



## wwPDB EM Validation Summary Report ⓘ

Feb 13, 2024 – 10:03 PM EST

PDB ID : 3J77  
EMDB ID : EMD-5976  
Title : Structures of yeast 80S ribosome-tRNA complexes in the rotated and non-rotated conformations (Class II - rotated ribosome with 1 tRNA)  
Authors : Svidritskiy, E.; Brilot, A.F.; Koh, C.S.; Grigorieff, N.; Korostelev, A.A.  
Deposited on : 2014-05-29  
Resolution : 6.20 Å (reported)  
Based on initial models : 3J3B, 3U5B, 3U5E, 4GD1, 3U5C, 3U5D

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:

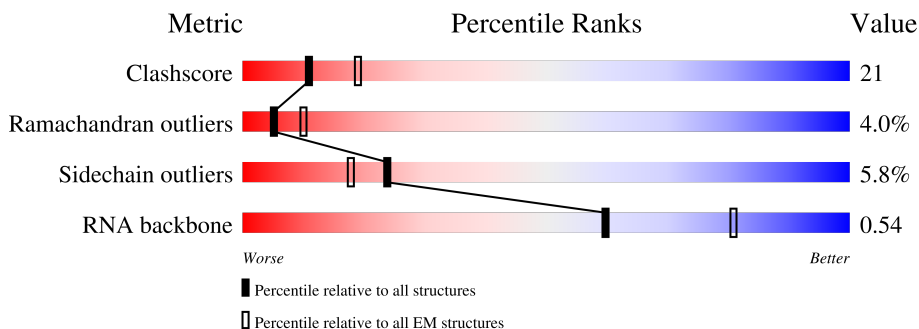
EMDB validation analysis : 0.0.1.dev70  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

# 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 6.20 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	L1	217	
2	L2	254	
3	L3	387	
4	L4	362	
5	L5	297	
6	L6	176	
7	L7	244	

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Mol	Chain	Length	Quality of chain
8	L8	256	
9	L9	191	
10	60	221	
11	61	174	
12	62	165	
13	63	199	
14	64	138	
15	65	204	
16	66	199	
17	67	184	
18	68	186	
19	69	189	
20	70	172	
21	71	160	
22	72	121	
23	73	137	
24	74	155	
25	75	142	
26	76	127	
27	77	136	
28	78	149	
29	79	59	
30	80	105	
31	81	113	
32	82	130	

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Mol	Chain	Length	Quality of chain
33	83	107	42% 53% 5% 7%
34	84	121	51% 38% 5% 7%
35	85	120	48% 49% 5% 7%
36	86	100	44% 48% 11% 7%
37	87	88	51% 44% 8% 7%
38	88	78	51% 45% 14% 7%
39	89	51	49% 43% 6% 6%
40	90	128	25% 13% 59%
41	91	25	44% 52% 4% 4%
42	92	106	50% 46% 24% 7%
43	93	92	59% 38% 5% 7%
44	P0	312	21% 16% 13% 61%
45	RC	319	56% 41% 33% 7%
46	S0	252	36% 41% 15% 18%
47	S1	255	35% 38% 11% 16%
48	S2	254	46% 37% 10% 15%
49	S3	240	50% 36% 15% 8%
50	S4	261	43% 52% 23% 5%
51	S5	225	44% 42% 19% 6%
52	S6	236	48% 44% 33% 7%
53	S7	190	40% 47% 17% 8%
54	S8	200	46% 42% 29% 6%
55	S9	197	44% 46% 13% 6%
56	10	105	31% 50% 16% 10%
57	11	156	53% 44% 27% 9%


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Mol	Chain	Length	Quality of chain
58	12	143	
59	13	151	
60	14	137	
61	15	142	
62	16	143	
63	17	136	
64	18	146	
65	19	144	
66	20	121	
67	21	87	
68	22	130	
69	23	145	
70	24	135	
71	25	108	
72	26	119	
73	27	82	
74	28	67	
75	29	56	
76	30	63	
77	31	152	
78	1S	1798	
79	2S	3395	
80	8S	158	
81	5S	121	
82	MR	14	

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Mol	Chain	Length	Quality of chain
83	PT	77	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into three segments: a green segment on the left labeled '53%', a yellow segment in the middle labeled '39%', and a red segment on the right labeled '8%'. A small red dot is visible at the beginning of the bar.</p>

## 2 Entry composition [i](#)

There are 83 unique types of molecules in this entry. The entry contains 207751 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 60S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	L1	204	Total	C	N	O	S	0	0
			1609	1031	279	290	9		

- Molecule 2 is a protein called 60S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	L2	252	Total	C	N	O	S	0	0
			1918	1193	389	335	1		

- Molecule 3 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	L3	386	Total	C	N	O	S	0	0
			3082	1956	584	534	8		

- Molecule 4 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	L4	361	Total	C	N	O	S	0	0
			2750	1730	522	495	3		

- Molecule 5 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	L5	296	Total	C	N	O	S	0	0
			2376	1501	414	459	2		

- Molecule 6 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	L6	156	Total	C	N	O	S	0	0
			1240	800	222	217	1		

- Molecule 7 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	L7	222	1785	1151	324	309	1	0	0

- Molecule 8 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	L8	233	1818	1159	326	330	3	0	0

- Molecule 9 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	L9	191	1519	963	274	278	4	0	0

- Molecule 10 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	60	211	1718	1089	325	298	6	0	0

- Molecule 11 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	61	169	1354	847	253	250	4	0	0

- Molecule 12 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
12	62	150	737	437	150	150	0	0

- Molecule 13 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
13	63	193	1543	962	315	266	0	0

- Molecule 14 is a protein called 60S ribosomal protein L14.



Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	64	136	1054	675	199	178	2	0	0

- Molecule 15 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	65	203	1721	1077	361	282	1	0	0

- Molecule 16 is a protein called 60S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	66	197	1556	1003	289	263	1	0	0

- Molecule 17 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
17	67	183	1443	896	287	260	0	0

- Molecule 18 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	68	185	1442	908	290	242	2	0	0

- Molecule 19 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
19	69	188	1522	935	326	261	0	0

- Molecule 20 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	70	172	1446	930	267	245	4	0	0

- Molecule 21 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	71	159	1277	805	246	222	4	0	0

- Molecule 22 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	72	100	796	516	131	149		0	0

- Molecule 23 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	73	136	1004	628	189	180	7	0	0

- Molecule 24 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	74	135	1089	682	219	187	1	0	0

- Molecule 25 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	75	121	969	623	170	174	2	0	0

- Molecule 26 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	76	126	994	625	192	177		0	0

- Molecule 27 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	77	135	1093	710	202	181		0	0

- Molecule 28 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	78	148	1174	749	231	191	3	0	0

- Molecule 29 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	79	58	463	289	100	74		0	0

- Molecule 30 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	80	97	743	479	124	139	1	0	0

- Molecule 31 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	81	109	890	565	168	156	1	0	0

- Molecule 32 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	82	127	1020	647	205	167	1	0	0

- Molecule 33 is a protein called 60S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	83	106	851	540	165	145	1	0	0

- Molecule 34 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	84	112	881	546	179	152	4	0	0

- Molecule 35 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	85	119	Total	C	N	O	S	0	0
			970	615	186	168	1		

- Molecule 36 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	86	99	Total	C	N	O	S	0	0
			772	481	156	133	2		

- Molecule 37 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	87	87	Total	C	N	O	S	0	0
			682	414	148	115	5		

- Molecule 38 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	88	77	Total	C	N	O	0	0
			613	391	115	107		

- Molecule 39 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	89	50	Total	C	N	O	S	0	0
			437	272	97	66	2		

- Molecule 40 is a protein called 60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	90	52	Total	C	N	O	S	0	0
			418	259	86	68	5		

- Molecule 41 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	91	25	Total	C	N	O	S	0	0
			234	142	63	28	1		

- Molecule 42 is a protein called 60S ribosomal protein L42.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	92	105	Total	C	N	O	S	0	0
			848	534	170	139	5		

- Molecule 43 is a protein called 60S ribosomal protein L43.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	93	91	Total	C	N	O	S	0	0
			695	429	138	122	6		

- Molecule 44 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	P0	121	Total	C	N	O	S	0	0
			967	621	170	173	3		

- Molecule 45 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	RC	318	Total	C	N	O	S	0	0
			2445	1546	419	472	8		

- Molecule 46 is a protein called 40S ribosomal protein S0.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	S0	206	Total	C	N	O	S	0	0
			1612	1034	285	291	2		

- Molecule 47 is a protein called 40S ribosomal protein S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	S1	214	Total	C	N	O	S	0	0
			1709	1084	310	311	4		

- Molecule 48 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	S2	217	Total	C	N	O	S	0	0
			1635	1047	289	297	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
49	S3	223	Total	C	N	O	S	0	0
			1734	1101	313	314	6		

- Molecule 50 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	S4	260	Total	C	N	O	S	0	0
			2069	1316	389	361	3		

- Molecule 51 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	S5	206	Total	C	N	O	S	0	0
			1610	1007	300	300	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
52	S6	226	Total	C	N	O	S	0	0
			1820	1142	350	325	3		

- Molecule 53 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	S7	184	Total	C	N	O	0	0
			1481	951	265	265		

- Molecule 54 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	S8	188	Total	C	N	O	S	0	0
			1490	925	298	265	2		

- Molecule 55 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	S9	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		

- Molecule 56 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	10	96	817	529	133	153	2	0	0

- Molecule 57 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
57	11	155	1245	798	235	209	3	0	0

- Molecule 58 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
58	12	124	935	587	165	181	2	0	0

- Molecule 59 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
59	13	150	1193	759	224	208	2	0	0

- Molecule 60 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
60	14	127	942	578	186	175	3	0	0

- Molecule 61 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
61	15	124	991	631	187	166	7	0	0

- Molecule 62 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
62	16	141	1106	708	203	195	0	0

- Molecule 63 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
63	17	120	965	603	183	177	2	0	0

- Molecule 64 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
64	18	145	1193	743	237	211	2	0	0

- Molecule 65 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
65	19	143	1113	694	208	209	2	0	0

- Molecule 66 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
66	20	107	856	539	156	160	1	0	0

- Molecule 67 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
67	21	87	685	420	125	138	2	0	0

- Molecule 68 is a protein called 40S ribosomal protein S22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
68	22	129	1022	650	188	181	3	0	0

- Molecule 69 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
69	23	144	1122	708	220	192	2	0	0

- Molecule 70 is a protein called 40S ribosomal protein S24.



Mol	Chain	Residues	Atoms				AltConf	Trace
70	24	134	Total	C	N	O	0	0
			1074	676	208	190		

- Molecule 71 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms				AltConf	Trace
71	25	70	Total	C	N	O	0	0
			563	360	104	99		

- Molecule 72 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	26	97	Total	C	N	O	S	0	0
			769	475	160	129	5		

- Molecule 73 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	27	81	Total	C	N	O	S	0	0
			611	382	110	114	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
74	28	63	Total	C	N	O	S	0	0
			498	306	99	92	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
75	29	53	Total	C	N	O	S	0	0
			444	275	92	73	4		

- Molecule 76 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	30	60	Total	C	N	O	S	0	0
			475	299	98	77	1		

- Molecule 77 is a protein called 40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	31	71	Total	C	N	O	S	0	0
			498	309	93	92	4		

- Molecule 78 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	1S	1781	Total	C	N	O	P	0	0
			37949	16965	6715	12488	1781		

- Molecule 79 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	2S	3287	Total	C	N	O	P	0	0
			70300	31399	12658	22956	3287		

- Molecule 80 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	8S	158	Total	C	N	O	P	0	0
			3354	1500	586	1110	158		

- Molecule 81 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	5S	121	Total	C	N	O	P	0	0
			2580	1152	461	846	121		

- Molecule 82 is a RNA chain called messenger RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	MR	9	Total	C	N	O	P	0	0
			195	88	39	59	9		

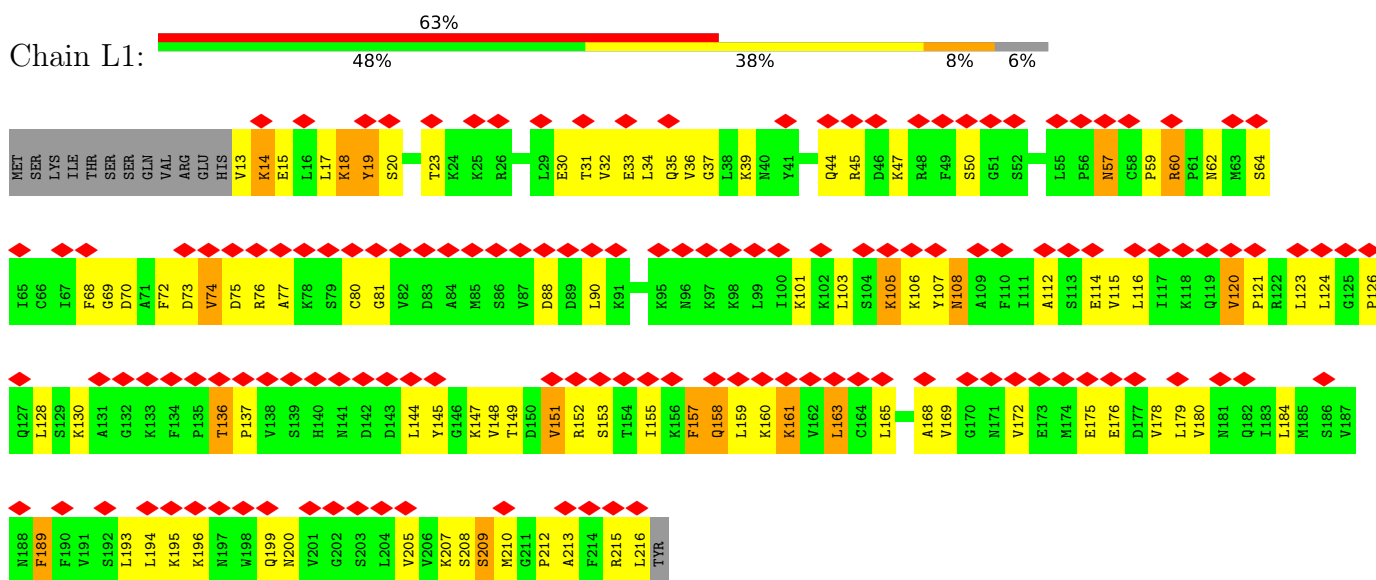
- Molecule 83 is a RNA chain called P/E-site initiator transfer RNA<sup>fMet</sup>.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	PT	77	Total	C	N	O	P	0	0
			1644	732	297	538	77		

