



wwPDB EM Validation Summary Report ⓘ

Nov 20, 2022 – 07:12 AM EST

PDB ID : 4V7E
EMDB ID : EMD-1780
Title : Model of the small subunit RNA based on a 5.5 Å cryo-EM map of *Triticum aestivum* translating 80S ribosome
Authors : Barrio-Garcia, C.; Armache, J.-P.; Jarasch, A.; Anger, A.M.; Villa, E.; Becker, T.; Bhushan, S.; Jossinet, F.; Habeck, M.; Dindar, G.; Franckenberg, S.; Marquez, V.; Mielke, T.; Thomm, M.; Berninghausen, O.; Beatrix, B.; Soeding, J.; Westhof, E.; Wilson, D.N.; Beckmann, R.
Deposited on : 2013-11-22
Resolution : 5.50 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev43
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) : 2.31.3

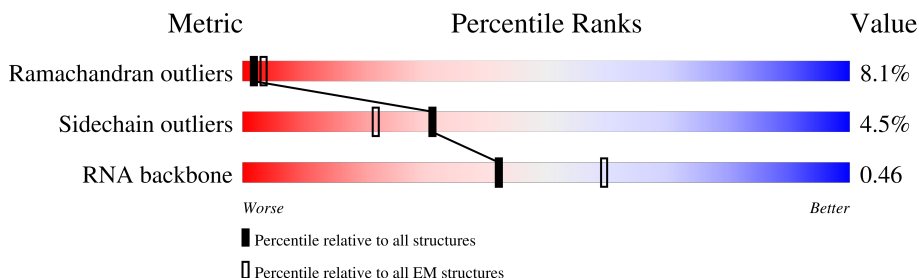
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.50 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	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 ≥ 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	Ad	1810	<div> <div>9%</div> <div>69%</div> <div>24%</div> </div>
2	Ae	75	<div> <div>29%</div> <div>71%</div> <div>25%</div> </div>
3	Af	11	<div> <div>9%</div> <div>82%</div> <div>73%</div> <div>18%</div> </div>
4	BY	138	<div> <div>51%</div> <div>88%</div> <div>10%</div> </div>
5	BI	220	<div> <div>14%</div> <div>28%</div> <div>70%</div> </div>
6	BK	183	<div> <div>26%</div> <div>44%</div> <div>5%</div> <div>48%</div> </div>
7	BM	171	<div> <div>47%</div> <div>61%</div> <div>9%</div> <div>28%</div> </div>
8	Bf	155	<div> <div>25%</div> <div>35%</div> <div>11%</div> <div>54%</div> </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	BX	142	
10	Bg	380	
11	BD	208	
12	BE	265	
13	BF	191	
14	BQ	149	
15	BU	128	
16	BO	151	
17	BS	152	
18	BN	151	
19	BL	160	
20	BT	146	
21	BP	154	
22	BZ	108	
23	Bc	65	
24	BW	130	
25	Bd	56	
26	Bb	86	
27	Be	62	
28	BA	260	
29	BR	141	
30	BB	262	
31	BV	82	
32	Ba	133	
33	BJ	195	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
34	BC	263	
35	BG	245	
36	BH	189	
37	CG	257	
38	CT	164	
39	CZ	136	
40	Cz	216	
41	CA	261	
42	CJ	180	
43	CH	190	
44	CV	140	
45	CN	200	
46	Ca	144	
47	CQ	188	
48	CD	304	
49	CR	209	
50	CP	171	
51	CX	152	
52	CW	162	
53	CY	150	
54	Cr	147	
55	Cc	112	
56	Cd	123	
57	Ce	133	
58	Cj	94	

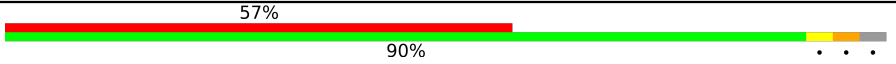
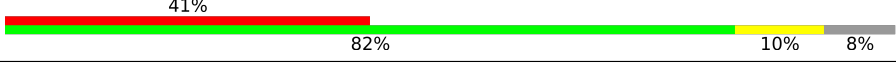
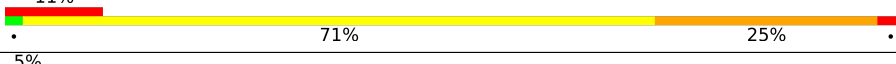
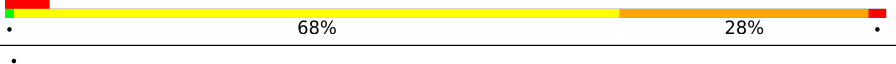
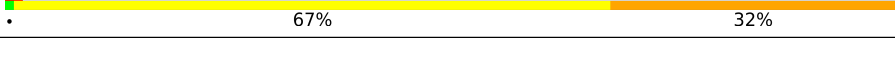
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
59	Cl	51	
60	Co	105	
61	CM	134	
62	CS	178	
63	CU	130	
64	Ci	112	
65	CK	166	
66	Cu	110	
66	Cv	110	
67	Cs	113	
67	Ct	113	
68	Ch	124	
69	CF	244	
70	Cq	319	
71	CB	389	
72	CC	405	
73	CO	206	
74	Cp	92	
75	CI	224	
76	Cn	25	
77	Cm	53	
78	CL	208	
79	CE	219	
80	Cf	111	
81	Ck	69	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
82	Cb	60	
83	Cg	119	
84	Aa	3391	
85	Ac	160	
86	Ab	120	

2 Entry composition

There are 86 unique types of molecules in this entry. The entry contains 212263 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Ad	1762	Total	C	N	O	P	0	0
			37584	16788	6708	12327	1761		

- Molecule 2 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	Ae	75	Total	C	N	O	P	0	0
			1595	712	280	529	74		

- Molecule 3 is a RNA chain called 5'-R(*AP*AP*AP*AP*GP*AP*CP*UP*UP*CP*A)-3'.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Af	11	Total	C	N	O	P	0	0
			232	106	45	71	10		

- Molecule 4 is a protein called 40S ribosomal protein S24E.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	BY	138	Total	C	N	O	S	0	0
			1108	703	212	189	4		

- Molecule 5 is a protein called 40S ribosomal protein S8E.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	BI	66	Total	C	N	O	S	0	0
			533	330	105	95	3		

- Molecule 6 is a protein called 40S ribosomal protein S10E.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	BK	96	Total	C	N	O	S	0	0
			818	535	137	143	3		

- Molecule 7 is a protein called 40S ribosomal protein S12E.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	BM	123	Total	C	N	O	S	0	0
			924	577	159	179	9		

- Molecule 8 is a protein called 40S ribosomal protein S31e.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Bf	71	Total	C	N	O	S	0	0
			577	367	107	98	5		

- Molecule 9 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	BX	142	Total	C	N	O	S	0	0
			1103	698	214	187	4		

- Molecule 10 is a protein called RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Bg	380	Total	C	N	O	S	0	0
			2929	1813	530	567	19		

- Molecule 11 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	BD	208	Total	C	N	O	S	0	0
			1629	1029	294	297	9		

- Molecule 12 is a protein called 40S ribosomal protein S4E.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	BE	200	Total	C	N	O	S	0	0
			1607	1030	290	283	4		

- Molecule 13 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	BF	191	Total	C	N	O	S	0	0
			1489	928	281	273	7		

- Molecule 14 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	BQ	126	Total	C	N	O	S	0	0
			1017	648	195	170	4		

- Molecule 15 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	BU	128	Total	C	N	O	S	0	0
			982	613	176	187	6		

- Molecule 16 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	BO	119	Total	C	N	O	S	0	0
			899	550	178	167	4		

- Molecule 17 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	BS	152	Total	C	N	O	S	0	0
			1240	772	248	213	7		

- Molecule 18 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	BN	121	Total	C	N	O	S	0	0
			977	627	180	167	3		

- Molecule 19 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	BL	85	Total	C	N	O	S	0	0
			688	435	134	115	4		

- Molecule 20 is a protein called 40S ribosomal protein S19E.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	BT	146	Total	C	N	O	S	0	0
			1155	726	218	207	4		

- Molecule 21 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	BP	91	Total	C	N	O	S	0	0
			711	457	130	120	4		

- Molecule 22 is a protein called 40S ribosomal protein S25E.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	BZ	100	Total	C	N	O	S	0	0
			779	489	146	144			

- Molecule 23 is a protein called 40S ribosomal protein S28E.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Bc	58	Total	C	N	O	S	0	0
			454	281	86	84	3		

- Molecule 24 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	BW	130	Total	C	N	O	S	0	0
			1042	667	189	181	5		

- Molecule 25 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Bd	48	Total	C	N	O	S	0	0
			379	233	77	63	6		

- Molecule 26 is a protein called 40S ribosomal protein S27E.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Bb	86	Total	C	N	O	S	0	0
			663	414	119	122	8		

- Molecule 27 is a protein called 40S ribosomal protein S30E.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Be	60	Total	C	N	O	S	0	0
			469	289	104	75	1		

