



## wwPDB EM Validation Summary Report ⓘ

Nov 7, 2024 – 04:51 pm GMT

PDB ID : 8P60  
EMDB ID : EMD-17457  
Title : Spraguea lophii ribosome dimer  
Authors : Gil Diez, P.; McLaren, M.; Isupov, M.N.; Daum, B.; Connors, R.; Williams, B.  
Deposited on : 2023-05-24  
Resolution : 14.30 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev113  
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) : 2.39

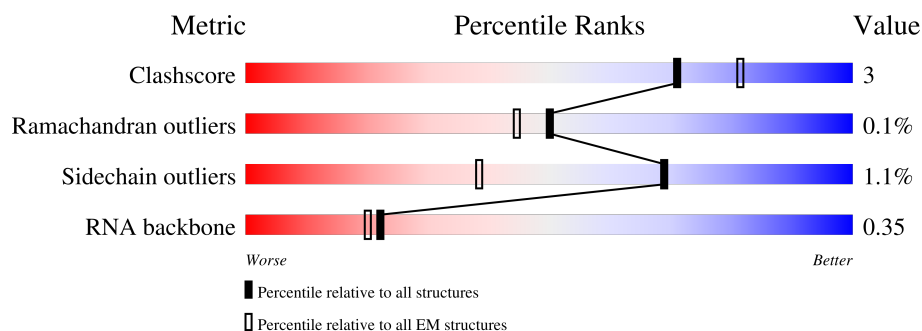
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 14.30 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	K50	2618	<div> <div>9%</div> <div>62%</div> <div>29%</div> <div>5%</div> </div>
1	L50	2618	<div> <div>5%</div> <div>62%</div> <div>29%</div> <div>5%</div> </div>
2	K70	119	<div> <div>18%</div> <div>59%</div> <div>36%</div> <div>5%</div> </div>
2	L70	119	<div> <div>60%</div> <div>35%</div> <div>5%</div> </div>
3	KA0	246	<div> <div>40%</div> <div>96%</div> </div>
3	LA0	246	<div> <div>40%</div> <div>96%</div> </div>
4	KAA	147	<div> <div>35%</div> <div>93%</div> <div>7%</div> </div>

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Mol	Chain	Length	Quality of chain
4	LAA	147	<div> <div>31%</div> <div>93%</div> <div>7%</div> </div>
5	KB0	392	<div> <div>45%</div> <div>94%</div> <div>..</div> </div>
5	LB0	392	<div> <div>49%</div> <div>94%</div> <div>..</div> </div>
6	KC0	328	<div> <div>53%</div> <div>95%</div> <div>..</div> </div>
6	LC0	328	<div> <div>41%</div> <div>96%</div> <div>..</div> </div>
7	KCC	110	<div> <div>64%</div> <div>88%</div> <div>.. 10%</div> </div>
7	LCC	110	<div> <div>65%</div> <div>88%</div> <div>.. 10%</div> </div>
8	KD0	291	<div> <div>63%</div> <div>94%</div> <div>..</div> </div>
8	LD0	291	<div> <div>53%</div> <div>94%</div> <div>..</div> </div>
9	KDD	110	<div> <div>47%</div> <div>98%</div> <div>..</div> </div>
9	LDD	110	<div> <div>43%</div> <div>99%</div> <div>.</div> </div>
10	KE0	171	<div> <div>84%</div> <div>90%</div> <div>5% ..</div> </div>
10	LE0	171	<div> <div>80%</div> <div>90%</div> <div>5% ..</div> </div>
11	KEE	139	<div> <div>50%</div> <div>93%</div> <div>..</div> </div>
11	LEE	139	<div> <div>41%</div> <div>93%</div> <div>..</div> </div>
12	KF0	235	<div> <div>65%</div> <div>95%</div> <div>..</div> </div>
12	LF0	235	<div> <div>56%</div> <div>95%</div> <div>..</div> </div>
13	KFF	111	<div> <div>69%</div> <div>97%</div> <div>.</div> </div>
13	LFF	111	<div> <div>59%</div> <div>97%</div> <div>.</div> </div>
14	KG0	206	<div> <div>70%</div> <div>93%</div> <div>..</div> </div>
14	LG0	206	<div> <div>73%</div> <div>94%</div> <div>..</div> </div>
15	KGG	106	<div> <div>36%</div> <div>93%</div> <div>..</div> </div>
15	LGG	106	<div> <div>40%</div> <div>92%</div> <div>5% ..</div> </div>
16	KH0	187	<div> <div>57%</div> <div>94%</div> <div>..</div> </div>
16	LH0	187	<div> <div>56%</div> <div>94%</div> <div>..</div> </div>

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Mol	Chain	Length	Quality of chain
17	KHH	119	69% 95% 5%
17	LHH	119	56% 95% 5%
18	KI0	218	47% 98% .
18	LI0	218	47% 97% .
19	KII	98	56% 93% 6% .
19	LII	98	58% 94% 5% .
20	KJ0	171	58% 92% 6% .
20	LJ0	171	65% 92% 6% .
21	KJJ	92	26% 90% 7% .
21	LJJ	92	14% 90% 7% .
22	KL0	165	55% 92% 8% .
22	LL0	165	46% 91% 8% ..
23	KLL	52	31% 98% .
23	LLL	52	17% 98% .
24	KM0	115	91% 97% .
24	LM0	115	93% 96% .
25	KMM	127	14% 41% 59%
25	LMM	127	21% 41% 59%
26	KN0	204	. 95% .
26	LN0	204	. 95% .
27	KO0	198	52% 97% .
27	LO0	198	51% 97% .
28	KOO	104	16% 93% .
28	LOO	104	38% 92% .
29	KP0	167	53% 87% 8%

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Mol	Chain	Length	Quality of chain
29	LP0	167	<div> <div>38%</div> <div>89%</div> <div>8%</div> </div>
30	KPP	89	<div> <div>31%</div> <div>92%</div> <div>...</div> </div>
30	LPP	89	<div> <div>44%</div> <div>92%</div> <div>...</div> </div>
31	KQ0	183	<div> <div>63%</div> <div>96%</div> <div>...</div> </div>
31	LQ0	183	<div> <div>50%</div> <div>96%</div> <div>...</div> </div>
32	KR0	168	<div> <div>52%</div> <div>96%</div> <div>...</div> </div>
32	LR0	168	<div> <div>54%</div> <div>96%</div> <div>...</div> </div>
33	KS0	171	<div> <div>79%</div> <div>96%</div> <div>...</div> </div>
33	LS0	171	<div> <div>67%</div> <div>96%</div> <div>...</div> </div>
34	KT0	158	<div> <div>63%</div> <div>91%</div> <div>7%</div> </div>
34	LT0	158	<div> <div>49%</div> <div>91%</div> <div>7%</div> </div>
35	KU0	113	<div> <div>64%</div> <div>86%</div> <div>12%</div> </div>
35	LU0	113	<div> <div>65%</div> <div>86%</div> <div>12%</div> </div>
36	KV0	142	<div> <div>37%</div> <div>98%</div> <div>...</div> </div>
36	LV0	142	<div> <div>58%</div> <div>98%</div> <div>...</div> </div>
37	KW0	131	<div> <div>44%</div> <div>67%</div> <div>10%</div> <div>22%</div> </div>
37	LW0	131	<div> <div>56%</div> <div>67%</div> <div>10%</div> <div>22%</div> </div>
38	KX0	113	<div> <div>51%</div> <div>96%</div> <div>...</div> </div>
38	LX0	113	<div> <div>49%</div> <div>96%</div> <div>...</div> </div>
39	KY0	131	<div> <div>57%</div> <div>96%</div> <div>...</div> </div>
39	LY0	131	<div> <div>57%</div> <div>96%</div> <div>...</div> </div>
40	KZ0	153	<div> <div>58%</div> <div>76%</div> <div>23%</div> </div>
40	LZ0	153	<div> <div>57%</div> <div>76%</div> <div>23%</div> </div>
41	MD1	151	<div> <div>62%</div> <div>94%</div> <div>6%</div> </div>
41	MD2	151	<div> <div>71%</div> <div>94%</div> <div>6%</div> </div>

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Mol	Chain	Length	Quality of chain
42	R60	1368	
42	S60	1368	
43	RA0	233	
43	SA0	233	
44	RAA	102	
44	SAA	102	
45	RB0	230	
45	SB0	230	
46	RBB	82	
46	SBB	82	
47	RC0	248	
47	SC0	248	
48	RCC	65	
48	SCC	65	
49	RD0	242	
49	SD0	242	
50	RDD	65	
50	SDD	65	
51	RE0	280	
51	SE0	280	
52	REE	60	
52	SEE	60	
53	RF0	195	
53	SF0	195	
54	RFF	150	

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Mol	Chain	Length	Quality of chain
54	SFF	150	
55	RG0	230	
55	SG0	230	
56	RGG	326	
56	SGG	326	
57	RH0	164	
57	SH0	164	
58	RI0	173	
58	SI0	173	
59	RJ0	184	
59	SJ0	184	
60	RK0	107	
60	SK0	107	
61	RL0	155	
61	SL0	155	
62	RM0	130	
62	SM0	130	
63	RN0	143	
63	SN0	143	
64	RO0	135	
64	SO0	135	
65	RQ0	143	
65	SQ0	143	
66	RR0	120	
66	SR0	120	

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Mol	Chain	Length	Quality of chain
67	RS0	160	
67	SS0	160	
68	RT0	143	
68	ST0	143	
69	RU0	119	
69	SU0	119	
70	RV0	67	
70	SV0	67	
71	RW0	128	
71	SW0	128	
72	RX0	141	
72	SX0	141	
73	RY0	146	
73	SY0	146	
74	RZ0	128	
74	SZ0	128	
75	RP0	163	
75	SP0	163	



## 2 Entry composition

There are 76 unique types of molecules in this entry. The entry contains 343629 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called RNA 28S.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L50	2499	Total	C	N	O	P	0	0
			53655	23950	9876	17330	2499		
1	K50	2499	Total	C	N	O	P	0	0
			53655	23950	9876	17330	2499		

- Molecule 2 is a RNA chain called RNA 5S.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L70	119	Total	C	N	O	P	0	0
			2542	1136	459	828	119		
2	K70	119	Total	C	N	O	P	0	0
			2542	1136	459	828	119		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	LA0	245	Total	C	N	O	S	0	0
			1889	1189	361	334	5		
3	KA0	245	Total	C	N	O	S	0	0
			1889	1189	361	334	5		

- Molecule 4 is a protein called Ribosomal protein L18e/L15P.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	LAA	147	Total	C	N	O	S	0	0
			1167	738	229	194	6		
4	KAA	147	Total	C	N	O	S	0	0
			1167	738	229	194	6		

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	LB0	383	Total	C	N	O	S	0	0
			3039	1926	559	543	11		
5	KB0	383	Total	C	N	O	S	0	0
			3039	1926	559	543	11		

- Molecule 6 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LC0	327	Total	C	N	O	S	0	0
			2604	1629	478	485	12		
6	KC0	327	Total	C	N	O	S	0	0
			2604	1629	478	485	12		

- Molecule 7 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LCC	99	Total	C	N	O	S	0	0
			781	504	126	148	3		
7	KCC	99	Total	C	N	O	S	0	0
			781	504	126	148	3		

- Molecule 8 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LD0	281	Total	C	N	O	S	0	0
			2298	1451	410	426	11		
8	KD0	281	Total	C	N	O	S	0	0
			2298	1451	410	426	11		

- Molecule 9 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LDD	109	Total	C	N	O	S	0	0
			895	575	163	154	3		
9	KDD	109	Total	C	N	O	S	0	0
			895	575	163	154	3		

- Molecule 10 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LE0	165	Total	C	N	O	S	0	0
			1371	879	227	262	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
10	KE0	165	Total	C	N	O	S	0	0
			1371	879	227	262	3		

- Molecule 11 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LEE	135	Total	C	N	O	S	0	0
			1090	697	205	182	6		
11	KEE	135	Total	C	N	O	S	0	0
			1090	697	205	182	6		

- Molecule 12 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LF0	231	Total	C	N	O	S	0	0
			1933	1234	342	350	7		
12	KF0	231	Total	C	N	O	S	0	0
			1933	1234	342	350	7		

- Molecule 13 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LFF	111	Total	C	N	O	S	0	0
			893	567	159	162	5		
13	KFF	111	Total	C	N	O	S	0	0
			893	567	159	162	5		

- Molecule 14 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LG0	199	Total	C	N	O	S	0	0
			1590	1015	275	290	10		
14	KG0	199	Total	C	N	O	S	0	0
			1590	1015	275	290	10		

- Molecule 15 is a protein called Ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LGG	104	Total	C	N	O	S	0	0
			819	504	169	139	7		
15	KGG	104	Total	C	N	O	S	0	0
			819	504	169	139	7		

- Molecule 16 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LH0	183	Total	C	N	O	S	0	0
			1477	951	252	266	8		
16	KH0	183	Total	C	N	O	S	0	0
			1477	951	252	266	8		

- Molecule 17 is a protein called Ribosomal L29 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LHH	119	Total	C	N	O	S	0	0
			992	626	188	175	3		
17	KHH	119	Total	C	N	O	S	0	0
			992	626	188	175	3		

- Molecule 18 is a protein called S60 ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LI0	217	Total	C	N	O	S	0	0
			1750	1096	333	308	13		
18	KI0	217	Total	C	N	O	S	0	0
			1750	1096	333	308	13		

- Molecule 19 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LII	97	Total	C	N	O	S	0	0
			784	496	146	136	6		
19	KII	97	Total	C	N	O	S	0	0
			784	496	146	136	6		

- Molecule 20 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LJ0	167	Total	C	N	O	S	0	0
			1332	847	242	236	7		
20	KJ0	167	Total	C	N	O	S	0	0
			1332	847	242	236	7		

- Molecule 21 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LJJ	89	Total	C	N	O	S	0	0
			701	427	146	118	10		
21	KJJ	89	Total	C	N	O	S	0	0
			701	427	146	118	10		

- Molecule 22 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LL0	164	Total	C	N	O	S	0	0
			1353	857	252	232	12		
22	KL0	164	Total	C	N	O	S	0	0
			1353	857	252	232	12		

- Molecule 23 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LLL	51	Total	C	N	O	S	0	0
			427	272	87	65	3		
23	KLL	51	Total	C	N	O	S	0	0
			427	272	87	65	3		

- Molecule 24 is a protein called Transposase.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LM0	115	Total	C	N	O	S	0	0
			927	588	151	183	5		
24	KM0	115	Total	C	N	O	S	0	0
			927	588	151	183	5		

- Molecule 25 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LMM	52	Total	C	N	O	S	0	0
			427	264	89	70	4		
25	KMM	52	Total	C	N	O	S	0	0
			427	264	89	70	4		

- Molecule 26 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LN0	203	Total	C	N	O	S	0	0
			1688	1055	346	276	11		

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Mol	Chain	Residues	Atoms					AltConf	Trace
26	KN0	203	Total	C	N	O	S	0	0
			1688	1055	346	276	11		

- Molecule 27 is a protein called Ribosomal protein L13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LO0	198	Total	C	N	O	S	0	0
			1598	1018	286	280	14		
27	KO0	198	Total	C	N	O	S	0	0
			1598	1018	286	280	14		

- Molecule 28 is a protein called 60S ribosomal protein L44.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LOO	100	Total	C	N	O	S	0	0
			801	504	163	130	4		
28	KOO	100	Total	C	N	O	S	0	0
			801	504	163	130	4		

- Molecule 29 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LP0	154	Total	C	N	O	S	0	0
			1238	794	225	213	6		
29	KP0	154	Total	C	N	O	S	0	0
			1238	794	225	213	6		

- Molecule 30 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LPP	87	Total	C	N	O	S	0	0
			684	427	131	116	10		
30	KPP	87	Total	C	N	O	S	0	0
			684	427	131	116	10		

- Molecule 31 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LQ0	182	Total	C	N	O	S	0	0
			1491	950	270	266	5		
31	KQ0	182	Total	C	N	O	S	0	0
			1491	950	270	266	5		

- Molecule 32 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LR0	164	Total	C	N	O	S	0	0
			1336	832	261	236	7		
32	KR0	164	Total	C	N	O	S	0	0
			1336	832	261	236	7		

- Molecule 33 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LS0	170	Total	C	N	O	S	0	0
			1400	898	241	256	5		
33	KS0	170	Total	C	N	O	S	0	0
			1400	898	241	256	5		

- Molecule 34 is a protein called 60s ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	LT0	156	Total	C	N	O	S	0	0
			1270	808	233	224	5		
34	KT0	156	Total	C	N	O	S	0	0
			1270	808	233	224	5		

- Molecule 35 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	LU0	100	Total	C	N	O	S	0	0
			810	526	135	147	2		
35	KU0	100	Total	C	N	O	S	0	0
			810	526	135	147	2		

- Molecule 36 is a protein called Ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	LV0	141	Total	C	N	O	S	0	0
			1057	663	200	189	5		
36	KV0	141	Total	C	N	O	S	0	0
			1057	663	200	189	5		

- Molecule 37 is a protein called Ribosomal protein L24E.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	LW0	102	Total	C	N	O	S	0	0
			832	539	143	147	3		
37	KW0	102	Total	C	N	O	S	0	0
			832	539	143	147	3		

- Molecule 38 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	LX0	112	Total	C	N	O	S	0	0
			874	562	156	155	1		
38	KX0	112	Total	C	N	O	S	0	0
			874	562	156	155	1		

- Molecule 39 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	LY0	131	Total	C	N	O	S	0	0
			1048	658	197	186	7		
39	KY0	131	Total	C	N	O	S	0	0
			1048	658	197	186	7		

- Molecule 40 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	LZ0	118	Total	C	N	O	S	0	0
			963	618	172	169	4		
40	KZ0	118	Total	C	N	O	S	0	0
			963	618	172	169	4		

- Molecule 41 is a protein called DNL-type domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	MD1	151	Total	C	N	O	S	0	0
			1229	776	201	241	11		
41	MD2	151	Total	C	N	O	S	0	0
			1229	776	201	241	11		

- Molecule 42 is a RNA chain called RNA 16S.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	S60	1354	Total	C	N	O	P	0	0
			29181	13024	5463	9340	1354		

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Mol	Chain	Residues	Atoms					AltConf	Trace
42	R60	1354	Total	C	N	O	P	0	0
			29181	13024	5463	9340	1354		

- Molecule 43 is a protein called 40S ribosomal protein S0.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	SA0	220	Total	C	N	O	S	0	0
			1725	1091	292	328	14		
43	RA0	220	Total	C	N	O	S	0	0
			1725	1091	292	328	14		

- Molecule 44 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	SAA	101	Total	C	N	O	S	0	0
			827	513	163	145	6		
44	RAA	101	Total	C	N	O	S	0	0
			827	513	163	145	6		

- Molecule 45 is a protein called 40S ribosomal protein S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	SB0	204	Total	C	N	O	S	0	0
			1609	1018	286	298	7		
45	RB0	204	Total	C	N	O	S	0	0
			1609	1018	286	298	7		

- Molecule 46 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	SBB	81	Total	C	N	O	S	0	0
			627	394	108	116	9		
46	RBB	81	Total	C	N	O	S	0	0
			627	394	108	116	9		

- Molecule 47 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	SC0	226	Total	C	N	O	S	0	0
			1727	1099	300	321	7		
47	RC0	226	Total	C	N	O	S	0	0
			1727	1099	300	321	7		

- Molecule 48 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SCC	62	Total	C	N	O	S	0	0
			476	295	86	91	4		
48	RCC	62	Total	C	N	O	S	0	0
			476	295	86	91	4		

- Molecule 49 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SD0	216	Total	C	N	O	S	0	0
			1700	1085	300	307	8		
49	RD0	216	Total	C	N	O	S	0	0
			1700	1085	300	307	8		

- Molecule 50 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SDD	65	Total	C	N	O	S	0	0
			550	345	102	96	7		
50	RDD	65	Total	C	N	O	S	0	0
			550	345	102	96	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SE0	260	Total	C	N	O	S	0	0
			2044	1297	361	379	7		
51	RE0	260	Total	C	N	O	S	0	0
			2044	1297	361	379	7		

- Molecule 52 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	SEE	56	Total	C	N	O	0	0
			447	284	89	74		
52	REE	56	Total	C	N	O	0	0
			447	284	89	74		

- Molecule 53 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SF0	192	Total	C	N	O	S	0	0
			1509	953	275	275	6		
53	RF0	192	Total	C	N	O	S	0	0
			1509	953	275	275	6		

- Molecule 54 is a protein called Ubiquitin/40s ribosomal protein S27a fusion.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SFF	58	Total	C	N	O	S	0	0
			422	261	77	79	5		
54	RFF	58	Total	C	N	O	S	0	0
			417	259	74	79	5		

- Molecule 55 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SG0	229	Total	C	N	O	S	0	0
			1836	1179	325	328	4		
55	RG0	229	Total	C	N	O	S	0	0
			1836	1179	325	328	4		

- Molecule 56 is a protein called Guanine nucleotide binding protein beta subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SGG	319	Total	C	N	O	S	0	0
			2478	1558	411	494	15		
56	RGG	319	Total	C	N	O	S	0	0
			2478	1558	411	494	15		

- Molecule 57 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SH0	163	Total	C	N	O	S	0	0
			1335	855	219	255	6		
57	RH0	163	Total	C	N	O	S	0	0
			1335	855	219	255	6		

- Molecule 58 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SI0	167	Total	C	N	O	S	0	0
			1347	834	266	240	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
58	RI0	167	Total	C	N	O	S	0	0
			1347	834	266	240	7		

- Molecule 59 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SJ0	168	Total	C	N	O	S	0	0
			1379	880	252	243	4		
59	RJ0	168	Total	C	N	O	S	0	0
			1379	880	252	243	4		

- Molecule 60 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SK0	88	Total	C	N	O	S	0	0
			737	472	127	135	3		
60	RK0	88	Total	C	N	O	S	0	0
			737	472	127	135	3		

- Molecule 61 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SL0	150	Total	C	N	O	S	0	0
			1229	790	217	216	6		
61	RL0	150	Total	C	N	O	S	0	0
			1229	790	217	216	6		

- Molecule 62 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SM0	113	Total	C	N	O	S	0	0
			876	553	156	162	5		
62	RM0	113	Total	C	N	O	S	0	0
			876	553	156	162	5		

- Molecule 63 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SN0	142	Total	C	N	O	S	0	0
			1130	728	196	202	4		
63	RN0	142	Total	C	N	O	S	0	0
			1130	728	196	202	4		

- Molecule 64 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SO0	129	Total	C	N	O	S	0	0
			983	606	191	183	3		
64	RO0	129	Total	C	N	O	S	0	0
			983	606	191	183	3		

- Molecule 65 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SQ0	142	Total	C	N	O	S	0	0
			1143	726	204	207	6		
65	RQ0	142	Total	C	N	O	S	0	0
			1143	726	204	207	6		

- Molecule 66 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SR0	119	Total	C	N	O	S	0	0
			974	613	172	186	3		
66	RR0	119	Total	C	N	O	S	0	0
			974	613	172	186	3		

- Molecule 67 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SS0	144	Total	C	N	O	S	0	0
			1150	720	220	207	3		
67	RS0	144	Total	C	N	O	S	0	0
			1150	720	220	207	3		

- Molecule 68 is a protein called 40S Ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	ST0	142	Total	C	N	O	S	0	0
			1161	741	208	211	1		
68	RT0	142	Total	C	N	O	S	0	0
			1161	741	208	211	1		

- Molecule 69 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SU0	100	Total	C	N	O	S	0	0
			809	515	144	143	7		
69	RU0	100	Total	C	N	O	S	0	0
			809	515	144	143	7		

- Molecule 70 is a protein called Ribosomal protein S21E.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SV0	65	Total	C	N	O	S	0	0
			521	319	96	101	5		
70	RV0	65	Total	C	N	O	S	0	0
			521	319	96	101	5		

- Molecule 71 is a protein called 40S ribosomal protein S15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SW0	128	Total	C	N	O	S	0	0
			1022	639	195	180	8		
71	RW0	128	Total	C	N	O	S	0	0
			1022	639	195	180	8		

- Molecule 72 is a protein called Ribosomal protein S12/S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SX0	140	Total	C	N	O	S	0	0
			1098	692	216	186	4		
72	RX0	140	Total	C	N	O	S	0	0
			1098	692	216	186	4		

- Molecule 73 is a protein called 40s ribosomal protein s24.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SY0	136	Total	C	N	O	S	0	0
			1118	693	215	204	6		
73	RY0	136	Total	C	N	O	S	0	0
			1118	693	215	204	6		

- Molecule 74 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SZ0	76	Total	C	N	O	S	0	0
			633	403	116	113	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
74	RZ0	76	Total	C	N	O	S	0	0
			633	403	116	113	1		

- Molecule 75 is a protein called Ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	SP0	117	Total	C	N	O	S	0	0
			950	598	172	173	7		
75	RP0	117	Total	C	N	O	S	0	0
			950	598	172	173	7		

- Molecule 76 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
76	LGG	1	Total	Zn	0
			1	1	
76	LJJ	1	Total	Zn	0
			1	1	
76	LMM	1	Total	Zn	0
			1	1	
76	LOO	1	Total	Zn	0
			1	1	
76	LPP	1	Total	Zn	0
			1	1	
76	SAA	1	Total	Zn	0
			1	1	
76	SBB	1	Total	Zn	0
			1	1	
76	SDD	1	Total	Zn	0
			1	1	
76	SFF	1	Total	Zn	0
			1	1	
76	KGG	1	Total	Zn	0
			1	1	
76	KJJ	1	Total	Zn	0
			1	1	
76	KMM	1	Total	Zn	0
			1	1	
76	KOO	1	Total	Zn	0
			1	1	
76	KPP	1	Total	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
76	RAA	1	Total 1	Zn 1	0
76	RBB	1	Total 1	Zn 1	0
76	RDD	1	Total 1	Zn 1	0
76	RFF	1	Total 1	Zn 1	0



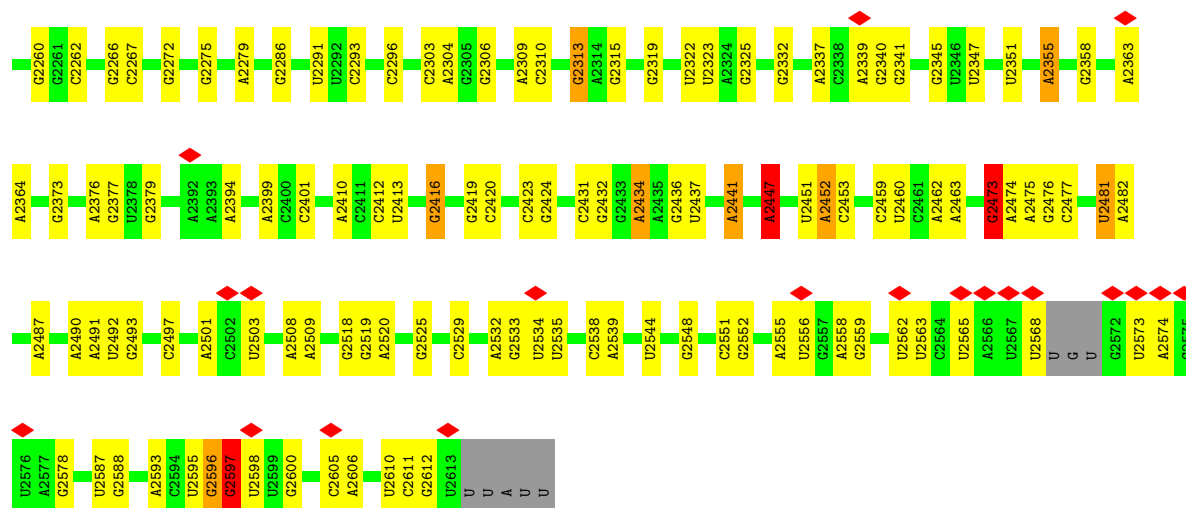
### 3 Residue-property plots

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.

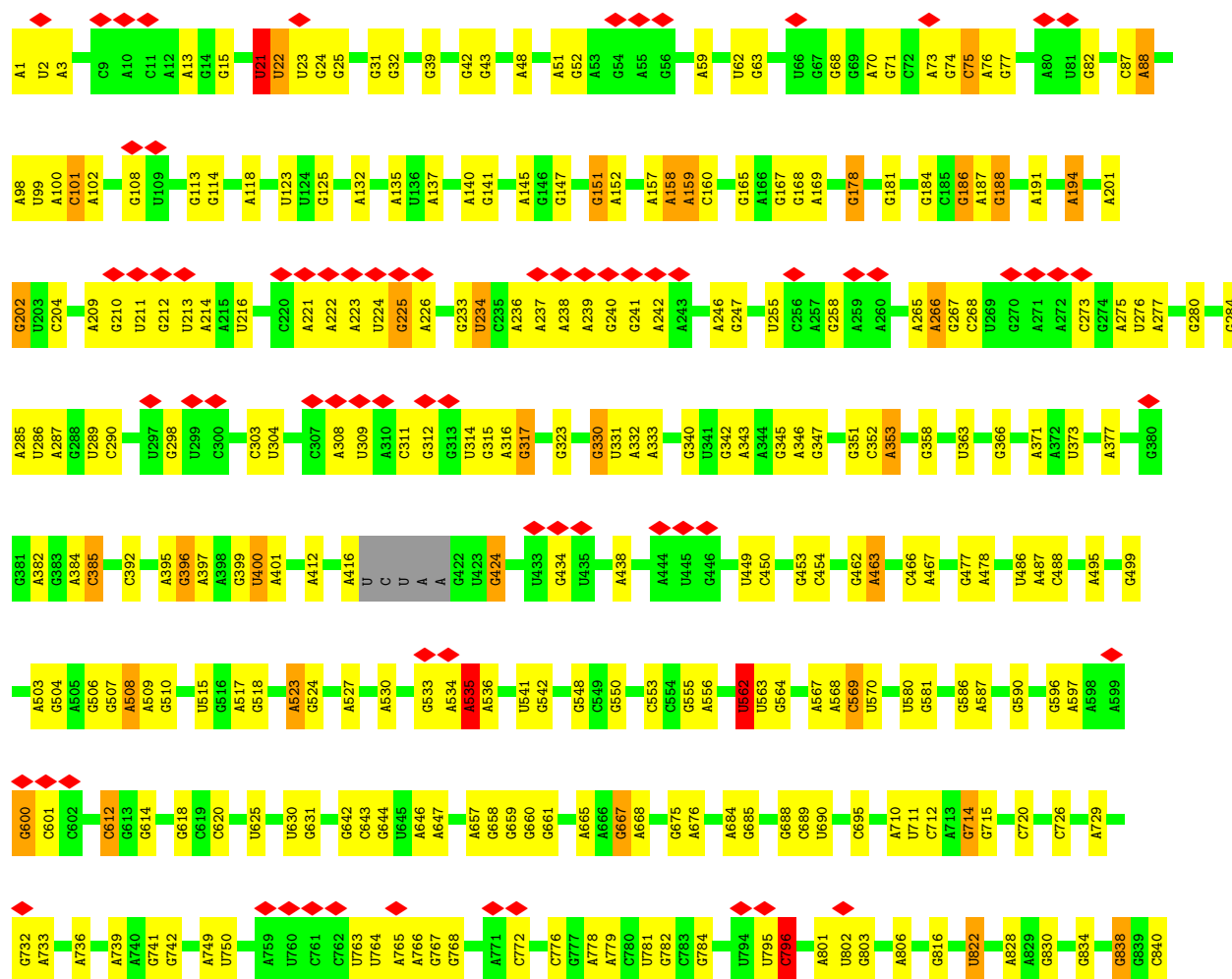
#### • Molecule 1: RNA 28S



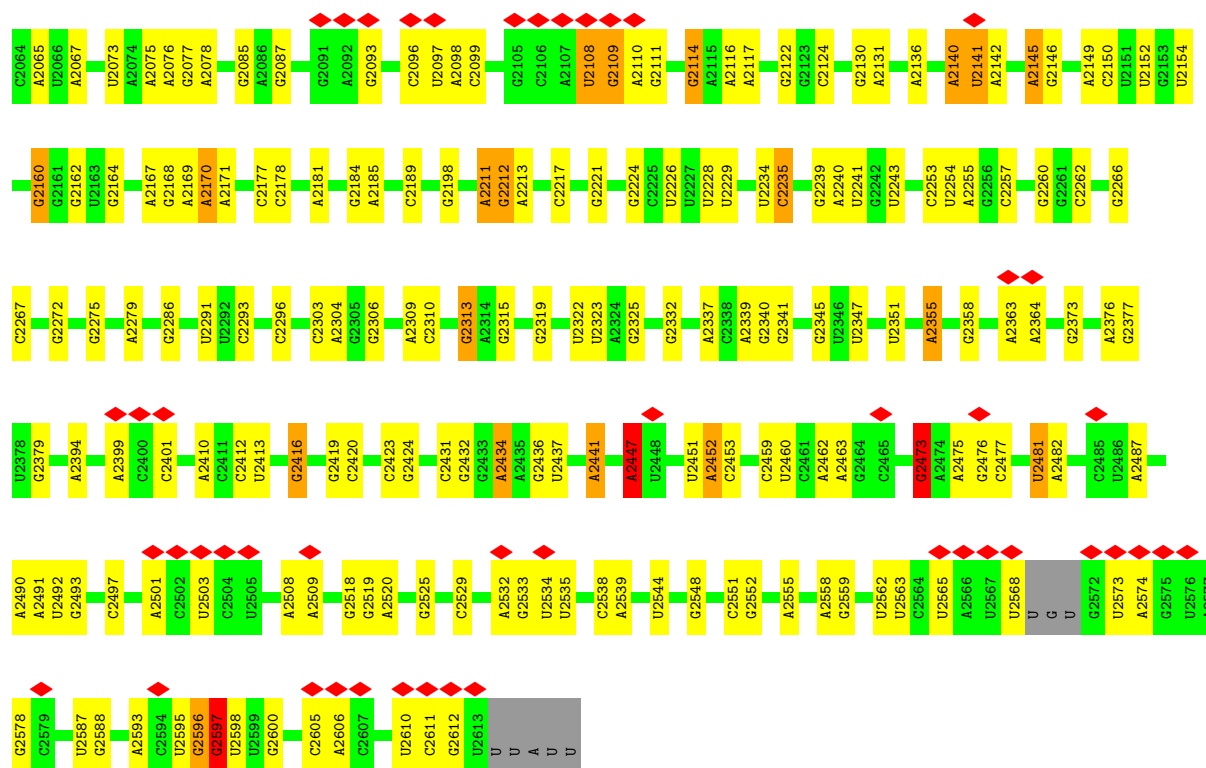




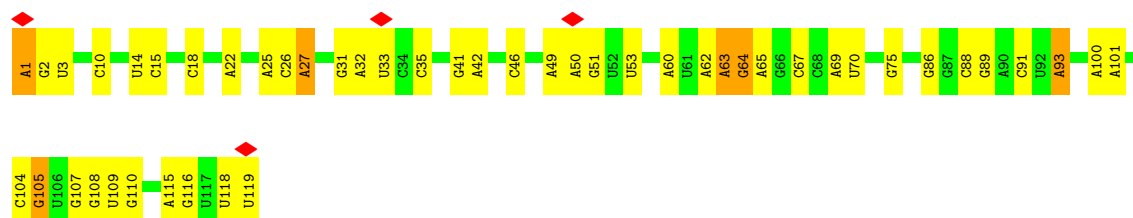
• Molecule 1: RNA 28S



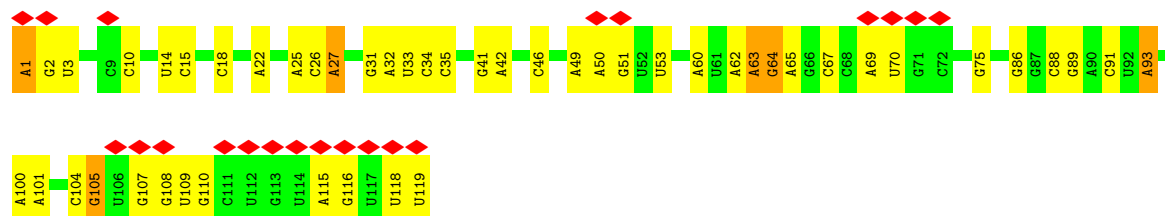




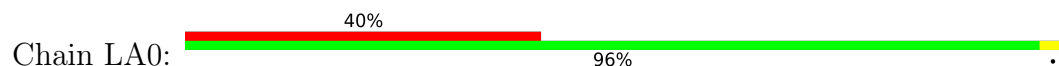
• Molecule 2: RNA 5S

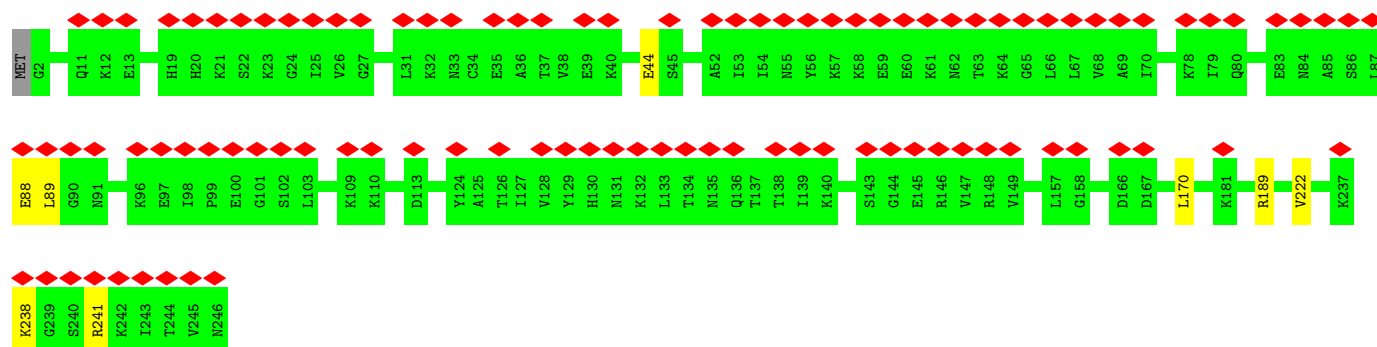


• Molecule 2: RNA 5S



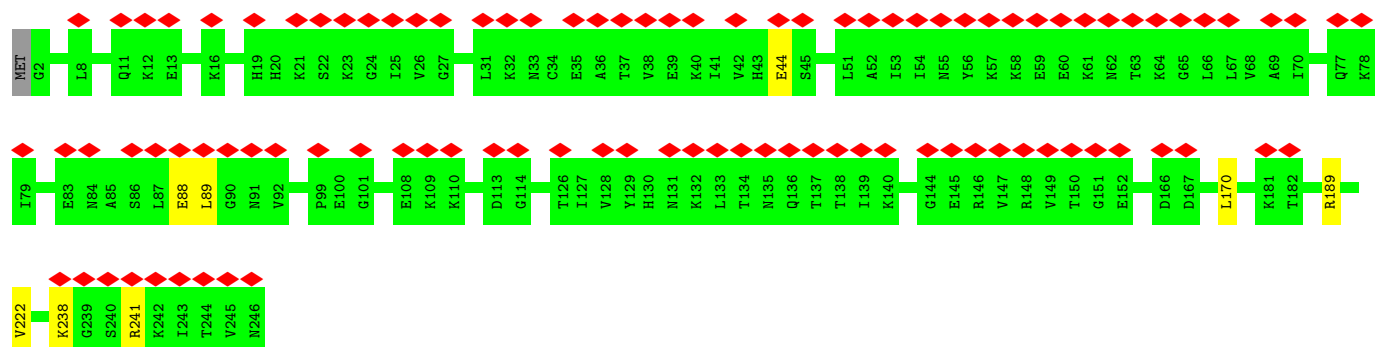
• Molecule 3: 60S ribosomal protein L8





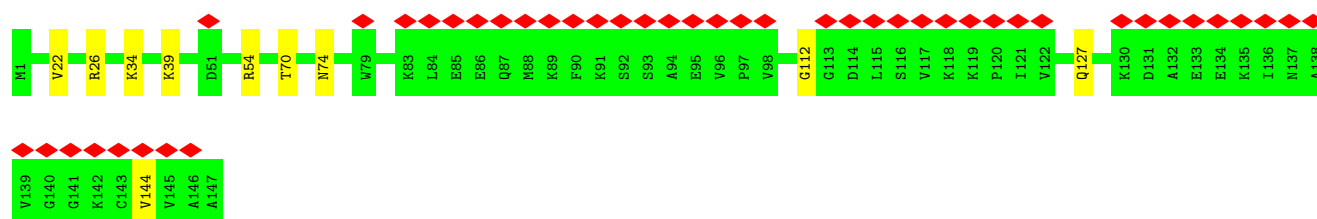
- Molecule 3: 60S ribosomal protein L8

Chain KA0: 40% 96%



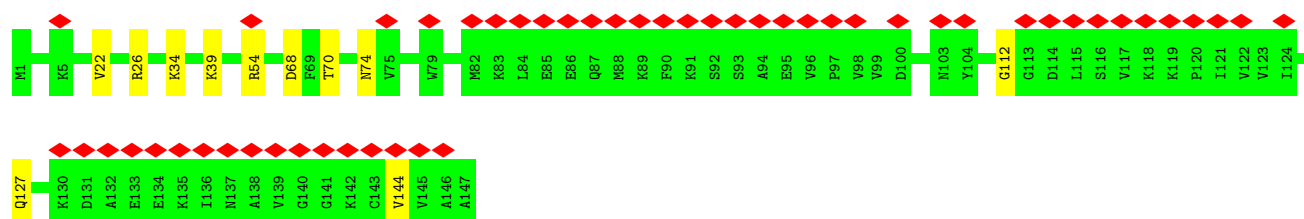
- Molecule 4: Ribosomal protein L18e/L15P

