



wwPDB EM Validation Summary Report ⓘ

Apr 21, 2025 – 03:37 PM EDT

PDB ID : 9AZC / pdb_00009azc
EMDB ID : EMD-44014
Title : In situ human 80S ribosome (Consensus map)
Authors : Wei, Z.; Yong, X.
Deposited on : 2024-03-11
Resolution : 2.19 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:

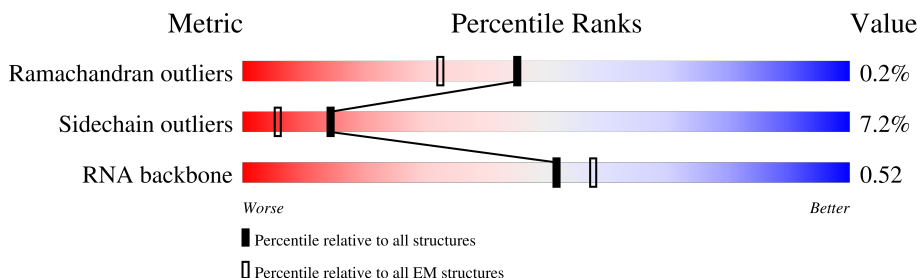
EMDB validation analysis : 0.0.1.dev117
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.42

1 Overall quality at a glance

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

The reported resolution of this entry is 2.19 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	CD	36	<div> <div>97%</div> <div>92% 8%</div> </div>
2	CI	31	<div> <div>77%</div> <div>90% 10%</div> </div>
3	LR	187	<div> <div>84%</div> <div>97% .</div> </div>
4	SE	262	<div> <div>92%</div> <div>90% 10%</div> </div>
5	SI	206	<div> <div>91%</div> <div>93% 7%</div> </div>
6	SL	153	<div> <div>85%</div> <div>91% 9%</div> </div>
7	SX	141	<div> <div>96%</div> <div>94% 6%</div> </div>
8	SG	237	<div> <div>98%</div> <div>90% 10%</div> </div>

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Mol	Chain	Length	Quality of chain
9	SJ	185	98% 94% 6%
10	SY	131	99% 89% 11%
11	Se	58	98% 88% 12%
12	SA	221	100% 95% 5%
13	SB	214	100% 96% .
14	SH	186	99% 90% 10%
15	SV	83	98% 89% 11%
16	Sa	102	100% 92% 8%
17	SC	222	97% 92% 8%
18	SN	150	99% 95% 5%
19	SO	140	100% 95% 5%
20	SW	129	94% 92% 8%
21	Sb	83	100% 95% 5%
22	L5	3740	96% 77% 22% .
23	L7	120	98% 90% 10%
24	L8	156	89% 81% 19%
25	LA	248	100% 94% 6%
26	LB	402	85% 95% .
27	LC	368	93% 95% 5%
28	LD	293	100% 94% 5%
29	LE	236	94% 94% 6%
30	LF	225	100% 98% .
31	LG	241	100% 95% 5%
32	LH	190	99% 93% 7%
33	LI	202	93% 93% 6%

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Mol	Chain	Length	Quality of chain
34	LJ	176	<div>100%</div> <div>93% 7%</div>
35	LL	210	<div>99%</div> <div>95% 5%</div>
36	LM	139	<div>98%</div> <div>94% 6%</div>
37	LN	203	<div>99%</div> <div>98%</div>
38	LO	201	<div>92%</div> <div>96%</div>
39	LP	153	<div>75%</div> <div>95% 5%</div>
40	LQ	187	<div>99%</div> <div>98%</div>
41	LS	175	<div>99%</div> <div>92% 8%</div>
42	LT	159	<div>96%</div> <div>96%</div>
43	LU	101	<div>70%</div> <div>90% 10%</div>
44	LV	131	<div>100%</div> <div>98%</div>
45	LX	120	<div>73%</div> <div>97%</div>
46	LY	134	<div>77%</div> <div>96%</div>
47	LZ	135	<div>99%</div> <div>91% 9%</div>
48	La	147	<div>95%</div> <div>99%</div>
49	Lb	109	<div>96%</div> <div>95% 5%</div>
50	Lc	98	<div>98%</div> <div>93% 6%</div>
51	Ld	107	<div>74%</div> <div>92% 8%</div>
52	Le	128	<div>91%</div> <div>98%</div>
53	Lf	109	<div>98%</div> <div>94% 6%</div>
54	Lg	114	<div>96%</div> <div>95% 5%</div>
55	Lh	122	<div>78%</div> <div>94% 6%</div>
56	Li	102	<div>100%</div> <div>97%</div>
57	Lj	86	<div>83%</div> <div>91% 9%</div>
58	Lk	69	<div>78%</div> <div>96%</div>

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Mol	Chain	Length	Quality of chain
59	Ll	50	<div>76%</div> <div>92%</div> <div>8%</div>
60	Lm	52	<div>100%</div> <div>98%</div> <div>.</div>
61	Ln	24	<div>100%</div> <div>88%</div> <div>12%</div>
62	Lo	105	<div>100%</div> <div>92%</div> <div>8%</div>
63	Lp	91	<div>100%</div> <div>96%</div> <div>.</div>
64	Lr	125	<div>96%</div> <div>90%</div> <div>10%</div>
65	SR	135	<div>100%</div> <div>88%</div> <div>12%</div>
66	SD	227	<div>100%</div> <div>92%</div> <div>8%</div>
67	SF	189	<div>100%</div> <div>91%</div> <div>8%</div> <div>.</div>
68	SK	98	<div>100%</div> <div>91%</div> <div>9%</div>
69	SP	121	<div>100%</div> <div>90%</div> <div>9%</div> <div>.</div>
70	SQ	144	<div>100%</div> <div>90%</div> <div>10%</div>
71	SS	145	<div>100%</div> <div>96%</div> <div>.</div>
72	ST	143	<div>100%</div> <div>93%</div> <div>7%</div>
73	SU	104	<div>100%</div> <div>92%</div> <div>8%</div>
74	Sc	64	<div>100%</div> <div>91%</div> <div>9%</div>
75	Sd	55	<div>100%</div> <div>89%</div> <div>11%</div>
76	Sg	313	<div>100%</div> <div>91%</div> <div>9%</div>
77	SM	122	<div>100%</div> <div>89%</div> <div>11%</div>
78	SZ	75	<div>100%</div> <div>88%</div> <div>12%</div>
79	Sf	67	<div>100%</div> <div>91%</div> <div>9%</div>
80	S2	1740	<div>99%</div> <div>76%</div> <div>24%</div> <div>.</div>
81	AT	76	<div>100%</div> <div>62%</div> <div>36%</div> <div>.</div>
82	CF	441	<div>100%</div> <div>91%</div> <div>9%</div>
83	Pt	74	<div>97%</div> <div>80%</div> <div>20%</div>

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Mol	Chain	Length	Quality of chain
84	Lt	141	<div><div></div><div>100%</div><div>95%</div><div>5%</div></div>
85	Ls	196	<div><div></div><div>100%</div><div>94%</div><div>6%</div></div>
86	LW	118	<div><div></div><div>100%</div><div>93%</div><div>7%</div></div>

2 Entry composition

There are 88 unique types of molecules in this entry. The entry contains 224908 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 Serbp1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	CD	36	Total	C	N	O	S	0	0
			284	177	47	59	1		

- Molecule 2 is a protein called NAC-beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	CI	31	Total	C	N	O	S	0	0
			245	151	54	39	1		

- Molecule 3 is a protein called 60S ribosomal protein L19.

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

- Molecule 4 is a protein called Small ribosomal subunit protein eS4, X isoform.

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

- Molecule 5 is a protein called 40S ribosomal protein S8.

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

- Molecule 6 is a protein called 40S ribosomal protein S11.

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

- Molecule 7 is a protein called 40S ribosomal protein S23.

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

- Molecule 8 is a protein called 40S ribosomal protein S6.

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

- Molecule 9 is a protein called 40S ribosomal protein S9.

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

- Molecule 10 is a protein called 40S ribosomal protein S24.

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

- Molecule 11 is a protein called Small ribosomal subunit protein eS30.

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

- Molecule 12 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	SA	221	Total	C	N	O	S	0	0
			1741	1106	305	322	8		

- Molecule 13 is a protein called 40S ribosomal protein S3a.

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

- Molecule 14 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	SH	186	Total	C	N	O	S	0	0
			1497	956	274	266	1		

- Molecule 15 is a protein called 40S ribosomal protein S21.

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

- Molecule 16 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Sa	102	Total	C	N	O	S	0	0
			821	512	171	133	5		

- Molecule 17 is a protein called 40S ribosomal protein S2.

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

- Molecule 18 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SN	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 19 is a protein called Small ribosomal subunit protein uS11.

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

- Molecule 20 is a protein called 40S ribosomal protein S15a.

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

- Molecule 21 is a protein called Small ribosomal subunit protein eS27.

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

- Molecule 22 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	L5	3740	Total	C	N	O	P	0	0
			79860	35549	14585	25987	3739		

- Molecule 23 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	L7	120	Total	C	N	O	P	0	0
			2561	1141	456	844	120		

- Molecule 24 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	L8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 25 is a protein called 60S ribosomal protein L8.

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

- Molecule 26 is a protein called Large ribosomal subunit protein uL3.

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

- Molecule 27 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LC	368	Total	C	N	O	S	0	0
			2927	1840	583	489	15		

- Molecule 28 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 29 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LE	236	Total	C	N	O	S	0	0
			1904	1222	361	317	4		

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

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

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

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

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

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

- Molecule 33 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LI	202	Total	C	N	O	S	0	0
			1634	1037	314	269	14		

- Molecule 34 is a protein called 60S ribosomal protein L11.

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

- Molecule 35 is a protein called Large ribosomal subunit protein eL13.

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

- Molecule 36 is a protein called 60S ribosomal protein L14.

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

- Molecule 37 is a protein called 60S ribosomal protein L15.

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

- Molecule 38 is a protein called 60S ribosomal protein L13a.

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

- Molecule 39 is a protein called 60S ribosomal protein L17.

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

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

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

- Molecule 41 is a protein called 60S ribosomal protein L18a.

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

- Molecule 42 is a protein called 60S ribosomal protein L21.

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

- Molecule 43 is a protein called Heparin-binding protein HBp15.

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

- Molecule 44 is a protein called 60S ribosomal protein L23.

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

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

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

- Molecule 46 is a protein called 60S ribosomal protein L26.

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

- Molecule 47 is a protein called 60S ribosomal protein L27.

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

- Molecule 48 is a protein called 60S ribosomal protein L27a.

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

- Molecule 49 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Lb	109	Total	C	N	O	S	0	0
			876	546	189	137	4		

- Molecule 50 is a protein called 60S ribosomal protein L30.

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

- Molecule 51 is a protein called 60S ribosomal protein L31.

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

- Molecule 52 is a protein called 60S ribosomal protein L32.

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

- Molecule 53 is a protein called 60S ribosomal protein L35a.

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

- Molecule 54 is a protein called 60S ribosomal protein L34.

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

- Molecule 55 is a protein called 60S ribosomal protein L35.

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

- Molecule 56 is a protein called 60S ribosomal protein L36.

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

- Molecule 57 is a protein called 60S ribosomal protein L37.

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

- Molecule 58 is a protein called 60S ribosomal protein L38.

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

- Molecule 59 is a protein called 60S ribosomal protein L39.

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

- Molecule 60 is a protein called Large ribosomal subunit protein eL40.

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

- Molecule 61 is a protein called 60S ribosomal protein L41.

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

- Molecule 62 is a protein called 60S ribosomal protein L36a.

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

- Molecule 63 is a protein called 60S ribosomal protein L37a.

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

- Molecule 64 is a protein called 60S ribosomal protein L28.

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

- Molecule 65 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SR	135	Total	C	N	O	S	0	0
			1090	685	202	198	5		

- Molecule 66 is a protein called Small ribosomal subunit protein uS3.

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

- Molecule 67 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SF	189	Total	C	N	O	S	0	0
			1495	934	284	270	7		

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

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

- Molecule 69 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SP	121	Total	C	N	O	S	0	0
			985	623	185	170	7		

- Molecule 70 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SQ	144	Total	C	N	O	S	0	0
			1142	726	216	197	3		

- Molecule 71 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SS	145	Total	C	N	O	S	0	0
			1198	751	242	203	2		

- Molecule 72 is a protein called 40S ribosomal protein S19.

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

- Molecule 73 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SU	104	Total	C	N	O	S	0	0
			821	514	155	148	4		

- Molecule 74 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Sc	64	Total	C	N	O	S	0	0
			506	308	102	94	2		

- Molecule 75 is a protein called 40S ribosomal protein S29.

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

- Molecule 76 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 77 is a protein called Small ribosomal subunit protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	SM	122	Total	C	N	O	S	0	0
			940	590	164	177	9		

- Molecule 78 is a protein called Small ribosomal subunit protein eS25.

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

- Molecule 79 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Sf	67	Total	C	N	O	S	0	0
			548	346	102	93	7		

- Molecule 80 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	S2	1740	Total	C	N	O	P	0	0
			36898	16459	6599	12101	1739		

- Molecule 81 is a RNA chain called AT site tRNA.

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

- Molecule 82 is a protein called eEF1A.

Mol	Chain	Residues	Atoms						AltConf	Trace
82	CF	441	Total	C	N	O	P	S	0	0
			3383	2148	581	636	1	17		

- Molecule 83 is a RNA chain called P site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Pt	74	Total	C	N	O	P	0	0
			1576	705	286	512	73		

- Molecule 84 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Lt	141	Total	C	N	O	S	0	0
			1046	652	191	199	4		

- Molecule 85 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	Ls	196	Total	C	N	O	S	0	0
			1496	952	259	276	9		

- Molecule 86 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	LW	118	Total	C	N	O	S	0	0
			965	604	199	158	4		

- Molecule 87 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
87	Sa	1	Total	Zn	0
			1	1	
87	Lg	1	Total	Zn	0
			1	1	
87	Lj	1	Total	Zn	0
			1	1	
87	Lm	1	Total	Zn	0
			1	1	
87	Lo	1	Total	Zn	0
			1	1	
87	Lp	1	Total	Zn	0
			1	1	

- Molecule 88 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
88	L5	214	Total	Mg	0
			214	214	
88	L7	3	Total	Mg	0
			3	3	
88	L8	3	Total	Mg	0
			3	3	

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Mol	Chain	Residues	Atoms		AltConf
88	LA	1	Total 1	Mg 1	0
88	LP	1	Total 1	Mg 1	0
88	LV	1	Total 1	Mg 1	0
88	Le	1	Total 1	Mg 1	0
88	Lg	2	Total 2	Mg 2	0
88	S2	29	Total 29	Mg 29	0

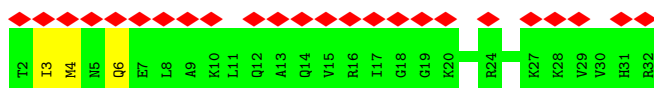
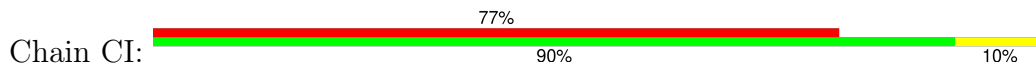
3 Residue-property plots

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

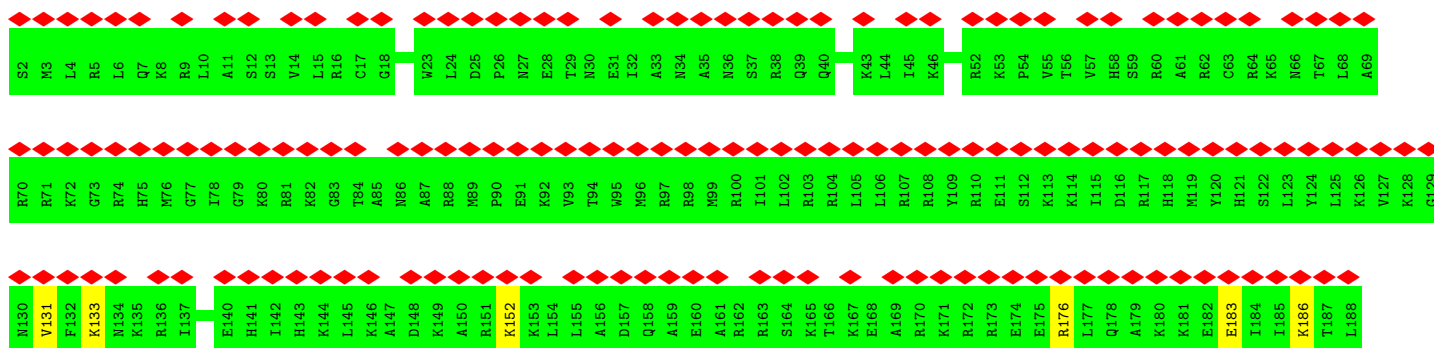
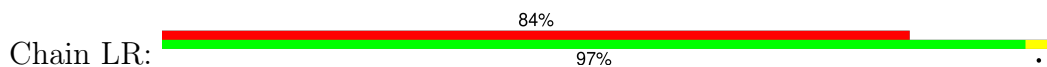
- Molecule 1: Serbp1



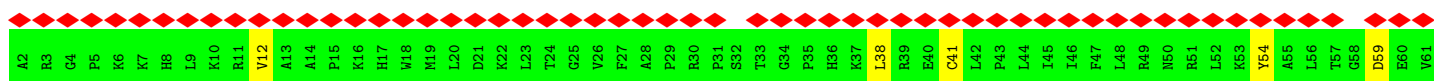
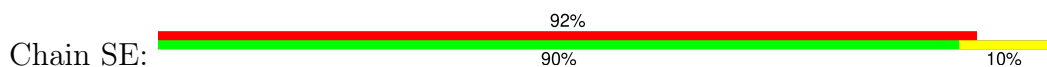
- Molecule 2: NAC-beta

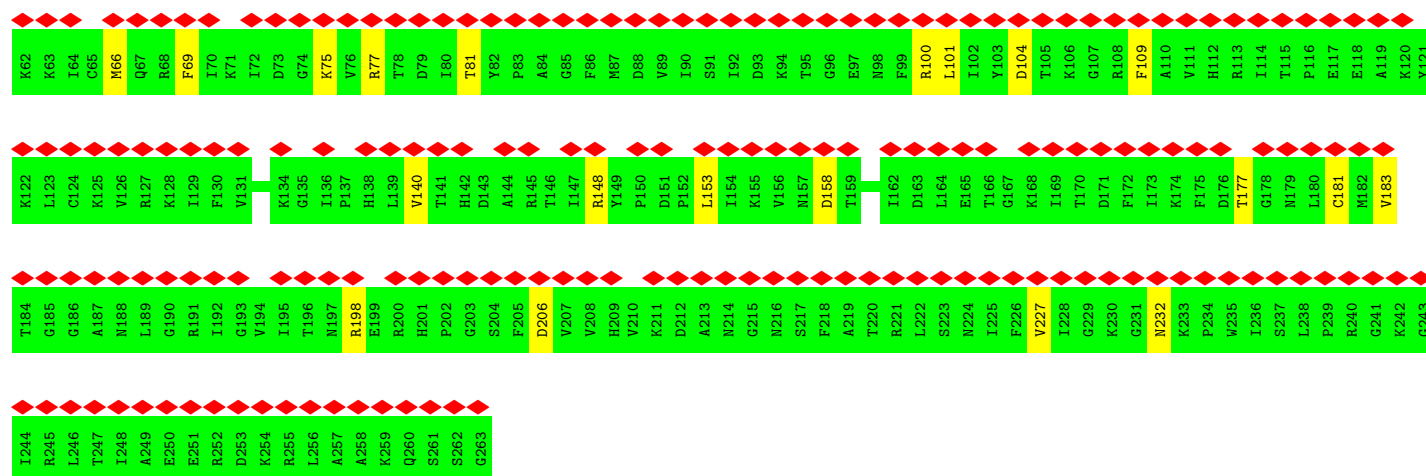


- Molecule 3: 60S ribosomal protein L19

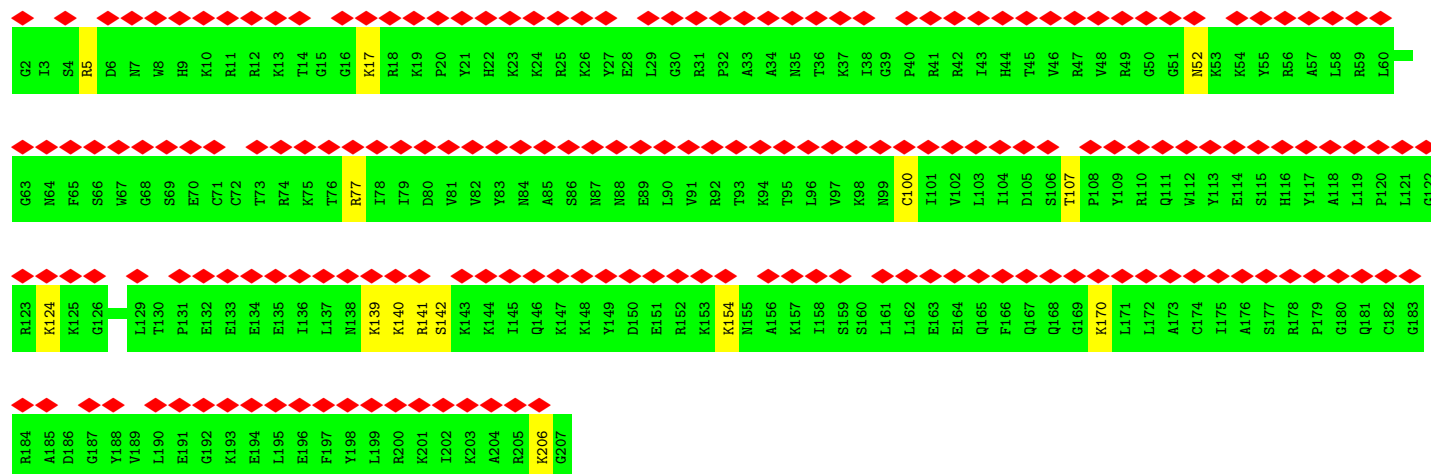


- Molecule 4: Small ribosomal subunit protein eS4, X isoform

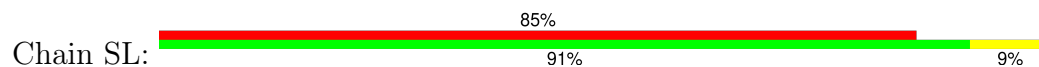




• Molecule 5: 40S ribosomal protein S8

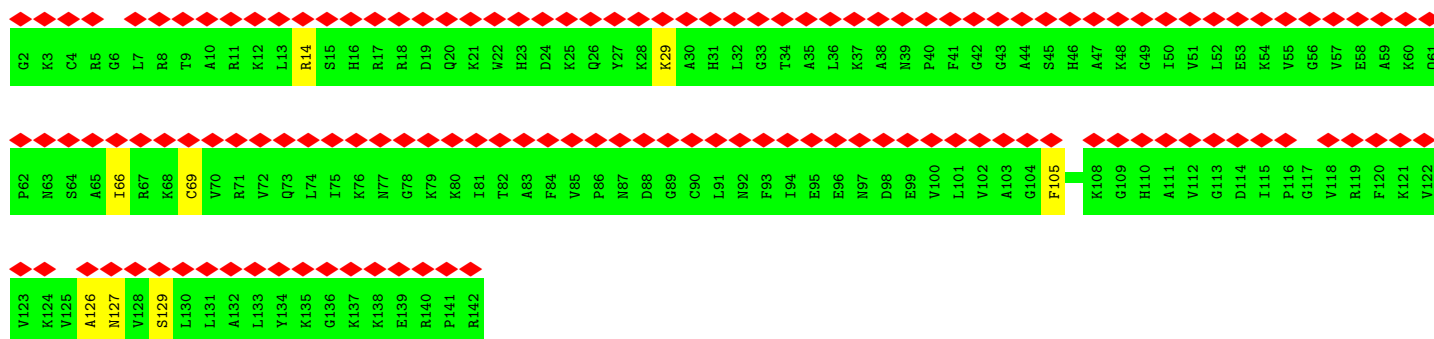


• Molecule 6: 40S ribosomal protein S11

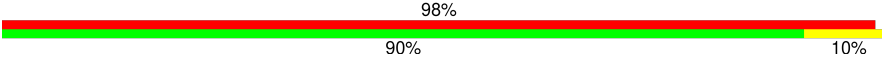


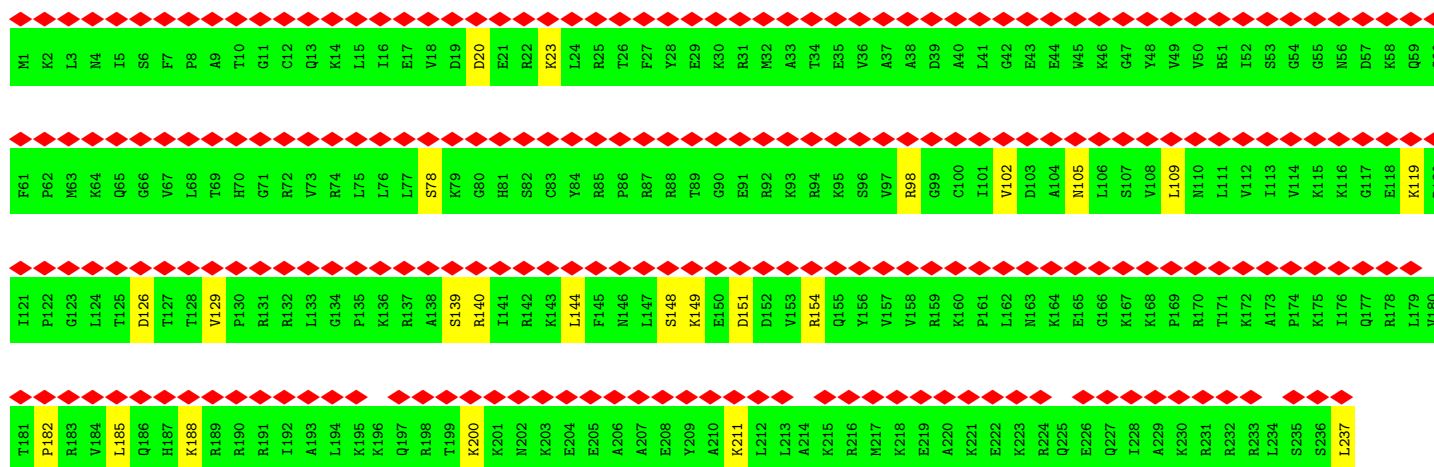
• Molecule 7: 40S ribosomal protein S23

Chain SX: 



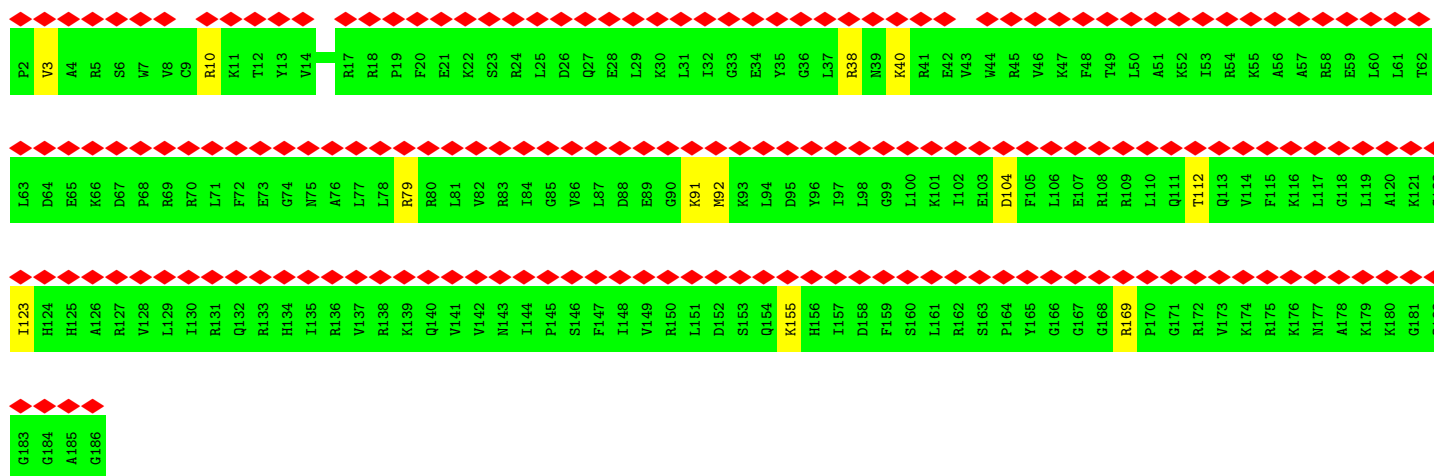
• Molecule 8: 40S ribosomal protein S6

Chain SG: 