- Molecule 28 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BA	197	Total	C	N	O	S	0	0
			1537	969	280	278	10		

- Molecule 29 is a protein called 40S ribosomal protein S17E.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	BR	116	Total	C	N	O	S	0	0
			945	589	178	171	7		

- Molecule 30 is a protein called 40S ribosomal protein S1E.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	BB	211	Total	C	N	O	S	0	0
			1707	1089	308	302	8		

- Molecule 31 is a protein called 40S ribosomal protein S21E.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BV	76	Total	C	N	O	S	0	0
			601	371	112	115	3		

- Molecule 32 is a protein called 40S ribosomal protein S26E.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Ba	93	Total	C	N	O	S	0	0
			753	461	163	122	7		

- Molecule 33 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BJ	187	Total	C	N	O	S	0	0
			1525	959	305	256	5		

- Molecule 34 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BC	214	Total	C	N	O	S	0	0
			1665	1074	297	287	7		

- Molecule 35 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BG	231	Total	C	N	O	S	0	0
			1867	1164	367	328	8		

- Molecule 36 is a protein called 40S ribosomal protein S7E.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BH	184	Total	C	N	O	S	0	0
			1508	962	278	266	2		

- Molecule 37 is a protein called 60S ribosomal protein L8E.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	CG	237	Total	C	N	O	S	0	0
			1906	1226	351	322	7		

- Molecule 38 is a protein called 60S ribosomal protein L21E.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	CT	160	Total	C	N	O	S	0	0
			1288	814	251	219	4		

- Molecule 39 is a protein called 60S ribosomal protein L27E.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	CZ	136	Total	C	N	O	S	0	0
			1090	704	205	176	5		

- Molecule 40 is a protein called 60S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Cz	216	Total	C	N	O	S	0	0
			1718	1092	309	304	13		

- Molecule 41 is a protein called 60S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	CA	255	Total	C	N	O	S	0	0
			1946	1210	399	328	9		

- Molecule 42 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	CJ	170	Total	C	N	O	S	0	0
			1380	869	256	246	9		

- Molecule 43 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	CH	190	Total	C	N	O	S	0	0
			1500	947	270	277	6		

- Molecule 44 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	CV	140	Total	C	N	O	S	0	0
			1048	658	199	181	10		

- Molecule 45 is a protein called 60S ribosomal protein L15E.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	CN	194	Total	C	N	O	S	0	0
			1630	1027	342	257	4		

- Molecule 46 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Ca	144	Total	C	N	O	S	0	0
			1114	710	223	175	6		

- Molecule 47 is a protein called 60S ribosomal protein L18E.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	CQ	163	Total	C	N	O	S	0	0
			1284	810	248	219	7		

- Molecule 48 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	CD	304	Total	C	N	O	S	0	0
			2444	1531	440	466	7		

- Molecule 49 is a protein called 60S ribosomal protein L19E.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	CR	189	Total	C	N	O	S	0	0
			1569	972	330	257	10		

- Molecule 50 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	CP	171	Total	C	N	O	S	0	0
			1372	852	271	244	5		

- Molecule 51 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	CX	122	Total	C	N	O	S	0	0
			987	634	178	173	2		

- Molecule 52 is a protein called 60S ribosomal protein L24E.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	CW	75	Total	C	N	O	S	0	0
			635	408	126	97	4		

- Molecule 53 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	CY	130	Total	C	N	O	S	0	0
			1048	647	220	178	3		

- Molecule 54 is a protein called 60S ribosomal protein L28E.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	Cr	73	Total	C	N	O	S	0	0
			576	364	107	103	2		

- Molecule 55 is a protein called 60S ribosomal protein L30E.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Cc	112	Total	C	N	O	S	0	0
			857	540	149	161	7		

- Molecule 56 is a protein called 60S ribosomal protein L31E.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Cd	120	Total	C	N	O	S	0	0
			960	598	186	173	3		

- Molecule 57 is a protein called 60S ribosomal protein L32E.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	Ce	133	Total	C	N	O	S	0	0
			1103	696	216	185	6		

- Molecule 58 is a protein called 60S ribosomal protein L37E.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Cj	94	Total	C	N	O	S	0	0
			755	459	166	123	7		

- Molecule 59 is a protein called 60S ribosomal protein L39E.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	Cl	51	Total	C	N	O	S	0	0
			460	291	100	67	2		

- Molecule 60 is a protein called 60S ribosomal protein L44E.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	Co	105	Total	C	N	O	S	0	0
			851	535	166	144	6		

- Molecule 61 is a protein called 60S ribosomal protein L14E.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	CM	134	Total	C	N	O	S	0	0
			1081	690	201	185	5		

- Molecule 62 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	CS	167	Total	C	N	O	S	0	0
			1419	916	263	233	7		

- Molecule 63 is a protein called 60S ribosomal protein L22E.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	CU	108	Total	C	N	O	S	0	0
			864	551	155	156	2		

- Molecule 64 is a protein called 60S ribosomal protein L36E.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Ci	77	Total	C	N	O	S	0	0
			613	383	128	100	2		

- Molecule 65 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	CK	128	Total	C	N	O	S	0	0
			960	602	177	177	4		

- Molecule 66 is a protein called 60S ribosomal protein P1.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Cu	58	Total	C	N	O	S	0	0
			432	283	69	79	1		
66	Cv	58	Total	C	N	O	S	0	0
			432	283	69	79	1		

- Molecule 67 is a protein called Acidic ribosomal protein P2.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Cs	59	Total	C	N	O	S	0	0
			441	278	69	90	4		
67	Ct	59	Total	C	N	O	S	0	0
			441	278	69	90	4		

- Molecule 68 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Ch	124	Total	C	N	O	S	0	0
			1012	636	202	173	1		

- Molecule 69 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	CF	244	Total	C	N	O	S	0	0
			1984	1271	368	339	6		

- Molecule 70 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Cq	262	Total	C	N	O	S	0	0
			1993	1278	330	377	8		

- Molecule 71 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	CB	389	Total	C	N	O	S	0	0
			3139	1997	584	540	18		

- Molecule 72 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	CC	372	Total	C	N	O	S	0	0
			2898	1823	556	510	9		

- Molecule 73 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	CO	206	Total	C	N	O	S	0	0
			1650	1045	320	274	11		

- Molecule 74 is a protein called 60S ribosomal protein L43E.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Cp	92	Total	C	N	O	S	0	0
			715	447	137	124	7		

- Molecule 75 is a protein called 60S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	CI	184	Total	C	N	O	S	0	0
			1490	941	290	247	12		

- Molecule 76 is a protein called 60S ribosomal protein L41E.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Cn	25	Total	C	N	O	S	0	0
			238	145	62	28	3		

- Molecule 77 is a protein called 60S ribosomal protein L40E.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Cm	52	Total	C	N	O	S	0	0
			428	267	90	66	5		

- Molecule 78 is a protein called 60S ribosomal protein L13E.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	CL	208	Total	C	N	O	S	0	0
			1691	1061	338	286	6		

- Molecule 79 is a protein called 60S ribosomal protein L6E.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	CE	219	Total	C	N	O	S	0	0
			1731	1106	314	307	4		

- Molecule 80 is a protein called 60S ribosomal protein L33E.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Cf	111	Total	C	N	O	S	0	0
			891	561	170	156	4		

- Molecule 81 is a protein called 60S ribosomal protein L38E.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Ck	69	Total	C	N	O	S	0	0
			564	360	104	97	3		

- Molecule 82 is a protein called 60S ribosomal protein L29E.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	Cb	58	Total	C	N	O	S	0	0
			477	288	103	85	1		

- Molecule 83 is a protein called 60S ribosomal protein L34E.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Cg	110	Total	C	N	O	S	0	0
			897	567	182	146	2		

- Molecule 84 is a RNA chain called 60S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Aa	3391	Total	C	N	O	P	0	0
			72601	32373	13241	23598	3389		

- Molecule 85 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	Ac	160	Total	C	N	O	P	0	0
			3408	1522	614	1113	159		

