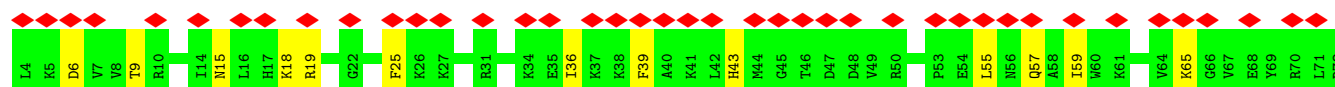
- Molecule 66: Large ribosomal subunit protein eL29



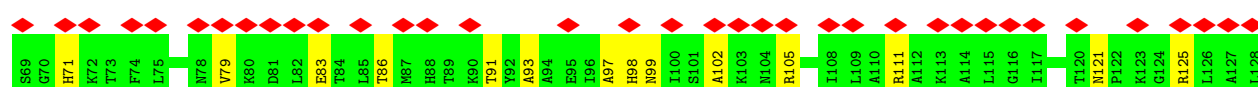
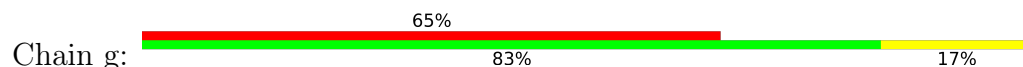
- Molecule 67: Large ribosomal subunit protein eL30



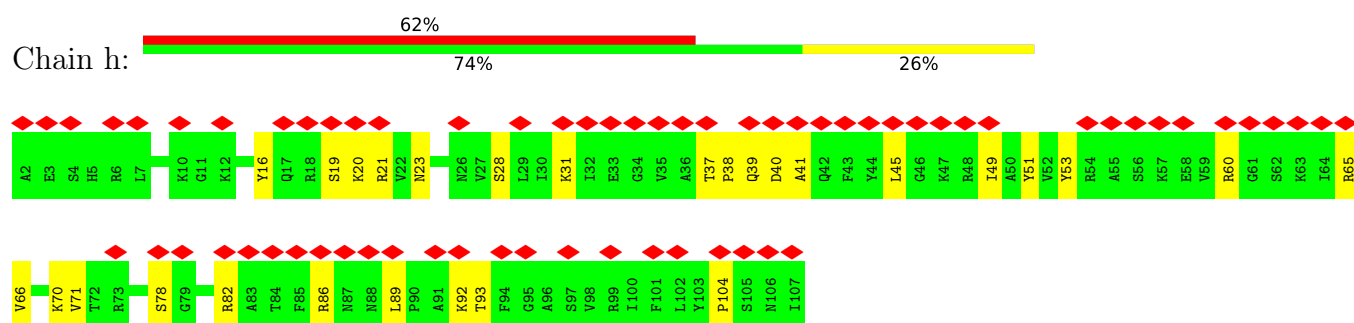
- Molecule 68: Large ribosomal subunit protein eL31A



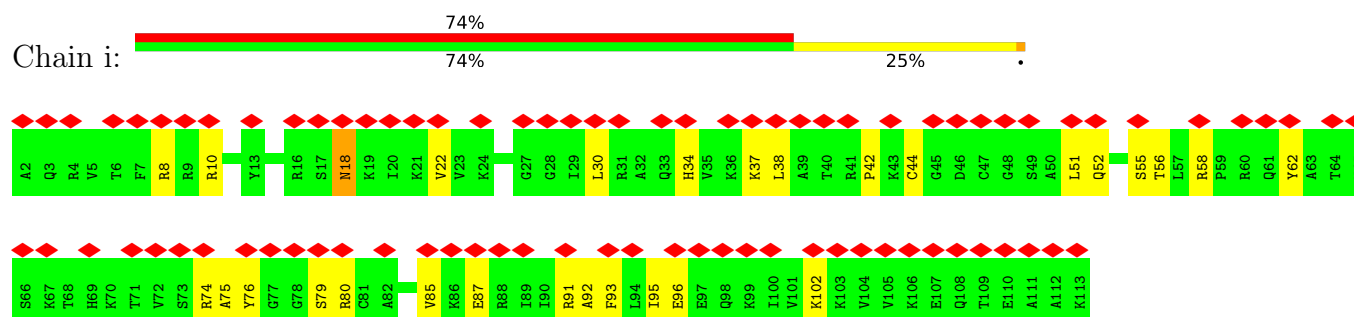
- Molecule 69: Large ribosomal subunit protein eL32



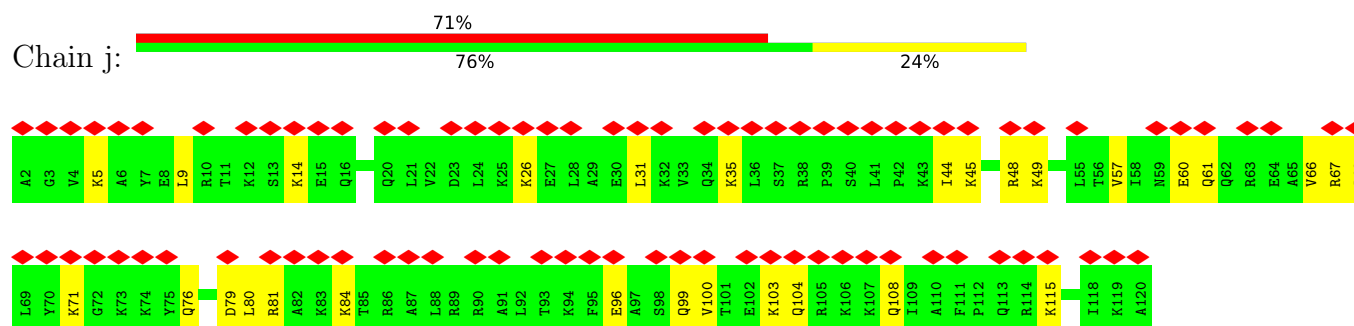
- Molecule 70: Large ribosomal subunit protein eL33A



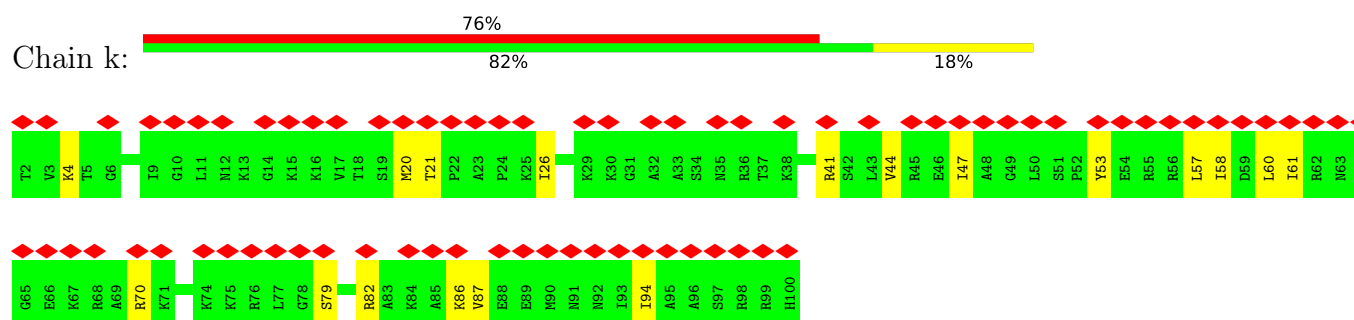
- Molecule 71: Large ribosomal subunit protein eL34A



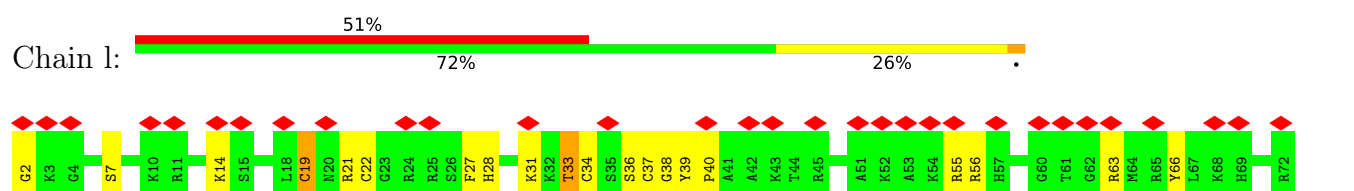
- Molecule 72: Large ribosomal subunit protein uL29A

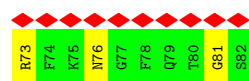


- Molecule 73: Large ribosomal subunit protein eL36A

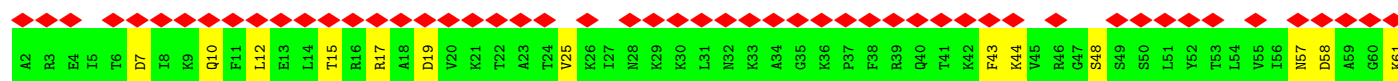
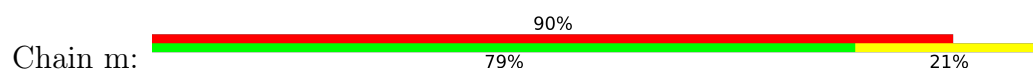


- Molecule 74: Large ribosomal subunit protein eL37A

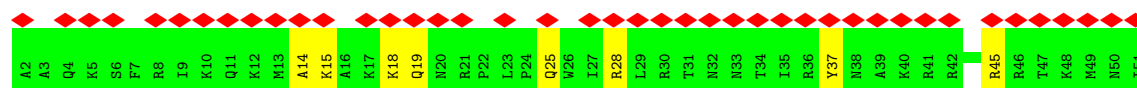
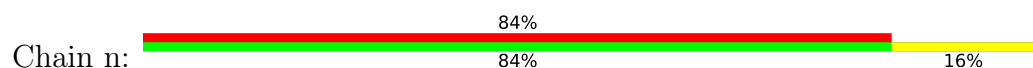




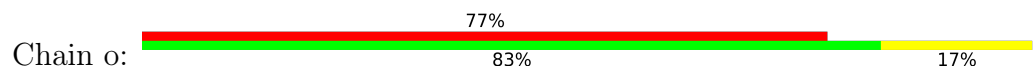
- Molecule 75: Large ribosomal subunit protein eL38



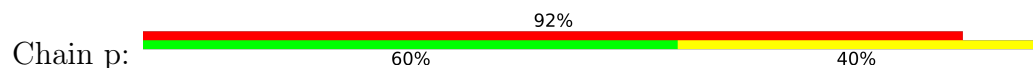
- Molecule 76: Large ribosomal subunit protein eL39



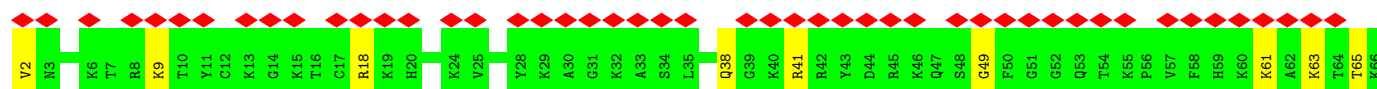
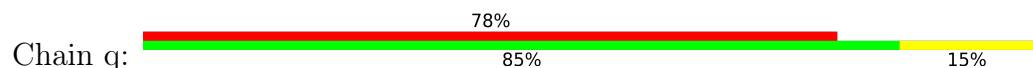
- Molecule 77: Large ribosomal subunit protein eL40A