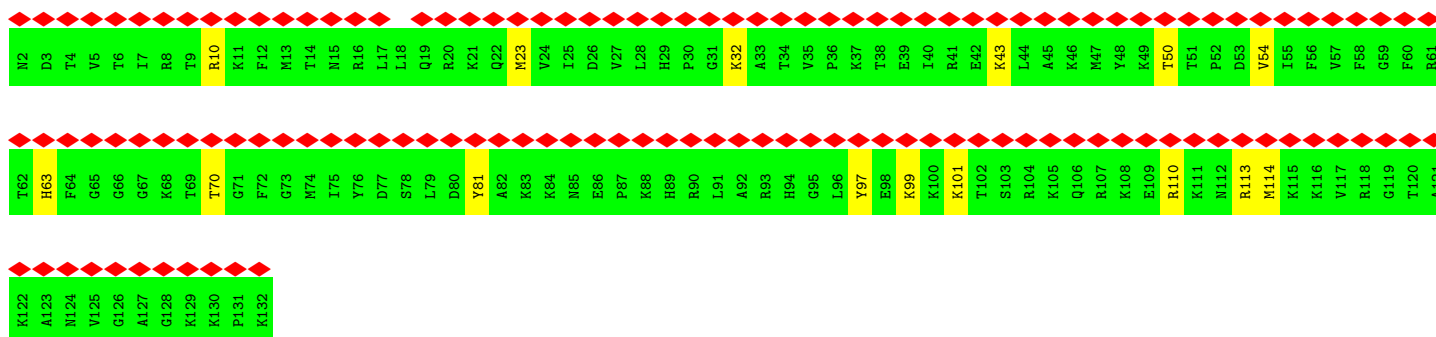
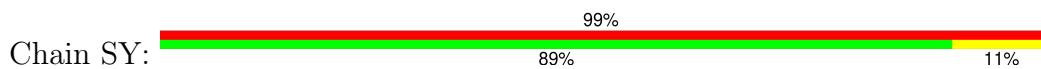


• Molecule 9: 40S ribosomal protein S9

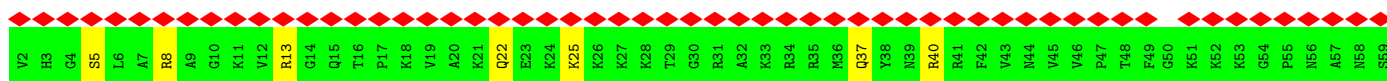
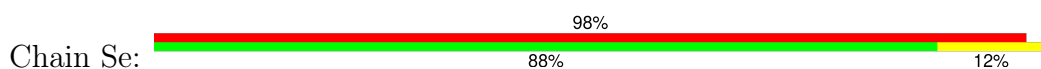
Chain SJ: 



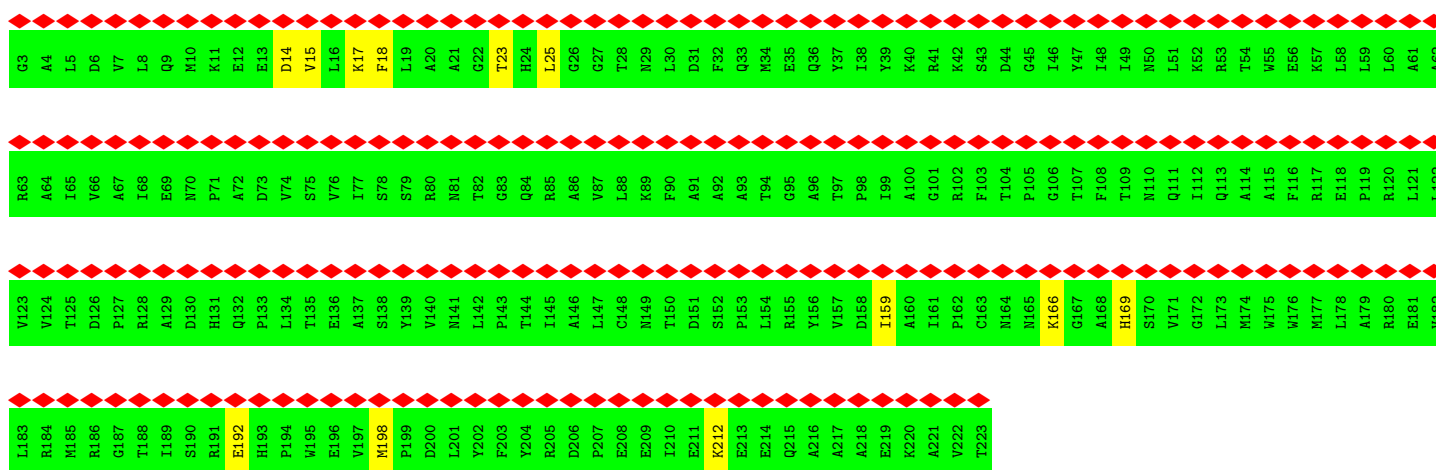
• Molecule 10: 40S ribosomal protein S24



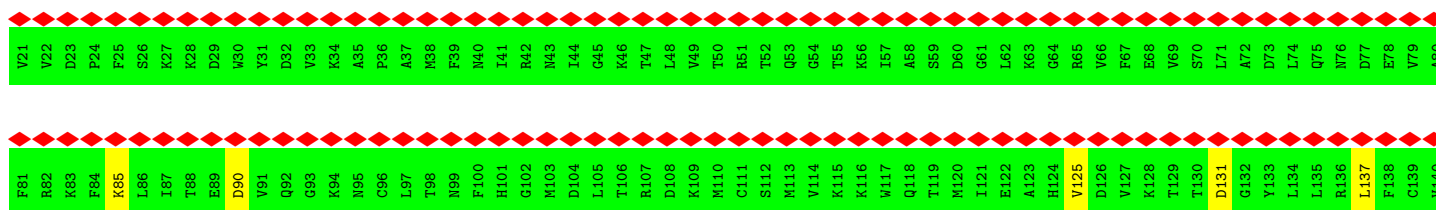
- Molecule 11: Small ribosomal subunit protein eS30

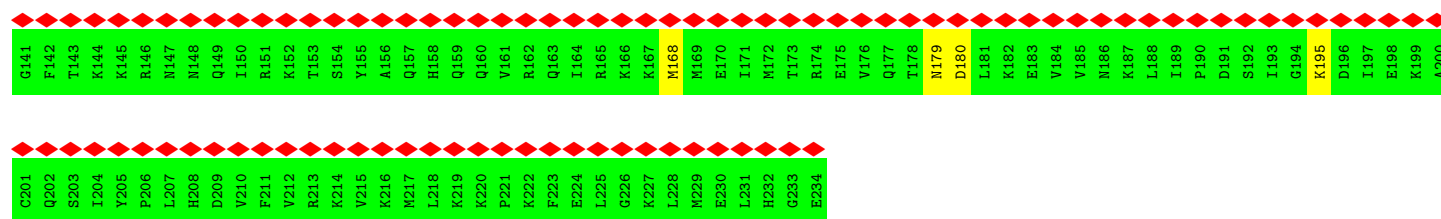


- Molecule 12: 40S ribosomal protein SA

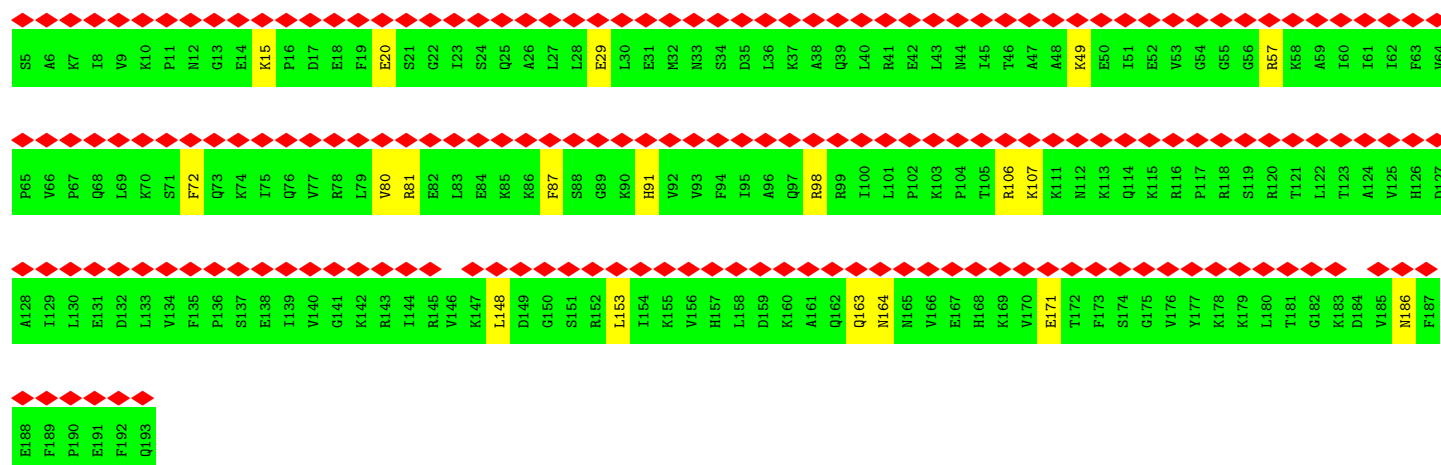
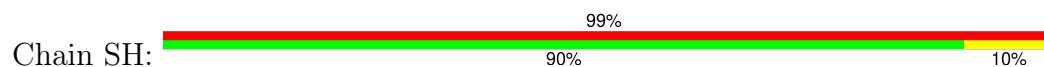


- Molecule 13: 40S ribosomal protein S3a

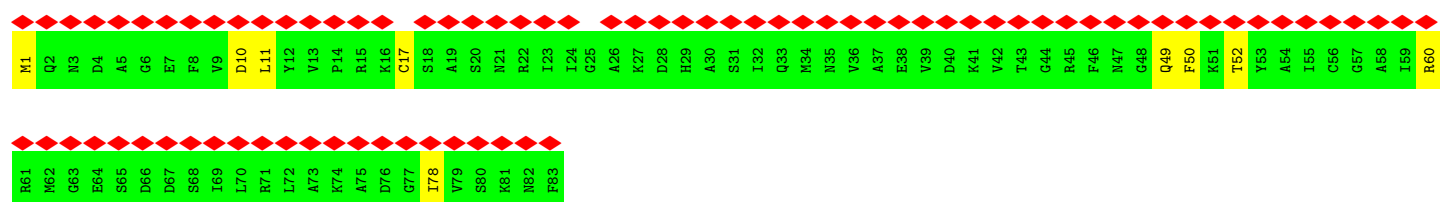
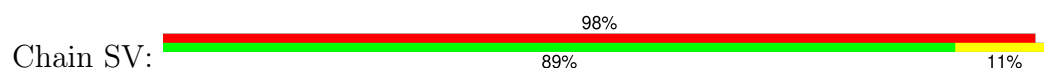




• Molecule 14: 40S ribosomal protein S7



• Molecule 15: 40S ribosomal protein S21

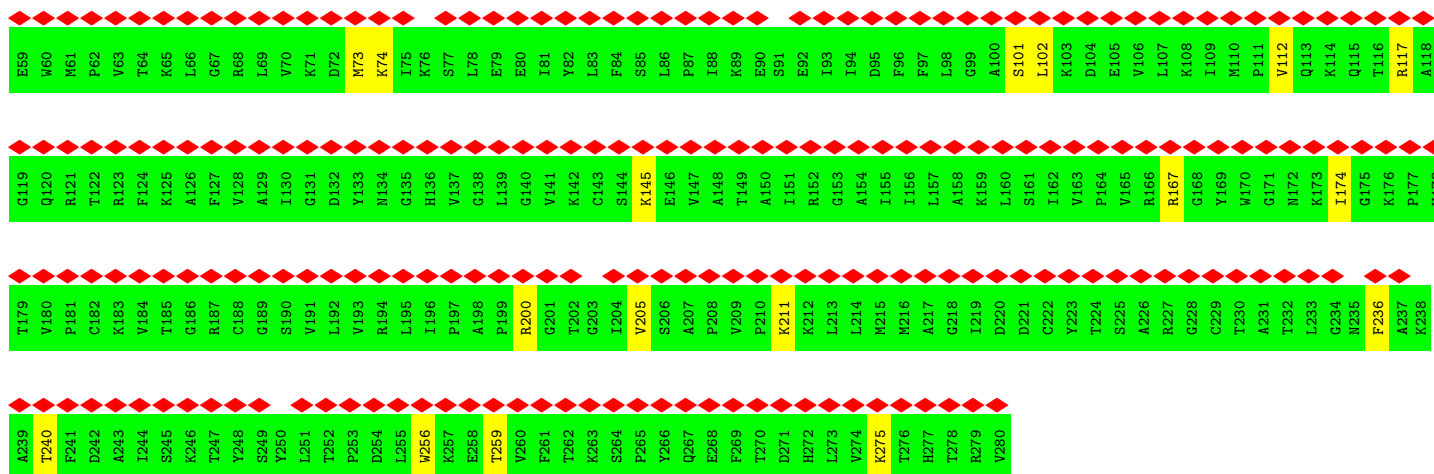


• Molecule 16: 40S ribosomal protein S26

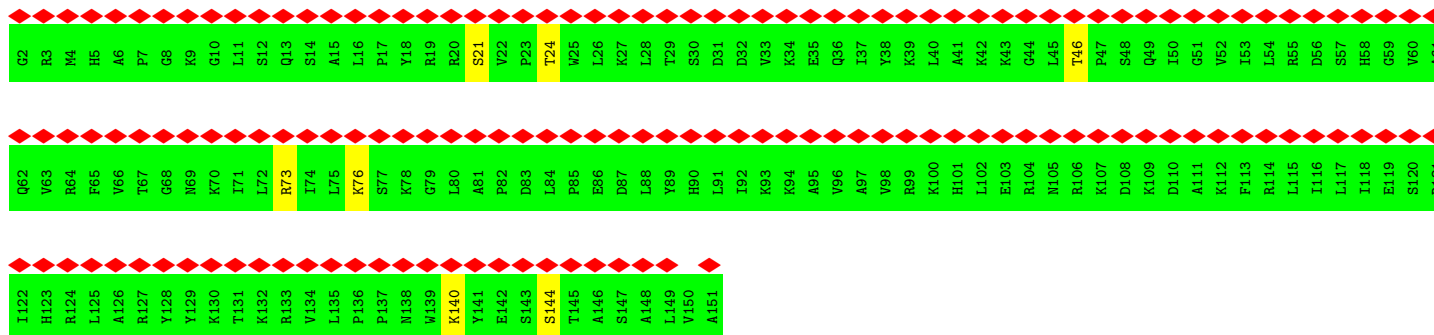


• Molecule 17: 40S ribosomal protein S2

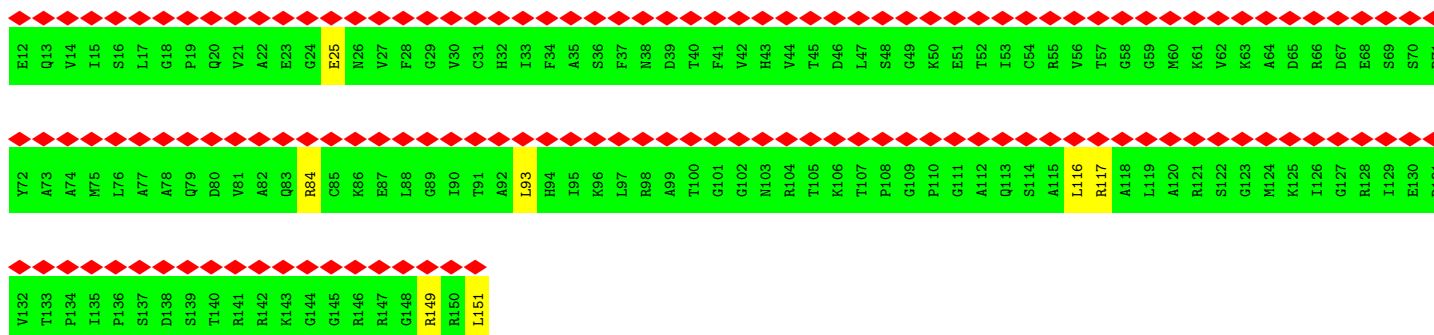




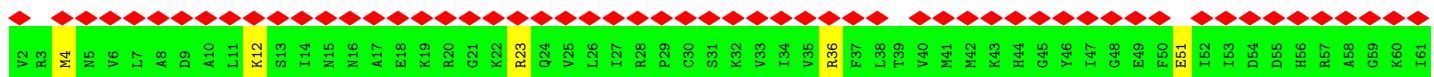
• Molecule 18: 40S ribosomal protein S13



• Molecule 19: Small ribosomal subunit protein uS11

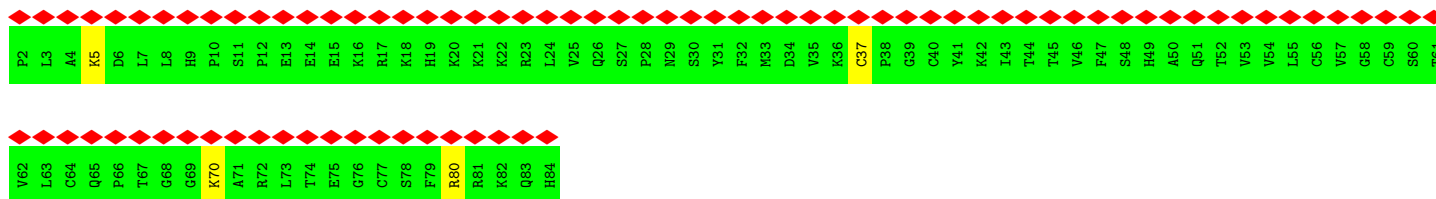


• Molecule 20: 40S ribosomal protein S15a

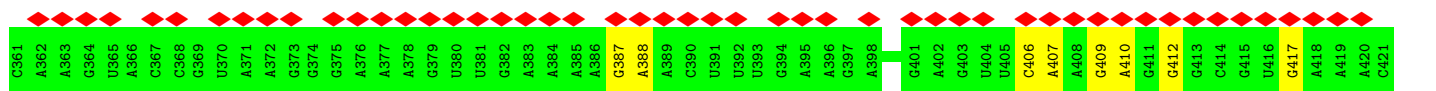
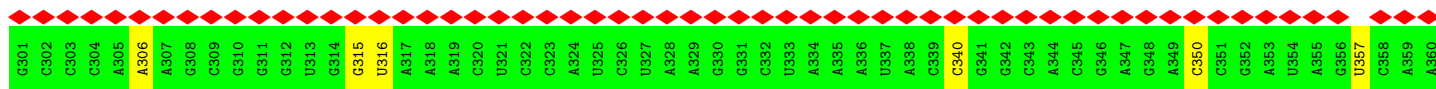
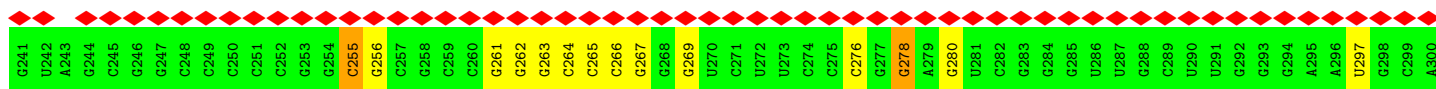
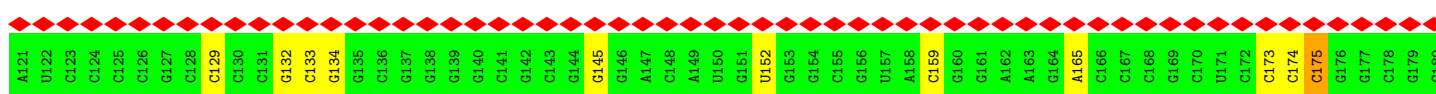
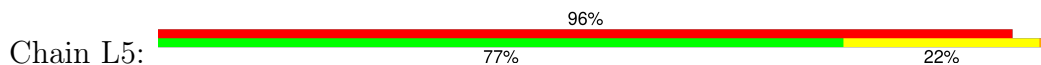




- Molecule 21: Small ribosomal subunit protein eS27



- Molecule 22: 28S rRNA

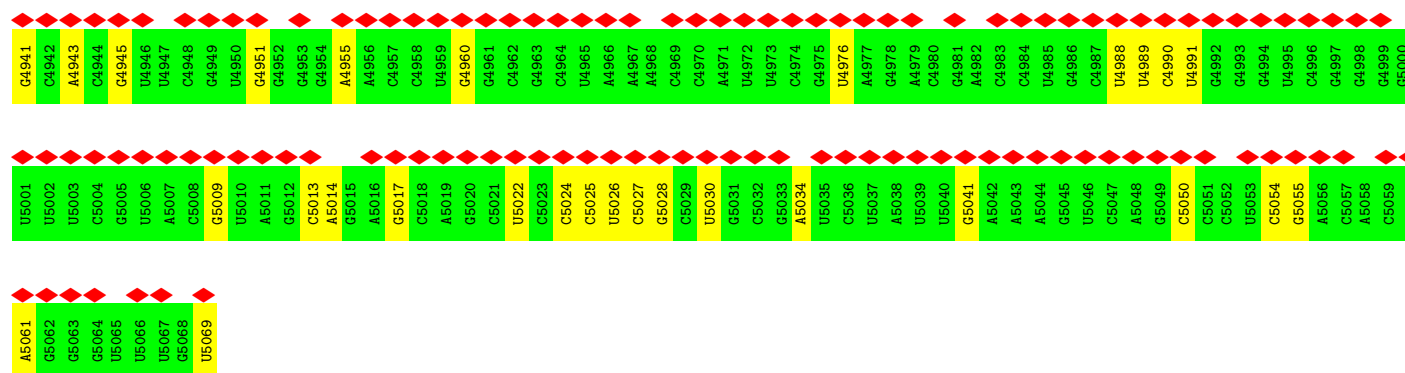


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C1607	G1487	A1547	A1427	C1367	A1307	U1247	C1176	C988	G928	G726	G666	U484
G1608	G1488	G1548	U1428	A1368	C1308	G1248	U1177	U989	A929	C727	A667	C485
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C1610	G1490	G1550	C1430	G1370	C1310	G1250	U1179	C991	C931	G729	C669	G487
C1611	C1491	C1551	C1431	A1371	G1311	G1251	C1180	C992	A932	G730	G670	G488
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A1621	C1501	G1561	C1441	U1381	G1321	G1261	C1190	G1064	G942	G740	G680	C498
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A1623	A1503	A1563	A1443	G1383	A1323	A1263	C1192	G1066	A944	G742	G682	G500
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A1631	U1511	G1571	G1451	A1391	C1331	G1271	G1200	G1074	G952	U750	G508	G508
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A1638	A1518	U1578	C1458	A1398	G1338	G1278	G1207	C1081	G959	G757	C515	C515
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C1661	C1541	U1601	C1481	A1421	G1361	C1301	U1241	G1170	U982	C922	A660	A660
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G1663	G1543	C1603	C1483	U1423	C1363	A1303	C1243	C1172	C984	C924	C662	C662
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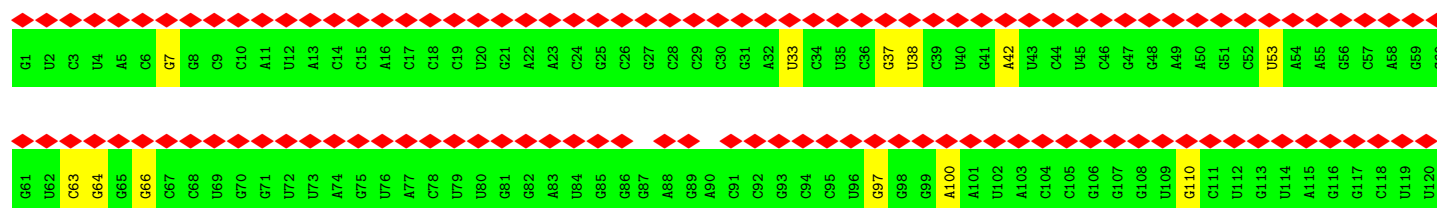
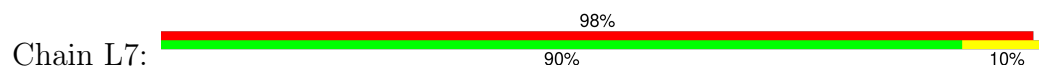
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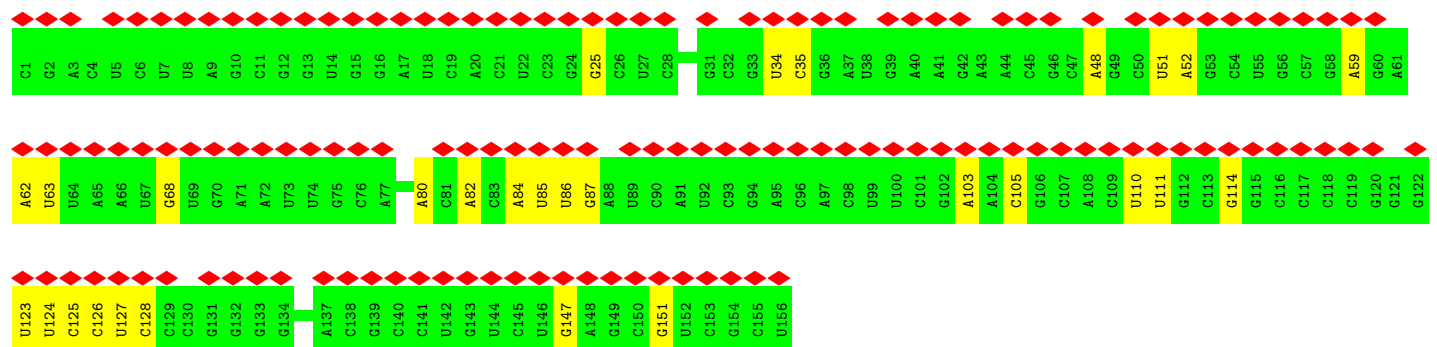
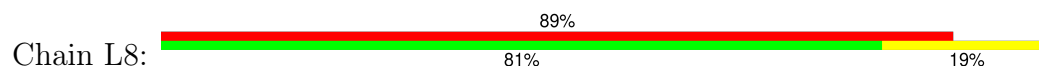
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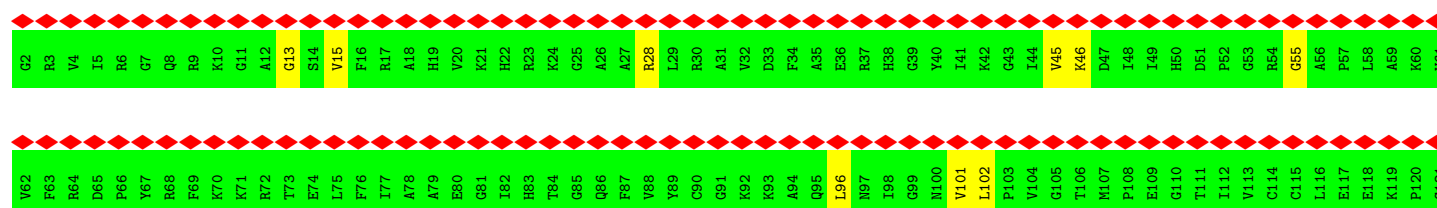
• Molecule 23: 5S rRNA