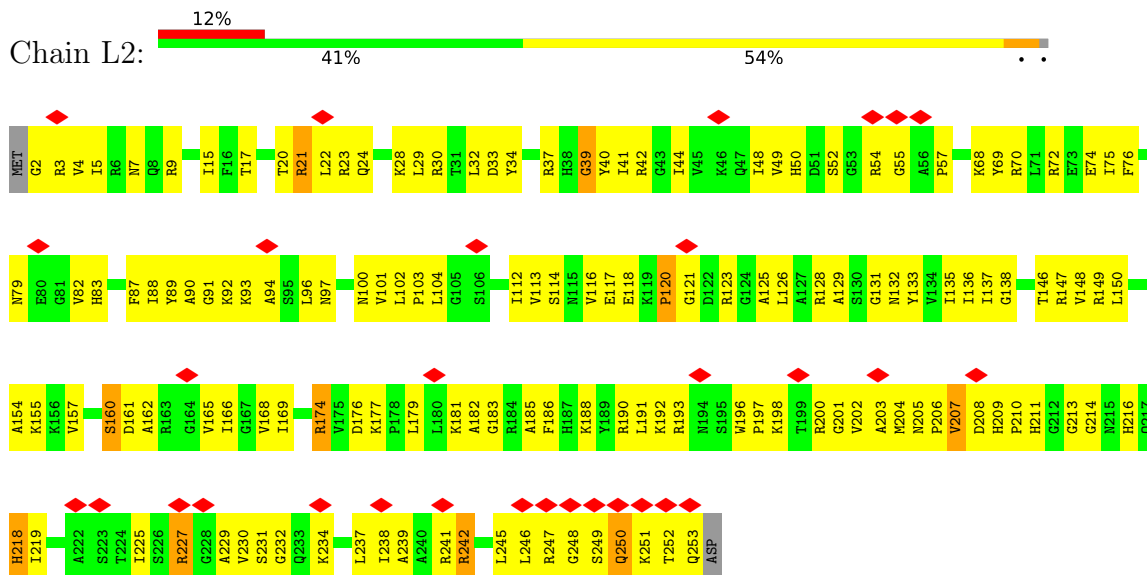
### 3 Residue-property plots

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: 60S ribosomal protein L1



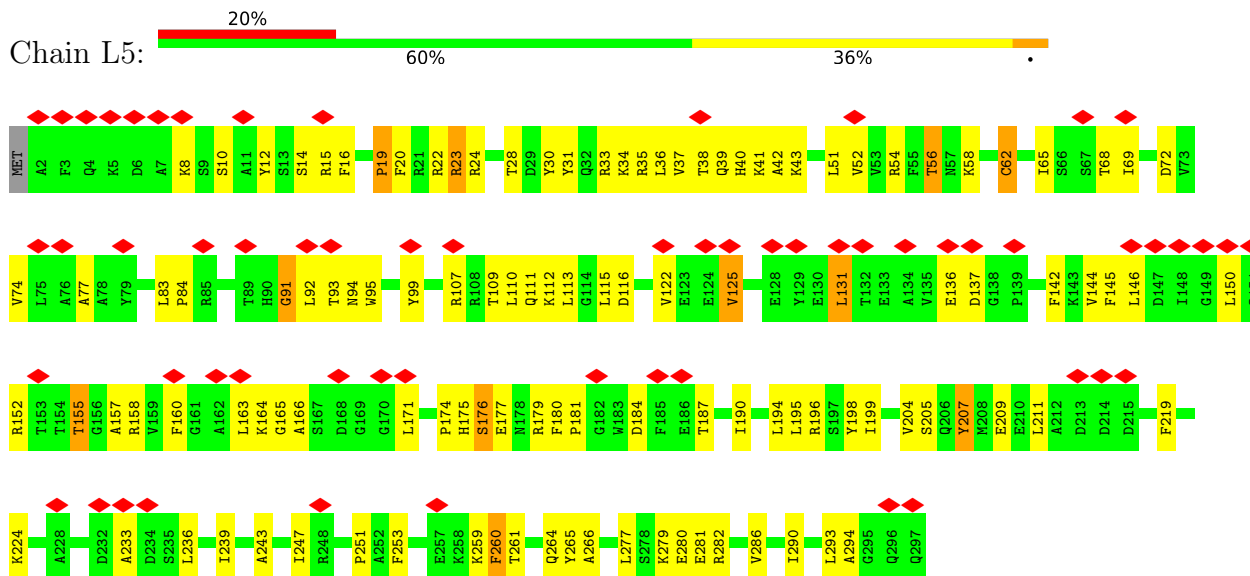
- Molecule 2: 60S ribosomal protein L2



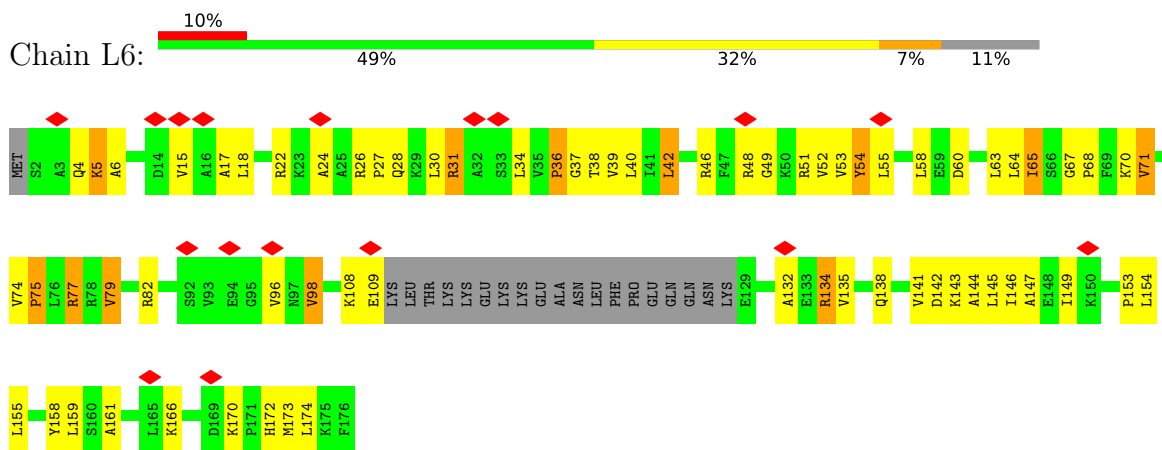
- Molecule 3: 60S ribosomal protein L3



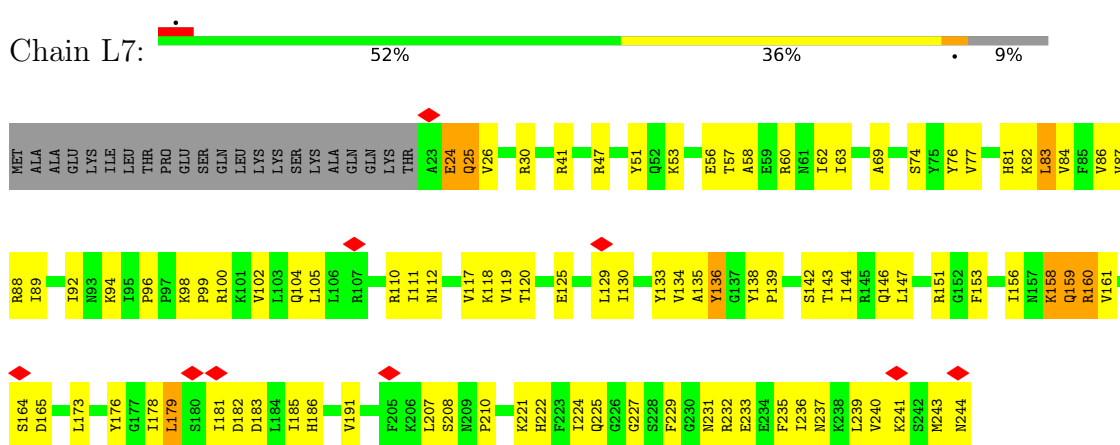
- Molecule 5: 60S ribosomal protein L5



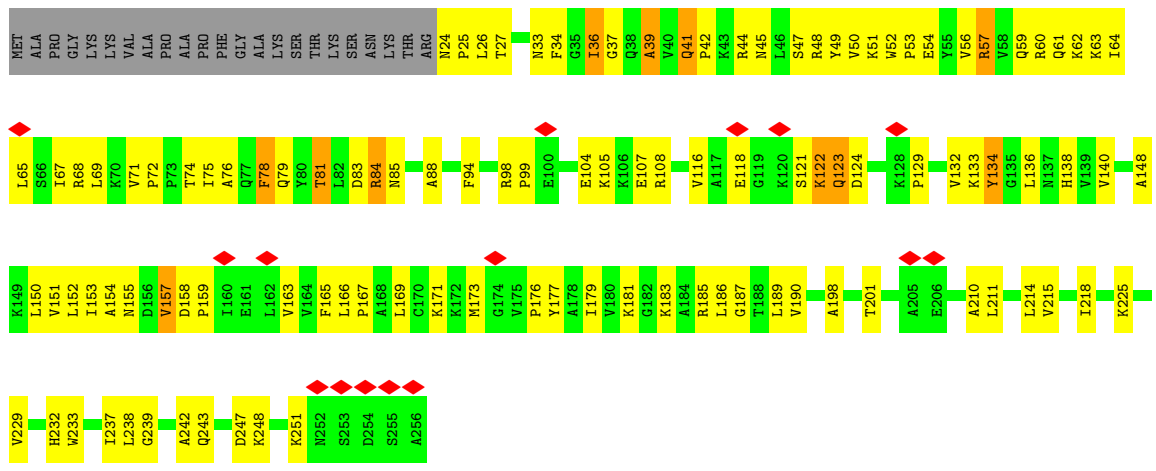
- Molecule 6: 60S ribosomal protein L6



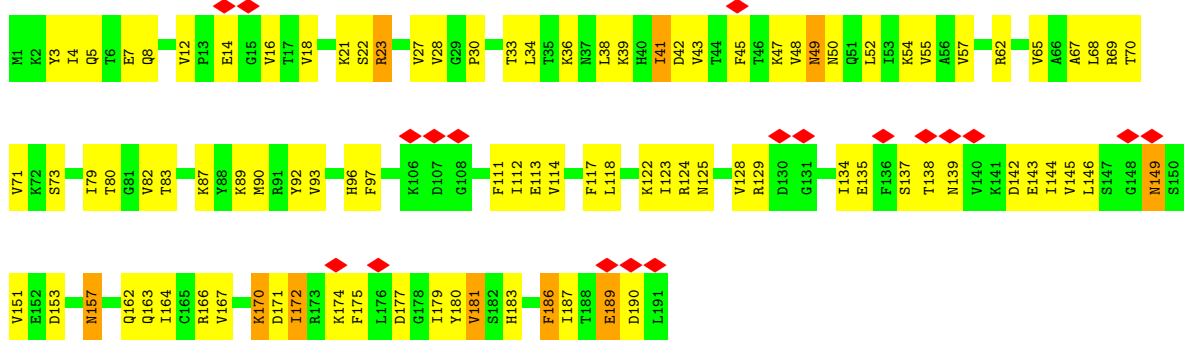
- Molecule 7: 60S ribosomal protein L7



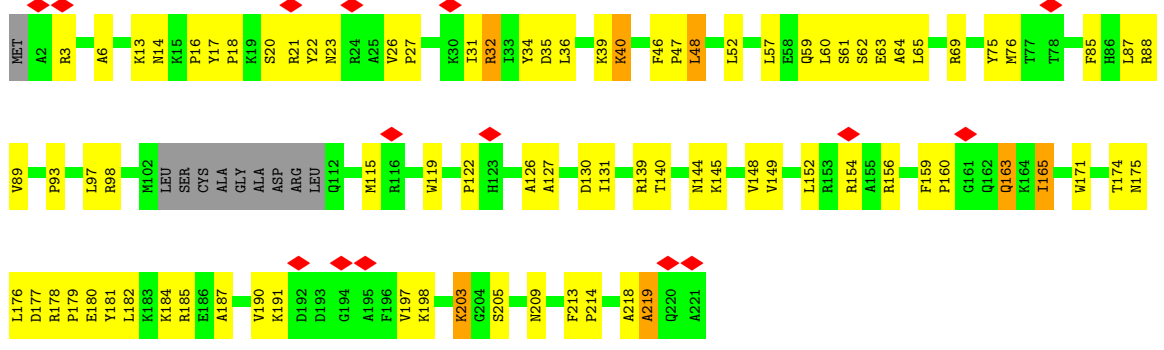
- Molecule 8: 60S ribosomal protein L8



• Molecule 9: 60S ribosomal protein L9

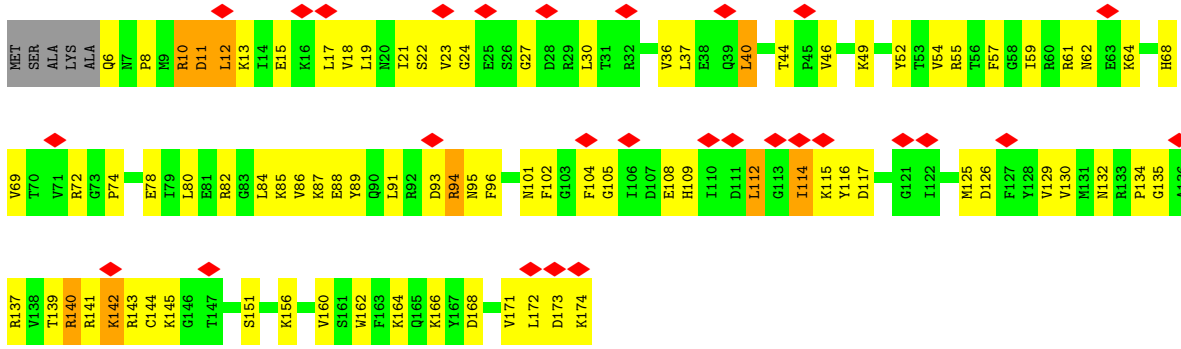


• Molecule 10: 60S ribosomal protein L10

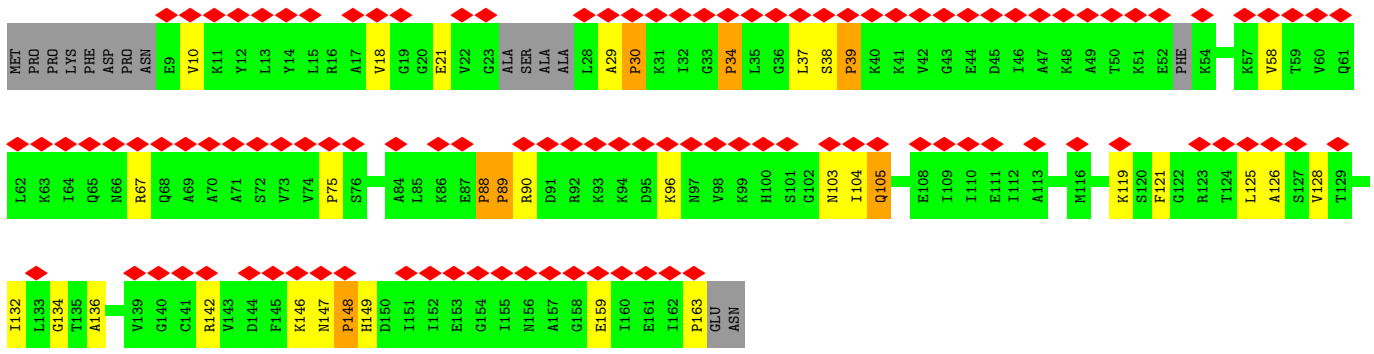
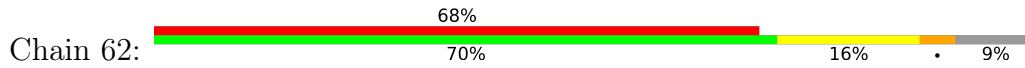


• Molecule 11: 60S ribosomal protein L11

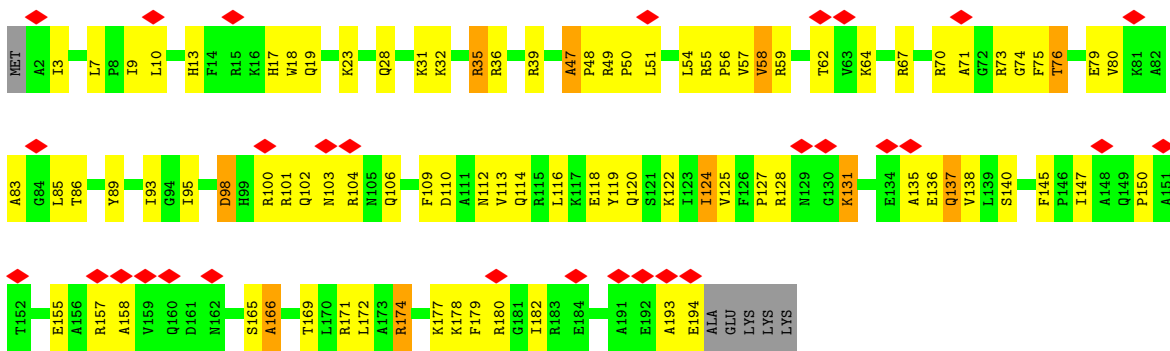




• Molecule 12: 60S ribosomal protein L12



• Molecule 13: 60S ribosomal protein L13

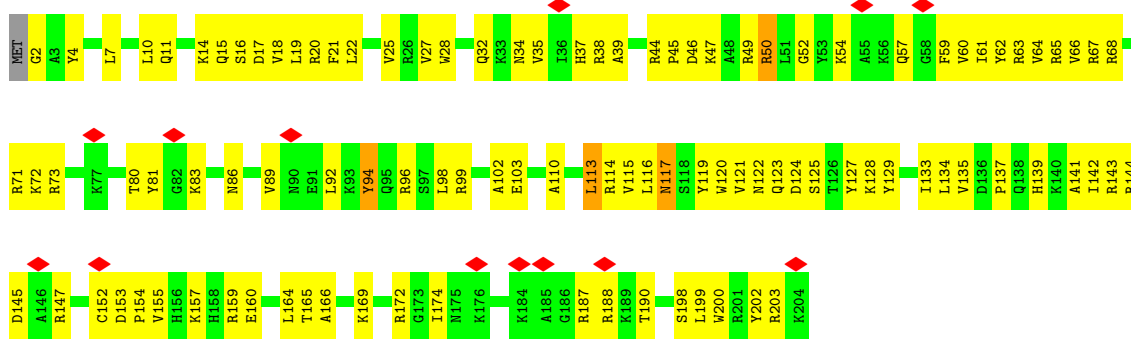


• Molecule 14: 60S ribosomal protein L14

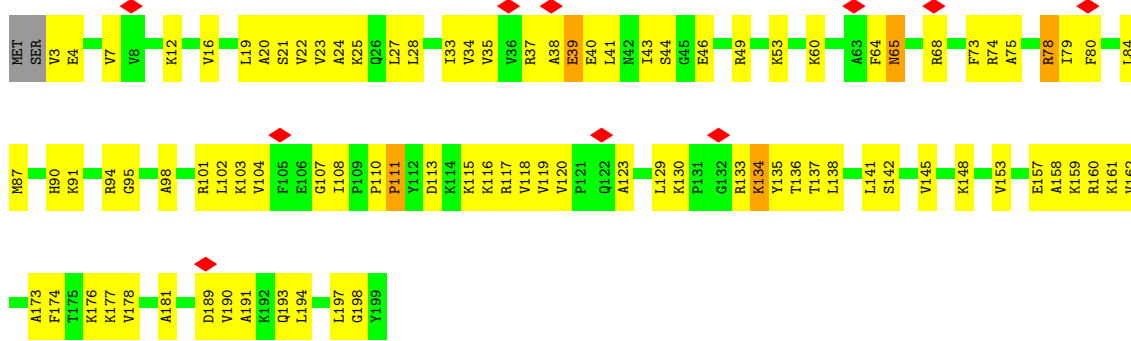




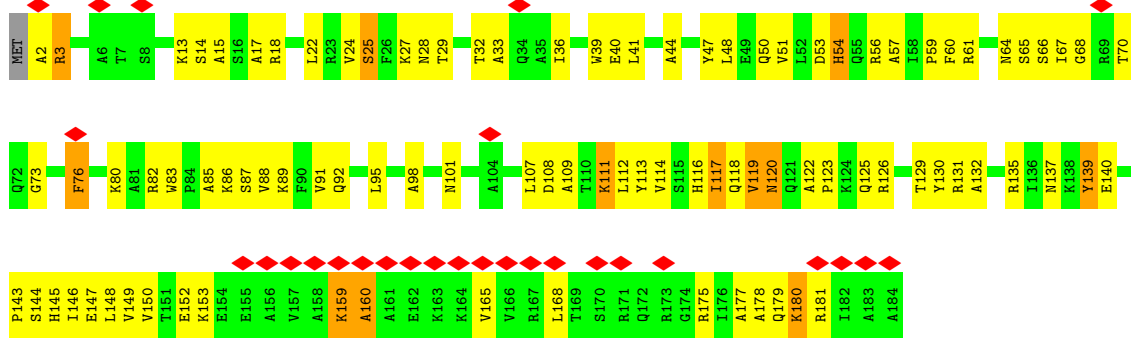
• Molecule 15: 60S ribosomal protein L15



• Molecule 16: 60S ribosomal protein L16

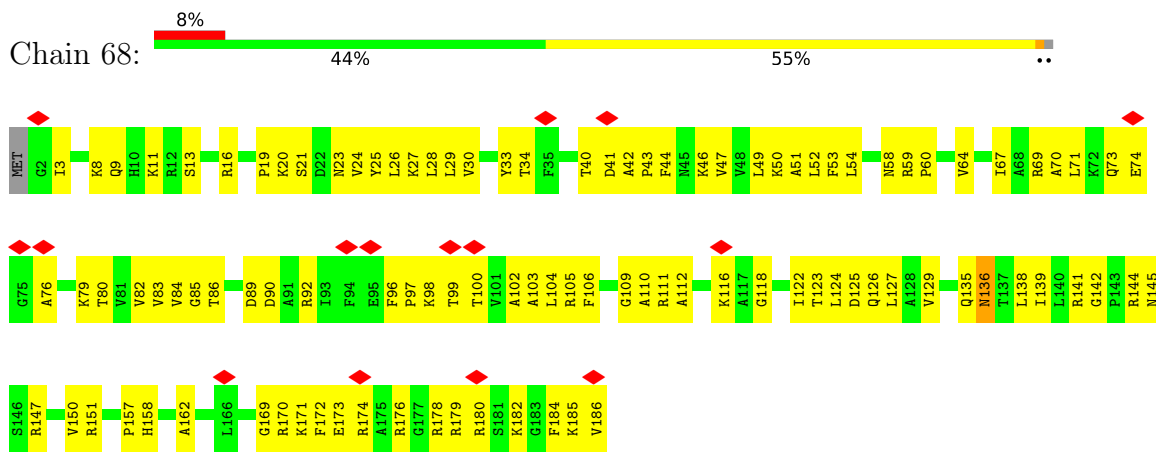


• Molecule 17: 60S ribosomal protein L17

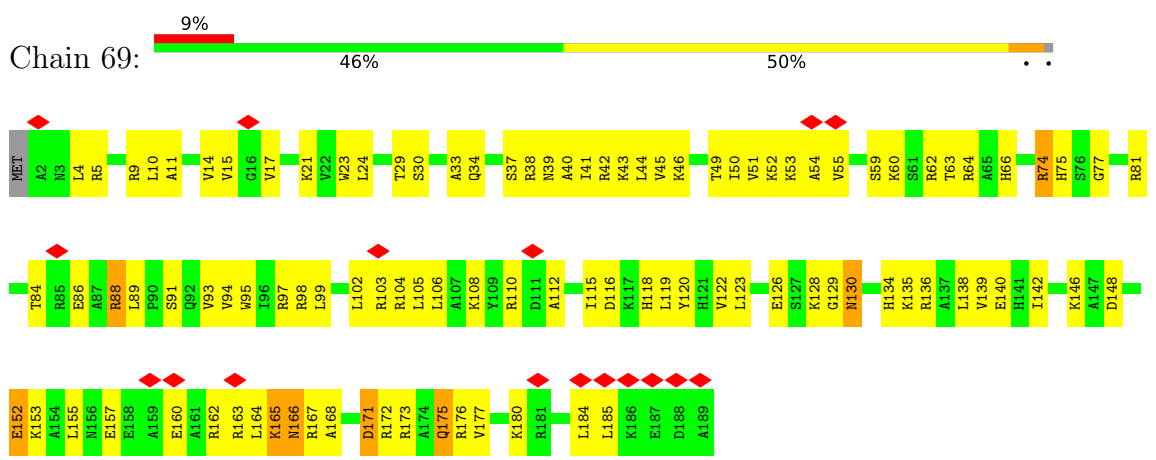


• Molecule 18: 60S ribosomal protein L18

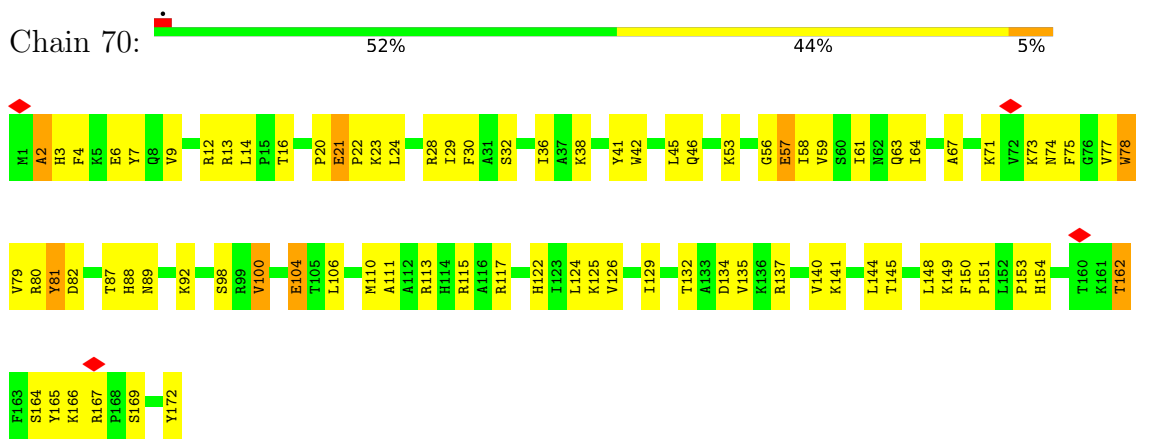




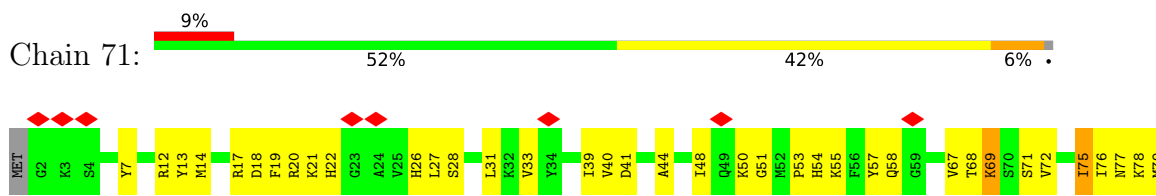
• Molecule 19: 60S ribosomal protein L19