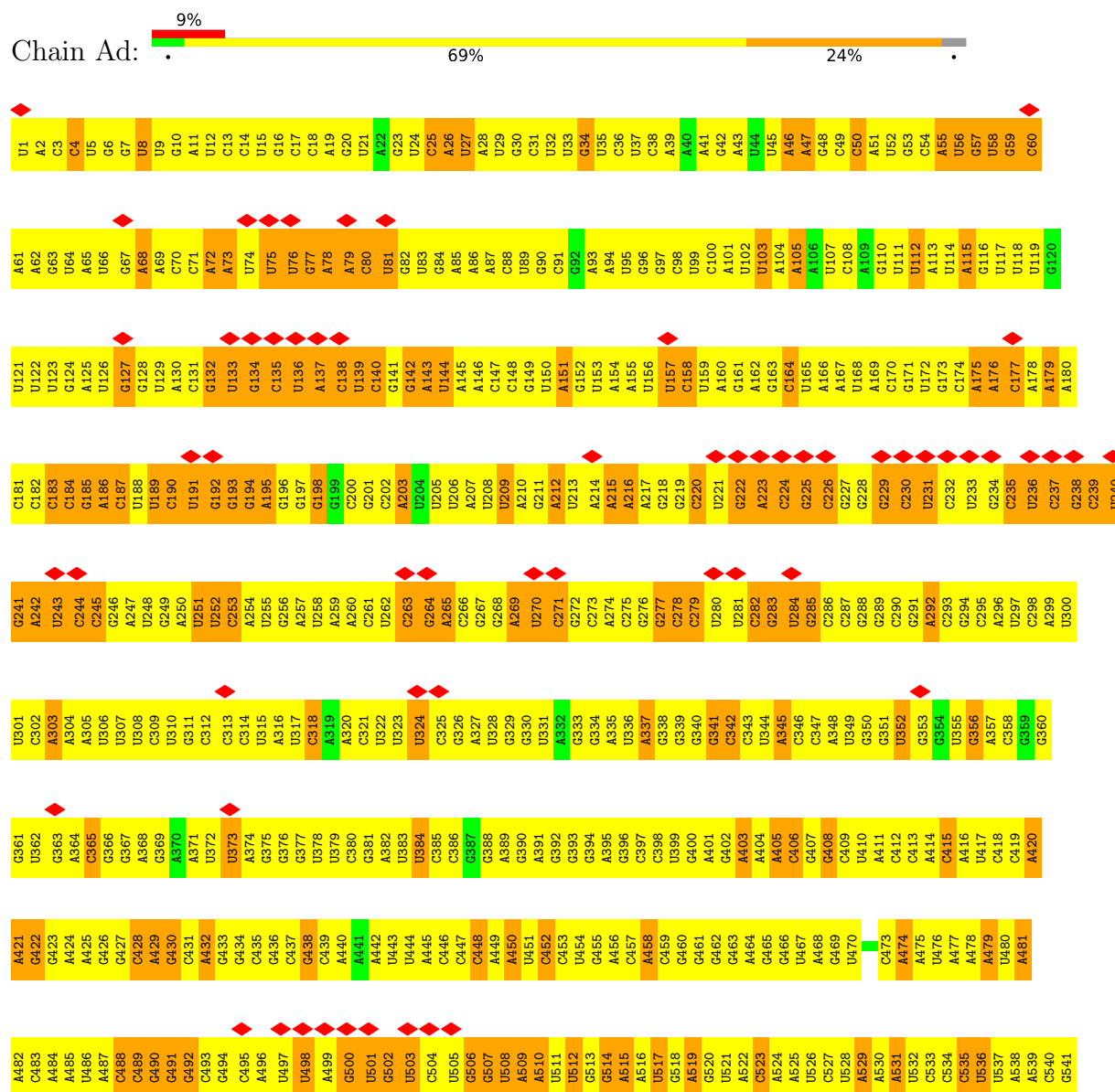
- Molecule 86 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	Ab	120	Total	C	N	O	P	0	0
			2561	1144	461	837	119		

3 Residue-property plots

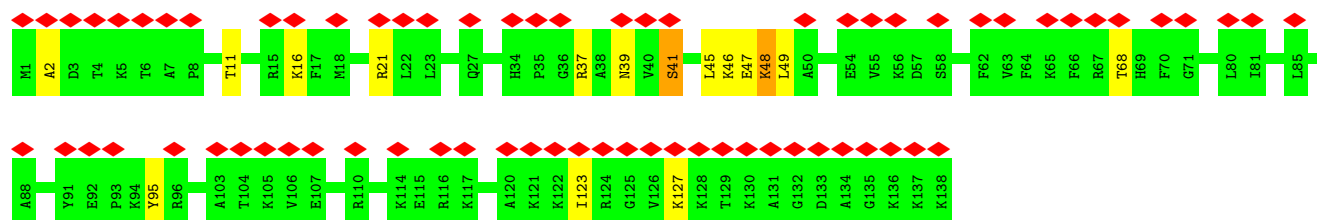
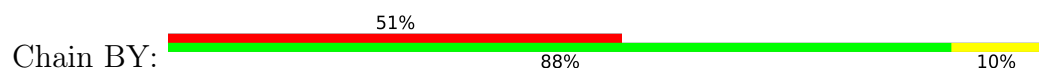
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 18S ribosomal RNA

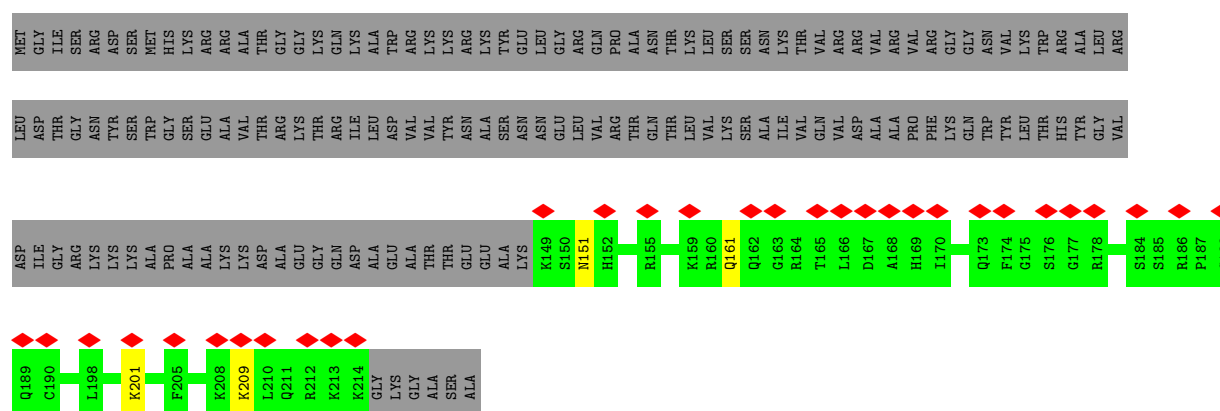


U1262	C1263	G1264	U1265	A1266	C1267	U1268	C1269	U1270	U1271	U1272	U1273	G1274	G1275	U1276	G1277	U1278	U1279	U1280	C1281	C1282	C1283	U1284	U1285	U1286	U1287	C1288	U1289	U1290	A1291	U1292	U1293	U1294	G1295	U1296	U1297	C1298	U1299	A1300	C1301	C1302	C1303	A1304	U1305	U1306	U1307	U1308	U1309	C1310	U1311	G1312	G1313	U1314	U1315	U1316	A1317	U1318	U1319	C1320	C1321
G1202	G1203	G1204	G1205	G1206	A1207	A1208	C1209	U1210	U1211	U1212	C1213	C1214	A1215	G1216	G1217	U1218	C1219	C1220	A1221	G1222	A1223	C1224	U1225	U1226	A1227	G1228	C1229	U1230	G1231	G1232	U1233	A1234	U1235	U1236	U1237	A1238	C1239	A1240	G1241	A1242	C1243	U1244	G1245	A1246	U1247	U1248	G1249	C1250	U1251	C1252	U1253	U1254	U1255	U1256	U1257	U1258	G1259	A1260	U1261
A1142	A1143	A1144	G1145	G1146	A1147	A1148	U1149	U1150	G1151	A1152	C1153	G1154	G1155	A1156	A1157	G1158	G1159	G1160	C1161	A1162	C1163	C1164	A1165	C1166	C1167	A1168	G1169	G1170	C1171	G1172	U1173	G1174	G1175	A1176	G1177	C1178	C1179	U1180	G1181	C1182	G1183	C1184	U1185	U1186	A1187	A1188	U1189	U1190	U1191	G1192	A1193	C1194	U1195	C1196	A1197	A1198	C1199	A1200	C1201
C1082	C1083	U1084	U1085	A1086	U1087	G1088	A1089	G1090	A1091	A1092	A1093	U1094	C1095	A1096	A1097	A1098	G1099	U1100	C1101	U1102	U1103	U1104	G1105	G1106	G1107	U1108	U1109	C1110	C1111	G1112	G1113	G1114	G1115	G1116	G1117	A1118	G1119	U1120	A1121	U1122	G1123	G1124	U1125	C1126	G1127	U1128	A1129	A1130	G1131	G1132	C1133	U1134	G1135	U1136	A1137	A1138	C1139	U1140	U1141
U1022	C1023	A1024	A1025	U1026	C1027	A1028	U1029	A1030	A1031	A1032	C1033	G1034	A1035	U1036	G1037	C1038	C1039	G1040	A1041	C1042	C1043	A1044	G1045	G1046	G1047	A1048	U1049	G1050	G1051	G1052	C1053	G1054	G1055	U1056	U1057	G1058	U1059	U1060	G1061	C1062	U1063	U1064	A1065	U1066	A1067	G1068	U1069	A1070	C1071	U1072	C1073	C1074	G1075	C1076	C1077	G1078	C1079	C1080	A1081
G962	U963	U964	U965	U966	C967	A968	U969	U970	A971	A972	U973	C974	A975	U976	G977	A978	U979	C980	G981	A982	A983	A984	G985	U986	U987	G988	G989	G990	G991	G992	C993	U994	C995	G996	A997	A998	G999	A1000	C1001	G1002	A1003	U1004	C1005	A1006	G1007	U1008	U1009	A1010	C1011	C1012	G1013	U1014	C1015	C1016	U1017	A1018	G1019	U1020	C1021
C902	A903	G904	A905	G906	G907	U908	G909	A910	A911	A912	U913	U914	C915	U916	U917	G918	G919	A920	U921	U922	U923	A924	U925	G926	A927	U928	A929	G930	A931	C932	G933	A934	C935	C936	A937	A938	C939	U940	G941	C942	G943	A944	A945	A946	G947	C948	U949	U950	U951	U952	G953	C954	C955	A956	A957	A958	G959	A960	U961
G842	G843	C844	C845	U846	U847	C848	G849	G850	G851	A852	U853	U854	C855	G856	A857	G858	U859	A860	A861	U862	G863	A864	U865	U866	A867	A868	U869	A870	G871	G872	G873	A874	C875	A876	G877	U878	C879	G880	G881	G882	G883	G884	C885	A886	U887	U888	C889	G890	U891	A892	U893	U894	U895	A896	A897	U898	A899	G900	U901
U722	C723	U724	U725	U726	C727	C728	C729	G730	G731	G732	U733	C734	G735	U736	U737	U738	U739	U740	C741	C742	G743	G744	C745	U746	U747	C748	G749	U750	U751	C752	C753	U754	U755	U756	G757	A758	A759	G760	A761	A762	A763	U764	U765	A766	G767	A768	G769	U770	U771	C772	U773	C774	A775	A776	A777	G778	A780	A781	
U602	A603	U604	A605	U606	U607	U608	A609	A610	G611	U612	U613	G614	U615	U616	G617	C618	A619	G620	U621	U622	A623	A624	A625	A626	A627	G628	C629	G630	C631	G632	U633	A634	G635	U636	U637	G638	G639	A640	C641	U642	U643	U644	G645	U646	G647	C648	C649	G650	G651	G	U	C	C	G	U	C	G	U	
A542	G543	G544	A545	U546	C547	C548	A549	U550	U551	G552	G553	A554	G555	G556	G557	C558	A559	A560	G561	U562	C563	U564	G565	G566	G567	G568	C569	C570	A571	G572	C573	A574	G575	C576	C577	U578	C579	G580	G581	U582	A583	A584	U585	U586	C587	C588	A589	G590	C591	U592	C593	C594	A595	C596	U597	A598	G599	C600	G601