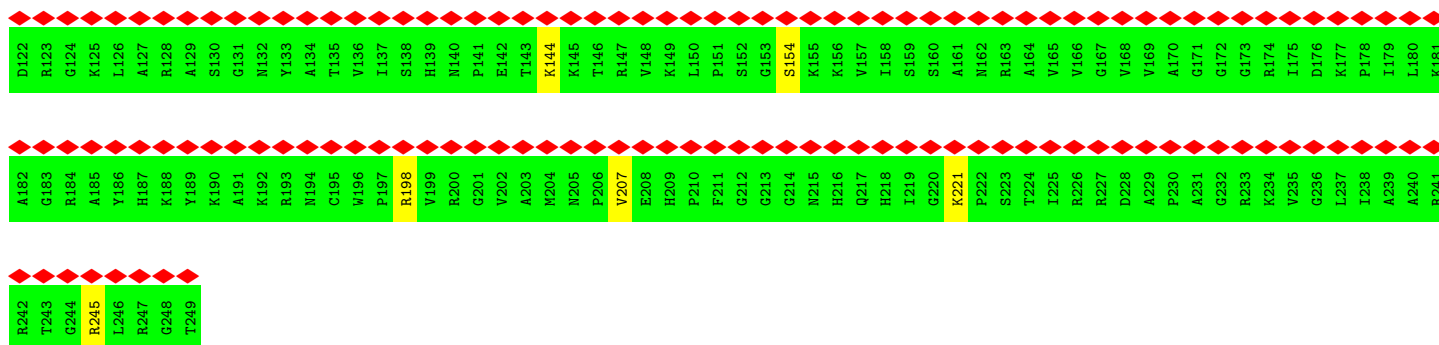


• Molecule 24: 5.8S rRNA

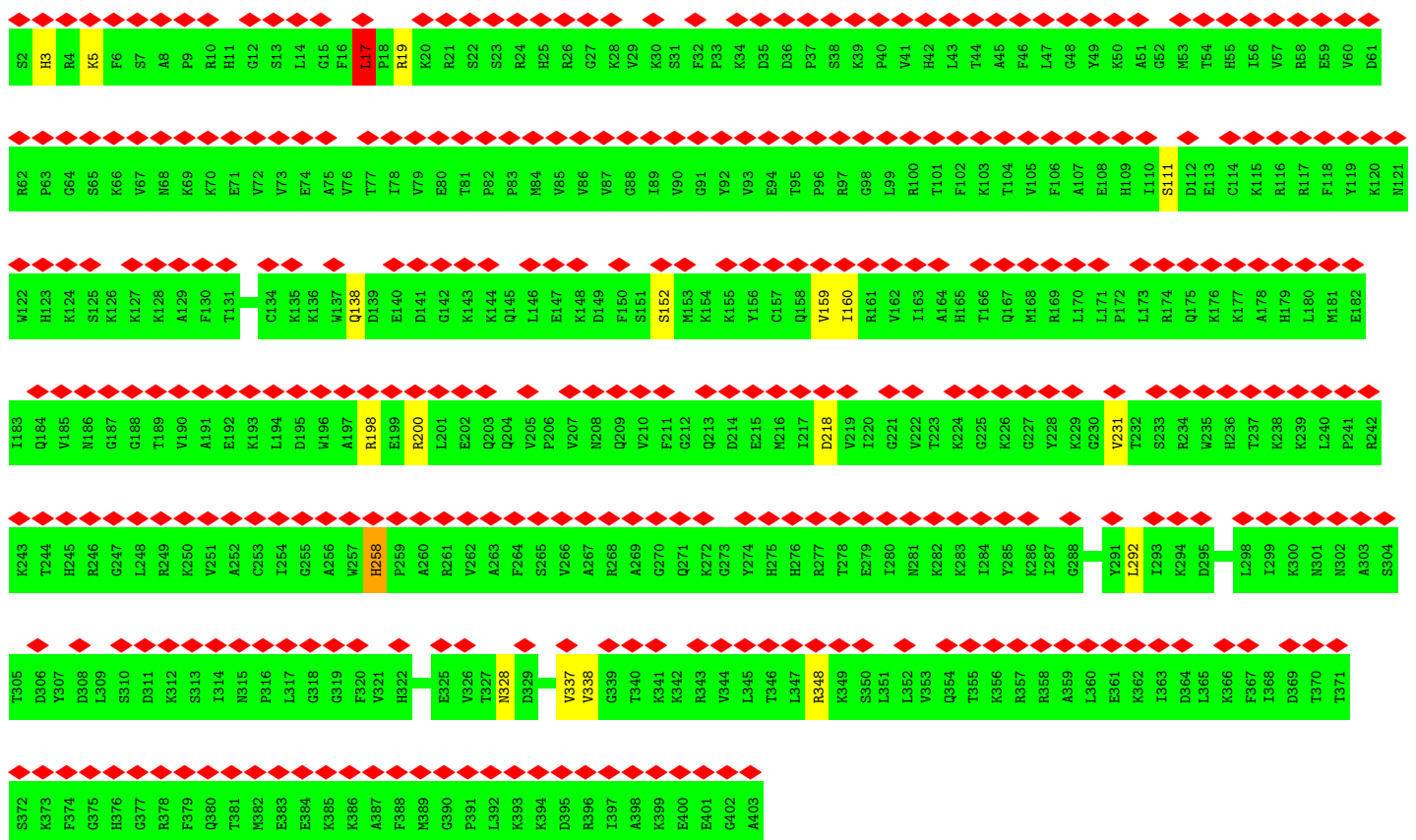
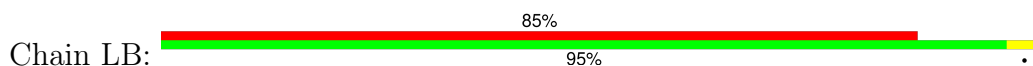


• Molecule 25: 60S ribosomal protein L8

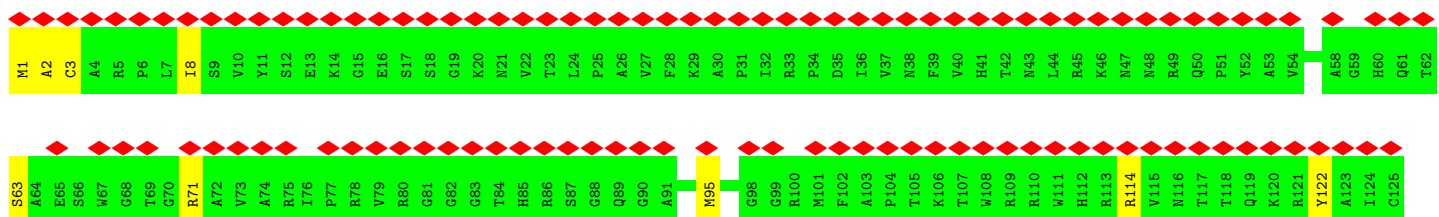


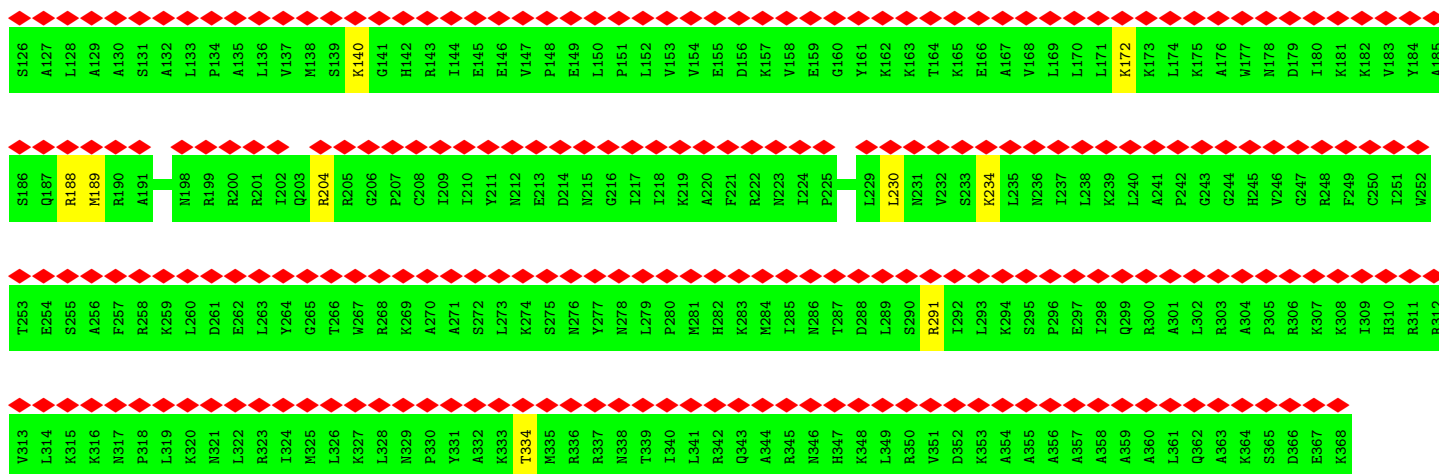


- Molecule 26: Large ribosomal subunit protein uL3

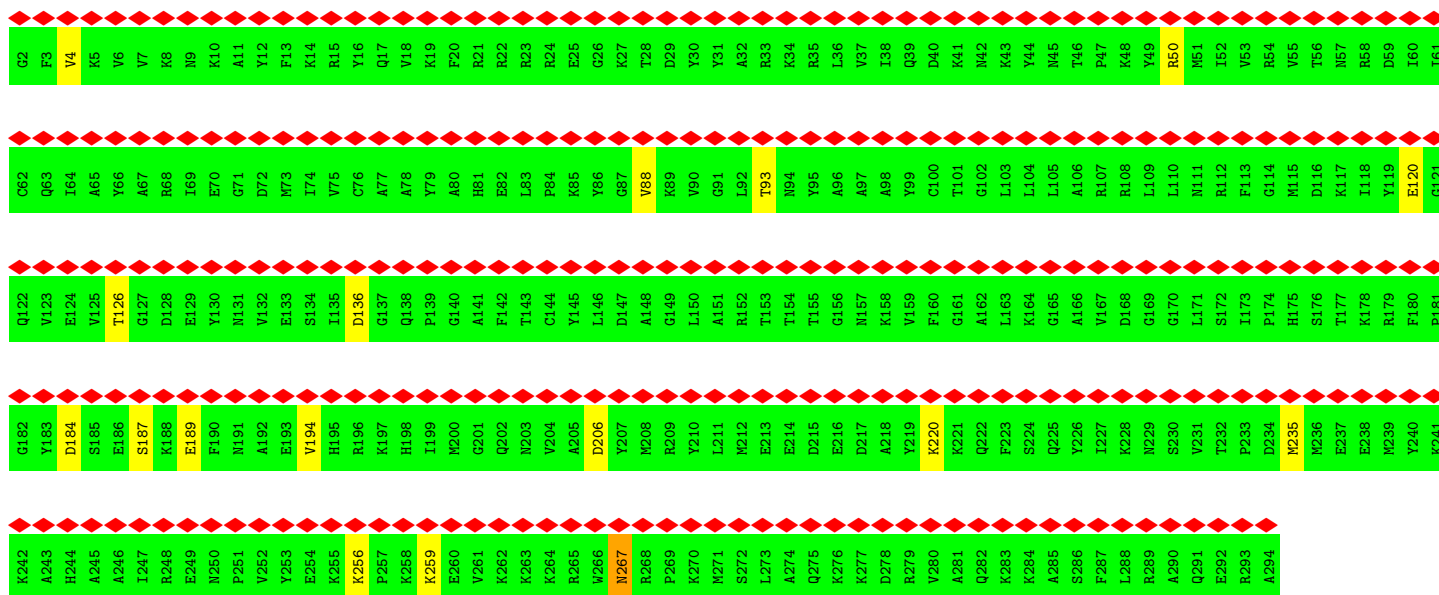


- Molecule 27: 60S ribosomal protein L4



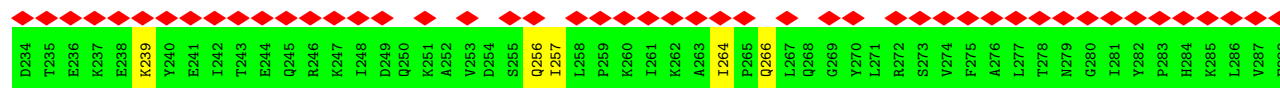


- Molecule 28: Large ribosomal subunit protein uL18

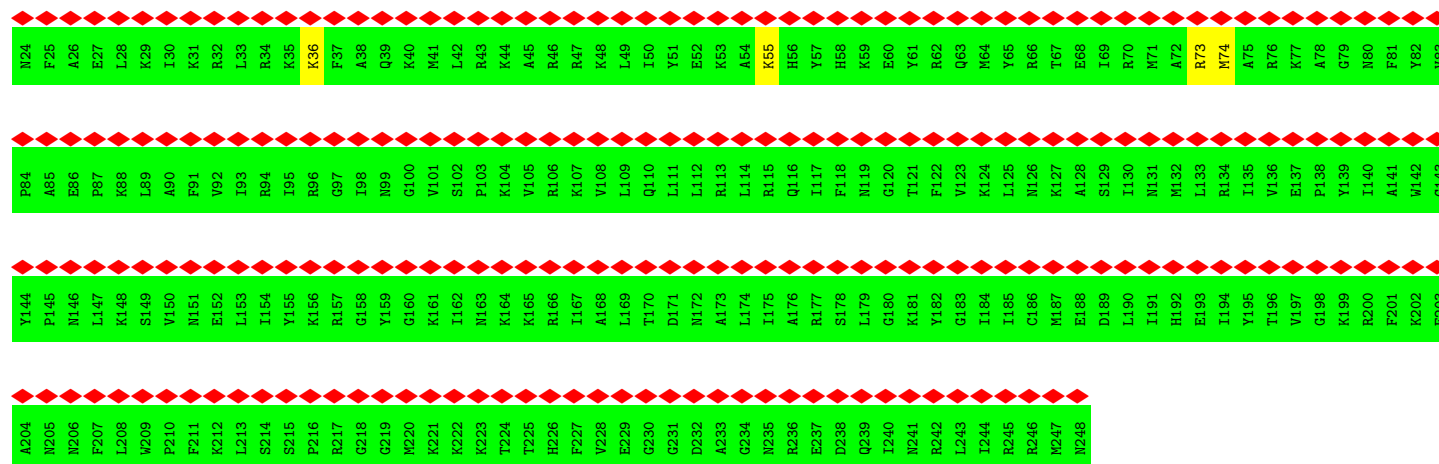


- Molecule 29: 60S ribosomal protein L6

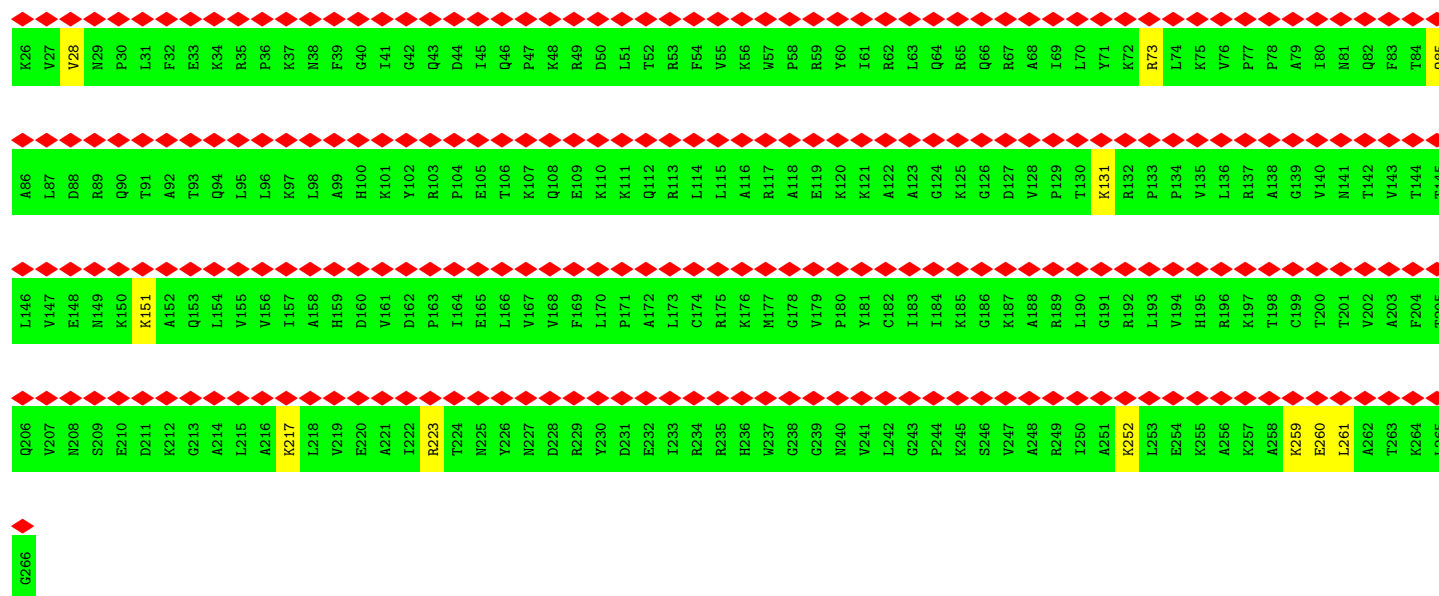




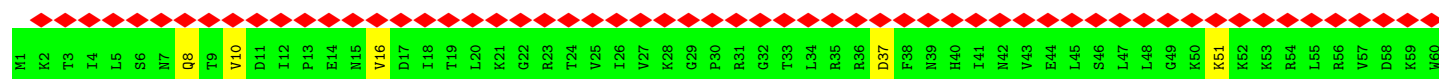
• Molecule 30: 60S ribosomal protein L7

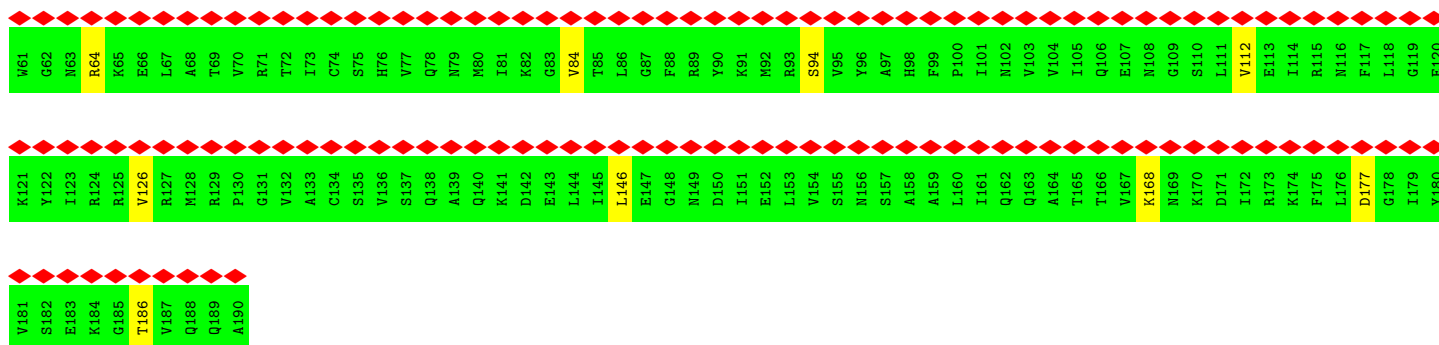


• Molecule 31: 60S ribosomal protein L7a

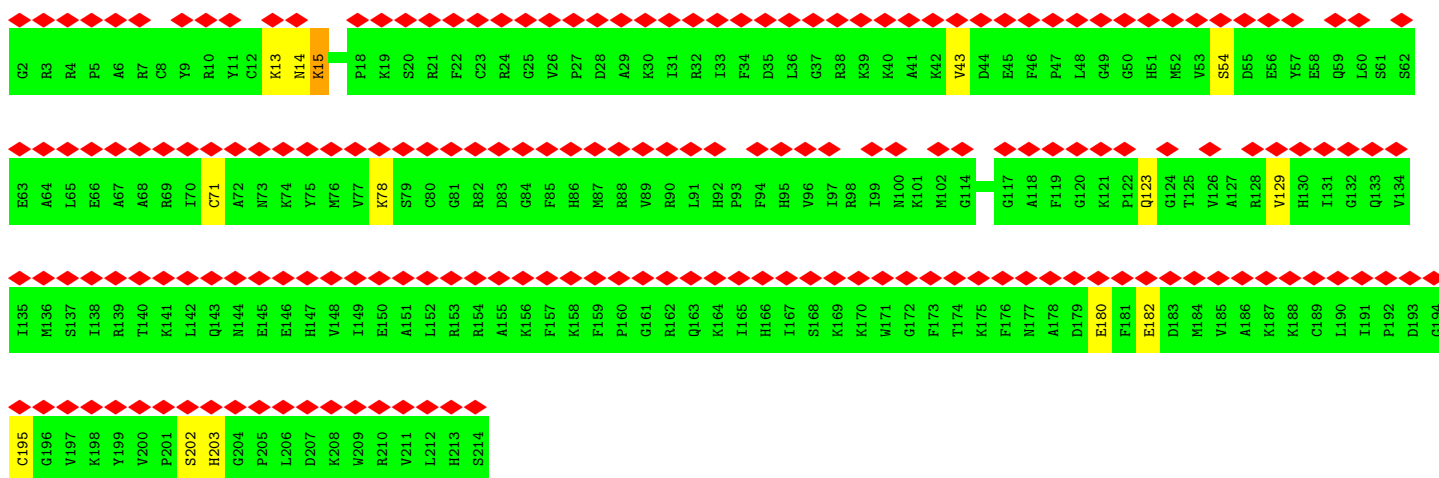


• Molecule 32: 60S ribosomal protein L9

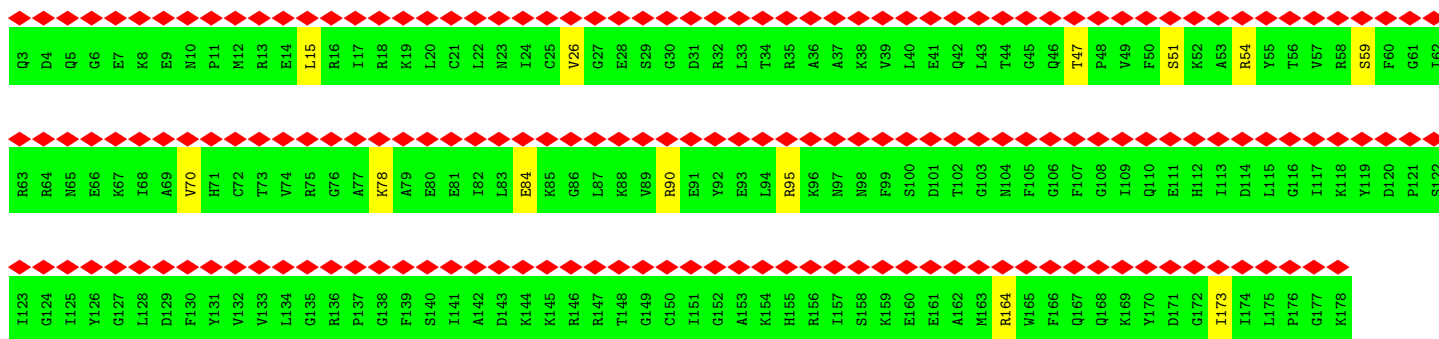




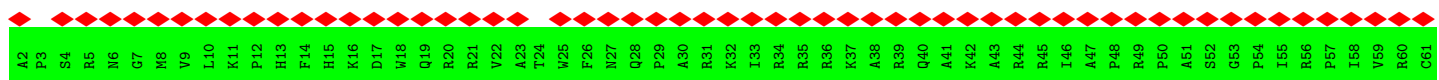
• Molecule 33: 60S ribosomal protein L10-like

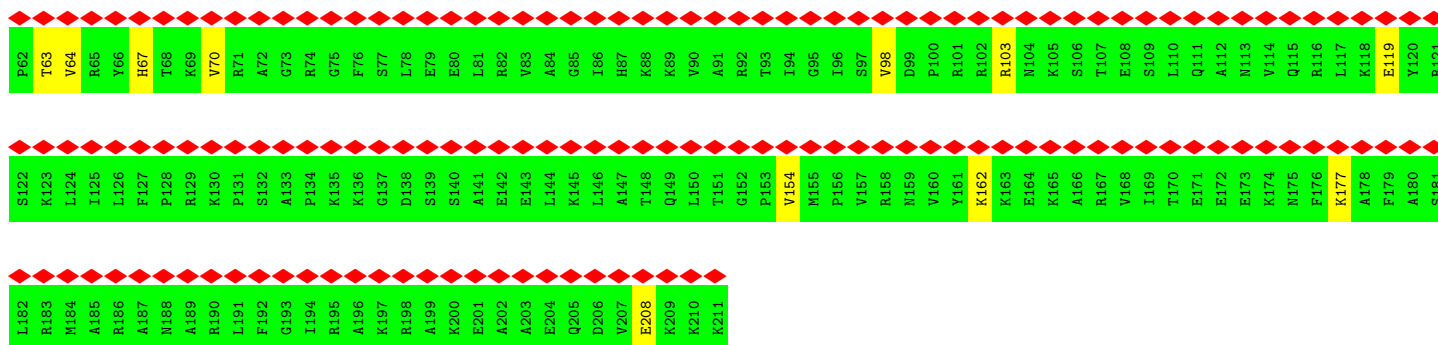


• Molecule 34: 60S ribosomal protein L11

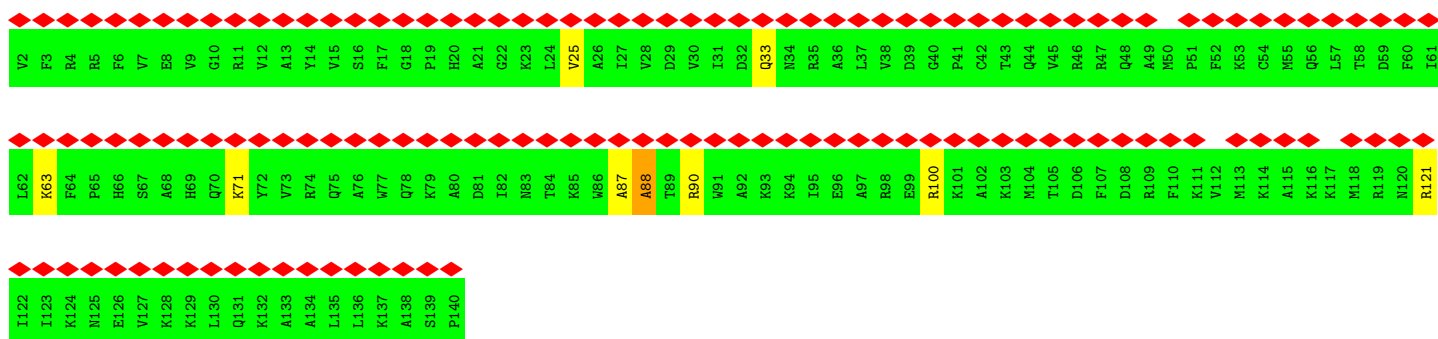


• Molecule 35: Large ribosomal subunit protein eL13

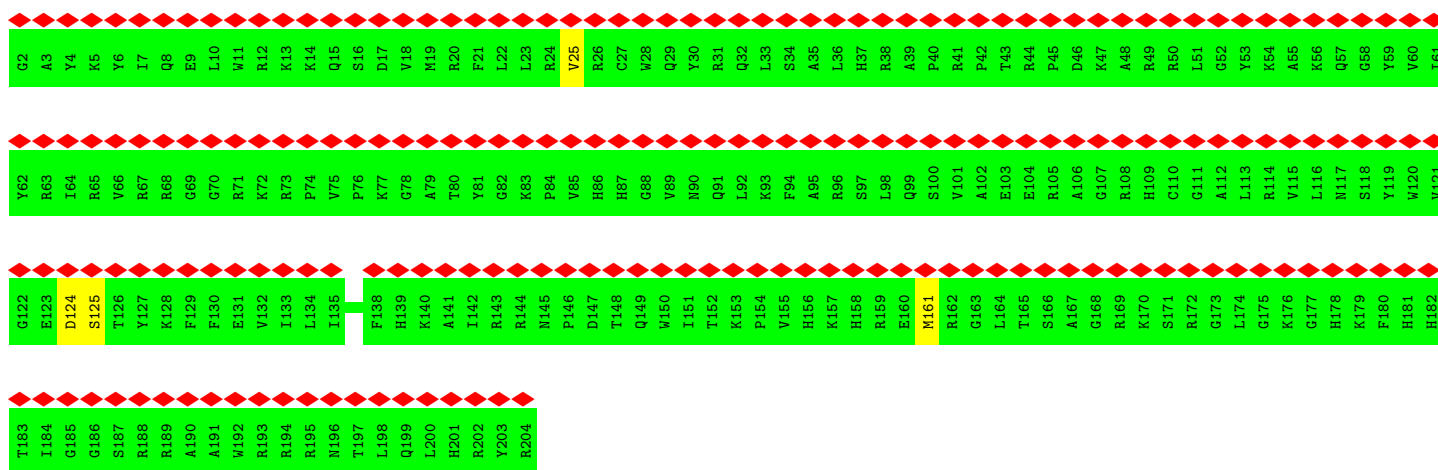




• Molecule 36: 60S ribosomal protein L14

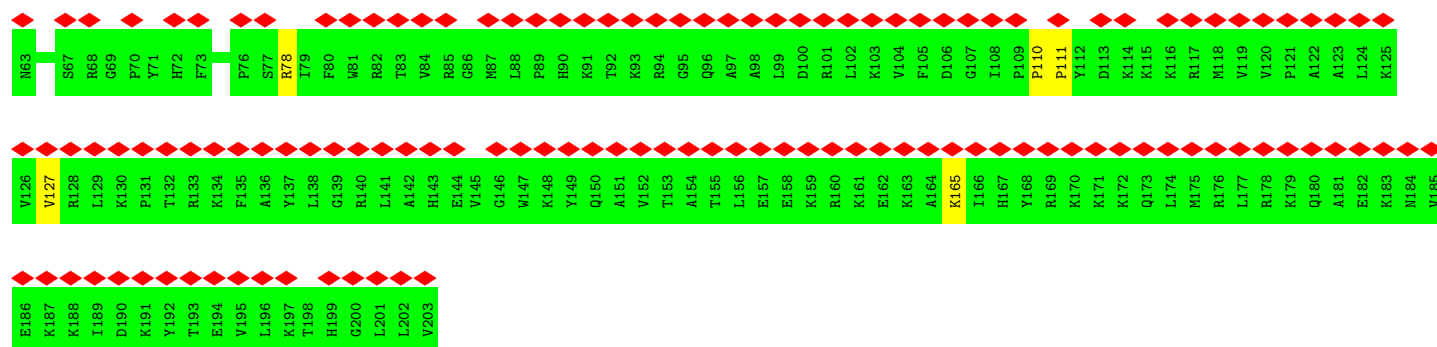


• Molecule 37: 60S ribosomal protein L15



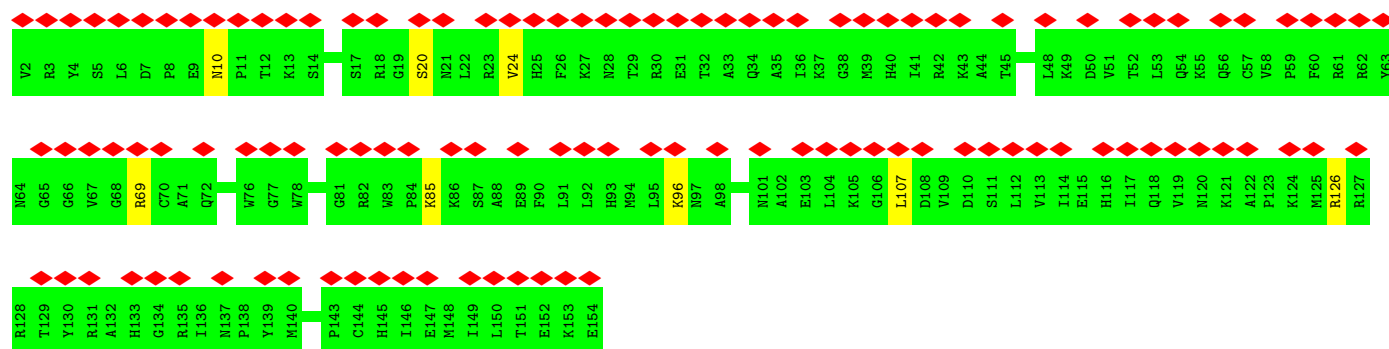
• Molecule 38: 60S ribosomal protein L13a