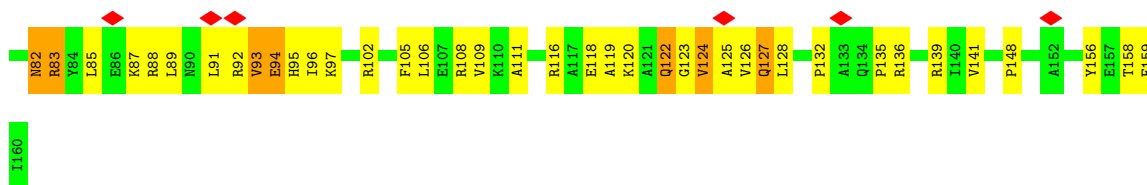


• Molecule 20: 60S ribosomal protein L20

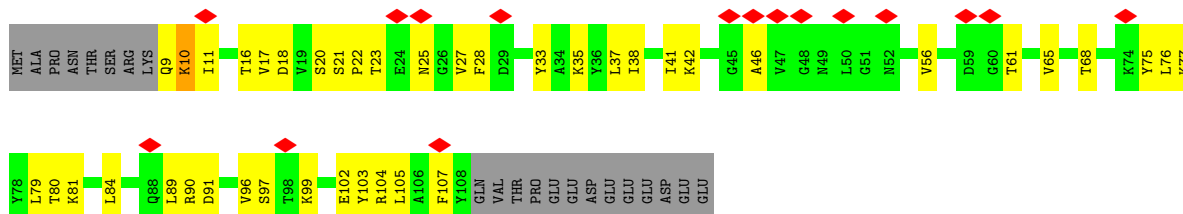


• Molecule 21: 60S ribosomal protein L21

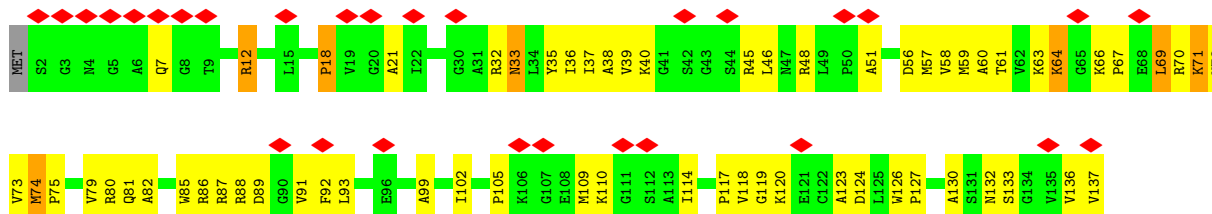




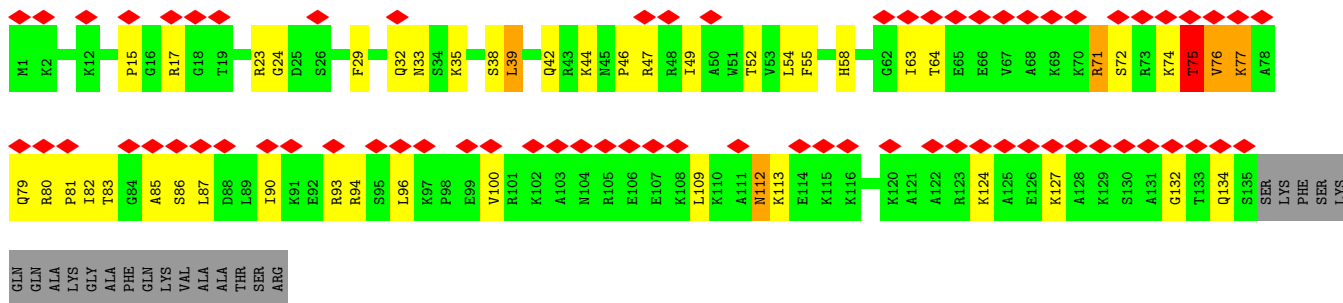
• Molecule 22: 60S ribosomal protein L22



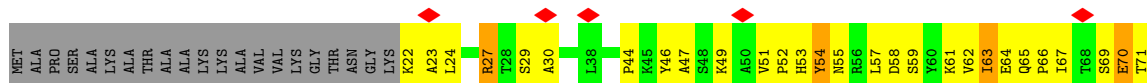
• Molecule 23: 60S ribosomal protein L23

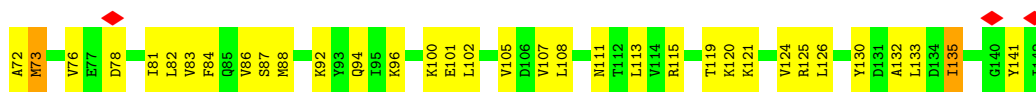


• Molecule 24: 60S ribosomal protein L24

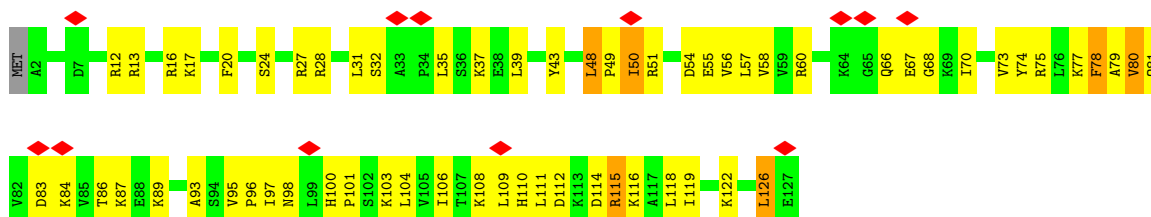


• Molecule 25: 60S ribosomal protein L25

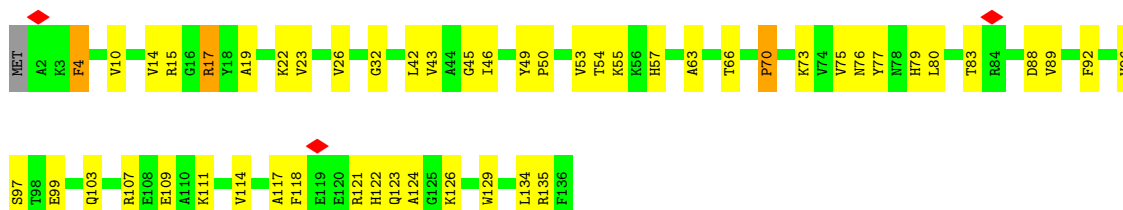




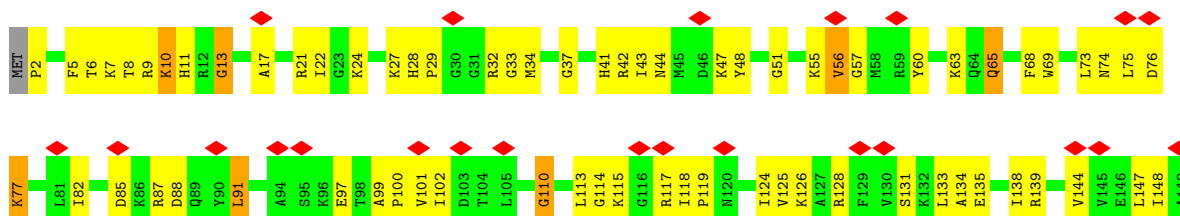
- Molecule 26: 60S ribosomal protein L26



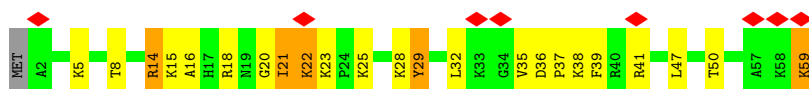
- Molecule 27: 60S ribosomal protein L27



- Molecule 28: 60S ribosomal protein L28

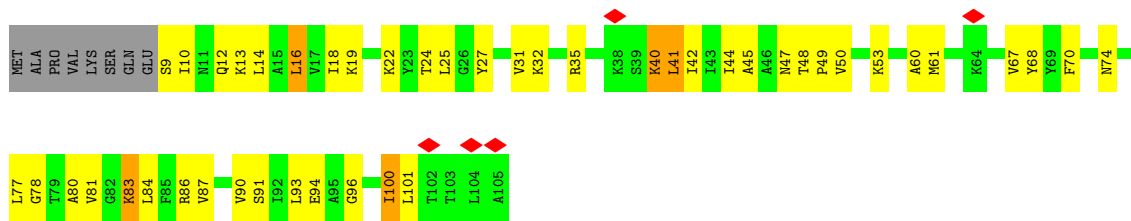


- Molecule 29: 60S ribosomal protein L29

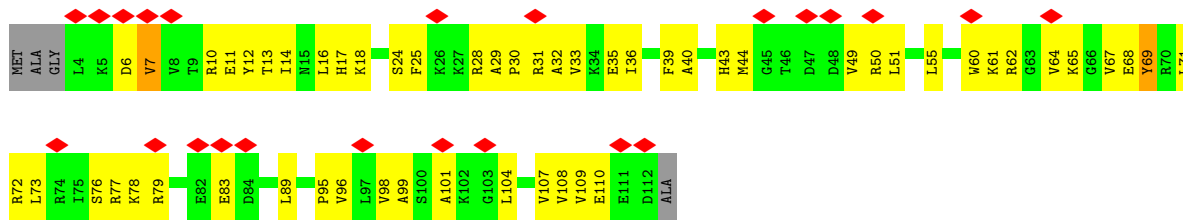


- Molecule 30: 60S ribosomal protein L30

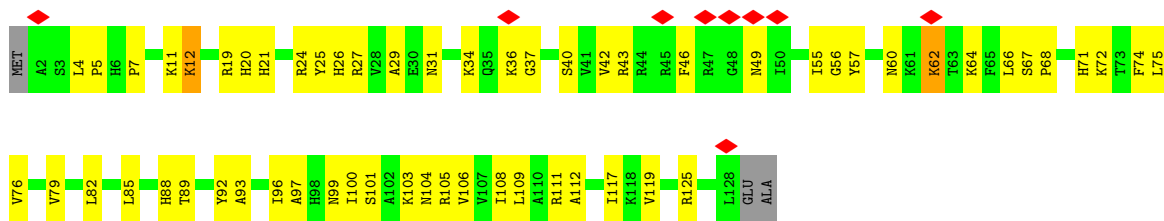




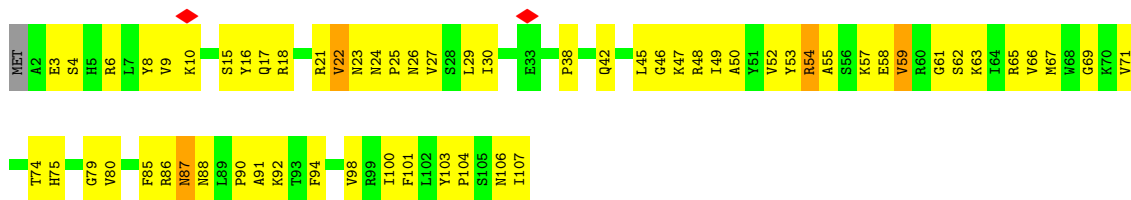
• Molecule 31: 60S ribosomal protein L31



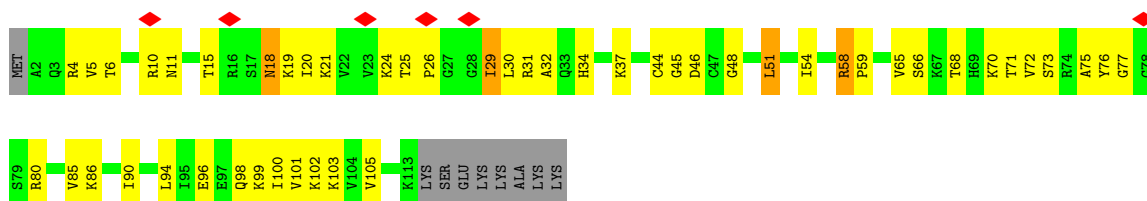
• Molecule 32: 60S ribosomal protein L32



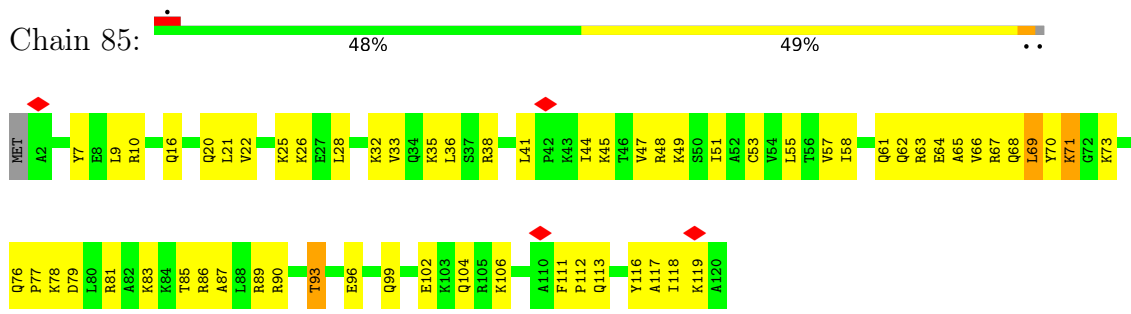
• Molecule 33: 60S ribosomal protein L33



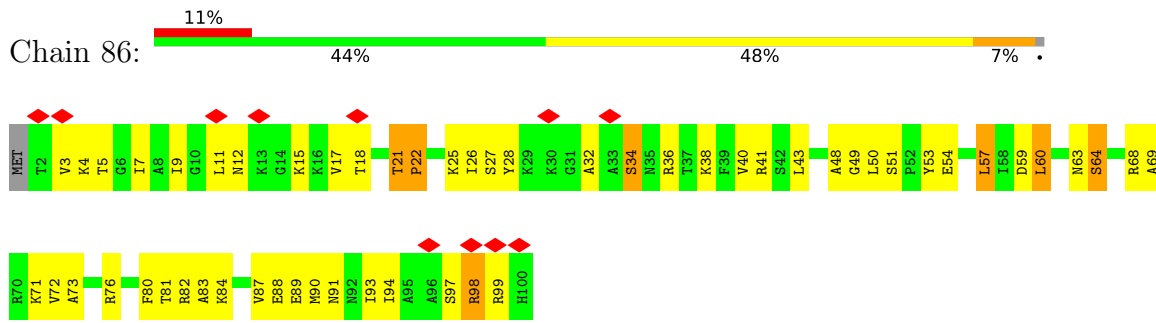
• Molecule 34: 60S ribosomal protein L34



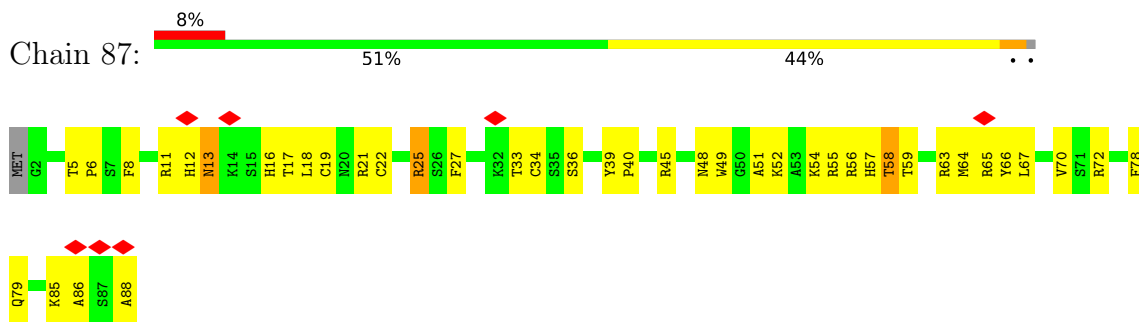
• Molecule 35: 60S ribosomal protein L35



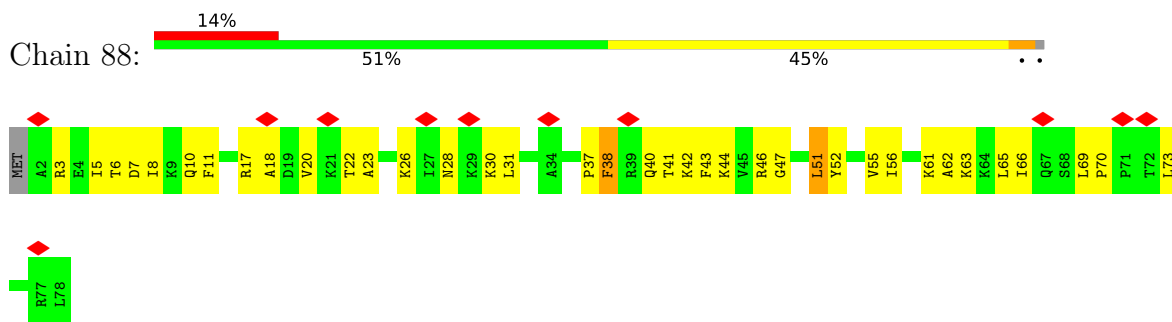
• Molecule 36: 60S ribosomal protein L36



• Molecule 37: 60S ribosomal protein L37

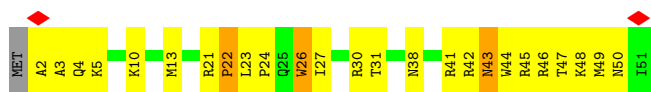


• Molecule 38: 60S ribosomal protein L38

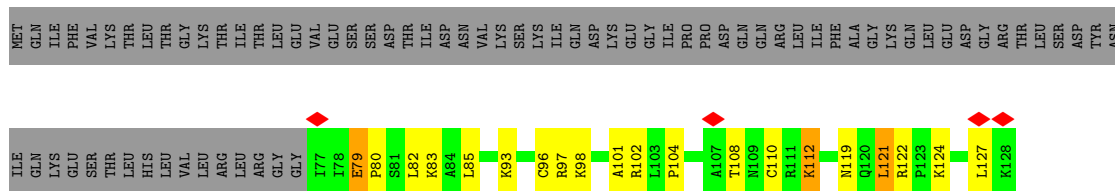


• Molecule 39: 60S ribosomal protein L39

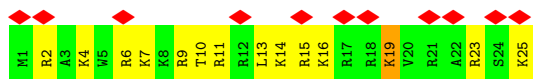




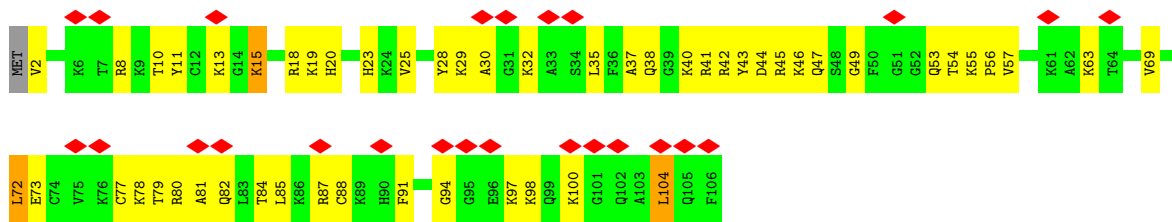
• Molecule 40: 60S ribosomal protein L40