Chain LAA: 31% 93% 7%

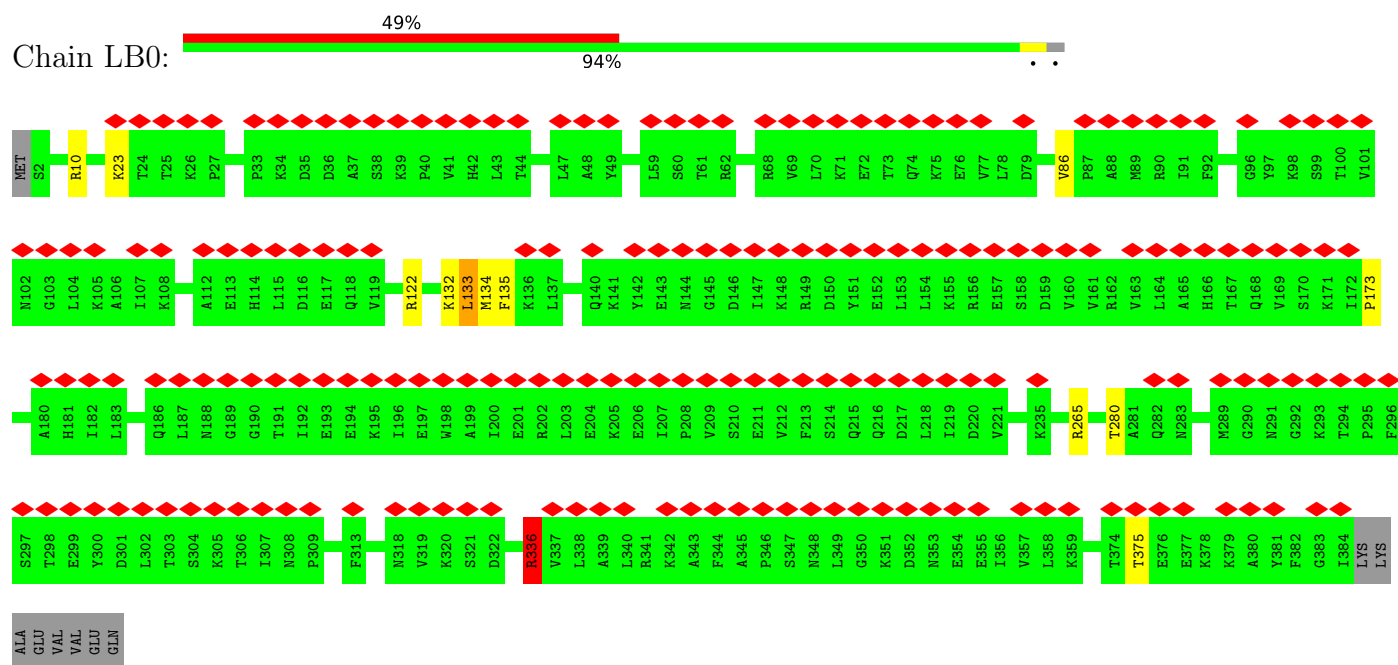


- Molecule 4: Ribosomal protein L18e/L15P

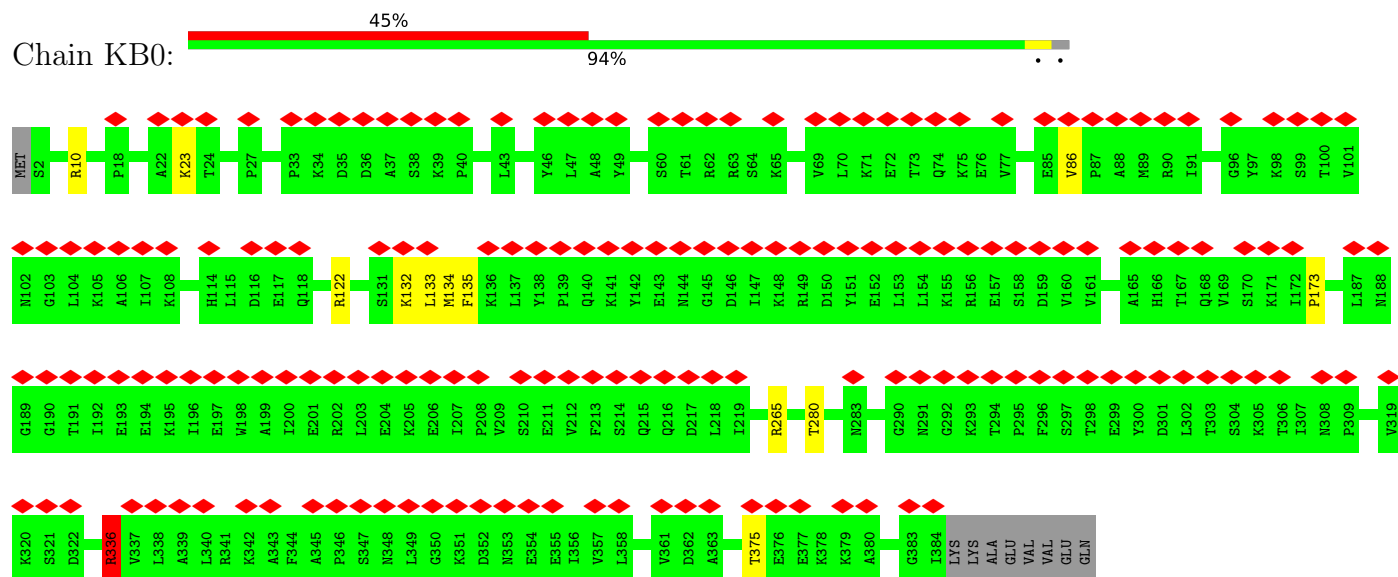
Chain KAA: 35% 93% 7%



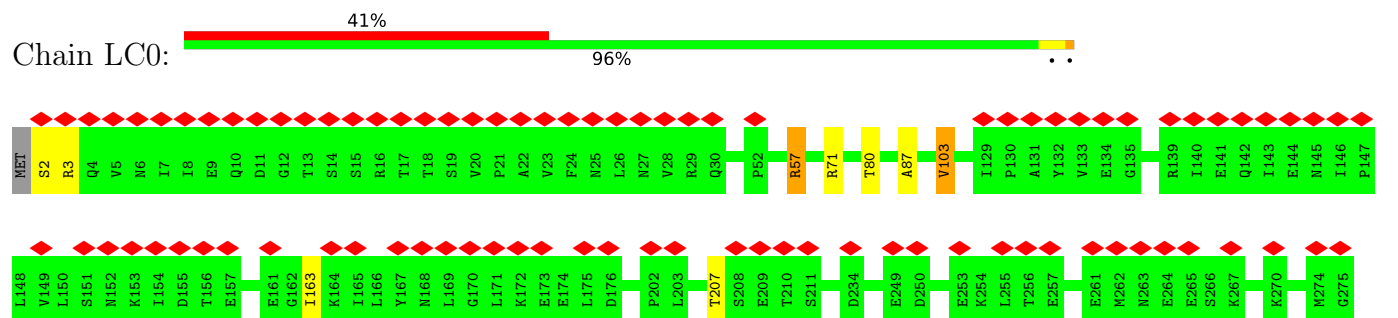
- Molecule 5: 60S ribosomal protein L3

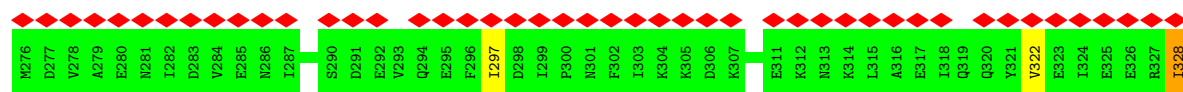


• Molecule 5: 60S ribosomal protein L3

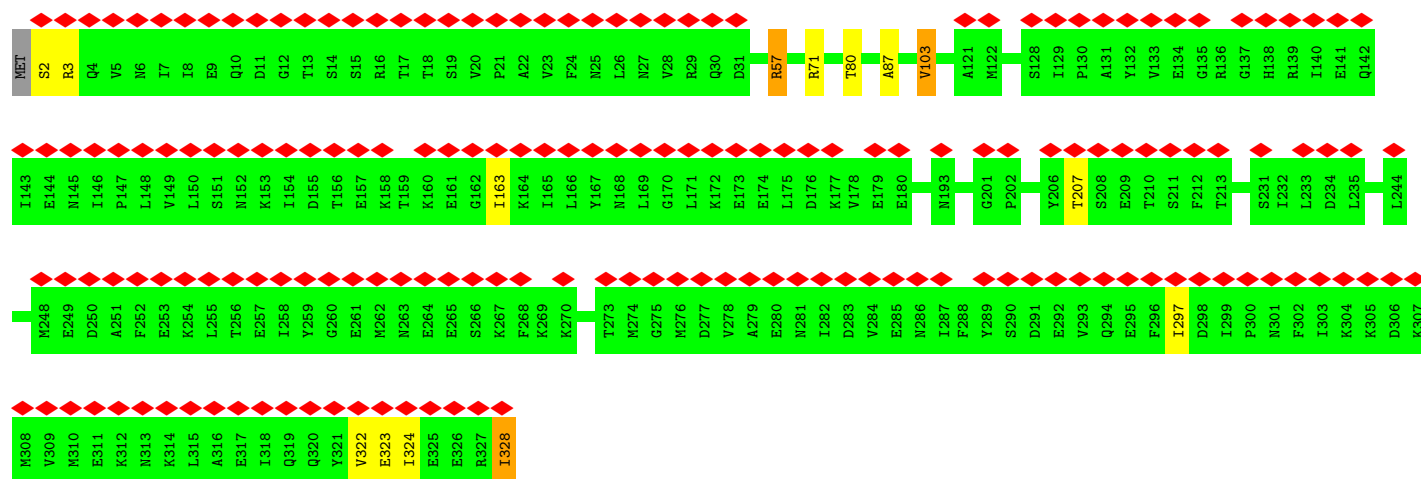


• Molecule 6: 60S ribosomal protein L4

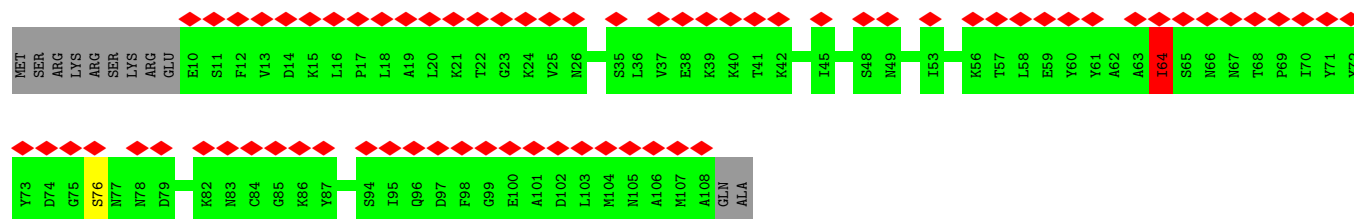
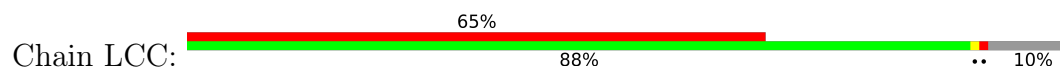




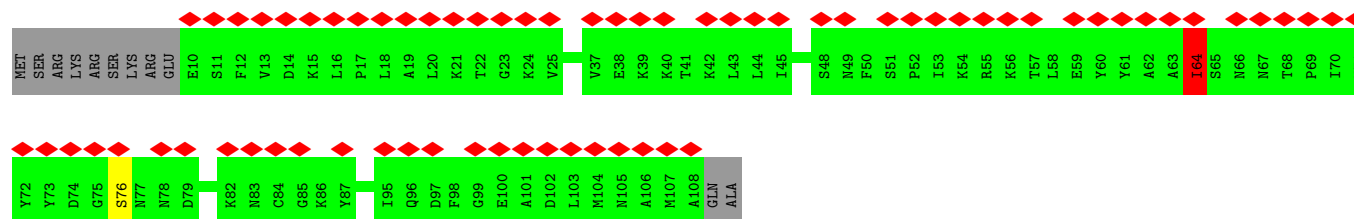
• Molecule 6: 60S ribosomal protein L4



• Molecule 7: 60S ribosomal protein L3



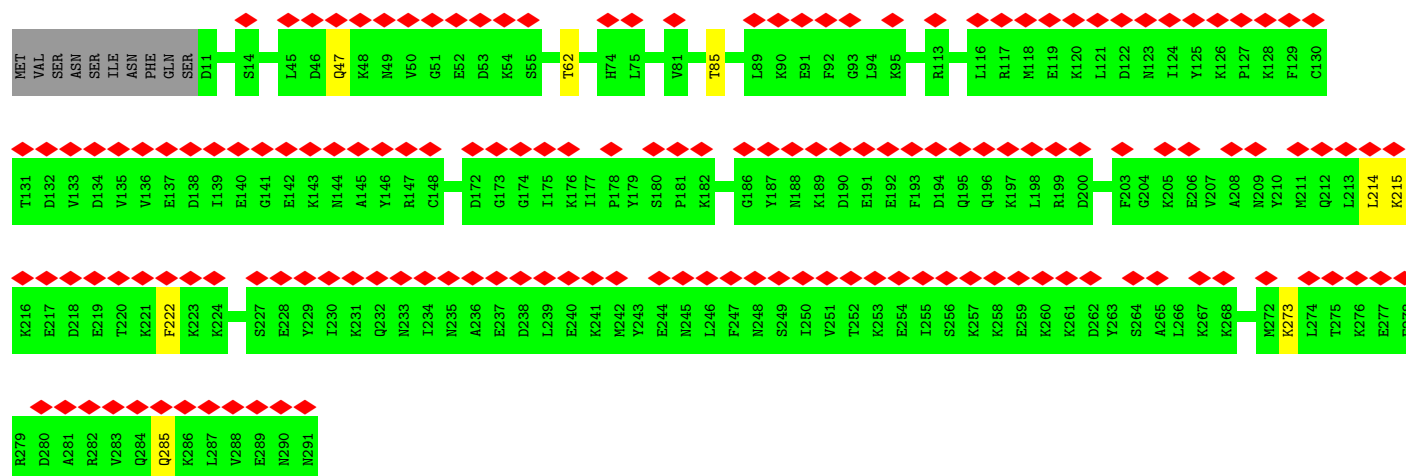
• Molecule 8: 60S ribosomal protein L5



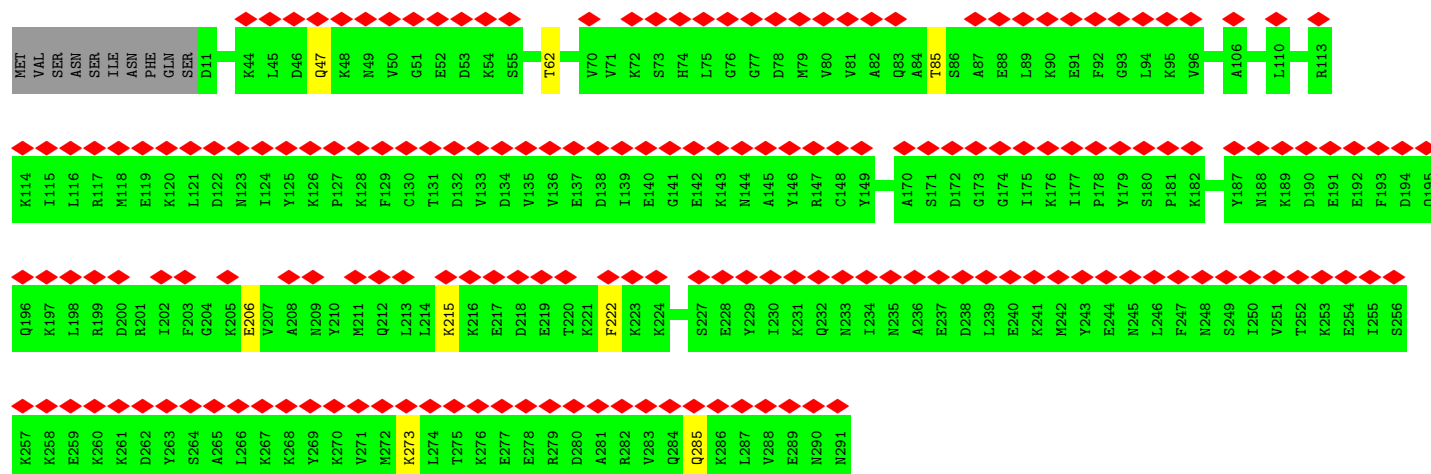
• Molecule 9: 60S ribosomal protein L6



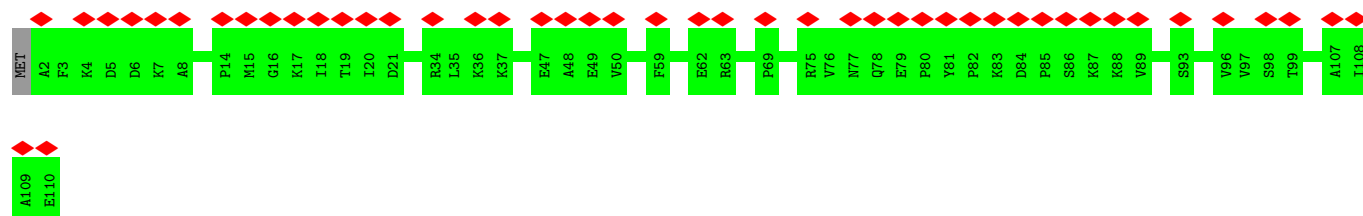




• Molecule 8: 60S ribosomal protein L5

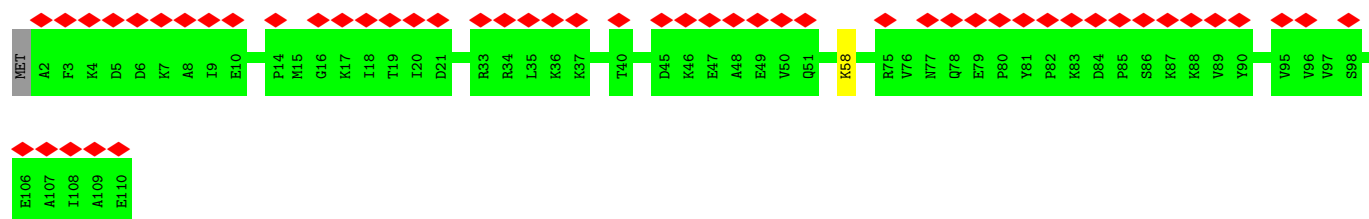


• Molecule 9: 60S ribosomal protein L31

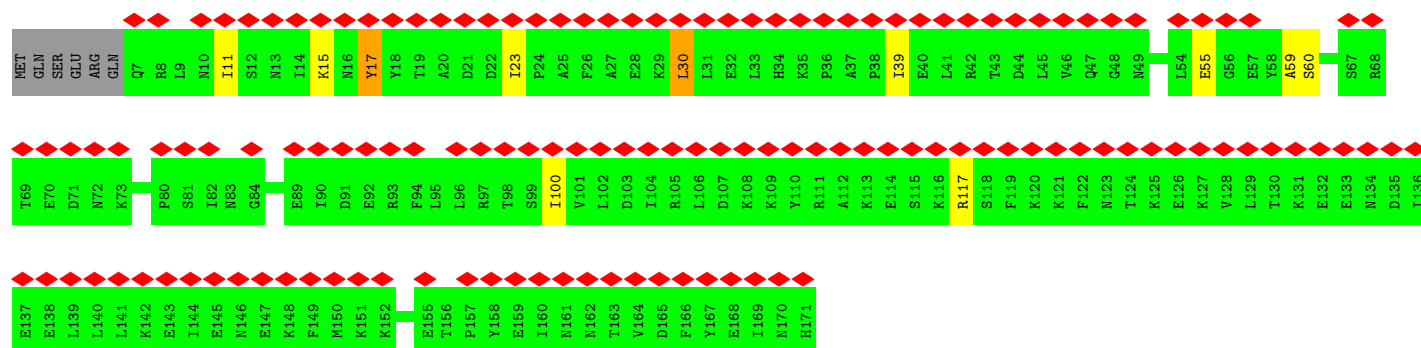
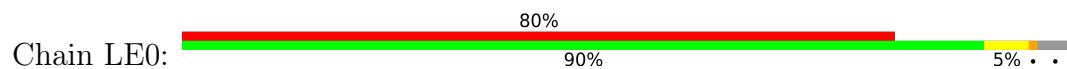


• Molecule 9: 60S ribosomal protein L31

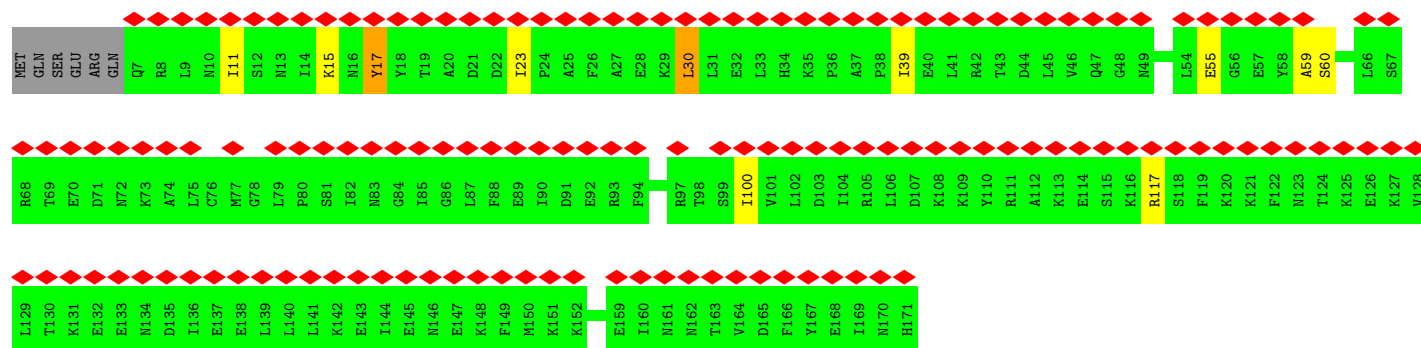
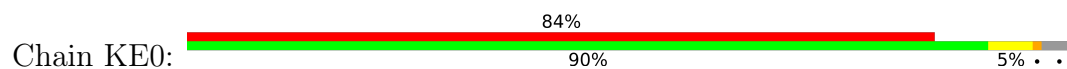




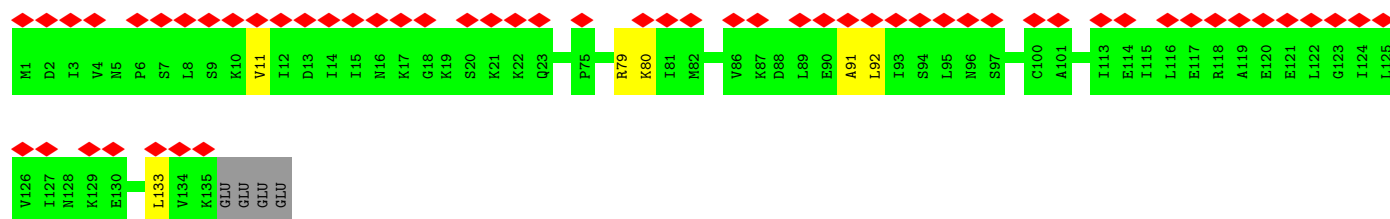
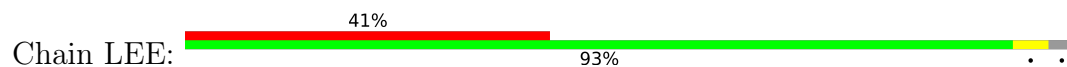
- Molecule 10: 60S ribosomal protein L6



- Molecule 10: 60S ribosomal protein L6

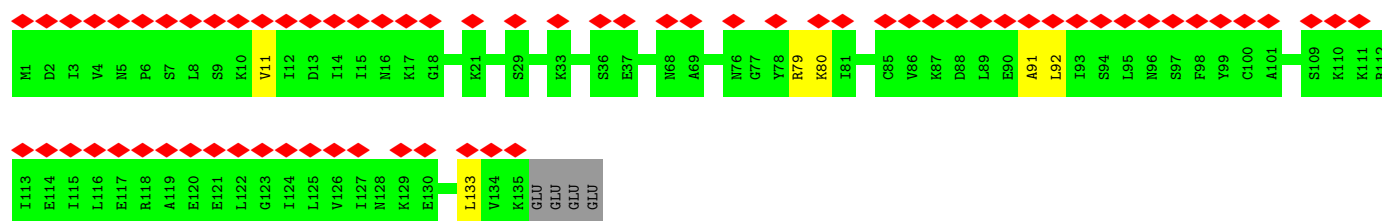


- Molecule 11: 60S ribosomal protein L32



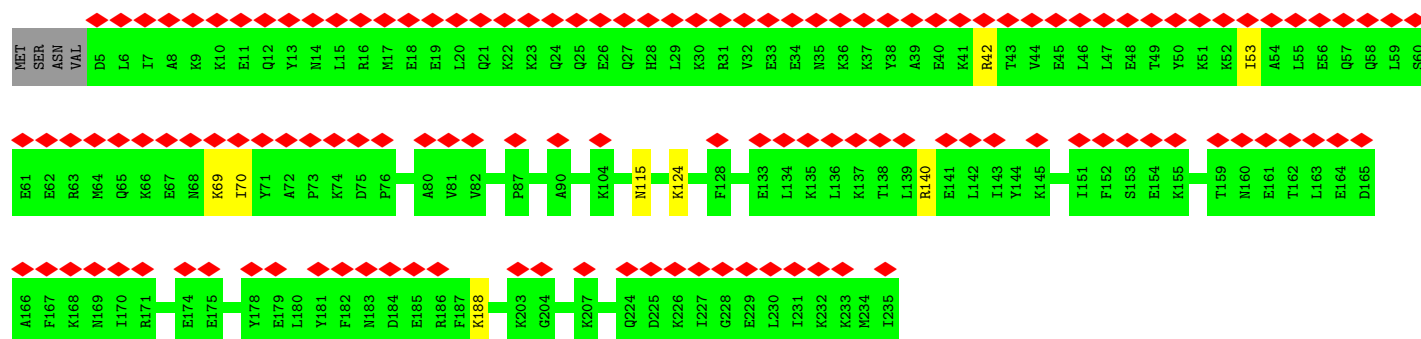
- Molecule 11: 60S ribosomal protein L32

Chain KEE: 



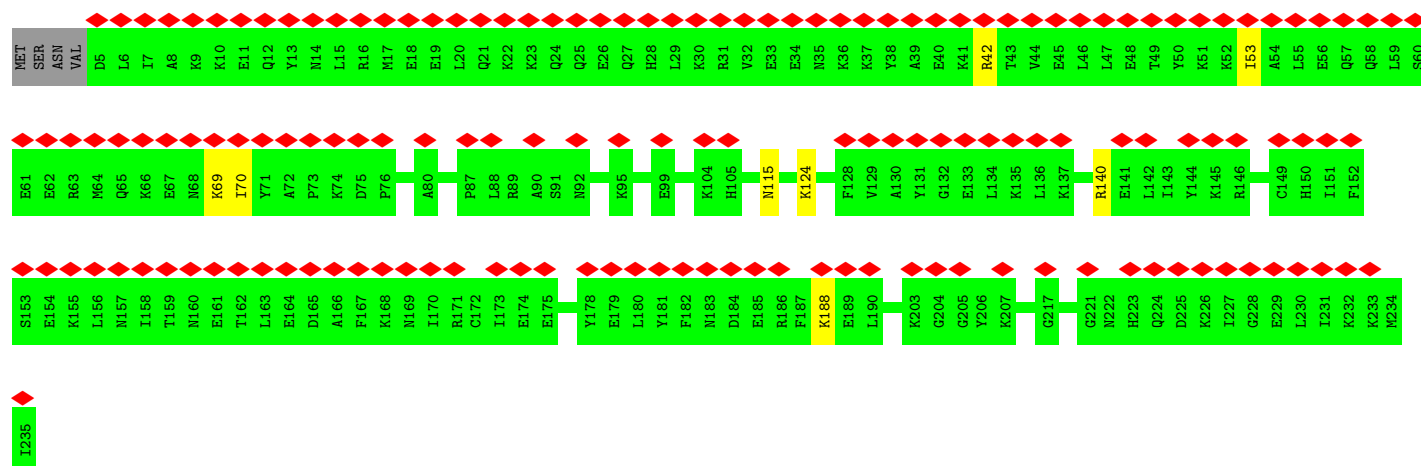
• Molecule 12: 60S ribosomal protein L7

Chain LF0: 



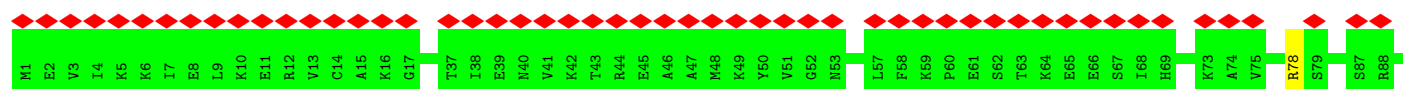
• Molecule 12: 60S ribosomal protein L7

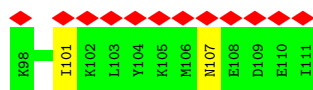
Chain KF0: 



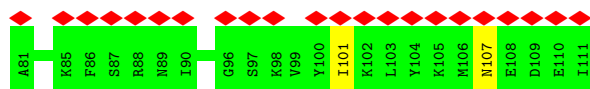
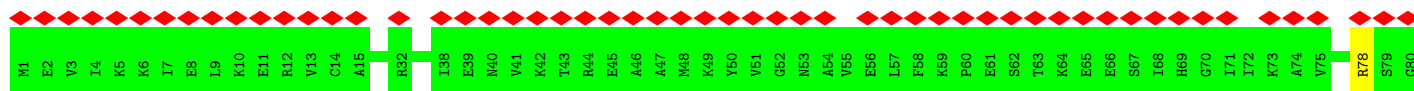
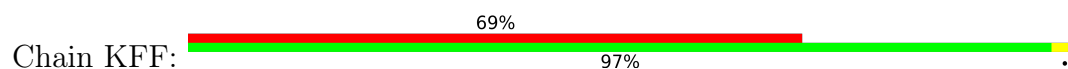
• Molecule 13: 60S ribosomal protein L35a

Chain LFF: 

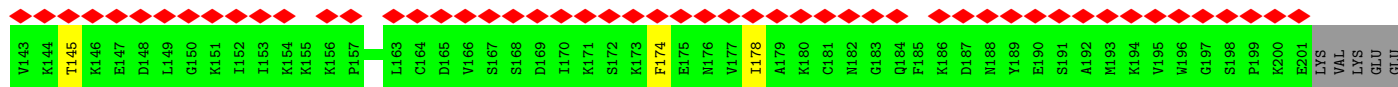
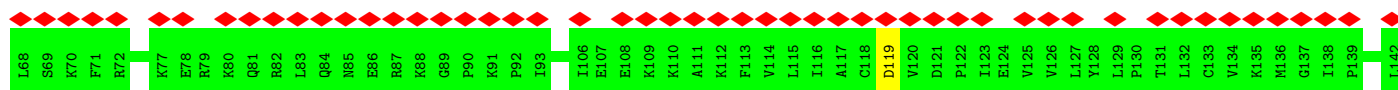
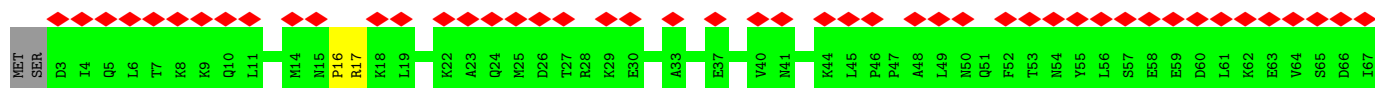
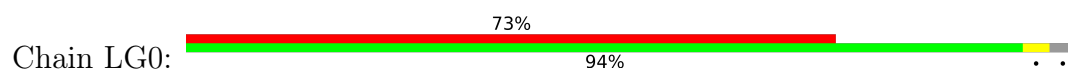




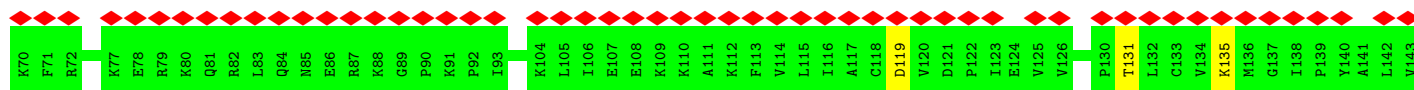
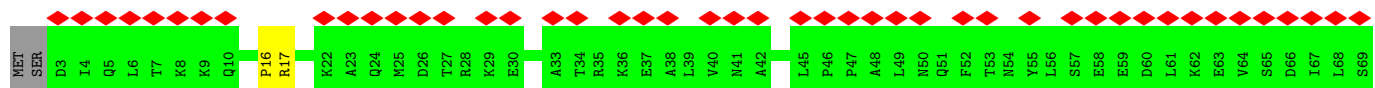
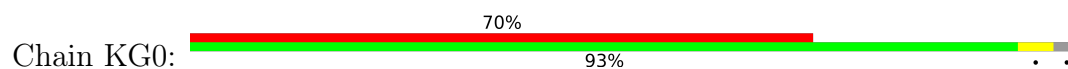
- Molecule 13: 60S ribosomal protein L35a