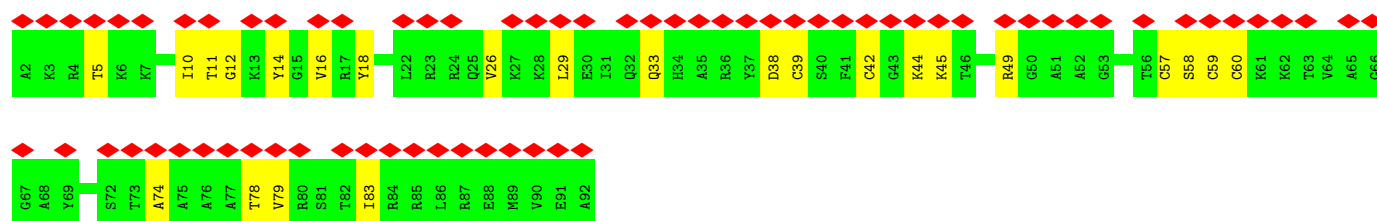
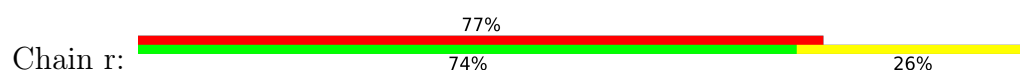
- Molecule 78: Large ribosomal subunit protein eL41A



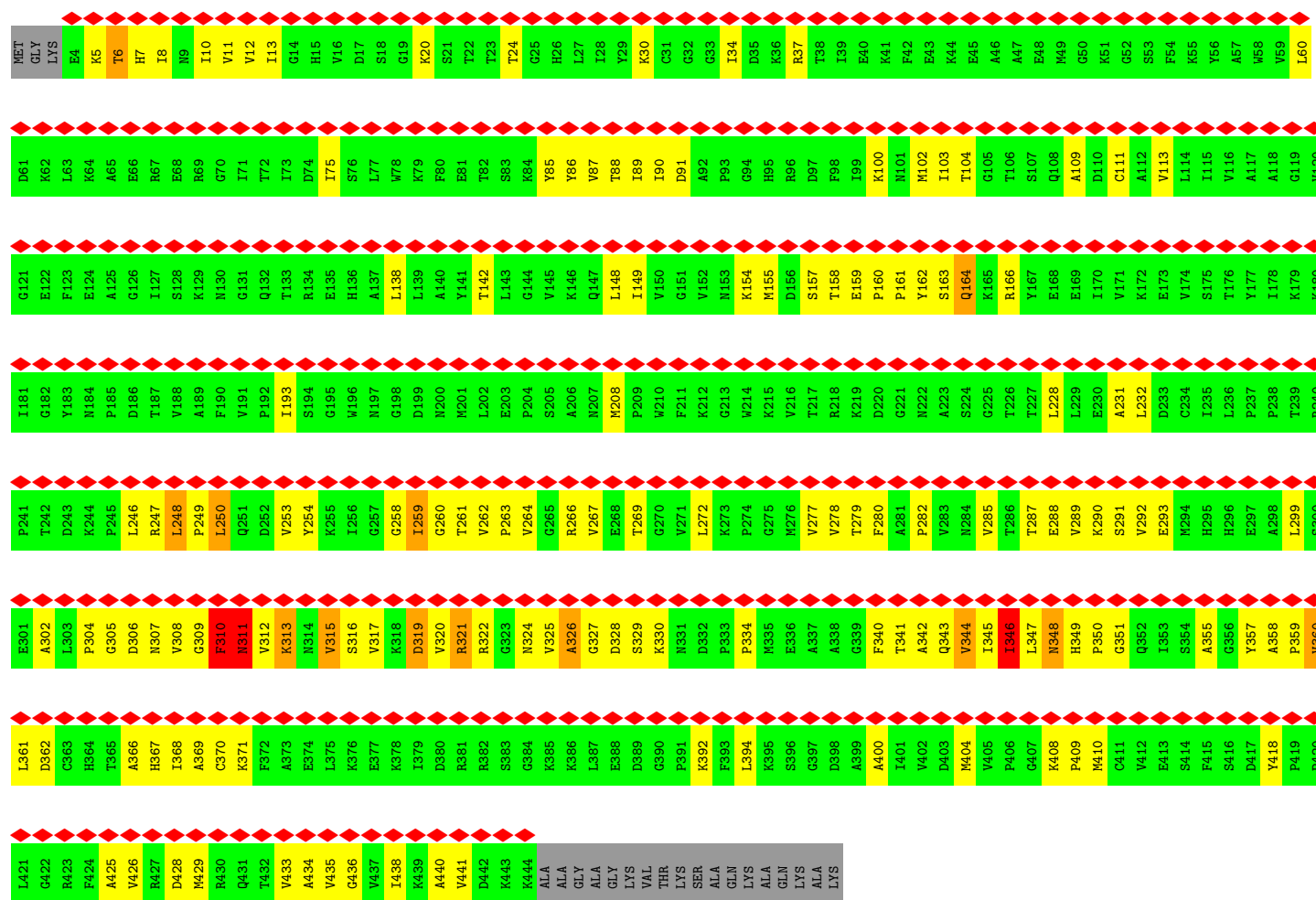
- Molecule 79: Large ribosomal subunit protein eL42A



- Molecule 80: Large ribosomal subunit protein eL43A



• Molecule 81: Elongation factor 1-alpha 1



G842	G843	G844	G845	G846	S847	H848	S849	K850	M851	V852	A853	E854	V855	D856	M857	K858	E859	A860	L861	A862	S863	G864	Q865	P866	P867	P868	L869	T870	S871	R872	E873	Q756	Q757	R758	V759	Q760	T761	G762	E763	D764	R765	E766	T767	M768	D769	V770	P771	N772	A773	R774	L775	M776	E777	M778	D779	A780	R841				
K661	Q662	K663	A664	I665	V666	K667	V668	T669	N670	M671	E672	F673	G674	V675	P676	G677	T678	S679	K680	P681	Q682	L683	T684	E685	I686	I687	L688	T689	Q690	S691	L692	S693	S694	R695	T696	A697	V698	E699	G700	L701	N702	G703	A704	G705	K706	S707	T708	L709	I710	N711	V712	L713	T714	G715	E716	L717	L718	P719	T720		
F601	L602	D603	N604	V605	C606	E607	V608	I609	T610	N611	V612	E613	G614	L615	K616	L617	R618	R619	Y620	K621	G622	N623	F624	T625	L626	E627	V628	F629	N630	C631	P632	L633	A634	K635	A636	V637	E638	E639	L640	S641	N642	T643	D644	L645	E646	F647	K648	V649	P650	E651	P652	L653	T654	L655	E656	V657	V658	K659	T660		
S541	A542	L543	S544	G545	G546	W547	K548	M549	K550	L551	A552	L553	A554	R555	A556	V557	L558	R559	N560	A561	D562	L563	L564	L565	L566	D567	E568	F569	T570	N571	H572	L573	D574	T575	V576	N577	V578	A579	V580	L581	V582	N583	Y584	L585	N586	T587	C588	G589	T590	T591	S592	L593	T594	L595	S596	H597	D598	S599	V600		
D481	G482	F483	P484	T485	Q486	E487	E488	C489	R490	T491	V492	Y493	V494	E495	H496	D497	L498	D499	G500	T501	H502	S503	D504	T505	S506	V507	L508	D509	C510	V511	F512	E513	S514	G515	V516	G517	T518	K519	E520	A521	I522	K523	D524	K525	L526	I527	E528	F529	G530	F531	T532	D533	E534	M535	I536	A537	M538	P539	I540		
D421	D422	E423	E424	D425	Q426	E427	E428	D429	L430	C431	M432	C433	E434	F435	S436	L437	A438	Y439	G440	A441	K442	L443	L444	L445	M446	K447	T448	Q449	L450	R451	L452	K453	R454	A455	R456	R457	Y458	G459	L460	C461	G462	P463	M464	G465	C466	G467	K468	S469	T470	L471	M472	R473	A474	L475	A476	N477	G478	Q479	V480		
V361	E362	Y363	I364	A365	A366	I367	G368	A369	L370	L371	I372	D373	E374	R375	I376	I377	D378	Q379	Q380	A381	G382	F383	T384	H385	I386	T387	P388	Y389	K390	T391	I392	F393	L394	H395	E396	K397	K398	A399	K400	D401	L402	L403	D404	E405	F406	R407	K408	R409	A410	V411	D412	M413	L414	P415	V416	G417	P418	M419	F420		
A301	D302	P303	E304	A305	R306	E307	V308	T309	L310	R311	A312	L313	K314	T315	L316	R317	R318	V319	G320	N321	V322	G323	E324	D325	D326	A327	I328	P329	E330	V331	S332	H333	A334	G335	D336	V337	S338	T339	T340	L341	Q342	V343	V344	N345	E346	L347	L348	K349	D350	E351	T352	V353	A354	S355	R356	F357	K358	I359	V360		
N121	P122	V123	A124	I125	K126	A127	L128	L129	P130	H131	A132	L133	T134	M135	A136	I136	V137	E138	T139	M140	K141	V142	Q143	E144	K145	I146	A147	I148	L149	A150	A151	I152	S153	A154	C155	M156	V157	D157	A158	A159	K160	D161	Q162	V163	A164	L165	R166	M167	P168	E169	L170	I171	T172	P173	V174	L175	S176	E177	N178	V179	D180
K61	T62	A63	N64	A65	A66	M67	Q68	A69	V70	A71	H72	I73	A74	N75	Q76	S77	N78	L79	P81	S82	E83	E84	P85	Y86	I87	V88	Q89	L90	V91	P92	A93	I94	C95	T96	N97	A98	G99	N100	K101	D102	K103	E104	I105	Q106	S107	V108	A109	S110	E111	T112	L113	I114	S115	I116	V117	N118	A119	V120			