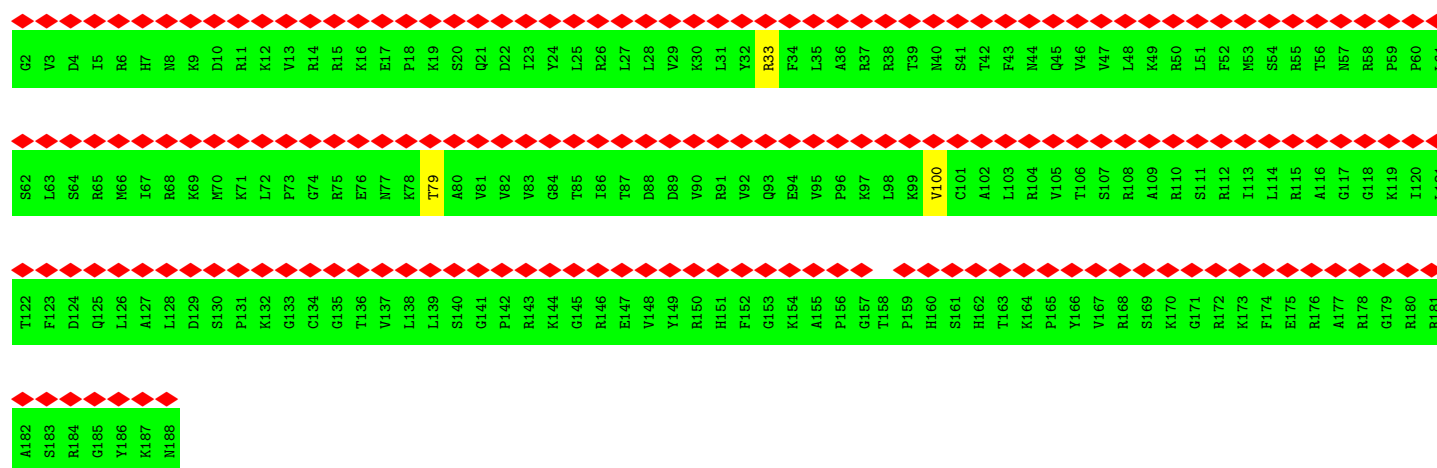
• Molecule 39: 60S ribosomal protein L17

Chain LP:



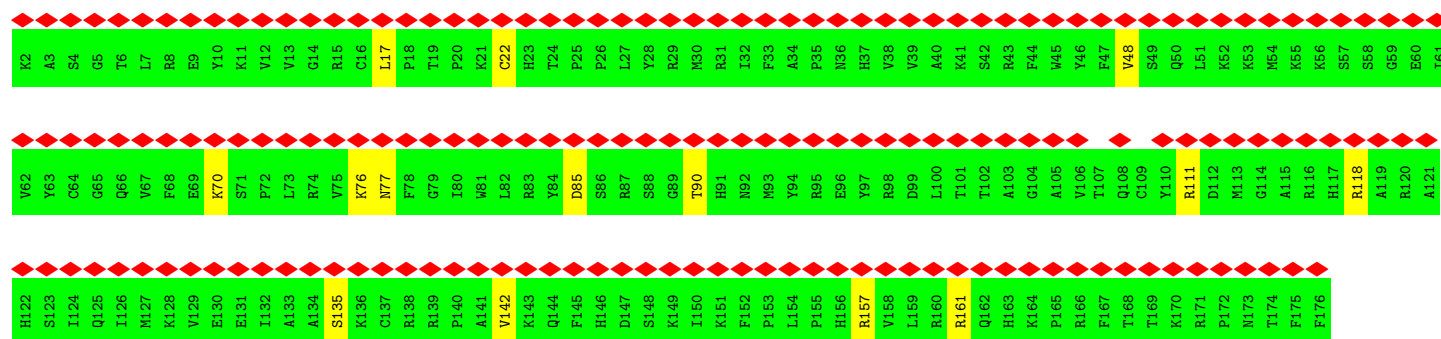
• Molecule 40: 60S ribosomal protein L18

Chain LQ:

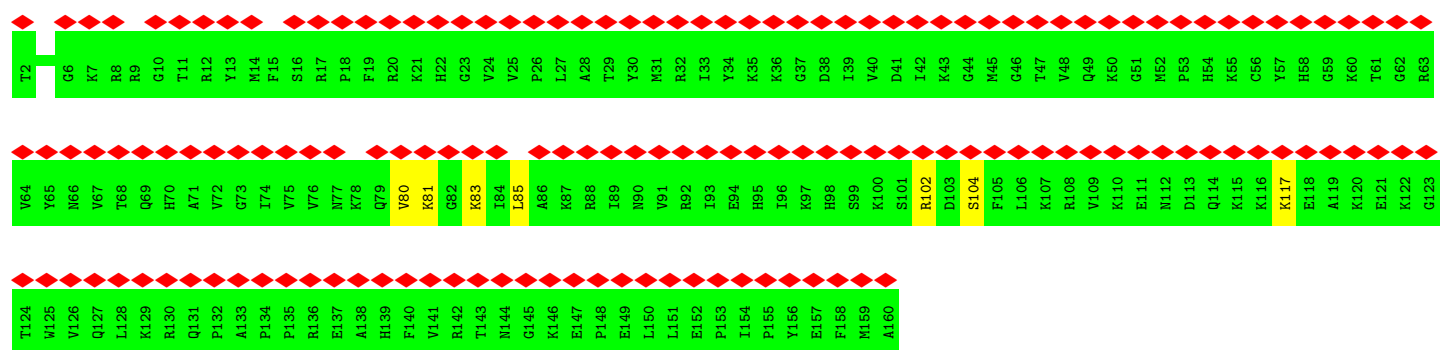


• Molecule 41: 60S ribosomal protein L18a

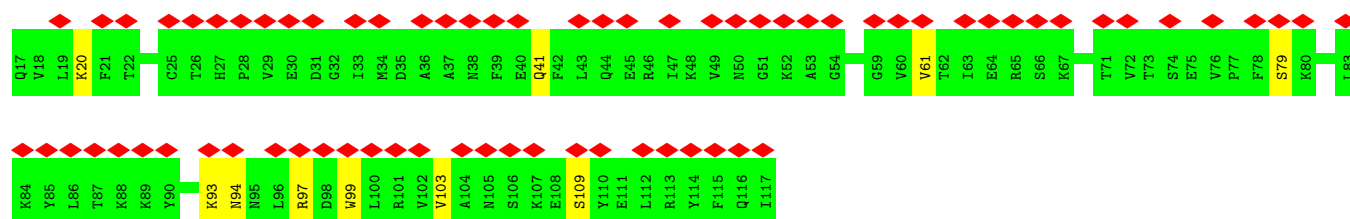
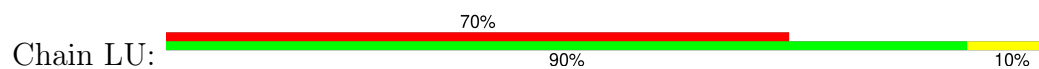
Chain LS:



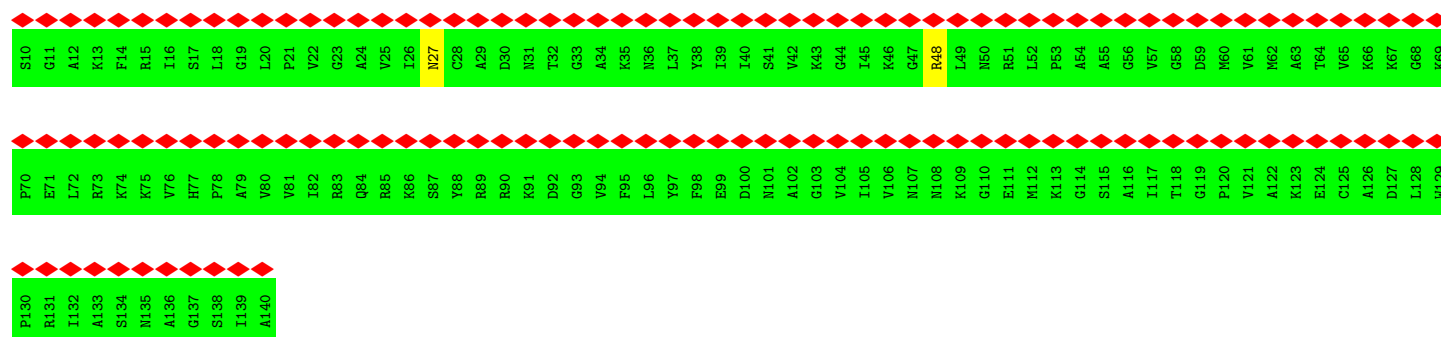
• Molecule 42: 60S ribosomal protein L21



• Molecule 43: Heparin-binding protein HBp15

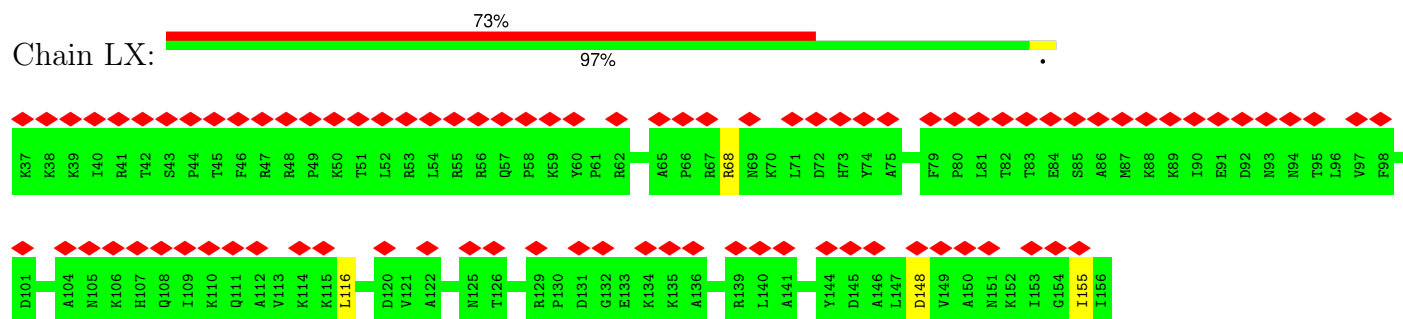


• Molecule 44: 60S ribosomal protein L23



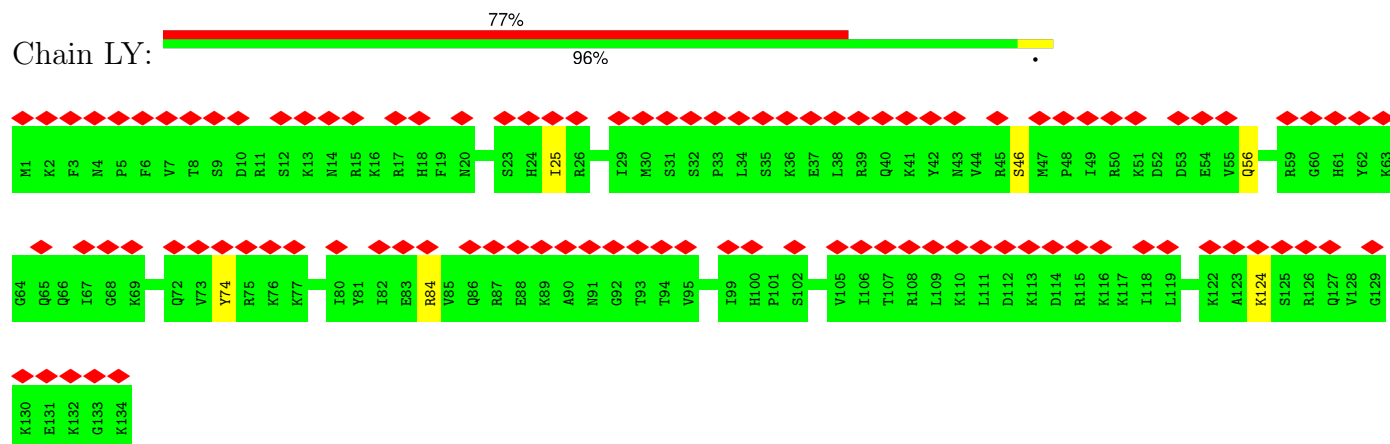
- Molecule 45: 60S ribosomal protein L23a

Chain LX:



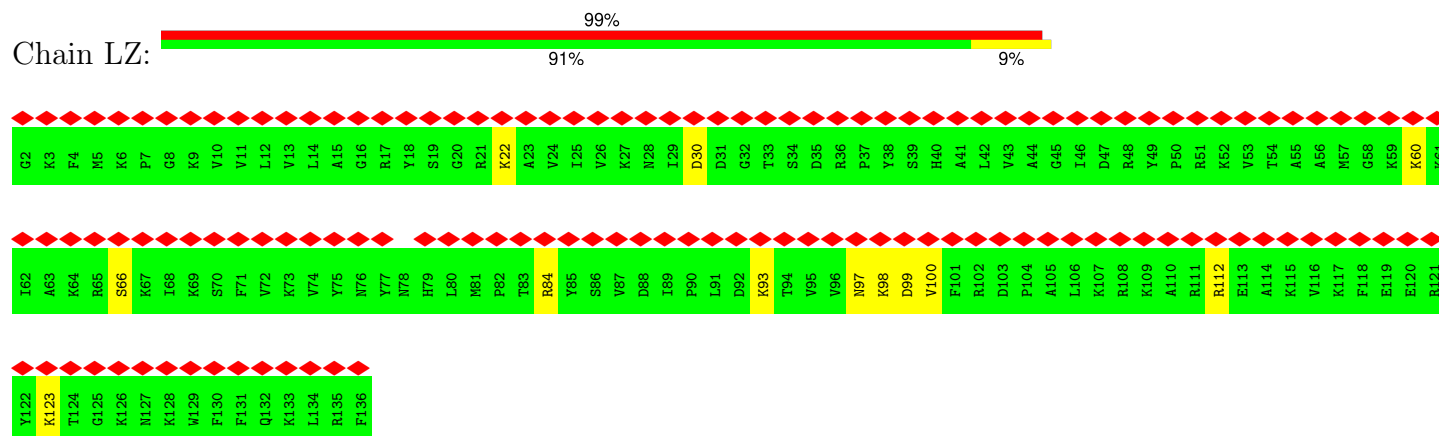
- Molecule 46: 60S ribosomal protein L26

Chain LY:



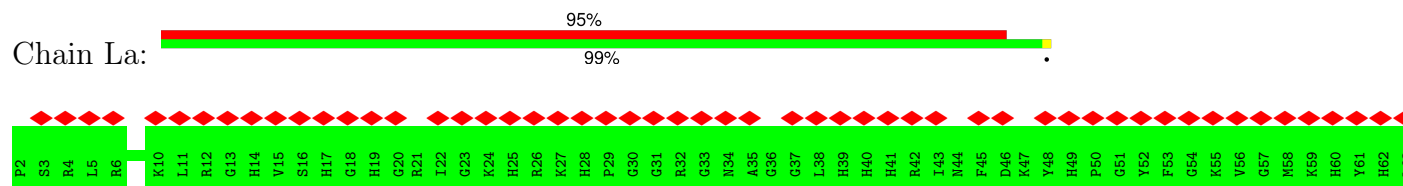
- Molecule 47: 60S ribosomal protein L27

Chain LZ:



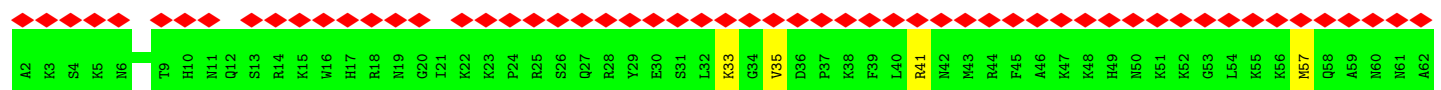
- Molecule 48: 60S ribosomal protein L27a

Chain La:





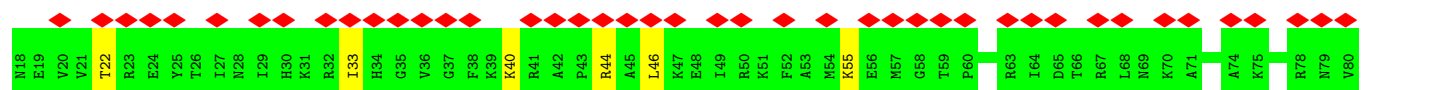
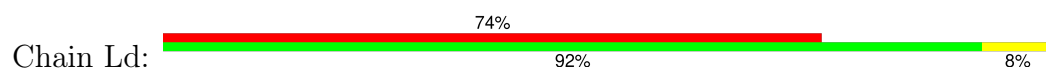
• Molecule 49: 60S ribosomal protein L29



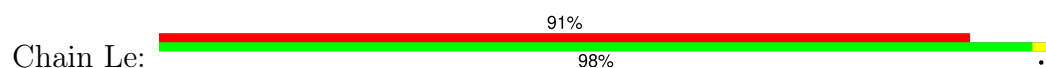
• Molecule 50: 60S ribosomal protein L30

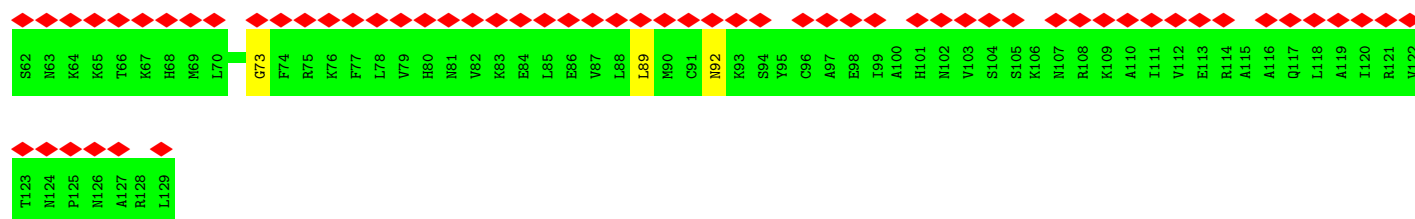


• Molecule 51: 60S ribosomal protein L31

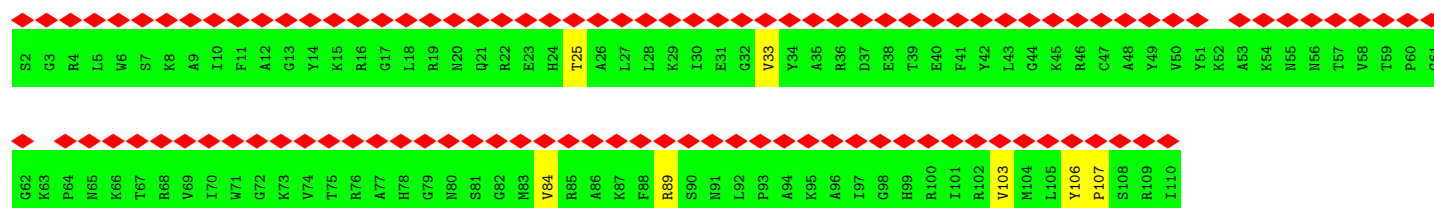


• Molecule 52: 60S ribosomal protein L32





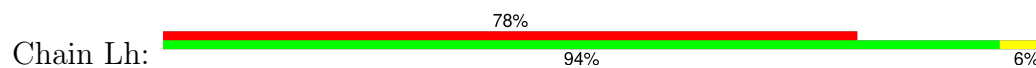
- Molecule 53: 60S ribosomal protein L35a



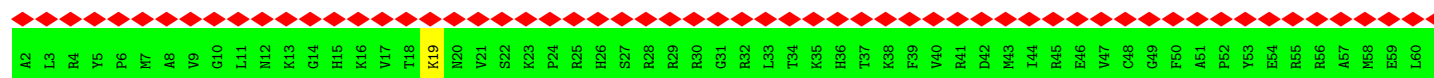
- Molecule 54: 60S ribosomal protein L34

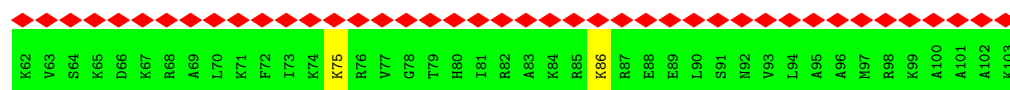


- Molecule 55: 60S ribosomal protein L35

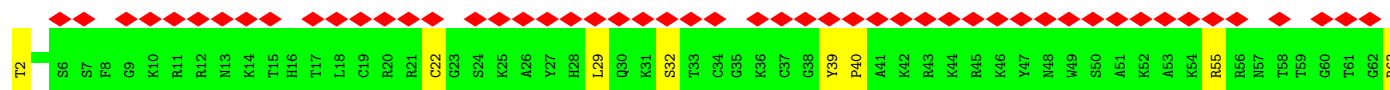
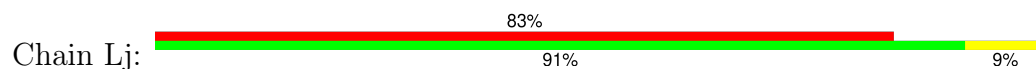


- Molecule 56: 60S ribosomal protein L36

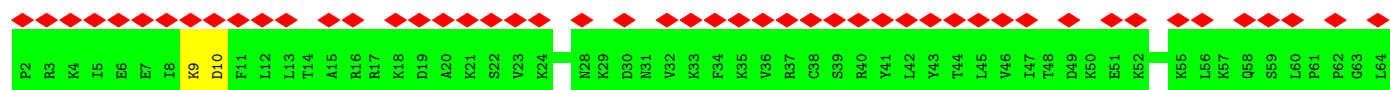
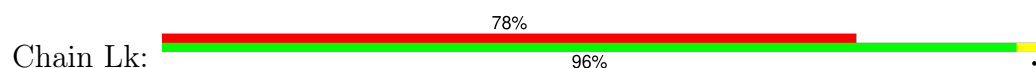




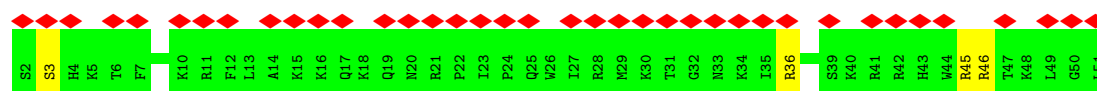
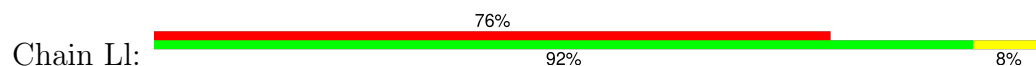
- Molecule 57: 60S ribosomal protein L37



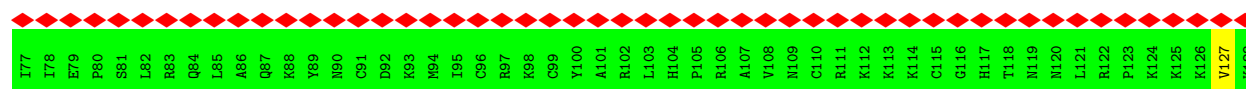
- Molecule 58: 60S ribosomal protein L38



- Molecule 59: 60S ribosomal protein L39



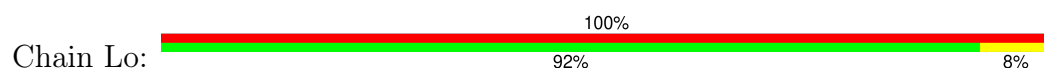
- Molecule 60: Large ribosomal subunit protein eL40



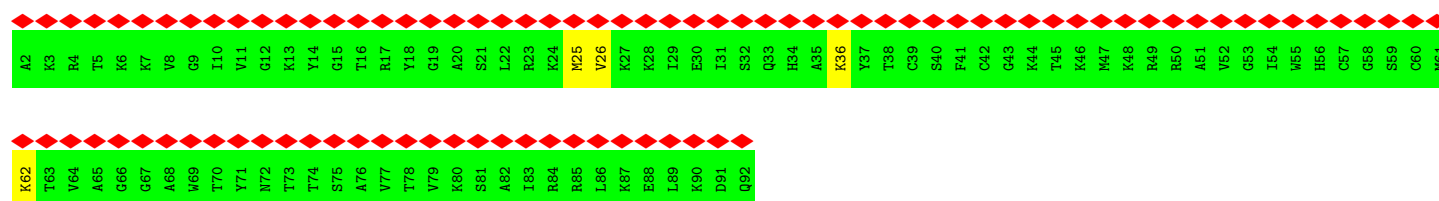
- Molecule 61: 60S ribosomal protein L41