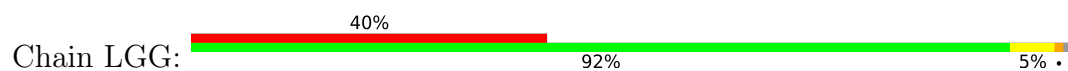
- Molecule 14: 60S ribosomal protein L8



- Molecule 14: 60S ribosomal protein L8

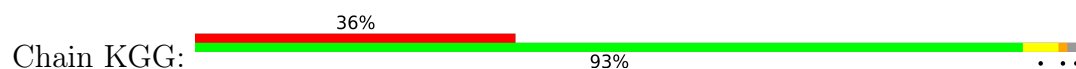


- Molecule 15: Ribosomal protein L34

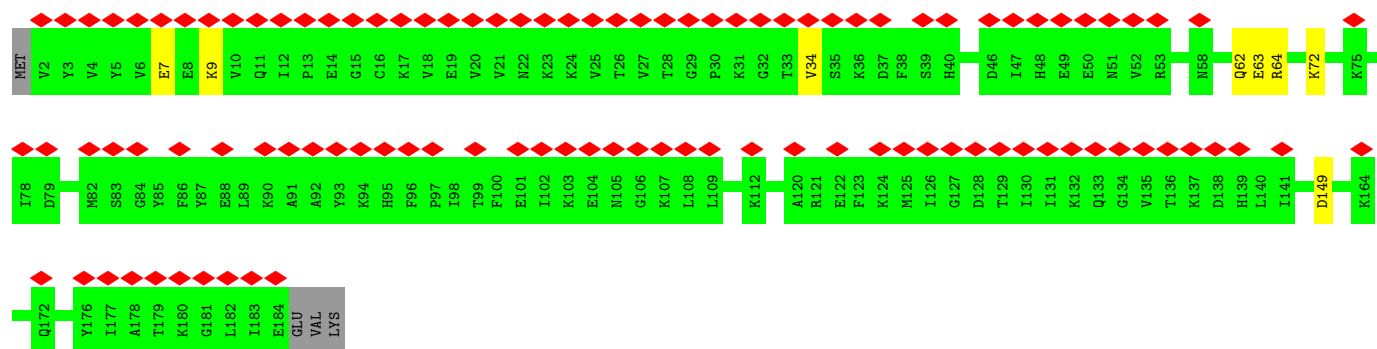




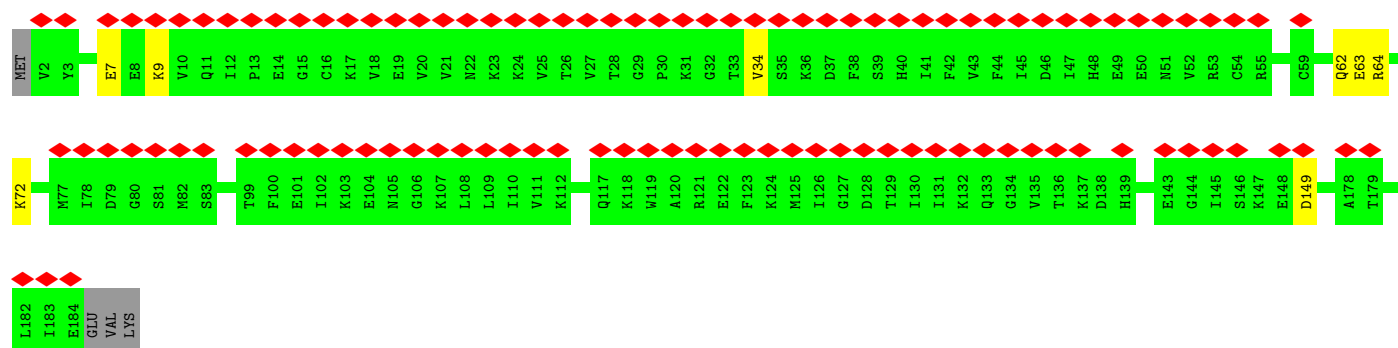
- Molecule 15: Ribosomal protein L34



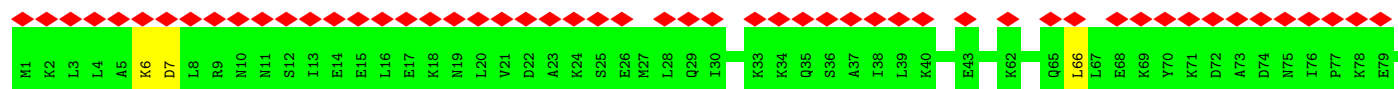
- Molecule 16: 60S ribosomal protein L9

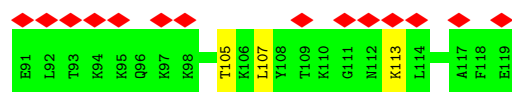


- Molecule 16: 60S ribosomal protein L9

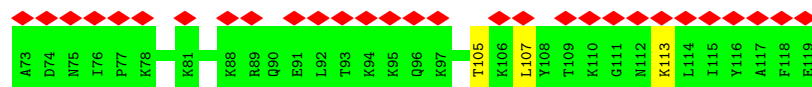
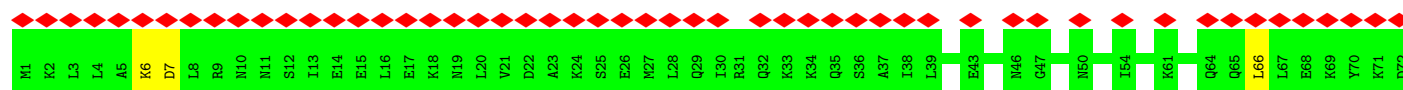
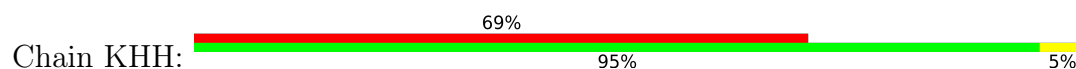


- Molecule 17: Ribosomal L29 protein

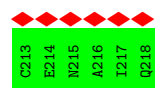
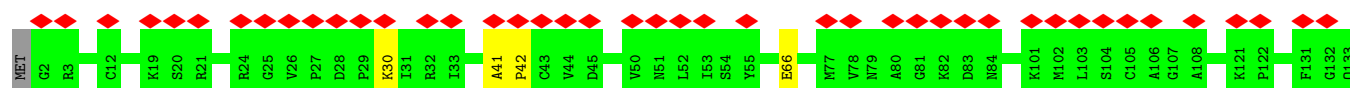




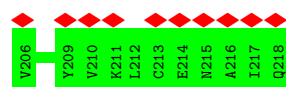
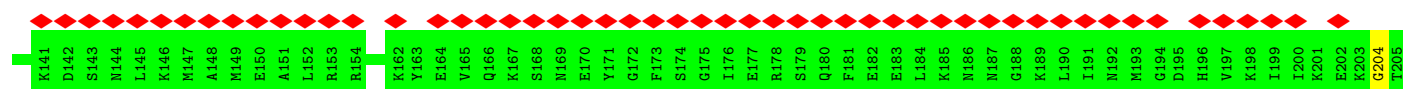
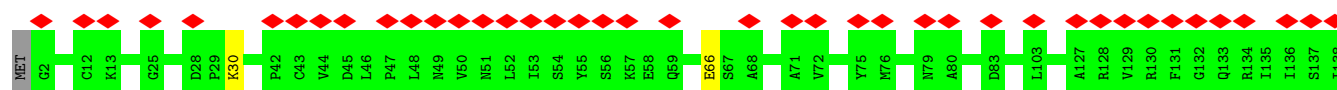
- Molecule 17: Ribosomal L29 protein



- Molecule 18: S60 ribosomal protein L10

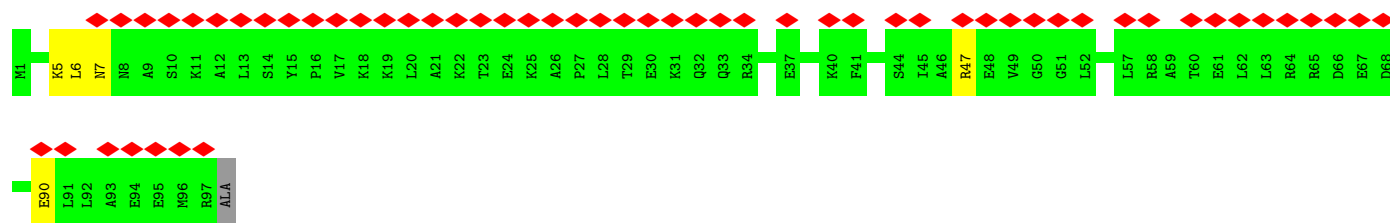


- Molecule 18: S60 ribosomal protein L10



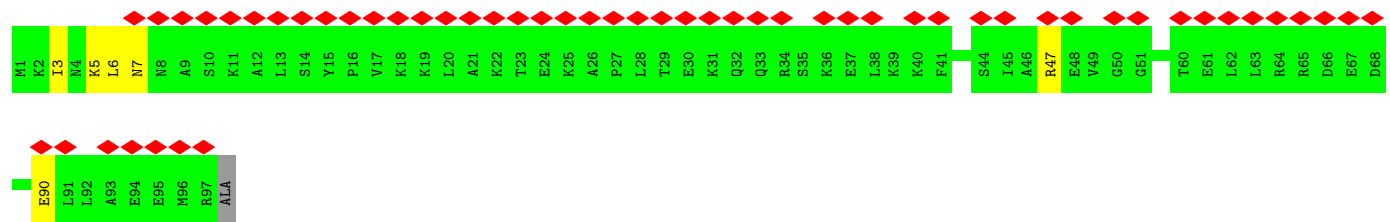
- Molecule 19: 60S ribosomal protein L36





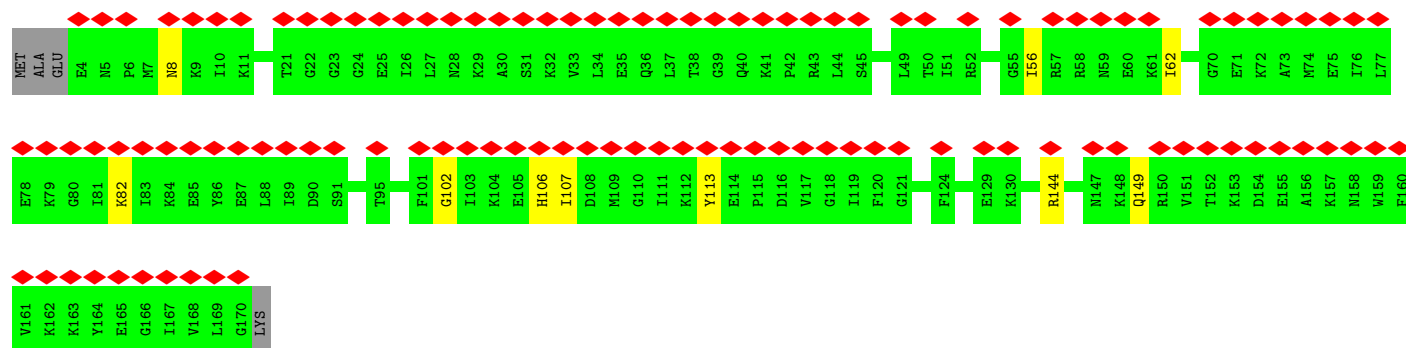
- Molecule 19: 60S ribosomal protein L36

Chain KII: 56% 93% 6% •



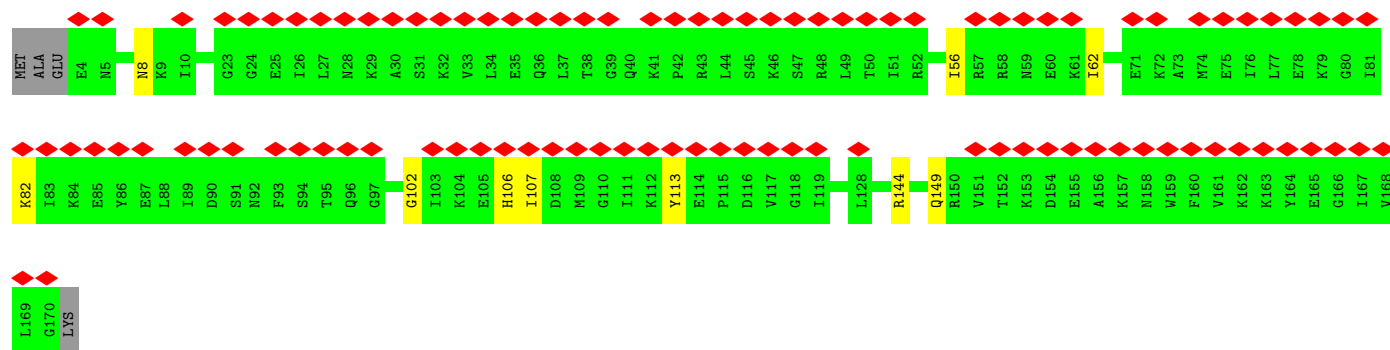
- Molecule 20: 60S ribosomal protein L11

Chain LJ0: 65% 92% 6% •

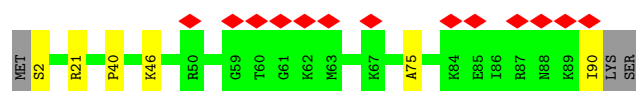


- Molecule 20: 60S ribosomal protein L11

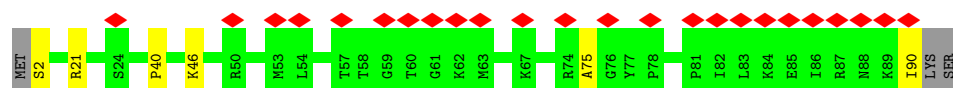
Chain KJ0: 58% 92% 6% •



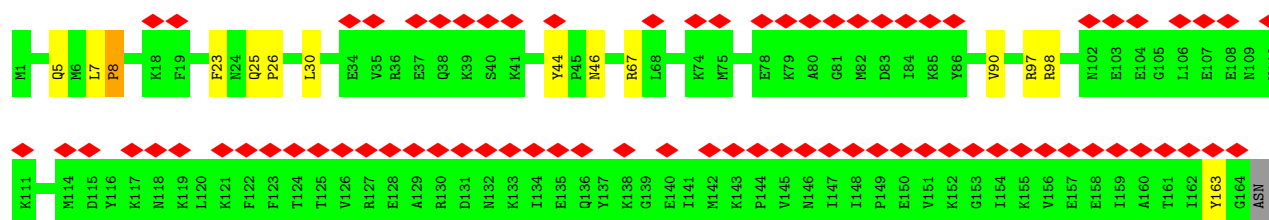
- Molecule 21: 60S ribosomal protein L37



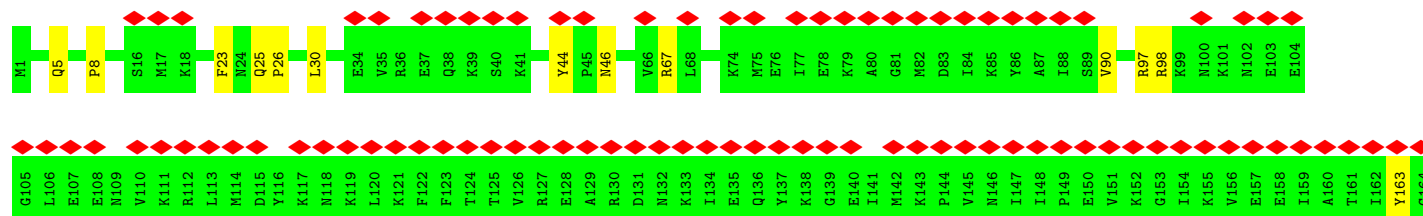
- Molecule 21: 60S ribosomal protein L37



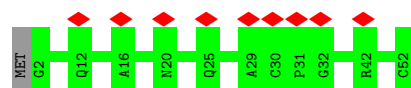
- Molecule 22: 60S ribosomal protein L13



- Molecule 22: 60S ribosomal protein L13



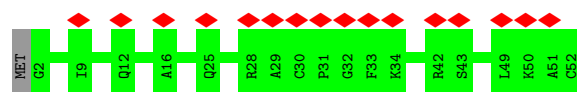
- Molecule 23: 60S ribosomal protein L39



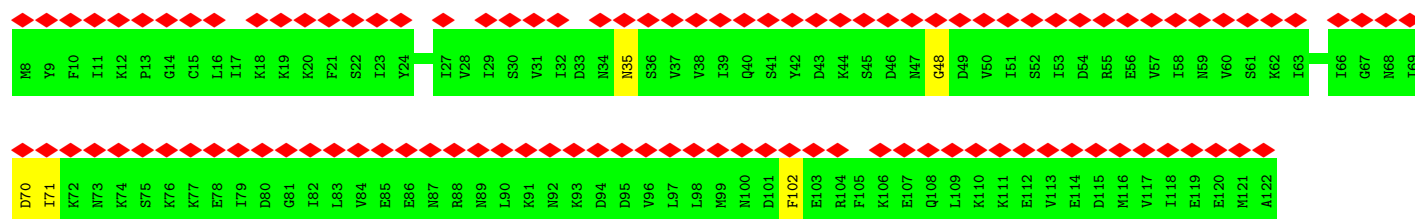
- Molecule 23: 60S ribosomal protein L39







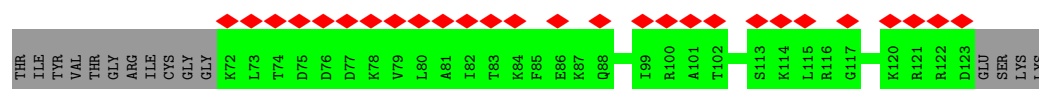
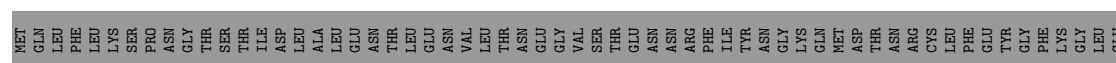
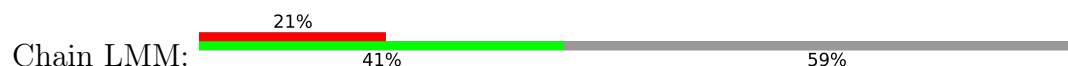
• Molecule 24: Transposase



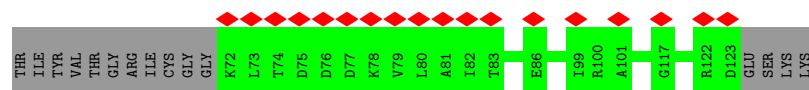
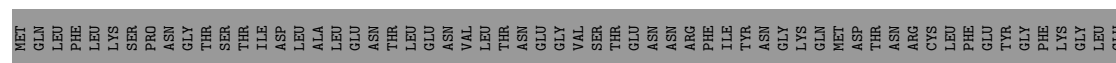
• Molecule 24: Transposase



• Molecule 25: Ubiquitin



• Molecule 25: Ubiquitin



• Molecule 26: Ribosomal protein L15

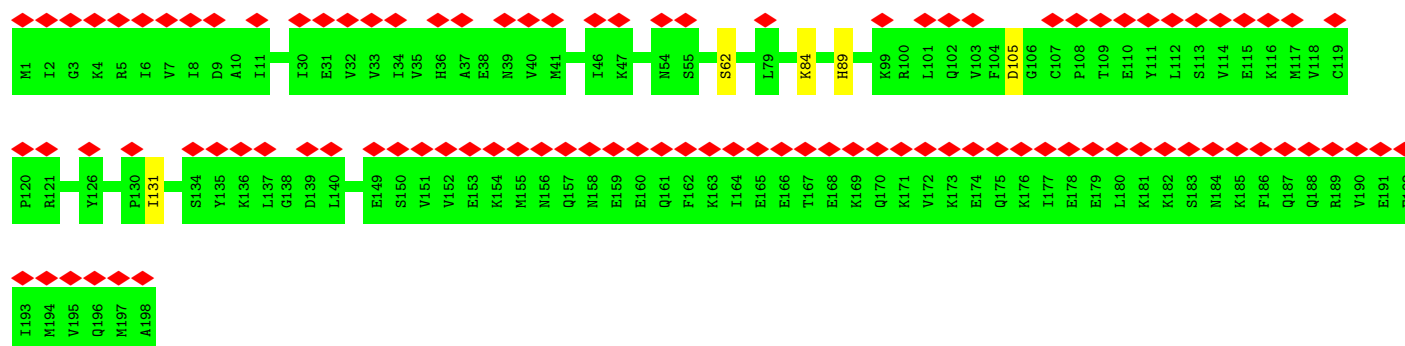




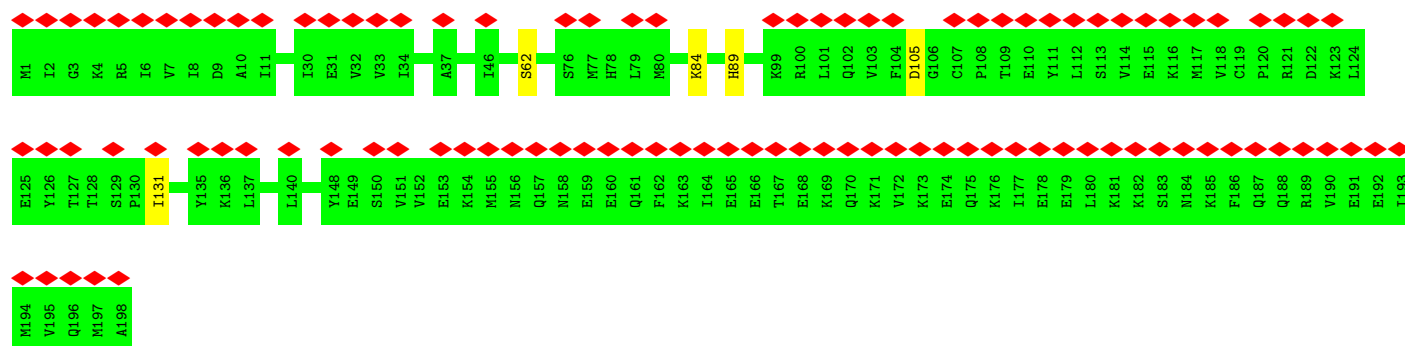
- Molecule 26: Ribosomal protein L15



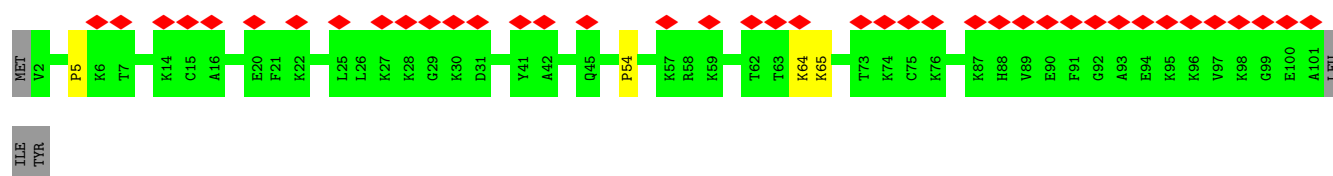
- Molecule 27: Ribosomal protein L13A



- Molecule 27: Ribosomal protein L13A

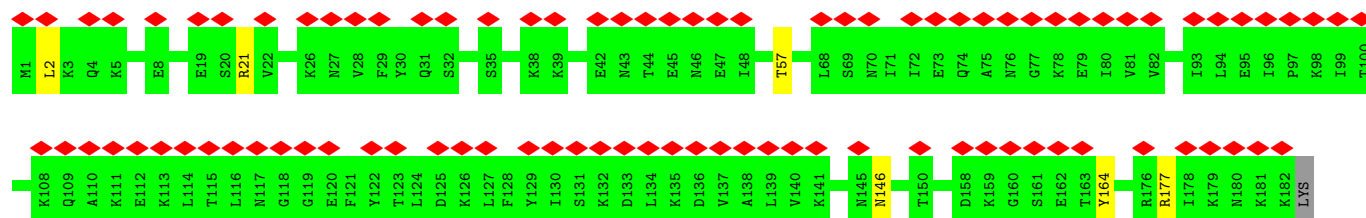


- Molecule 28: 60S ribosomal protein L44



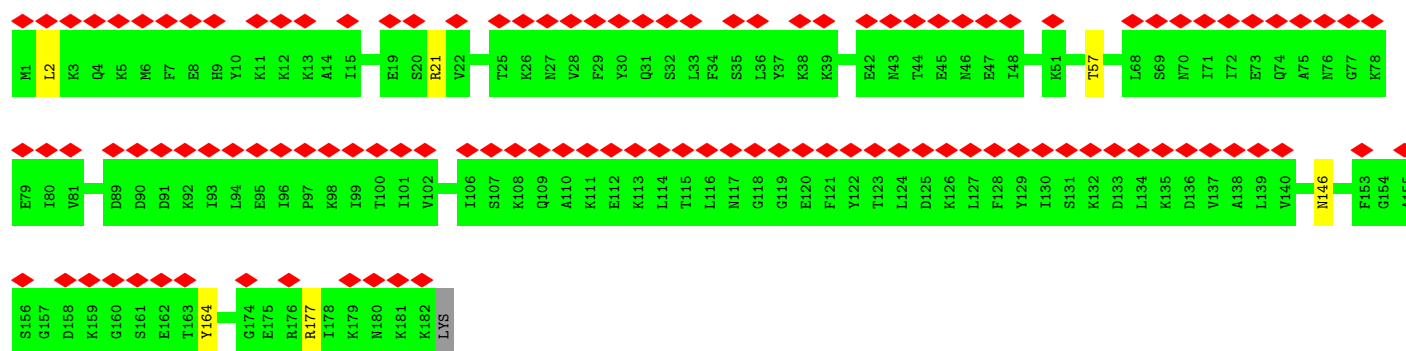


Chain LQ0: 



- Molecule 31: 60S ribosomal protein L18

Chain KQ0: 



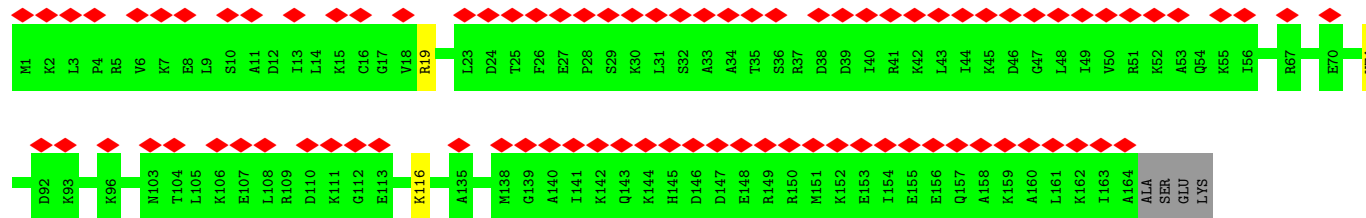
- Molecule 32: 60S ribosomal protein L19

Chain LR0: 



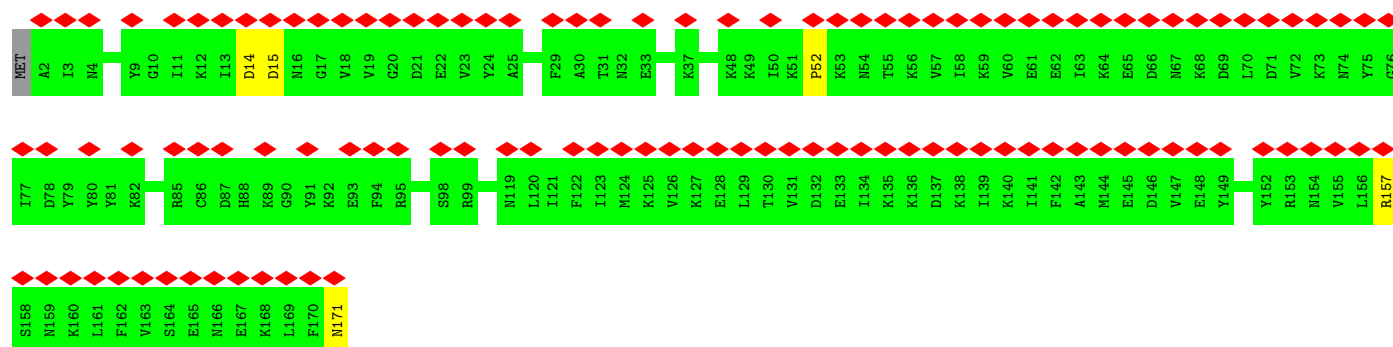
- Molecule 32: 60S ribosomal protein L19

Chain KR0: 

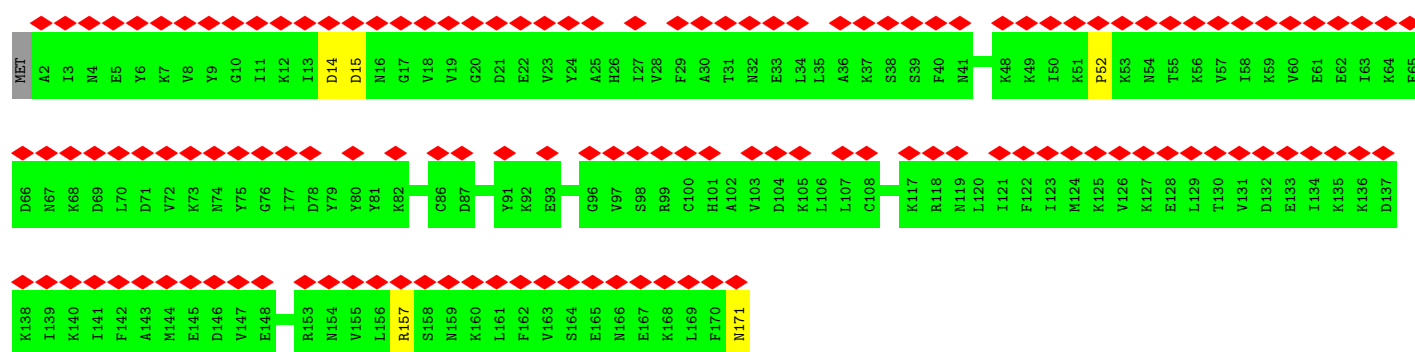
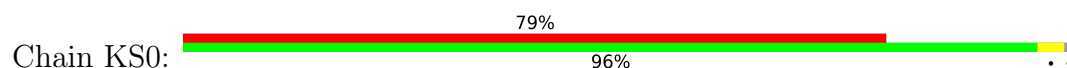


- Molecule 33: 60S ribosomal protein L20

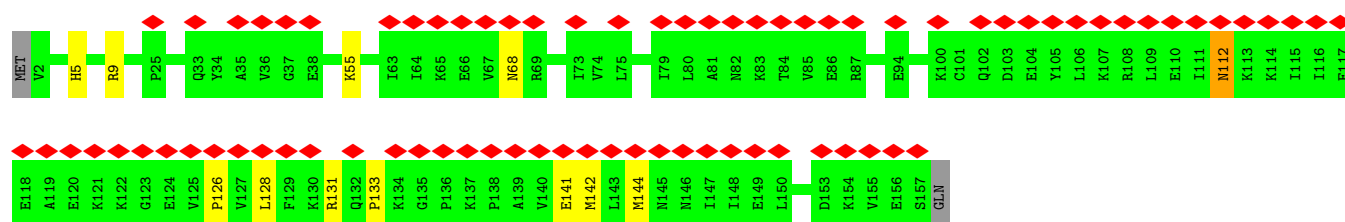
Chain LS0: 



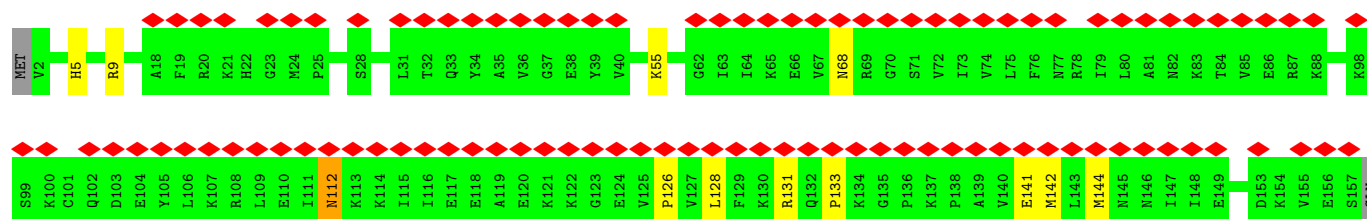
• Molecule 33: 60S ribosomal protein L20



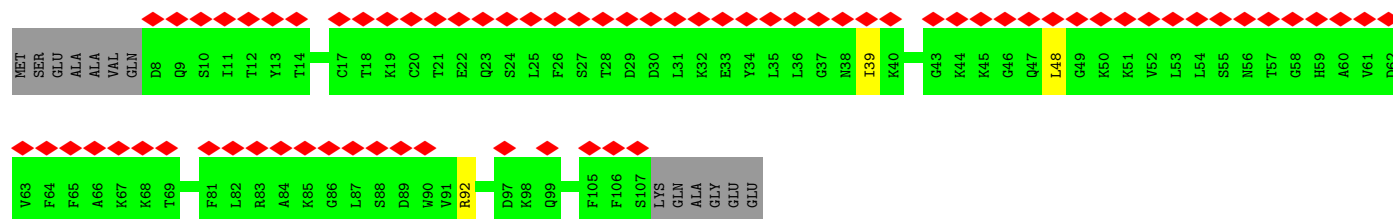
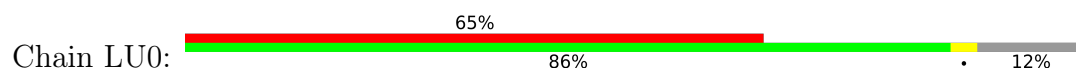
• Molecule 34: 60s ribosomal protein L21



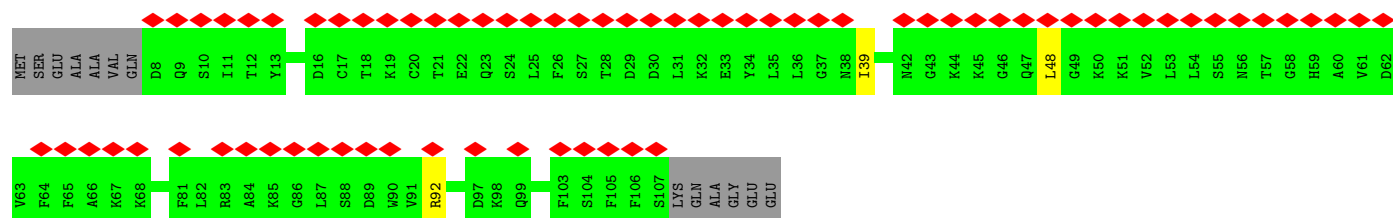
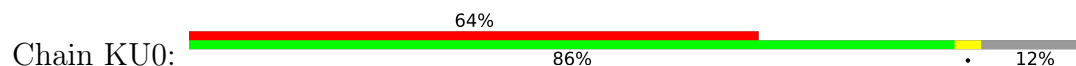
• Molecule 34: 60s ribosomal protein L21



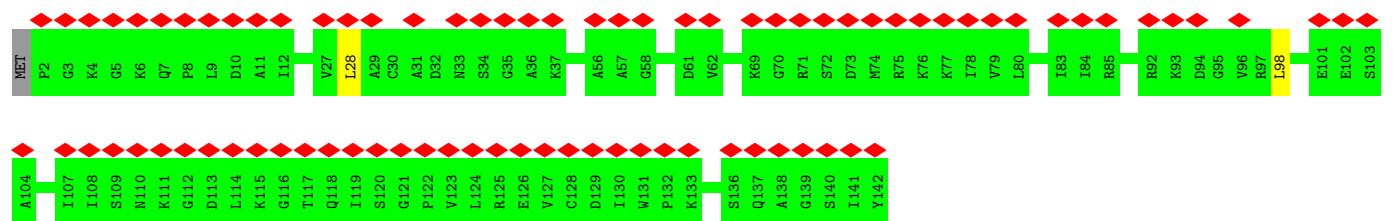
• Molecule 35: 60S ribosomal protein L22



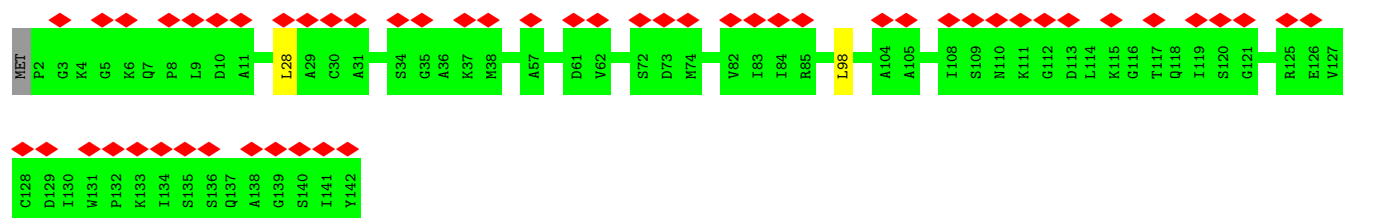
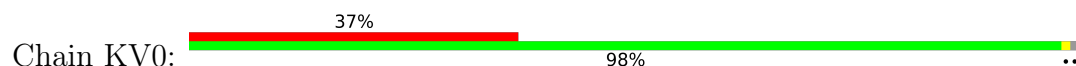
- Molecule 35: 60S ribosomal protein L22



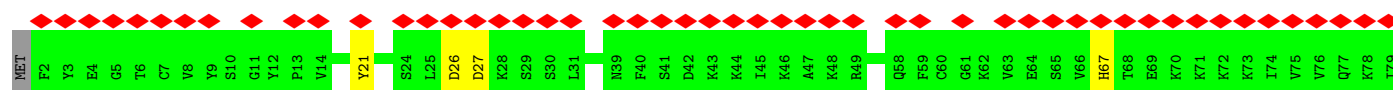
- Molecule 36: Ribosomal protein L23

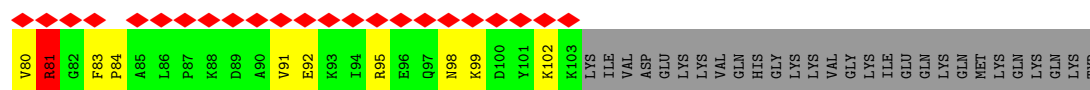


- Molecule 36: Ribosomal protein L23

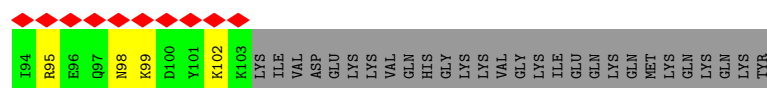
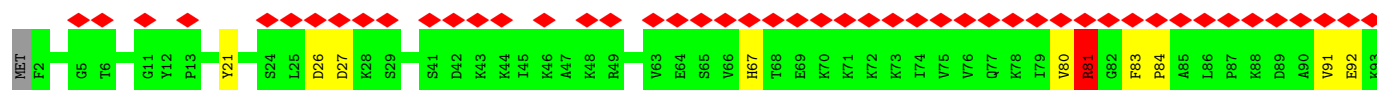
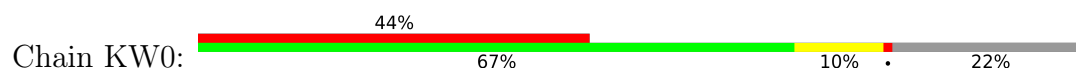


- Molecule 37: Ribosomal protein L24E

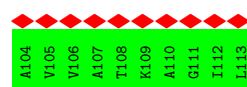
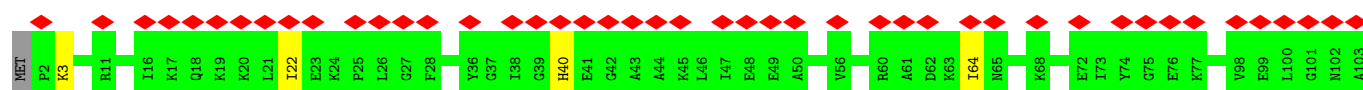




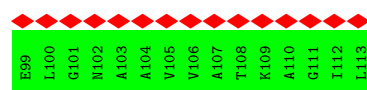
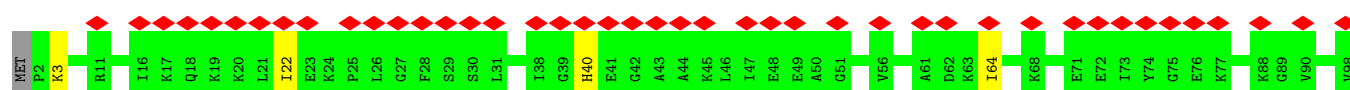
- Molecule 37: Ribosomal protein L24E



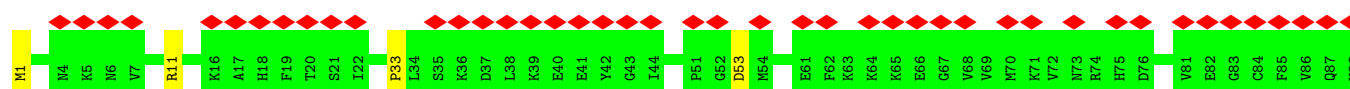
- Molecule 38: 60S ribosomal protein L23a



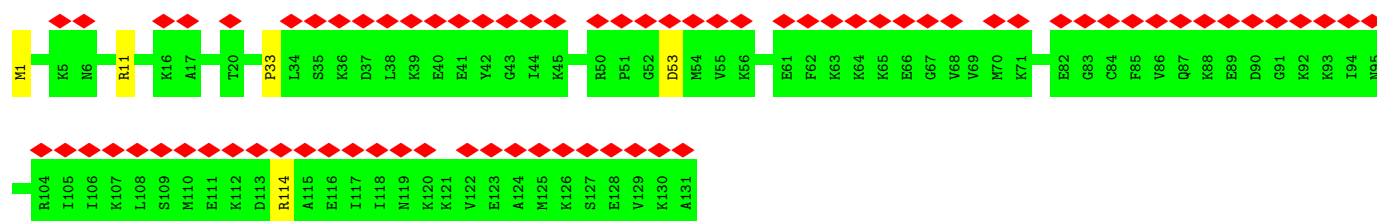
- Molecule 38: 60S ribosomal protein L23a