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	27708	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.588	Depositor
Minimum map value	-0.320	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.033	Depositor
Recommended contour level	0.219	Depositor
Map size (\AA)	528.0, 528.0, 528.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.32, 1.32, 1.32	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	2	0.07	0/42211	0.17	0/65773
2	SA	0.16	0/1754	0.39	0/2361
3	SB	0.20	0/1625	0.42	0/2197
4	SC	0.12	0/769	0.35	0/1039
5	SD	0.15	0/883	0.49	0/1199
6	SE	0.13	0/936	0.36	0/1259
7	SF	0.18	0/1125	0.45	0/1510
8	SG	0.14	0/971	0.45	0/1303
9	SH	0.16	0/1207	0.39	1/1623 (0.1%)
10	SI	0.12	0/1130	0.34	0/1517
11	SJ	0.14	0/807	0.55	1/1091 (0.1%)
12	SK	0.17	0/661	0.54	0/888
13	SL	0.10	0/493	0.28	0/663
14	SM	0.12	0/452	0.36	0/600
15	SN	0.18	0/567	0.49	0/764
16	SO	0.18	0/2436	0.50	2/3318 (0.1%)
17	SP	0.11	0/1644	0.31	0/2249
18	SQ	0.14	0/1823	0.37	0/2447
19	SR	0.12	0/1656	0.35	0/2251
20	SS	0.11	0/2097	0.33	0/2823
21	ST	0.11	0/1839	0.32	0/2460
22	SU	0.17	0/1498	0.41	1/2019 (0.0%)
23	SV	0.13	0/1501	0.32	0/2006
24	SW	0.10	0/1504	0.30	0/2016
25	SX	0.10	0/1168	0.30	0/1575
26	SY	0.10	0/1215	0.27	0/1638
27	SZ	0.13	0/901	0.35	0/1217
28	Sa	0.13	0/682	0.42	0/921
29	Sb	0.10	0/1038	0.29	0/1395
30	Sc	0.16	0/1139	0.34	0/1518
31	Sd	0.12	0/1087	0.33	0/1449
32	Se	0.12	0/761	0.39	0/1016
33	Sf	0.09	0/620	0.28	0/838
34	Sg	0.10	0/480	0.28	0/639

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	s	0.11	0/1805	0.27	2/2809 (0.1%)
36	t	0.07	0/1796	0.16	0/2799
37	B	0.05	0/2883	0.11	0/4491
38	C	0.05	0/3746	0.12	0/5832
39	T	0.09	0/1532	0.29	0/2043
40	Y	0.10	0/850	0.30	0/1152
41	A	0.08	0/76303	0.19	0/118956
42	D	0.09	0/1933	0.26	0/2598
43	E	0.09	0/3146	0.26	0/4228
44	F	0.09	0/2800	0.26	0/3790
45	G	0.11	0/2400	0.30	0/3239
46	H	0.14	0/1329	0.35	0/1794
47	I	0.11	0/1821	0.27	0/2451
48	J	0.13	0/1836	0.34	0/2481
49	K	0.13	0/1529	0.34	0/2060
50	L	0.11	0/1801	0.29	0/2416
51	M	0.13	0/1367	0.38	0/1834
52	N	0.12	0/1568	0.29	0/2106
53	O	0.09	0/1068	0.22	0/1438
54	P	0.08	0/1757	0.22	0/2354
55	Q	0.13	0/1585	0.28	0/2128
56	R	0.14	0/1439	0.29	0/1938
57	S	0.10	0/1465	0.25	0/1965
58	U	0.09	0/1473	0.27	0/1980
59	V	0.11	0/1296	0.30	0/1739
60	W	0.13	0/812	0.42	0/1099
61	X	0.14	0/1018	0.33	0/1369
62	Z	0.10	0/979	0.32	0/1321
63	a	0.10	0/995	0.26	0/1329
64	b	0.12	0/1106	0.31	0/1485
65	c	0.09	0/1200	0.27	0/1607
66	d	0.09	0/473	0.24	0/629
67	e	0.12	0/745	0.33	0/1001
68	f	0.09	0/890	0.25	0/1196
69	g	0.07	0/1034	0.21	0/1385
70	h	0.10	0/868	0.26	0/1168
71	i	0.11	0/890	0.29	0/1189
72	j	0.15	0/978	0.36	1/1301 (0.1%)
73	k	0.10	0/772	0.28	0/1026
74	l	0.36	1/660 (0.2%)	0.47	0/875
75	m	0.14	0/618	0.34	0/826
76	n	0.09	0/443	0.24	0/588
77	o	0.12	0/416	0.34	0/553

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	p	0.13	0/230	0.36	0/296
79	q	0.09	0/836	0.26	0/1104
80	r	0.17	0/701	0.40	0/934
81	x	0.54	0/3449	0.82	5/4667 (0.1%)
82	v	0.26	1/7611 (0.0%)	0.63	6/10322 (0.1%)
All	All	0.13	2/228932 (0.0%)	0.28	19/335473 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
81	x	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
82	v	648	LYS	C-N	-5.99	1.24	1.33
74	l	33	THR	C-N	5.71	1.41	1.33

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
81	x	311	ASN	CA-C-N	-7.95	107.66	121.97
81	x	311	ASN	C-N-CA	-7.95	107.66	121.97
11	SJ	101	LYS	N-CA-C	-7.19	103.71	114.64
82	v	180	ASP	N-CA-C	-7.18	103.15	110.97
35	s	76	C	C4'-C3'-O3'	6.83	119.65	109.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
81	x	159	GLU	Peptide

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	2	37739	0	18988	437	0
2	SA	1729	0	1812	39	0
3	SB	1605	0	1669	52	0
4	SC	752	0	719	29	0
5	SD	875	0	878	27	0
6	SE	916	0	941	19	0
7	SF	1105	0	1166	64	0
8	SG	961	0	999	39	0
9	SH	1188	0	1218	44	0
10	SI	1112	0	1124	34	0
11	SJ	797	0	863	27	0
12	SK	651	0	682	15	0
13	SL	491	0	524	13	0
14	SM	442	0	432	12	0
15	SN	556	0	549	15	0
16	SO	2383	0	2332	115	0
17	SP	1603	0	1610	35	0
18	SQ	1798	0	1890	40	0
19	SR	1626	0	1715	41	0
20	SS	2056	0	2140	47	0
21	ST	1815	0	1894	44	0
22	SU	1473	0	1555	35	0
23	SV	1476	0	1501	47	0
24	SW	1479	0	1556	37	0
25	SX	1142	0	1209	13	0
26	SY	1192	0	1255	21	0
27	SZ	891	0	883	29	0
28	Sa	673	0	662	21	0
29	Sb	1021	0	1060	30	0
30	Sc	1121	0	1196	37	0
31	Sd	1073	0	1132	23	0
32	Se	750	0	799	18	0
33	Sf	610	0	633	8	0
34	Sg	472	0	521	9	0
35	s	1616	0	824	82	0
36	t	1606	0	816	9	0
37	B	2579	0	1304	30	0
38	C	3353	0	1695	33	0
39	T	1515	0	1606	29	0
40	Y	836	0	706	16	0
41	A	68170	0	34260	1138	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	D	1899	0	1957	57	0
43	E	3075	0	3142	70	0
44	F	2748	0	2859	40	0
45	G	2351	0	2294	38	0
46	H	1307	0	1377	39	0
47	I	1784	0	1862	33	0
48	J	1804	0	1877	40	0
49	K	1508	0	1572	27	0
50	L	1764	0	1804	42	0
51	M	1346	0	1370	37	0
52	N	1543	0	1608	30	0
53	O	1053	0	1149	26	0
54	P	1720	0	1779	41	0
55	Q	1555	0	1659	29	0
56	R	1416	0	1433	27	0
57	S	1441	0	1543	30	0
58	U	1437	0	1475	32	0
59	V	1272	0	1312	29	0
60	W	796	0	812	22	0
61	X	1003	0	1048	22	0
62	Z	964	0	1025	20	0
63	a	984	0	1075	20	0
64	b	1080	0	1122	31	0
65	c	1169	0	1211	19	0
66	d	462	0	491	7	0
67	e	737	0	792	18	0
68	f	876	0	912	14	0
69	g	1013	0	1077	19	0
70	h	850	0	880	21	0
71	i	880	0	945	23	0
72	j	969	0	1078	20	0
73	k	766	0	844	11	0
74	l	645	0	649	29	0
75	m	612	0	682	12	0
76	n	436	0	475	7	0
77	o	410	0	446	8	0
78	p	229	0	273	10	0
79	q	824	0	892	12	0
80	r	694	0	738	20	0
81	x	3379	0	3433	296	0
82	v	7476	0	7414	439	0
All	All	213525	0	159704	3968	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 11.

The worst 5 of 3968 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)
81:x:280:PHE:HB3	81:x:324:ASN:CG	1.48	1.35
35:s:77:A:C5	81:x:293:GLU:HG3	1.76	1.20
81:x:346:ILE:HA	81:x:434:ALA:CA	1.72	1.18
81:x:280:PHE:CD1	81:x:324:ASN:HB2	1.80	1.16
30:Sc:63:GLN:HB3	30:Sc:64:PRO:HD2	1.23	1.14