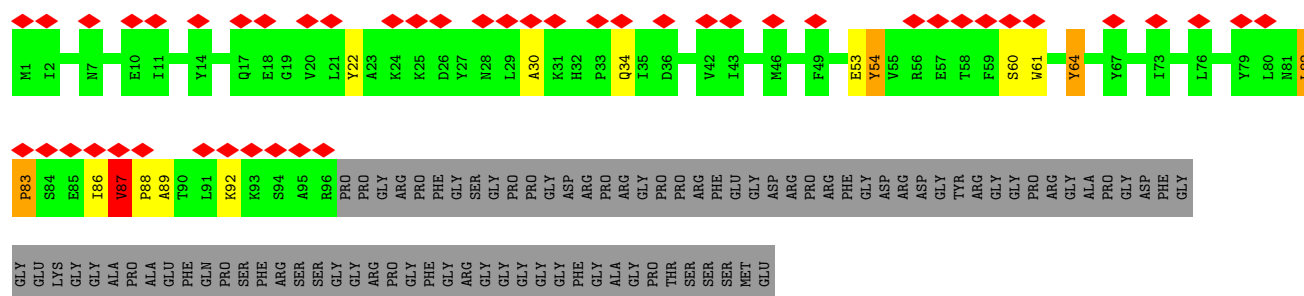
- Molecule 4: 40S ribosomal protein S24E



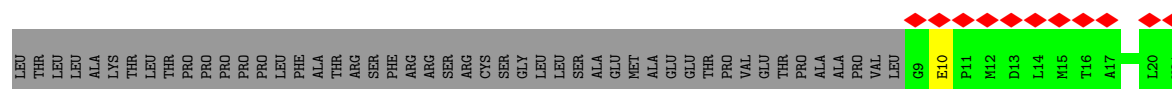
- Molecule 5: 40S ribosomal protein S8E

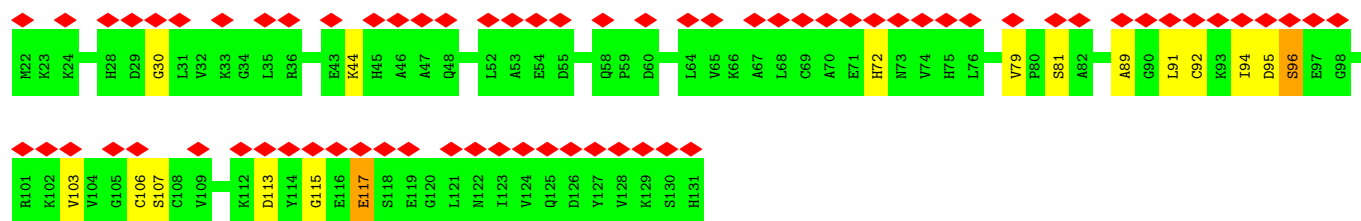


- Molecule 6: 40S ribosomal protein S10E

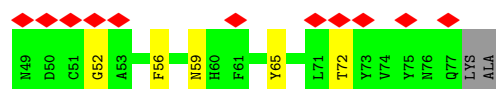
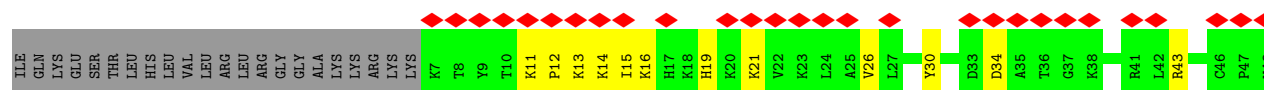
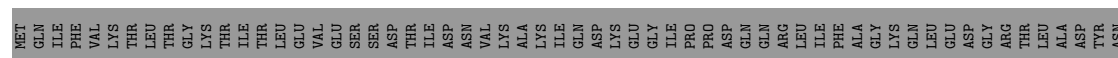
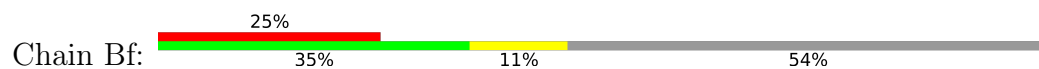


- Molecule 7: 40S ribosomal protein S12E

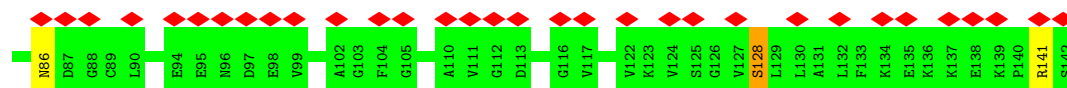
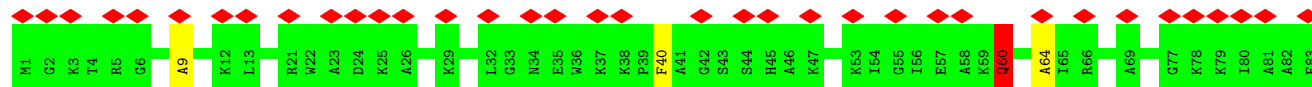




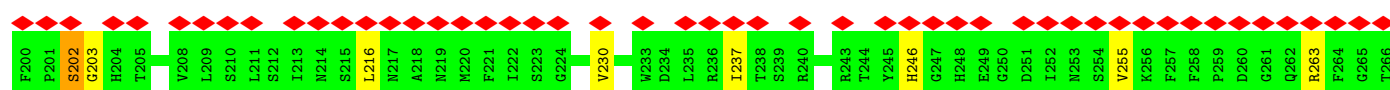
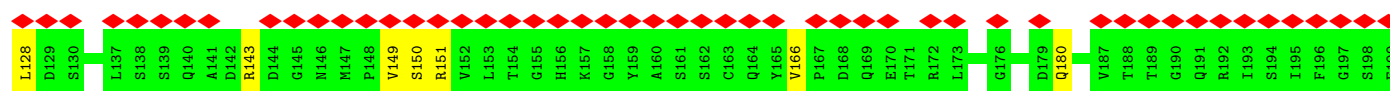
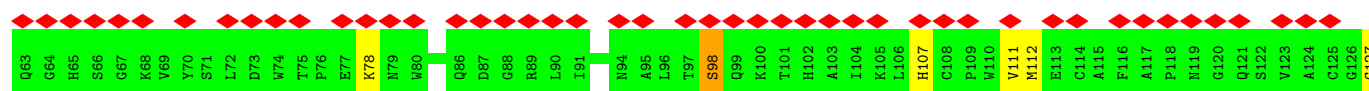
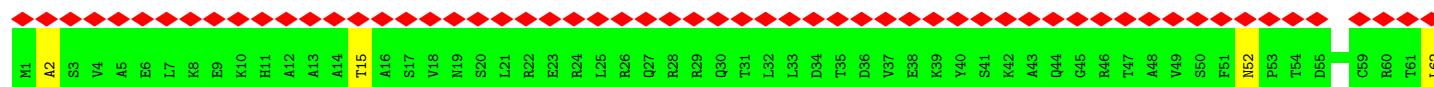
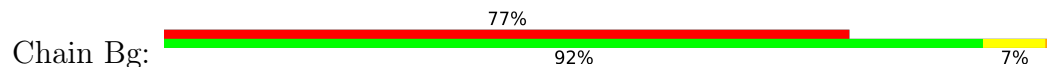
• Molecule 8: 40S ribosomal protein S31e