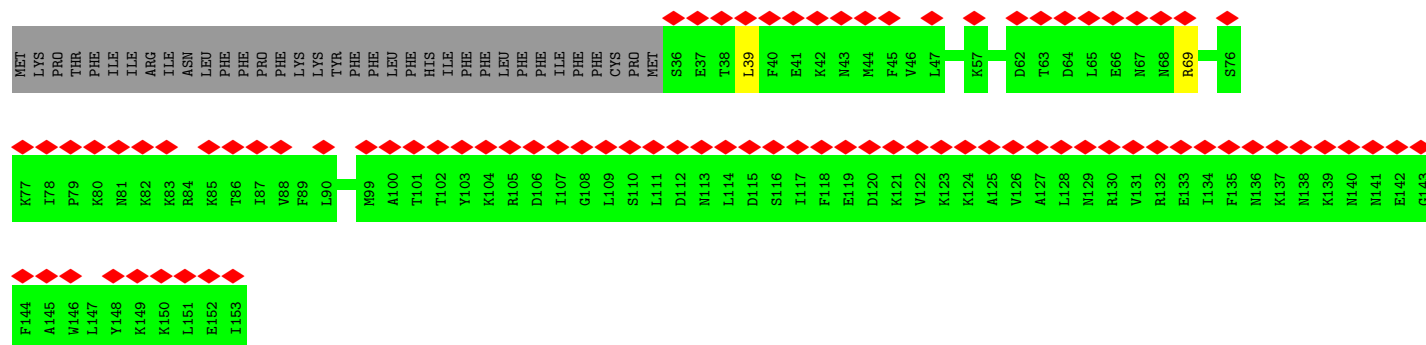
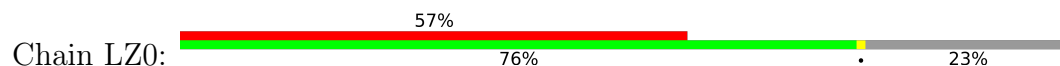
- Molecule 39: 60S ribosomal protein L26



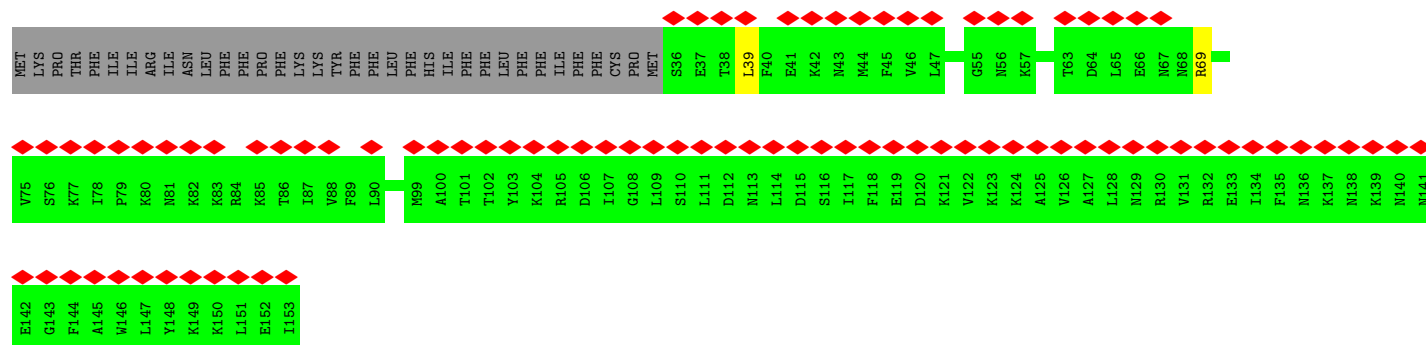
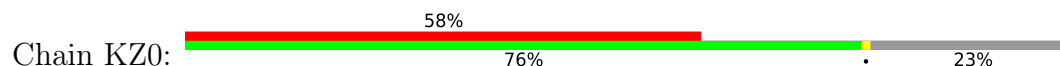
- Molecule 39: 60S ribosomal protein L26



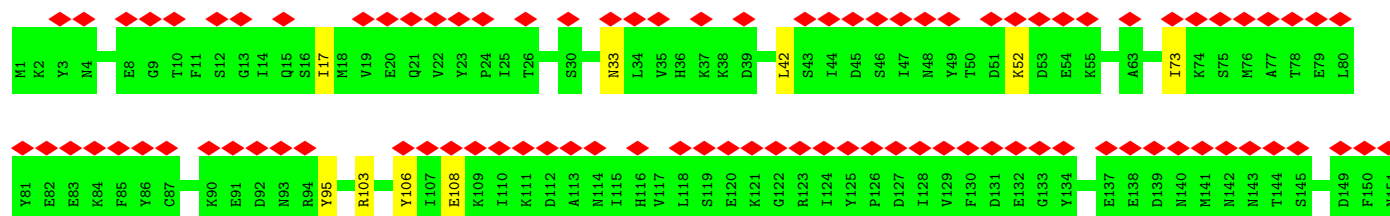
• Molecule 40: 60S ribosomal protein L27



• Molecule 40: 60S ribosomal protein L27

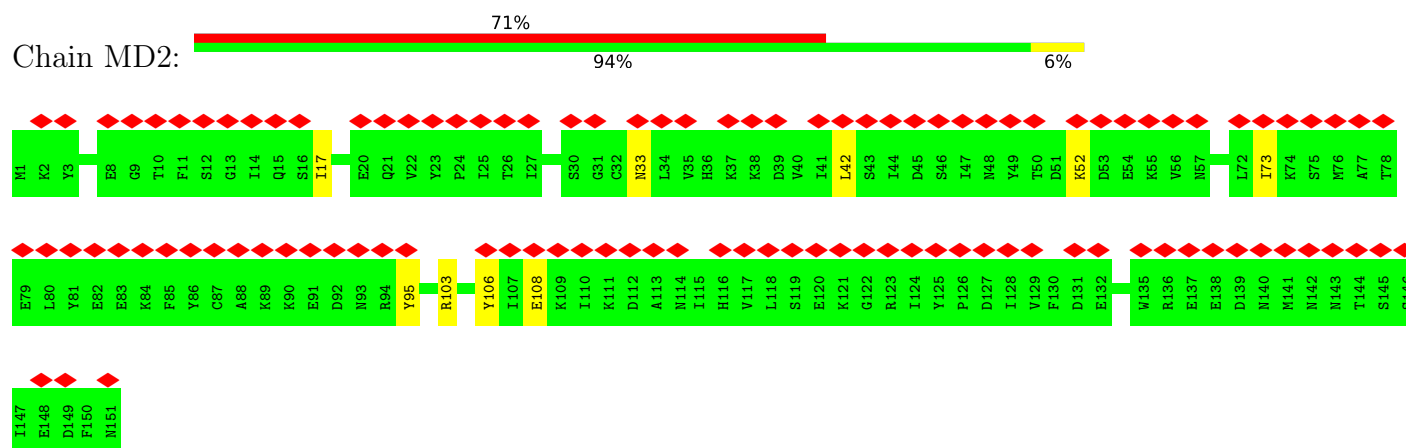


• Molecule 41: DNL-type domain-containing protein

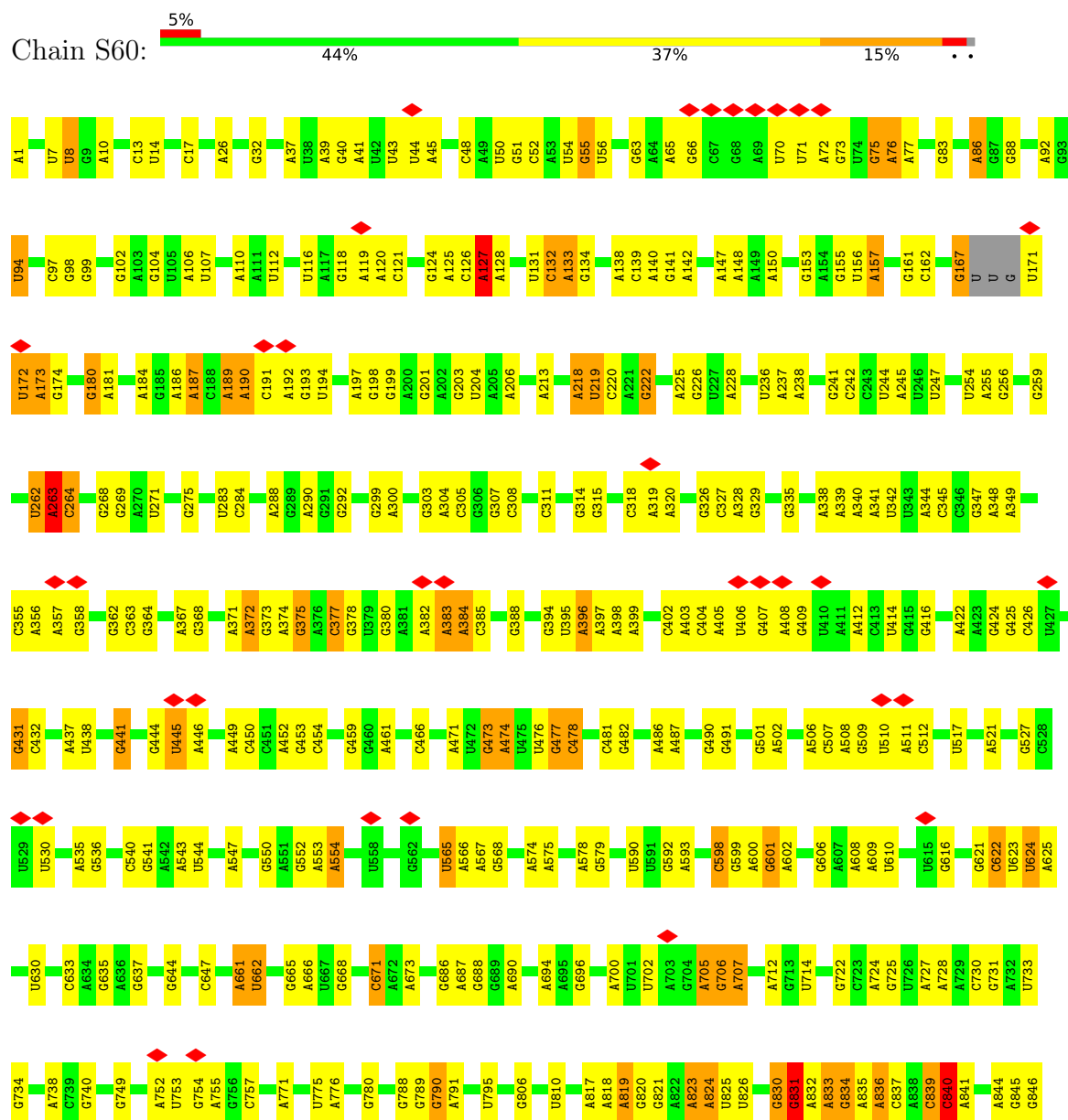


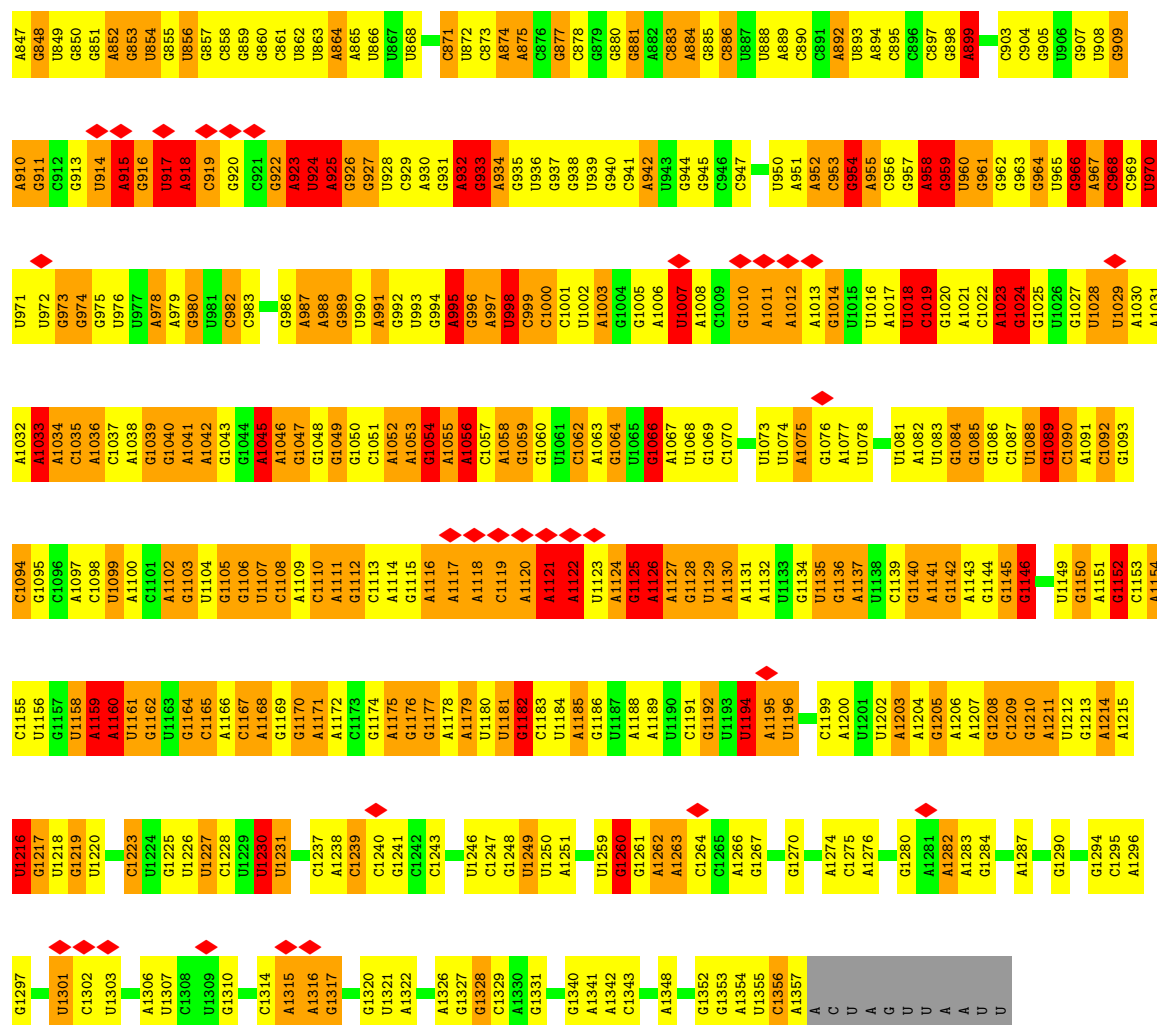


- Molecule 41: DNL-type domain-containing protein

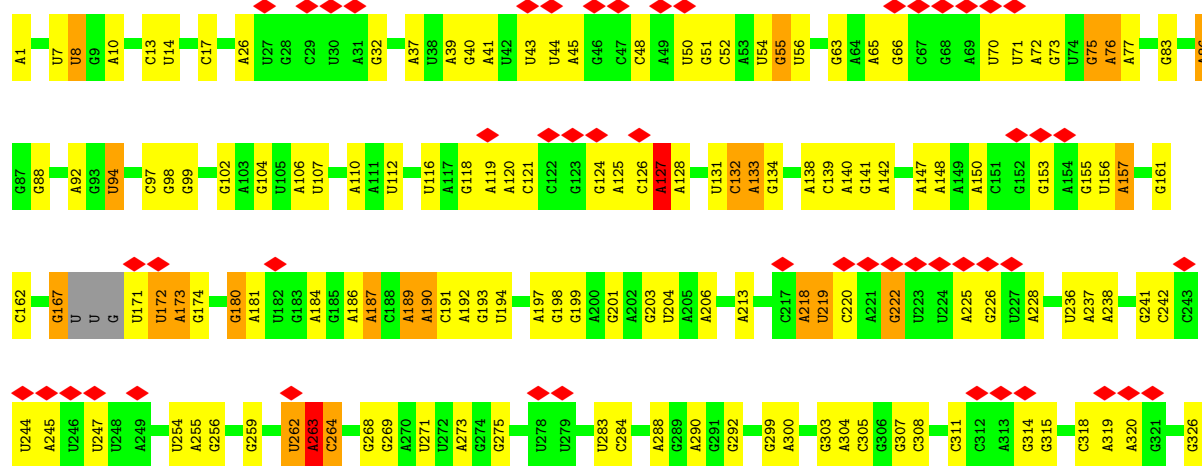


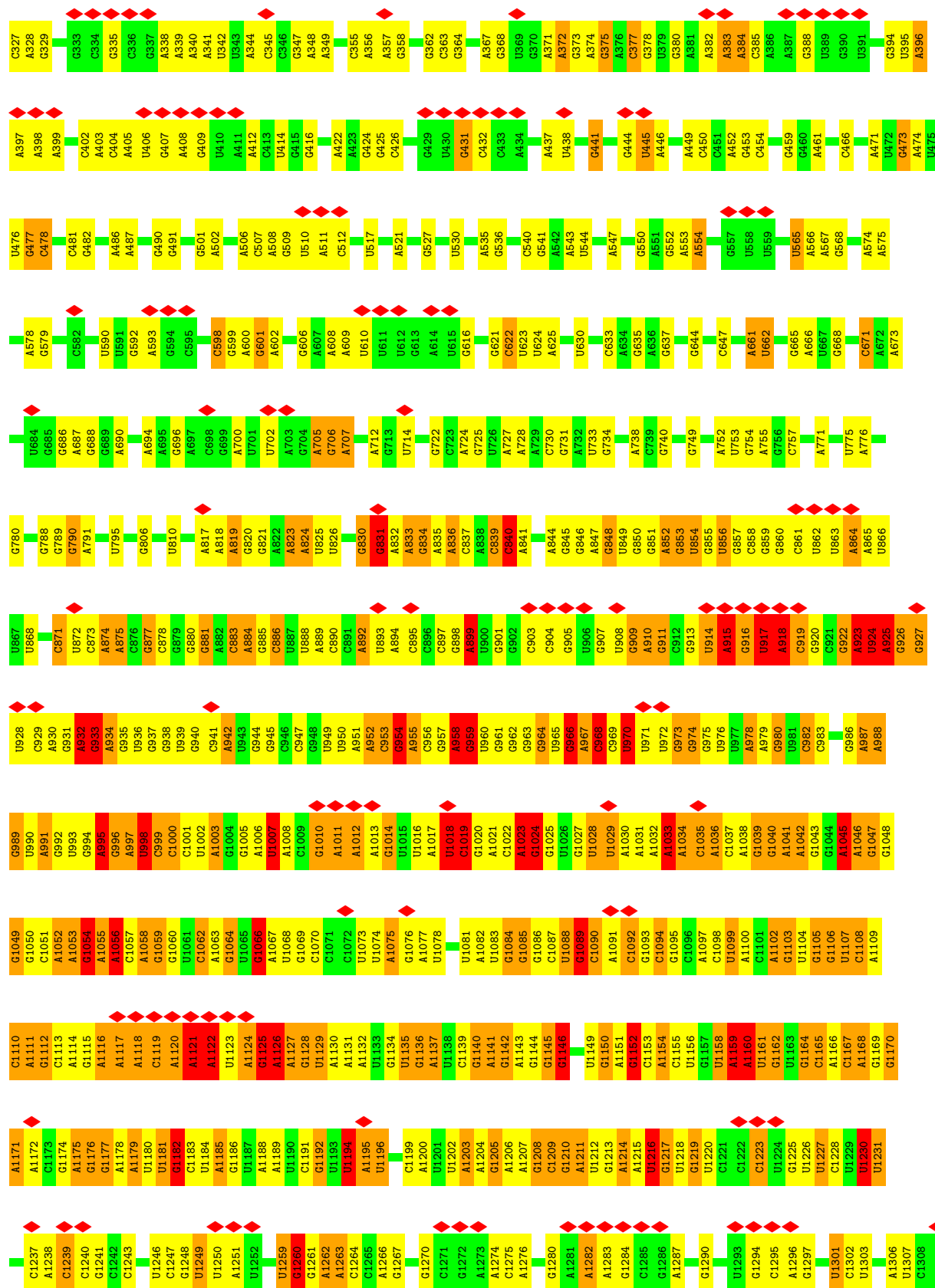
- Molecule 42: RNA 16S





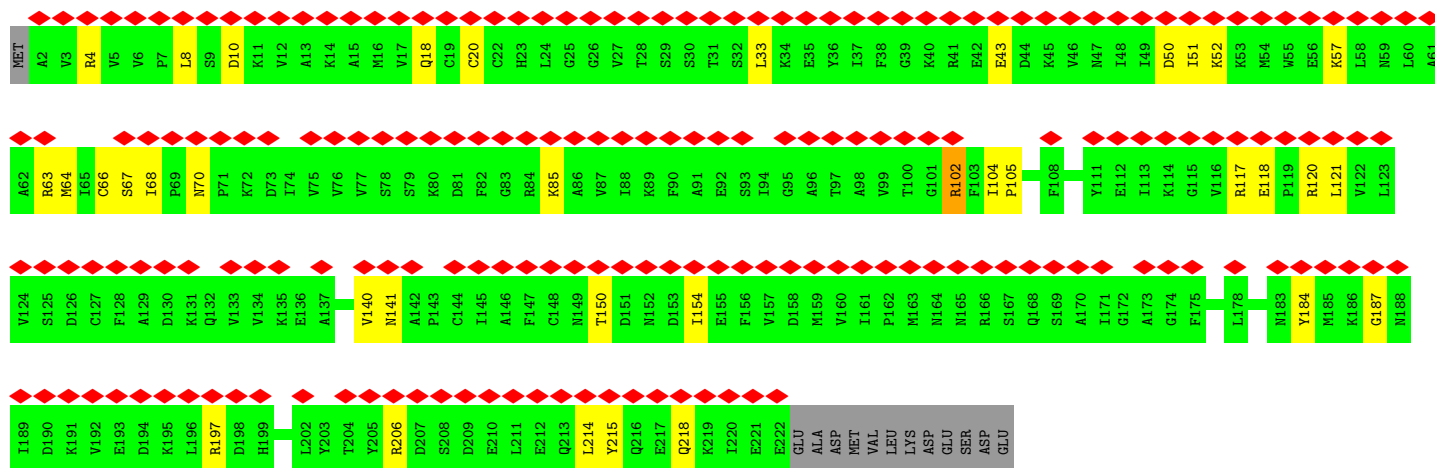
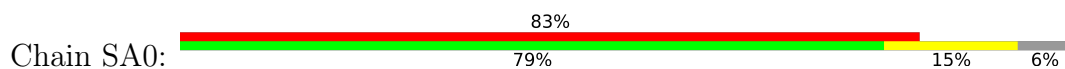
• Molecule 42: RNA 16S



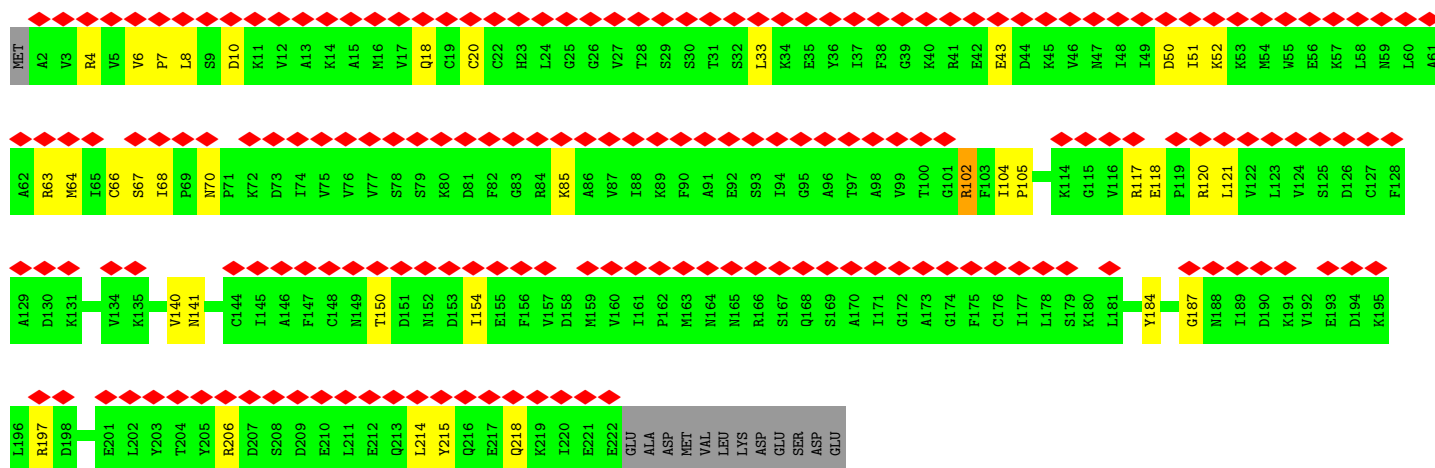
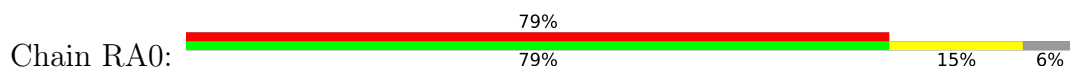




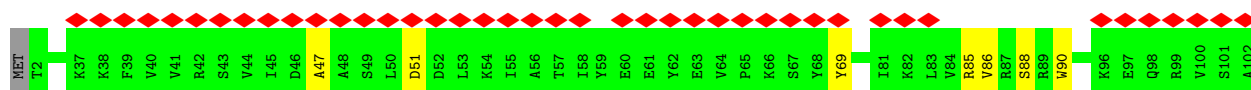
- Molecule 43: 40S ribosomal protein S0



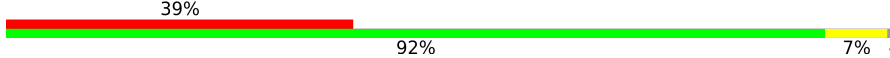
- Molecule 43: 40S ribosomal protein S0

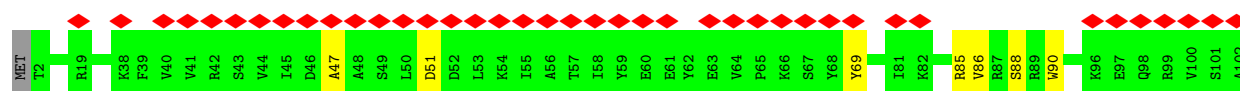


- Molecule 44: 40S ribosomal protein S26



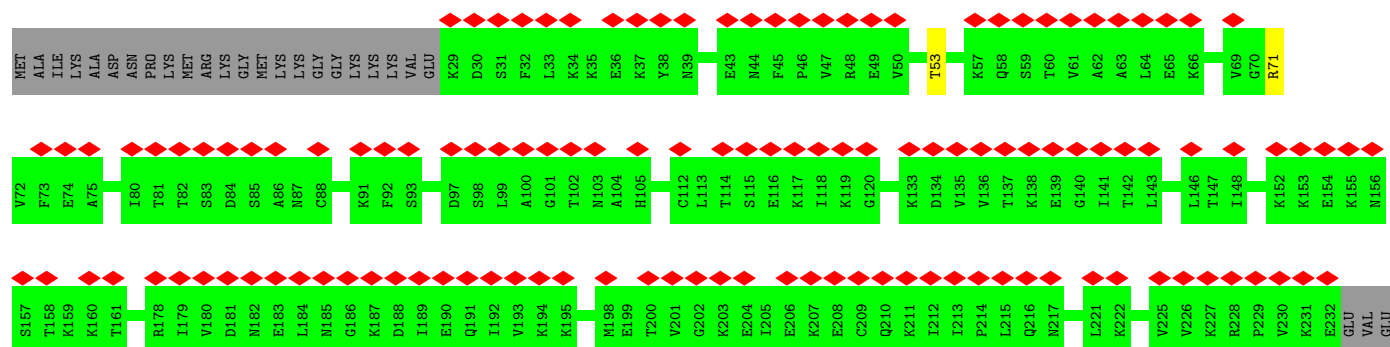
- Molecule 44: 40S ribosomal protein S26

Chain RAA: 



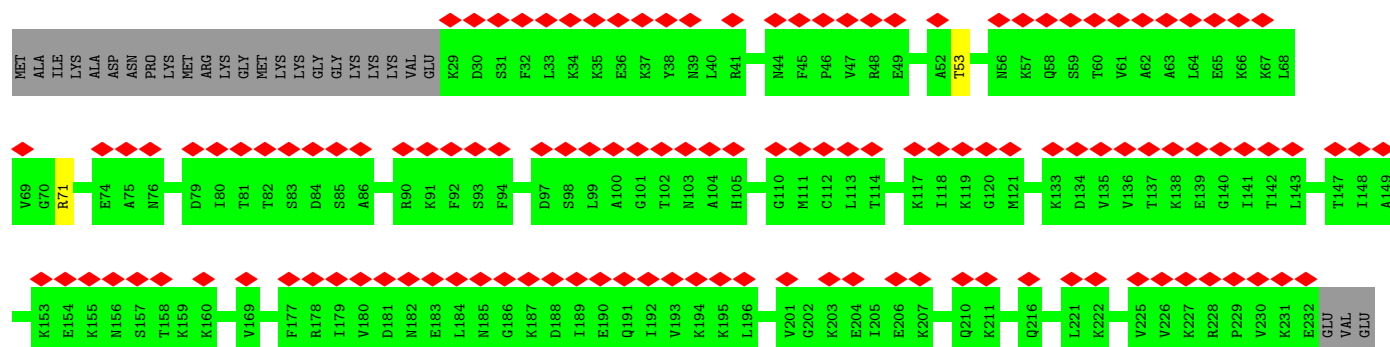
• Molecule 45: 40S ribosomal protein S1

Chain SB0: 



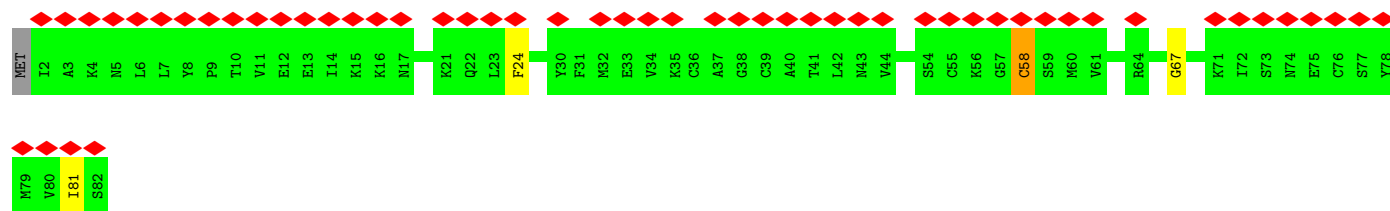
• Molecule 45: 40S ribosomal protein S1

Chain RB0: 



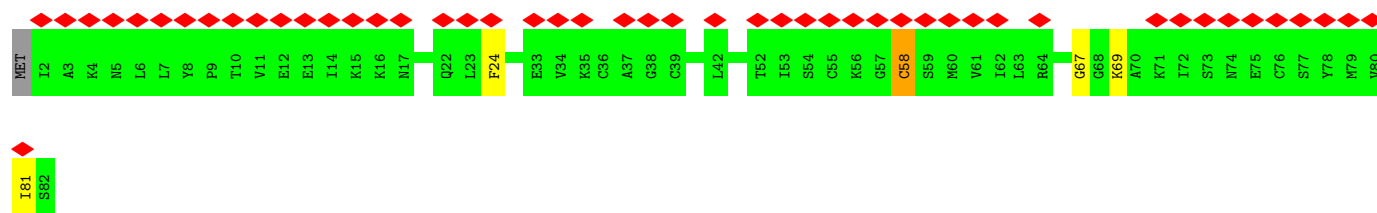
• Molecule 46: 40S ribosomal protein S27

Chain SBB: 

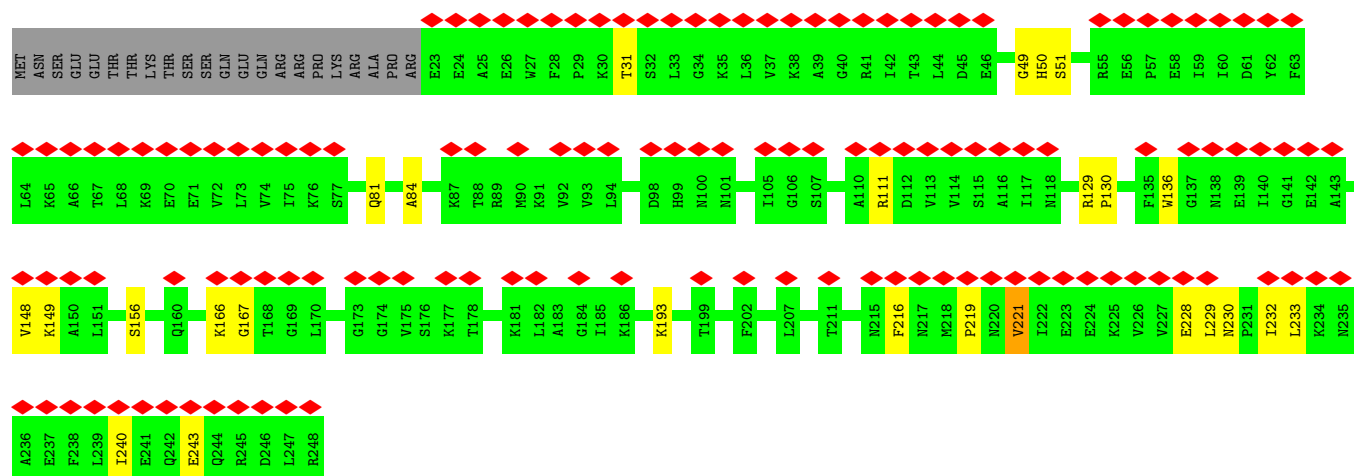
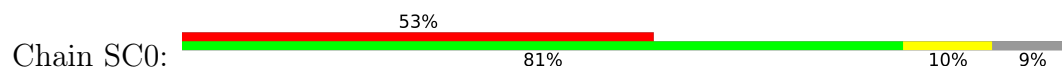


• Molecule 46: 40S ribosomal protein S27

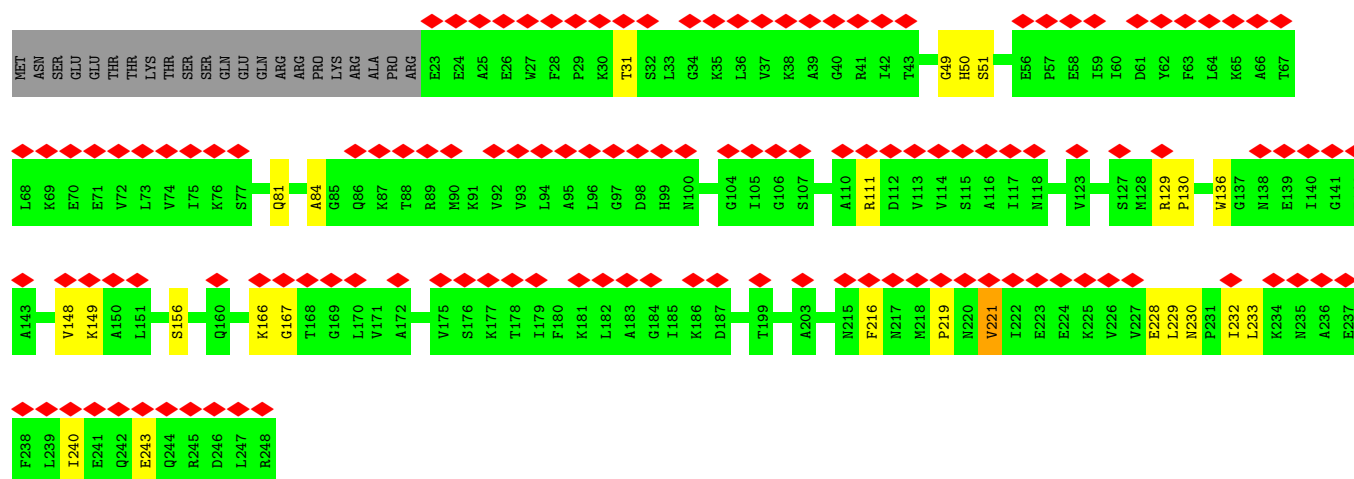
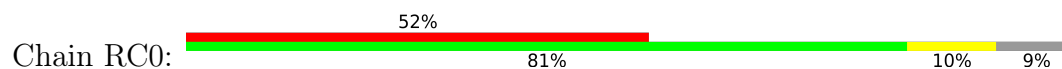
Chain RBB: 



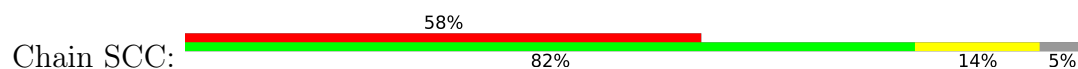
• Molecule 47: 40S ribosomal protein S2




• Molecule 47: 40S ribosomal protein S2

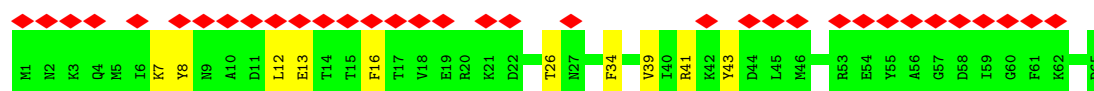


• Molecule 48: 40S ribosomal protein S28




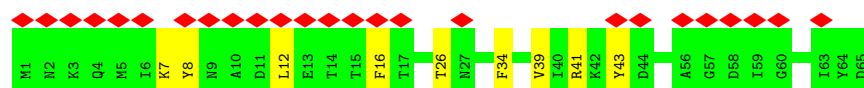


Chain SDD: 