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	
2	SA	220/222 (99%)	208 (94%)	11 (5%)	1 (0%)	24	57
3	SB	204/206 (99%)	186 (91%)	13 (6%)	5 (2%)	4	28
4	SC	90/92 (98%)	76 (84%)	12 (13%)	2 (2%)	5	30
5	SD	119/121 (98%)	99 (83%)	20 (17%)	0	100	100
6	SE	115/117 (98%)	104 (90%)	11 (10%)	0	100	100
7	SF	139/141 (99%)	130 (94%)	7 (5%)	2 (1%)	9	38
8	SG	119/121 (98%)	108 (91%)	11 (9%)	0	100	100
9	SH	143/145 (99%)	137 (96%)	6 (4%)	0	100	100
10	SI	141/143 (99%)	132 (94%)	8 (6%)	1 (1%)	18	51
11	SJ	98/100 (98%)	87 (89%)	11 (11%)	0	100	100
12	SK	80/108 (74%)	64 (80%)	14 (18%)	2 (2%)	4	28
13	SL	61/63 (97%)	58 (95%)	3 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	SM	51/53 (96%)	47 (92%)	4 (8%)	0	100	100
15	SN	71/73 (97%)	49 (69%)	21 (30%)	1 (1%)	9	38
16	SO	310/312 (99%)	285 (92%)	24 (8%)	1 (0%)	36	65
17	SP	204/206 (99%)	191 (94%)	12 (6%)	1 (0%)	24	57
18	SQ	222/232 (96%)	203 (91%)	19 (9%)	0	100	100
19	SR	214/216 (99%)	204 (95%)	10 (5%)	0	100	100
20	SS	256/258 (99%)	240 (94%)	16 (6%)	0	100	100
21	ST	226/228 (99%)	220 (97%)	5 (2%)	1 (0%)	30	61
22	SU	182/184 (99%)	170 (93%)	11 (6%)	1 (0%)	24	57
23	SV	183/200 (92%)	172 (94%)	11 (6%)	0	100	100
24	SW	182/184 (99%)	176 (97%)	6 (3%)	0	100	100
25	SX	140/142 (99%)	132 (94%)	7 (5%)	1 (1%)	18	51
26	SY	148/150 (99%)	142 (96%)	6 (4%)	0	100	100
27	SZ	125/127 (98%)	113 (90%)	12 (10%)	0	100	100
28	Sa	85/87 (98%)	77 (91%)	8 (9%)	0	100	100
29	Sb	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	16	49
30	Sc	142/144 (99%)	136 (96%)	4 (3%)	2 (1%)	9	38
31	Sd	132/134 (98%)	126 (96%)	6 (4%)	0	100	100
32	Se	92/94 (98%)	79 (86%)	13 (14%)	0	100	100
33	Sf	79/81 (98%)	76 (96%)	3 (4%)	0	100	100
34	Sg	58/60 (97%)	53 (91%)	5 (9%)	0	100	100
39	T	186/188 (99%)	184 (99%)	2 (1%)	0	100	100
40	Y	124/126 (98%)	111 (90%)	11 (9%)	2 (2%)	7	36
42	D	249/251 (99%)	239 (96%)	10 (4%)	0	100	100
43	E	384/386 (100%)	370 (96%)	14 (4%)	0	100	100
44	F	359/361 (99%)	348 (97%)	11 (3%)	0	100	100
45	G	292/294 (99%)	279 (96%)	13 (4%)	0	100	100
46	H	163/175 (93%)	151 (93%)	12 (7%)	0	100	100
47	I	220/223 (99%)	216 (98%)	4 (2%)	0	100	100
48	J	231/233 (99%)	217 (94%)	13 (6%)	1 (0%)	30	61
49	K	189/191 (99%)	181 (96%)	8 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
50	L	216/218 (99%)	207 (96%)	9 (4%)	0	100	100
51	M	167/169 (99%)	157 (94%)	10 (6%)	0	100	100
52	N	191/193 (99%)	178 (93%)	11 (6%)	2 (1%)	12	45
53	O	134/136 (98%)	128 (96%)	6 (4%)	0	100	100
54	P	201/203 (99%)	196 (98%)	5 (2%)	0	100	100
55	Q	195/197 (99%)	189 (97%)	6 (3%)	0	100	100
56	R	181/183 (99%)	172 (95%)	9 (5%)	0	100	100
57	S	183/185 (99%)	175 (96%)	7 (4%)	1 (0%)	24	57
58	U	169/171 (99%)	161 (95%)	8 (5%)	0	100	100
59	V	157/159 (99%)	149 (95%)	8 (5%)	0	100	100
60	W	98/100 (98%)	89 (91%)	9 (9%)	0	100	100
61	X	134/136 (98%)	133 (99%)	1 (1%)	0	100	100
62	Z	119/121 (98%)	113 (95%)	6 (5%)	0	100	100
63	a	123/125 (98%)	120 (98%)	3 (2%)	0	100	100
64	b	133/135 (98%)	127 (96%)	6 (4%)	0	100	100
65	c	146/148 (99%)	138 (94%)	8 (6%)	0	100	100
66	d	56/58 (97%)	54 (96%)	2 (4%)	0	100	100
67	e	94/96 (98%)	92 (98%)	2 (2%)	0	100	100
68	f	107/109 (98%)	102 (95%)	5 (5%)	0	100	100
69	g	125/127 (98%)	124 (99%)	1 (1%)	0	100	100
70	h	104/106 (98%)	97 (93%)	7 (7%)	0	100	100
71	i	110/112 (98%)	104 (94%)	6 (6%)	0	100	100
72	j	117/119 (98%)	114 (97%)	3 (3%)	0	100	100
73	k	97/99 (98%)	93 (96%)	4 (4%)	0	100	100
74	l	79/81 (98%)	74 (94%)	5 (6%)	0	100	100
75	m	75/77 (97%)	69 (92%)	6 (8%)	0	100	100
76	n	48/50 (96%)	47 (98%)	1 (2%)	0	100	100
77	o	50/52 (96%)	48 (96%)	2 (4%)	0	100	100
78	p	23/25 (92%)	23 (100%)	0	0	100	100
79	q	101/103 (98%)	96 (95%)	5 (5%)	0	100	100
80	r	89/91 (98%)	84 (94%)	5 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
81	x	439/462 (95%)	402 (92%)	30 (7%)	7 (2%)	7	36
82	v	975/1044 (93%)	872 (89%)	99 (10%)	4 (0%)	30	61
All	All	12391/12691 (98%)	11622 (94%)	730 (6%)	39 (0%)	37	65

5 of 39 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	SC	83	PRO
4	SC	88	PRO
7	SF	39	VAL
7	SF	40	GLU
12	SK	33	LYS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	SA	182/182 (100%)	182 (100%)	0	100	100
3	SB	172/173 (99%)	170 (99%)	2 (1%)	63	73
4	SC	77/85 (91%)	76 (99%)	1 (1%)	61	72
5	SD	88/98 (90%)	87 (99%)	1 (1%)	65	74
6	SE	95/98 (97%)	95 (100%)	0	100	100
7	SF	117/117 (100%)	117 (100%)	0	100	100
8	SG	105/110 (96%)	104 (99%)	1 (1%)	68	75
9	SH	127/128 (99%)	127 (100%)	0	100	100
10	SI	115/115 (100%)	114 (99%)	1 (1%)	70	76
11	SJ	93/93 (100%)	93 (100%)	0	100	100
12	SK	67/89 (75%)	67 (100%)	0	100	100
13	SL	55/56 (98%)	55 (100%)	0	100	100
14	SM	47/47 (100%)	46 (98%)	1 (2%)	47	65
15	SN	56/64 (88%)	56 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	SO	250/257 (97%)	247 (99%)	3 (1%)	63	73
17	SP	170/173 (98%)	170 (100%)	0	100	100
18	SQ	200/205 (98%)	198 (99%)	2 (1%)	68	75
19	SR	175/175 (100%)	173 (99%)	2 (1%)	65	74
20	SS	220/220 (100%)	220 (100%)	0	100	100
21	ST	189/195 (97%)	189 (100%)	0	100	100
22	SU	163/165 (99%)	163 (100%)	0	100	100
23	SV	148/161 (92%)	148 (100%)	0	100	100
24	SW	156/157 (99%)	155 (99%)	1 (1%)	78	79
25	SX	126/127 (99%)	126 (100%)	0	100	100
26	SY	127/127 (100%)	126 (99%)	1 (1%)	73	77
27	SZ	81/96 (84%)	80 (99%)	1 (1%)	63	73
28	Sa	71/74 (96%)	71 (100%)	0	100	100
29	Sb	110/110 (100%)	110 (100%)	0	100	100
30	Sc	119/119 (100%)	119 (100%)	0	100	100
31	Sd	112/112 (100%)	111 (99%)	1 (1%)	70	76
32	Se	81/81 (100%)	81 (100%)	0	100	100
33	Sf	70/70 (100%)	70 (100%)	0	100	100
34	Sg	50/51 (98%)	50 (100%)	0	100	100
39	T	152/153 (99%)	152 (100%)	0	100	100
40	Y	56/108 (52%)	56 (100%)	0	100	100
42	D	190/193 (98%)	190 (100%)	0	100	100
43	E	319/322 (99%)	316 (99%)	3 (1%)	70	76
44	F	288/288 (100%)	287 (100%)	1 (0%)	86	83
45	G	241/243 (99%)	239 (99%)	2 (1%)	73	77
46	H	139/154 (90%)	139 (100%)	0	100	100
47	I	186/187 (100%)	186 (100%)	0	100	100
48	J	187/191 (98%)	187 (100%)	0	100	100
49	K	168/171 (98%)	168 (100%)	0	100	100
50	L	185/185 (100%)	184 (100%)	1 (0%)	81	80
51	M	145/147 (99%)	144 (99%)	1 (1%)	76	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	N	154/154 (100%)	153 (99%)	1 (1%)	78	79
53	O	107/107 (100%)	106 (99%)	1 (1%)	70	76
54	P	175/175 (100%)	175 (100%)	0	100	100
55	Q	160/160 (100%)	160 (100%)	0	100	100
56	R	138/145 (95%)	138 (100%)	0	100	100
57	S	150/150 (100%)	149 (99%)	1 (1%)	76	78
58	U	155/155 (100%)	153 (99%)	2 (1%)	61	72
59	V	135/136 (99%)	134 (99%)	1 (1%)	76	78
60	W	87/87 (100%)	87 (100%)	0	100	100
61	X	104/104 (100%)	104 (100%)	0	100	100
62	Z	104/105 (99%)	104 (100%)	0	100	100
63	a	108/108 (100%)	108 (100%)	0	100	100
64	b	112/115 (97%)	111 (99%)	1 (1%)	70	76
65	c	117/118 (99%)	117 (100%)	0	100	100
66	d	46/46 (100%)	46 (100%)	0	100	100
67	e	81/81 (100%)	81 (100%)	0	100	100
68	f	92/96 (96%)	92 (100%)	0	100	100
69	g	107/109 (98%)	107 (100%)	0	100	100
70	h	90/90 (100%)	90 (100%)	0	100	100
71	i	95/95 (100%)	94 (99%)	1 (1%)	65	74
72	j	104/104 (100%)	103 (99%)	1 (1%)	68	75
73	k	80/81 (99%)	79 (99%)	1 (1%)	61	72
74	l	67/67 (100%)	66 (98%)	1 (2%)	57	70
75	m	68/68 (100%)	68 (100%)	0	100	100
76	n	45/45 (100%)	45 (100%)	0	100	100
77	o	45/47 (96%)	45 (100%)	0	100	100
78	p	22/23 (96%)	22 (100%)	0	100	100
79	q	87/88 (99%)	87 (100%)	0	100	100
80	r	71/71 (100%)	71 (100%)	0	100	100
81	x	366/379 (97%)	349 (95%)	17 (5%)	24	51
82	v	789/890 (89%)	777 (98%)	12 (2%)	57	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	10331/10671 (97%)	10265 (99%)	66 (1%)	76 79

5 of 66 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
82	v	475	ILE
82	v	660	THR
82	v	880	MET
50	L	140	THR
45	G	221	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 107 such sidechains are listed below:

Mol	Chain	Res	Type
52	N	12	ASN
57	S	23	ASN
82	v	395	HIS
53	O	56	GLN
54	P	117	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1768/1799 (98%)	408 (23%)	40 (2%)
35	s	74/77 (96%)	32 (43%)	0
36	t	74/75 (98%)	18 (24%)	0
37	B	120/121 (99%)	9 (7%)	1 (0%)
38	C	157/158 (99%)	26 (16%)	1 (0%)
41	A	3180/3394 (93%)	506 (15%)	9 (0%)
All	All	5373/5624 (95%)	999 (18%)	51 (0%)

5 of 999 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	4	C
1	2	25	C
1	2	26	A
1	2	34	G

5 of 51 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	1256	A
1	2	1557	U
41	A	3004	C
1	2	1273	G
1	2	1382	A

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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

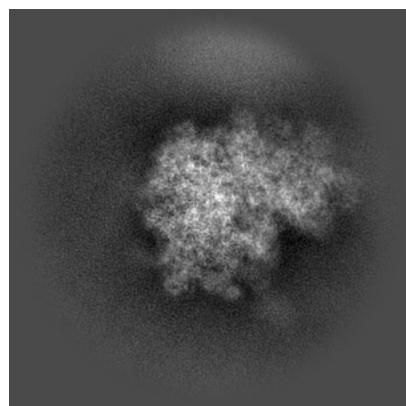
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38657. These allow visual inspection of the internal detail of the map and identification of artifacts.