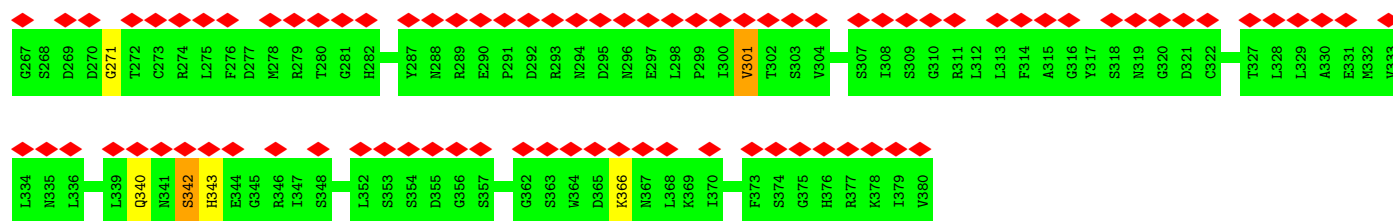


• Molecule 9: 40S ribosomal protein S12

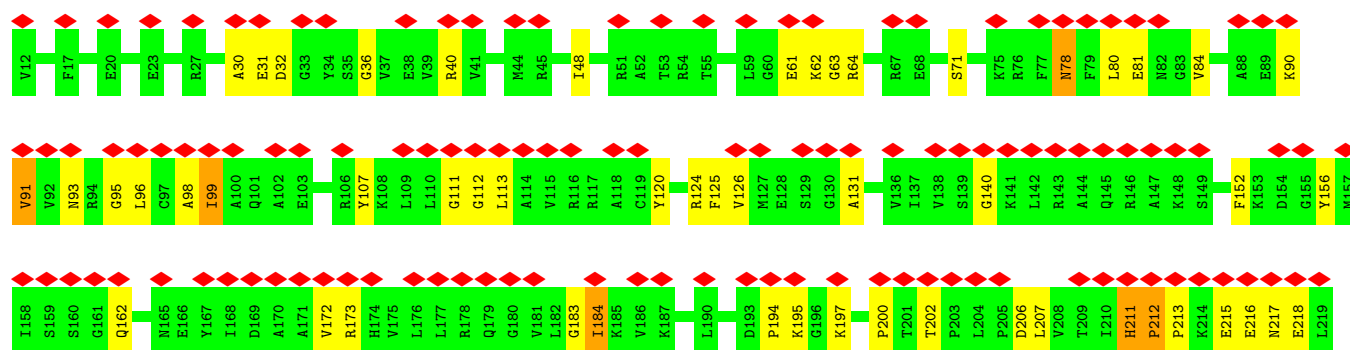
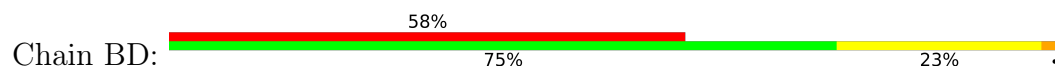


• Molecule 10: RACK1

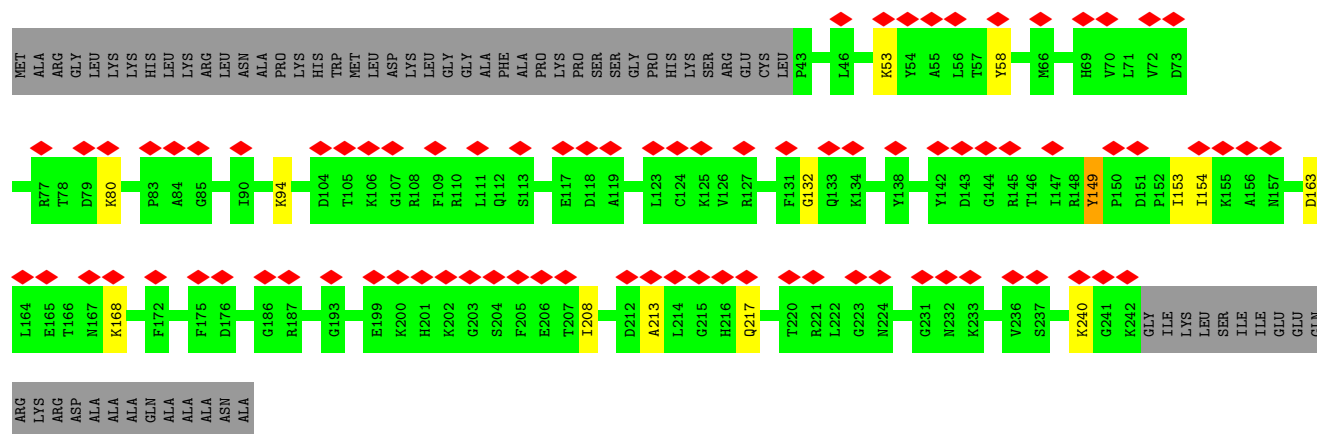
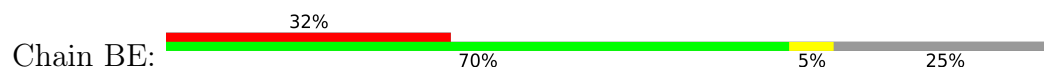




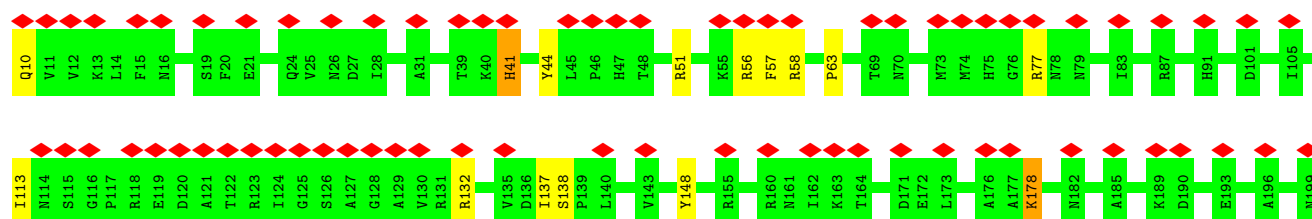
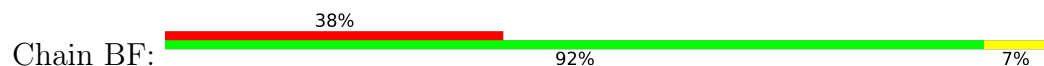
• Molecule 11: 40S ribosomal protein S3



• Molecule 12: 40S ribosomal protein S4E

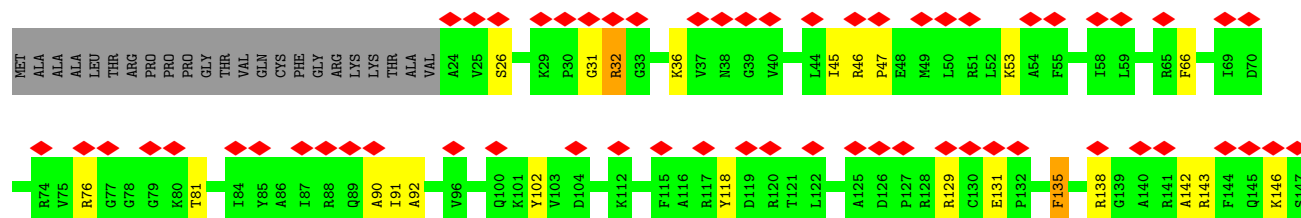
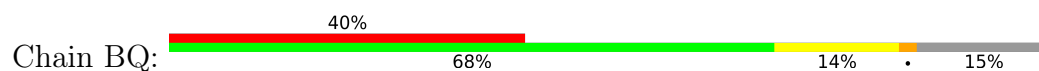