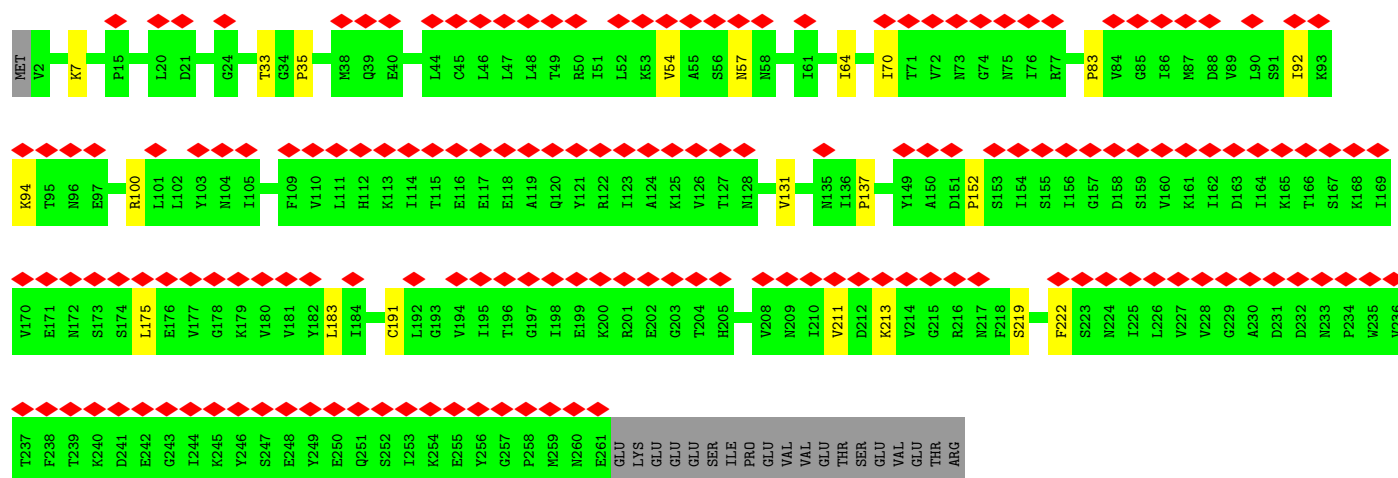
- Molecule 50: 40S ribosomal protein S29

Chain RDD: 



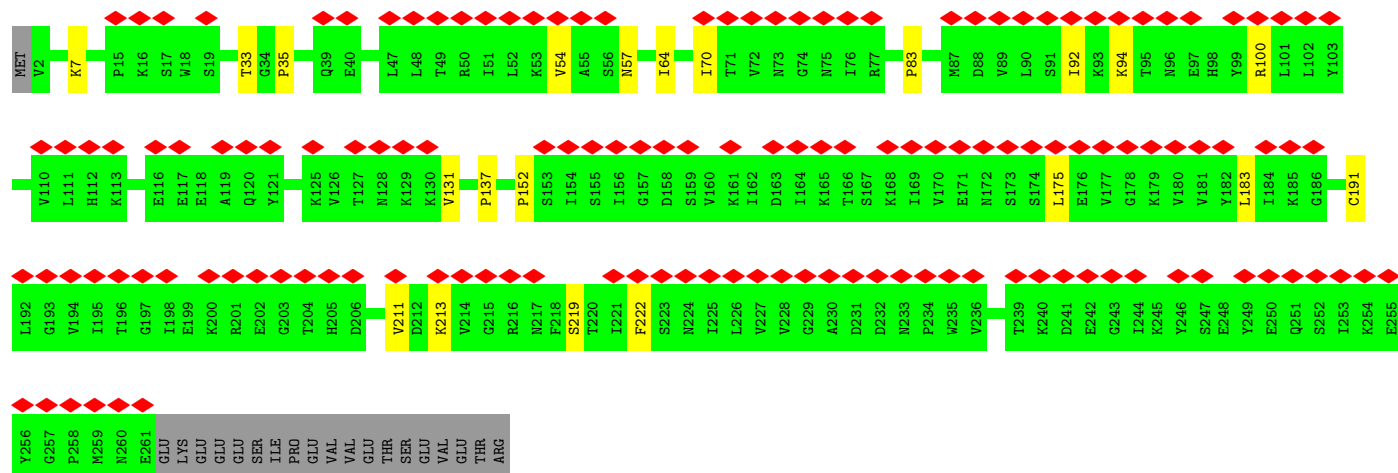
- Molecule 51: 40S ribosomal protein S4

Chain SE0: 



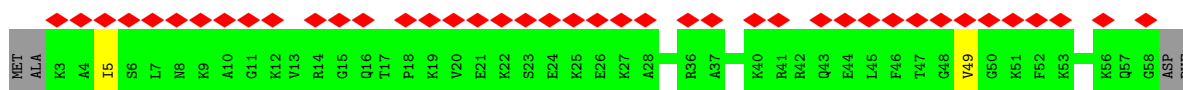
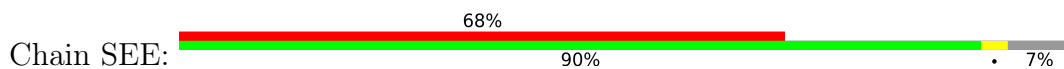
- Molecule 51: 40S ribosomal protein S4

Chain RE0: 

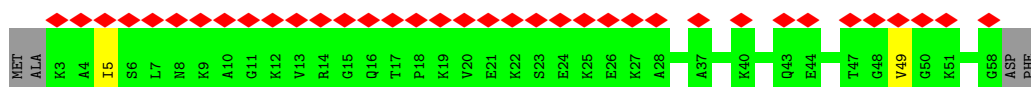




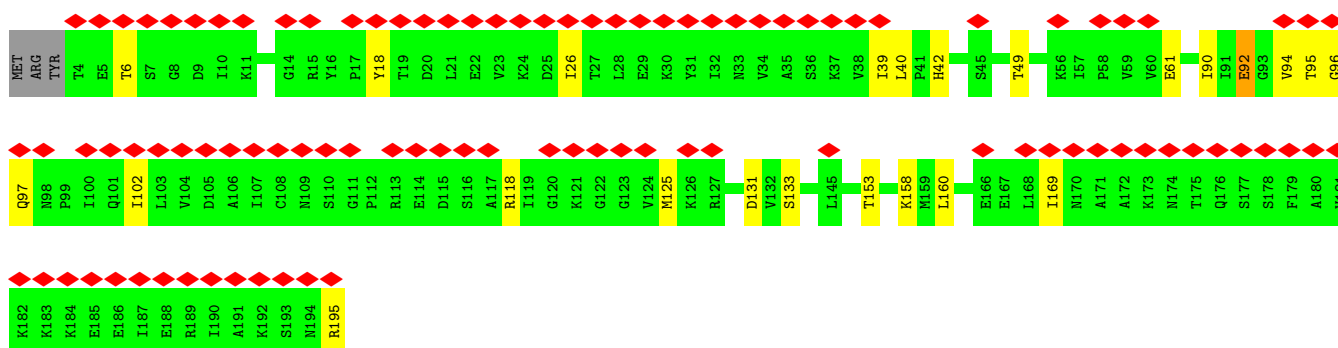
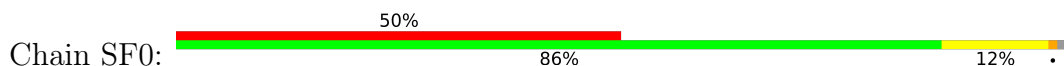
- Molecule 52: 40S ribosomal protein S30



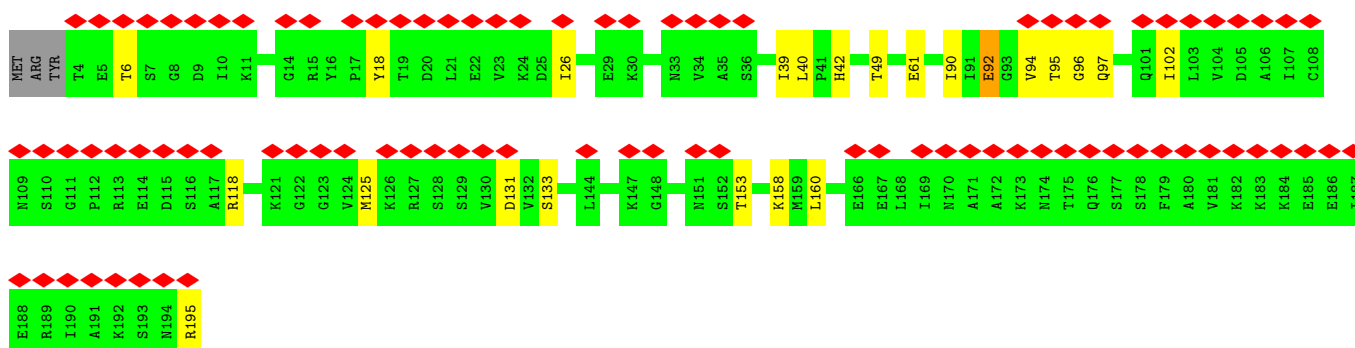
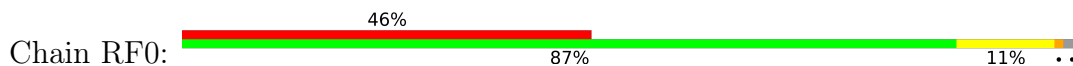
- Molecule 52: 40S ribosomal protein S30



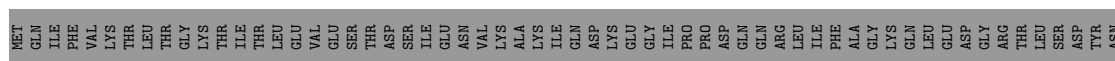
- Molecule 53: 40S ribosomal protein S5



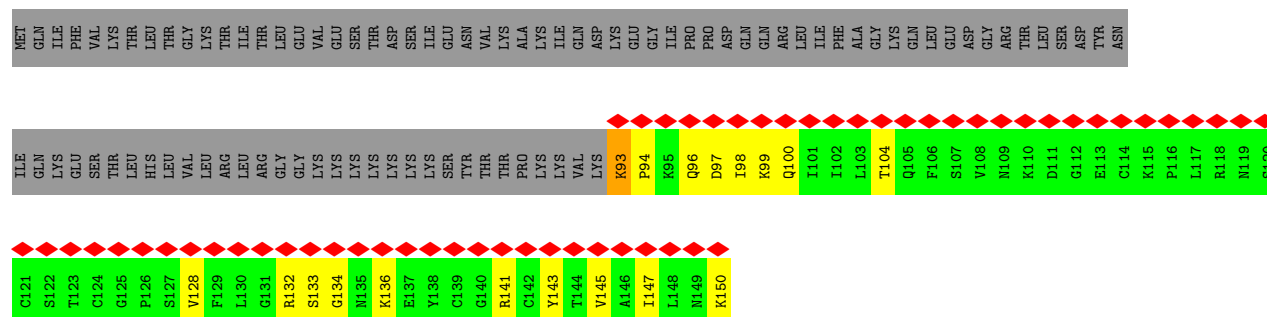
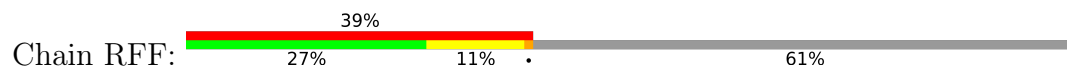
- Molecule 53: 40S ribosomal protein S5



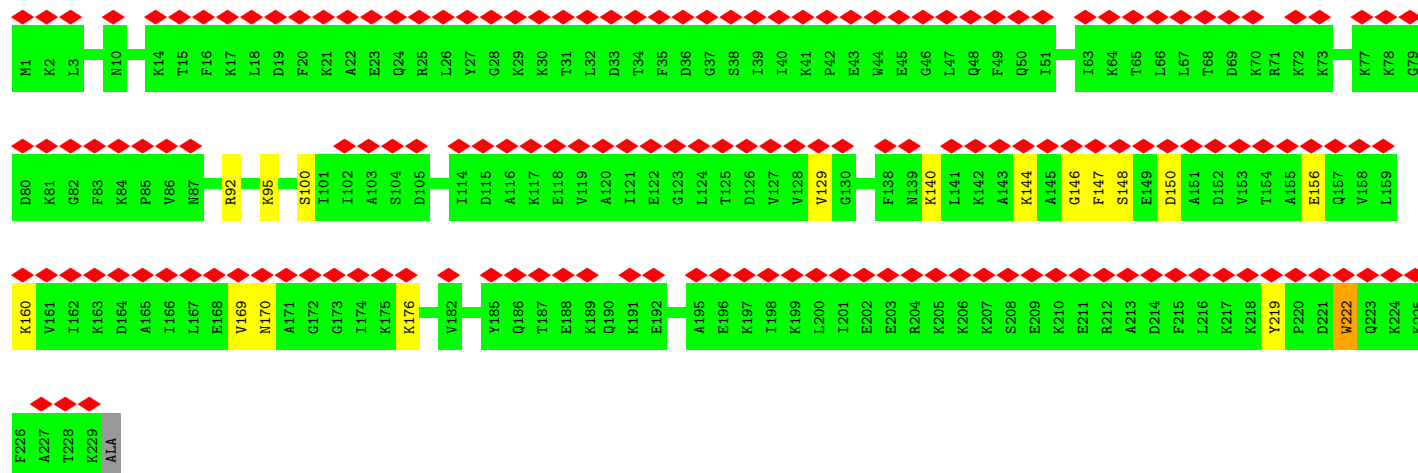
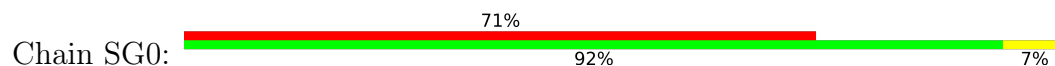
- Molecule 54: Ubiquitin/40s ribosomal protein S27a fusion



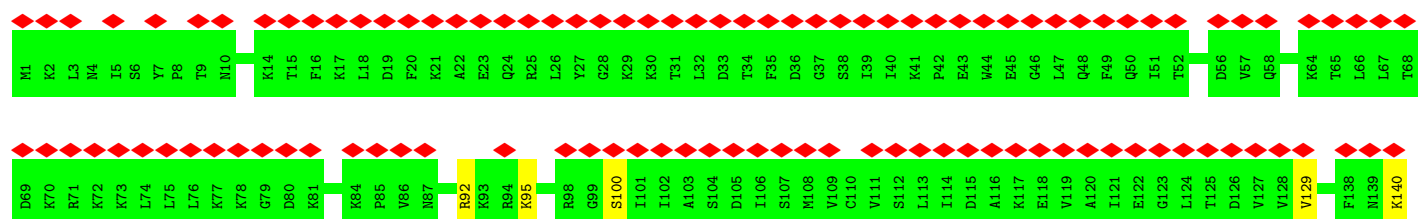
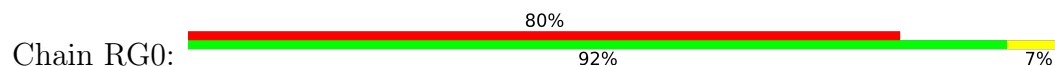
- Molecule 54: Ubiquitin/40s ribosomal protein S27a fusion

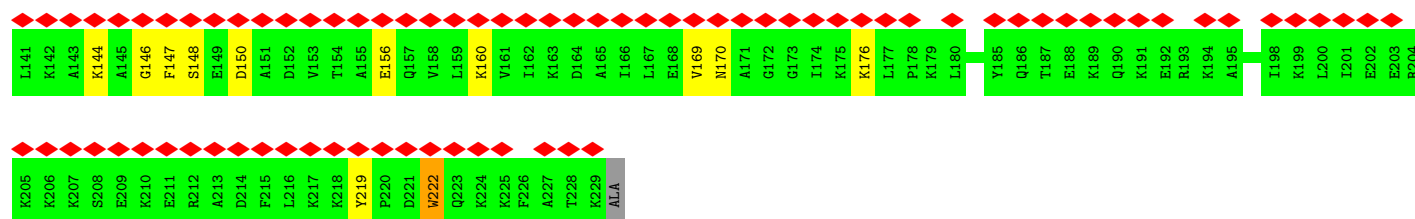


- Molecule 55: 40S ribosomal protein S6



- Molecule 55: 40S ribosomal protein S6





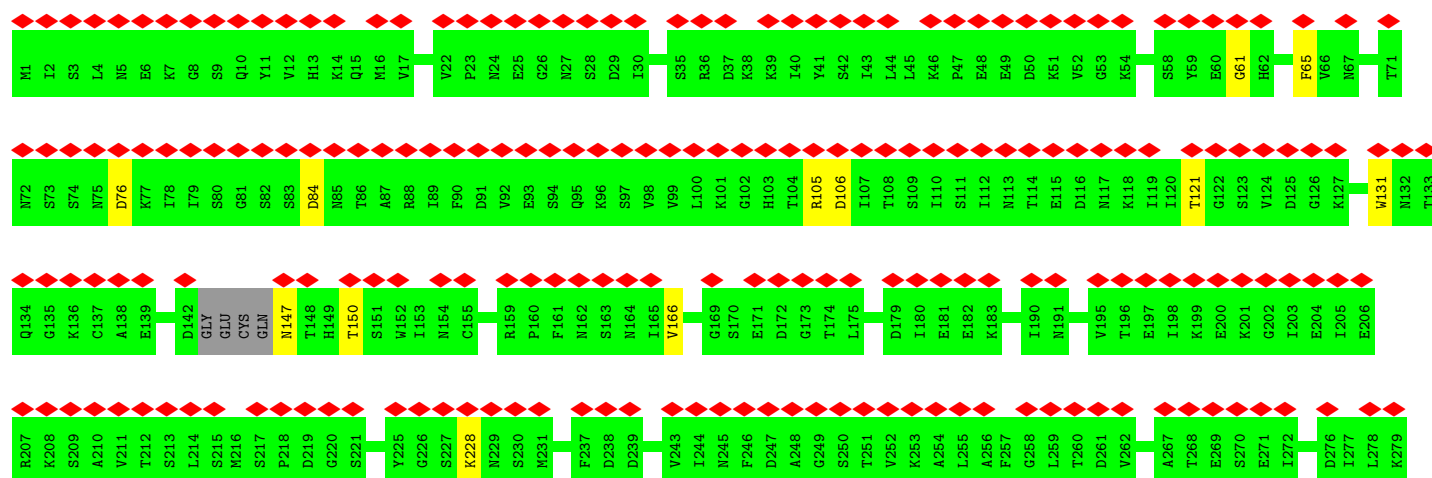
• Molecule 56: Guanine nucleotide binding protein beta subunit

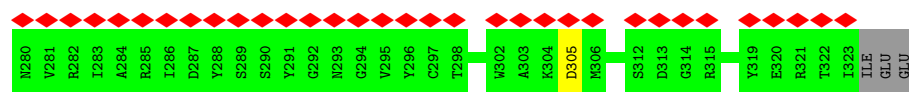
Chain SGG:



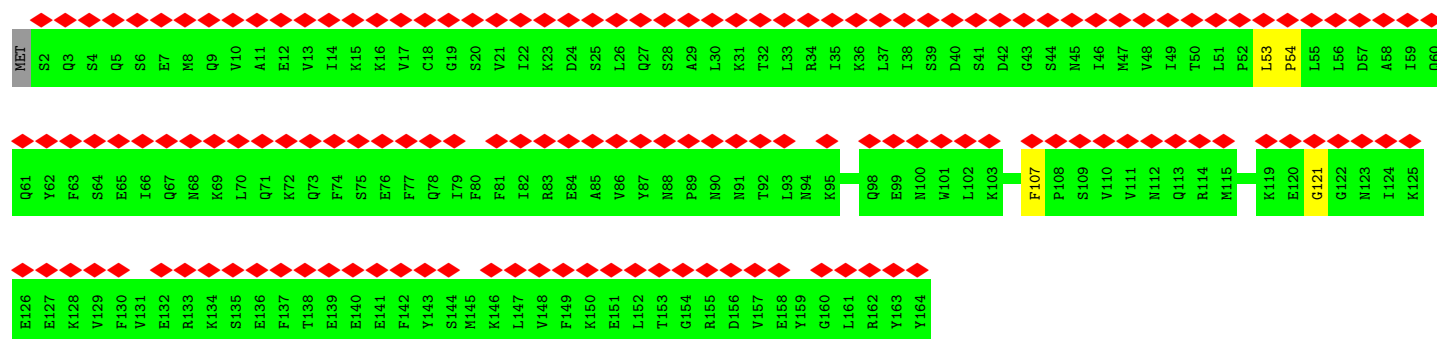
• Molecule 56: Guanine nucleotide binding protein beta subunit

Chain RGC:

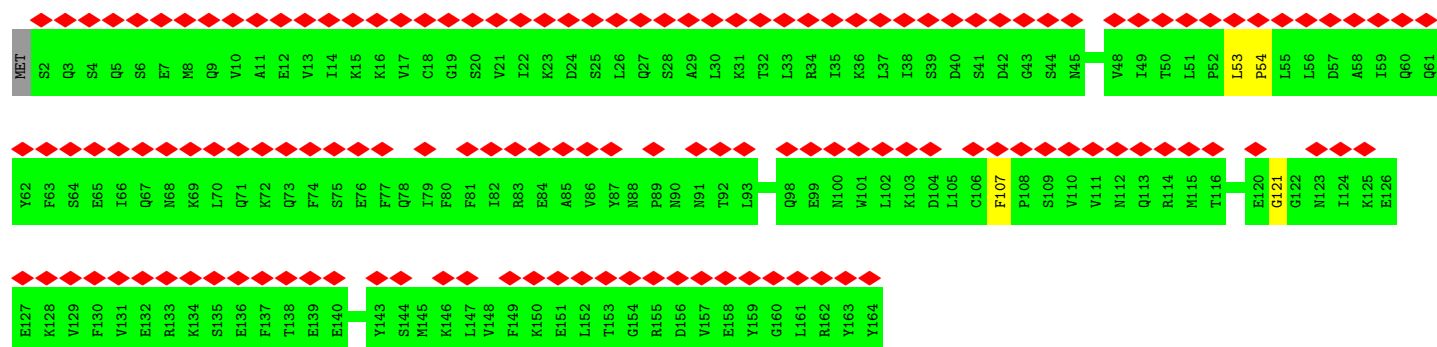




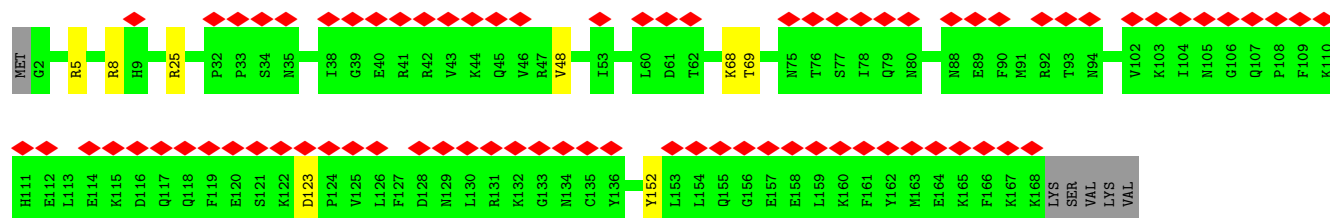
- Molecule 57: 40S ribosomal protein S7



- Molecule 57: 40S ribosomal protein S7

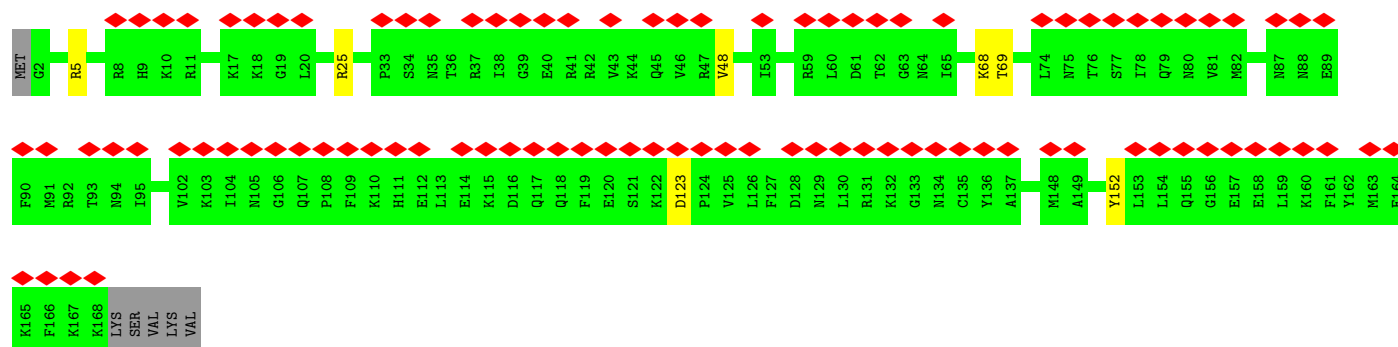


- Molecule 58: 40S ribosomal protein S8



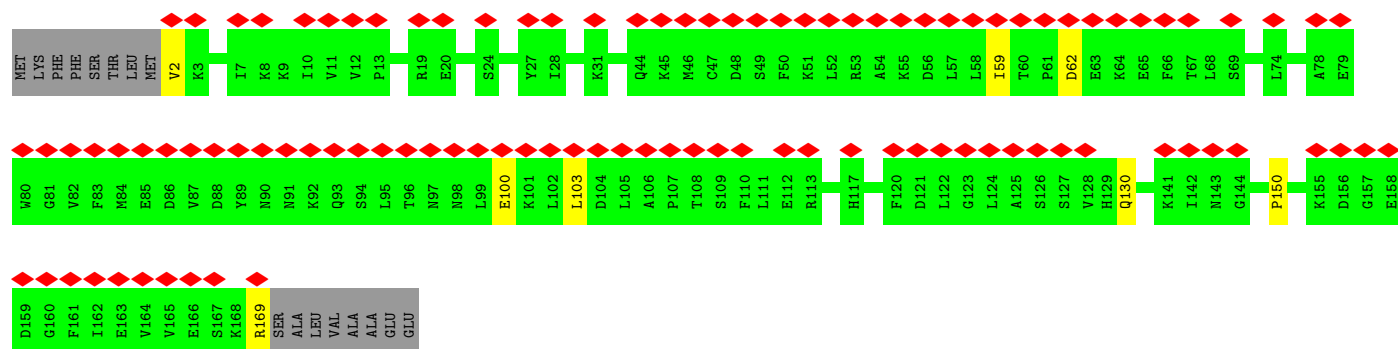
- Molecule 58: 40S ribosomal protein S8





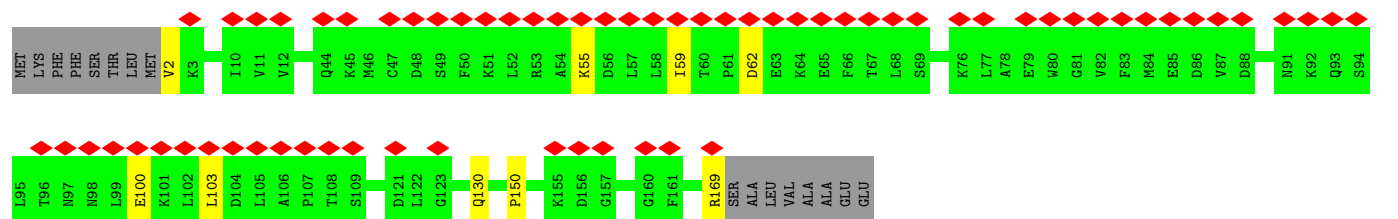
- Molecule 59: 40S ribosomal protein S9

Chain SJ0: 56% 87% 9%



- Molecule 59: 40S ribosomal protein S9

Chain RJ0: 36% 86% 5% 9%




- Molecule 60: 40S ribosomal protein S10

Chain SK0: 76% 75% 7% 18%



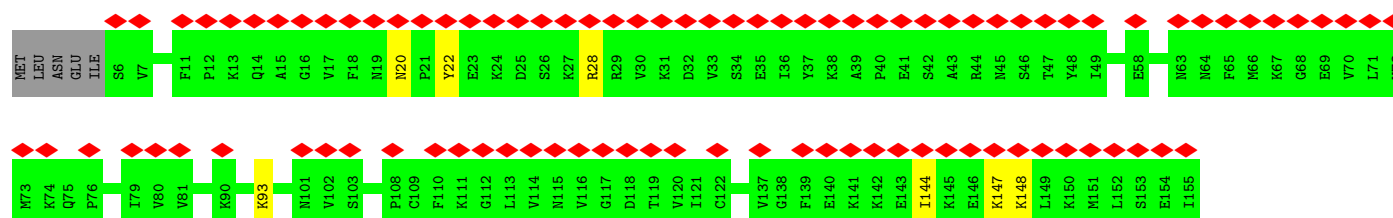
- Molecule 60: 40S ribosomal protein S10

Chain RK0: 



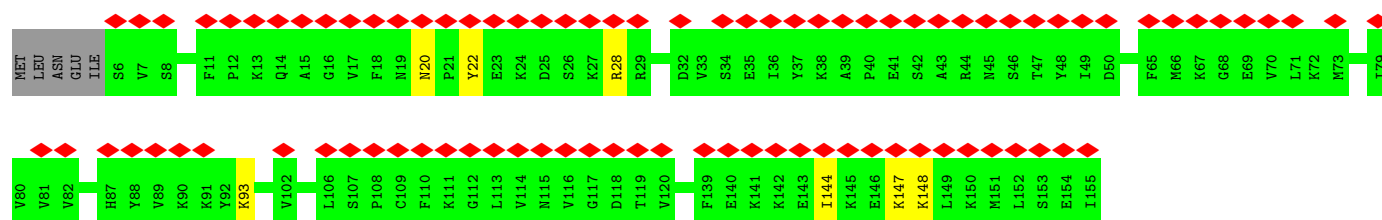
- Molecule 61: 40S ribosomal protein S11

Chain SL0: 




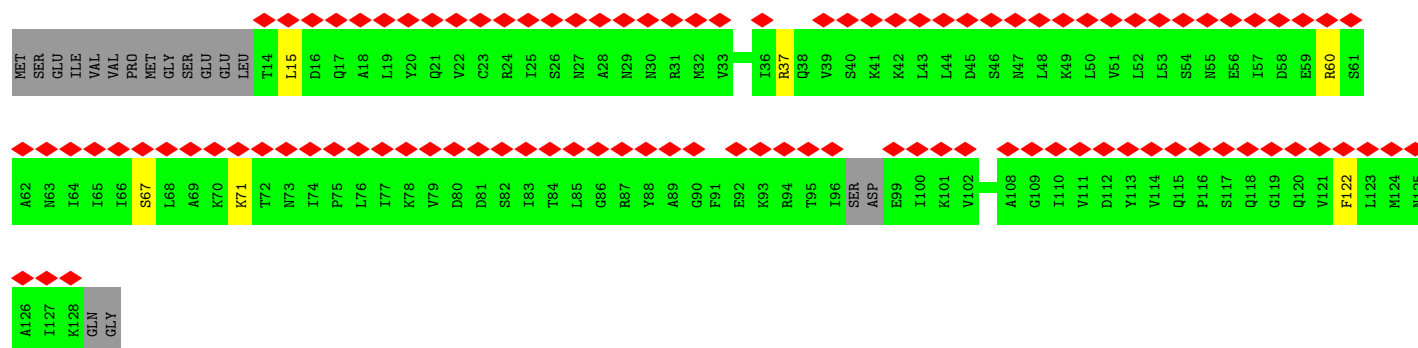
- Molecule 61: 40S ribosomal protein S11

Chain RL0: 




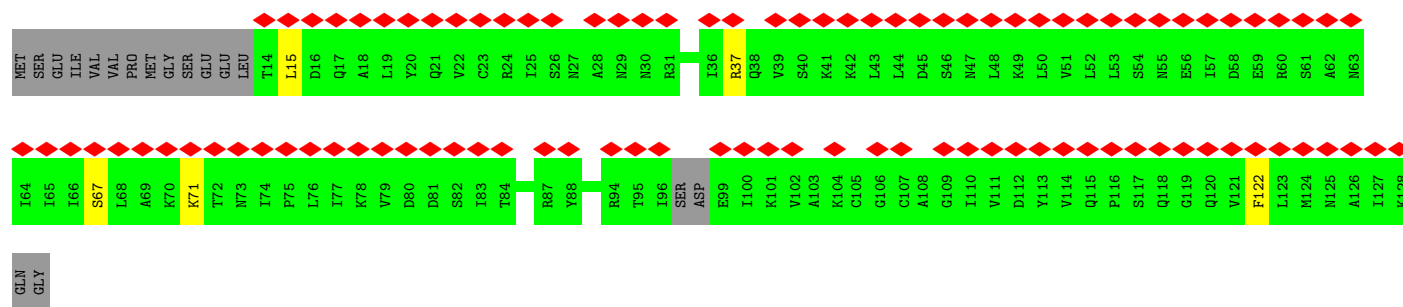
- Molecule 62: 40S ribosomal protein S12

Chain SM0: 

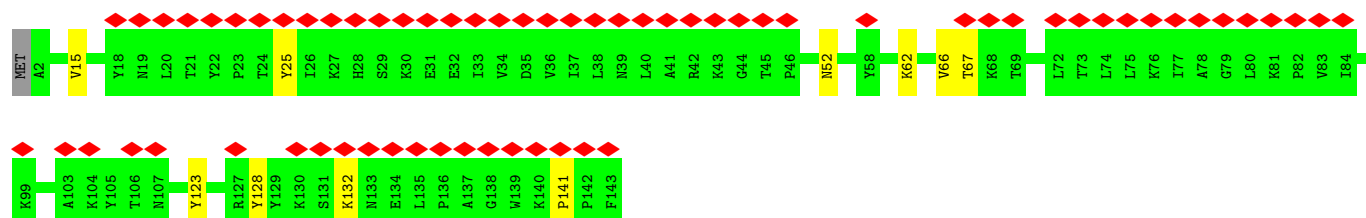


- Molecule 62: 40S ribosomal protein S12

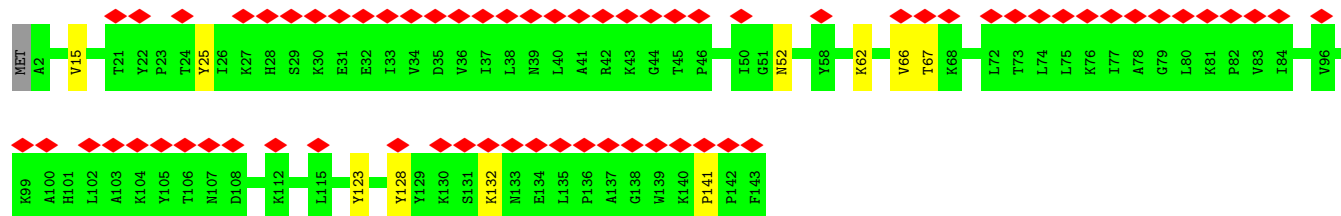
Chain RM0: 



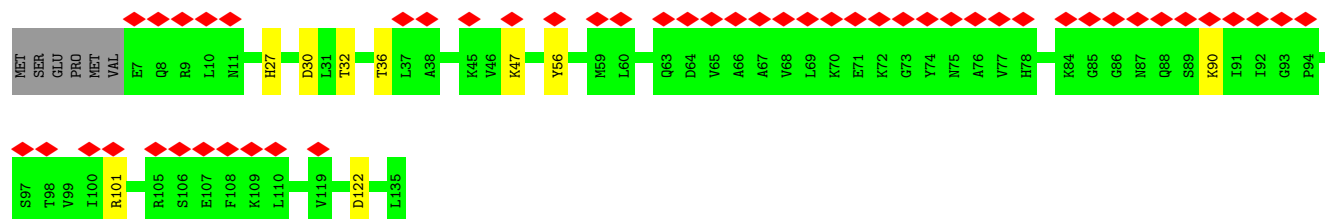
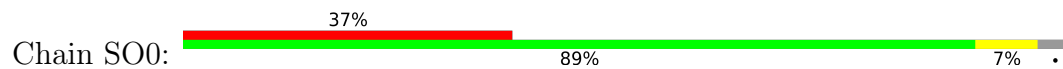
- Molecule 63: 40S ribosomal protein S13



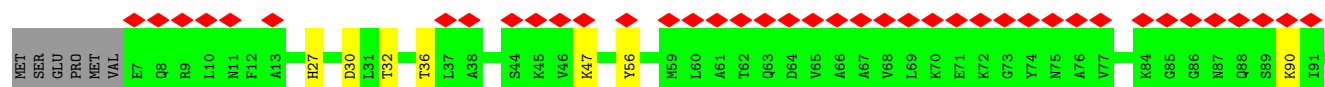
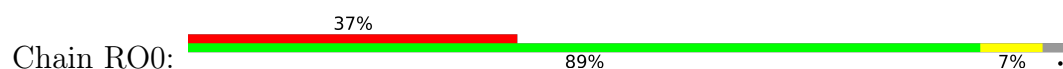
- Molecule 63: 40S ribosomal protein S13

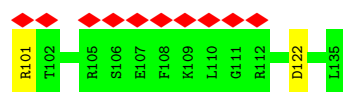


- Molecule 64: 40S ribosomal protein S14

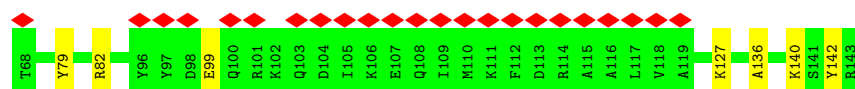
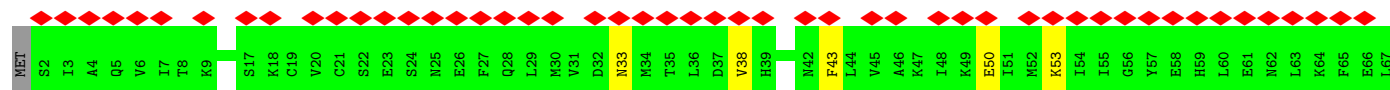


- Molecule 64: 40S ribosomal protein S14

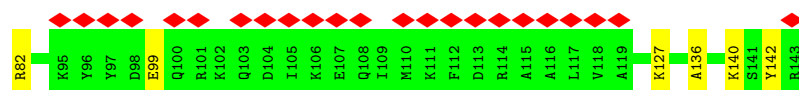
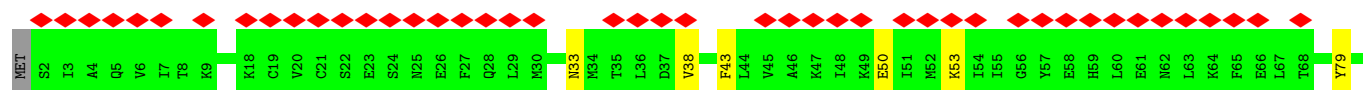




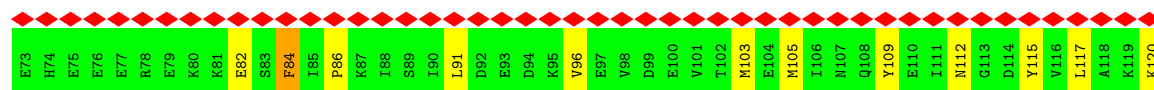
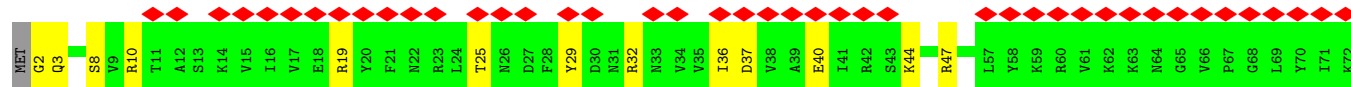
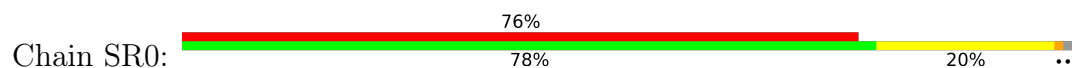
- Molecule 65: 40S ribosomal protein S16