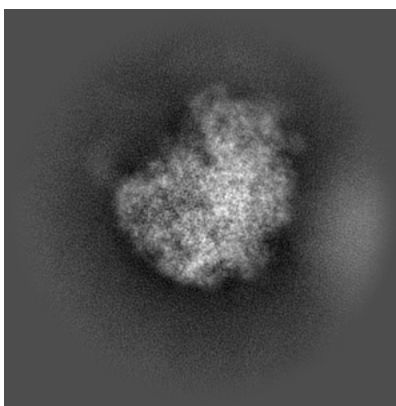
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

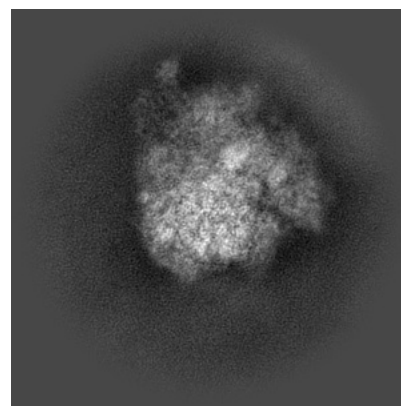
6.1.1 Primary map



X

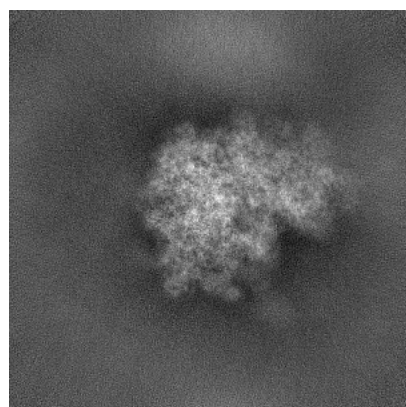


Y

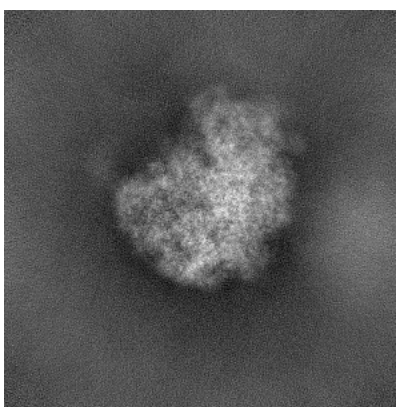


Z

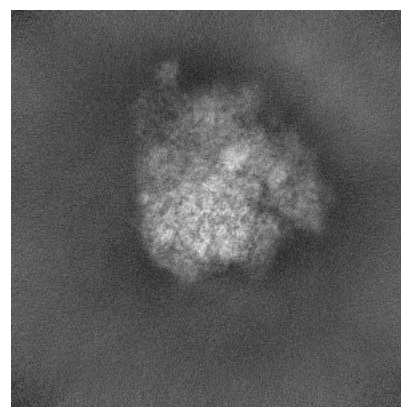
6.1.2 Raw map



X



Y

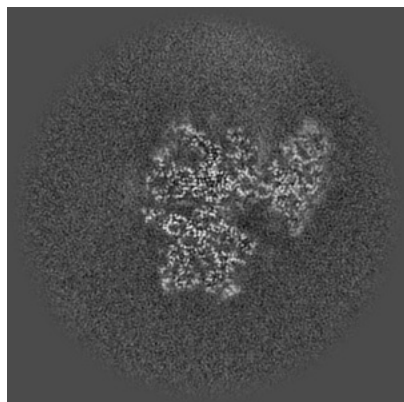


Z

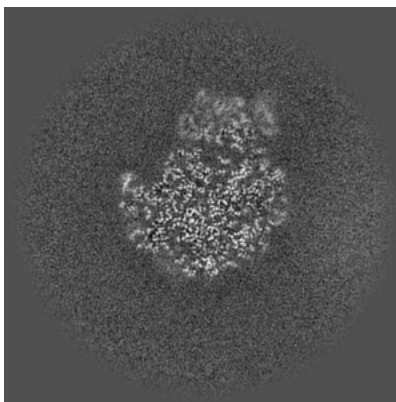
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

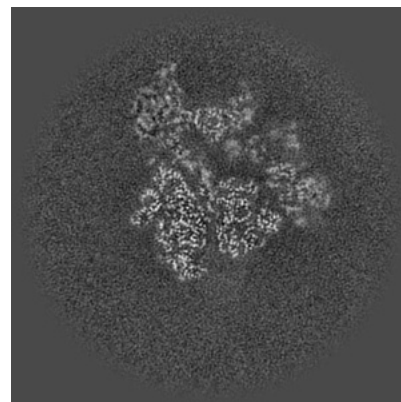
6.2.1 Primary map



X Index: 200

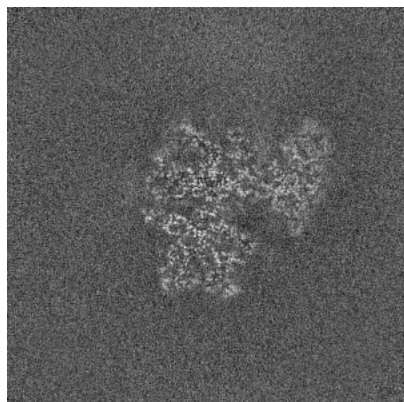


Y Index: 200

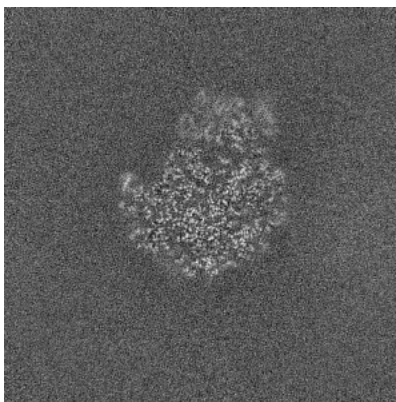


Z Index: 200

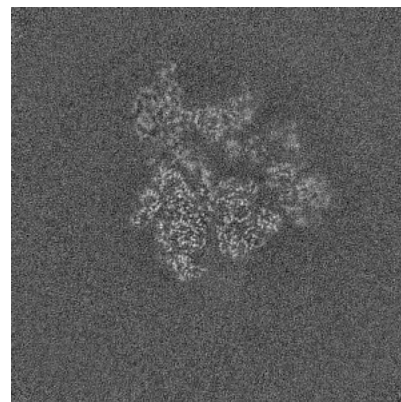
6.2.2 Raw map



X Index: 200



Y Index: 200

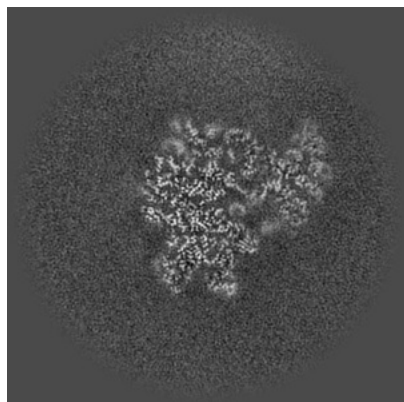


Z Index: 200

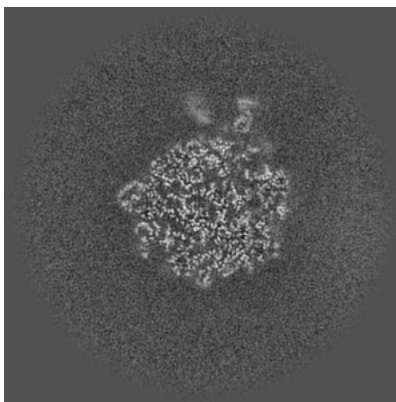
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

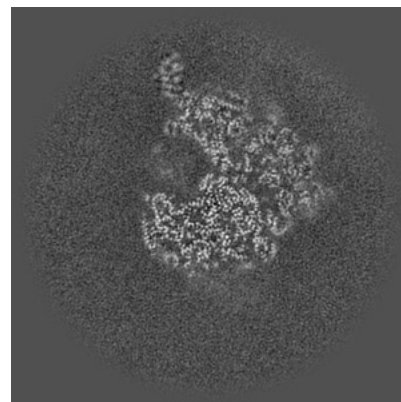
6.3.1 Primary map



X Index: 194

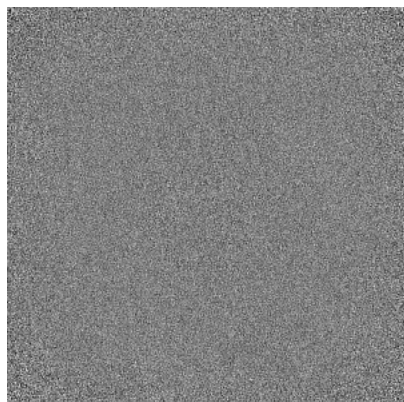


Y Index: 184

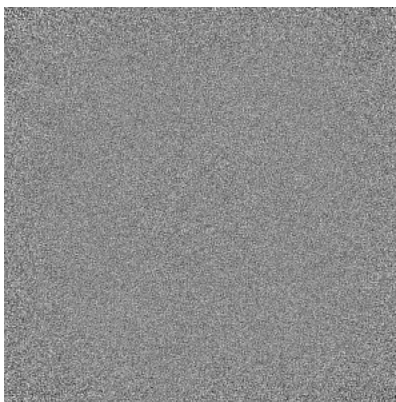


Z Index: 222

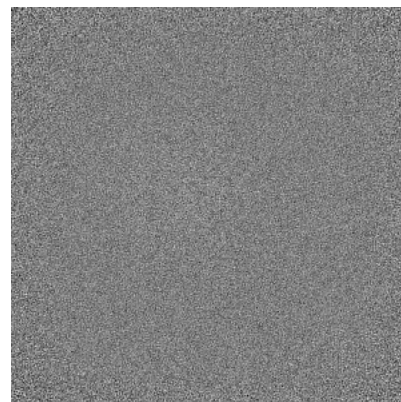
6.3.2 Raw map



X Index: 0



Y Index: 0

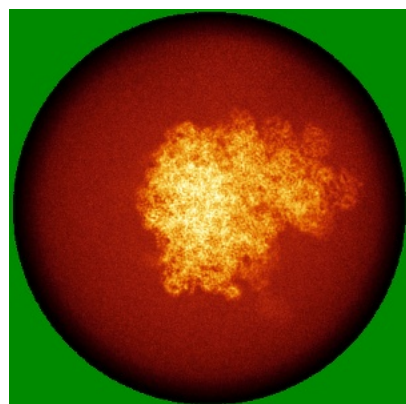


Z Index: 0

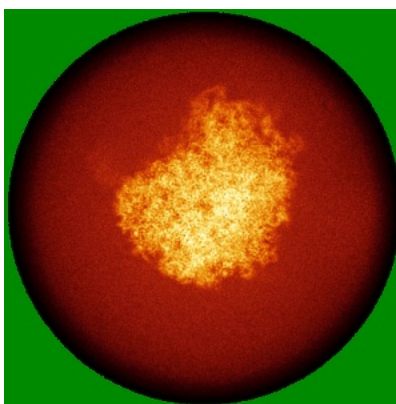
The images above show the largest variance slices of the map in three orthogonal directions.