• Molecule 41: 60S ribosomal protein L41



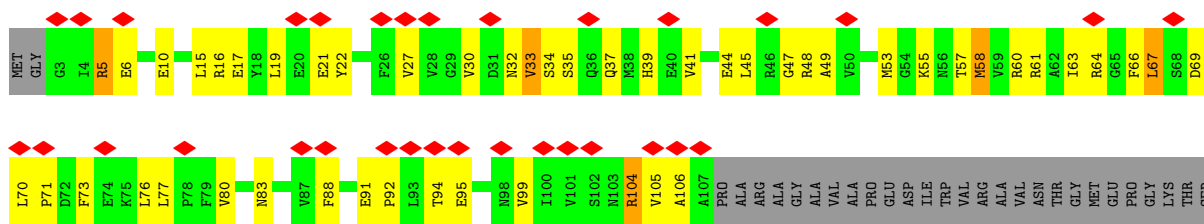
• Molecule 42: 60S ribosomal protein L42



• Molecule 43: 60S ribosomal protein L43



• Molecule 44: 60S acidic ribosomal protein P0



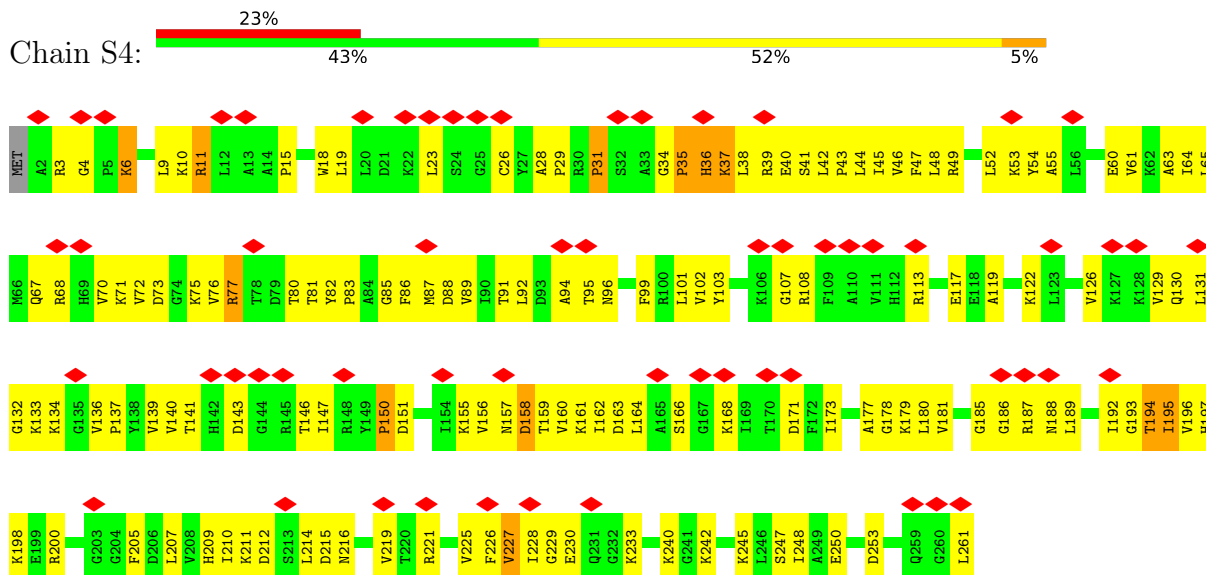




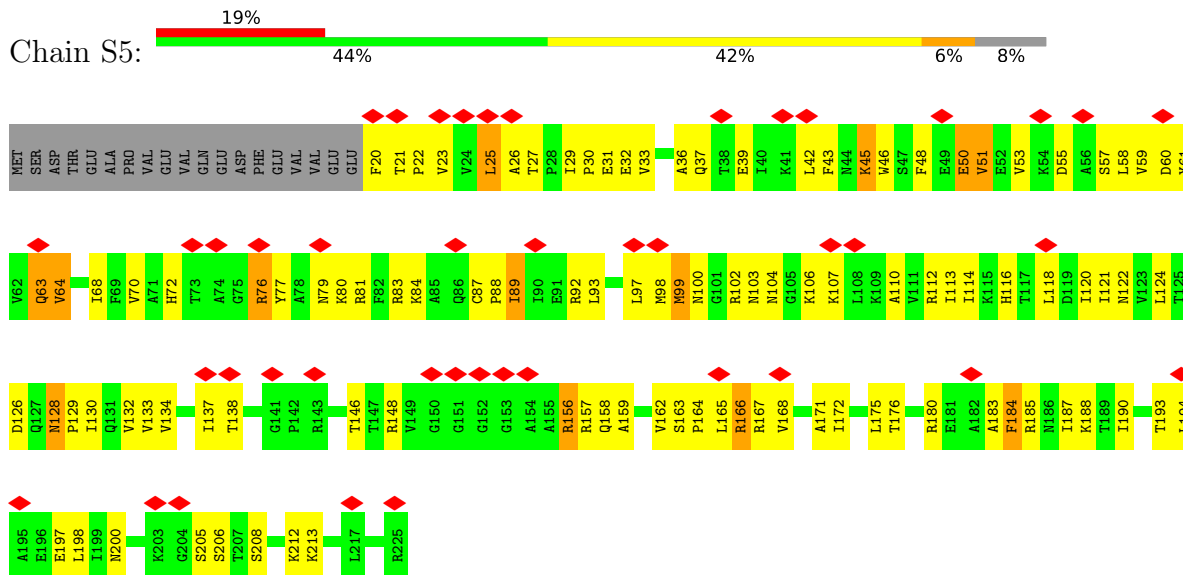


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THR  
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GLU  
ALA  
GLN  
ALA  
GLU  
PRO  
VAL  
GLU  
ALA

• Molecule 50: 40S ribosomal protein S4

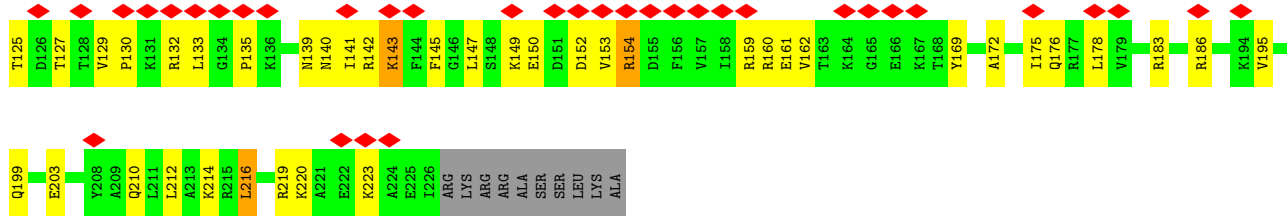


• Molecule 51: 40S ribosomal protein S5

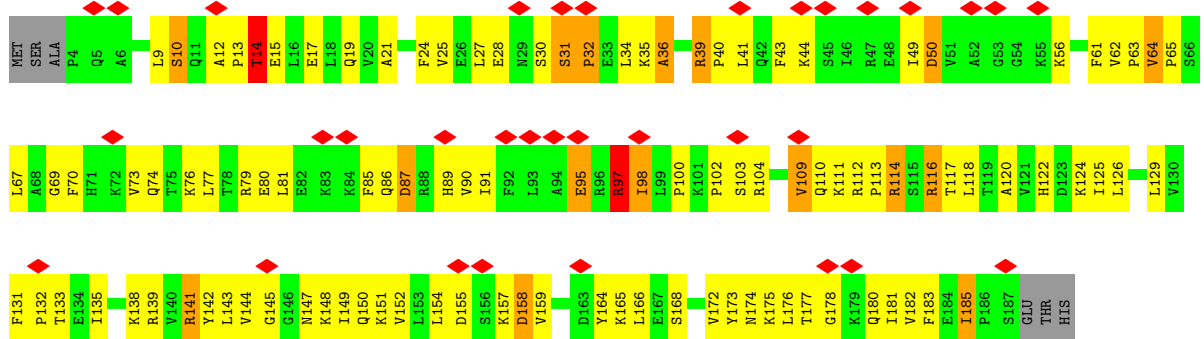


• Molecule 52: 40S ribosomal protein S6

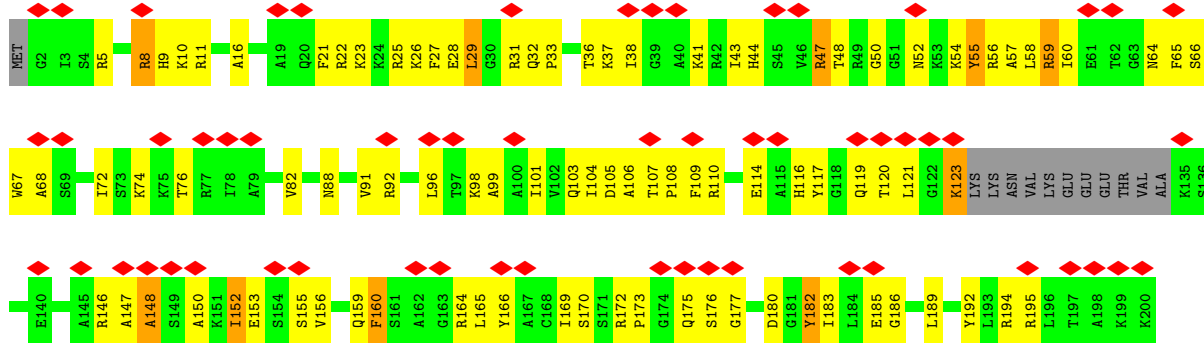




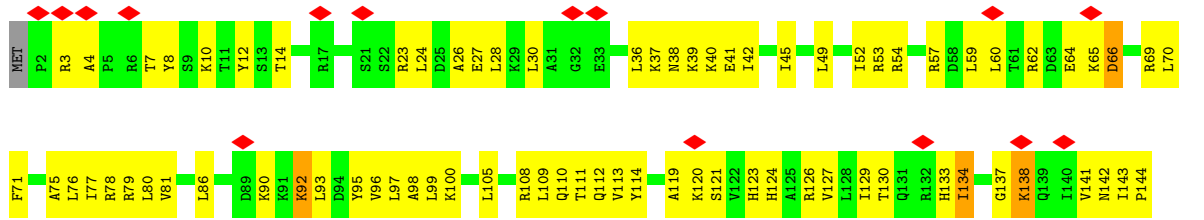
• Molecule 53: 40S ribosomal protein S7

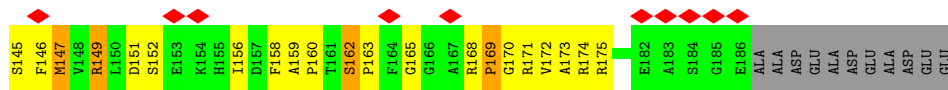


• Molecule 54: 40S ribosomal protein S8

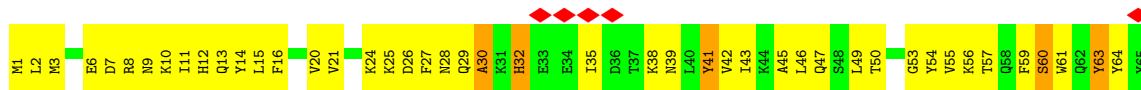
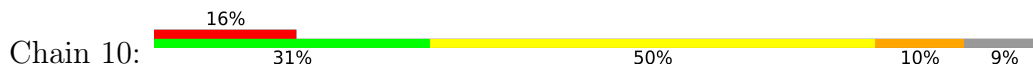


• Molecule 55: 40S ribosomal protein S9

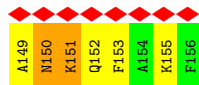




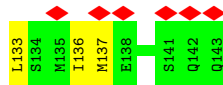
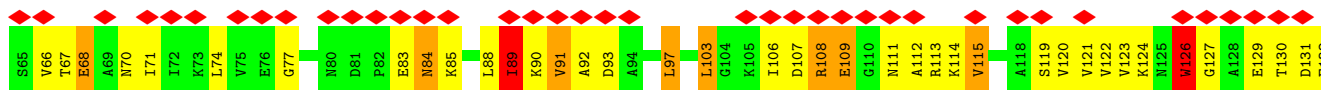
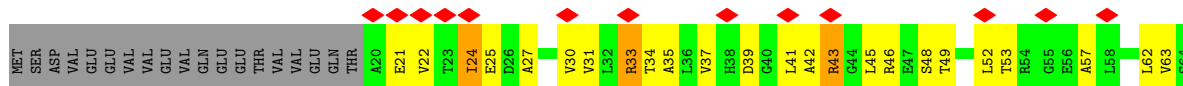
• Molecule 56: 40S ribosomal protein S10



• Molecule 57: 40S ribosomal protein S11

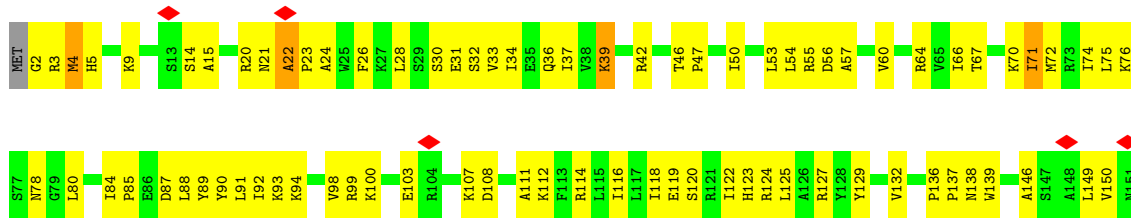


• Molecule 58: 40S ribosomal protein S12

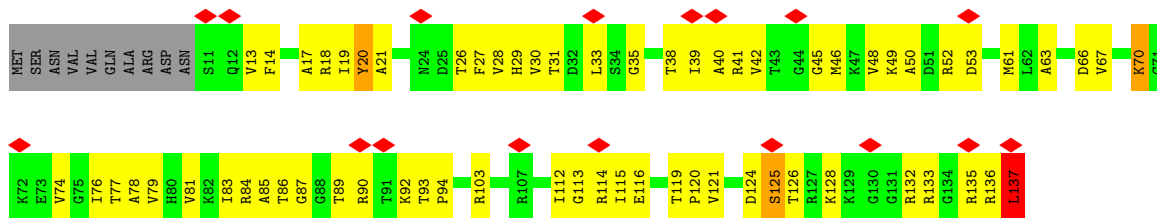


• Molecule 59: 40S ribosomal protein S13

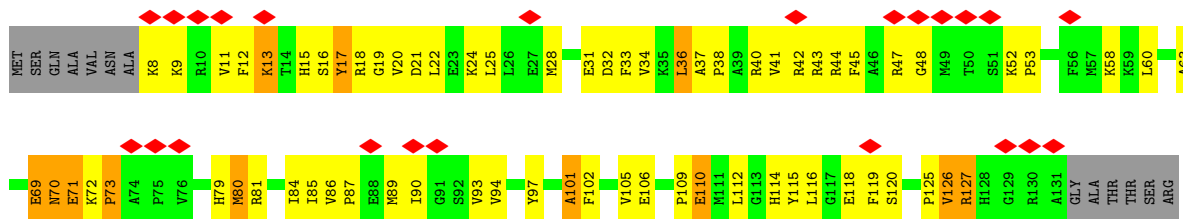




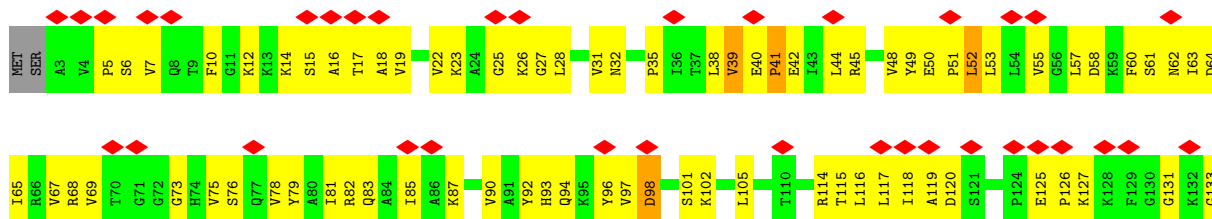
• Molecule 60: 40S ribosomal protein S14



• Molecule 61: 40S ribosomal protein S15

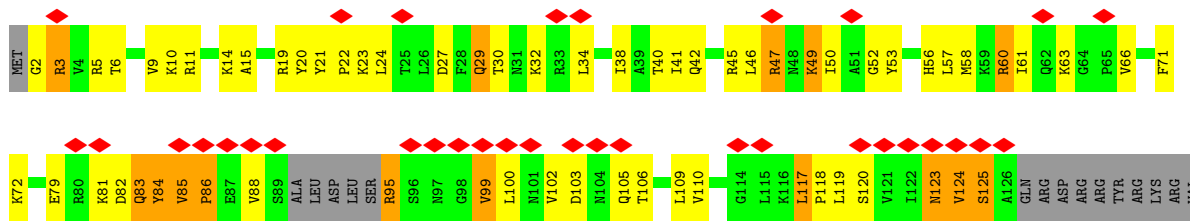


• Molecule 62: 40S ribosomal protein S16

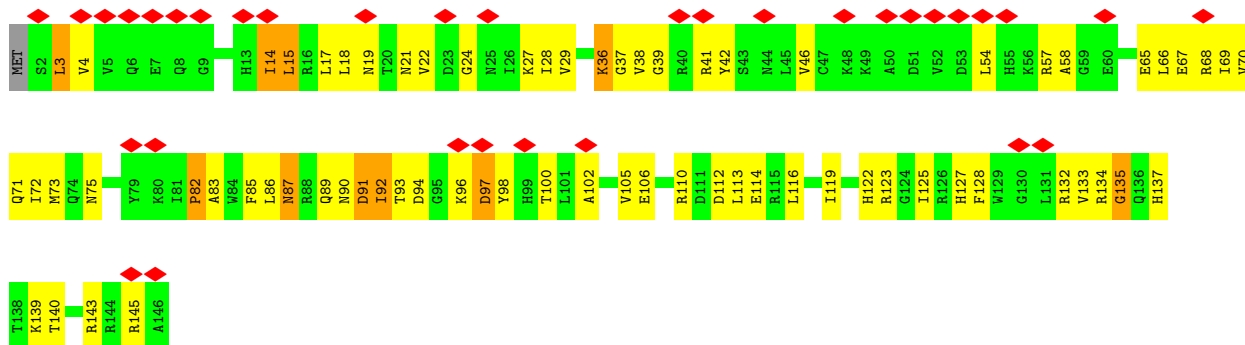


• Molecule 63: 40S ribosomal protein S17

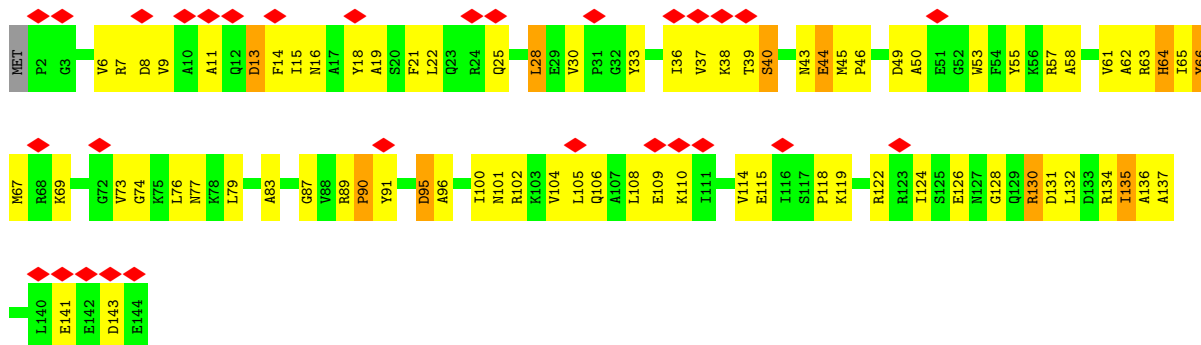




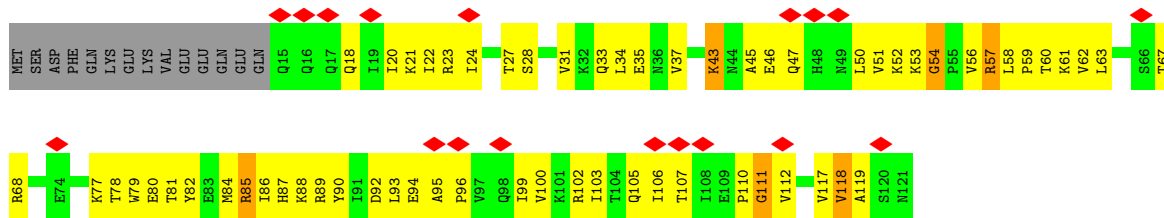
• Molecule 64: 40S ribosomal protein S18