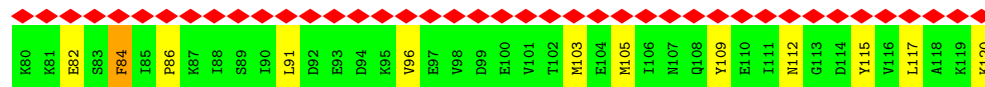
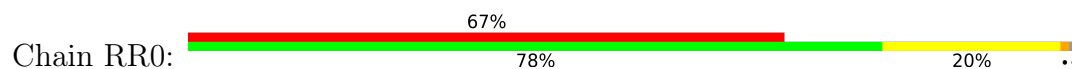
- Molecule 65: 40S ribosomal protein S16



- Molecule 66: 40S ribosomal protein S17

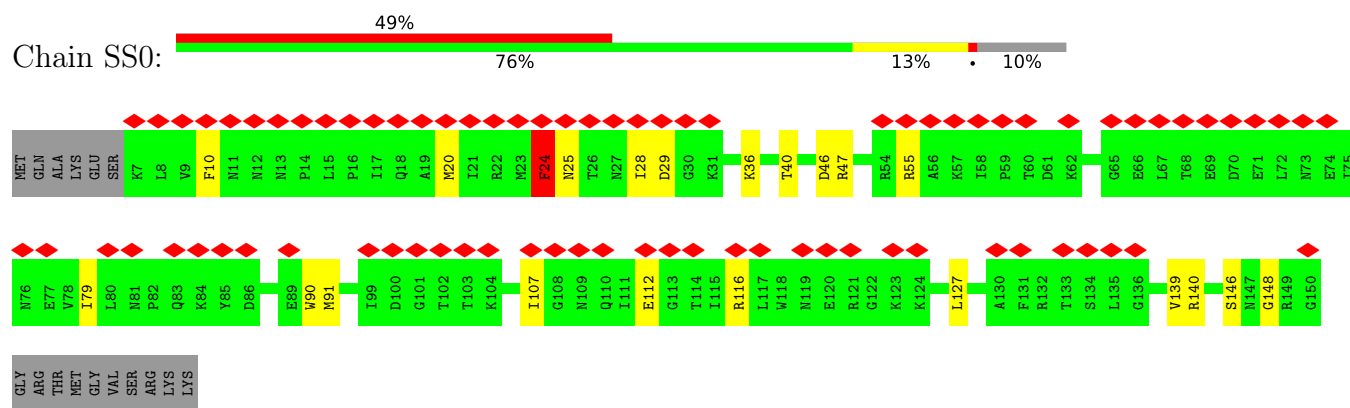


- Molecule 66: 40S ribosomal protein S17

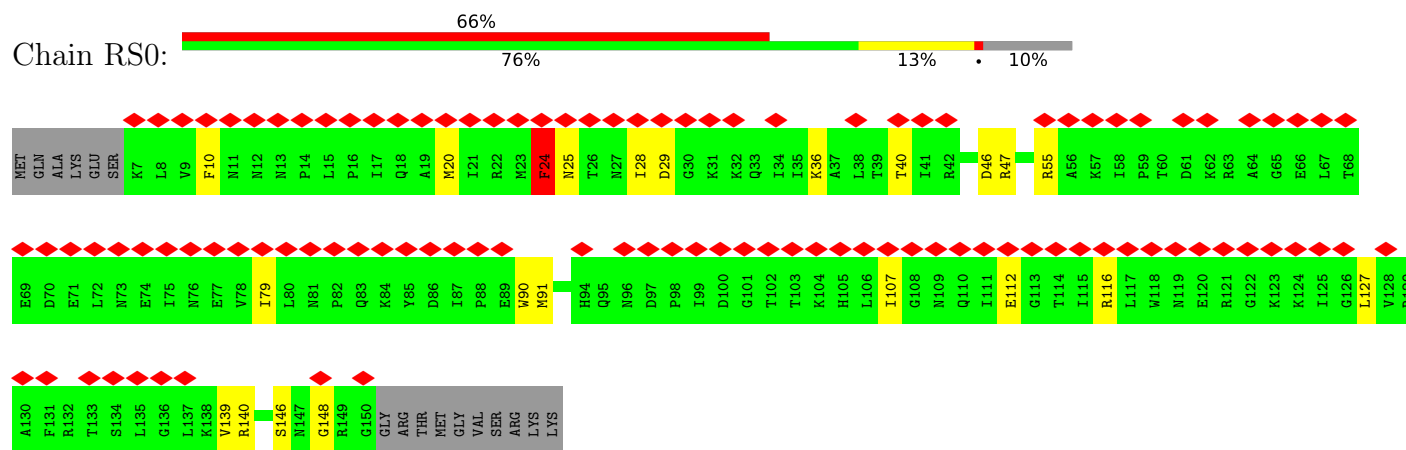


- Molecule 67: 40S ribosomal protein S18

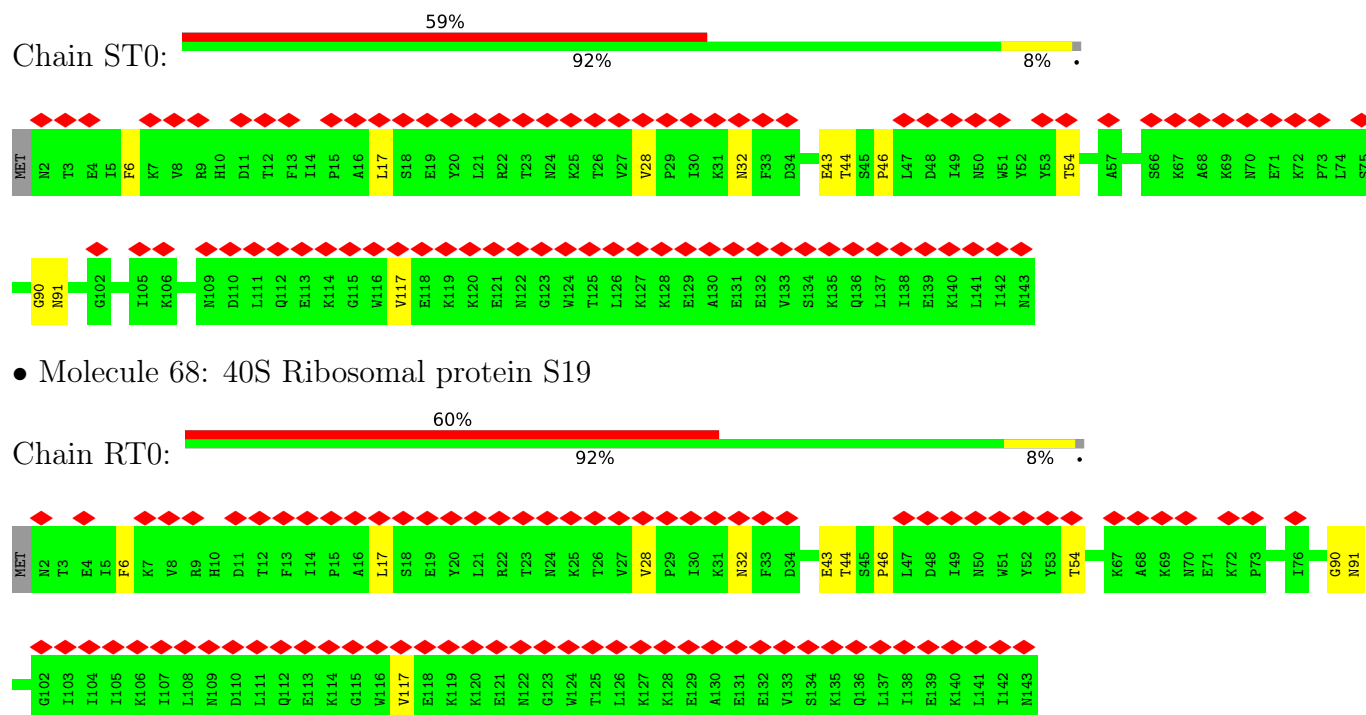




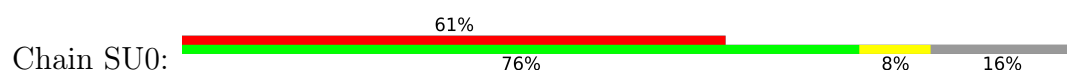
- Molecule 67: 40S ribosomal protein S18



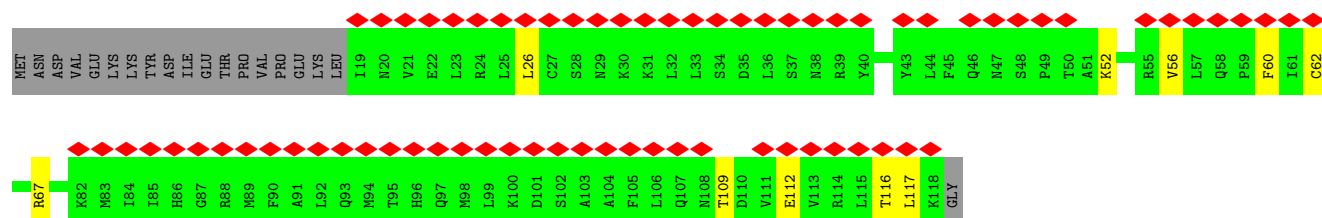
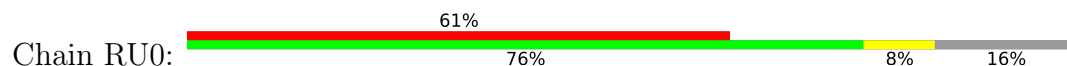
- Molecule 68: 40S Ribosomal protein S19



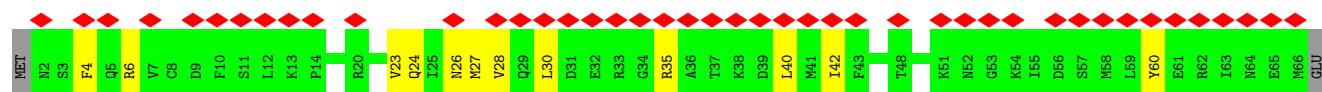
- Molecule 69: 40S ribosomal protein S20



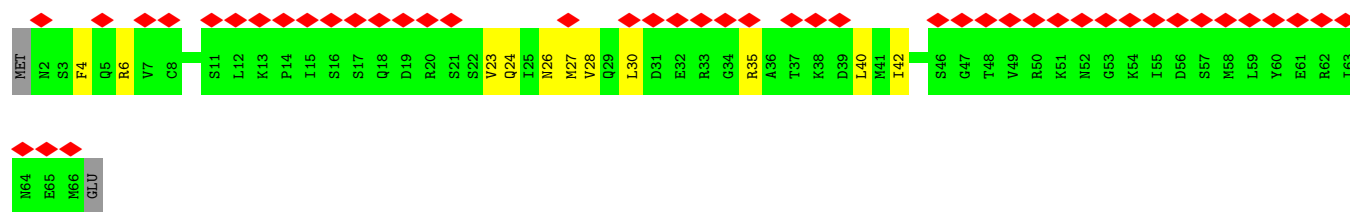
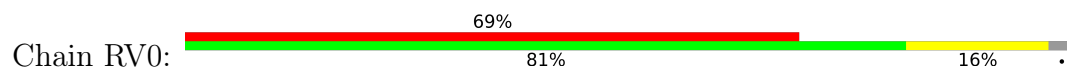
- Molecule 69: 40S ribosomal protein S20



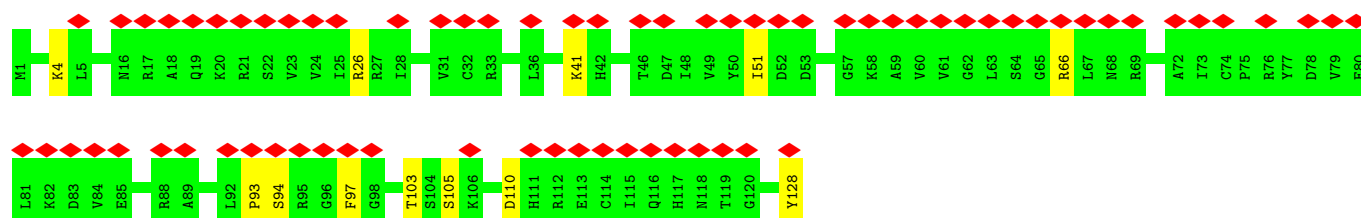
- Molecule 70: Ribosomal protein S21E



- Molecule 70: Ribosomal protein S21E

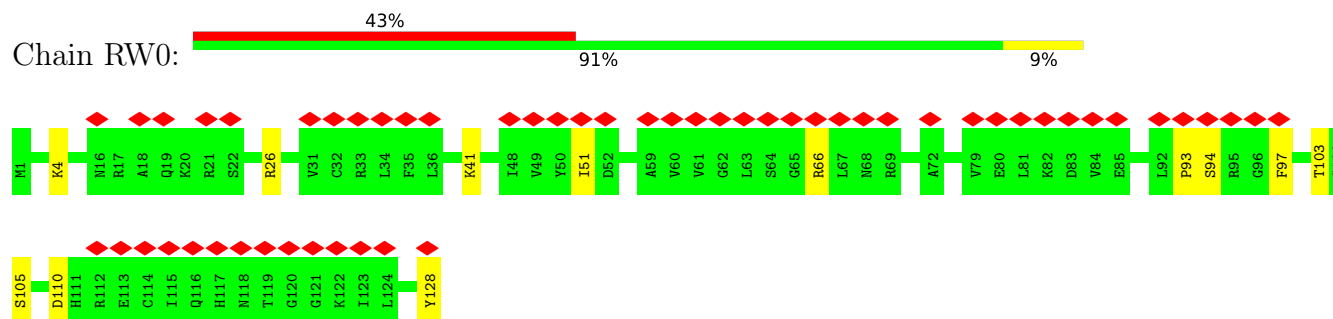


- Molecule 71: 40S ribosomal protein S15A



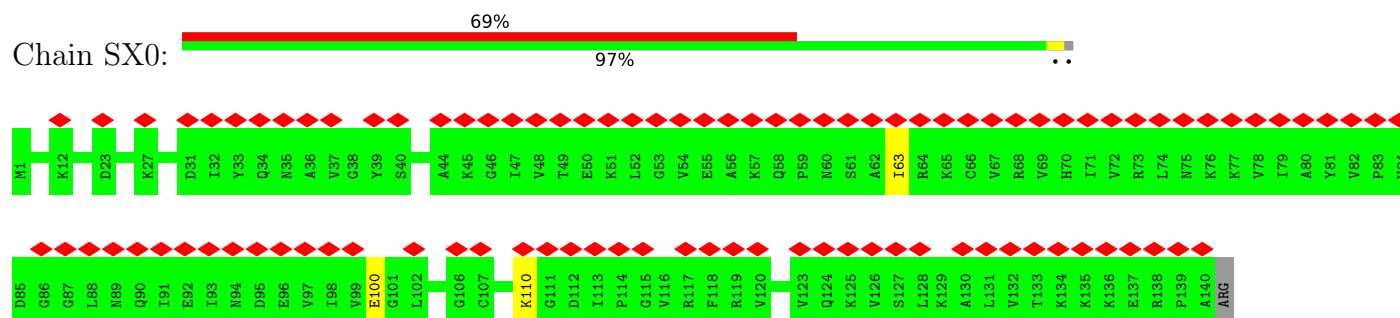
## ● Molecule 71: 40S ribosomal protein S15A

Chain RW0:



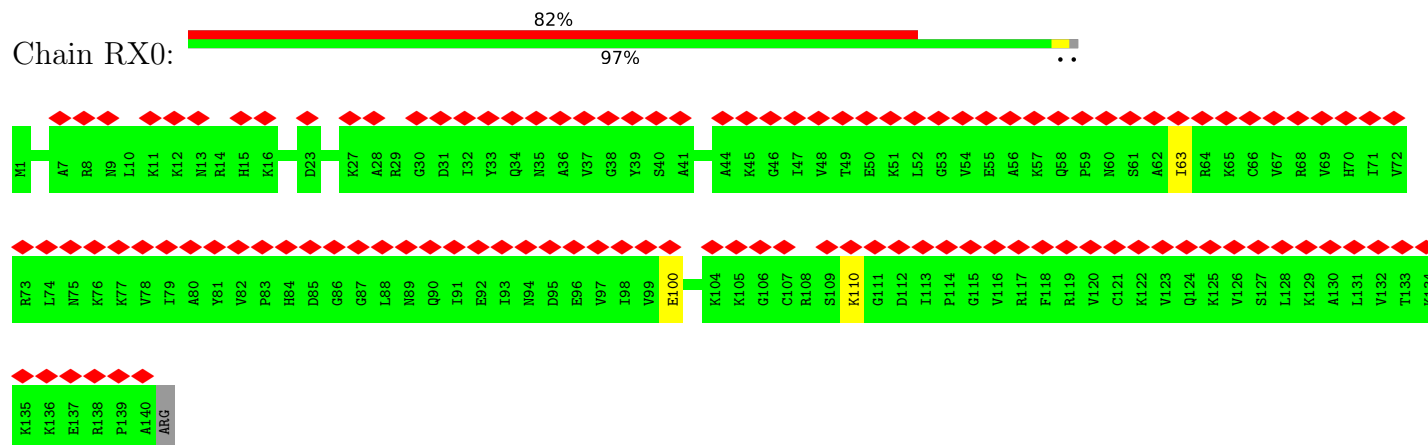
## ● Molecule 72: Ribosomal protein S12/S23

Chain SX0:



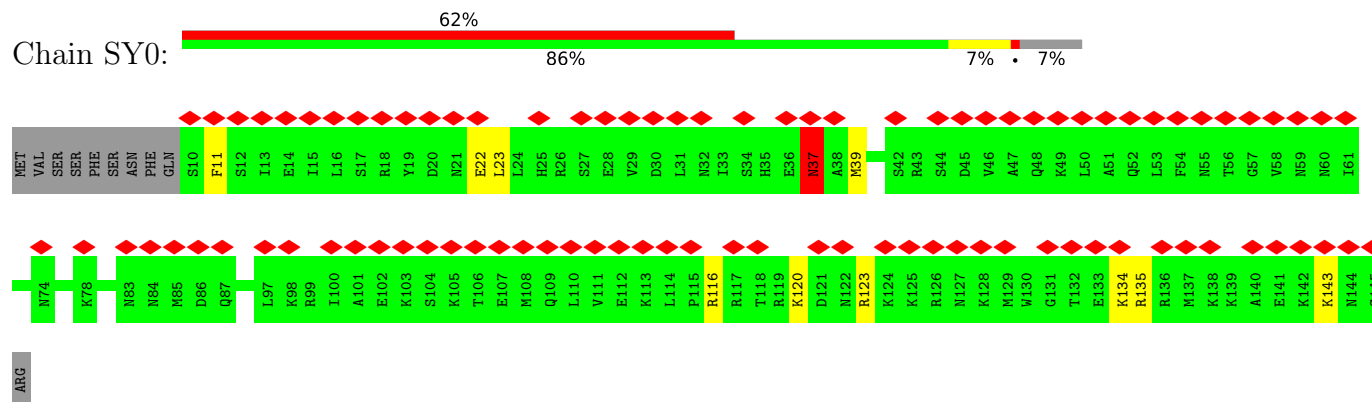
## ● Molecule 72: Ribosomal protein S12/S23

Chain RX0:



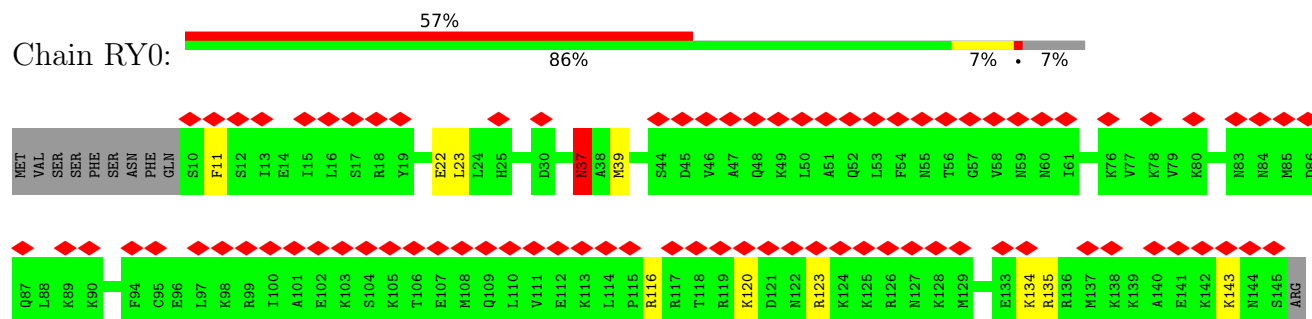
## ● Molecule 73: 40s ribosomal protein s24

Chain SY0:



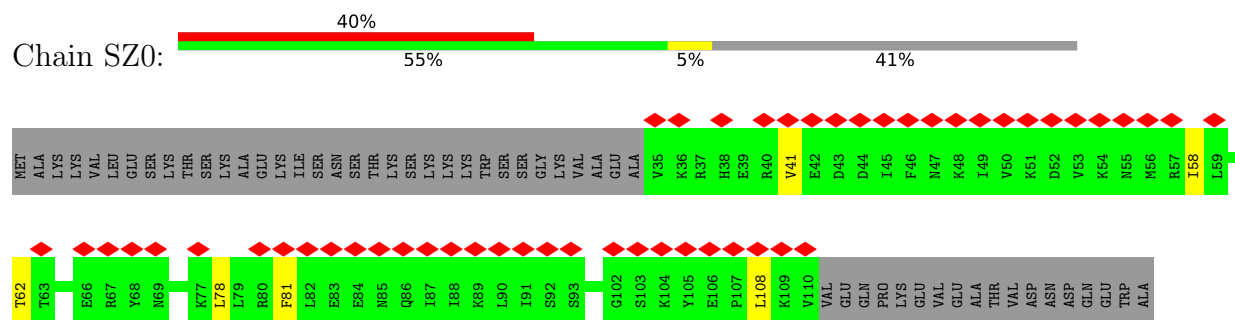
- Molecule 73: 40s ribosomal protein s24

Chain RY0:



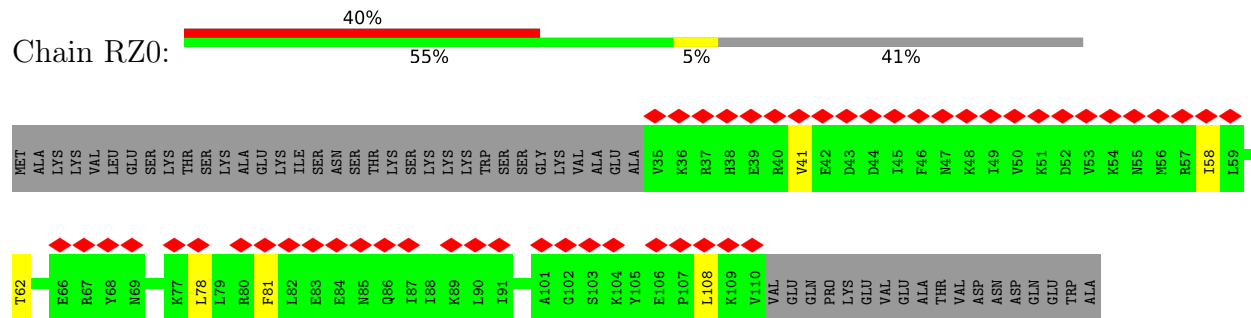
- Molecule 74: 40S ribosomal protein S25

Chain SZ0:



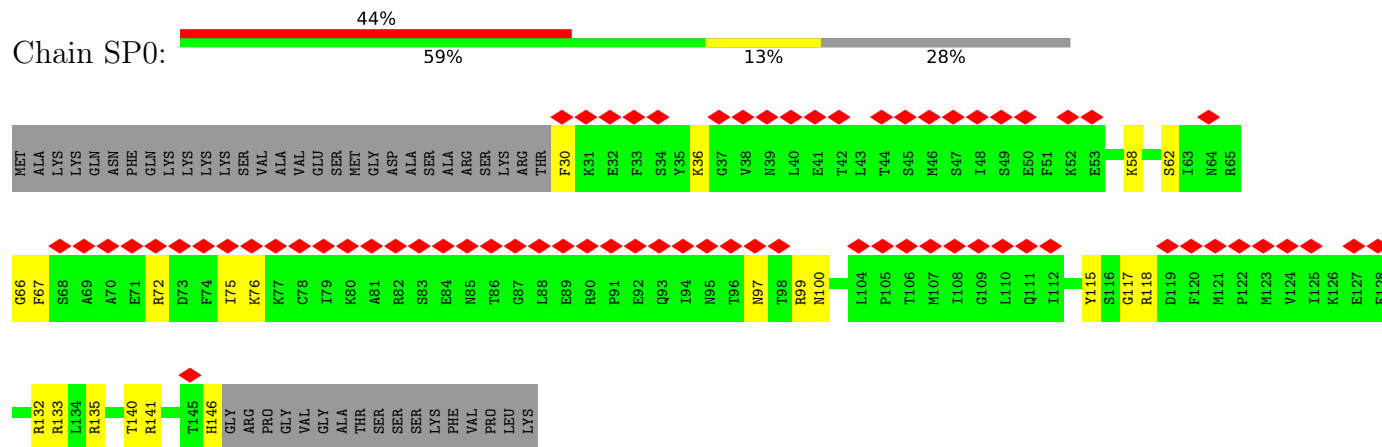
- Molecule 74: 40S ribosomal protein S25

Chain RZ0:

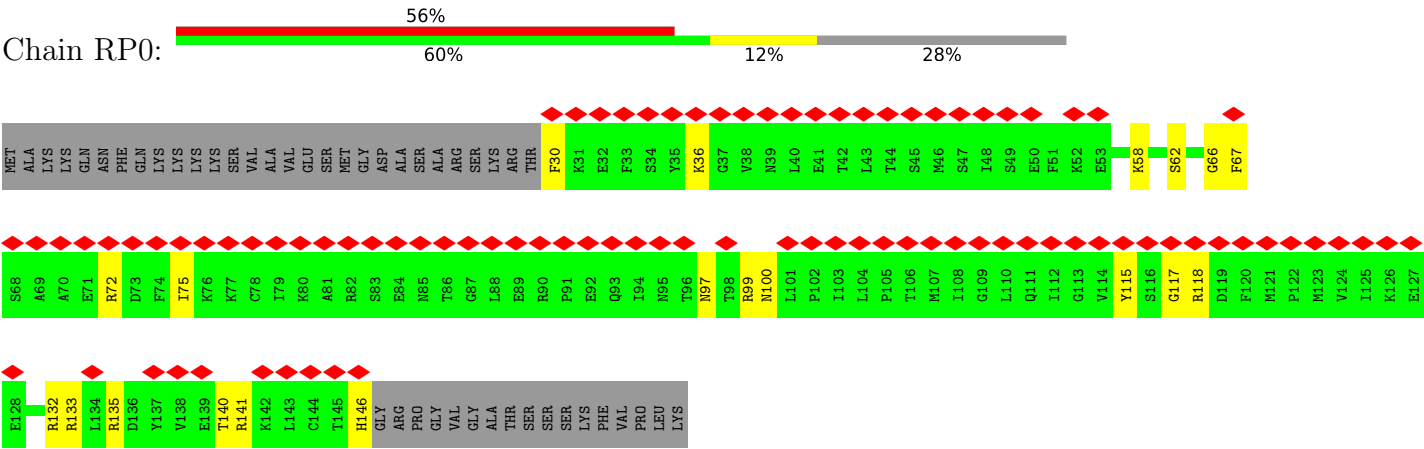


- Molecule 75: Ribosomal protein S19

Chain SP0:



- Molecule 75: Ribosomal protein S19



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of subtomograms used	1344	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	120, 120	Depositor
Minimum defocus (nm)	2500	Depositor
Maximum defocus (nm)	6000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k), GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.850	Depositor
Minimum map value	-1.211	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.118	Depositor
Recommended contour level	0.58	Depositor
Map size ( $\text{\AA}$ )	772.8, 772.8, 772.8	wwPDB
Map dimensions	168, 168, 168	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	4.6, 4.6, 4.6	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

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	K50	0.75	1/60107 (0.0%)	1.19	160/93753 (0.2%)
1	L50	0.75	1/60107 (0.0%)	1.19	160/93753 (0.2%)
2	K70	0.75	1/2844 (0.0%)	1.11	6/4429 (0.1%)
2	L70	0.75	1/2844 (0.0%)	1.11	6/4429 (0.1%)
3	KA0	0.32	0/1926	0.74	0/2590
3	LA0	0.32	0/1926	0.74	0/2590
4	KAA	0.34	0/1191	0.66	0/1586
4	LAA	0.34	0/1191	0.66	0/1586
5	KB0	0.32	0/3092	0.70	1/4144 (0.0%)
5	LB0	0.32	0/3092	0.70	1/4144 (0.0%)
6	KC0	0.33	0/2646	0.75	1/3555 (0.0%)
6	LC0	0.33	0/2646	0.75	1/3555 (0.0%)
7	KCC	0.32	0/794	0.62	0/1067
7	LCC	0.32	0/794	0.62	0/1067
8	KD0	0.28	0/2328	0.67	0/3098
8	LD0	0.28	0/2328	0.67	0/3098
9	KDD	0.30	0/913	0.66	0/1223
9	LDD	0.30	0/913	0.66	0/1223
10	KE0	0.28	0/1394	0.65	0/1875
10	LE0	0.28	0/1394	0.65	0/1875
11	KEE	0.32	0/1108	0.69	0/1477
11	LEE	0.32	0/1108	0.69	0/1477
12	KF0	0.30	0/1963	0.68	0/2618
12	LF0	0.30	0/1963	0.68	0/2618
13	KFF	0.33	0/906	0.70	0/1207
13	LFF	0.33	0/906	0.70	0/1207
14	KG0	0.28	0/1612	0.63	0/2163
14	LG0	0.28	0/1612	0.63	0/2163
15	KGG	0.34	0/825	0.78	1/1090 (0.1%)
15	LGG	0.34	0/825	0.78	1/1090 (0.1%)
16	KH0	0.30	0/1503	0.65	0/2018
16	LH0	0.30	0/1503	0.65	0/2018

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
17	KHH	0.28	0/999	0.65	0/1324
17	LHH	0.28	0/999	0.65	0/1324
18	KI0	0.32	0/1781	0.69	0/2382
18	LI0	0.32	0/1781	0.69	0/2382
19	KII	0.29	0/790	0.59	0/1041
19	LII	0.29	0/790	0.59	0/1041
20	KJ0	0.30	0/1350	0.66	0/1797
20	LJ0	0.30	0/1350	0.66	0/1797
21	KJJ	0.40	0/710	0.82	2/932 (0.2%)
21	LJJ	0.40	0/710	0.83	2/932 (0.2%)
22	KL0	0.30	0/1374	0.76	1/1827 (0.1%)
22	LL0	0.30	0/1374	0.77	1/1827 (0.1%)
23	KLL	0.34	0/435	0.72	0/576
23	LLL	0.34	0/435	0.72	0/576
24	KM0	0.32	0/935	0.66	0/1251
24	LM0	0.32	0/935	0.65	0/1251
25	KMM	0.41	0/431	0.68	0/568
25	LMM	0.41	0/431	0.68	0/568
26	KN0	0.35	0/1722	0.74	1/2297 (0.0%)
26	LN0	0.35	0/1722	0.74	1/2297 (0.0%)
27	KO0	0.30	0/1626	0.65	0/2168
27	LO0	0.30	0/1626	0.65	0/2168
28	KOO	0.34	0/811	0.69	0/1071
28	LOO	0.34	0/811	0.70	0/1071
29	KP0	0.31	0/1262	0.77	0/1689
29	LP0	0.31	0/1262	0.77	0/1689
30	KPP	0.40	0/693	0.78	2/918 (0.2%)
30	LPP	0.40	0/693	0.78	2/918 (0.2%)
31	KQ0	0.30	0/1512	0.64	0/2014
31	LQ0	0.30	0/1512	0.64	0/2014
32	KR0	0.31	0/1352	0.65	1/1790 (0.1%)
32	LR0	0.31	0/1352	0.65	1/1790 (0.1%)
33	KS0	0.30	0/1422	0.67	0/1898
33	LS0	0.30	0/1422	0.66	0/1898
34	KT0	0.31	0/1294	0.68	0/1736
34	LT0	0.31	0/1294	0.68	0/1736
35	KU0	0.31	0/826	0.67	0/1104
35	LU0	0.30	0/826	0.67	0/1104
36	KV0	0.31	0/1068	0.70	0/1429
36	LV0	0.31	0/1068	0.70	0/1429
37	KW0	0.43	0/849	0.72	0/1129
37	LW0	0.43	0/849	0.72	0/1129
38	KX0	0.28	0/883	0.67	0/1175



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
38	LX0	0.28	0/883	0.67	0/1175
39	KY0	0.29	0/1058	0.69	1/1399 (0.1%)
39	LY0	0.29	0/1058	0.69	1/1399 (0.1%)
40	KZ0	0.29	0/976	0.73	1/1302 (0.1%)
40	LZ0	0.29	0/976	0.73	1/1302 (0.1%)
41	MD1	0.66	0/1249	0.87	1/1677 (0.1%)
41	MD2	0.66	0/1249	0.87	1/1677 (0.1%)
42	R60	1.40	347/32725 (1.1%)	1.41	369/51066 (0.7%)
42	S60	1.40	351/32725 (1.1%)	1.41	376/51066 (0.7%)
43	RA0	0.36	1/1751 (0.1%)	0.64	0/2358
43	SA0	0.35	1/1751 (0.1%)	0.64	0/2358
44	RAA	0.38	0/839	0.73	0/1120
44	SAA	0.38	0/839	0.72	0/1120
45	RB0	0.29	0/1623	0.67	0/2169
45	SB0	0.29	0/1623	0.67	0/2169
46	RBB	0.47	1/634 (0.2%)	0.65	0/844
46	SBB	0.47	1/634 (0.2%)	0.65	0/844
47	RC0	0.31	0/1751	0.69	2/2359 (0.1%)
47	SC0	0.31	0/1751	0.69	2/2359 (0.1%)
48	RCC	0.33	0/480	0.73	0/644
48	SCC	0.32	0/480	0.73	0/644
49	RD0	0.30	0/1721	0.66	0/2304
49	SD0	0.30	0/1721	0.66	0/2304
50	RDD	0.40	0/559	0.75	1/742 (0.1%)
50	SDD	0.40	0/559	0.75	1/742 (0.1%)
51	RE0	0.32	0/2080	0.72	2/2804 (0.1%)
51	SE0	0.32	0/2080	0.72	2/2804 (0.1%)
52	REE	0.35	0/453	0.74	1/596 (0.2%)
52	SEE	0.36	0/453	0.74	1/596 (0.2%)
53	RF0	0.31	0/1527	0.69	0/2045
53	SF0	0.31	0/1527	0.68	0/2045
54	RFF	0.43	0/422	0.66	0/568
54	SFF	0.43	0/427	0.68	0/573
55	RG0	0.29	0/1864	0.68	0/2485
55	SG0	0.29	0/1864	0.68	0/2485
56	RGG	0.34	0/2517	0.71	1/3397 (0.0%)
56	SGG	0.34	0/2517	0.71	1/3397 (0.0%)
57	RH0	0.31	0/1356	0.66	0/1820
57	SH0	0.31	0/1356	0.66	0/1820
58	RI0	0.33	0/1369	0.67	0/1825
58	SI0	0.33	0/1369	0.67	0/1825
59	RJ0	0.33	0/1403	0.68	0/1880
59	SJ0	0.33	0/1403	0.68	0/1880

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
60	RK0	0.29	0/750	0.71	0/1009
60	SK0	0.29	0/750	0.71	0/1009
61	RL0	0.32	0/1252	0.72	2/1672 (0.1%)
61	SL0	0.32	0/1252	0.72	2/1672 (0.1%)
62	RM0	0.32	0/881	0.71	0/1182
62	SM0	0.32	0/881	0.71	0/1182
63	RN0	0.38	0/1154	0.78	0/1557
63	SN0	0.38	0/1154	0.78	0/1557
64	RO0	0.33	0/993	0.72	0/1326
64	SO0	0.32	0/993	0.72	0/1326
65	RQ0	0.33	0/1163	0.74	3/1556 (0.2%)
65	SQ0	0.32	0/1163	0.74	3/1556 (0.2%)
66	RR0	0.64	0/985	0.97	2/1315 (0.2%)
66	SR0	0.64	0/985	0.97	2/1315 (0.2%)
67	RS0	0.34	0/1165	0.74	0/1566
67	SS0	0.34	0/1165	0.74	0/1566
68	RT0	0.34	0/1181	0.75	1/1585 (0.1%)
68	ST0	0.34	0/1181	0.75	1/1585 (0.1%)
69	RU0	0.33	0/824	0.74	2/1110 (0.2%)
69	SU0	0.33	0/824	0.74	2/1110 (0.2%)
70	RV0	0.33	0/525	0.66	0/700
70	SV0	0.33	0/525	0.66	0/700
71	RW0	0.32	0/1037	0.71	0/1389
71	SW0	0.32	0/1037	0.71	0/1389
72	RX0	0.31	0/1113	0.70	0/1486
72	SX0	0.31	0/1113	0.70	0/1486
73	RY0	0.30	0/1131	0.72	1/1503 (0.1%)
73	SY0	0.30	0/1131	0.72	1/1503 (0.1%)
74	RZ0	0.33	0/640	0.75	0/855
74	SZ0	0.33	0/640	0.75	0/855
75	RP0	0.33	0/964	0.71	0/1289
75	SP0	0.33	0/964	0.71	0/1289
All	All	0.77	706/366789 (0.2%)	1.06	1139/533031 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
6	KC0	0	1
6	LC0	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
13	KFF	0	1
13	LFF	0	1
15	KGG	0	1
15	LGG	0	1
All	All	0	6

The worst 5 of 706 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	S60	934	A	P-O5'	10.41	1.70	1.59
42	R60	934	A	P-O5'	10.38	1.70	1.59
42	R60	988	A	N9-C4	-8.53	1.32	1.37
42	S60	988	A	N9-C4	-8.53	1.32	1.37
43	RA0	20	CYS	C-N	8.45	1.53	1.34

The worst 5 of 1139 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	R60	1356	C	O5'-P-OP1	-18.09	89.00	110.70
42	S60	1356	C	O5'-P-OP1	-18.08	89.00	110.70
42	S60	910	A	P-O3'-C3'	-11.69	105.67	119.70
42	R60	910	A	P-O3'-C3'	-11.66	105.71	119.70
42	S60	850	G	C5-N7-C8	-11.29	98.66	104.30

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	KC0	87	ALA	Peptide
13	KFF	101	ILE	Peptide
6	LC0	87	ALA	Peptide
13	LFF	101	ILE	Peptide
15	LGG	77	GLY	Peptide