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

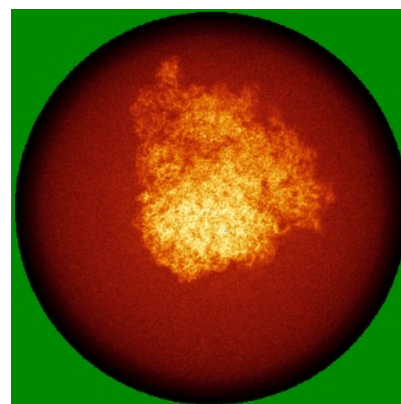
6.4.1 Primary map



X

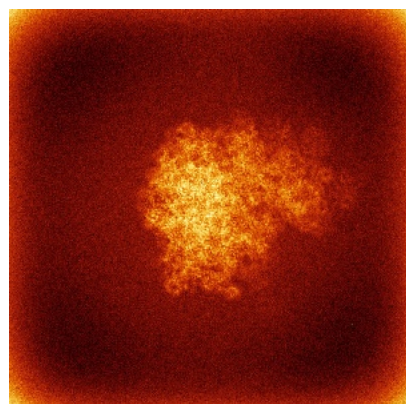


Y

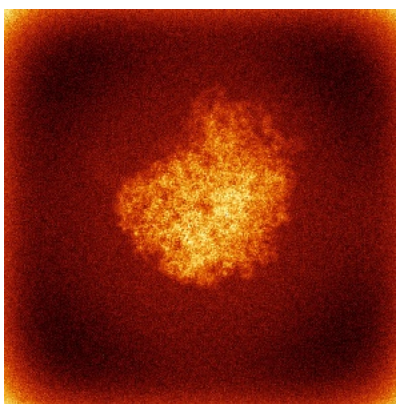


Z

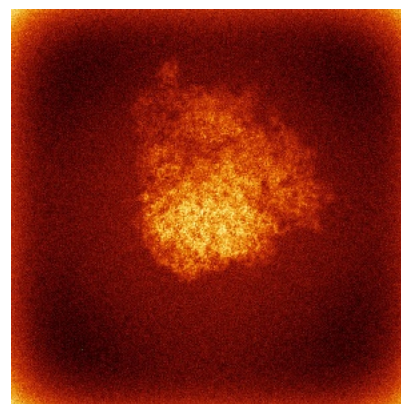
6.4.2 Raw map



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.

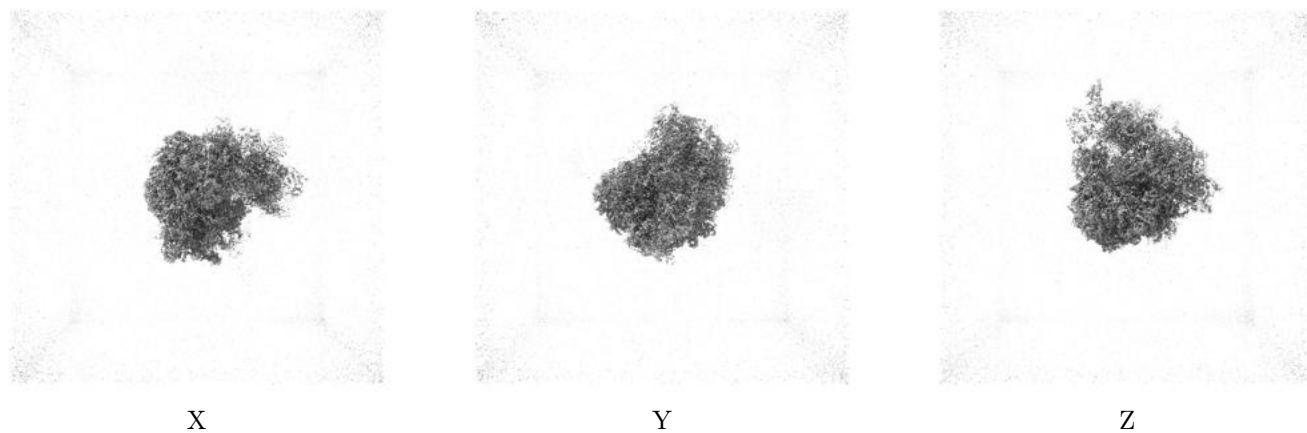
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.219. 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.

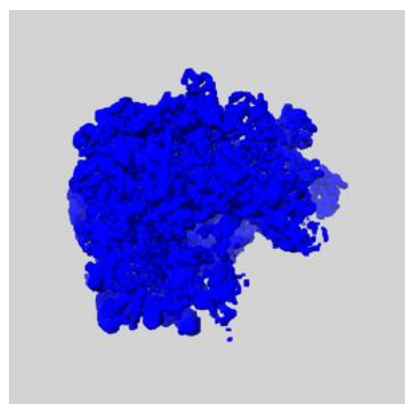
6.6 Mask visualisation [i](#)

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

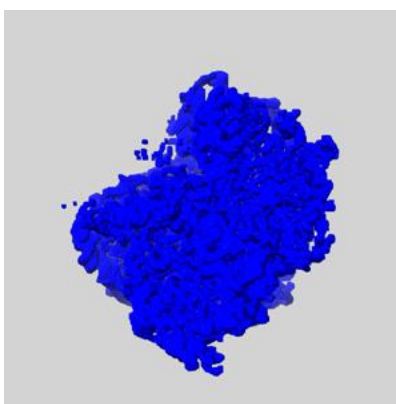
A mask typically either:

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

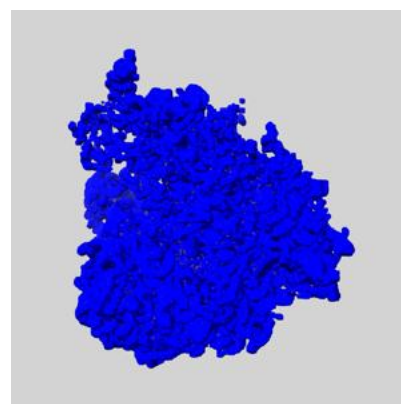
6.6.1 emd_38657_msk_1.map [i](#)