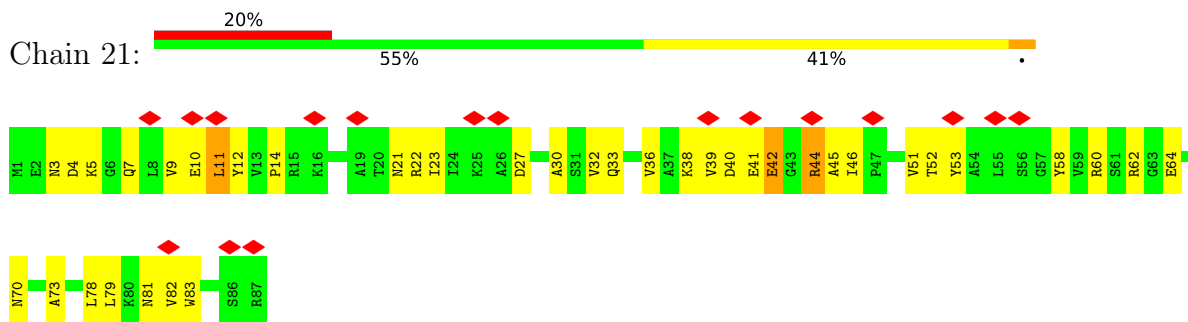
• Molecule 65: 40S ribosomal protein S19



• Molecule 66: 40S ribosomal protein S20



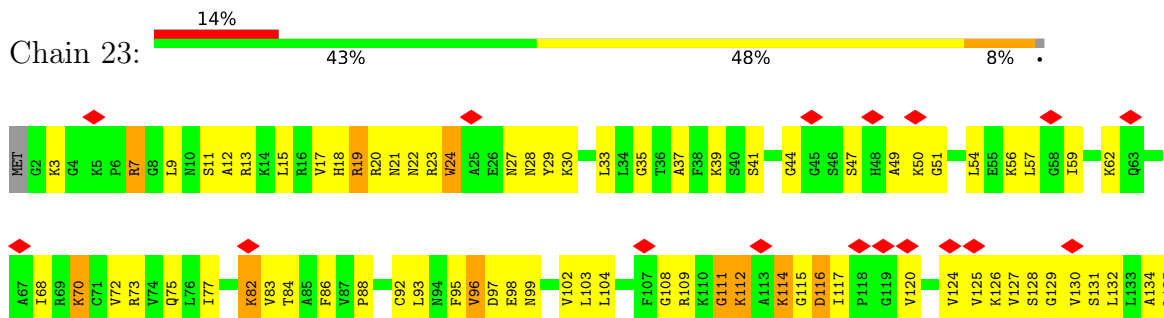
• Molecule 67: 40S ribosomal protein S21



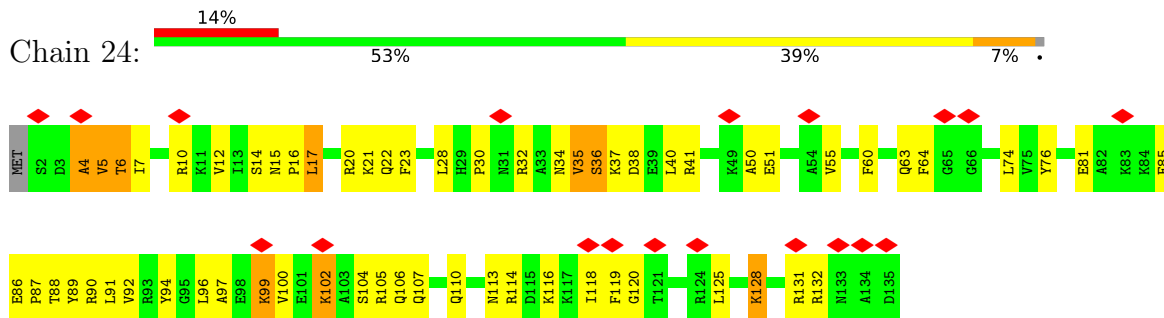
• Molecule 68: 40S ribosomal protein S22



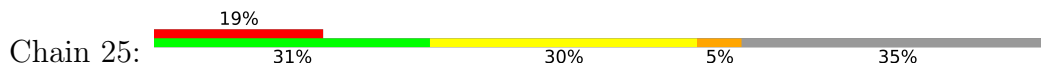
• Molecule 69: 40S ribosomal protein S23

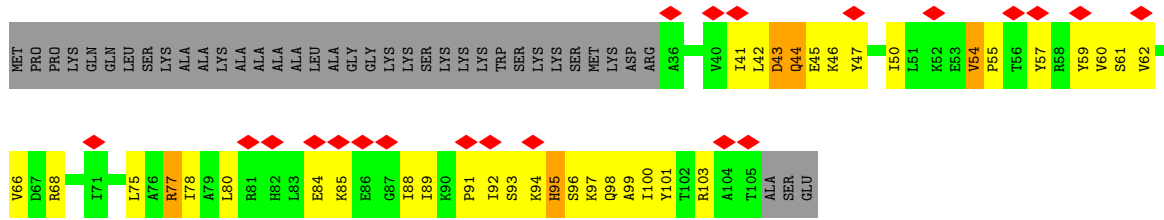


• Molecule 70: 40S ribosomal protein S24

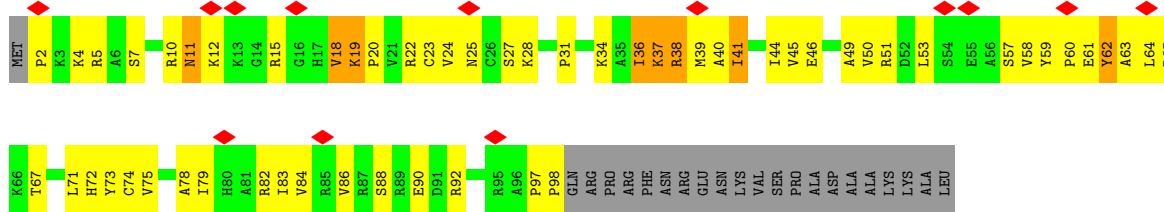


• Molecule 71: 40S ribosomal protein S25

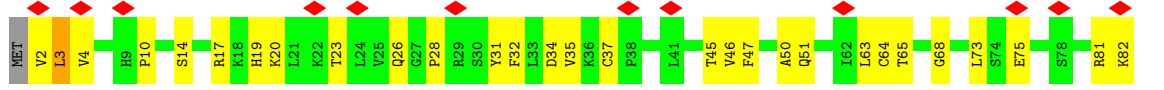




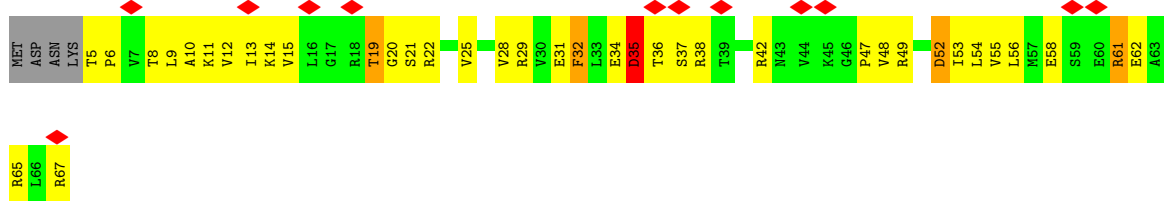
• Molecule 72: 40S ribosomal protein S26



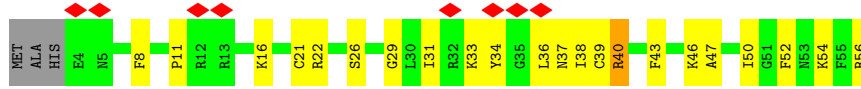
• Molecule 73: 40S ribosomal protein S27



• Molecule 74: 40S ribosomal protein S28

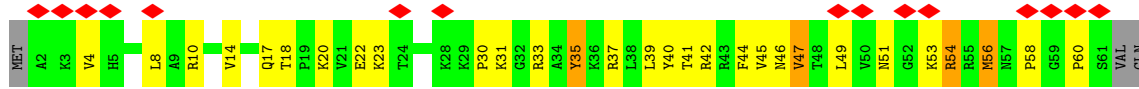


• Molecule 75: 40S ribosomal protein S29

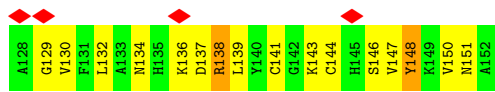
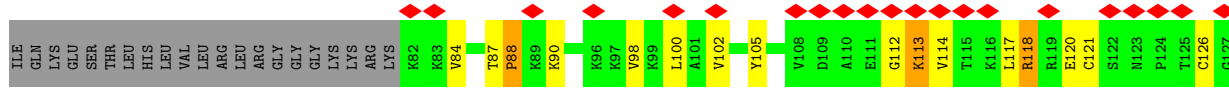


• Molecule 76: 40S ribosomal protein S30

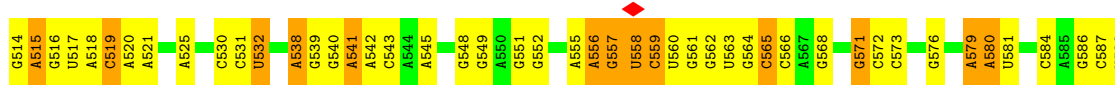
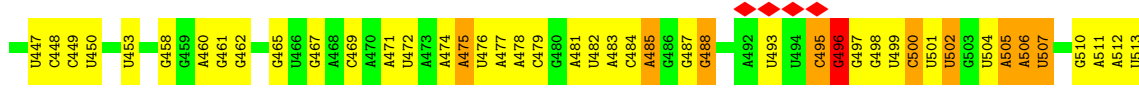
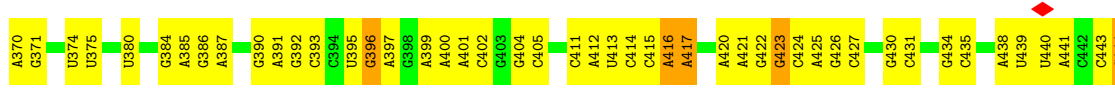
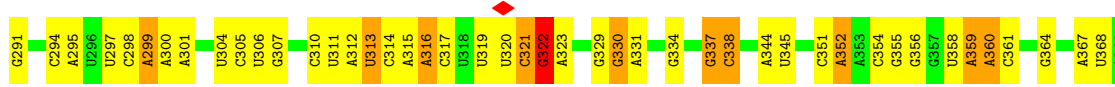
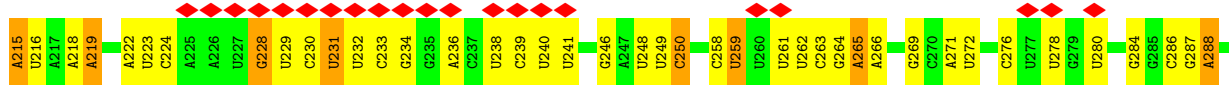
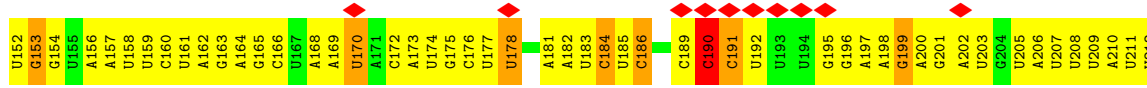
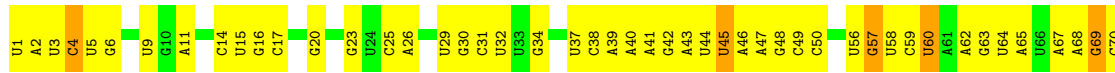




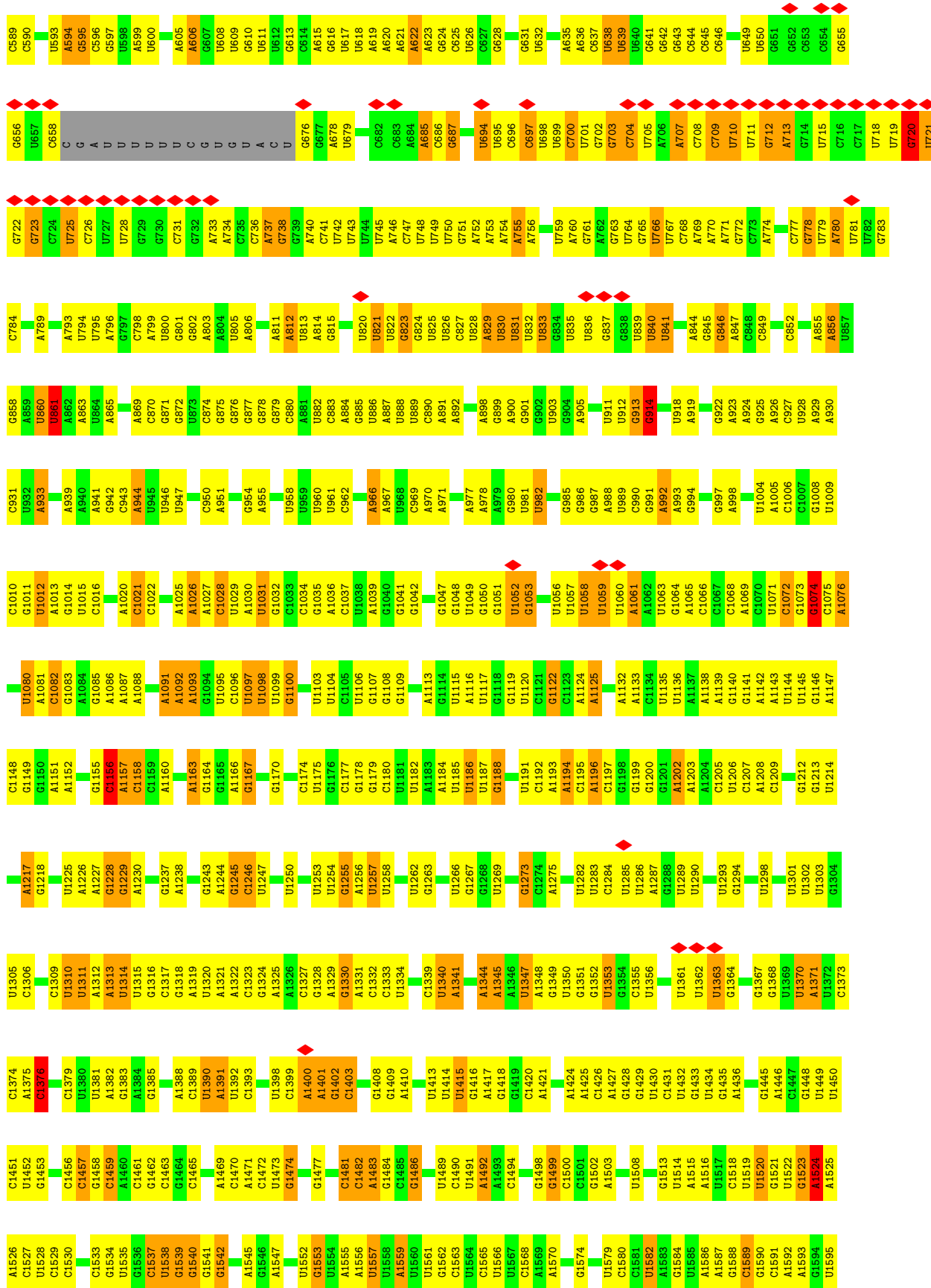
• Molecule 77: 40S ribosomal protein S31