## 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	K50	53655	0	26955	121	0
1	L50	53655	0	26955	121	0
2	K70	2542	0	1282	9	0
2	L70	2542	0	1282	8	0
3	KA0	1889	0	1985	12	0
3	LA0	1889	0	1985	12	0
4	KAA	1167	0	1214	7	0
4	LAA	1167	0	1214	6	0
5	KB0	3039	0	3183	5	0
5	LB0	3039	0	3183	6	0
6	KC0	2604	0	2638	11	0
6	LC0	2604	0	2638	10	0
7	KCC	781	0	803	2	0
7	LCC	781	0	803	2	0
8	KD0	2298	0	2384	7	0
8	LD0	2298	0	2384	7	0
9	KDD	895	0	948	1	0
9	LDD	895	0	948	0	0
10	KE0	1371	0	1389	15	0
10	LE0	1371	0	1389	14	0
11	KEE	1090	0	1173	11	0
11	LEE	1090	0	1173	11	0
12	KF0	1933	0	2011	10	0
12	LF0	1933	0	2011	10	0
13	KFF	893	0	945	2	0
13	LFF	893	0	945	2	0
14	KG0	1590	0	1709	5	0
14	LG0	1590	0	1709	4	0
15	KGG	819	0	882	2	0
15	LGG	819	0	882	3	0
16	KH0	1477	0	1528	3	0
16	LH0	1477	0	1528	3	0
17	KHH	992	0	1097	5	0
17	LHH	992	0	1097	5	0
18	KI0	1750	0	1797	2	0
18	LI0	1750	0	1797	3	0
19	KII	784	0	874	4	0
19	LII	784	0	874	3	0
20	KJ0	1332	0	1411	12	0
20	LJ0	1332	0	1411	12	0
21	KJJ	701	0	753	4	0
21	LJJ	701	0	753	4	0
22	KL0	1353	0	1433	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	LL0	1353	0	1433	5	0
23	KLL	427	0	468	0	0
23	LLL	427	0	468	0	0
24	KM0	927	0	961	4	0
24	LM0	927	0	961	5	0
25	KMM	427	0	461	0	0
25	LMM	427	0	461	0	0
26	KN0	1688	0	1752	5	0
26	LN0	1688	0	1752	5	0
27	KO0	1598	0	1681	3	0
27	LO0	1598	0	1681	3	0
28	KOO	801	0	886	3	0
28	LOO	801	0	886	4	0
29	KP0	1238	0	1304	4	0
29	LP0	1238	0	1304	3	0
30	KPP	684	0	720	2	0
30	LPP	684	0	720	2	0
31	KQ0	1491	0	1587	6	0
31	LQ0	1491	0	1587	7	0
32	KR0	1336	0	1430	1	0
32	LR0	1336	0	1430	0	0
33	KS0	1400	0	1450	1	0
33	LS0	1400	0	1450	1	0
34	KT0	1270	0	1321	16	0
34	LT0	1270	0	1321	16	0
35	KU0	810	0	834	1	0
35	LU0	810	0	834	1	0
36	KV0	1057	0	1139	1	0
36	LV0	1057	0	1139	1	0
37	KW0	832	0	873	45	0
37	LW0	832	0	873	45	0
38	KX0	874	0	956	5	0
38	LX0	874	0	956	5	0
39	KY0	1048	0	1135	2	0
39	LY0	1048	0	1135	2	0
40	KZ0	963	0	1022	2	0
40	LZ0	963	0	1022	2	0
41	MD1	1229	0	1216	10	0
41	MD2	1229	0	1216	9	0
42	R60	29181	0	14605	318	0
42	S60	29181	0	14604	321	0
43	RA0	1725	0	1750	140	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	SA0	1725	0	1750	138	0
44	RAA	827	0	859	17	0
44	SAA	827	0	859	17	0
45	RB0	1609	0	1728	6	0
45	SB0	1609	0	1728	6	0
46	RBB	627	0	651	4	0
46	SBB	627	0	651	3	0
47	RC0	1727	0	1802	95	0
47	SC0	1727	0	1802	94	0
48	RCC	476	0	488	17	0
48	SCC	476	0	488	17	0
49	RD0	1700	0	1815	32	0
49	SD0	1700	0	1815	32	0
50	RDD	550	0	542	28	0
50	SDD	550	0	542	30	0
51	RE0	2044	0	2116	26	0
51	SE0	2044	0	2116	26	0
52	REE	447	0	483	1	0
52	SEE	447	0	483	1	0
53	RF0	1509	0	1604	39	0
53	SF0	1509	0	1604	41	0
54	RFF	417	0	402	42	0
54	SFF	422	0	412	44	0
55	RG0	1836	0	1972	40	0
55	SG0	1836	0	1972	39	0
56	RGG	2478	0	2458	24	0
56	SGG	2478	0	2458	24	0
57	RH0	1335	0	1356	2	0
57	SH0	1335	0	1356	2	0
58	RI0	1347	0	1379	9	0
58	SI0	1347	0	1379	10	0
59	RJ0	1379	0	1436	16	0
59	SJ0	1379	0	1436	15	0
60	RK0	737	0	746	16	0
60	SK0	737	0	746	16	0
61	RL0	1229	0	1302	5	0
61	SL0	1229	0	1302	5	0
62	RM0	876	0	937	6	0
62	SM0	876	0	937	5	0
63	RN0	1130	0	1189	10	0
63	SN0	1130	0	1189	10	0
64	RO0	983	0	1028	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
64	SO0	983	0	1028	14	0
65	RQ0	1143	0	1171	20	0
65	SQ0	1143	0	1171	21	0
66	RR0	974	0	1003	99	0
66	SR0	974	0	1003	98	0
67	RS0	1150	0	1207	32	0
67	SS0	1150	0	1207	33	0
68	RT0	1161	0	1219	10	0
68	ST0	1161	0	1219	10	0
69	RU0	809	0	838	14	0
69	SU0	809	0	838	14	0
70	RV0	521	0	525	74	0
70	SV0	521	0	525	74	0
71	RW0	1022	0	1052	20	0
71	SW0	1022	0	1052	19	0
72	RX0	1098	0	1183	3	0
72	SX0	1098	0	1183	3	0
73	RY0	1118	0	1166	13	0
73	SY0	1118	0	1166	13	0
74	RZ0	633	0	678	14	0
74	SZ0	633	0	678	14	0
75	RP0	950	0	984	56	0
75	SP0	950	0	984	59	0
76	KGG	1	0	0	0	0
76	KJJ	1	0	0	0	0
76	KMM	1	0	0	0	0
76	KOO	1	0	0	0	0
76	KPP	1	0	0	0	0
76	LGG	1	0	0	0	0
76	LJJ	1	0	0	0	0
76	LMM	1	0	0	0	0
76	LOO	1	0	0	0	0
76	LPP	1	0	0	0	0
76	RAA	1	0	0	0	0
76	RBB	1	0	0	0	0
76	RDD	1	0	0	0	0
76	RFF	1	0	0	0	0
76	SAA	1	0	0	0	0
76	SBB	1	0	0	0	0
76	SDD	1	0	0	0	0
76	SFF	1	0	0	0	0
All	All	343629	0	266537	1984	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

The worst 5 of 1984 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:SA0:70:ASN:HB2	47:SC0:240:ILE:CD1	1.35	1.54
43:RA0:70:ASN:HB2	47:RC0:240:ILE:CD1	1.35	1.49
47:SC0:51:SER:HB2	70:SV0:6:ARG:NH2	1.30	1.45
47:RC0:51:SER:HB2	70:RV0:6:ARG:NH2	1.30	1.42
49:SD0:238:PRO:C	66:SR0:19:ARG:HH12	1.27	1.38

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	KA0	243/246 (99%)	236 (97%)	7 (3%)	0	100	100
3	LA0	243/246 (99%)	236 (97%)	7 (3%)	0	100	100
4	KAA	145/147 (99%)	142 (98%)	3 (2%)	0	100	100
4	LAA	145/147 (99%)	142 (98%)	3 (2%)	0	100	100
5	KB0	381/392 (97%)	372 (98%)	9 (2%)	0	100	100
5	LB0	381/392 (97%)	372 (98%)	9 (2%)	0	100	100
6	KC0	325/328 (99%)	313 (96%)	11 (3%)	1 (0%)	37	73
6	LC0	325/328 (99%)	313 (96%)	11 (3%)	1 (0%)	37	73
7	KCC	97/110 (88%)	94 (97%)	2 (2%)	1 (1%)	13	49
7	LCC	97/110 (88%)	94 (97%)	2 (2%)	1 (1%)	13	49
8	KD0	279/291 (96%)	274 (98%)	5 (2%)	0	100	100
8	LD0	279/291 (96%)	274 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	KDD	107/110 (97%)	104 (97%)	3 (3%)	0	100	100
9	LDD	107/110 (97%)	104 (97%)	3 (3%)	0	100	100
10	KE0	163/171 (95%)	154 (94%)	9 (6%)	0	100	100
10	LE0	163/171 (95%)	154 (94%)	9 (6%)	0	100	100
11	KEE	133/139 (96%)	127 (96%)	6 (4%)	0	100	100
11	LEE	133/139 (96%)	127 (96%)	6 (4%)	0	100	100
12	KF0	229/235 (97%)	224 (98%)	5 (2%)	0	100	100
12	LF0	229/235 (97%)	224 (98%)	5 (2%)	0	100	100
13	KFF	109/111 (98%)	106 (97%)	3 (3%)	0	100	100
13	LFF	109/111 (98%)	106 (97%)	3 (3%)	0	100	100
14	KG0	197/206 (96%)	194 (98%)	3 (2%)	0	100	100
14	LG0	197/206 (96%)	194 (98%)	3 (2%)	0	100	100
15	KGG	102/106 (96%)	96 (94%)	5 (5%)	1 (1%)	13	49
15	LGG	102/106 (96%)	96 (94%)	5 (5%)	1 (1%)	13	49
16	KH0	181/187 (97%)	177 (98%)	4 (2%)	0	100	100
16	LH0	181/187 (97%)	177 (98%)	4 (2%)	0	100	100
17	KHH	117/119 (98%)	109 (93%)	8 (7%)	0	100	100
17	LHH	117/119 (98%)	109 (93%)	8 (7%)	0	100	100
18	KI0	215/218 (99%)	213 (99%)	2 (1%)	0	100	100
18	LI0	215/218 (99%)	214 (100%)	1 (0%)	0	100	100
19	KII	95/98 (97%)	91 (96%)	4 (4%)	0	100	100
19	LII	95/98 (97%)	91 (96%)	4 (4%)	0	100	100
20	KJ0	165/171 (96%)	156 (94%)	9 (6%)	0	100	100
20	LJ0	165/171 (96%)	156 (94%)	9 (6%)	0	100	100
21	KJJ	87/92 (95%)	86 (99%)	1 (1%)	0	100	100
21	LJJ	87/92 (95%)	86 (99%)	1 (1%)	0	100	100
22	KL0	162/165 (98%)	155 (96%)	6 (4%)	1 (1%)	22	60
22	LL0	162/165 (98%)	155 (96%)	6 (4%)	1 (1%)	22	60
23	KLL	49/52 (94%)	48 (98%)	1 (2%)	0	100	100
23	LLL	49/52 (94%)	48 (98%)	1 (2%)	0	100	100
24	KM0	113/115 (98%)	106 (94%)	6 (5%)	1 (1%)	14	52

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
24	LM0	113/115 (98%)	106 (94%)	6 (5%)	1 (1%)	14	52
25	KMM	50/127 (39%)	50 (100%)	0	0	100	100
25	LMM	50/127 (39%)	50 (100%)	0	0	100	100
26	KN0	201/204 (98%)	195 (97%)	6 (3%)	0	100	100
26	LN0	201/204 (98%)	195 (97%)	6 (3%)	0	100	100
27	KO0	196/198 (99%)	193 (98%)	3 (2%)	0	100	100
27	LO0	196/198 (99%)	193 (98%)	3 (2%)	0	100	100
28	KOO	98/104 (94%)	96 (98%)	2 (2%)	0	100	100
28	LOO	98/104 (94%)	96 (98%)	2 (2%)	0	100	100
29	KP0	152/167 (91%)	145 (95%)	7 (5%)	0	100	100
29	LP0	152/167 (91%)	145 (95%)	7 (5%)	0	100	100
30	KPP	85/89 (96%)	80 (94%)	4 (5%)	1 (1%)	11	44
30	LPP	85/89 (96%)	80 (94%)	4 (5%)	1 (1%)	11	44
31	KQ0	180/183 (98%)	175 (97%)	5 (3%)	0	100	100
31	LQ0	180/183 (98%)	175 (97%)	5 (3%)	0	100	100
32	KR0	162/168 (96%)	160 (99%)	2 (1%)	0	100	100
32	LR0	162/168 (96%)	160 (99%)	2 (1%)	0	100	100
33	KS0	168/171 (98%)	159 (95%)	9 (5%)	0	100	100
33	LS0	168/171 (98%)	159 (95%)	9 (5%)	0	100	100
34	KT0	154/158 (98%)	145 (94%)	9 (6%)	0	100	100
34	LT0	154/158 (98%)	145 (94%)	9 (6%)	0	100	100
35	KU0	98/113 (87%)	93 (95%)	5 (5%)	0	100	100
35	LU0	98/113 (87%)	93 (95%)	5 (5%)	0	100	100
36	KV0	139/142 (98%)	137 (99%)	2 (1%)	0	100	100
36	LV0	139/142 (98%)	137 (99%)	2 (1%)	0	100	100
37	KW0	100/131 (76%)	93 (93%)	6 (6%)	1 (1%)	13	49
37	LW0	100/131 (76%)	93 (93%)	6 (6%)	1 (1%)	13	49
38	KX0	110/113 (97%)	106 (96%)	4 (4%)	0	100	100
38	LX0	110/113 (97%)	106 (96%)	4 (4%)	0	100	100
39	KY0	129/131 (98%)	123 (95%)	6 (5%)	0	100	100
39	LY0	129/131 (98%)	123 (95%)	6 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	KZ0	116/153 (76%)	116 (100%)	0	0	100	100
40	LZ0	116/153 (76%)	116 (100%)	0	0	100	100
41	MD1	149/151 (99%)	144 (97%)	5 (3%)	0	100	100
41	MD2	149/151 (99%)	144 (97%)	5 (3%)	0	100	100
43	RA0	218/233 (94%)	206 (94%)	12 (6%)	0	100	100
43	SA0	218/233 (94%)	206 (94%)	12 (6%)	0	100	100
44	RAA	99/102 (97%)	98 (99%)	1 (1%)	0	100	100
44	SAA	99/102 (97%)	98 (99%)	1 (1%)	0	100	100
45	RB0	202/230 (88%)	197 (98%)	5 (2%)	0	100	100
45	SB0	202/230 (88%)	197 (98%)	5 (2%)	0	100	100
46	RBB	79/82 (96%)	77 (98%)	2 (2%)	0	100	100
46	SBB	79/82 (96%)	77 (98%)	2 (2%)	0	100	100
47	RC0	224/248 (90%)	220 (98%)	4 (2%)	0	100	100
47	SC0	224/248 (90%)	220 (98%)	4 (2%)	0	100	100
48	RCC	60/65 (92%)	57 (95%)	3 (5%)	0	100	100
48	SCC	60/65 (92%)	57 (95%)	3 (5%)	0	100	100
49	RD0	214/242 (88%)	212 (99%)	2 (1%)	0	100	100
49	SD0	214/242 (88%)	212 (99%)	2 (1%)	0	100	100
50	RDD	63/65 (97%)	58 (92%)	5 (8%)	0	100	100
50	SDD	63/65 (97%)	58 (92%)	5 (8%)	0	100	100
51	RE0	258/280 (92%)	247 (96%)	11 (4%)	0	100	100
51	SE0	258/280 (92%)	247 (96%)	11 (4%)	0	100	100
52	REE	54/60 (90%)	53 (98%)	1 (2%)	0	100	100
52	SEE	54/60 (90%)	53 (98%)	1 (2%)	0	100	100
53	RF0	190/195 (97%)	181 (95%)	9 (5%)	0	100	100
53	SF0	190/195 (97%)	180 (95%)	10 (5%)	0	100	100
54	RFF	56/150 (37%)	52 (93%)	4 (7%)	0	100	100
54	SFF	56/150 (37%)	52 (93%)	4 (7%)	0	100	100
55	RG0	227/230 (99%)	214 (94%)	13 (6%)	0	100	100
55	SG0	227/230 (99%)	214 (94%)	13 (6%)	0	100	100
56	RGG	315/326 (97%)	295 (94%)	19 (6%)	1 (0%)	37	73

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
56	SGG	315/326 (97%)	295 (94%)	19 (6%)	1 (0%)	37	73
57	RH0	161/164 (98%)	156 (97%)	4 (2%)	1 (1%)	22	60
57	SH0	161/164 (98%)	156 (97%)	4 (2%)	1 (1%)	22	60
58	RI0	165/173 (95%)	161 (98%)	4 (2%)	0	100	100
58	SI0	165/173 (95%)	161 (98%)	4 (2%)	0	100	100
59	RJ0	166/184 (90%)	165 (99%)	1 (1%)	0	100	100
59	SJ0	166/184 (90%)	165 (99%)	1 (1%)	0	100	100
60	RK0	86/107 (80%)	81 (94%)	4 (5%)	1 (1%)	11	44
60	SK0	86/107 (80%)	81 (94%)	4 (5%)	1 (1%)	11	44
61	RL0	148/155 (96%)	141 (95%)	7 (5%)	0	100	100
61	SL0	148/155 (96%)	141 (95%)	7 (5%)	0	100	100
62	RM0	109/130 (84%)	106 (97%)	3 (3%)	0	100	100
62	SM0	109/130 (84%)	106 (97%)	3 (3%)	0	100	100
63	RN0	140/143 (98%)	134 (96%)	6 (4%)	0	100	100
63	SN0	140/143 (98%)	134 (96%)	6 (4%)	0	100	100
64	RO0	127/135 (94%)	120 (94%)	7 (6%)	0	100	100
64	SO0	127/135 (94%)	120 (94%)	7 (6%)	0	100	100
65	RQ0	140/143 (98%)	134 (96%)	6 (4%)	0	100	100
65	SQ0	140/143 (98%)	134 (96%)	6 (4%)	0	100	100
66	RR0	117/120 (98%)	113 (97%)	4 (3%)	0	100	100
66	SR0	117/120 (98%)	113 (97%)	4 (3%)	0	100	100
67	RS0	142/160 (89%)	137 (96%)	4 (3%)	1 (1%)	19	57
67	SS0	142/160 (89%)	137 (96%)	4 (3%)	1 (1%)	19	57
68	RT0	140/143 (98%)	140 (100%)	0	0	100	100
68	ST0	140/143 (98%)	140 (100%)	0	0	100	100
69	RU0	98/119 (82%)	94 (96%)	4 (4%)	0	100	100
69	SU0	98/119 (82%)	94 (96%)	4 (4%)	0	100	100
70	RV0	63/67 (94%)	62 (98%)	1 (2%)	0	100	100
70	SV0	63/67 (94%)	62 (98%)	1 (2%)	0	100	100
71	RW0	126/128 (98%)	124 (98%)	2 (2%)	0	100	100
71	SW0	126/128 (98%)	124 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
72	RX0	138/141 (98%)	136 (99%)	2 (1%)	0	100	100
72	SX0	138/141 (98%)	136 (99%)	2 (1%)	0	100	100
73	RY0	134/146 (92%)	121 (90%)	11 (8%)	2 (2%)	8	40
73	SY0	134/146 (92%)	122 (91%)	10 (8%)	2 (2%)	8	40
74	RZ0	74/128 (58%)	69 (93%)	5 (7%)	0	100	100
74	SZ0	74/128 (58%)	69 (93%)	5 (7%)	0	100	100
75	RP0	115/163 (71%)	113 (98%)	2 (2%)	0	100	100
75	SP0	115/163 (71%)	113 (98%)	2 (2%)	0	100	100
All	All	21258/22938 (93%)	20523 (96%)	709 (3%)	26 (0%)	50	83

5 of 26 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
15	LGG	78	GLY
73	SY0	134	LYS
15	KGG	78	GLY
73	RY0	134	LYS
30	LPP	18	TYR

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	KA0	202/203 (100%)	199 (98%)	3 (2%)	60	75
3	LA0	202/203 (100%)	199 (98%)	3 (2%)	60	75
4	KAA	123/123 (100%)	119 (97%)	4 (3%)	33	52
4	LAA	123/123 (100%)	119 (97%)	4 (3%)	33	52
5	KB0	328/336 (98%)	319 (97%)	9 (3%)	40	58
5	LB0	328/336 (98%)	319 (97%)	9 (3%)	40	58
6	KC0	277/278 (100%)	274 (99%)	3 (1%)	70	80
6	LC0	277/278 (100%)	274 (99%)	3 (1%)	70	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	KCC	87/97 (90%)	85 (98%)	2 (2%)	45	64
7	LCC	87/97 (90%)	85 (98%)	2 (2%)	45	64
8	KD0	251/261 (96%)	249 (99%)	2 (1%)	79	85
8	LD0	251/261 (96%)	249 (99%)	2 (1%)	79	85
9	KDD	99/100 (99%)	99 (100%)	0	100	100
9	LDD	99/100 (99%)	99 (100%)	0	100	100
10	KE0	153/159 (96%)	150 (98%)	3 (2%)	50	68
10	LE0	153/159 (96%)	150 (98%)	3 (2%)	50	68
11	KEE	118/122 (97%)	118 (100%)	0	100	100
11	LEE	118/122 (97%)	118 (100%)	0	100	100
12	KF0	212/216 (98%)	211 (100%)	1 (0%)	86	89
12	LF0	212/216 (98%)	211 (100%)	1 (0%)	86	89
13	KFF	98/98 (100%)	98 (100%)	0	100	100
13	LFF	98/98 (100%)	98 (100%)	0	100	100
14	KG0	183/190 (96%)	183 (100%)	0	100	100
14	LG0	183/190 (96%)	183 (100%)	0	100	100
15	KGG	88/90 (98%)	86 (98%)	2 (2%)	45	64
15	LGG	88/90 (98%)	86 (98%)	2 (2%)	45	64
16	KH0	165/169 (98%)	161 (98%)	4 (2%)	44	62
16	LH0	165/169 (98%)	161 (98%)	4 (2%)	44	62
17	KHH	110/110 (100%)	109 (99%)	1 (1%)	75	83
17	LHH	110/110 (100%)	109 (99%)	1 (1%)	75	83
18	KI0	188/189 (100%)	188 (100%)	0	100	100
18	LI0	188/189 (100%)	188 (100%)	0	100	100
19	KII	84/84 (100%)	82 (98%)	2 (2%)	44	62
19	LII	84/84 (100%)	82 (98%)	2 (2%)	44	62
20	KJ0	146/149 (98%)	144 (99%)	2 (1%)	62	75
20	LJ0	146/149 (98%)	144 (99%)	2 (1%)	62	75
21	KJJ	78/81 (96%)	77 (99%)	1 (1%)	65	77
21	LJJ	78/81 (96%)	77 (99%)	1 (1%)	65	77
22	KL0	148/149 (99%)	142 (96%)	6 (4%)	26	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	LL0	148/149 (99%)	142 (96%)	6 (4%)	26	47
23	KLL	46/47 (98%)	46 (100%)	0	100	100
23	LLL	46/47 (98%)	46 (100%)	0	100	100
24	KM0	110/110 (100%)	110 (100%)	0	100	100
24	LM0	110/110 (100%)	110 (100%)	0	100	100
25	KMM	46/112 (41%)	46 (100%)	0	100	100
25	LMM	46/112 (41%)	46 (100%)	0	100	100
26	KN0	175/176 (99%)	171 (98%)	4 (2%)	45	64
26	LN0	175/176 (99%)	171 (98%)	4 (2%)	45	64
27	KO0	178/178 (100%)	177 (99%)	1 (1%)	84	88
27	LO0	178/178 (100%)	177 (99%)	1 (1%)	84	88
28	KOO	85/89 (96%)	85 (100%)	0	100	100
28	LOO	85/89 (96%)	85 (100%)	0	100	100
29	KP0	135/147 (92%)	132 (98%)	3 (2%)	47	65
29	LP0	135/147 (92%)	132 (98%)	3 (2%)	47	65
30	KPP	75/77 (97%)	73 (97%)	2 (3%)	40	58
30	LPP	75/77 (97%)	73 (97%)	2 (3%)	40	58
31	KQ0	165/166 (99%)	165 (100%)	0	100	100
31	LQ0	165/166 (99%)	165 (100%)	0	100	100
32	KR0	142/145 (98%)	141 (99%)	1 (1%)	81	87
32	LR0	142/145 (98%)	141 (99%)	1 (1%)	81	87
33	KS0	155/156 (99%)	152 (98%)	3 (2%)	52	69
33	LS0	155/156 (99%)	152 (98%)	3 (2%)	52	69
34	KT0	140/142 (99%)	138 (99%)	2 (1%)	62	75
34	LT0	140/142 (99%)	138 (99%)	2 (1%)	62	75
35	KU0	89/98 (91%)	88 (99%)	1 (1%)	70	80
35	LU0	89/98 (91%)	88 (99%)	1 (1%)	70	80
36	KV0	113/114 (99%)	112 (99%)	1 (1%)	75	83
36	LV0	113/114 (99%)	112 (99%)	1 (1%)	75	83
37	KW0	93/120 (78%)	89 (96%)	4 (4%)	25	46
37	LW0	93/120 (78%)	89 (96%)	4 (4%)	25	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	KX0	92/93 (99%)	91 (99%)	1 (1%)	70	80
38	LX0	92/93 (99%)	91 (99%)	1 (1%)	70	80
39	KY0	116/116 (100%)	114 (98%)	2 (2%)	56	72
39	LY0	116/116 (100%)	114 (98%)	2 (2%)	56	72
40	KZ0	106/141 (75%)	106 (100%)	0	100	100
40	LZ0	106/141 (75%)	106 (100%)	0	100	100
41	MD1	139/139 (100%)	139 (100%)	0	100	100
41	MD2	139/139 (100%)	139 (100%)	0	100	100
43	RA0	194/206 (94%)	191 (98%)	3 (2%)	60	75
43	SA0	194/206 (94%)	191 (98%)	3 (2%)	60	75
44	RAA	92/93 (99%)	92 (100%)	0	100	100
44	SAA	92/93 (99%)	92 (100%)	0	100	100
45	RB0	182/203 (90%)	182 (100%)	0	100	100
45	SB0	182/203 (90%)	182 (100%)	0	100	100
46	RBB	72/73 (99%)	71 (99%)	1 (1%)	62	75
46	SBB	72/73 (99%)	71 (99%)	1 (1%)	62	75
47	RC0	187/209 (90%)	185 (99%)	2 (1%)	70	80
47	SC0	187/209 (90%)	185 (99%)	2 (1%)	70	80
48	RCC	51/54 (94%)	51 (100%)	0	100	100
48	SCC	51/54 (94%)	51 (100%)	0	100	100
49	RD0	189/215 (88%)	189 (100%)	0	100	100
49	SD0	189/215 (88%)	189 (100%)	0	100	100
50	RDD	57/57 (100%)	57 (100%)	0	100	100
50	SDD	57/57 (100%)	57 (100%)	0	100	100
51	RE0	231/251 (92%)	229 (99%)	2 (1%)	75	83
51	SE0	231/251 (92%)	229 (99%)	2 (1%)	75	83
52	REE	44/47 (94%)	44 (100%)	0	100	100
52	SEE	44/47 (94%)	44 (100%)	0	100	100
53	RF0	167/170 (98%)	163 (98%)	4 (2%)	44	62
53	SF0	167/170 (98%)	163 (98%)	4 (2%)	44	62
54	RFF	45/136 (33%)	44 (98%)	1 (2%)	47	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
54	SFF	46/136 (34%)	45 (98%)	1 (2%)	47	65
55	RG0	199/199 (100%)	195 (98%)	4 (2%)	50	68
55	SG0	199/199 (100%)	195 (98%)	4 (2%)	50	68
56	RGG	282/288 (98%)	278 (99%)	4 (1%)	62	75
56	SGG	282/288 (98%)	278 (99%)	4 (1%)	62	75
57	RH0	153/154 (99%)	153 (100%)	0	100	100
57	SH0	153/154 (99%)	153 (100%)	0	100	100
58	RI0	147/153 (96%)	147 (100%)	0	100	100
58	SI0	147/153 (96%)	147 (100%)	0	100	100
59	RJ0	152/165 (92%)	150 (99%)	2 (1%)	65	77
59	SJ0	152/165 (92%)	150 (99%)	2 (1%)	65	77
60	RK0	83/99 (84%)	82 (99%)	1 (1%)	67	78
60	SK0	83/99 (84%)	82 (99%)	1 (1%)	67	78
61	RL0	140/145 (97%)	139 (99%)	1 (1%)	81	87
61	SL0	140/145 (97%)	139 (99%)	1 (1%)	81	87
62	RM0	99/114 (87%)	99 (100%)	0	100	100
62	SM0	99/114 (87%)	99 (100%)	0	100	100
63	RN0	126/127 (99%)	126 (100%)	0	100	100
63	SN0	126/127 (99%)	126 (100%)	0	100	100
64	RO0	102/108 (94%)	101 (99%)	1 (1%)	73	82
64	SO0	102/108 (94%)	101 (99%)	1 (1%)	73	82
65	RQ0	120/121 (99%)	119 (99%)	1 (1%)	79	85
65	SQ0	120/121 (99%)	119 (99%)	1 (1%)	79	85
66	RR0	109/111 (98%)	108 (99%)	1 (1%)	75	83
66	SR0	109/111 (98%)	108 (99%)	1 (1%)	75	83
67	RS0	125/138 (91%)	124 (99%)	1 (1%)	79	85
67	SS0	125/138 (91%)	124 (99%)	1 (1%)	79	85
68	RT0	129/130 (99%)	127 (98%)	2 (2%)	58	73
68	ST0	129/130 (99%)	127 (98%)	2 (2%)	58	73
69	RU0	92/110 (84%)	92 (100%)	0	100	100
69	SU0	92/110 (84%)	92 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
70	RV0	61/63 (97%)	61 (100%)	0	100	100
70	SV0	61/63 (97%)	61 (100%)	0	100	100
71	RW0	111/111 (100%)	110 (99%)	1 (1%)	75	83
71	SW0	111/111 (100%)	110 (99%)	1 (1%)	75	83
72	RX0	115/116 (99%)	115 (100%)	0	100	100
72	SX0	115/116 (99%)	115 (100%)	0	100	100
73	RY0	126/136 (93%)	121 (96%)	5 (4%)	27	47
73	SY0	126/136 (93%)	121 (96%)	5 (4%)	27	47
74	RZ0	73/118 (62%)	73 (100%)	0	100	100
74	SZ0	73/118 (62%)	73 (100%)	0	100	100
75	RP0	107/144 (74%)	106 (99%)	1 (1%)	75	83
75	SP0	107/144 (74%)	106 (99%)	1 (1%)	75	83
All	All	19001/20268 (94%)	18785 (99%)	216 (1%)	69	80

5 of 216 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	KB0	23	LYS
20	KJ0	106	HIS
59	RJ0	130	GLN
5	KB0	133	LEU
10	KE0	15	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	K50	2494/2618 (95%)	738 (29%)	103 (4%)
1	L50	2494/2618 (95%)	738 (29%)	102 (4%)
2	K70	118/119 (99%)	36 (30%)	4 (3%)
2	L70	118/119 (99%)	36 (30%)	4 (3%)
42	R60	1352/1368 (98%)	518 (38%)	70 (5%)
42	S60	1352/1368 (98%)	517 (38%)	70 (5%)
All	All	7928/8210 (96%)	2583 (32%)	353 (4%)

5 of 2583 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L50	2	U
1	L50	3	A
1	L50	13	A
1	L50	15	G
1	L50	21	U

5 of 353 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	K50	1454	U
42	R60	127	A
1	K50	1614	G
1	K50	2060	A
42	R60	355	C

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

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

## 5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

Of 18 ligands modelled in this entry, 18 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 ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

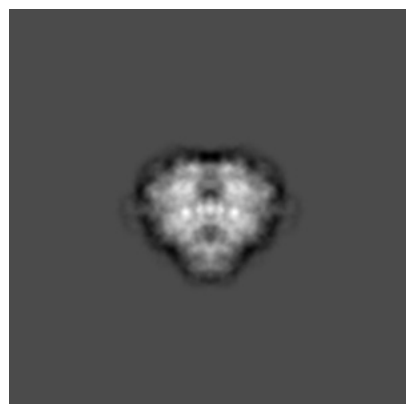
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-17457. These allow visual inspection of the internal detail of the map and identification of artifacts.

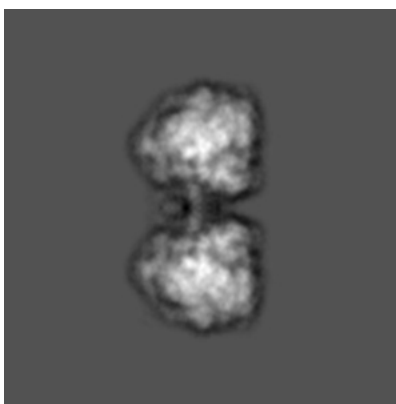
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

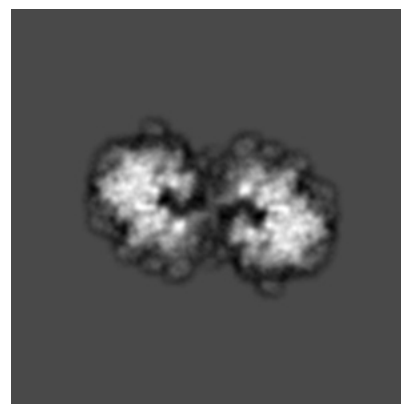
#### 6.1.1 Primary map



X

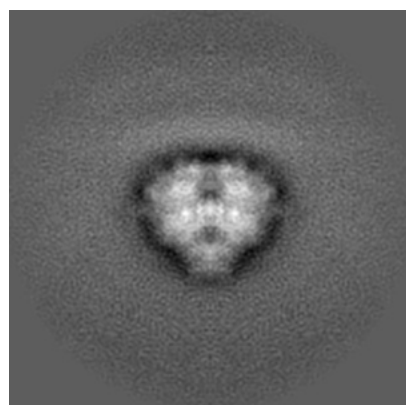


Y

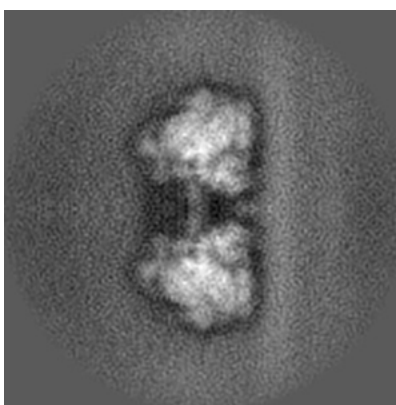


Z

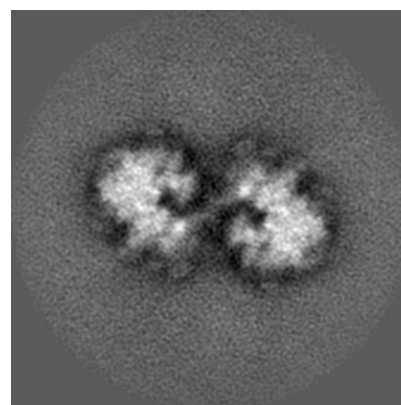
#### 6.1.2 Raw map



X



Y



Z

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

## 6.2 Central slices [i](#)

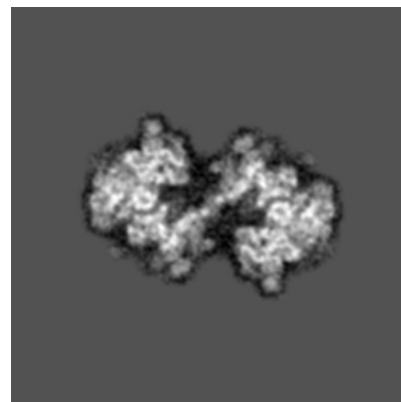
### 6.2.1 Primary map



X Index: 84

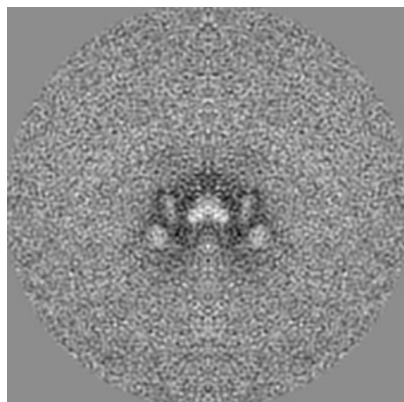


Y Index: 84

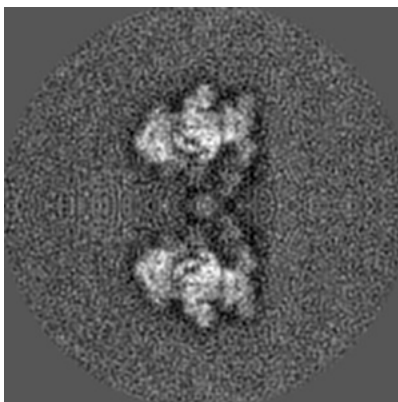


Z Index: 84

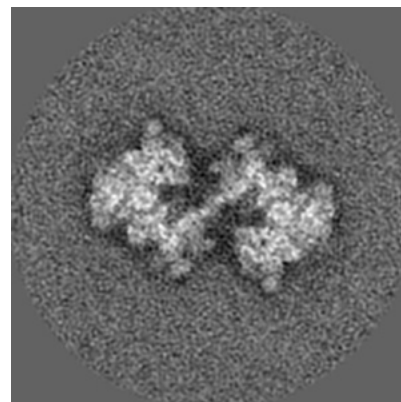
### 6.2.2 Raw map



X Index: 84



Y Index: 84

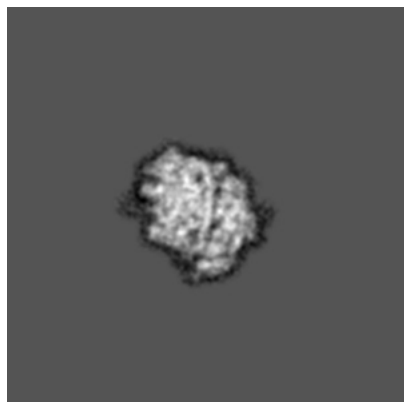


Z Index: 84

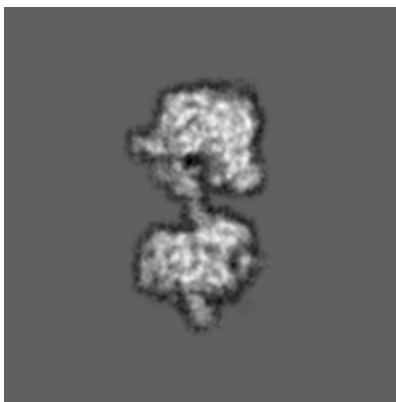
The images above show central slices of the map in three orthogonal directions.