• Molecule 13: 40S ribosomal protein S7

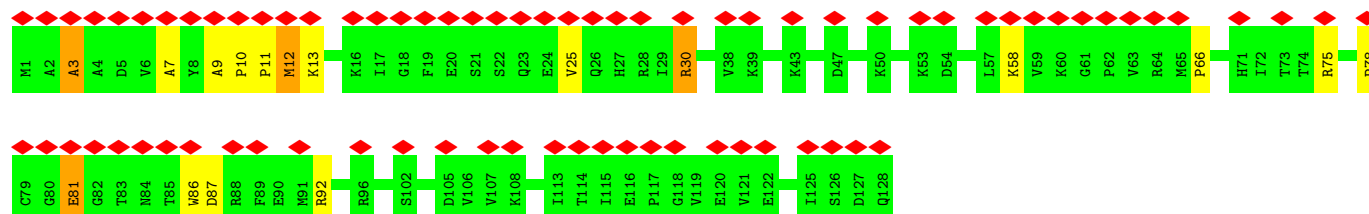
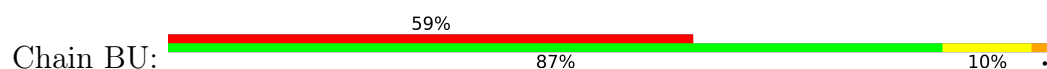




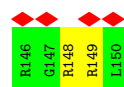
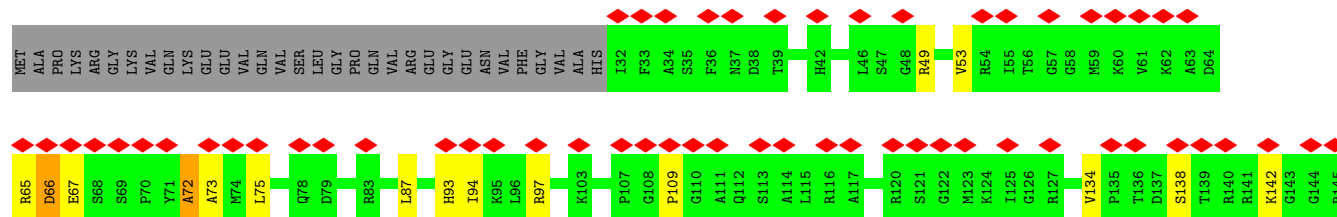
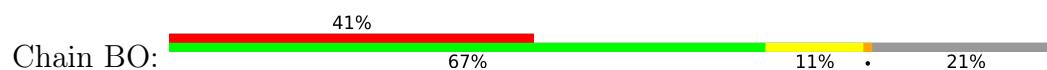
• Molecule 14: 40S ribosomal protein S9



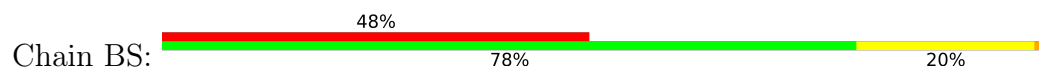
• Molecule 15: 40S ribosomal protein S10

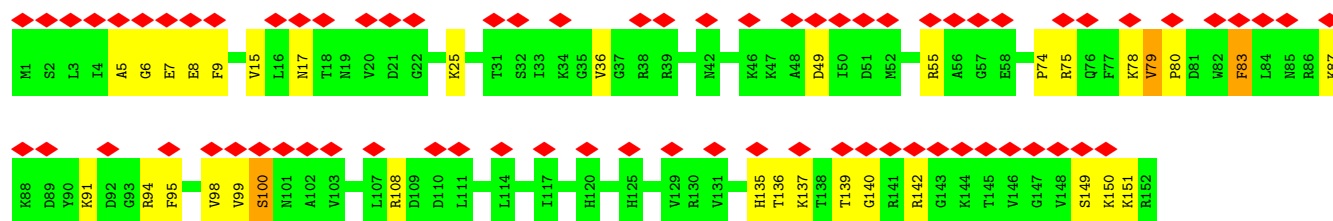


• Molecule 16: 40S ribosomal protein S11

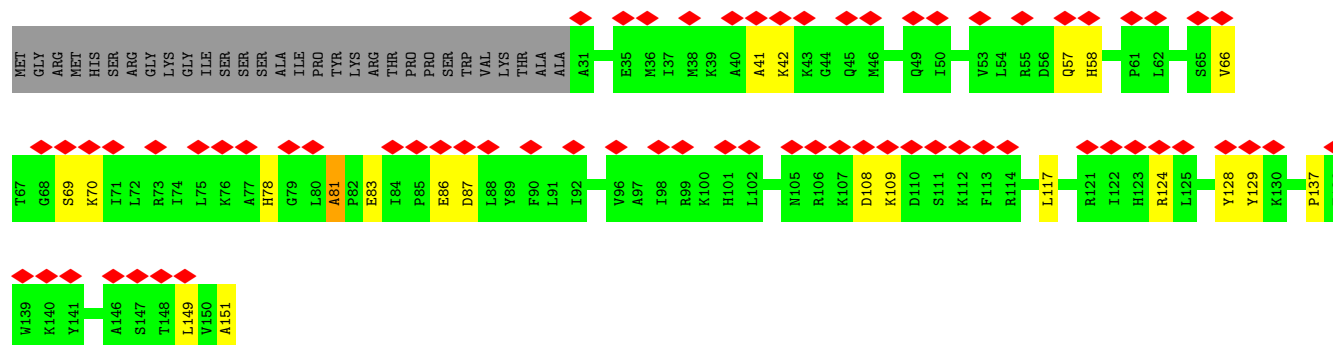


• Molecule 17: 40S ribosomal protein S13

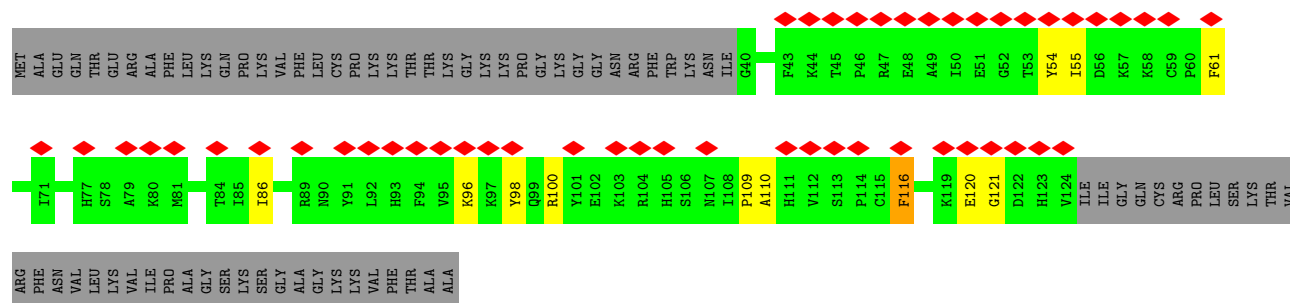




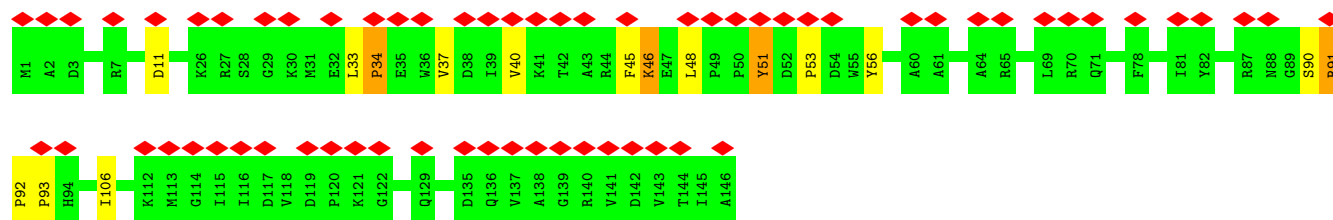
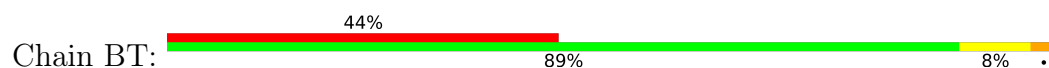
• Molecule 18: 40S ribosomal protein S15