X



Y

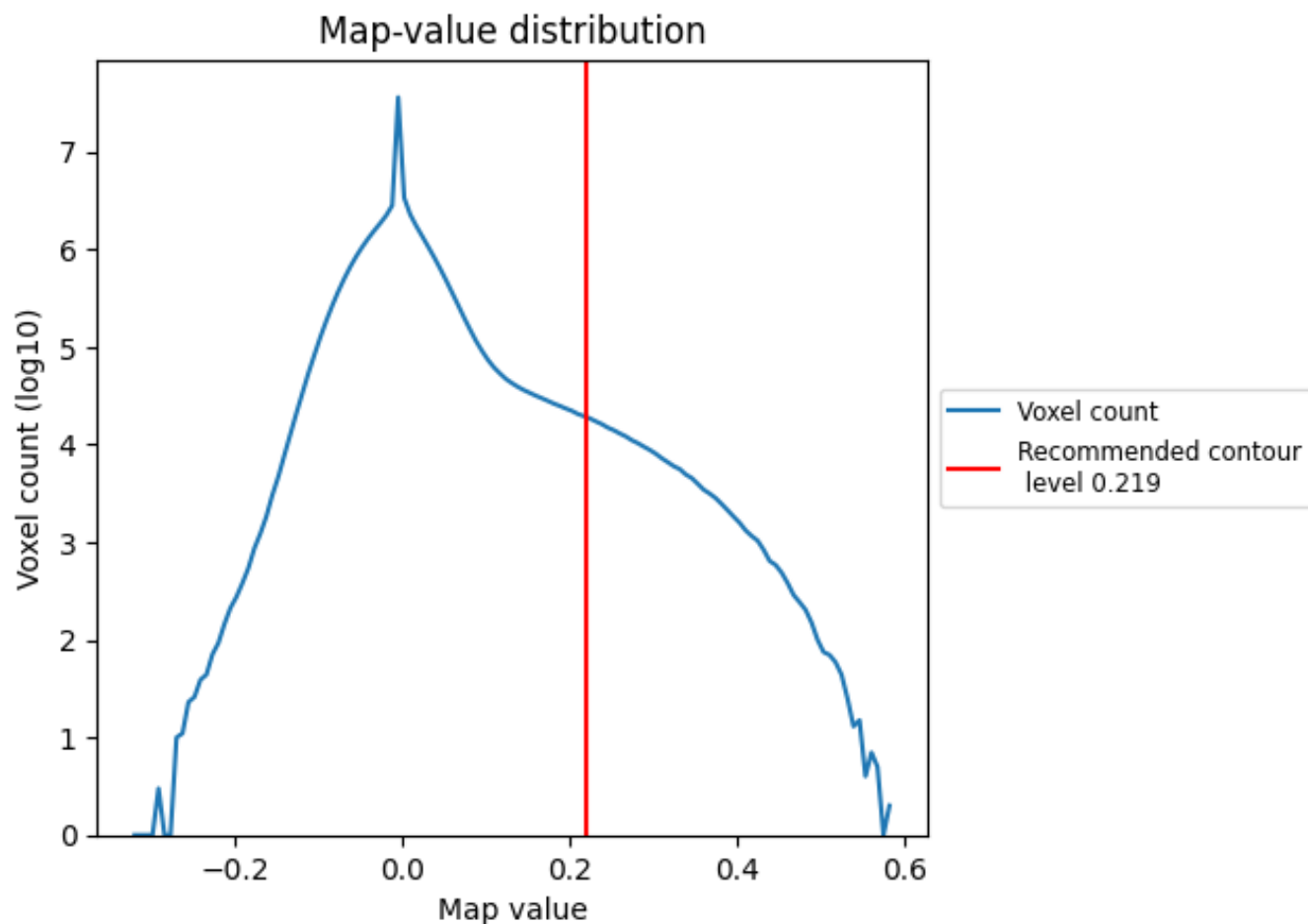


Z

7 Map analysis [i](#)

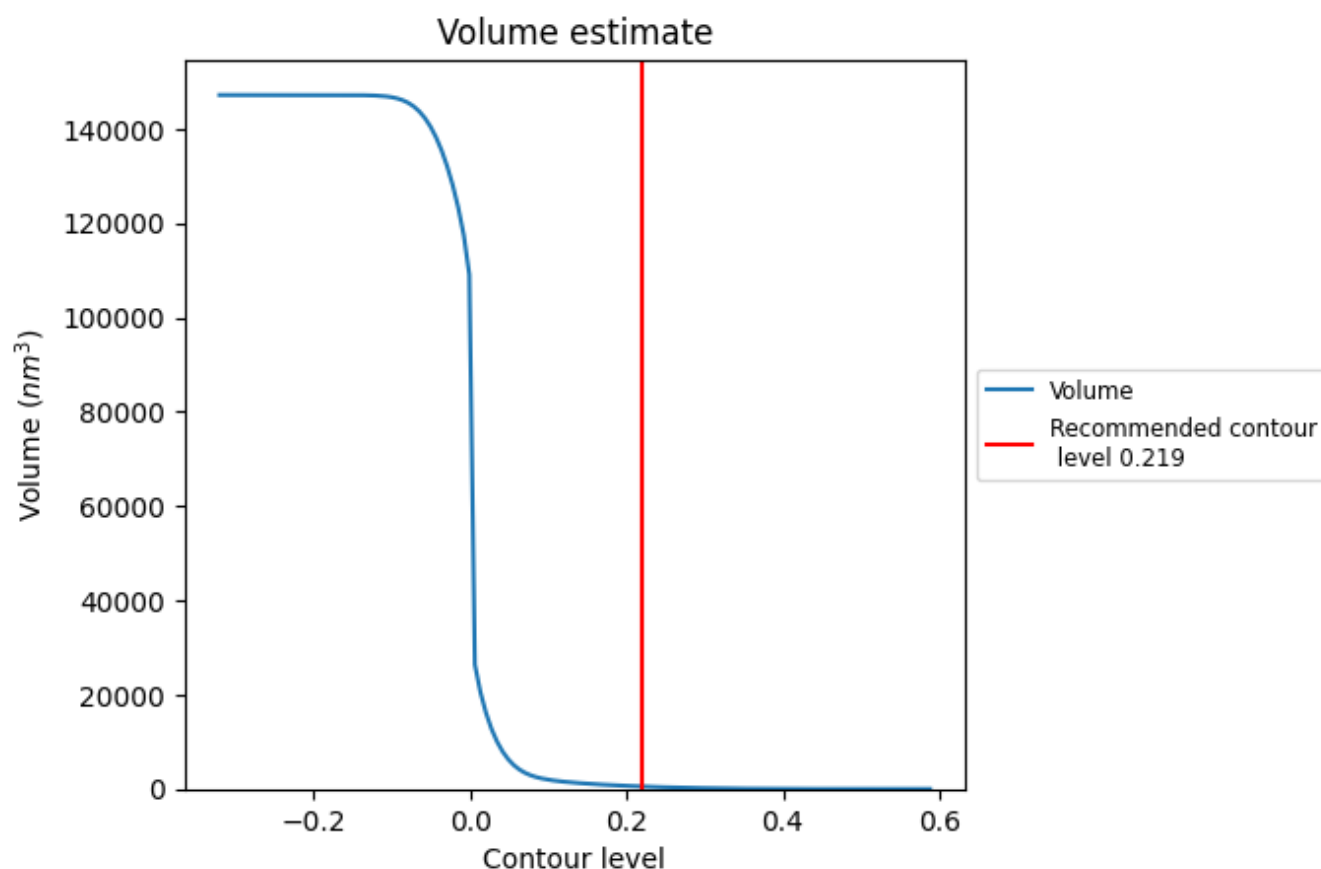
This section contains the results of statistical analysis of the map.

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.

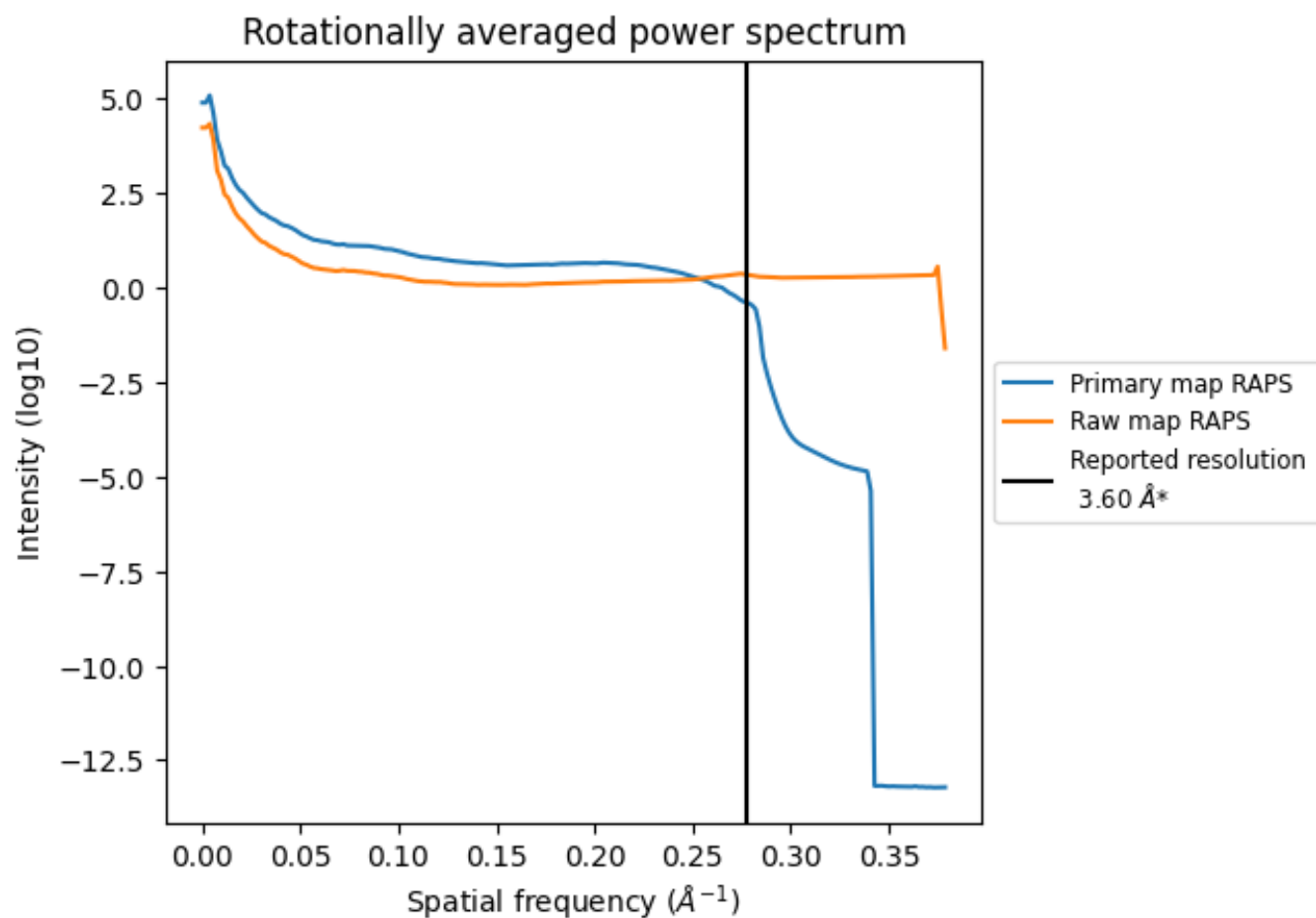
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 529 nm^3 ; this corresponds to an approximate mass of 478 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

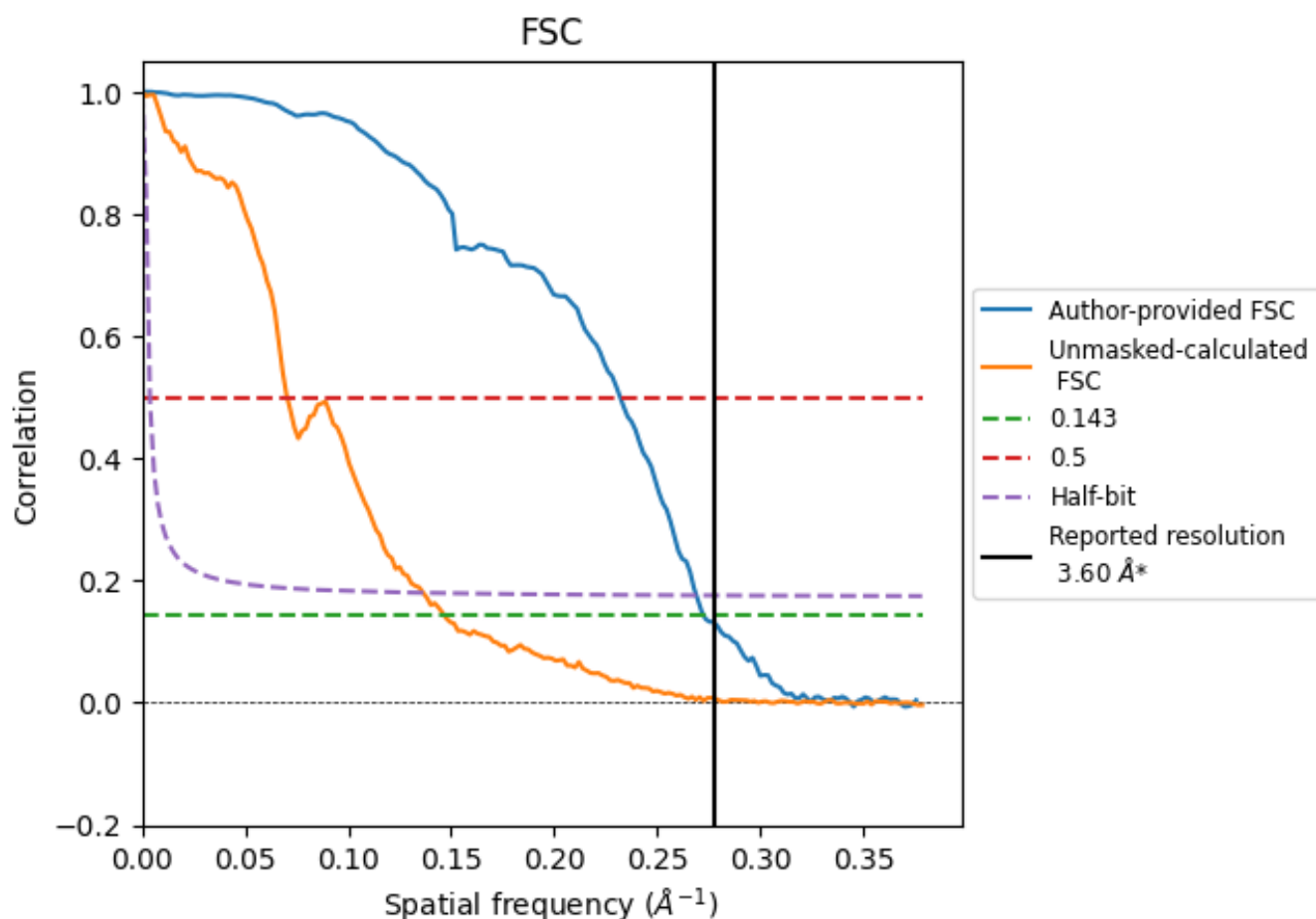


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

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 0.278 Å⁻¹

8.2 Resolution estimates [i](#)

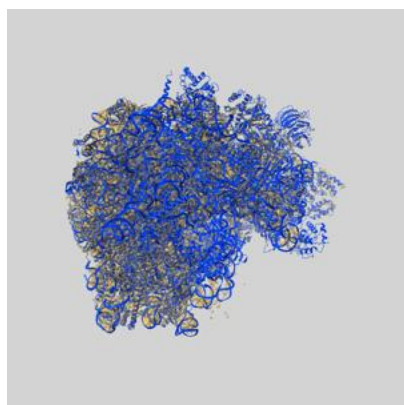
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.67	4.31	3.72
Unmasked-calculated*	6.82	14.22	7.33

*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 6.82 differs from the reported value 3.6 by more than 10 %

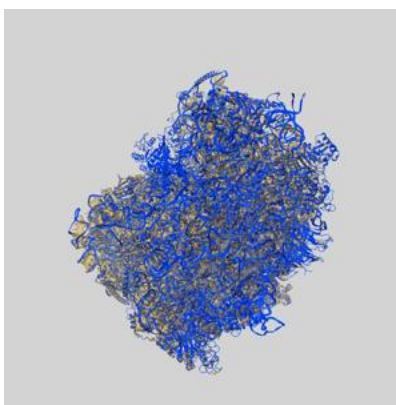
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-38657 and PDB model 8Z71. Per-residue inclusion information can be found in section 3 on page 19.