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

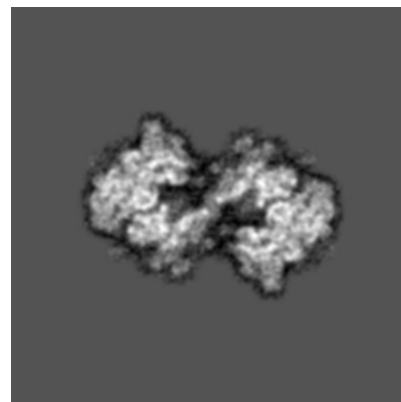
### 6.3.1 Primary map



X Index: 114

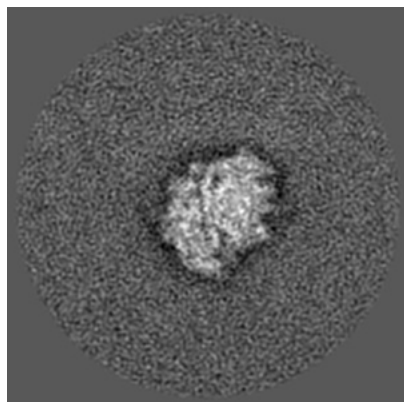


Y Index: 76

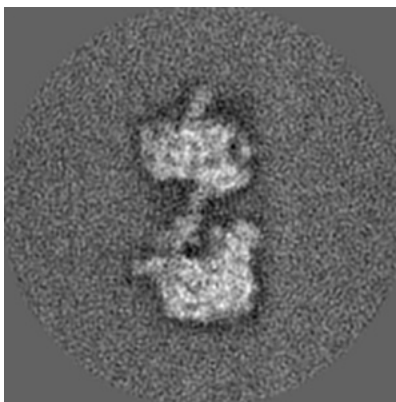


Z Index: 83

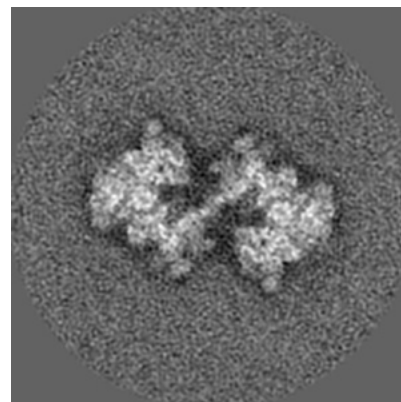
### 6.3.2 Raw map



X Index: 55



Y Index: 92



Z Index: 84

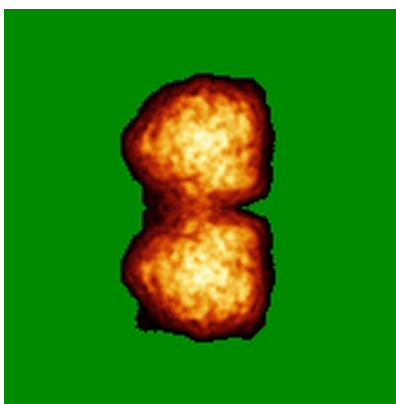
The images above show the largest variance slices of the map in three orthogonal directions.

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

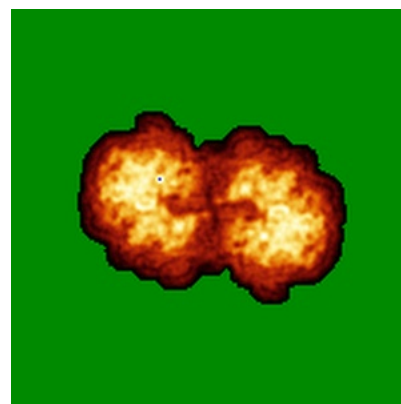
### 6.4.1 Primary map



X

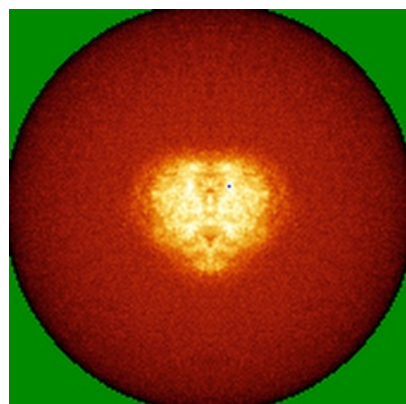


Y

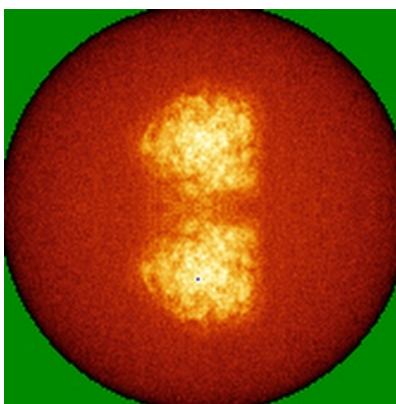


Z

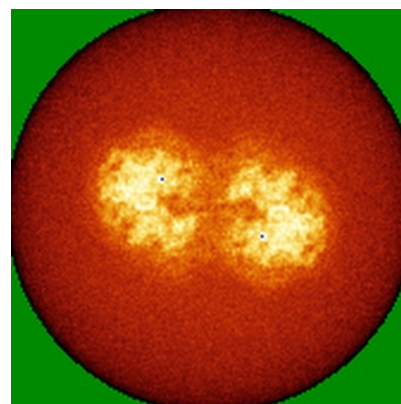
### 6.4.2 Raw map



X



Y



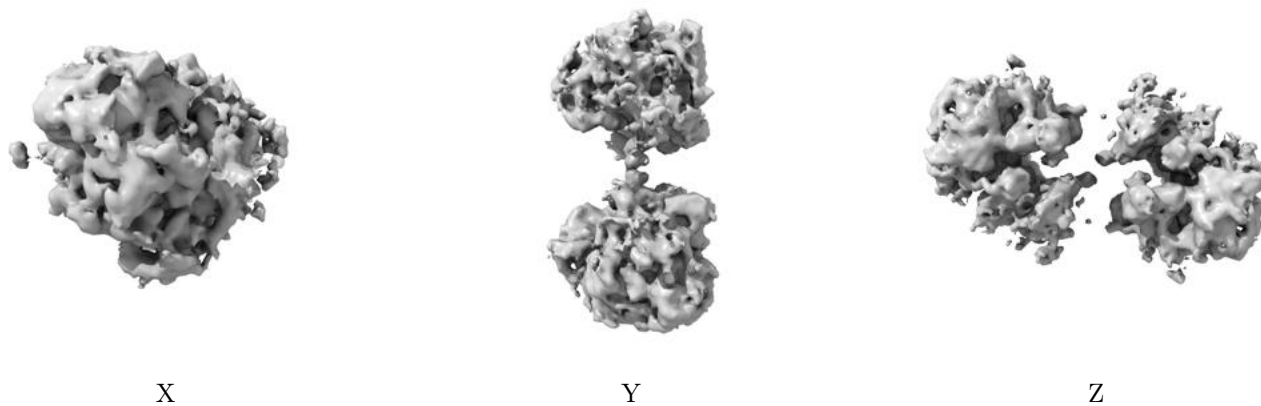
Z

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.



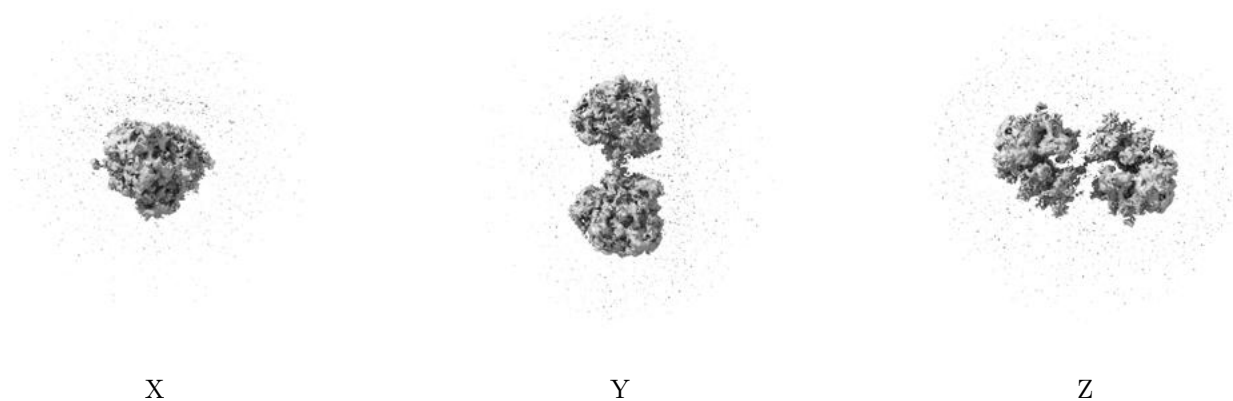
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.58. 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.

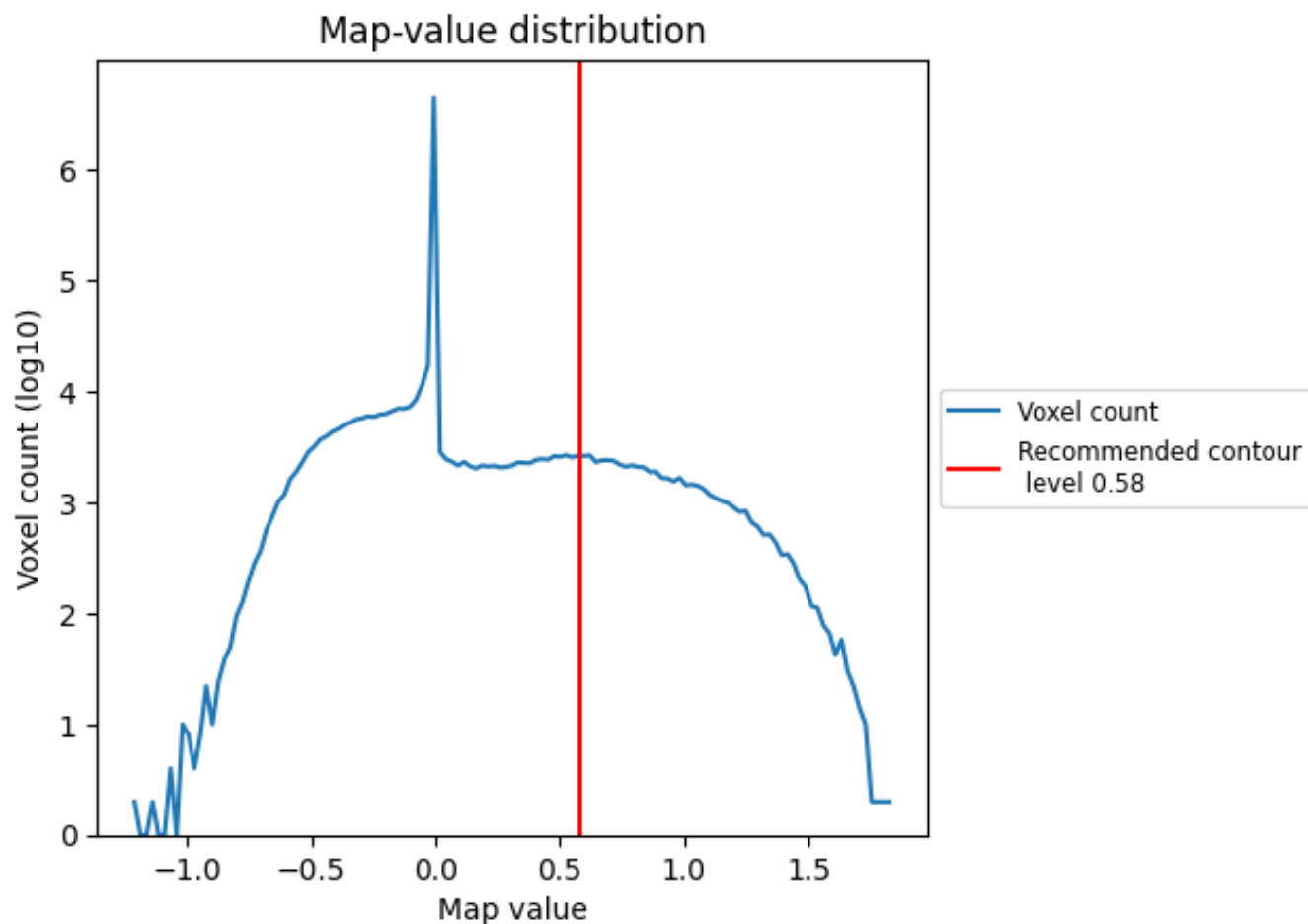
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

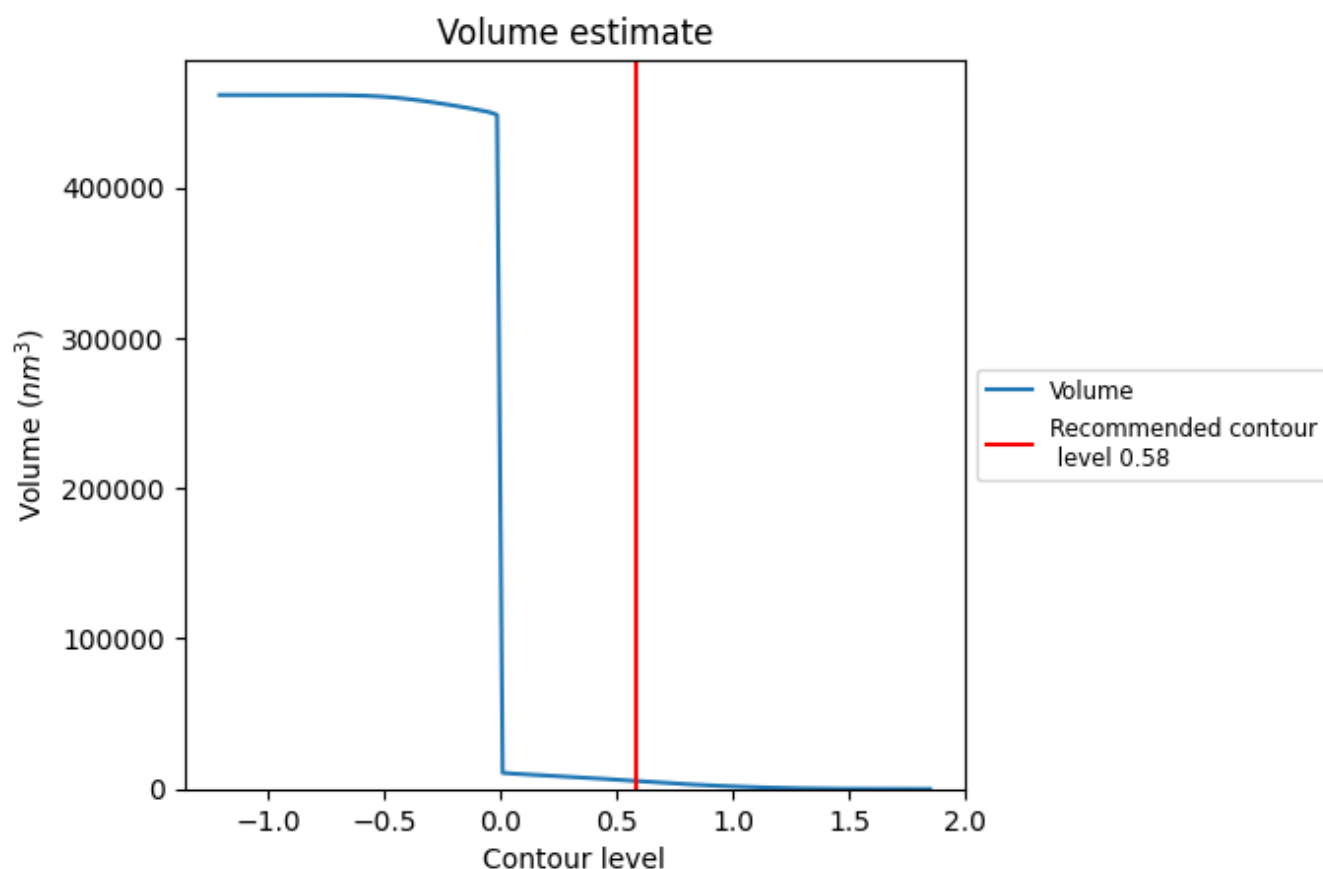
This section contains the results of statistical analysis of the map.

### 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.

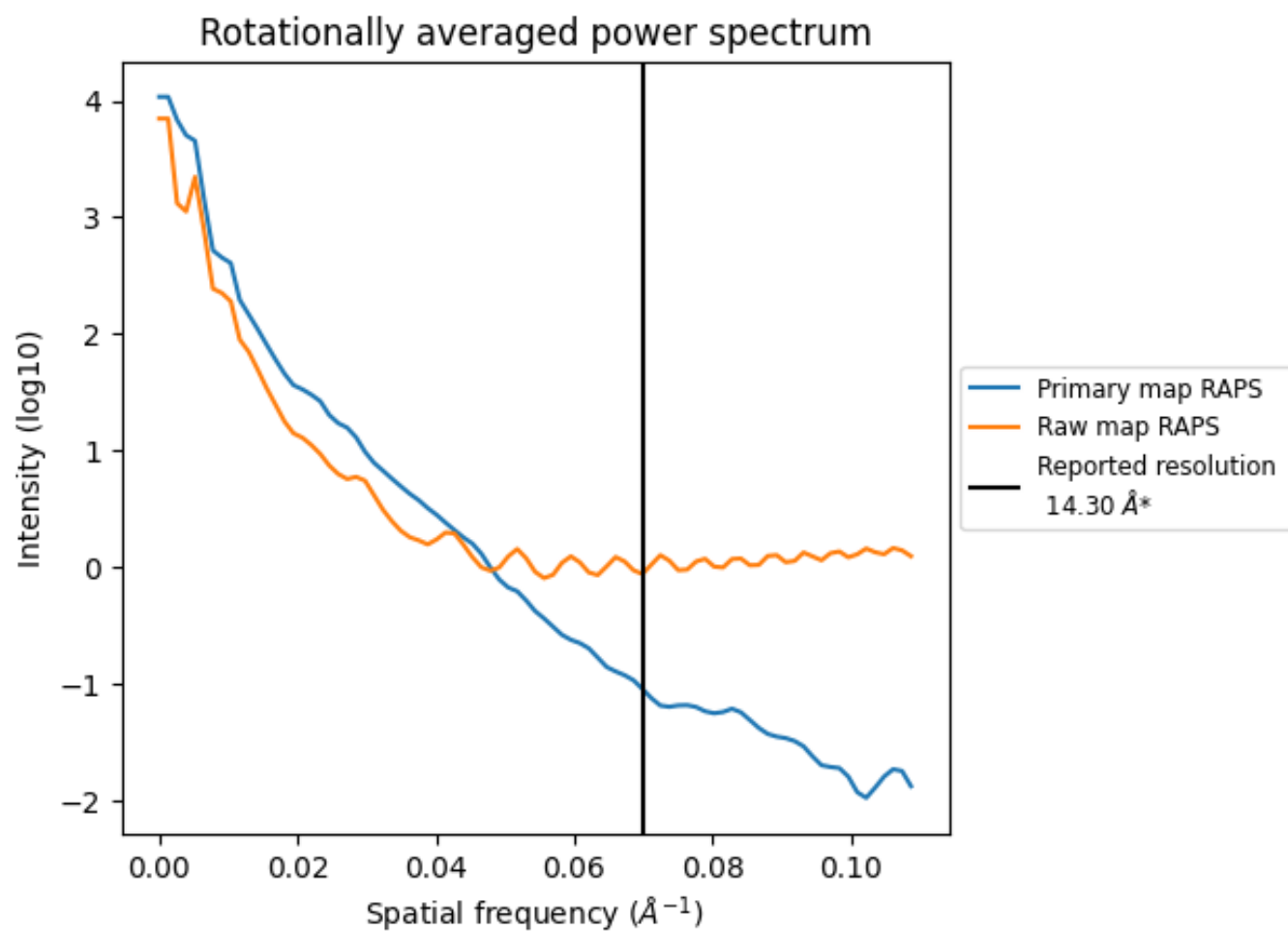
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5294 nm<sup>3</sup>; this corresponds to an approximate mass of 4782 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 ⓘ

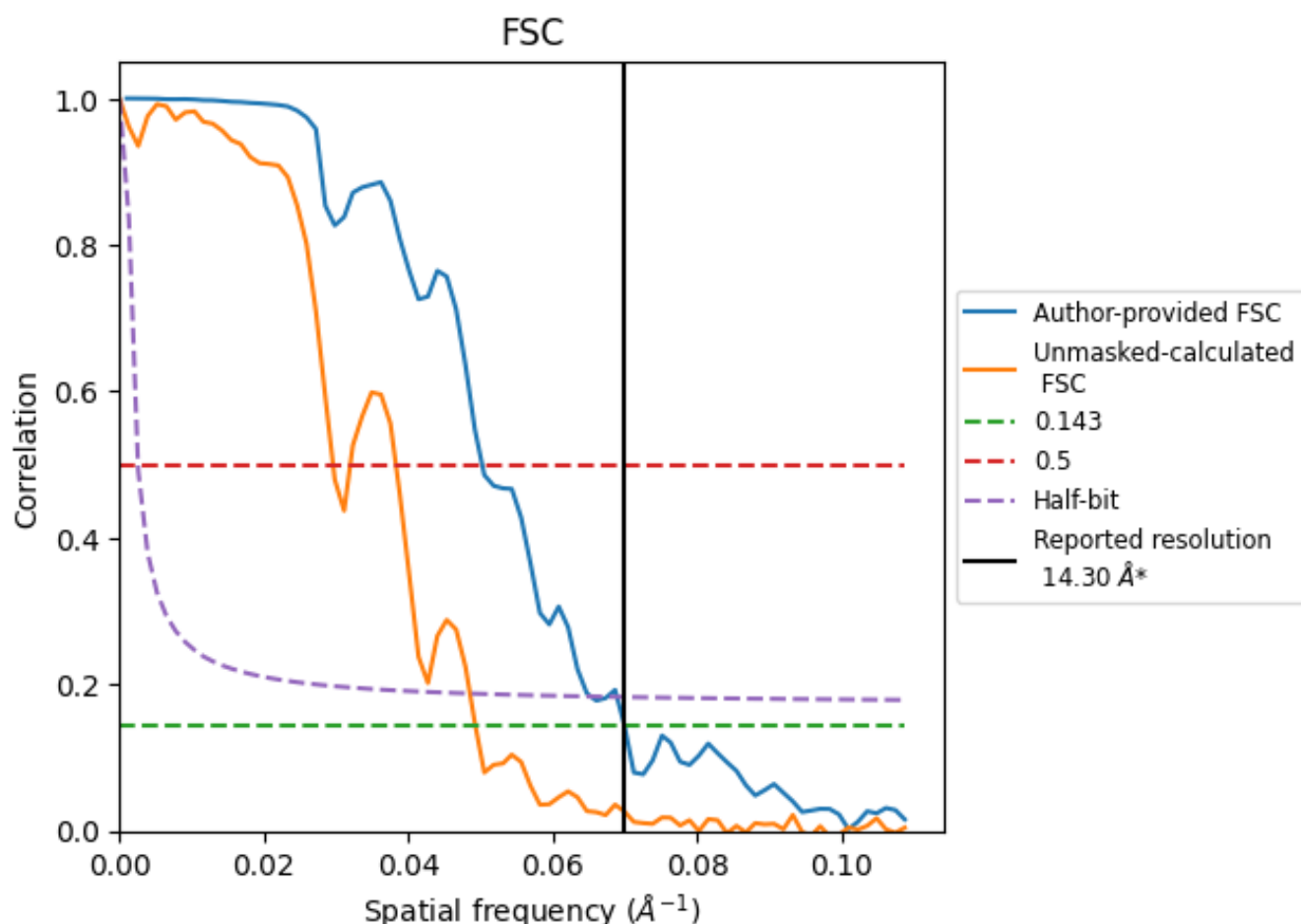


\*Reported resolution corresponds to spatial frequency of 0.070  $\text{\AA}^{-1}$

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

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.070 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

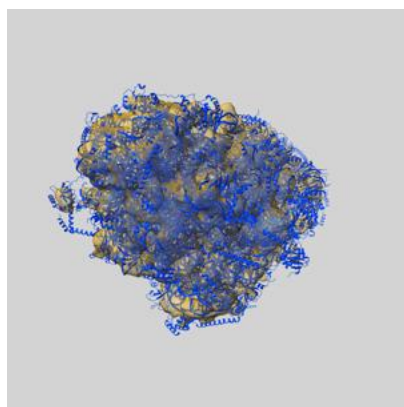
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	14.30	-	-
Author-provided FSC curve	14.31	19.92	15.31
Unmasked-calculated*	20.33	33.90	20.62

\*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 20.33 differs from the reported value 14.3 by more than 10 %

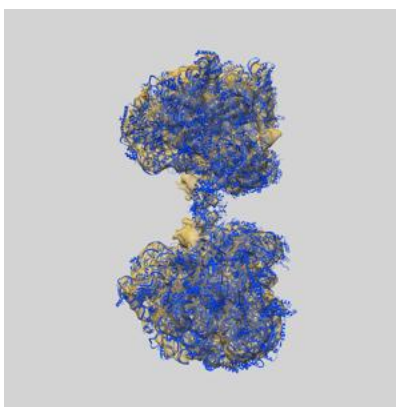
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-17457 and PDB model 8P60. Per-residue inclusion information can be found in section 3 on page 25.

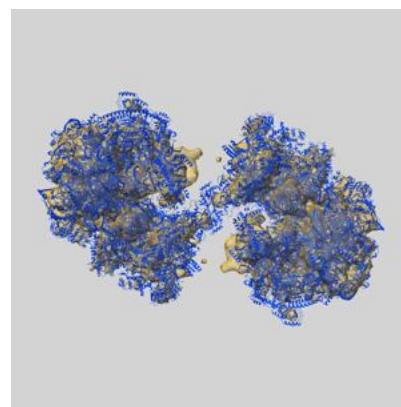
### 9.1 Map-model overlay [i](#)



X



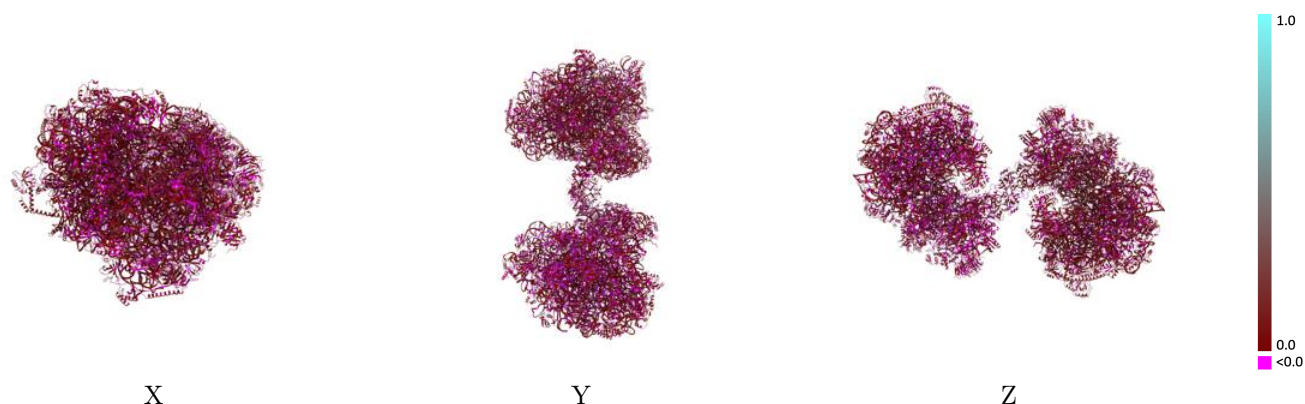
Y



Z

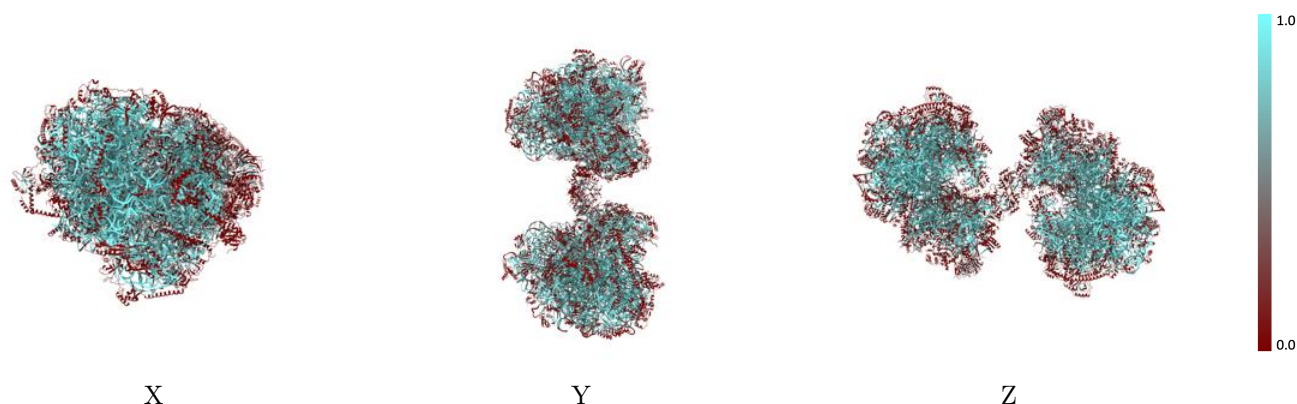
The images above show the 3D surface view of the map at the recommended contour level 0.58 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 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.

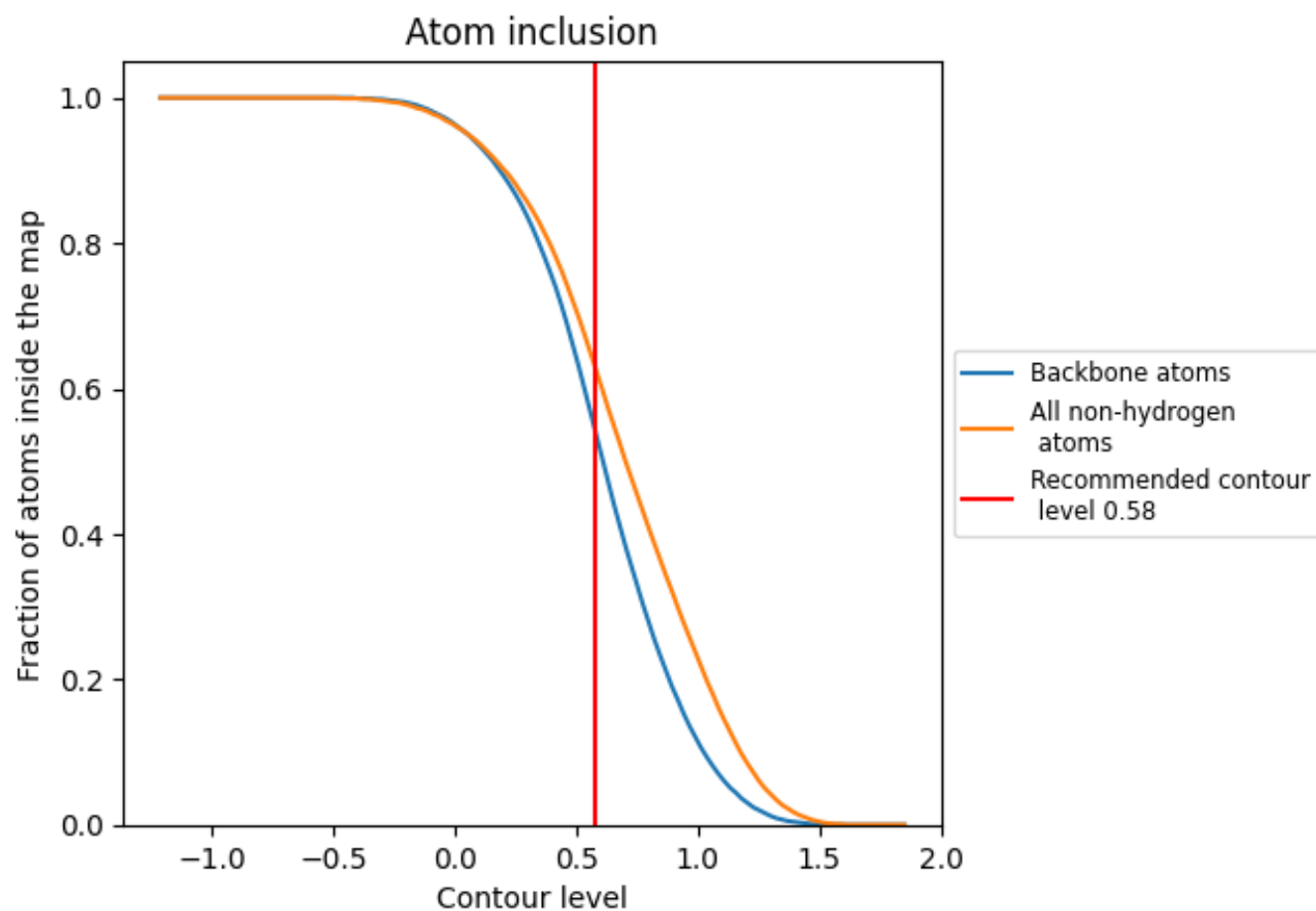
## 9.3 Atom inclusion mapped to coordinate model [i](#)



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 (0.58).









































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 54% of all backbone atoms, 63% 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 (0.58) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6260	 0.0540
K50	 0.8580	 0.0630
K70	 0.7670	 0.0610
KA0	 0.5520	 0.0200
KAA	 0.6240	 0.0140
KB0	 0.5200	 0.0110
KC0	 0.4360	 0.0230
KCC	 0.2870	 0.0540
KD0	 0.3260	 0.0420
KDD	 0.4740	 0.0260
KE0	 0.1230	 0.0420
KEE	 0.4530	 0.0270
KF0	 0.3250	 0.0420
KFF	 0.2800	 0.0500
KG0	 0.2560	 0.0580
KGK	 0.5730	 -0.0070
KH0	 0.3900	 0.0390
KHH	 0.2960	 0.0600
KI0	 0.5110	 -0.0030
KII	 0.4200	 0.0400
KJ0	 0.3960	 0.0380
KJJ	 0.6830	 -0.0090
KL0	 0.4180	 0.0410
KLL	 0.6380	 0.0030
KM0	 0.0800	 0.0500
KMM	 0.6050	 0.0210
KN0	 0.9390	 -0.0100
KO0	 0.4170	 0.0420
KOO	 0.8010	 0.0230
KP0	 0.4330	 0.0310
KPP	 0.6120	 0.0370
KQ0	 0.3460	 0.0270
KR0	 0.4390	 0.0290
KS0	 0.2010	 0.0370
KT0	 0.3500	 0.0200



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Chain	Atom inclusion	Q-score
KU0	 0.2750	 0.0620
KV0	 0.6120	 0.0110
KW0	 0.4180	 0.0120
KX0	 0.4740	 0.0360
KY0	 0.3800	 0.0290
KZ0	 0.2300	 0.0570
L50	 0.9000	 0.0850
L70	 0.8660	 0.0940
LA0	 0.5590	 0.0370
LAA	 0.6880	 0.0230
LB0	 0.4720	 0.0150
LC0	 0.5420	 0.0370
LCC	 0.2740	 0.0730
LD0	 0.4090	 0.0460
LDD	 0.5280	 0.0200
LE0	 0.1580	 0.0650
LEE	 0.5620	 0.0310
LF0	 0.3910	 0.0650
LFF	 0.3930	 0.0430
LG0	 0.2280	 0.0480
LGG	 0.5520	 -0.0050
LH0	 0.3950	 0.0480
LHH	 0.3930	 0.0350
LI0	 0.4970	 0.0350
LII	 0.4230	 0.0440
LJ0	 0.3090	 0.0450
LJJ	 0.7950	 0.0110
LL0	 0.5090	 0.0270
LLL	 0.7060	 -0.0100
LM0	 0.0820	 0.0860
LMM	 0.4270	 0.0060
LN0	 0.9350	 -0.0060
LO0	 0.4440	 0.0560
LOO	 0.5440	 0.0230
LP0	 0.5800	 0.0310
LPP	 0.4830	 0.0260
LQ0	 0.4650	 0.0530
LR0	 0.4090	 0.0300
LS0	 0.3030	 0.0660
LT0	 0.4470	 0.0340
LU0	 0.2700	 0.0540
LV0	 0.4030	 0.0280

































































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Chain	Atom inclusion	Q-score
LW0	0.2350	0.0290
LX0	0.4970	0.0050
LY0	0.3750	0.0250
LZ0	0.2290	0.0520
MD1	0.3180	0.0670
MD2	0.2550	0.0530
R60	0.8020	0.0570
RA0	0.1510	0.0330
RAA	0.5920	0.0270
RB0	0.3410	0.0420
RBB	0.3870	0.0380
RC0	0.3840	0.0320
RCC	0.4480	0.0420
RD0	0.2490	0.0300
RDD	0.5530	0.0150
RE0	0.4410	0.0280
REE	0.3780	0.0110
RF0	0.5270	0.0390
RFF	0.0000	0.0240
RG0	0.1790	0.0430
RGG	0.2130	0.0330
RH0	0.1090	0.0540
RI0	0.3660	0.0280
RJ0	0.5560	0.0190
RK0	0.1440	0.0310
RL0	0.3810	0.0260
RM0	0.1100	0.0270
RN0	0.4650	0.0160
RO0	0.5900	0.0200
RP0	0.1940	0.0270
RQ0	0.4880	0.0270
RR0	0.3250	0.0450
RS0	0.2330	0.0480
RT0	0.3610	0.0260
RU0	0.2610	0.0370
RV0	0.2720	0.0440
RW0	0.5430	-0.0050
RX0	0.1600	-0.0150
RY0	0.3650	0.0420
RZ0	0.2810	0.0740
S60	0.8830	0.0860
SA0	0.1240	0.0520

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Chain	Atom inclusion	Q-score
SAA	 0.5660	 0.0280
SB0	 0.3380	 0.0610
SBB	 0.2980	 0.0560
SC0	 0.3530	 0.0580
SCC	 0.3280	 0.0550
SD0	 0.1760	 0.0560
SDD	 0.4240	 0.0470
SE0	 0.3410	 0.0350
SEE	 0.2550	 0.0470
SF0	 0.4790	 0.0480
SFF	 0.0260	 0.0360
SG0	 0.2580	 0.0480
SGG	 0.2120	 0.0490
SH0	 0.0650	 0.0690
SI0	 0.4710	 0.0310
SJ0	 0.3660	 0.0420
SK0	 0.1040	 0.0580
SL0	 0.3580	 0.0360
SM0	 0.0600	 0.0490
SN0	 0.4900	 0.0320
SO0	 0.5760	 0.0340
SP0	 0.3560	 0.0630
SQ0	 0.4150	 0.0420
SR0	 0.2010	 0.0360
SS0	 0.4100	 0.0640
ST0	 0.3710	 0.0440
SU0	 0.2500	 0.0420
SV0	 0.2680	 0.0660
SW0	 0.4280	 0.0370
SX0	 0.2780	 0.0240
SY0	 0.2830	 0.0760
SZ0	 0.2860	 0.0740