• Molecule 19: 40S ribosomal protein S17

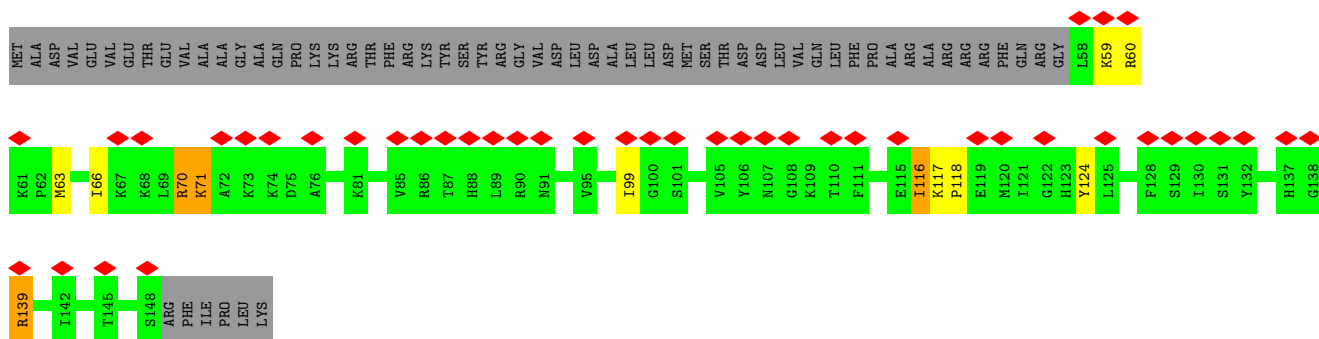


• Molecule 20: 40S ribosomal protein S19E

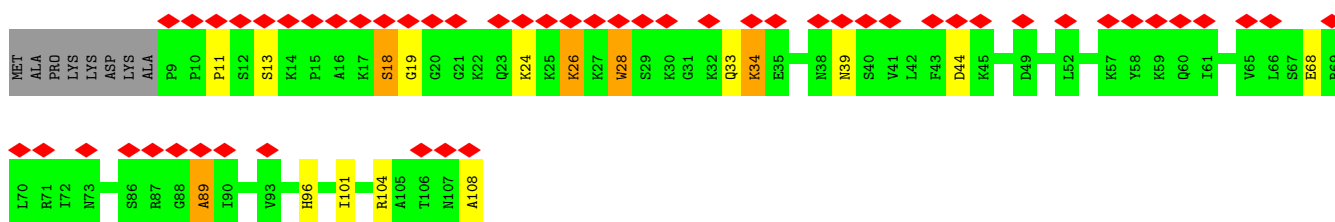
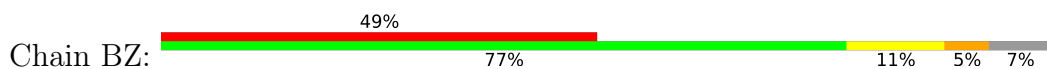


• Molecule 21: 40S ribosomal protein S19

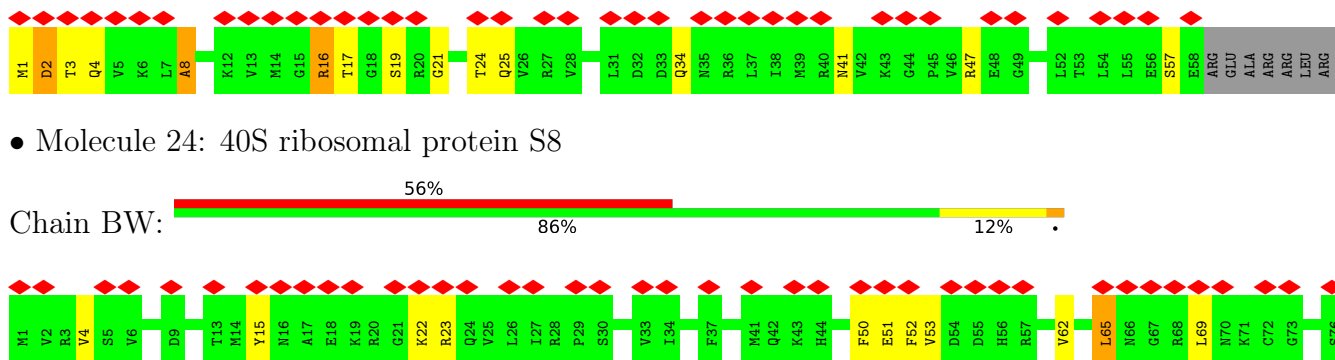




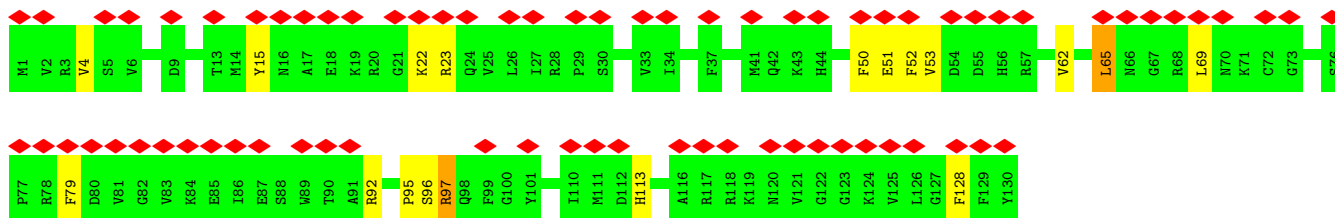
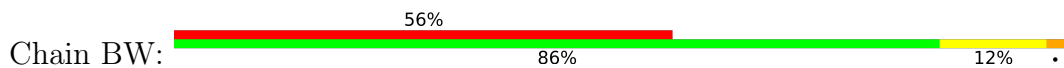
- Molecule 22: 40S ribosomal protein S25E



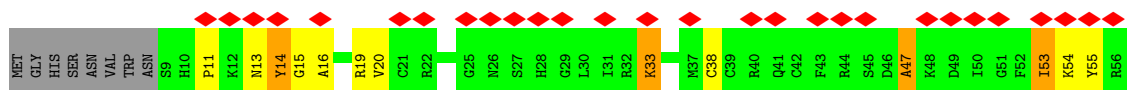
- Molecule 23: 40S ribosomal protein S28E



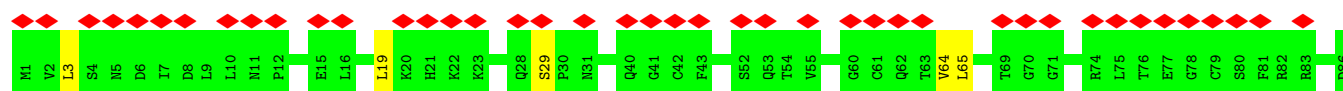
- Molecule 24: 40S ribosomal protein S8



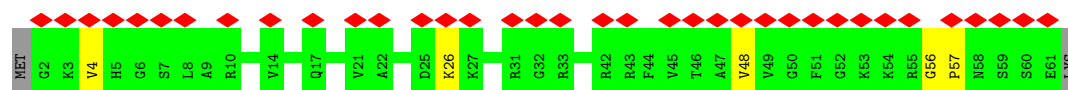
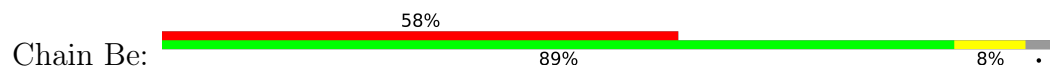
- Molecule 25: 40S ribosomal protein S14



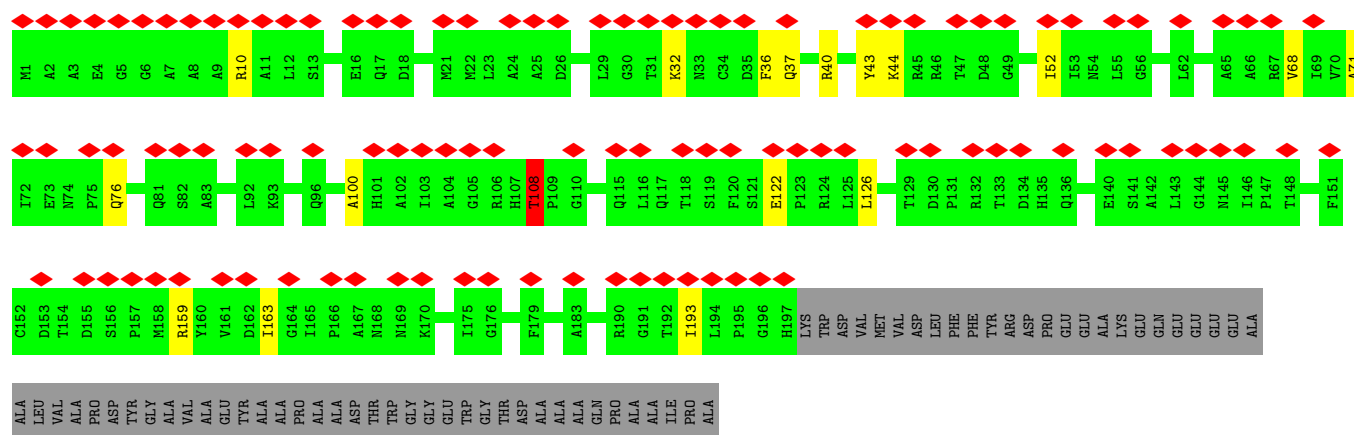
- Molecule 26: 40S ribosomal protein S27E



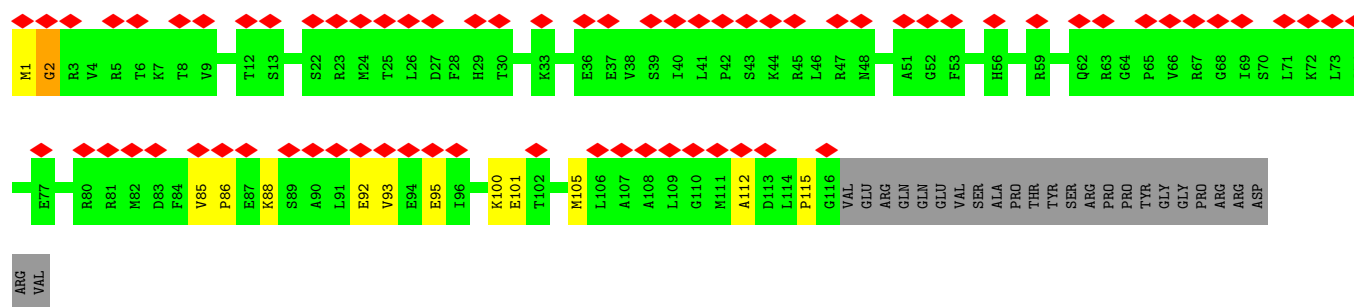
- Molecule 27: 40S ribosomal protein S30E