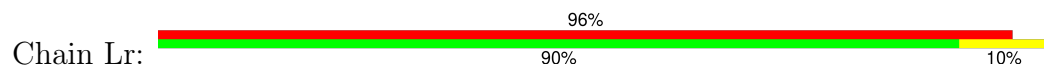
- Molecule 62: 60S ribosomal protein L36a



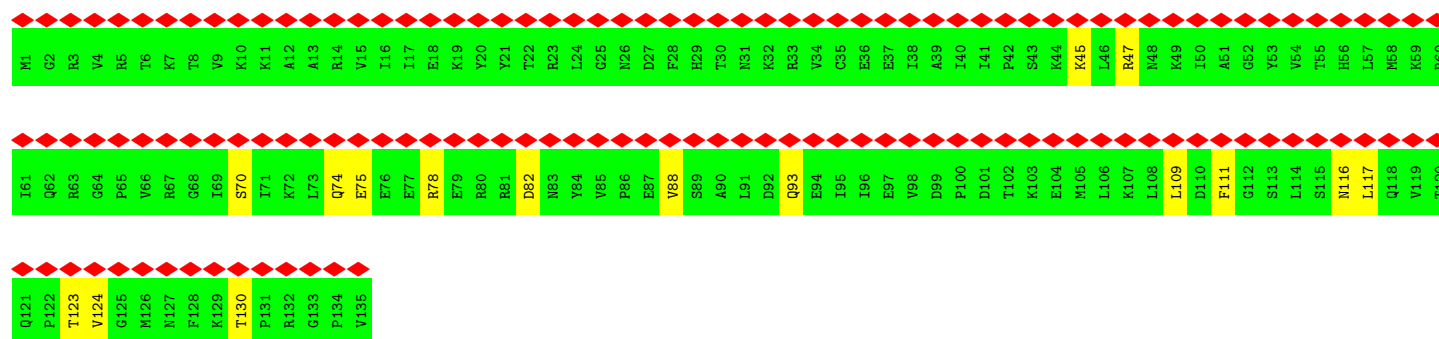
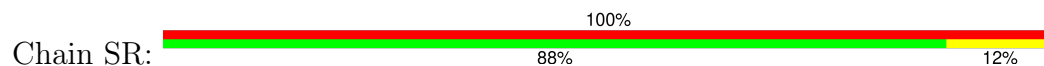
- Molecule 63: 60S ribosomal protein L37a



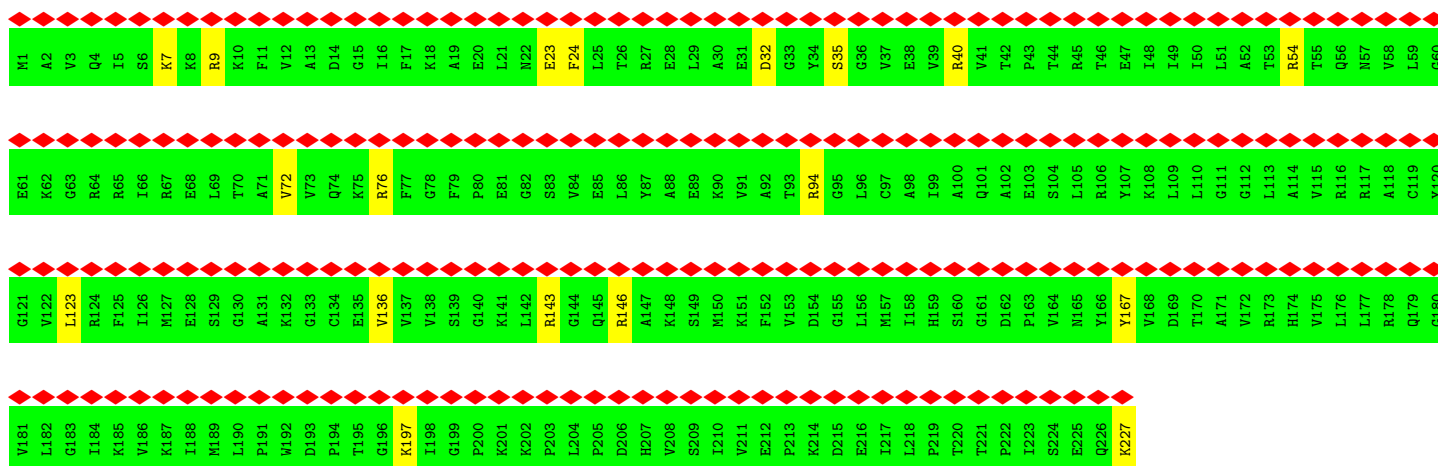
- Molecule 64: 60S ribosomal protein L28



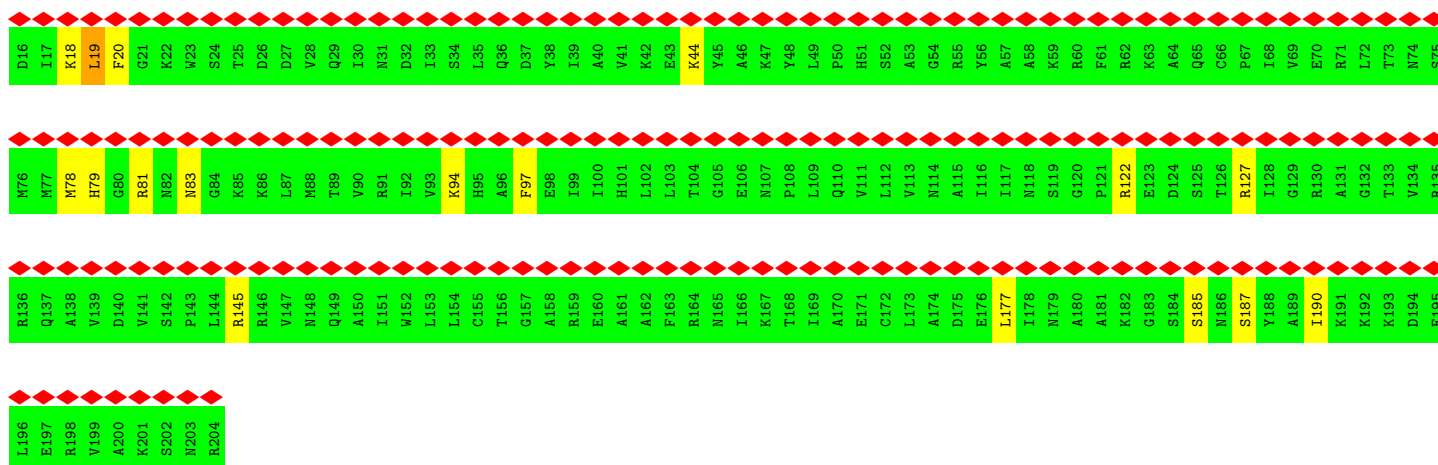
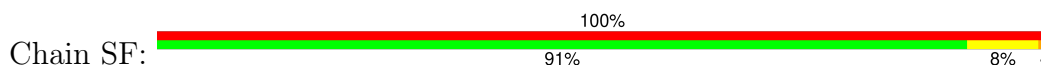
- Molecule 65: 40S ribosomal protein S17



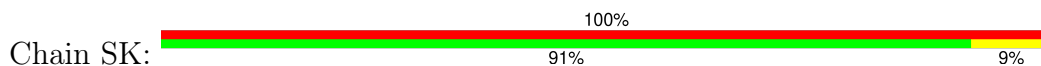
- Molecule 66: Small ribosomal subunit protein uS3



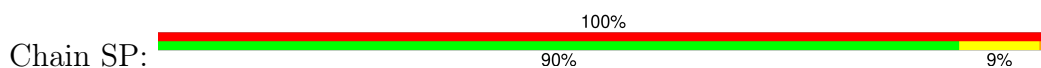
• Molecule 67: 40S ribosomal protein S5

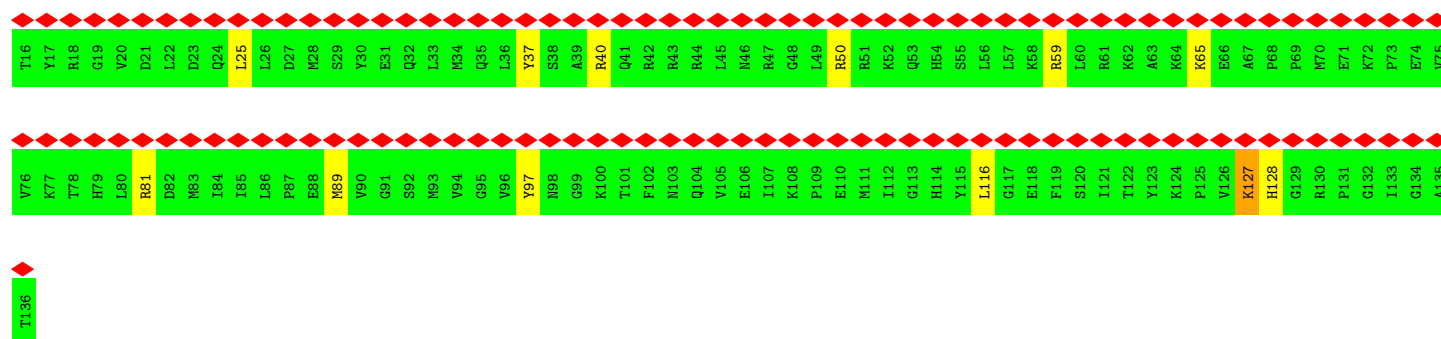


• Molecule 68: 40S ribosomal protein S10

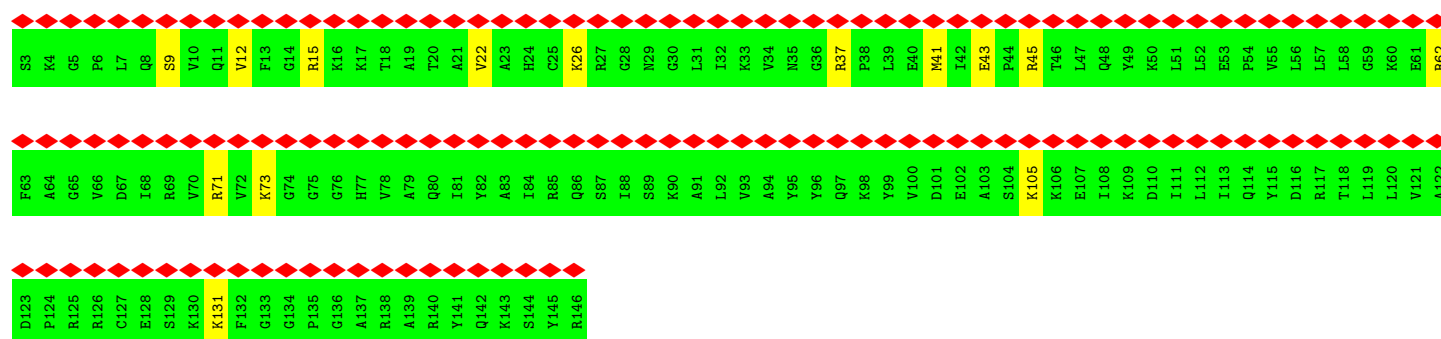


• Molecule 69: Small ribosomal subunit protein uS19

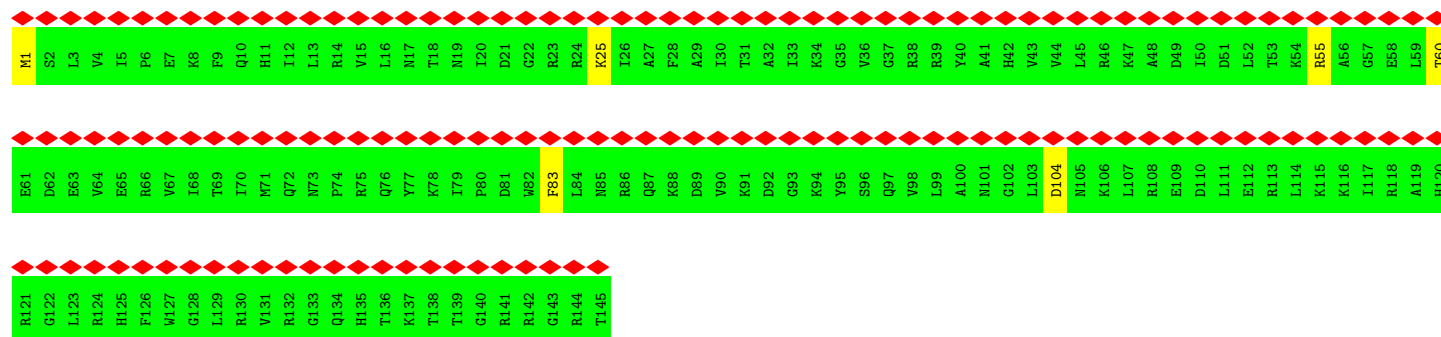




- Molecule 70: Small ribosomal subunit protein uS9

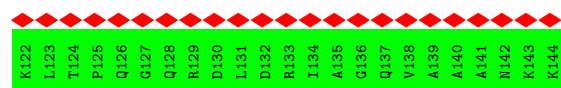


- Molecule 71: 40S ribosomal protein S18

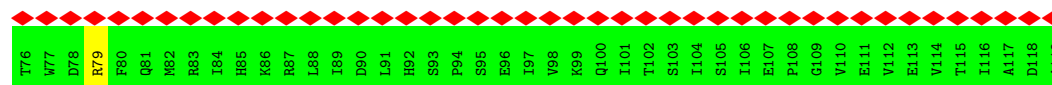
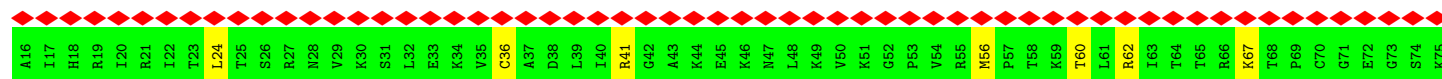


- Molecule 72: 40S ribosomal protein S19

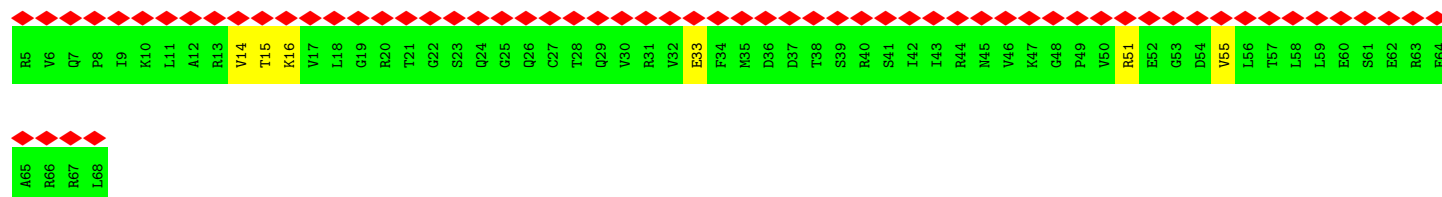
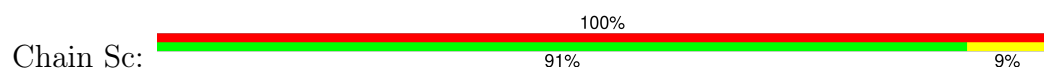




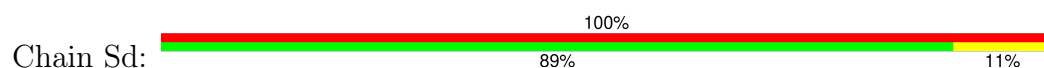
- Molecule 73: 40S ribosomal protein S20



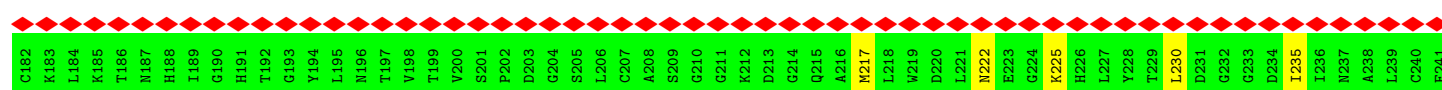
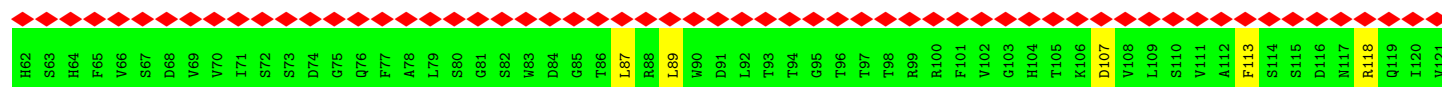
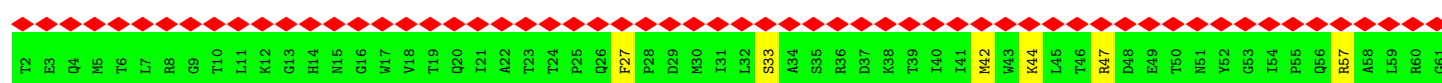
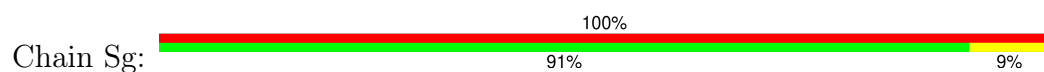
- Molecule 74: 40S ribosomal protein S28



- Molecule 75: 40S ribosomal protein S29

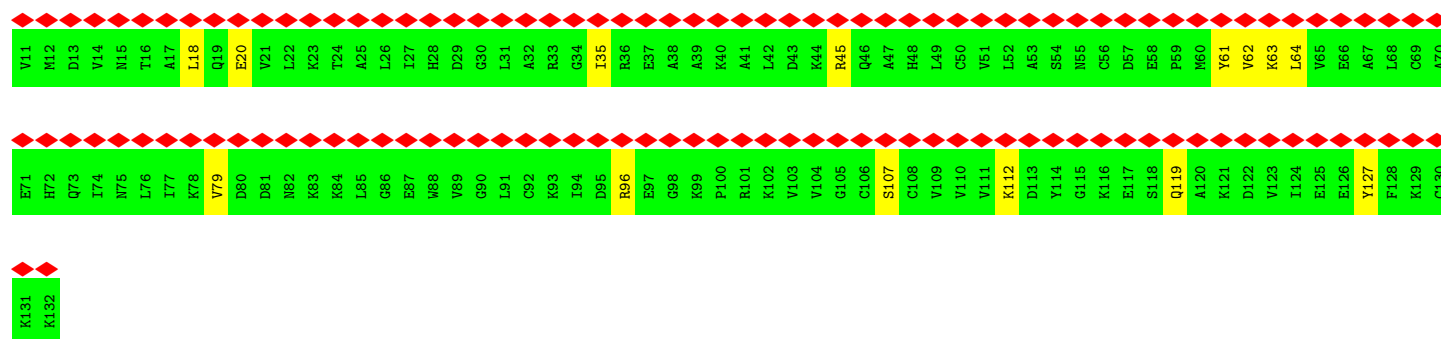
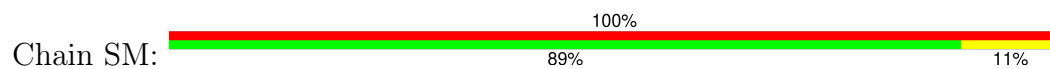


- Molecule 76: Receptor of activated protein C kinase 1

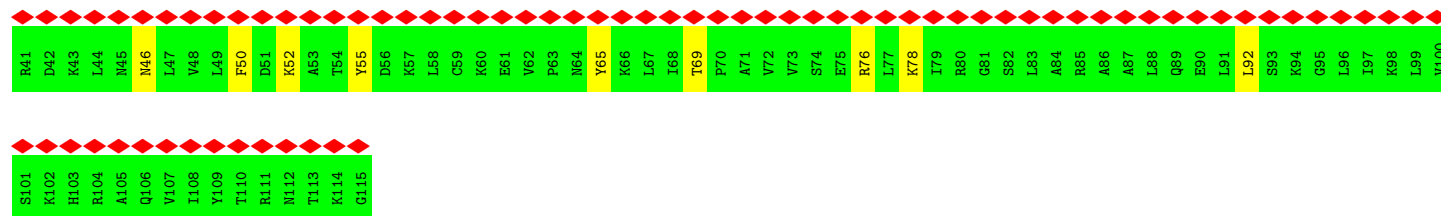
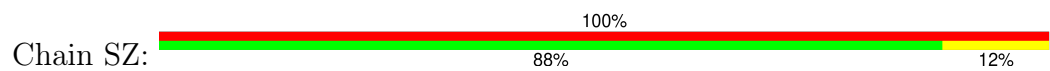




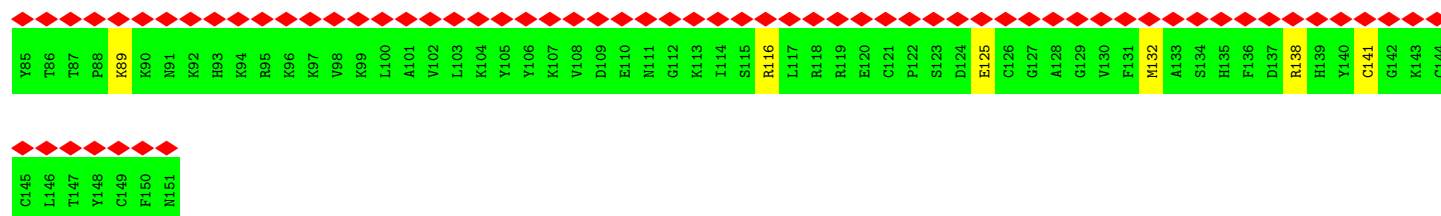
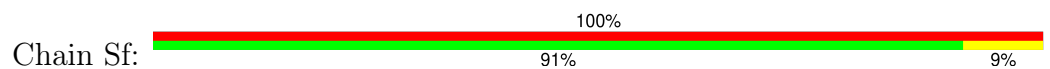
- Molecule 77: Small ribosomal subunit protein eS12



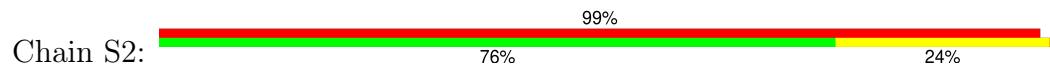
- Molecule 78: Small ribosomal subunit protein eS25



- Molecule 79: Ubiquitin-40S ribosomal protein S27a

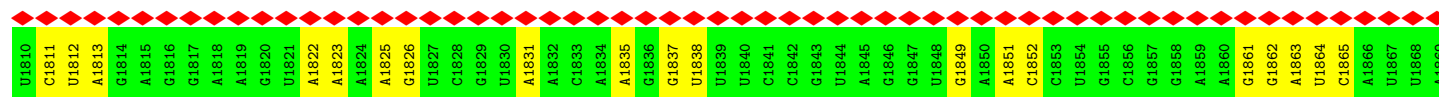
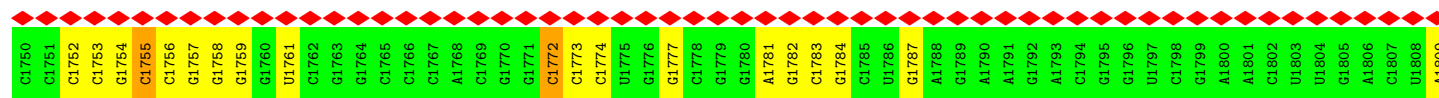


- Molecule 80: 18S rRNA

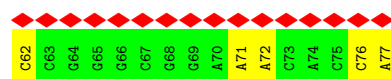
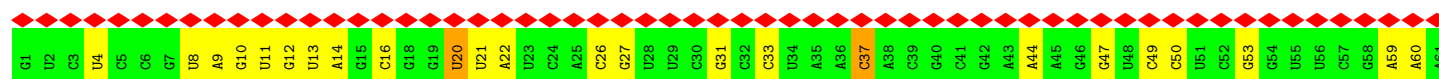


U1	A61	U121	A181	A302	C362	U422	G482	U542	G602	G662	C790	C850	G910
A2	G62	G122	C182	C303	A363	U423	C483	C543	C603	C663	C791	C851	C911
C3	U63	G123	G183	C304	A364	C424	A484	G544	A604	A664	C792	G852	C912
C4	A64	U124	G184	U305	C365	G425	A485	A545	A605	G665	G793	C853	A913
U5	C65	C125	G185	C306	U366	U426	A486	G546	G606	U666	A794	A854	U914
G6	G66	G126	G186	G307	U367	U427	U487	G547	U607	U667	A795	C855	U915
G7	C67	C127	G187	G308	U368	U428	U488	C548	C608	A668	G796	C856	U916
U8	A68	U128	C188	G309	C369	C429	A489	C549	U609	A669	C797	U857	U917
U9	C69	U129	C189	C310	G370	C430	A490	C550	G610	A670	G798	A858	U918
G10	G70	G130	G190	C311	A371	G431	C491	U551	G611	A671	U799	G859	A919
A11	G71	C131	A191	G312	U372	G432	C492	G552	U612	A672	U800	G860	A920
U12	C72	U132	C192	A313	G373	A433	A493	U553	G613	G673	U801	A861	G921
C13	C73	C133	C193	U314	G374	G434	C494	A554	C614	C674	A802	A862	A922
C14	G74	C134	C194	C315	U375	A435	U495	A555	C615	C675	C803	U863	G923
U15	G75	U135	C195	G316	A376	G436	C496	U556	A616	C676	U804	A864	G924
G16	U76	C136	C196	G317	G377	G437	C497	U557	G617	G677	U805	A865	G925
C17	A77	U137	U197	A318	U378	U438	C498	G558	C618	U678	U806	U866	A926
A18	C78	C138	U198	C319	C379	A439	G499	G559	A619	A679	G807	G867	C927
C19	A79	C139	C199	G320	G380	G440	A500	A560	G620	G680	A808	G868	G928
G20	G80	C140	G200	C321	C381	C441	C501	A561	C621	U681	A809	A869	G929
U21	U81	A141	C201	C322	G383	C442	C502	U562	C622	C682	A810	A870	C930
A22	G82	U143	G203	C323	U384	U443	C503	G563	G623	G683	A811	A871	C931
G23	A83	U143	G203	C324	G385	G444	G504	A564	C624	G684	A812	A872	G932
C24	A84	U144	G204	C325	G386	A445	G505	G565	G625	A685	A813	G873	G933
A25	A85	G145	G205	C326	C387	G446	G506	U566	G626	U686	U814	G874	G934
U26	C86	G146	G206	G327	U388	A447	G507	G567	U627	C687	U815	A875	G935
A27	U87	A147	G207	U328	A389	A448	A508	C568	A628	U688	A816	C876	G936
U28	G88	U148	G208	G329	C390	A449	G509	A569	A629	U689	G817	C877	C937
G29	C89	A149	A209	G330	C391	C450	G510	C570	U630	G690	A818	G878	A938
C30	G90	C151	G211	G331	A392	G451	U511	U571	U631	G691	G819	C879	U939
U31	A91	U152	C212	G332	U393	G452	A512	U572	C632	G692	U820	G880	U940
U32	A92	G153	G213	C333	G394	C453	G513	U573	C633	A693	G821	U881	C941
G33	U93	U154	U214	C334	G395	U454	U514	A574	A634	G694	U822	U882	G942
U34	G94	U154	G215	G335	U396	A455	G515	A575	G635	C695	U823	U883	U943
C35	G95	G155	C216	A336	G397	C456	A516	A576	C636	G696	C824	C884	A944
U36	C96	U156	G217	G337	U398	A457	C517	U577	U637	G697	A825	U885	U945
C37	U97	U157	A217	G338	A399	C458	G518	C578	C638	G698	A826	A886	U946
U38	C98	A158	U218	A339	C400	C459	A519	C579	C639	C730	A827	U887	U947
A39	A99	U159	U219	C340	A401	A460	A520	U580	A640	G731	G828	U888	C948
A40	U100	U160	U220	C341	C402	U461	A521	U581	A641	U732	C829	U889	G949
C41	U101	C162	U222	C342	G403	C462	A522	U582	C642	C733	A830	U890	C950
U43	A103	U163	C223	U343	G404	C463	A523	U583	A643	C734	G831	U891	C951
U44	A104	G164	G225	U344	U406	A464	U524	A584	G644	C735	G832	U892	G952
A45	U105	G165	G226	C346	G407	A465	A525	C585	C645	G736	C833	U893	C953
C46	C106	A166	U287	U347	A408	G466	A526	G586	G646	G737	C834	G894	U954
G47	A107	G167	G288	A348	C409	A468	A528	U588	A648	C739	C835	G895	A955
C48	C108	C168	C289	A349	C410	A469	A529	G589	U649	U746	G836	U896	G956
A49	U109	U169	U290	C350	G411	G470	U530	A590	A650	U747	G838	U898	G958
U50	A170	A171	C291	C351	G412	A471	A531	U591	U651	C748	C839	U899	G959
U51	U111	A172	A292	U352	G413	C472	C532	U592	U652	U749	C940	G900	U960
G52	G113	C173	C293	U353	A414	A473	A533	C593	A653	C750	G841	G901	G961
A54	U115	A174	G114	C354	A415	G474	G534	A594	U654	C752	C842	A903	A962
U55	U116	C175	U296	G355	A416	C475	G535	U596	G656	C753	C843	A904	C963
C56	U117	U176	A297	C356	C417	A476	A536	U596	G657	C754	U844	C905	A964
U57	C118	G177	G298	C357	A418	G477	C537	G597	U658	C755	G845	G906	U965
C58	U119	C178	A299	U359	A419	C478	U538	G598	U659	G756	G846	U907	U966
U59	U120	C179	A301	A360	G421	G480	U540	G600	C660	G757	A847	A908	C967
A60		G180		U361		C481	U541	G601	U661	G758	U848	U909	U968
													U969