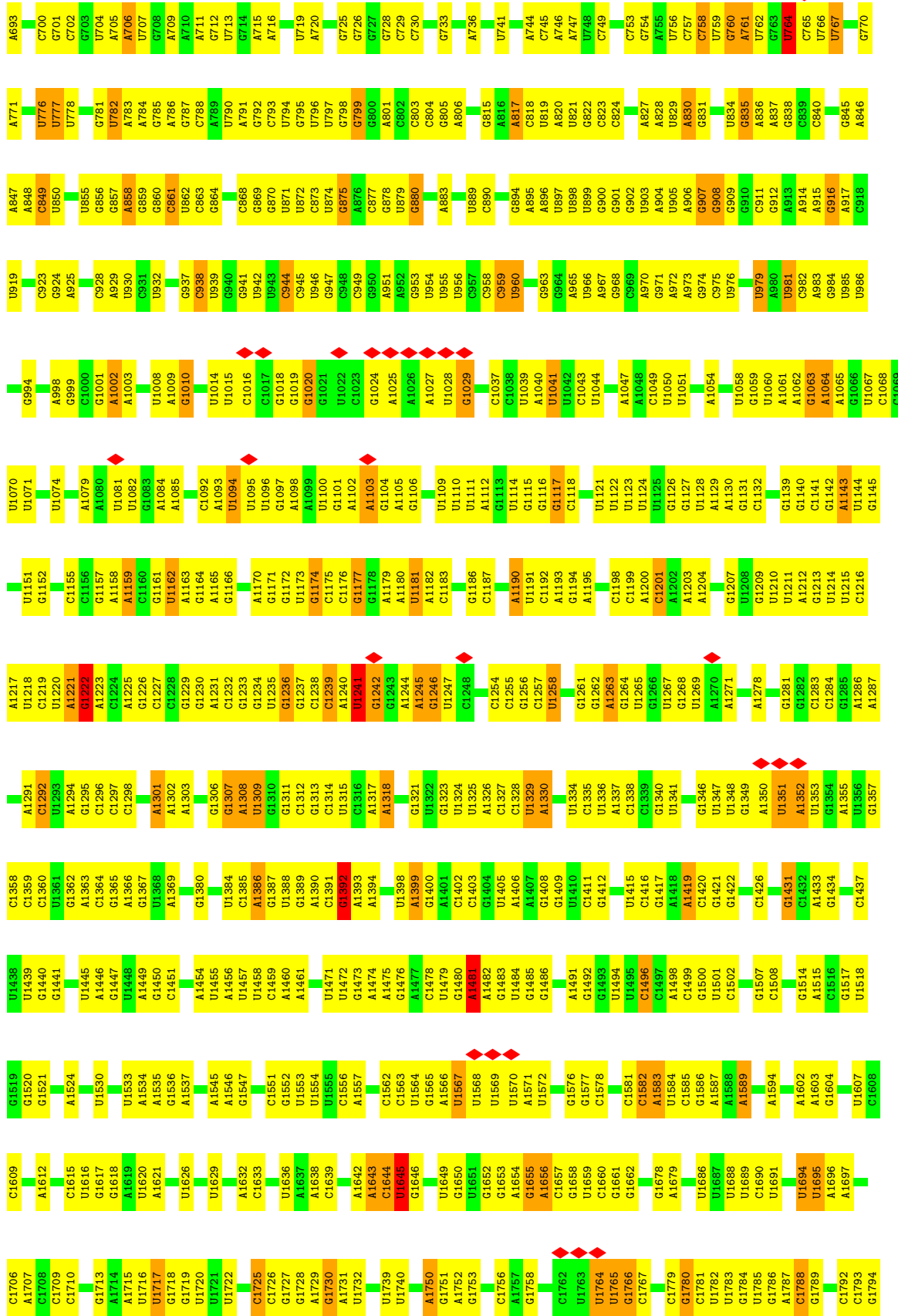
• Molecule 78: 18S ribosomal RNA



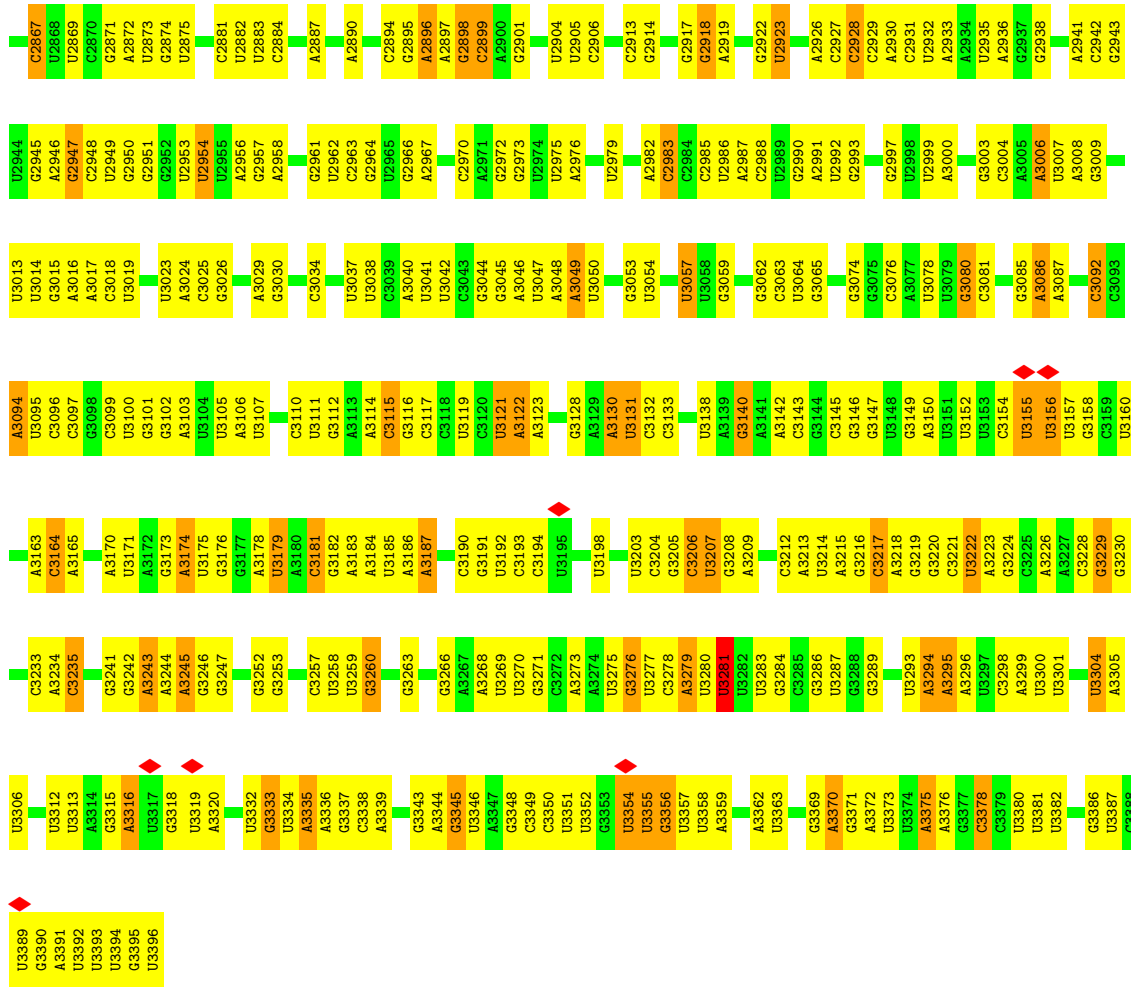




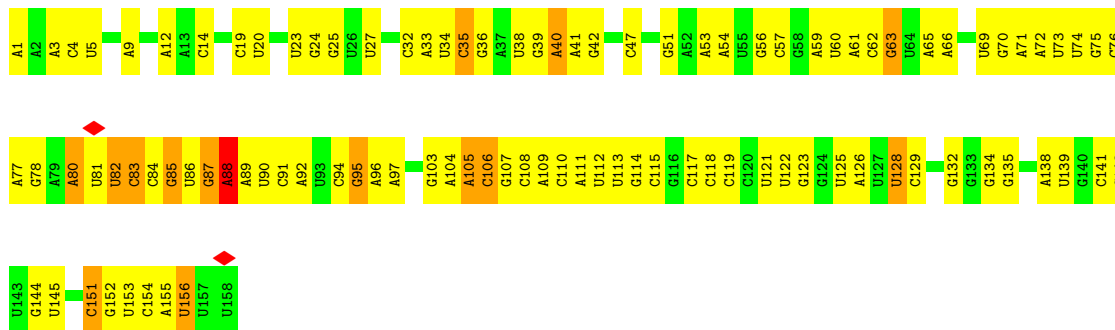






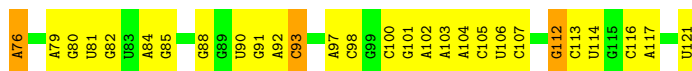


• Molecule 80: 5.8S ribosomal RNA

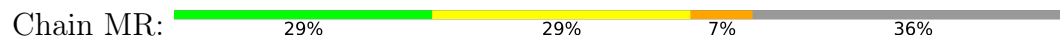


• Molecule 81: 5S ribosomal RNA

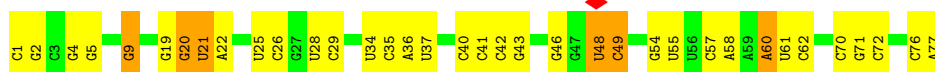




- Molecule 82: messenger RNA



- Molecule 83: P/E-site initiator transfer RNA<sup>fMet</sup>



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	25136	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	CTFFIND3, FREALIGN per micrograph	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	30	Depositor
Minimum defocus (nm)	1159	Depositor
Maximum defocus (nm)	4844	Depositor
Magnification	133333	Depositor
Image detector	FEI FALCON I (4k x 4k)	Depositor
Maximum map value	0.470	Depositor
Minimum map value	-0.182	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.048	Depositor
Recommended contour level	0.12	Depositor
Map size ( $\text{\AA}$ )	377.99997, 377.99997, 377.99997	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.05, 1.05, 1.05	Depositor

## 5 Model quality i

### 5.1 Standard geometry i

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	L1	0.59	0/1634	0.65	0/2195
2	L2	0.43	0/1952	0.56	0/2622
3	L3	0.48	0/3153	0.58	1/4239 (0.0%)
4	L4	0.46	0/2802	0.59	0/3792
5	L5	0.53	0/2426	0.58	0/3271
6	L6	0.51	0/1261	0.59	0/1694
7	L7	0.48	0/1822	0.58	0/2451
8	L8	0.49	0/1850	0.60	0/2495
9	L9	0.50	0/1540	0.59	0/2073
10	60	0.48	0/1754	0.56	0/2350
11	61	0.50	0/1375	0.55	0/1842
12	62	0.53	0/734	0.72	8/1015 (0.8%)
13	63	0.48	0/1568	0.58	0/2106
14	64	0.49	0/1069	0.58	0/1438
15	65	0.45	0/1758	0.54	0/2354
16	66	0.48	0/1586	0.56	0/2128
17	67	0.48	0/1466	0.60	0/1968
18	68	0.46	0/1466	0.61	0/1965
19	69	0.43	0/1539	0.58	0/2050
20	70	0.51	0/1482	0.53	0/1990
21	71	0.49	0/1301	0.56	0/1743
22	72	0.57	0/812	0.58	0/1099
23	73	0.47	0/1019	0.56	0/1369
24	74	0.54	0/1103	0.61	0/1458
25	75	0.49	0/984	0.63	0/1325
26	76	0.46	0/1005	0.58	0/1341
27	77	0.51	0/1119	0.53	0/1497
28	78	0.46	0/1205	0.62	0/1612
29	79	0.45	0/474	0.59	0/629
30	80	0.49	0/751	0.57	0/1008
31	81	0.48	0/904	0.59	0/1213
32	82	0.47	0/1041	0.58	0/1394
33	83	0.50	0/869	0.58	0/1168
34	84	0.46	0/891	0.56	0/1191



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
35	85	0.45	0/979	0.58	0/1301
36	86	0.47	0/779	0.60	0/1034
37	87	0.47	0/697	0.55	0/923
38	88	0.51	0/619	0.58	0/826
39	89	0.47	0/444	0.56	0/588
40	90	0.45	0/424	0.59	0/562
41	91	0.44	0/235	0.58	0/300
42	92	0.48	0/861	0.58	0/1136
43	93	0.45	0/702	0.56	0/934
44	P0	0.63	0/982	0.65	0/1320
45	RC	0.56	0/2498	0.62	0/3398
46	S0	0.54	0/1653	0.62	0/2261
47	S1	0.53	0/1735	0.62	0/2335
48	S2	0.49	0/1665	0.58	0/2263
49	S3	0.54	0/1759	0.59	0/2368
50	S4	0.50	0/2110	0.60	0/2839
51	S5	0.51	0/1630	0.61	0/2202
52	S6	0.51	0/1844	0.59	0/2464
53	S7	0.52	0/1506	0.60	0/2028
54	S8	0.51	0/1515	0.60	0/2021
55	S9	0.49	0/1519	0.63	0/2035
56	10	0.57	0/837	0.63	0/1131
57	11	0.53	0/1273	0.58	0/1712
58	12	0.59	0/943	0.70	0/1274
59	13	0.47	0/1216	0.61	0/1638
60	14	0.49	0/953	0.63	1/1279 (0.1%)
61	15	0.54	0/1012	0.64	0/1356
62	16	0.54	0/1126	0.63	0/1510
63	17	0.58	0/974	0.67	0/1304
64	18	0.51	0/1212	0.59	1/1628 (0.1%)
65	19	0.56	0/1131	0.62	0/1517
66	20	0.55	0/866	0.60	0/1169
67	21	0.50	0/694	0.59	0/935
68	22	0.49	0/1039	0.59	0/1395
69	23	0.45	0/1140	0.59	1/1518 (0.1%)
70	24	0.52	0/1088	0.58	0/1449
71	25	0.52	0/571	0.66	0/768
72	26	0.49	0/782	0.57	0/1047
73	27	0.51	0/621	0.58	0/838
74	28	0.50	0/500	0.61	0/670
75	29	0.55	0/454	0.60	0/602
76	30	0.51	0/483	0.60	0/643
77	31	0.57	0/505	0.69	1/682 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
78	1S	0.76	2/42445 (0.0%)	0.74	18/66138 (0.0%)
79	2S	0.71	6/78685 (0.0%)	0.72	23/122674 (0.0%)
80	8S	0.70	1/3747 (0.0%)	0.71	3/5832 (0.1%)
81	5S	0.70	2/2884 (0.1%)	0.69	0/4491
82	MR	0.86	0/219	0.82	0/339
83	PT	0.78	1/1836 (0.1%)	0.73	0/2859
All	All	0.64	12/223107 (0.0%)	0.68	57/327621 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
78	1S	1	35
79	2S	2	51
80	8S	0	4
81	5S	0	1
83	PT	0	1
All	All	3	92

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
78	1S	1	U	OP3-P	-6.85	1.52	1.61
83	PT	1	C	OP3-P	-6.77	1.53	1.61
80	8S	1	A	OP3-P	-6.77	1.53	1.61
81	5S	1	G	OP3-P	-6.76	1.53	1.61
79	2S	486	A	P-O5'	6.24	1.66	1.59

The worst 5 of 57 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
78	1S	1621	U	C2'-C3'-O3'	8.11	127.34	109.50
79	2S	65	A	C2'-C3'-O3'	7.44	125.86	109.50
80	8S	88	A	N9-C1'-C2'	7.40	123.62	114.00
79	2S	2545	C	N1-C1'-C2'	7.01	123.11	114.00
78	1S	720	G	N9-C1'-C2'	7.00	123.09	114.00

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
78	1S	1621	U	C3'
79	2S	65	A	C3'
79	2S	2512	C	C3'

5 of 92 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
78	1S	121	U	Sidechain
78	1S	143	G	Sidechain
78	1S	196	G	Sidechain
78	1S	50	C	Sidechain
78	1S	82	U	Sidechain

## 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L1	1609	0	1701	102	0
2	L2	1918	0	1987	149	0
3	L3	3082	0	3165	201	0
4	L4	2750	0	2863	193	0
5	L5	2376	0	2325	91	0
6	L6	1240	0	1326	74	0
7	L7	1785	0	1862	77	0
8	L8	1818	0	1908	115	0
9	L9	1519	0	1587	92	0
10	60	1718	0	1754	70	0
11	61	1354	0	1383	74	0
12	62	737	0	341	8	0
13	63	1543	0	1608	85	0
14	64	1054	0	1149	83	0
15	65	1721	0	1779	111	0
16	66	1556	0	1659	85	0
17	67	1443	0	1485	96	0
18	68	1442	0	1543	103	0
19	69	1522	0	1617	91	0
20	70	1446	0	1487	70	0
21	71	1277	0	1323	75	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	72	796	0	812	30	0
23	73	1004	0	1048	70	0
24	74	1089	0	1183	52	0
25	75	969	0	1036	57	0
26	76	994	0	1081	59	0
27	77	1093	0	1155	35	0
28	78	1174	0	1215	57	0
29	79	463	0	491	25	0
30	80	743	0	797	46	0
31	81	890	0	938	52	0
32	82	1020	0	1090	57	0
33	83	851	0	880	51	0
34	84	881	0	949	57	0
35	85	970	0	1078	55	0
36	86	772	0	849	45	0
37	87	682	0	687	43	0
38	88	613	0	682	30	0
39	89	437	0	475	21	0
40	90	418	0	459	17	0
41	91	234	0	284	10	0
42	92	848	0	918	55	0
43	93	695	0	738	28	0
44	P0	967	0	991	39	0
45	RC	2445	0	2401	108	0
46	S0	1612	0	1623	114	0
47	S1	1709	0	1784	152	0
48	S2	1635	0	1723	97	0
49	S3	1734	0	1817	96	0
50	S4	2069	0	2154	121	0
51	S5	1610	0	1675	128	0
52	S6	1820	0	1918	93	0
53	S7	1481	0	1572	113	0
54	S8	1490	0	1525	83	0
55	S9	1494	0	1573	108	0
56	10	817	0	804	62	0
57	11	1245	0	1314	62	0
58	12	935	0	975	57	0
59	13	1193	0	1255	66	0
60	14	942	0	979	69	0
61	15	991	0	1035	55	0
62	16	1106	0	1166	84	0
63	17	965	0	1026	75	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
64	18	1193	0	1222	62	0
65	19	1113	0	1124	66	0
66	20	856	0	917	56	0
67	21	685	0	672	36	0
68	22	1022	0	1060	67	0
69	23	1122	0	1196	85	0
70	24	1074	0	1132	56	0
71	25	563	0	603	38	0
72	26	769	0	818	51	0
73	27	611	0	633	19	0
74	28	498	0	535	35	0
75	29	444	0	436	26	0
76	30	475	0	525	36	0
77	31	498	0	441	23	0
78	1S	37949	0	19093	1032	0
79	2S	70300	0	35327	1725	0
80	8S	3354	0	1695	98	0
81	5S	2580	0	1304	68	0
82	MR	195	0	98	3	0
83	PT	1644	0	836	31	0
All	All	207751	0	153674	7427	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 21.

The worst 5 of 7427 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)
60:14:87:GLY:HA3	60:14:120:PRO:HG2	1.29	1.15
78:1S:1621:U:H3	78:1S:1623:C:H5''	1.11	1.12
79:2S:1235:U:H4'	79:2S:1236:G:H5'	1.31	1.11
79:2S:1238:C:H3'	79:2S:1239:C:H5''	1.26	1.11
60:14:52:ARG:HD3	78:1S:905:A:H5''	1.30	1.10

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	L1	202/217 (93%)	136 (67%)	54 (27%)	12 (6%)	1	17
2	L2	250/254 (98%)	198 (79%)	43 (17%)	9 (4%)	3	25
3	L3	384/387 (99%)	311 (81%)	58 (15%)	15 (4%)	3	23
4	L4	359/362 (99%)	293 (82%)	48 (13%)	18 (5%)	2	20
5	L5	294/297 (99%)	249 (85%)	38 (13%)	7 (2%)	6	33
6	L6	152/176 (86%)	131 (86%)	14 (9%)	7 (5%)	2	21
7	L7	220/244 (90%)	193 (88%)	21 (10%)	6 (3%)	5	31
8	L8	231/256 (90%)	191 (83%)	36 (16%)	4 (2%)	9	42
9	L9	189/191 (99%)	160 (85%)	25 (13%)	4 (2%)	7	36
10	60	207/221 (94%)	184 (89%)	21 (10%)	2 (1%)	15	54
11	61	167/174 (96%)	131 (78%)	29 (17%)	7 (4%)	3	22
12	62	144/165 (87%)	85 (59%)	34 (24%)	25 (17%)	0	2
13	63	191/199 (96%)	158 (83%)	27 (14%)	6 (3%)	4	27
14	64	134/138 (97%)	106 (79%)	21 (16%)	7 (5%)	2	19
15	65	201/204 (98%)	169 (84%)	29 (14%)	3 (2%)	10	45
16	66	195/199 (98%)	175 (90%)	18 (9%)	2 (1%)	15	54
17	67	181/184 (98%)	145 (80%)	31 (17%)	5 (3%)	5	30
18	68	183/186 (98%)	154 (84%)	25 (14%)	4 (2%)	6	35
19	69	186/189 (98%)	166 (89%)	17 (9%)	3 (2%)	9	44
20	70	170/172 (99%)	142 (84%)	25 (15%)	3 (2%)	8	40
21	71	157/160 (98%)	134 (85%)	16 (10%)	7 (4%)	2	21
22	72	98/121 (81%)	81 (83%)	15 (15%)	2 (2%)	7	38
23	73	134/137 (98%)	104 (78%)	26 (19%)	4 (3%)	4	28
24	74	133/155 (86%)	106 (80%)	21 (16%)	6 (4%)	2	21
25	75	119/142 (84%)	99 (83%)	17 (14%)	3 (2%)	5	32

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	76	124/127 (98%)	110 (89%)	10 (8%)	4 (3%)	4	26
27	77	133/136 (98%)	112 (84%)	17 (13%)	4 (3%)	4	28
28	78	146/149 (98%)	120 (82%)	17 (12%)	9 (6%)	1	16
29	79	56/59 (95%)	50 (89%)	4 (7%)	2 (4%)	3	25
30	80	95/105 (90%)	85 (90%)	8 (8%)	2 (2%)	7	36
31	81	107/113 (95%)	89 (83%)	16 (15%)	2 (2%)	8	38
32	82	125/130 (96%)	112 (90%)	10 (8%)	3 (2%)	6	33
33	83	104/107 (97%)	84 (81%)	17 (16%)	3 (3%)	4	29
34	84	110/121 (91%)	95 (86%)	15 (14%)	0	100	100
35	85	117/120 (98%)	106 (91%)	10 (8%)	1 (1%)	17	56
36	86	97/100 (97%)	79 (81%)	10 (10%)	8 (8%)	1	12
37	87	85/88 (97%)	74 (87%)	10 (12%)	1 (1%)	13	50
38	88	75/78 (96%)	66 (88%)	9 (12%)	0	100	100
39	89	48/51 (94%)	37 (77%)	9 (19%)	2 (4%)	3	22
40	90	50/128 (39%)	41 (82%)	8 (16%)	1 (2%)	7	38
41	91	23/25 (92%)	23 (100%)	0	0	100	100
42	92	103/106 (97%)	80 (78%)	20 (19%)	3 (3%)	4	29
43	93	89/92 (97%)	76 (85%)	11 (12%)	2 (2%)	6	35
44	P0	117/312 (38%)	102 (87%)	9 (8%)	6 (5%)	2	19
45	RC	316/319 (99%)	258 (82%)	51 (16%)	7 (2%)	6	35
46	S0	204/252 (81%)	152 (74%)	47 (23%)	5 (2%)	5	32
47	S1	212/255 (83%)	155 (73%)	41 (19%)	16 (8%)	1	13
48	S2	215/254 (85%)	186 (86%)	23 (11%)	6 (3%)	5	30
49	S3	221/240 (92%)	181 (82%)	29 (13%)	11 (5%)	2	20
50	S4	258/261 (99%)	201 (78%)	47 (18%)	10 (4%)	3	23
51	S5	204/225 (91%)	168 (82%)	29 (14%)	7 (3%)	3	25
52	S6	224/236 (95%)	194 (87%)	24 (11%)	6 (3%)	5	31
53	S7	182/190 (96%)	133 (73%)	34 (19%)	15 (8%)	1	12
54	S8	184/200 (92%)	146 (79%)	30 (16%)	8 (4%)	2	22
55	S9	183/197 (93%)	153 (84%)	22 (12%)	8 (4%)	2	22
56	10	94/105 (90%)	75 (80%)	11 (12%)	8 (8%)	1	11