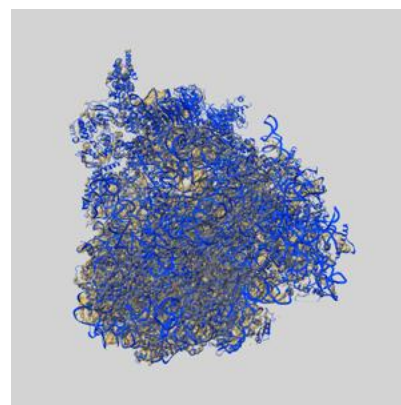
9.1 Map-model overlay [i](#)



X



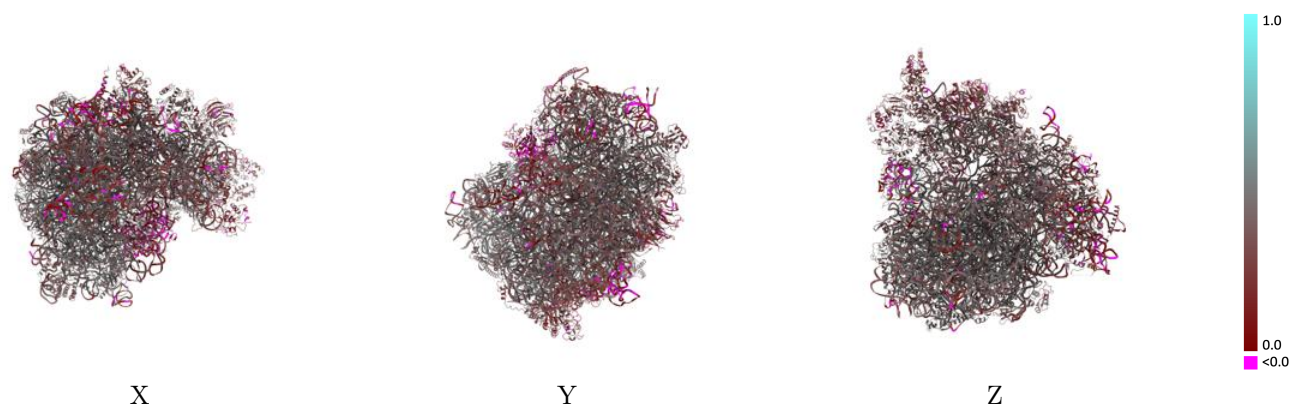
Y



Z

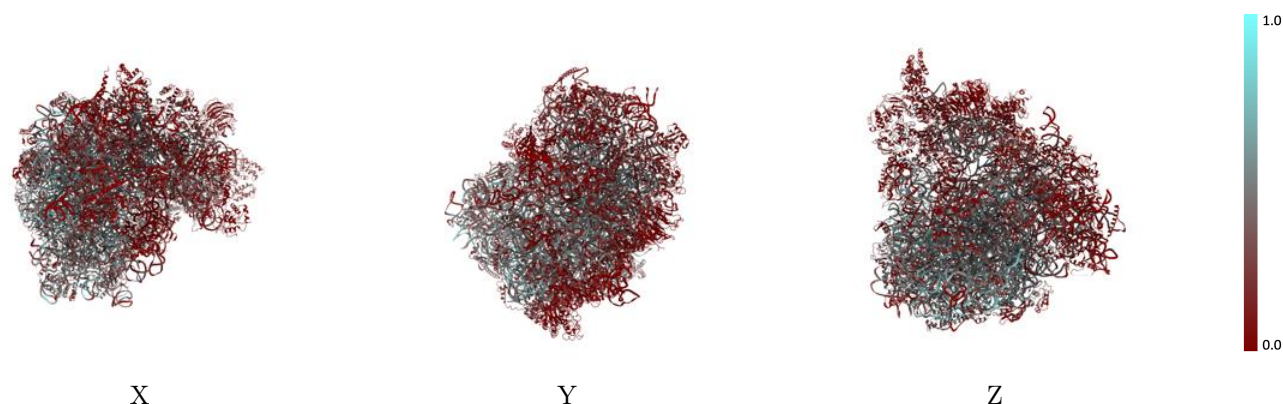
The images above show the 3D surface view of the map at the recommended contour level 0.219 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



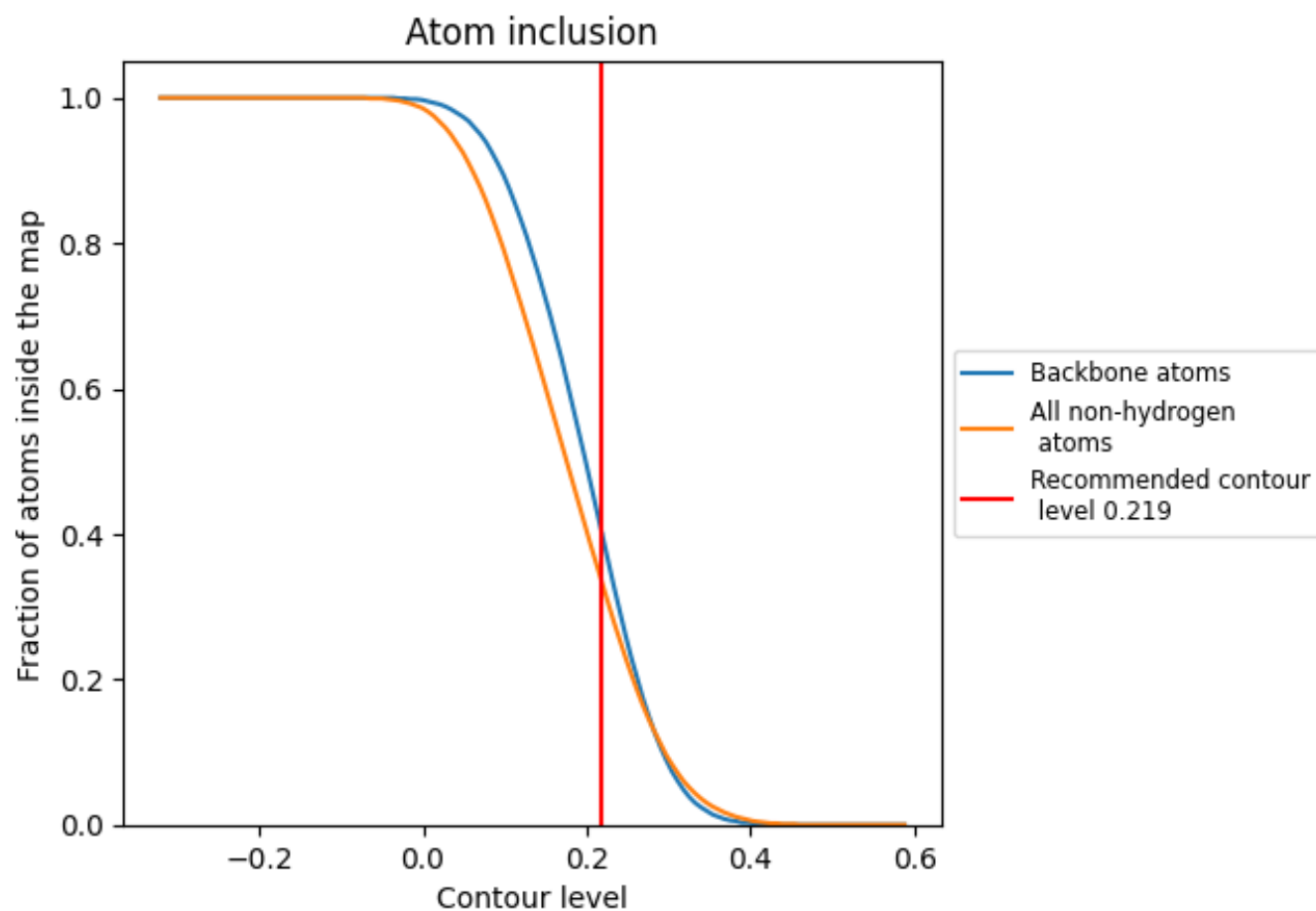
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.219).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 40% of all backbone atoms, 33% 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 (0.219) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3320	 0.3680
2	 0.3340	 0.3450
A	 0.4980	 0.3800
B	 0.5730	 0.4150
C	 0.5660	 0.4230
D	 0.3190	 0.4540
E	 0.3360	 0.4360
F	 0.3330	 0.4380
G	 0.2520	 0.3730
H	 0.2490	 0.3830
I	 0.3470	 0.4290
J	 0.2750	 0.3920
K	 0.2590	 0.4080
L	 0.2340	 0.4020
M	 0.1900	 0.3670
N	 0.3150	 0.4180
O	 0.3300	 0.4080
P	 0.3470	 0.4480
Q	 0.3550	 0.4290
R	 0.3710	 0.4370
S	 0.3330	 0.4440
SA	 0.0800	 0.3470
SB	 0.1300	 0.3570
SC	 0.0740	 0.3110
SD	 0.0020	 0.1860
SE	 0.0650	 0.3300
SF	 0.1200	 0.3580
SG	 0.1330	 0.3170
SH	 0.1620	 0.3570
SI	 0.1860	 0.3530
SJ	 0.0930	 0.3350
SK	 0.0680	 0.2740
SL	 0.1140	 0.3660
SM	 0.1820	 0.3910
SN	 0.0070	 0.2020















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Chain	Atom inclusion	Q-score
SO	 0.0300	 0.2220
SP	 0.1640	 0.3840
SQ	 0.1480	 0.3810
SR	 0.1830	 0.4040
SS	 0.0880	 0.3720
ST	 0.0530	 0.3030
SU	 0.1080	 0.3260
SV	 0.1640	 0.3950
SW	 0.1080	 0.3430
SX	 0.1980	 0.4200
SY	 0.2290	 0.4010
SZ	 0.1680	 0.4130
Sa	 0.1700	 0.3850
Sb	 0.2420	 0.4160
Sc	 0.1560	 0.4130
Sd	 0.0700	 0.3030
Se	 0.2360	 0.3890
Sf	 0.1270	 0.3890
Sg	 0.0720	 0.3290
T	 0.2840	 0.3940
U	 0.3340	 0.4400
V	 0.2880	 0.4340
W	 0.1830	 0.3410
X	 0.2620	 0.4420
Y	 0.1900	 0.3600
Z	 0.3130	 0.4230
a	 0.3120	 0.4290
b	 0.3150	 0.4150
c	 0.3480	 0.4440
d	 0.2700	 0.4130
e	 0.3150	 0.4250
f	 0.3240	 0.4250
g	 0.3470	 0.4540
h	 0.3760	 0.4570
i	 0.2940	 0.4330
j	 0.3200	 0.4060
k	 0.3010	 0.3970
l	 0.4100	 0.4600
m	 0.1770	 0.3790
n	 0.3180	 0.4380
o	 0.2600	 0.4190
p	 0.2790	 0.4390

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Chain	Atom inclusion	Q-score
q	 0.2800	 0.4300
r	 0.2900	 0.4210
s	 0.0110	 0.1650
t	 0.2130	 0.3140
v	 0.0850	 0.2830
x	 0.0010	 0.0850