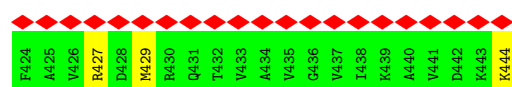
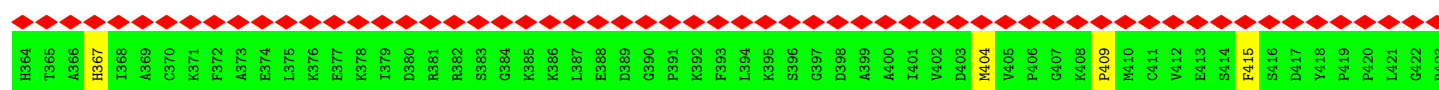
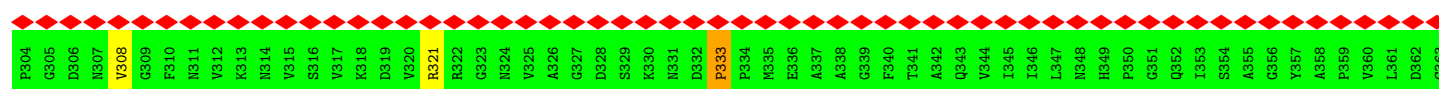
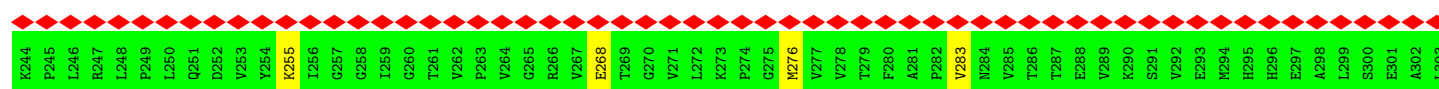
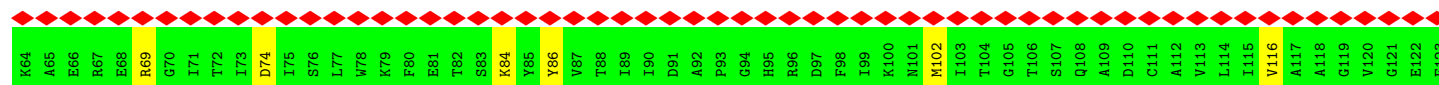
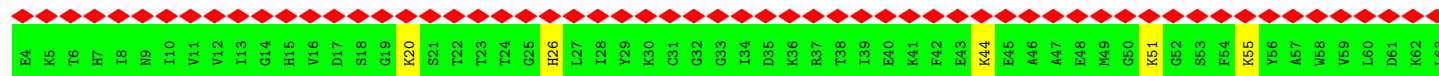
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U1694	C1634	C1094	A1034	C974
C1695	A1635	C1095	A1035	G975
C1696	G1636	G1096	G1036	G976
A1697	A1637	G1097	G1037	C977
C1698	G1638	G1098	U1038	G978
A1699	G1639	G1099	G1039	C979
C1700	A1640	A1100	G1040	A980
C1701	A1641	U1101	G1041	A981
G1702	A1642	G1102	A1042	G982
C1703	U1643	C1103	G1043	A983
C1704	C1644	G1104	G1044	C984
C1705	A1645	G1105	U1045	G985
G1706	C1646	G1106	U1046	G986
U1707	A1647	G1107	U1047	A987
C1708	G1648	G1108	G1048	C988
G1709	U1649	C1109	A1049	C989
A1650	C1650	U1110	A1050	A990
C1651	U1651	G1111	G1051	G991
G1652	C1652	U1112	A1052	A992
C1653	A1653	A1113	G1053	G993
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C1655	A1655	U1115	A1055	G995
G1656	U1656	C1116	U1056	A996
C1657	A1657	C1117	U1057	A997
G1658	U1658	C1118	A1058	A998
U1659	C1659	A1119	G1059	G999
C1660	A1660	U1120	A1060	C1000
A1661	U1661	G1121	U1061	A1001
U1662	C1662	A1122	A1062	U1002
G1663	G1663	C1123	G1063	U1003
A1664	U1664	C1124	C1064	U1004
G1665	C1665	C1125	G1065	G1005
C1666	U1666	G1126	U1066	C1006
G1667	A1667	C1127	C1067	C1007
U1668	C1668	C1128	G1068	A1008
G1669	U1669	G1129	U1069	A1009
C1670	A1670	A1130	G1070	G1010
U1671	G1671	G1131	G1071	A1011
G1672	U1672	C1132	U1072	A1012
C1673	C1673	A1133	U1073	U1013
U1674	A1674	G1134	C1074	G1014
A1675	C1675	C1135	C1075	U1015
G1676	U1676	U1136	G1076	U1016
C1677	A1677	U1137	A1077	U1017
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G1679	A1679	C1139	G1079	C1019
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A1681	C1681	G1141	U1081	U1021
U1682	U1682	G1142	A1082	U1022
C1683	G1683	A1143	A1083	A1023
G1684	U1684	A1144	A1084	A1024
A1685	C1685	A1145	G1085	U1025
G1686	U1686	C1146	G1086	C1026
C1687	A1687	G1147	U1087	A1027
U1688	C1688	A1148	U1088	A1028
G1689	U1689	A1149	G1089	G1029
U1690	A1630	G1090	A1030	G970
U1691	U1631	G1091	A1031	G971
U1692	G1632	G1092	C1032	A972
G1693	A1633	A1093	G1033	C973
U1694	C1634	C1094	A1034	C974
C1695	A1635	C1095	A1035	G975
C1696	G1636	G1096	G1036	G976
A1697	A1637	G1097	G1037	C977
C1698	G1638	G1098	U1038	G978
A1699	G1639	G1099	G1039	C979
C1700	A1640	A1100	G1040	A980
C1701	A1641	U1101	G1041	A981
G1702	A1642	G1102	A1042	G982
C1703	U1643	C1103	G1043	A983
C1704	C1644	G1104	G1044	C984
C1705	A1645	G1105	U1045	G985
G1706	C1646	G1106	U1046	G986
U1707	A1647	G1107	U1047	A987
C1708	G1648	G1108	G1048	C988
G1709	U1649	C1109	A1049	C989
A1650	C1650	U1110	A1050	A990
C1651	U1651	G1111	G1051	G991
G1652	C1652	U1112	A1052	A992
C1653	A1653	A1113	G1053	G993
U1654	G1654	U1114	G1054	C994
C1655	A1655	U1115	A1055	G995
G1656	U1656	C1116	U1056	A996
C1657	A1657	C1117	U1057	A997
G1658	U1658	C1118	A1058	A998
U1659	C1659	A1119	G1059	G999
C1660	A1660	U1120	A1060	C1000
A1661	U1661	G1121	U1061	A1001
U1662	C1662	A1122	A1062	U1002
G1663	G1663	C1123	G1063	U1003
A1664	U1664	C1124	C1064	U1004
G1665	C1665	C1125	G1065	G1005
C1666	U1666	G1126	U1066	C1006
G1667	A1667	C1127	C1067	C1007
U1668	C1668	C1128	G1068	A1008
G1669	U1669	G1129	U1069	A1009
C1670	A1670	A1130	G1070	G1010
U1671	G1671	G1131	G1071	A1011
G1672	U1672	C1132	U1072	A1012
C1673	C1673	A1133	U1073	U1013
U1674	A1674	G1134	C1074	G1014
A1675	C1675	C1135	C1075	U1015
G1676	U1676	U1136	G1076	U1016
C1677	A1677	U1137	A1077	U1017
U1678	C1678	C1138	C1078	U1018
G1679	A1679	C1139	G1079	C1019
C1680	U1680	G1140	A1080	A1020
A1681	C1681	G1141	U1081	U1021
U1682	U1682	G1142	A1082	U1022
C1683	G1683	A1143	A1083	A1023
G1684	U1684	A1144	A1084	A1024
A1685	C1685	A1145	G1085	U1025
G1686	U1686	C1146	G1086	C1026
C1687	A1687	G1147	U1087	A1027
U1688	C1688	A1148	U1088	A1028
G1689	U1689	A1149	G1089	G1029



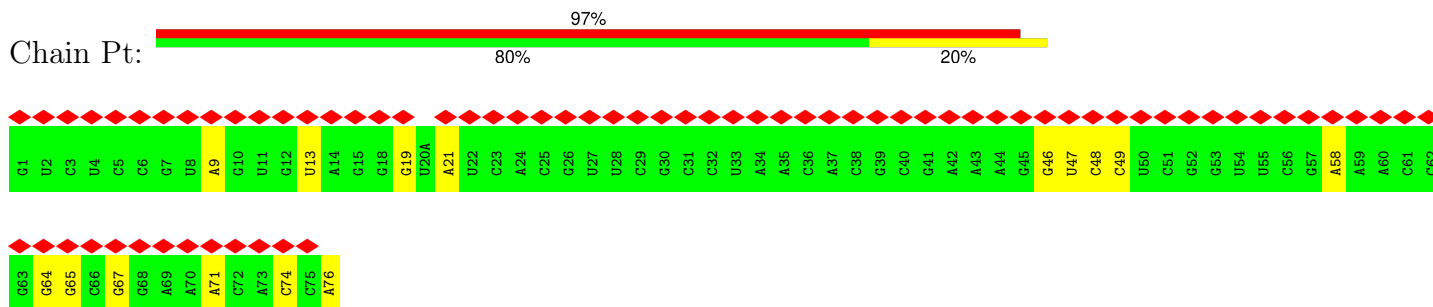
• Molecule 81: AT site tRNA



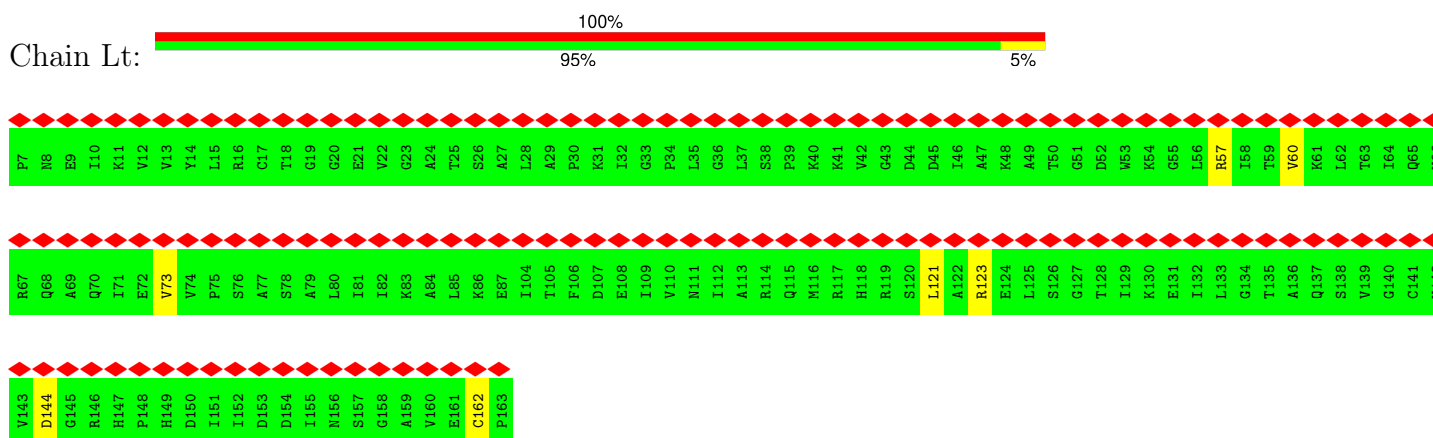
• Molecule 82: eEF1A



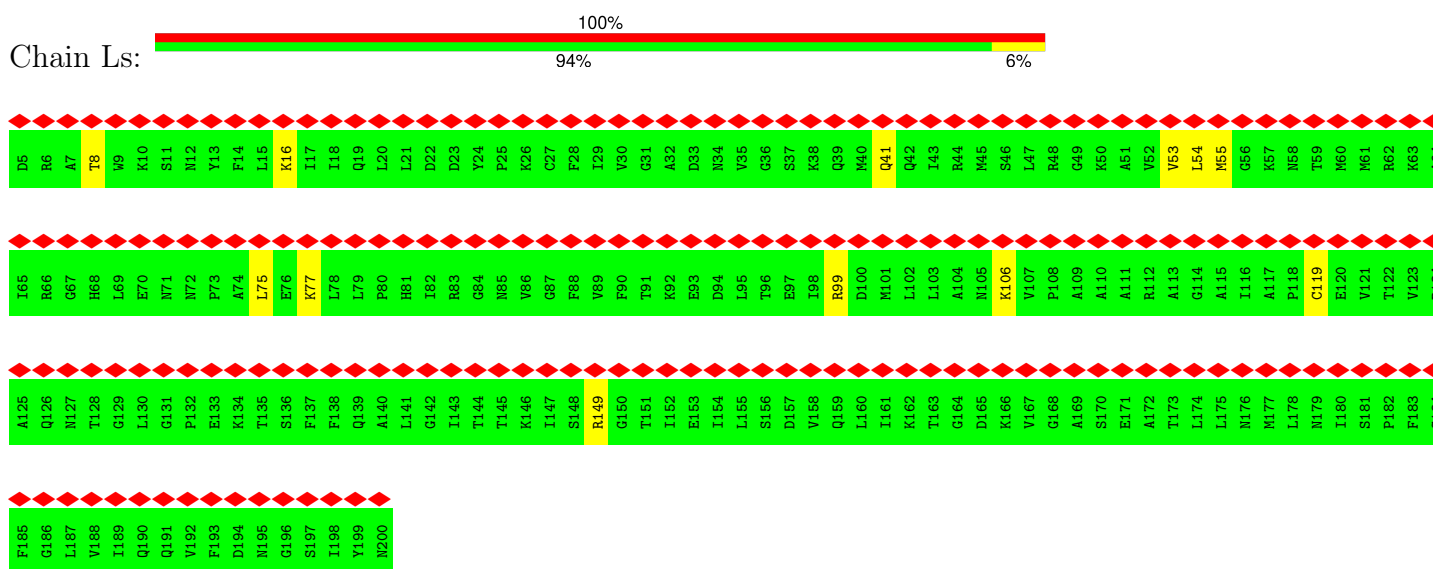
- Molecule 83: P site tRNA



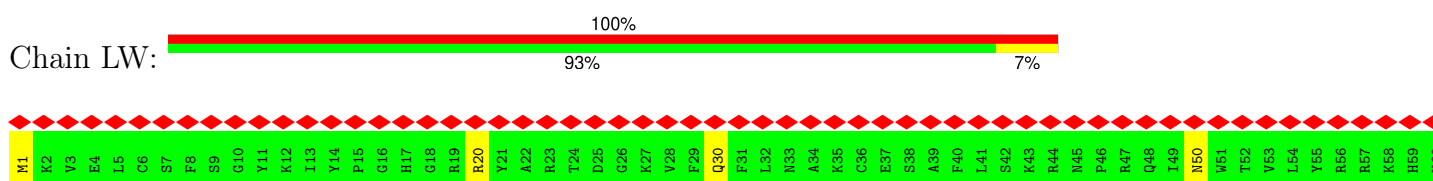
- Molecule 84: 60S ribosomal protein L12



- Molecule 85: 60S acidic ribosomal protein P0



- Molecule 86: 60S ribosomal protein L24



K61	G62	Q63	K70	R71	T72	R73	R74	A75	V76	K77	F78	Q79	R80	A81	I82	T83	G84	A85	S86	L87	A88	D89	I90	M91	A92	K93	R94	N95	Q96	K97	P98	E99	V100	R101	K102	A103	Q104	R105	E106	Q107	A108	I109	R110	A111	A112	K113	E114	A115	K116	K117	A118	K119	Q120	A121	S122	K123	K124
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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	1272627	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)	1200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.289	Depositor
Minimum map value	-0.724	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.024	Depositor
Recommended contour level	0.0729	Depositor
Map size (\AA)	615.16797, 615.16797, 615.16797	wwPDB
Map dimensions	576, 576, 576	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.068, 1.068, 1.068	Depositor

5 Model quality

5.1 Standard geometry

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

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	CD	0.38	0/290	0.64	0/391
2	CI	0.27	0/245	0.72	0/322
3	LR	0.27	0/1582	0.60	0/2091
4	SE	0.25	0/2118	0.55	0/2849
5	SI	0.26	0/1715	0.56	0/2287
6	SL	0.29	0/1268	0.58	0/1696
7	SX	0.27	0/1116	0.55	0/1490
8	SG	0.29	0/1946	0.61	0/2590
9	SJ	0.25	0/1550	0.57	0/2069
10	SY	0.25	0/1083	0.54	0/1438
11	Se	0.27	0/465	0.59	0/612
12	SA	0.28	0/1778	0.59	1/2416 (0.0%)
13	SB	0.26	0/1765	0.52	0/2362
14	SH	0.27	0/1519	0.58	2/2033 (0.1%)
15	SV	0.26	0/643	0.57	0/860
16	Sa	0.29	0/836	0.62	0/1121
17	SC	0.27	0/1762	0.55	0/2381
18	SN	0.25	0/1232	0.53	0/1656
19	SO	0.26	0/1062	0.59	0/1425
20	SW	0.26	0/1051	0.54	0/1406
21	Sb	0.27	0/665	0.54	0/891
22	L5	0.54	0/89312	0.88	91/139287 (0.1%)
23	L7	0.50	0/2861	0.81	0/4459
24	L8	0.54	0/3701	0.82	2/5766 (0.0%)
25	LA	0.33	0/1936	0.67	0/2596
26	LB	0.33	0/3306	0.61	1/4424 (0.0%)
27	LC	0.31	0/2981	0.62	1/4002 (0.0%)
28	LD	0.32	0/2428	0.57	2/3252 (0.1%)
29	LE	0.30	0/1942	0.60	0/2606
30	LF	0.33	0/1905	0.56	0/2539
31	LG	0.29	0/1960	0.55	0/2637
32	LH	0.31	0/1537	0.60	0/2066

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	LI	0.32	0/1673	0.58	0/2233
34	LJ	0.30	0/1433	0.59	0/1915
35	LL	0.29	0/1732	0.61	0/2315
36	LM	0.31	0/1161	0.58	0/1554
37	LN	0.33	0/1746	0.63	0/2338
38	LO	0.32	0/1682	0.57	0/2250
39	LP	0.33	0/1268	0.58	0/1701
40	LQ	0.32	0/1537	0.65	0/2052
41	LS	0.34	0/1493	0.61	0/2003
42	LT	0.32	0/1326	0.57	0/1770
43	LU	0.36	0/839	0.59	0/1126
44	LV	0.32	0/993	0.58	0/1332
45	LX	0.30	0/1002	0.56	0/1345
46	LY	0.31	0/1132	0.59	0/1504
47	LZ	0.34	0/1130	0.56	0/1507
48	La	0.32	0/1191	0.59	1/1591 (0.1%)
49	Lb	0.30	0/889	0.61	0/1175
50	Lc	0.37	0/774	0.69	3/1038 (0.3%)
51	Ld	0.30	0/903	0.60	0/1216
52	Le	0.34	0/1071	0.61	0/1429
53	Lf	0.35	0/895	0.67	0/1198
54	Lg	0.30	0/916	0.58	0/1220
55	Lh	0.29	0/1023	0.58	0/1351
56	Li	0.30	0/843	0.58	0/1115
57	Lj	0.34	0/720	0.66	0/952
58	Lk	0.30	0/575	0.54	0/761
59	Ll	0.30	0/454	0.62	0/599
60	Lm	0.30	0/435	0.56	0/575
61	Ln	0.26	0/231	0.74	0/294
62	Lo	0.33	0/876	0.62	0/1156
63	Lp	0.32	0/718	0.53	0/953
64	Lr	0.31	0/1017	0.60	0/1364
65	SR	0.28	0/1105	0.58	0/1484
66	SD	0.26	0/1793	0.54	0/2414
67	SF	0.28	0/1516	0.59	1/2037 (0.0%)
68	SK	0.27	0/851	0.55	0/1147
69	SP	0.26	0/1003	0.60	0/1342
70	SQ	0.26	0/1160	0.66	0/1553
71	SS	0.26	0/1216	0.59	0/1628
72	ST	0.25	0/1131	0.57	0/1515
73	SU	0.24	0/831	0.57	0/1115
74	Sc	0.26	0/508	0.64	0/680
75	Sd	0.26	0/470	0.54	0/623

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Sg	0.29	0/2493	0.59	1/3394 (0.0%)
77	SM	0.25	0/950	0.52	0/1275
78	SZ	0.26	0/604	0.69	0/810
79	Sf	0.24	0/560	0.58	0/745
80	S2	0.27	0/41242	0.82	38/64255 (0.1%)
81	AT	0.23	0/1805	0.85	5/2809 (0.2%)
82	CF	0.56	4/3442 (0.1%)	0.84	7/4656 (0.2%)
83	Pt	0.23	0/1761	0.79	0/2741
84	Lt	0.25	0/1058	0.58	0/1430
85	Ls	0.26	0/1519	0.53	1/2052 (0.0%)
86	LW	0.29	0/979	0.60	0/1295
All	All	0.41	4/241235 (0.0%)	0.77	157/353952 (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
1	CD	0	2
7	SX	0	1
14	SH	0	1
25	LA	0	1
26	LB	0	2
33	LI	0	1
35	LL	0	1
36	LM	0	2
38	LO	0	1
42	LT	0	1
53	Lf	0	2
55	Lh	0	1
57	Lj	0	1
64	Lr	0	1
67	SF	0	1
69	SP	0	1
70	SQ	0	1
78	SZ	0	1
All	All	0	22

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
82	CF	333	PRO	CG-CD	-23.55	0.72	1.50
82	CF	409	PRO	CB-CG	-11.35	0.93	1.50
82	CF	409	PRO	CG-CD	-7.02	1.27	1.50
82	CF	333	PRO	N-CA	5.04	1.55	1.47

The worst 5 of 157 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
82	CF	409	PRO	CA-CB-CG	-21.15	63.81	104.00
82	CF	409	PRO	N-CD-CG	-19.94	73.28	103.20
82	CF	333	PRO	CB-CG-CD	18.83	179.95	106.50
82	CF	333	PRO	N-CD-CG	-16.60	78.30	103.20
82	CF	333	PRO	CA-CB-CG	-15.13	75.26	104.00

There are no chirality outliers.