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
57	11	153/156 (98%)	118 (77%)	27 (18%)	8 (5%)	2	19
58	12	122/143 (85%)	81 (66%)	25 (20%)	16 (13%)	0	4
59	13	148/151 (98%)	129 (87%)	16 (11%)	3 (2%)	7	38
60	14	125/137 (91%)	92 (74%)	29 (23%)	4 (3%)	4	26
61	15	122/142 (86%)	88 (72%)	22 (18%)	12 (10%)	0	9
62	16	139/143 (97%)	113 (81%)	22 (16%)	4 (3%)	4	29
63	17	116/136 (85%)	93 (80%)	15 (13%)	8 (7%)	1	14
64	18	143/146 (98%)	117 (82%)	19 (13%)	7 (5%)	2	20
65	19	141/144 (98%)	119 (84%)	18 (13%)	4 (3%)	5	30
66	20	105/121 (87%)	82 (78%)	20 (19%)	3 (3%)	4	29
67	21	85/87 (98%)	71 (84%)	8 (9%)	6 (7%)	1	14
68	22	127/130 (98%)	110 (87%)	14 (11%)	3 (2%)	6	33
69	23	142/145 (98%)	107 (75%)	28 (20%)	7 (5%)	2	20
70	24	132/135 (98%)	109 (83%)	16 (12%)	7 (5%)	2	19
71	25	68/108 (63%)	44 (65%)	20 (29%)	4 (6%)	1	17
72	26	95/119 (80%)	69 (73%)	19 (20%)	7 (7%)	1	13
73	27	79/82 (96%)	59 (75%)	16 (20%)	4 (5%)	2	19
74	28	61/67 (91%)	52 (85%)	6 (10%)	3 (5%)	2	20
75	29	51/56 (91%)	40 (78%)	9 (18%)	2 (4%)	3	23
76	30	58/63 (92%)	47 (81%)	9 (16%)	2 (3%)	3	25
77	31	69/152 (45%)	42 (61%)	15 (22%)	12 (17%)	0	2
All	All	11463/12574 (91%)	9326 (81%)	1680 (15%)	457 (4%)	5	23

5 of 457 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L1	20	SER
1	L1	74	VAL
1	L1	151	VAL
3	L3	4	ARG
3	L3	5	LYS



### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	L1	185/198 (93%)	170 (92%)	15 (8%)	11	35
2	L2	194/196 (99%)	189 (97%)	5 (3%)	46	66
3	L3	322/323 (100%)	304 (94%)	18 (6%)	21	46
4	L4	288/289 (100%)	276 (96%)	12 (4%)	30	54
5	L5	244/245 (100%)	232 (95%)	12 (5%)	25	50
6	L6	134/153 (88%)	127 (95%)	7 (5%)	23	48
7	L7	186/205 (91%)	179 (96%)	7 (4%)	33	57
8	L8	191/208 (92%)	181 (95%)	10 (5%)	23	48
9	L9	171/171 (100%)	160 (94%)	11 (6%)	17	42
10	60	180/187 (96%)	172 (96%)	8 (4%)	28	53
11	61	147/150 (98%)	136 (92%)	11 (8%)	13	38
13	63	154/159 (97%)	143 (93%)	11 (7%)	14	39
14	64	107/109 (98%)	100 (94%)	7 (6%)	17	42
15	65	175/176 (99%)	168 (96%)	7 (4%)	31	55
16	66	160/162 (99%)	152 (95%)	8 (5%)	24	49
17	67	145/146 (99%)	137 (94%)	8 (6%)	21	47
18	68	150/151 (99%)	147 (98%)	3 (2%)	55	74
19	69	153/154 (99%)	146 (95%)	7 (5%)	27	52
20	70	156/156 (100%)	147 (94%)	9 (6%)	20	45
21	71	136/137 (99%)	129 (95%)	7 (5%)	24	48
22	72	87/107 (81%)	84 (97%)	3 (3%)	37	60
23	73	104/105 (99%)	97 (93%)	7 (7%)	16	41
24	74	114/129 (88%)	110 (96%)	4 (4%)	36	59
25	75	105/118 (89%)	97 (92%)	8 (8%)	13	37
26	76	109/110 (99%)	103 (94%)	6 (6%)	21	47
27	77	115/116 (99%)	110 (96%)	5 (4%)	29	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	78	118/119 (99%)	112 (95%)	6 (5%)	24	48
29	79	46/47 (98%)	42 (91%)	4 (9%)	10	31
30	80	81/88 (92%)	75 (93%)	6 (7%)	13	38
31	81	96/97 (99%)	91 (95%)	5 (5%)	23	48
32	82	109/111 (98%)	108 (99%)	1 (1%)	78	88
33	83	90/91 (99%)	84 (93%)	6 (7%)	16	41
34	84	95/103 (92%)	91 (96%)	4 (4%)	30	54
35	85	104/105 (99%)	96 (92%)	8 (8%)	13	37
36	86	81/82 (99%)	74 (91%)	7 (9%)	10	32
37	87	70/71 (99%)	65 (93%)	5 (7%)	14	39
38	88	68/69 (99%)	63 (93%)	5 (7%)	13	38
39	89	45/46 (98%)	42 (93%)	3 (7%)	16	41
40	90	47/116 (40%)	44 (94%)	3 (6%)	17	42
41	91	23/23 (100%)	22 (96%)	1 (4%)	29	53
42	92	90/91 (99%)	86 (96%)	4 (4%)	28	53
43	93	71/72 (99%)	71 (100%)	0	100	100
44	P0	105/254 (41%)	101 (96%)	4 (4%)	33	57
45	RC	261/262 (100%)	247 (95%)	14 (5%)	22	47
46	S0	173/210 (82%)	156 (90%)	17 (10%)	8	27
47	S1	191/224 (85%)	172 (90%)	19 (10%)	8	26
48	S2	176/205 (86%)	169 (96%)	7 (4%)	31	55
49	S3	182/195 (93%)	169 (93%)	13 (7%)	14	39
50	S4	221/222 (100%)	207 (94%)	14 (6%)	18	43
51	S5	173/191 (91%)	162 (94%)	11 (6%)	17	42
52	S6	193/201 (96%)	183 (95%)	10 (5%)	23	48
53	S7	165/170 (97%)	151 (92%)	14 (8%)	10	33
54	S8	150/161 (93%)	140 (93%)	10 (7%)	16	41
55	S9	158/166 (95%)	150 (95%)	8 (5%)	24	48
56	10	89/98 (91%)	82 (92%)	7 (8%)	12	36
57	11	136/137 (99%)	132 (97%)	4 (3%)	42	64
58	12	100/119 (84%)	88 (88%)	12 (12%)	5	20

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
59	13	127/128 (99%)	121 (95%)	6 (5%)	26	51
60	14	96/105 (91%)	92 (96%)	4 (4%)	30	54
61	15	104/118 (88%)	97 (93%)	7 (7%)	16	41
62	16	117/119 (98%)	112 (96%)	5 (4%)	29	53
63	17	109/124 (88%)	98 (90%)	11 (10%)	7	25
64	18	128/129 (99%)	117 (91%)	11 (9%)	10	32
65	19	115/116 (99%)	104 (90%)	11 (10%)	8	27
66	20	100/114 (88%)	92 (92%)	8 (8%)	12	35
67	21	74/74 (100%)	71 (96%)	3 (4%)	30	55
68	22	110/111 (99%)	103 (94%)	7 (6%)	17	42
69	23	119/120 (99%)	110 (92%)	9 (8%)	13	37
70	24	112/113 (99%)	106 (95%)	6 (5%)	22	47
71	25	61/89 (68%)	57 (93%)	4 (7%)	16	41
72	26	83/101 (82%)	78 (94%)	5 (6%)	19	44
73	27	70/71 (99%)	68 (97%)	2 (3%)	42	64
74	28	56/60 (93%)	52 (93%)	4 (7%)	14	39
75	29	47/49 (96%)	45 (96%)	2 (4%)	29	53
76	30	51/54 (94%)	47 (92%)	4 (8%)	12	36
77	31	43/135 (32%)	40 (93%)	3 (7%)	15	40
All	All	9641/10436 (92%)	9081 (94%)	560 (6%)	24	45

5 of 560 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
61	15	110	GLU
63	17	81	LYS
61	15	44	ARG
68	22	118	ARG
24	74	75	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 224 such sidechains are listed below:

Mol	Chain	Res	Type
33	83	42	GLN

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Mol	Chain	Res	Type
70	24	113	ASN
46	S0	30	GLN
70	24	22	GLN
65	19	16	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
78	1S	1779/1798 (98%)	336 (18%)	15 (0%)
79	2S	3282/3395 (96%)	472 (14%)	21 (0%)
80	8S	157/158 (99%)	22 (14%)	1 (0%)
81	5S	120/121 (99%)	11 (9%)	0
82	MR	8/14 (57%)	2 (25%)	0
83	PT	76/77 (98%)	9 (11%)	0
All	All	5422/5563 (97%)	852 (15%)	37 (0%)

5 of 852 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
78	1S	2	A
78	1S	4	C
78	1S	25	C
78	1S	26	A
78	1S	34	G

5 of 37 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
79	2S	2525	G
79	2S	3351	U
79	2S	2534	G
79	2S	3121	U
78	1S	1621	U

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

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

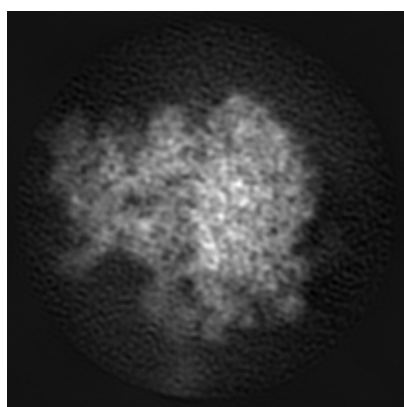
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5976. These allow visual inspection of the internal detail of the map and identification of artifacts.

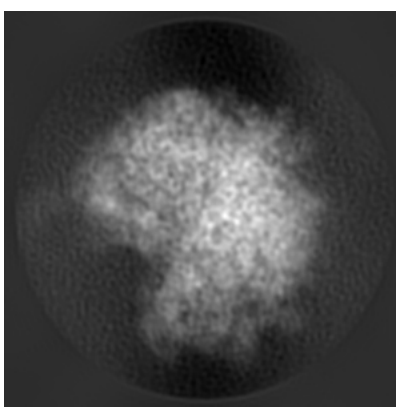
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

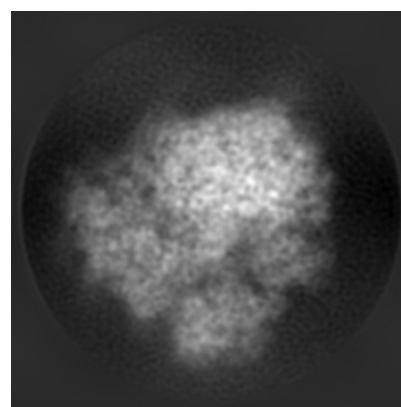
#### 6.1.1 Primary map



X



Y

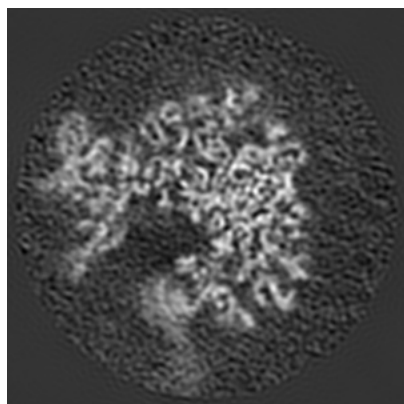


Z

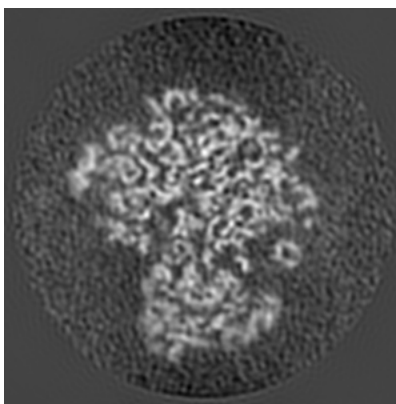
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

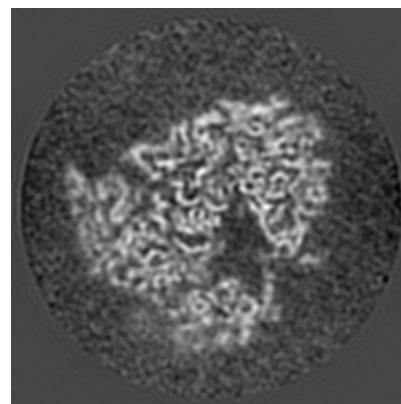
#### 6.2.1 Primary map



X Index: 180



Y Index: 180

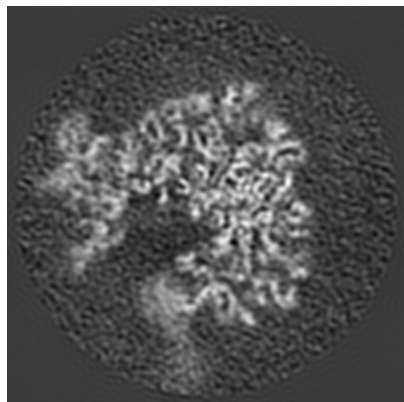


Z Index: 180

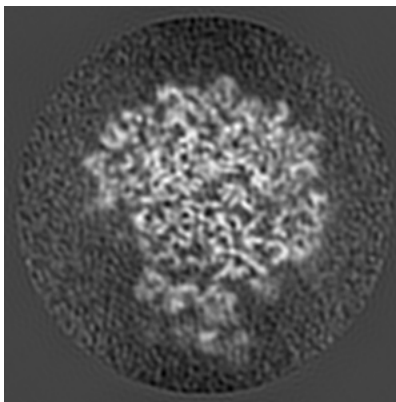
The images above show central slices of the map in three orthogonal directions.

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

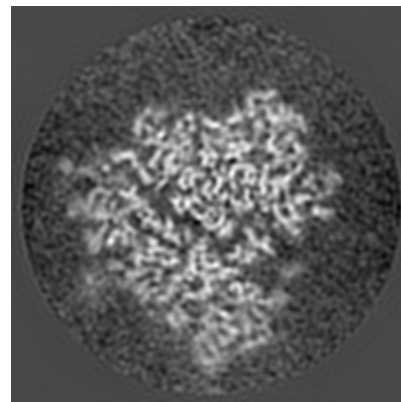
### 6.3.1 Primary map



X Index: 182



Y Index: 205

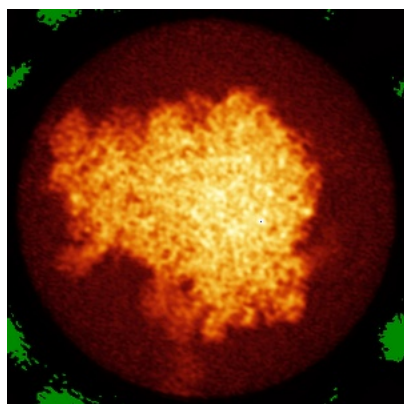


Z Index: 199

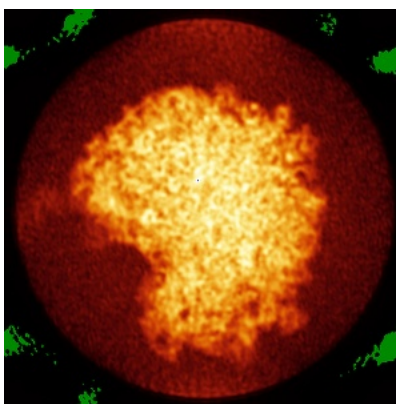
The images above show the largest variance slices of the map in three orthogonal directions.

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

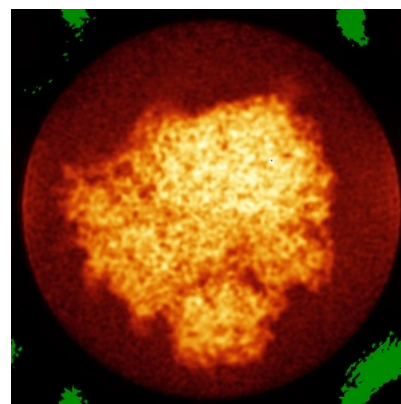
### 6.4.1 Primary map



X



Y



Z

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 0.12. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

## 6.6 Mask visualisation [i](#)

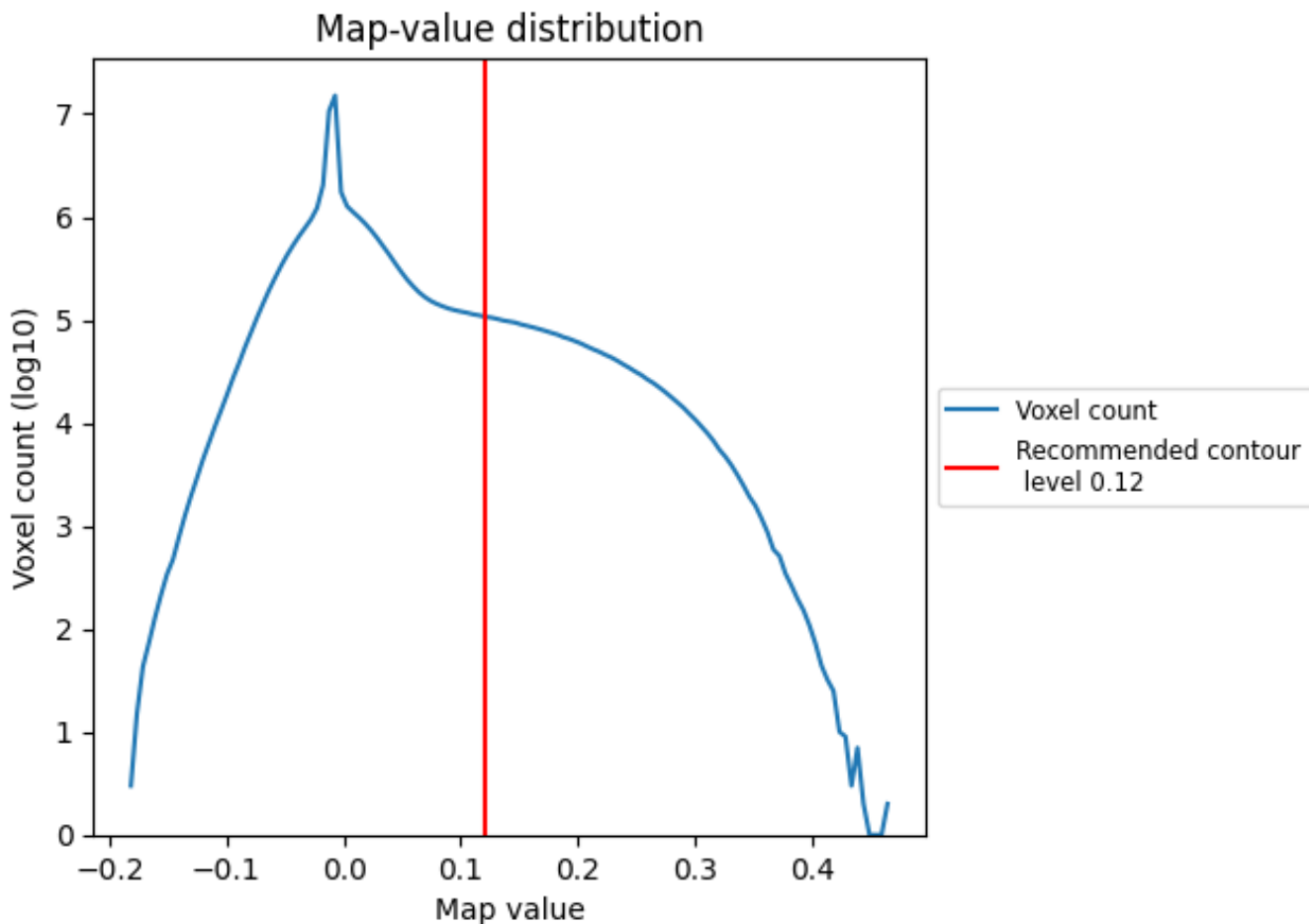
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