5 of 22 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	CD	11	CYS	Peptide
1	CD	9	PHE	Peptide
25	LA	13	GLY	Peptide
14	SH	15	LYS	Peptide
7	SX	126	ALA	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	CD	34/36 (94%)	27 (79%)	7 (21%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	CI	29/31 (94%)	27 (93%)	1 (3%)	1 (3%)	3	1
3	LR	185/187 (99%)	179 (97%)	6 (3%)	0	100	100
4	SE	260/262 (99%)	244 (94%)	16 (6%)	0	100	100
5	SI	204/206 (99%)	197 (97%)	7 (3%)	0	100	100
6	SL	151/153 (99%)	140 (93%)	11 (7%)	0	100	100
7	SX	139/141 (99%)	128 (92%)	10 (7%)	1 (1%)	19	19
8	SG	235/237 (99%)	223 (95%)	12 (5%)	0	100	100
9	SJ	183/185 (99%)	173 (94%)	9 (5%)	1 (0%)	25	28
10	SY	129/131 (98%)	121 (94%)	8 (6%)	0	100	100
11	Se	56/58 (97%)	52 (93%)	4 (7%)	0	100	100
12	SA	219/221 (99%)	198 (90%)	21 (10%)	0	100	100
13	SB	212/214 (99%)	207 (98%)	5 (2%)	0	100	100
14	SH	182/186 (98%)	163 (90%)	19 (10%)	0	100	100
15	SV	81/83 (98%)	75 (93%)	6 (7%)	0	100	100
16	Sa	100/102 (98%)	91 (91%)	8 (8%)	1 (1%)	13	12
17	SC	220/222 (99%)	204 (93%)	16 (7%)	0	100	100
18	SN	148/150 (99%)	146 (99%)	2 (1%)	0	100	100
19	SO	138/140 (99%)	128 (93%)	10 (7%)	0	100	100
20	SW	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
21	Sb	81/83 (98%)	70 (86%)	11 (14%)	0	100	100
25	LA	246/248 (99%)	222 (90%)	23 (9%)	1 (0%)	30	34
26	LB	400/402 (100%)	380 (95%)	20 (5%)	0	100	100
27	LC	366/368 (100%)	345 (94%)	21 (6%)	0	100	100
28	LD	291/293 (99%)	278 (96%)	13 (4%)	0	100	100
29	LE	232/236 (98%)	209 (90%)	23 (10%)	0	100	100
30	LF	223/225 (99%)	213 (96%)	10 (4%)	0	100	100
31	LG	239/241 (99%)	227 (95%)	12 (5%)	0	100	100
32	LH	188/190 (99%)	178 (95%)	10 (5%)	0	100	100
33	LI	198/202 (98%)	189 (96%)	8 (4%)	1 (0%)	25	28
34	LJ	174/176 (99%)	162 (93%)	12 (7%)	0	100	100
35	LL	208/210 (99%)	193 (93%)	15 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	LM	137/139 (99%)	129 (94%)	7 (5%)	1 (1%)	19	19
37	LN	201/203 (99%)	194 (96%)	6 (3%)	1 (0%)	25	28
38	LO	199/201 (99%)	192 (96%)	6 (3%)	1 (0%)	25	28
39	LP	151/153 (99%)	142 (94%)	9 (6%)	0	100	100
40	LQ	185/187 (99%)	178 (96%)	7 (4%)	0	100	100
41	LS	173/175 (99%)	164 (95%)	9 (5%)	0	100	100
42	LT	157/159 (99%)	149 (95%)	8 (5%)	0	100	100
43	LU	99/101 (98%)	84 (85%)	15 (15%)	0	100	100
44	LV	129/131 (98%)	125 (97%)	4 (3%)	0	100	100
45	LX	118/120 (98%)	117 (99%)	1 (1%)	0	100	100
46	LY	132/134 (98%)	129 (98%)	3 (2%)	0	100	100
47	LZ	133/135 (98%)	120 (90%)	13 (10%)	0	100	100
48	La	145/147 (99%)	139 (96%)	6 (4%)	0	100	100
49	Lb	105/109 (96%)	99 (94%)	6 (6%)	0	100	100
50	Lc	96/98 (98%)	88 (92%)	8 (8%)	0	100	100
51	Ld	105/107 (98%)	100 (95%)	5 (5%)	0	100	100
52	Le	126/128 (98%)	118 (94%)	6 (5%)	2 (2%)	8	6
53	Lf	107/109 (98%)	100 (94%)	6 (6%)	1 (1%)	14	14
54	Lg	112/114 (98%)	111 (99%)	1 (1%)	0	100	100
55	Lh	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
56	Li	100/102 (98%)	96 (96%)	4 (4%)	0	100	100
57	Lj	84/86 (98%)	79 (94%)	4 (5%)	1 (1%)	11	9
58	Lk	67/69 (97%)	65 (97%)	2 (3%)	0	100	100
59	Ll	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
60	Lm	50/52 (96%)	50 (100%)	0	0	100	100
61	Ln	22/24 (92%)	22 (100%)	0	0	100	100
62	Lo	103/105 (98%)	98 (95%)	5 (5%)	0	100	100
63	Lp	89/91 (98%)	85 (96%)	4 (4%)	0	100	100
64	Lr	123/125 (98%)	118 (96%)	5 (4%)	0	100	100
65	SR	133/135 (98%)	122 (92%)	10 (8%)	1 (1%)	16	16
66	SD	225/227 (99%)	205 (91%)	20 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
67	SF	187/189 (99%)	171 (91%)	16 (9%)	0	100	100
68	SK	96/98 (98%)	83 (86%)	11 (12%)	2 (2%)	5	3
69	SP	119/121 (98%)	112 (94%)	7 (6%)	0	100	100
70	SQ	142/144 (99%)	124 (87%)	18 (13%)	0	100	100
71	SS	143/145 (99%)	138 (96%)	5 (4%)	0	100	100
72	ST	141/143 (99%)	129 (92%)	11 (8%)	1 (1%)	19	19
73	SU	102/104 (98%)	96 (94%)	6 (6%)	0	100	100
74	Sc	62/64 (97%)	54 (87%)	8 (13%)	0	100	100
75	Sd	53/55 (96%)	50 (94%)	3 (6%)	0	100	100
76	Sg	311/313 (99%)	273 (88%)	38 (12%)	0	100	100
77	SM	120/122 (98%)	111 (92%)	8 (7%)	1 (1%)	16	16
78	SZ	73/75 (97%)	59 (81%)	14 (19%)	0	100	100
79	Sf	65/67 (97%)	54 (83%)	11 (17%)	0	100	100
82	CF	438/441 (99%)	415 (95%)	23 (5%)	0	100	100
84	Lt	137/141 (97%)	108 (79%)	28 (20%)	1 (1%)	19	19
85	Ls	194/196 (99%)	179 (92%)	15 (8%)	0	100	100
86	LW	114/118 (97%)	109 (96%)	5 (4%)	0	100	100
All	All	12149/12322 (99%)	11358 (94%)	772 (6%)	19 (0%)	45	52

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
37	LN	124	ASP
7	SX	127	ASN
36	LM	88	ALA
65	SR	124	VAL
68	SK	36	ALA

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	CD	31/31 (100%)	30 (97%)	1 (3%)	34	45
2	CI	25/25 (100%)	23 (92%)	2 (8%)	10	10
3	LR	166/166 (100%)	160 (96%)	6 (4%)	30	40
4	SE	224/224 (100%)	199 (89%)	25 (11%)	5	4
5	SI	178/178 (100%)	164 (92%)	14 (8%)	10	11
6	SL	137/137 (100%)	123 (90%)	14 (10%)	6	6
7	SX	113/113 (100%)	107 (95%)	6 (5%)	19	24
8	SG	207/207 (100%)	184 (89%)	23 (11%)	5	4
9	SJ	161/161 (100%)	150 (93%)	11 (7%)	13	15
10	SY	113/113 (100%)	98 (87%)	15 (13%)	3	2
11	Se	47/47 (100%)	40 (85%)	7 (15%)	2	2
12	SA	183/183 (100%)	172 (94%)	11 (6%)	16	19
13	SB	195/195 (100%)	186 (95%)	9 (5%)	23	30
14	SH	166/166 (100%)	150 (90%)	16 (10%)	7	6
15	SV	67/67 (100%)	58 (87%)	9 (13%)	3	2
16	Sa	89/89 (100%)	82 (92%)	7 (8%)	10	11
17	SC	188/188 (100%)	171 (91%)	17 (9%)	8	8
18	SN	130/130 (100%)	123 (95%)	7 (5%)	18	23
19	SO	110/110 (100%)	103 (94%)	7 (6%)	14	17
20	SW	112/112 (100%)	102 (91%)	10 (9%)	8	8
21	Sb	75/75 (100%)	71 (95%)	4 (5%)	19	24
25	LA	190/190 (100%)	177 (93%)	13 (7%)	13	15
26	LB	348/348 (100%)	329 (94%)	19 (6%)	18	22
27	LC	306/306 (100%)	289 (94%)	17 (6%)	17	21
28	LD	246/247 (100%)	230 (94%)	16 (6%)	14	16
29	LE	209/209 (100%)	195 (93%)	14 (7%)	13	15
30	LF	194/194 (100%)	190 (98%)	4 (2%)	48	63
31	LG	203/205 (99%)	192 (95%)	11 (5%)	18	23
32	LH	169/169 (100%)	155 (92%)	14 (8%)	9	9
33	LI	172/172 (100%)	159 (92%)	13 (8%)	11	12
34	LJ	148/148 (100%)	135 (91%)	13 (9%)	8	8
35	LL	176/176 (100%)	166 (94%)	10 (6%)	17	21

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	LM	118/118 (100%)	111 (94%)	7 (6%)	16	20
37	LN	171/171 (100%)	168 (98%)	3 (2%)	54	69
38	LO	173/173 (100%)	167 (96%)	6 (4%)	31	41
39	LP	134/134 (100%)	126 (94%)	8 (6%)	16	19
40	LQ	164/164 (100%)	161 (98%)	3 (2%)	54	69
41	LS	156/156 (100%)	142 (91%)	14 (9%)	8	8
42	LT	139/139 (100%)	133 (96%)	6 (4%)	25	32
43	LU	91/91 (100%)	81 (89%)	10 (11%)	5	4
44	LV	101/101 (100%)	99 (98%)	2 (2%)	50	65
45	LX	108/108 (100%)	104 (96%)	4 (4%)	29	39
46	LY	124/124 (100%)	118 (95%)	6 (5%)	21	28
47	LZ	117/117 (100%)	105 (90%)	12 (10%)	6	5
48	La	120/120 (100%)	119 (99%)	1 (1%)	79	88
49	Lb	88/90 (98%)	83 (94%)	5 (6%)	17	21
50	Lc	83/83 (100%)	77 (93%)	6 (7%)	12	13
51	Ld	98/98 (100%)	89 (91%)	9 (9%)	7	7
52	Le	114/114 (100%)	113 (99%)	1 (1%)	75	86
53	Lf	88/88 (100%)	84 (96%)	4 (4%)	23	30
54	Lg	98/98 (100%)	92 (94%)	6 (6%)	15	18
55	Lh	109/109 (100%)	103 (94%)	6 (6%)	18	22
56	Li	86/86 (100%)	83 (96%)	3 (4%)	31	41
57	Lj	73/73 (100%)	67 (92%)	6 (8%)	9	9
58	Lk	64/64 (100%)	61 (95%)	3 (5%)	22	29
59	Ll	47/47 (100%)	43 (92%)	4 (8%)	8	9
60	Lm	48/48 (100%)	47 (98%)	1 (2%)	48	63
61	Ln	23/23 (100%)	20 (87%)	3 (13%)	3	3
62	Lo	93/93 (100%)	85 (91%)	8 (9%)	8	9
63	Lp	74/74 (100%)	70 (95%)	4 (5%)	18	23
64	Lr	109/109 (100%)	98 (90%)	11 (10%)	6	6
65	SR	122/122 (100%)	107 (88%)	15 (12%)	4	3
66	SD	190/190 (100%)	172 (90%)	18 (10%)	7	7

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
67	SF	159/159 (100%)	143 (90%)	16 (10%)	6	6
68	SK	89/89 (100%)	82 (92%)	7 (8%)	10	11
69	SP	107/107 (100%)	95 (89%)	12 (11%)	5	4
70	SQ	119/119 (100%)	106 (89%)	13 (11%)	5	5
71	SS	126/126 (100%)	120 (95%)	6 (5%)	21	28
72	ST	113/113 (100%)	104 (92%)	9 (8%)	10	10
73	SU	94/94 (100%)	86 (92%)	8 (8%)	8	9
74	Sc	57/57 (100%)	51 (90%)	6 (10%)	5	5
75	Sd	48/48 (100%)	42 (88%)	6 (12%)	3	3
76	Sg	272/272 (100%)	244 (90%)	28 (10%)	6	5
77	SM	102/104 (98%)	89 (87%)	13 (13%)	3	3
78	SZ	66/66 (100%)	58 (88%)	8 (12%)	4	3
79	Sf	60/60 (100%)	54 (90%)	6 (10%)	6	6
82	CF	365/366 (100%)	327 (90%)	38 (10%)	5	5
84	Lt	112/115 (97%)	106 (95%)	6 (5%)	18	23
85	Ls	162/164 (99%)	151 (93%)	11 (7%)	13	15
86	LW	97/97 (100%)	89 (92%)	8 (8%)	9	9
All	All	10549/10562 (100%)	9788 (93%)	761 (7%)	14	13

5 of 761 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
51	Ld	55	LYS
67	SF	185	SER
54	Lg	105	LYS
51	Ld	46	LEU
64	Lr	60	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
37	LN	8	GLN
68	SK	7	ASN
86	LW	104	GLN
47	LZ	97	ASN

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Mol	Chain	Res	Type
69	SP	104	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
22	L5	3704/3740 (99%)	819 (22%)	23 (0%)
23	L7	119/120 (99%)	12 (10%)	0
24	L8	155/156 (99%)	28 (18%)	1 (0%)
80	S2	1715/1740 (98%)	408 (23%)	7 (0%)
81	AT	74/76 (97%)	27 (36%)	1 (1%)
83	Pt	72/74 (97%)	15 (20%)	0
All	All	5839/5906 (98%)	1309 (22%)	32 (0%)

5 of 1309 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
22	L5	2	G
22	L5	13	U
22	L5	25	A
22	L5	30	C
22	L5	39	A

5 of 32 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
80	S2	1355	C
80	S2	1434	C
22	L5	2416	G
22	L5	2033	A
80	S2	1781	A

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection.

RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
82	SEP	CF	163	82	8,9,10	1.61	1 (12%)	7,12,14	1.40	1 (14%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
82	SEP	CF	163	82	-	5/6/8/10	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
82	CF	163	SEP	P-O1P	3.54	1.61	1.50

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
82	CF	163	SEP	OG-CB-CA	3.12	111.18	108.14

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
82	CF	163	SEP	N-CA-CB-OG
82	CF	163	SEP	C-CA-CB-OG
82	CF	163	SEP	CB-OG-P-O1P
82	CF	163	SEP	CB-OG-P-O2P
82	CF	163	SEP	CB-OG-P-O3P

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 261 ligands modelled in this entry, 261 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
22	L5	12
80	S2	6
49	Lb	1
29	LE	1
86	LW	1
14	SH	1
83	Pt	1
84	Lt	1
33	LI	1
81	AT	1

The worst 5 of 26 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Lb	76:VAL	C	89:VAL	N	33.49
1	S2	753:C	O3'	785:C	P	27.14
1	LE	76:ALA	C	88:VAL	N	23.89
1	L5	2910:G	O3'	3584:C	P	21.19
1	S2	698:G	O3'	730:C	P	16.74

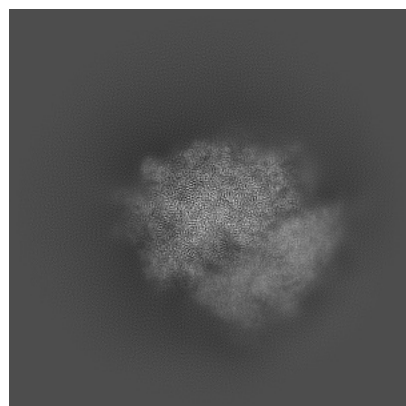
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-44014. These allow visual inspection of the internal detail of the map and identification of artifacts.

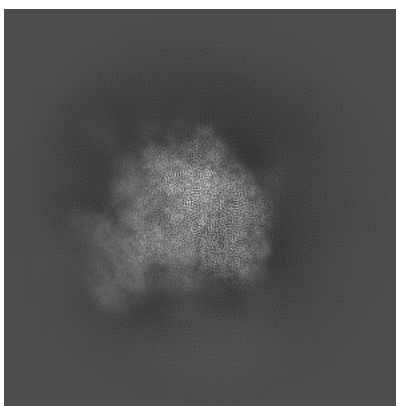
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

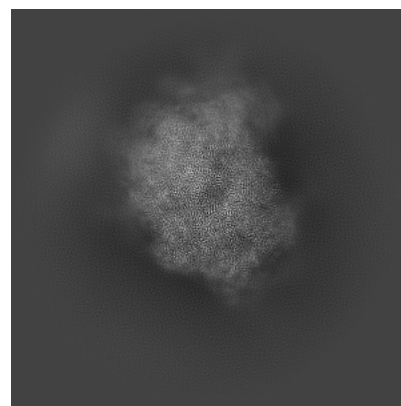
6.1.1 Primary map



X

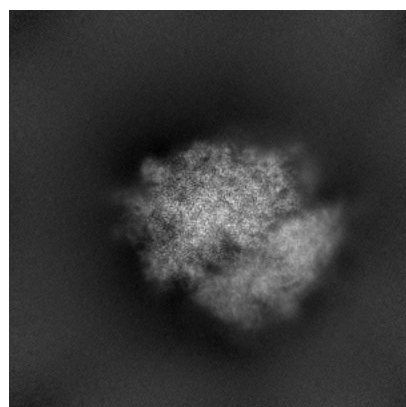


Y

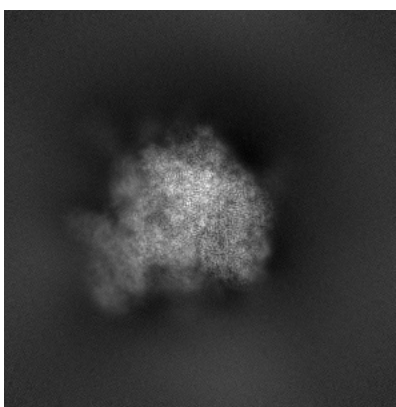


Z

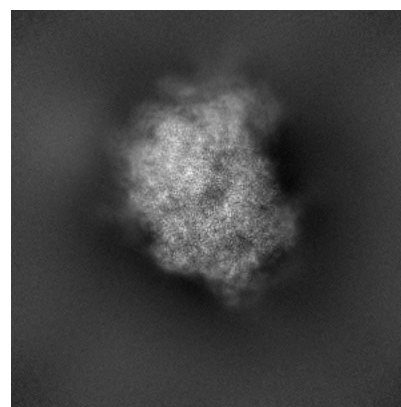
6.1.2 Raw map



X



Y

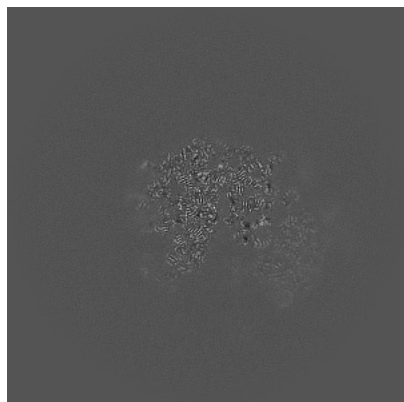


Z

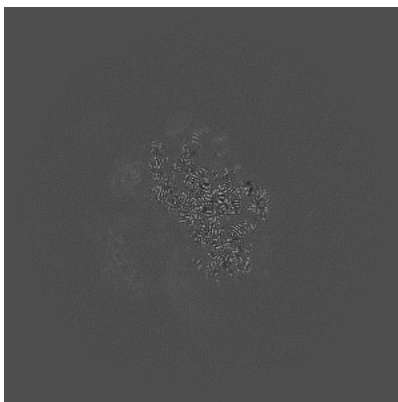
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

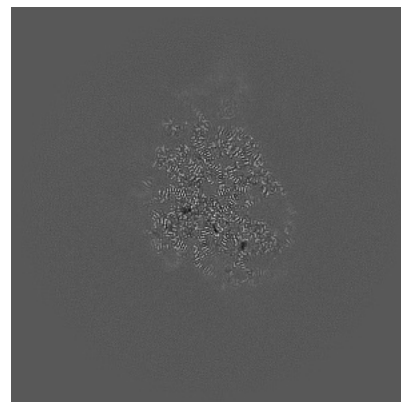
6.2.1 Primary map



X Index: 288

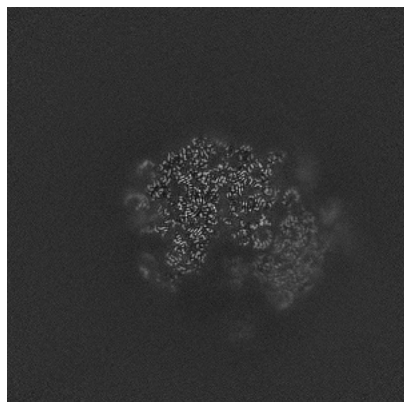


Y Index: 288

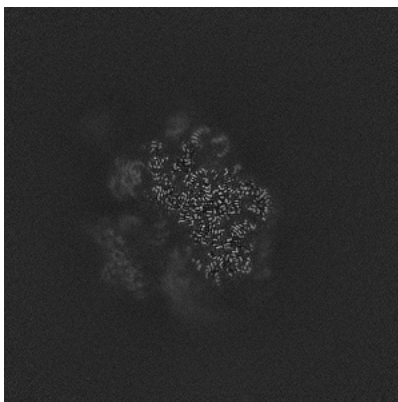


Z Index: 288

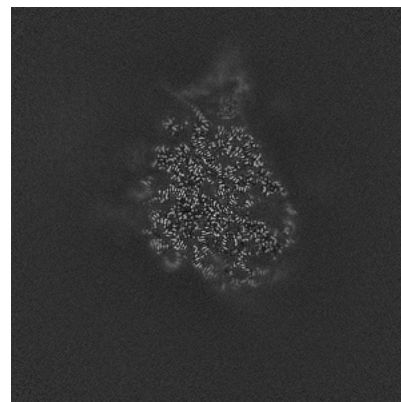
6.2.2 Raw map



X Index: 288



Y Index: 288

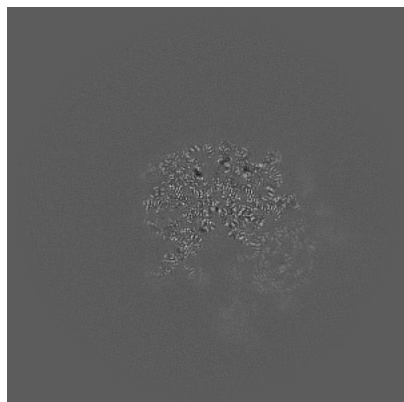


Z Index: 288

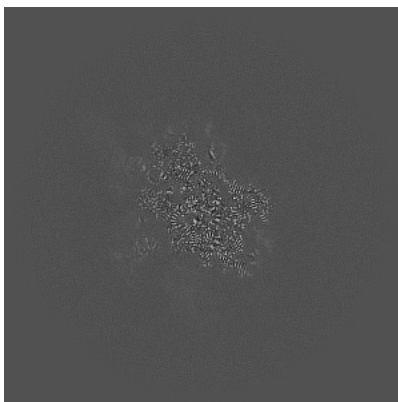
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

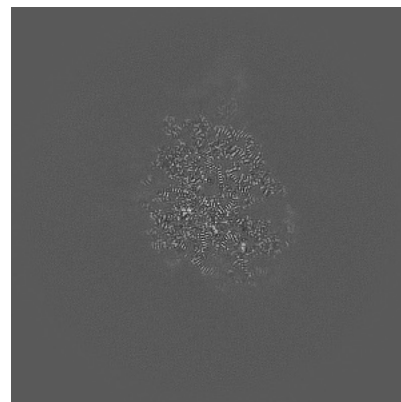
6.3.1 Primary map



X Index: 272

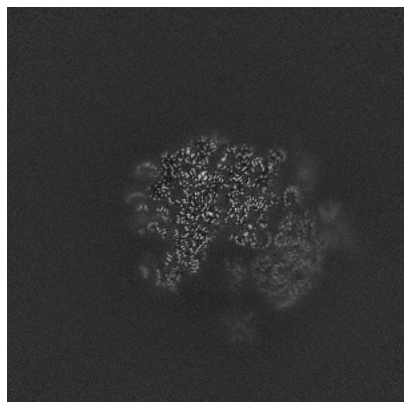


Y Index: 272

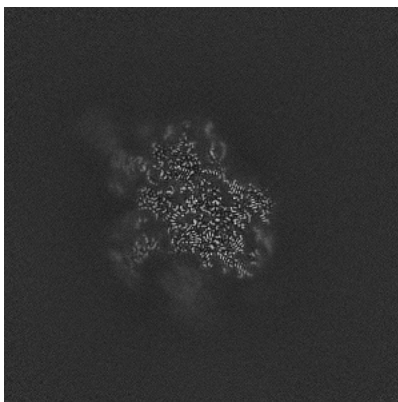


Z Index: 290

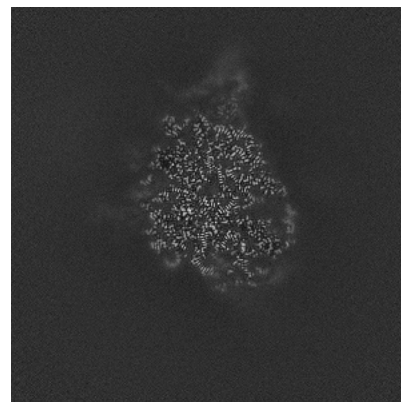
6.3.2 Raw map



X Index: 285



Y Index: 272

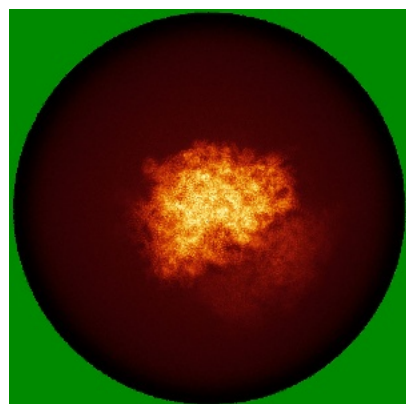


Z Index: 290

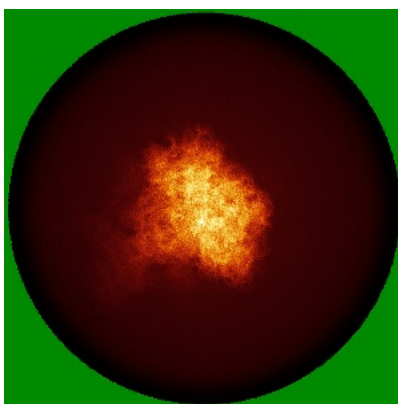
The images above show the largest variance slices of the map in three orthogonal directions.

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

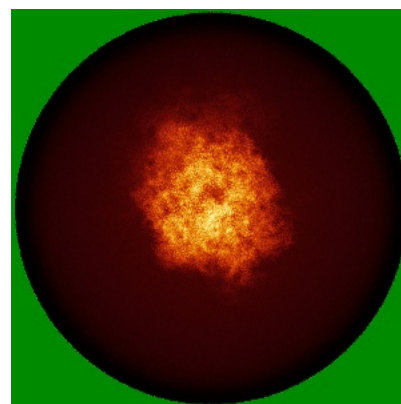
6.4.1 Primary map



X

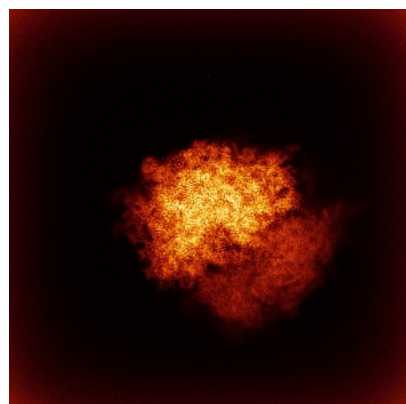


Y

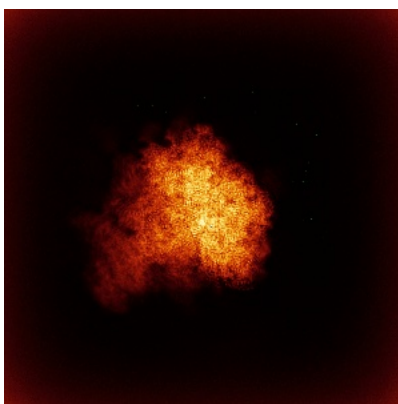


Z

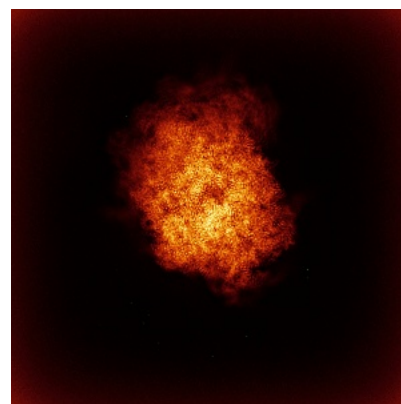
6.4.2 Raw map



X



Y

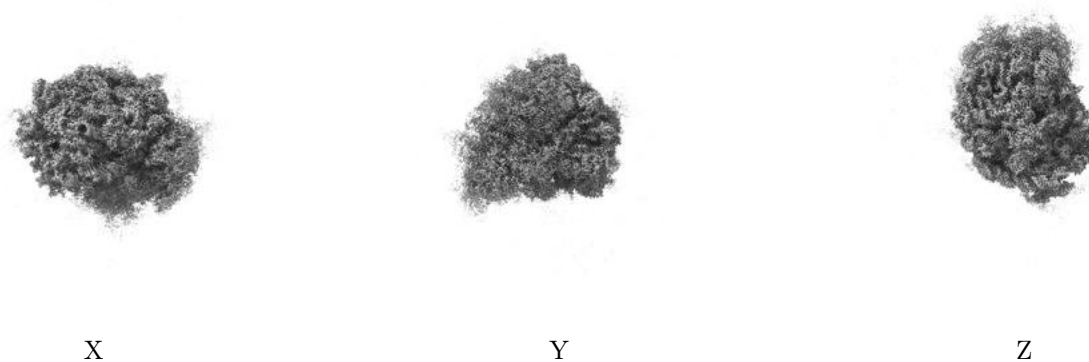


Z

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.

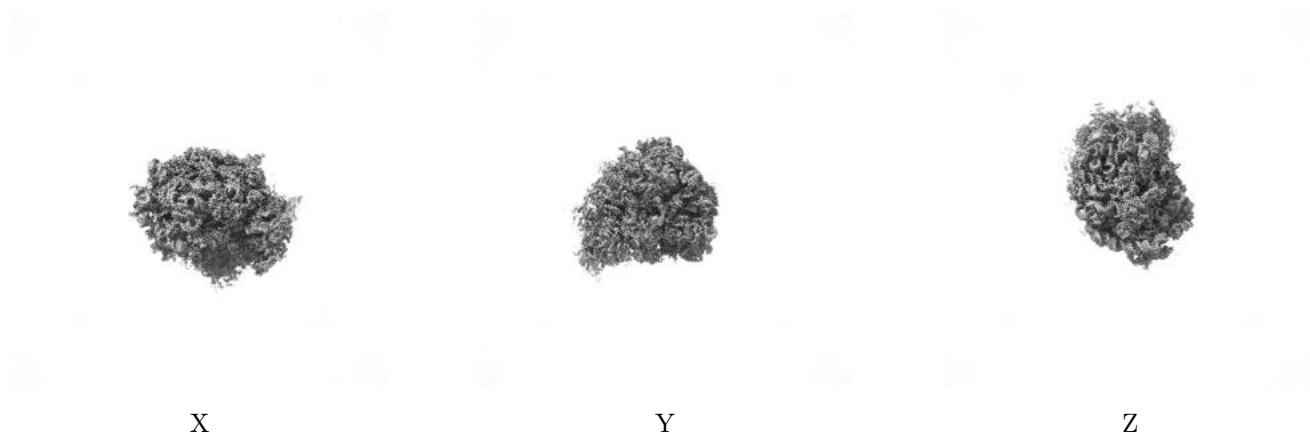
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0729. 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.