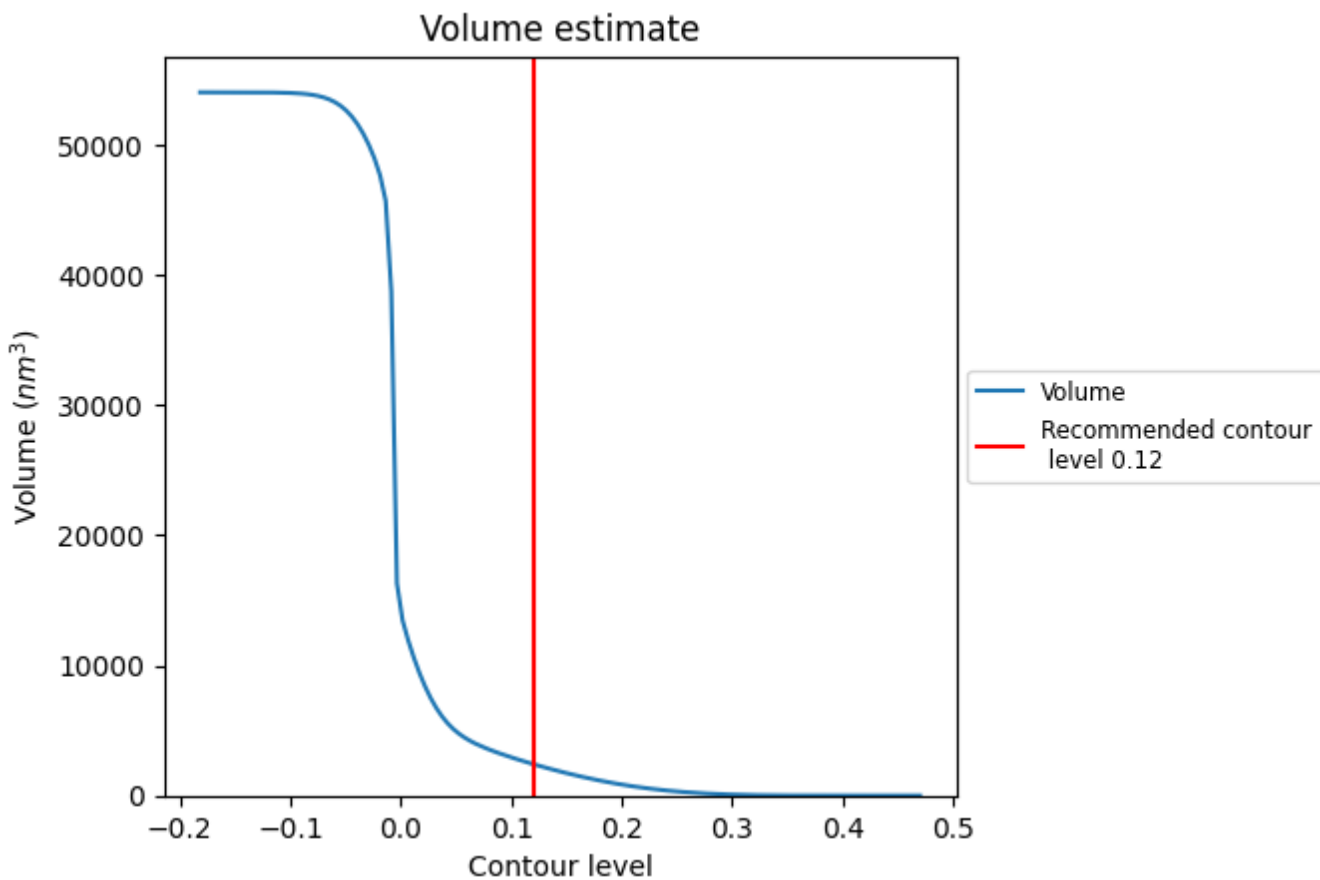
This section contains the results of statistical analysis of the map.

### 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.

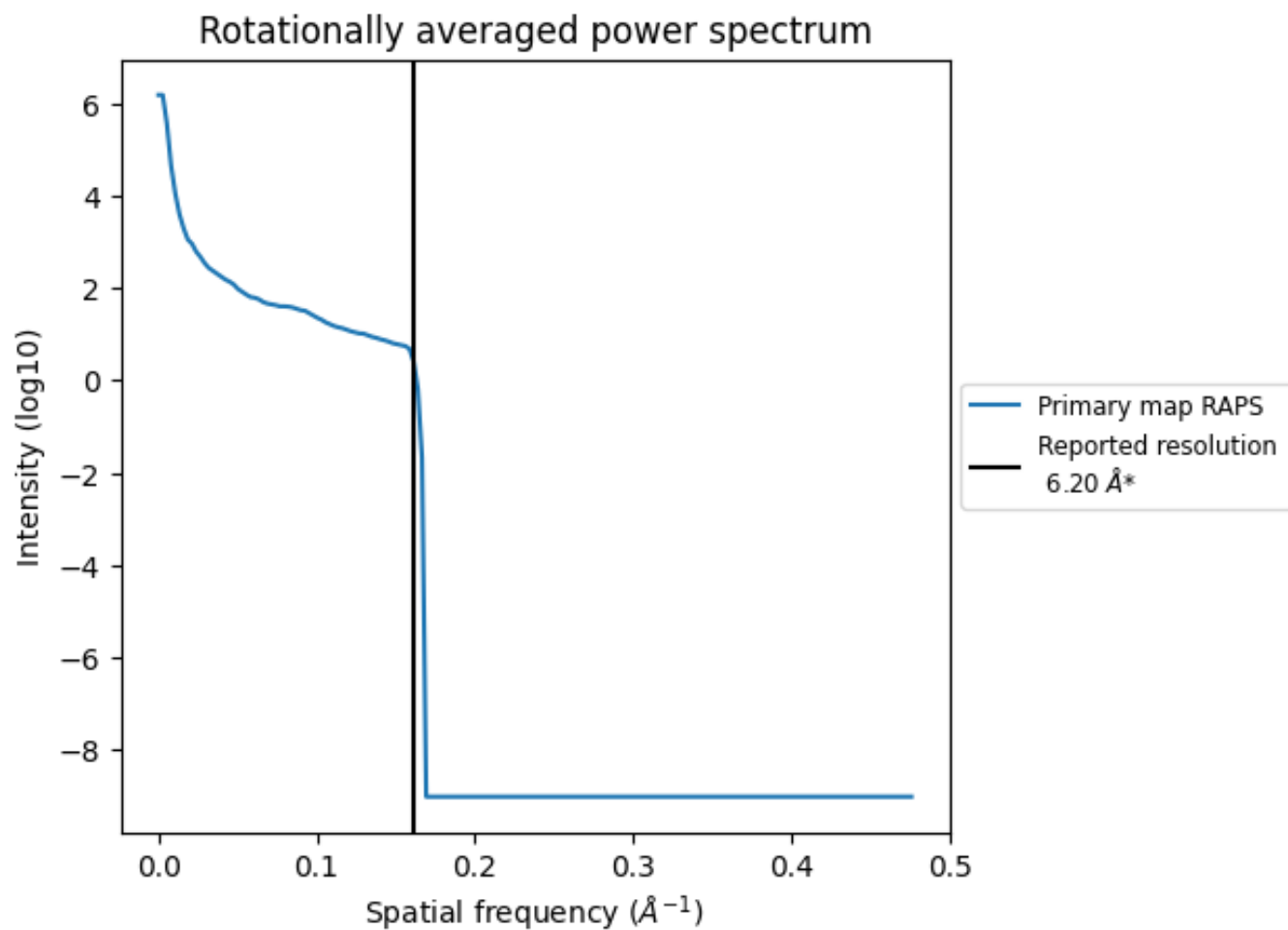
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2412 nm<sup>3</sup>; this corresponds to an approximate mass of 2179 kDa.

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

### 7.3 Rotationally averaged power spectrum i



\*Reported resolution corresponds to spatial frequency of 0.161 Å<sup>-1</sup>

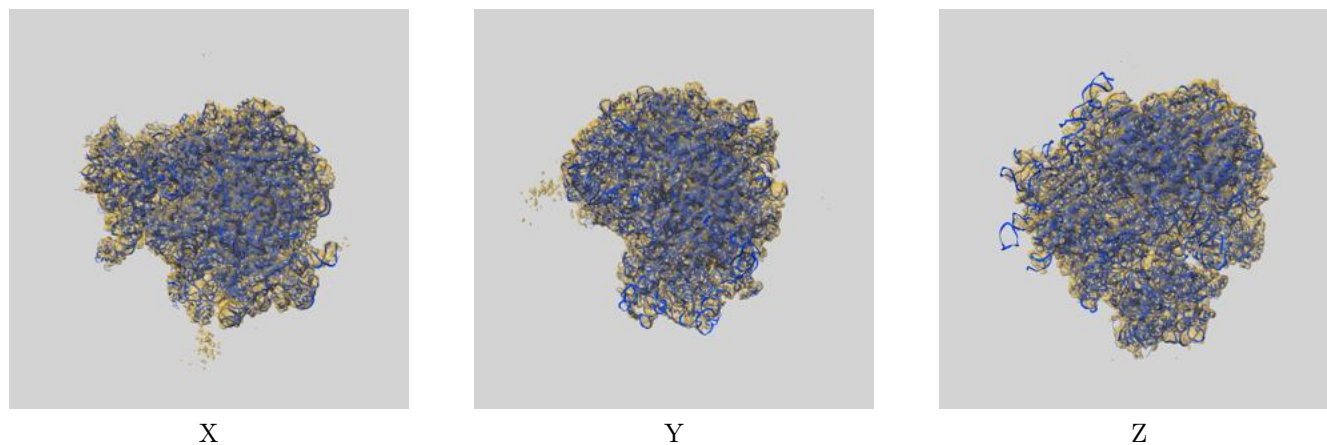
## 8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

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

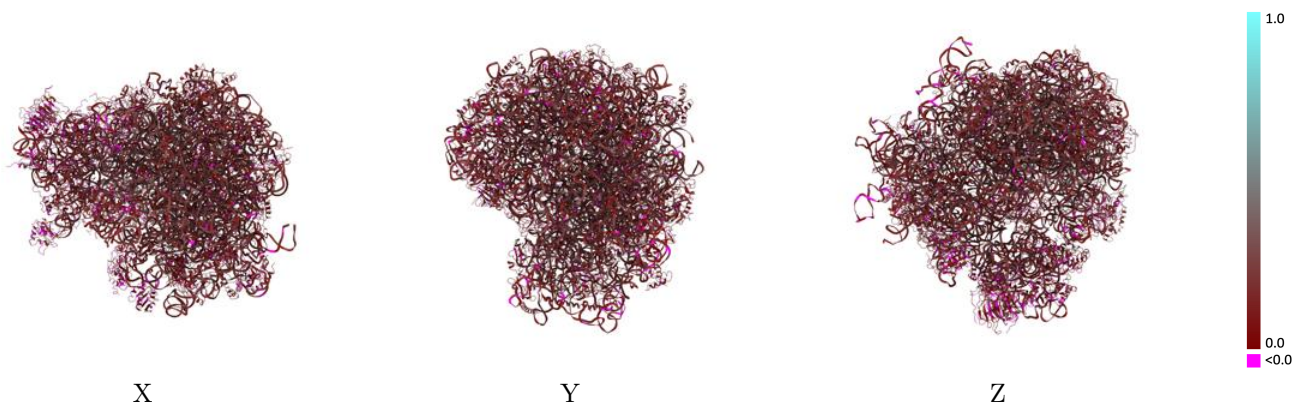
This section contains information regarding the fit between EMDB map EMD-5976 and PDB model 3J77. Per-residue inclusion information can be found in section 3 on page 19.

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



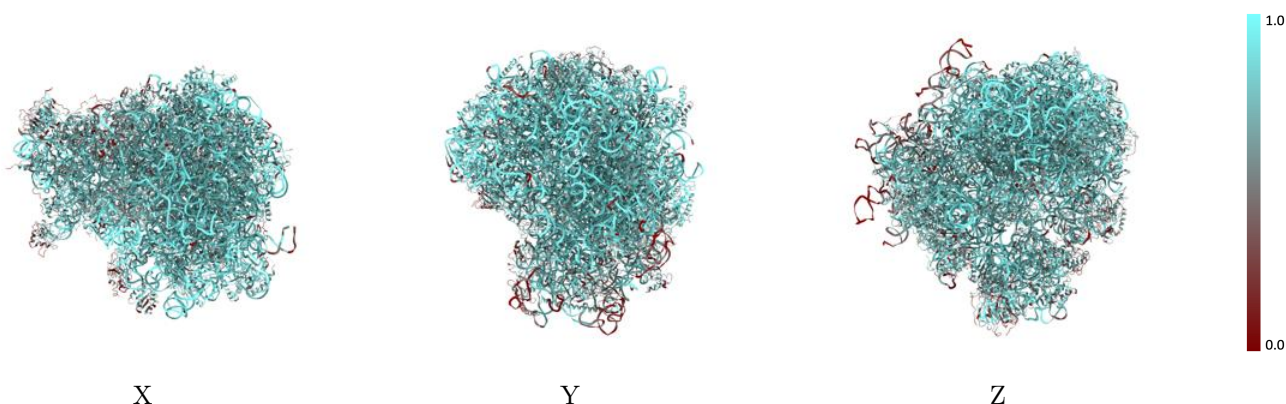
The images above show the 3D surface view of the map at the recommended contour level 0.12 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



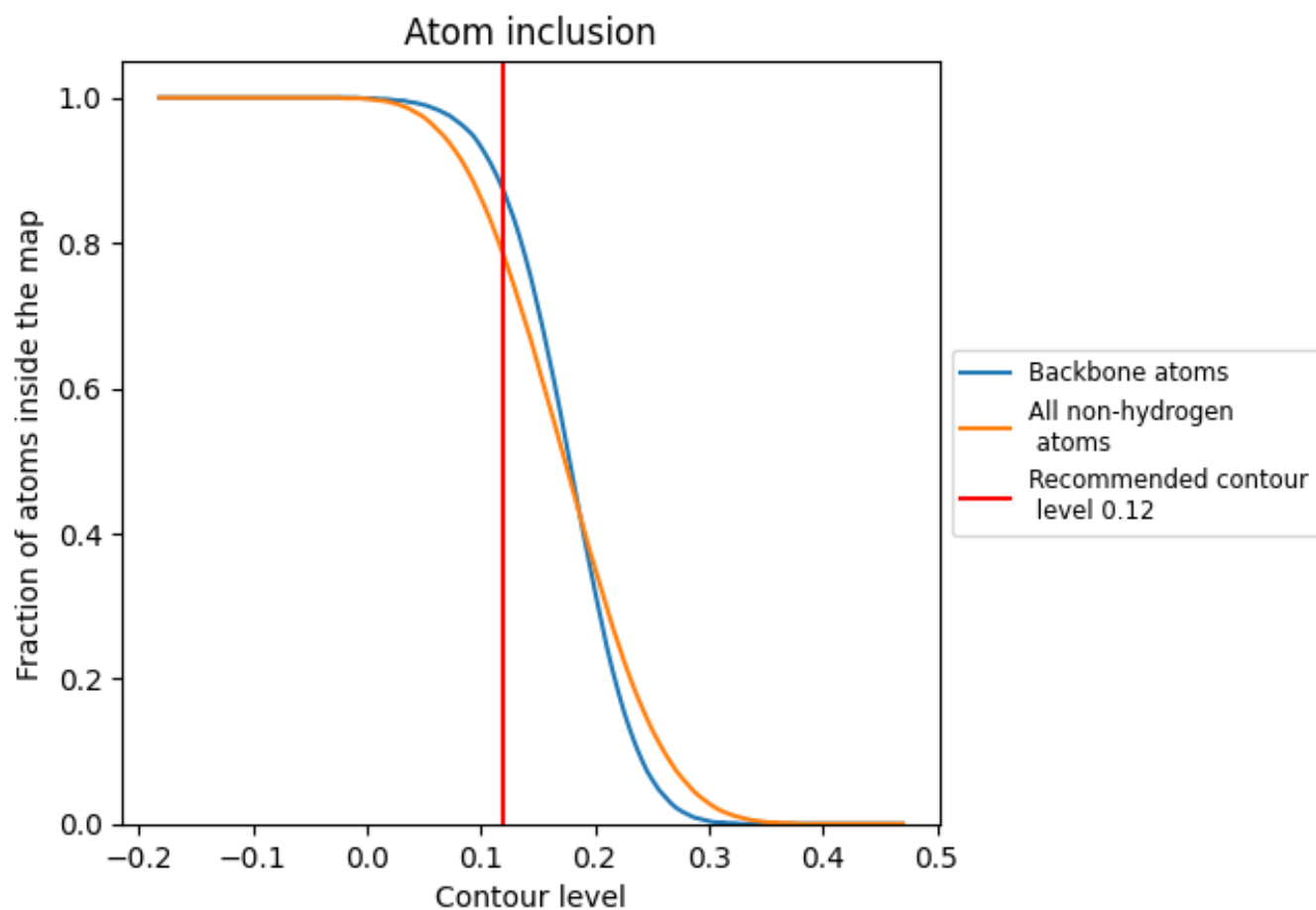
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.12).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 78% 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 (0.12) and Q-score for the entire model and for each chain.





















































































Chain	Atom inclusion	Q-score
All	 0.7830	 0.1910
10	 0.6750	 0.1370
11	 0.5250	 0.1720
12	 0.4140	 0.1440
13	 0.6960	 0.1710
14	 0.6580	 0.1690
15	 0.6610	 0.1590
16	 0.6220	 0.1210
17	 0.5500	 0.1440
18	 0.5820	 0.1520
19	 0.6060	 0.1260
1S	 0.8480	 0.2040
20	 0.6430	 0.1460
21	 0.6480	 0.1630
22	 0.6200	 0.1640
23	 0.5960	 0.1820
24	 0.6490	 0.1650
25	 0.5080	 0.1530
26	 0.6940	 0.1760
27	 0.6980	 0.1790
28	 0.5940	 0.1570
29	 0.7080	 0.1310
2S	 0.9110	 0.2210
30	 0.5900	 0.1880
31	 0.5330	 0.1380
5S	 0.9520	 0.2210
60	 0.7100	 0.1810
61	 0.6250	 0.1500
62	 0.2740	 0.1110
63	 0.6310	 0.1730
64	 0.7880	 0.1560
65	 0.6950	 0.1420
66	 0.7390	 0.1620
67	 0.6840	 0.1600
68	 0.6680	 0.1630



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Chain	Atom inclusion	Q-score
69	 0.6860	 0.1700
70	 0.7930	 0.1610
71	 0.6740	 0.1750
72	 0.6190	 0.1800
73	 0.5770	 0.1800
74	 0.4110	 0.1570
75	 0.7180	 0.1760
76	 0.7160	 0.1450
77	 0.7590	 0.1760
78	 0.6350	 0.1670
79	 0.6250	 0.1750
80	 0.7100	 0.1860
81	 0.6160	 0.1610
82	 0.7500	 0.1780
83	 0.7750	 0.1480
84	 0.7110	 0.1440
85	 0.7380	 0.1590
86	 0.6720	 0.1790
87	 0.7500	 0.1480
88	 0.6420	 0.1580
89	 0.7790	 0.1830
8S	 0.9430	 0.2260
90	 0.6880	 0.1540
91	 0.4370	 0.1200
92	 0.5610	 0.1820
93	 0.7130	 0.1730
L1	 0.2970	 0.1190
L2	 0.6670	 0.1650
L3	 0.6500	 0.1650
L4	 0.7260	 0.1720
L5	 0.6010	 0.1570
L6	 0.7020	 0.1600
L7	 0.7270	 0.1650
L8	 0.7230	 0.1740
L9	 0.7140	 0.1650
MR	 0.8560	 0.2450
P0	 0.5570	 0.1190
PT	 0.8740	 0.2160
RC	 0.5910	 0.1190
S0	 0.6540	 0.1710
S1	 0.6900	 0.1690
S2	 0.6680	 0.1760

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Chain	Atom inclusion	Q-score
S3	 0.6570	 0.1560
S4	 0.5840	 0.1530
S5	 0.6320	 0.1540
S6	 0.4970	 0.1500
S7	 0.5850	 0.1590
S8	 0.5550	 0.1580
S9	 0.6620	 0.1550