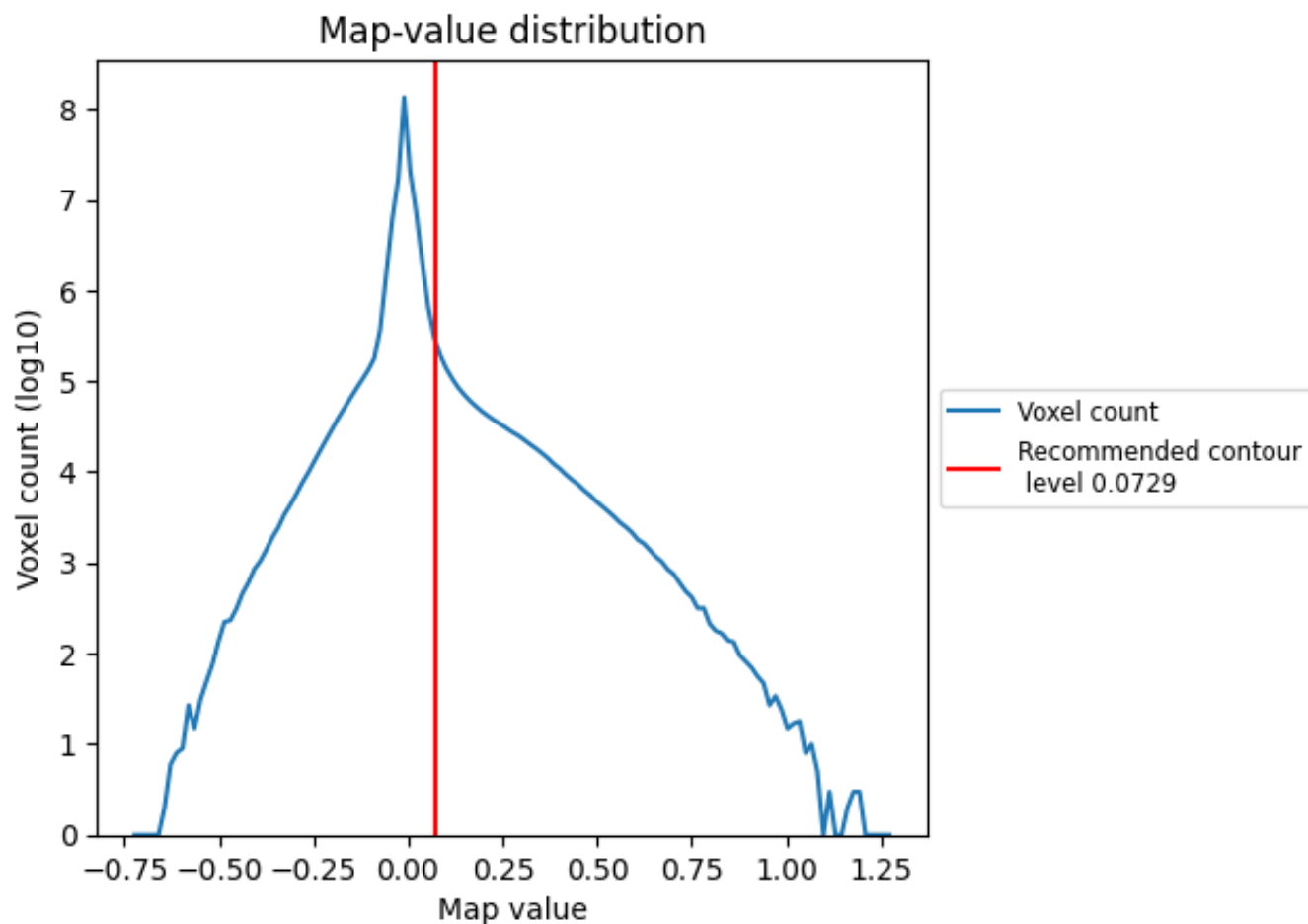
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

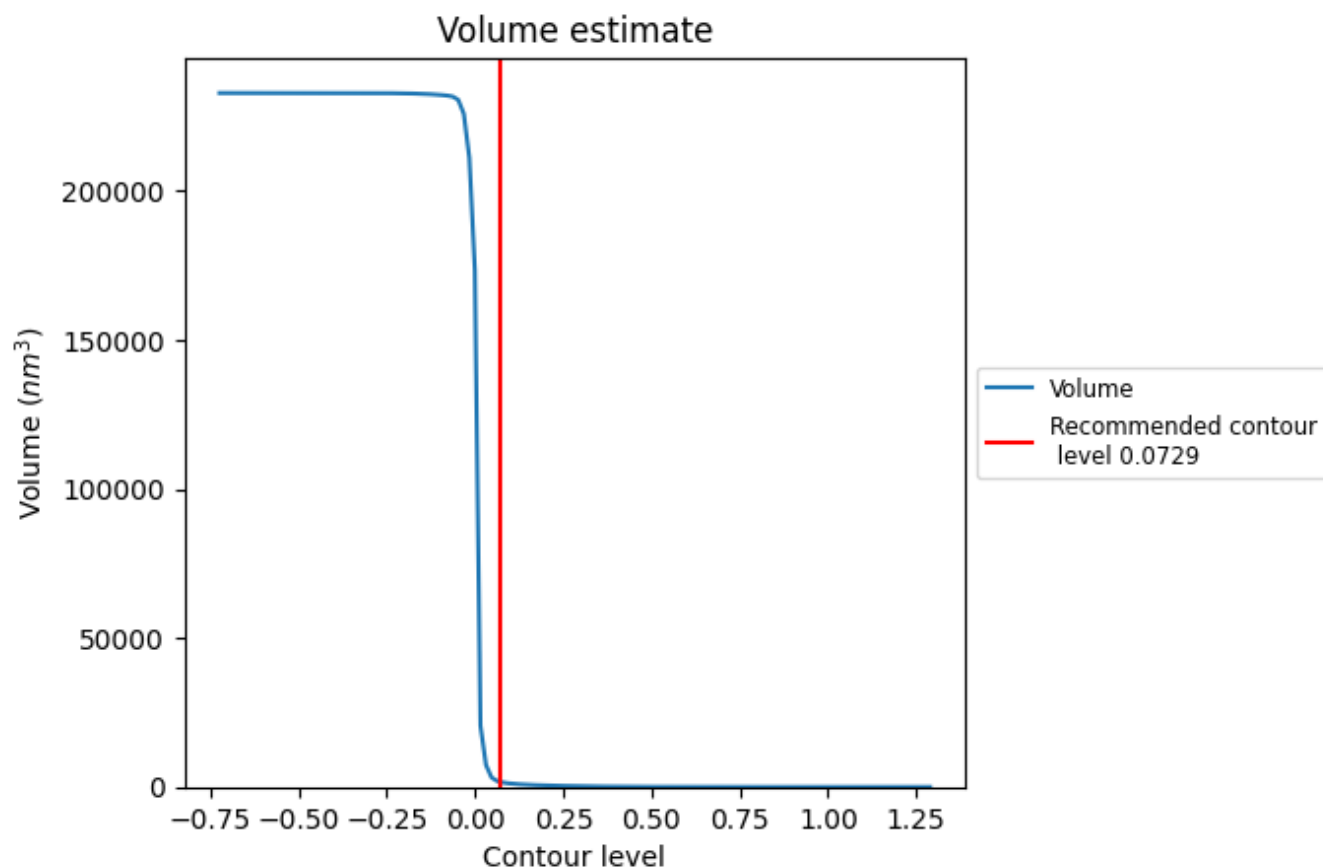
This section contains the results of statistical analysis of the map.

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.

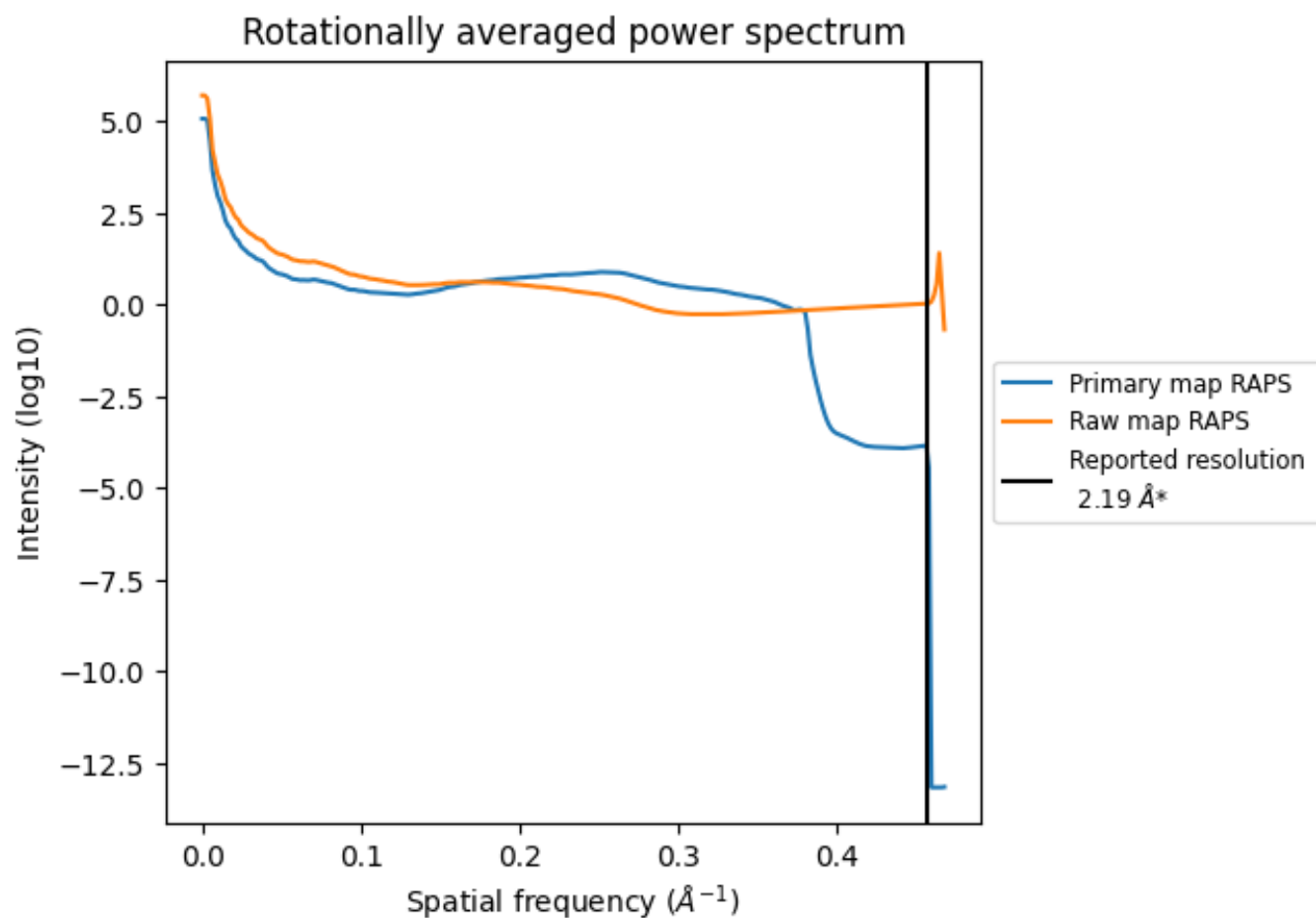
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1673 nm³; this corresponds to an approximate mass of 1511 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 ⓘ

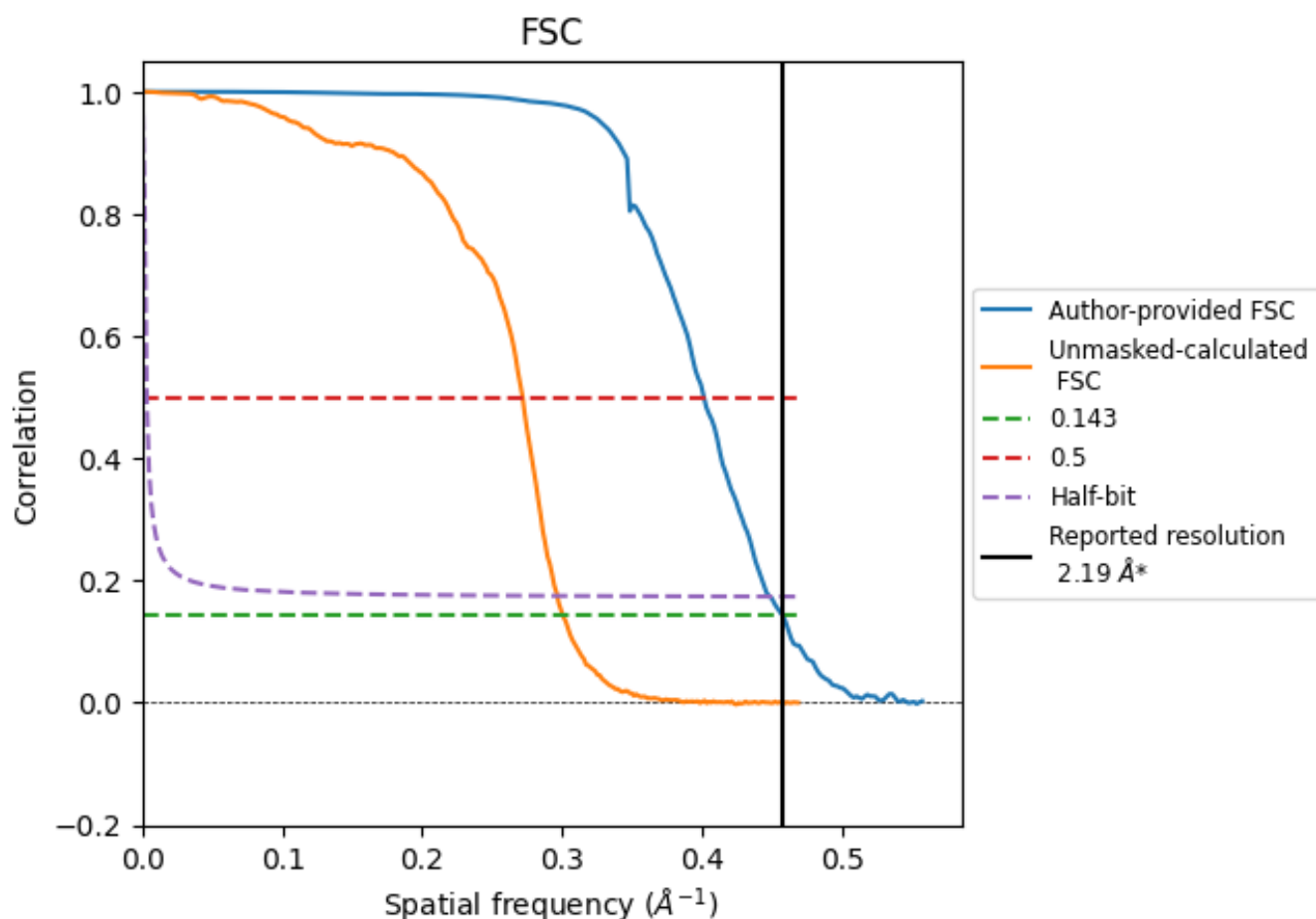


*Reported resolution corresponds to spatial frequency of 0.457 \AA^{-1}

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 0.457 \AA^{-1}

8.2 Resolution estimates [i](#)

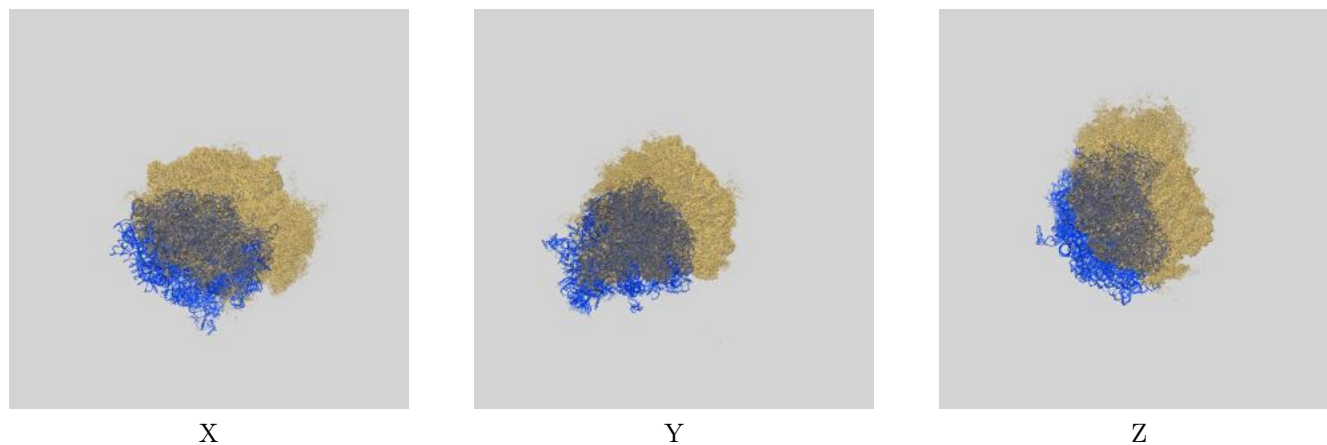
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.19	-	-
Author-provided FSC curve	2.19	2.49	2.23
Unmasked-calculated*	3.33	3.68	3.37

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.33 differs from the reported value 2.19 by more than 10 %

9 Map-model fit [i](#)

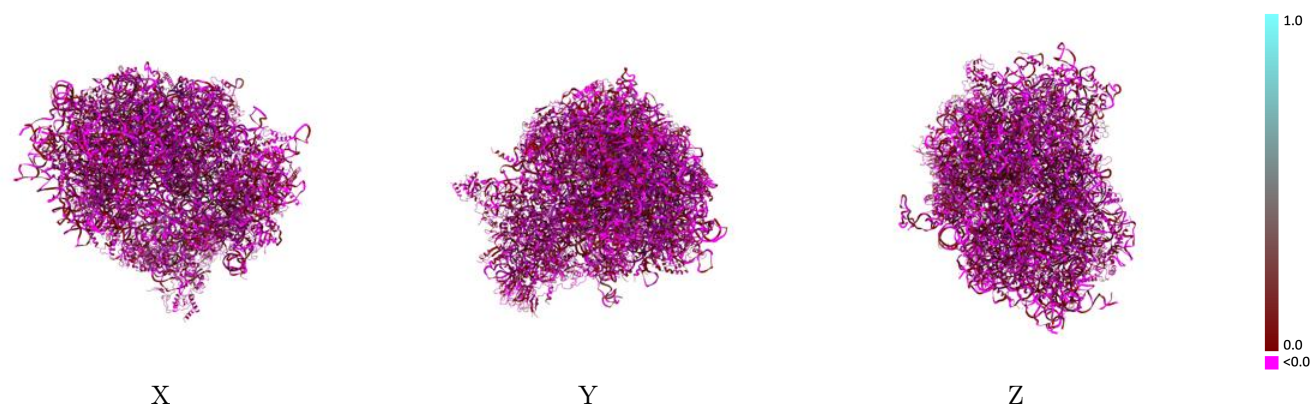
This section contains information regarding the fit between EMDB map EMD-44014 and PDB model 9AZC. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)



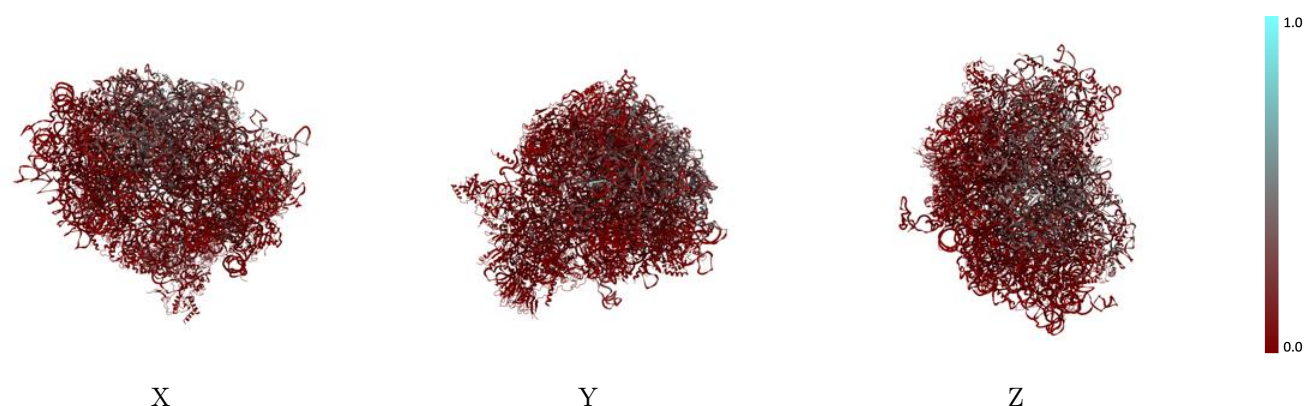
The images above show the 3D surface view of the map at the recommended contour level 0.0729 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



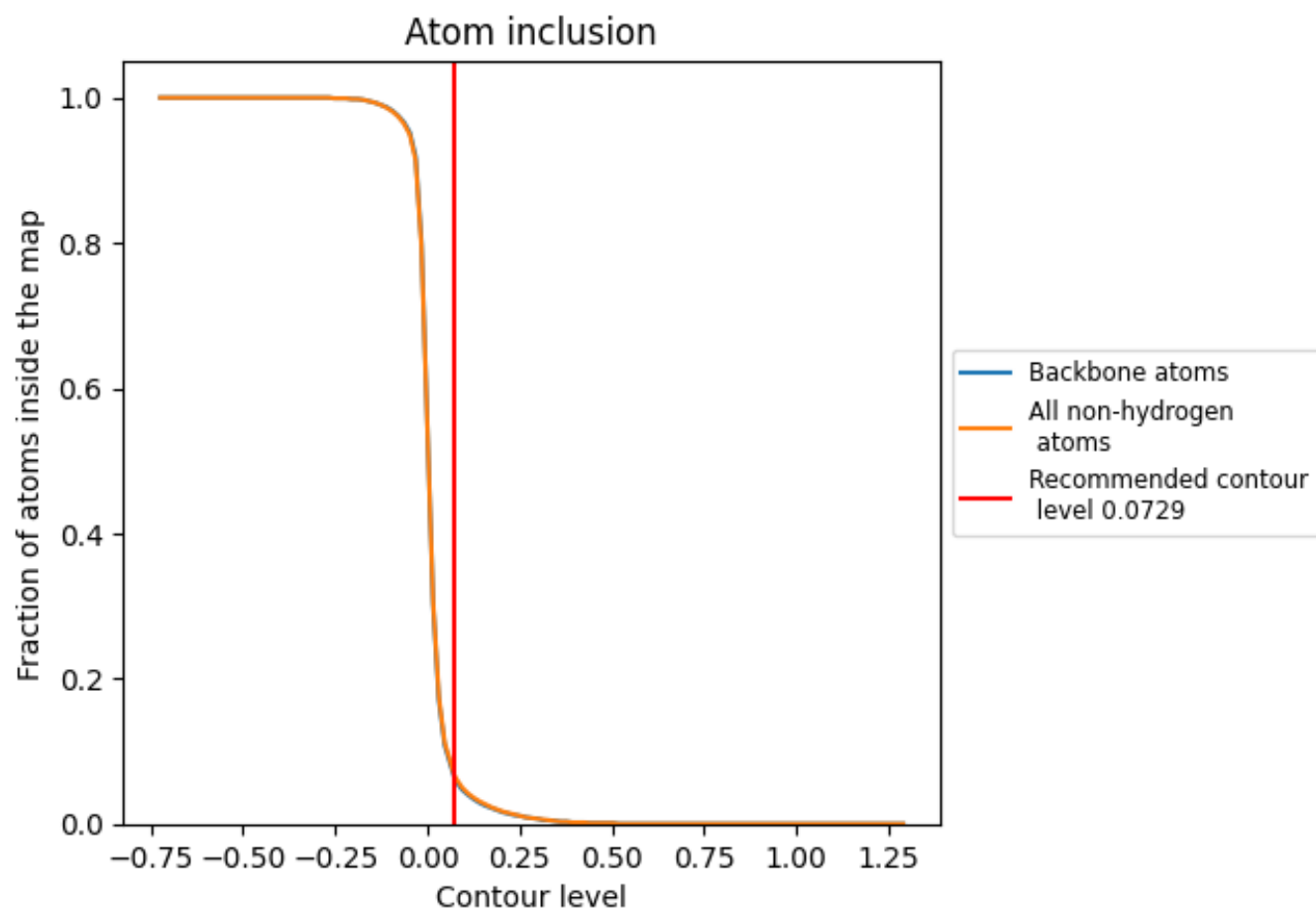
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0729).

9.4 Atom inclusion ⓘ



At the recommended contour level, 6% of all backbone atoms, 7% 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 (0.0729) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.0670	-0.0070
AT	0.0040	0.0030
CD	0.0210	-0.0590
CF	0.0020	-0.0020
CI	0.1770	-0.0580
L5	0.0880	-0.0090
L7	0.0440	0.0090
L8	0.1950	-0.0150
LA	0.0010	0.0160
LB	0.1910	-0.0120
LC	0.0590	-0.0080
LD	0.0000	-0.0100
LE	0.0560	0.0130
LF	0.0030	0.0000
LG	0.0000	0.0070
LH	0.0050	-0.0150
LI	0.0790	-0.0000
LJ	0.0000	-0.0110
LL	0.0120	-0.0010
LM	0.0440	0.0210
LN	0.0090	-0.0180
LO	0.1030	-0.0140
LP	0.2820	-0.0040
LQ	0.0050	-0.0050
LR	0.1750	-0.0410
LS	0.0390	0.0040
LT	0.0390	-0.0130
LU	0.3170	0.0110
LV	0.0000	-0.0040
LW	0.0020	-0.0250
LX	0.2610	0.0120
LY	0.2250	-0.0260
LZ	0.0240	-0.0110
La	0.0530	-0.0140
Lb	0.0470	-0.0010























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Chain	Atom inclusion	Q-score
Lc	0.0840	-0.0410
Ld	0.2660	-0.0100
Le	0.1290	-0.0110
Lf	0.0260	-0.0060
Lg	0.0760	-0.0070
Lh	0.2120	-0.0300
Li	0.0000	0.0060
Lj	0.1930	-0.0420
Lk	0.2100	-0.0120
Ll	0.2810	-0.0260
Lm	0.0410	-0.0210
Ln	0.0290	0.0380
Lo	0.0000	-0.0040
Lp	0.0020	-0.0250
Lr	0.0400	-0.0120
Ls	0.0000	-0.0010
Lt	0.0000	-0.0030
Pt	0.0490	0.0030
S2	0.0460	-0.0040
SA	0.0050	-0.0050
SB	0.0010	-0.0040
SC	0.0820	-0.0100
SD	0.0040	0.0110
SE	0.1150	-0.0150
SF	0.0000	-0.0130
SG	0.0380	-0.0040
SH	0.0220	-0.0190
SI	0.1190	-0.0110
SJ	0.0450	-0.0040
SK	0.0000	0.0110
SL	0.1810	-0.0380
SM	0.0000	-0.0100
SN	0.0220	-0.0160
SO	0.0000	0.0000
SP	0.0000	-0.0130
SQ	0.0000	-0.0190
SR	0.0000	-0.0220
SS	0.0000	0.0050
ST	0.0000	-0.0080
SU	0.0000	0.0060
SV	0.0450	0.0260
SW	0.0920	-0.0000

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Chain	Atom inclusion	Q-score
SX	 0.0800	 0.0000
SY	 0.0130	 -0.0100
SZ	 0.0000	 0.0050
Sa	 0.0250	 0.0020
Sb	 0.0170	 -0.0100
Sc	 0.0000	 -0.0270
Sd	 0.0000	 0.0170
Se	 0.0270	 -0.0120
Sf	 0.0000	 0.0110
Sg	 0.0000	 -0.0040