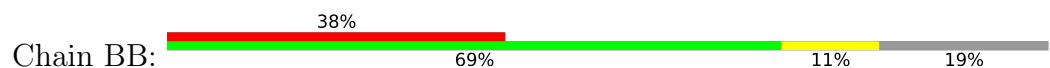
- Molecule 28: 40S ribosomal protein S2

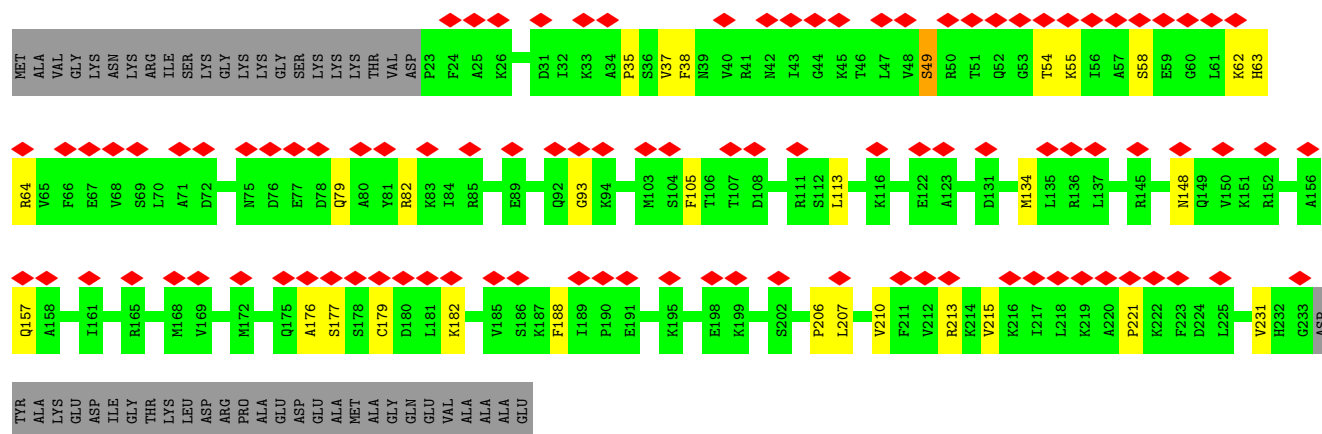


- Molecule 29: 40S ribosomal protein S17E

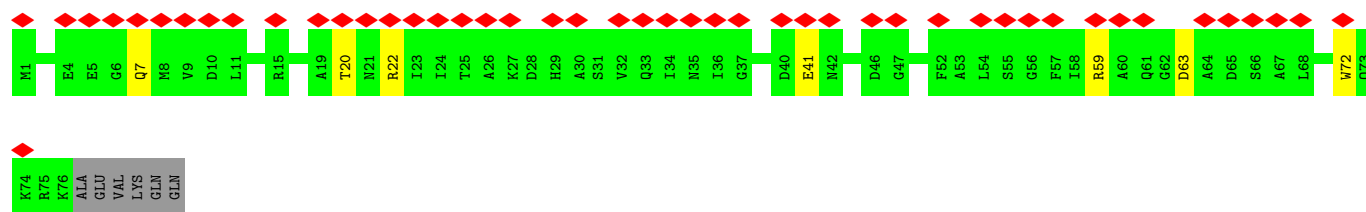
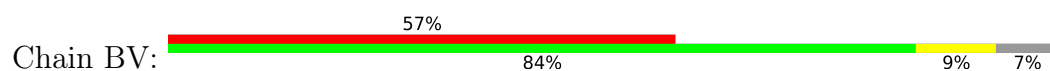


- Molecule 30: 40S ribosomal protein S1E

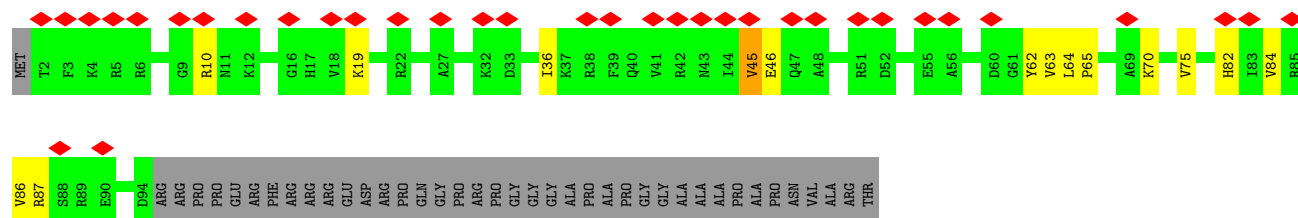




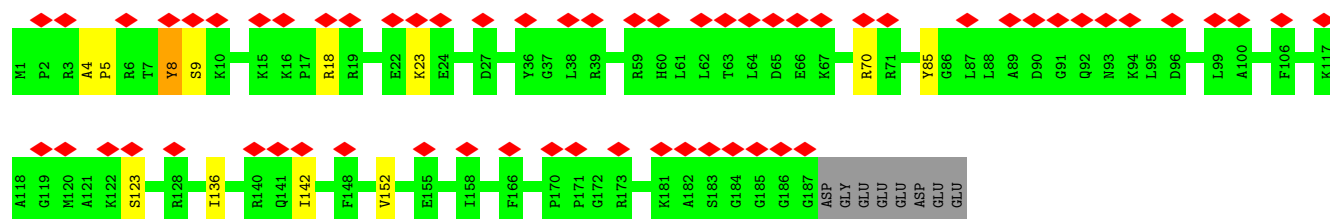
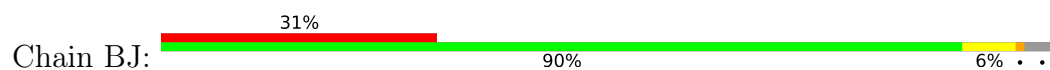
• Molecule 31: 40S ribosomal protein S21E



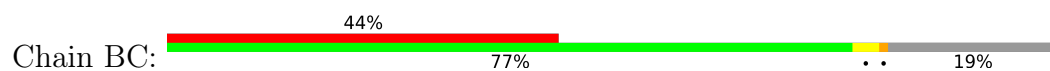
• Molecule 32: 40S ribosomal protein S26E

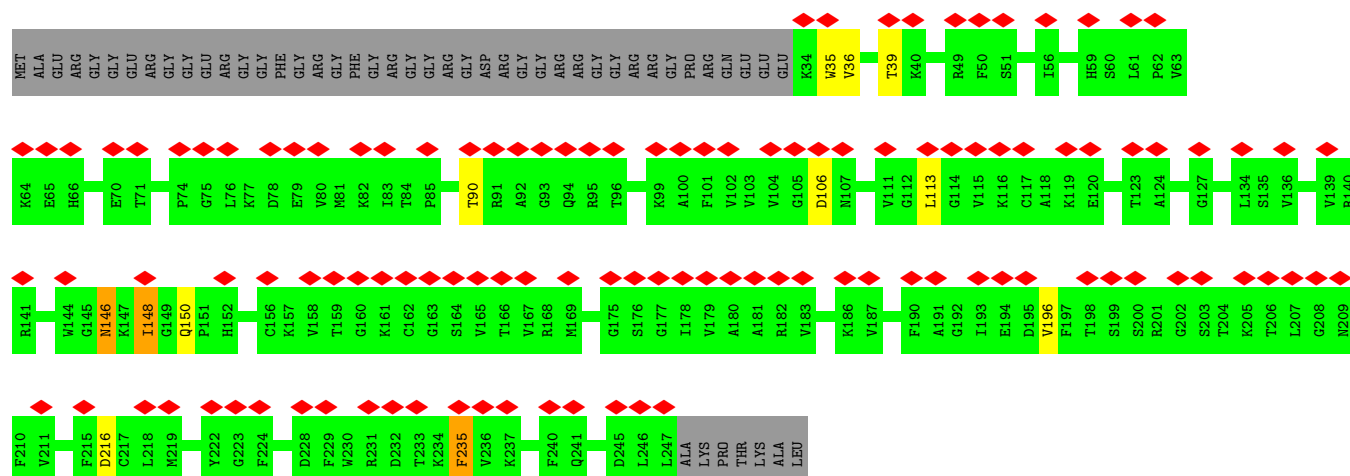


• Molecule 33: 40S ribosomal protein S4



• Molecule 34: 40S ribosomal protein S5





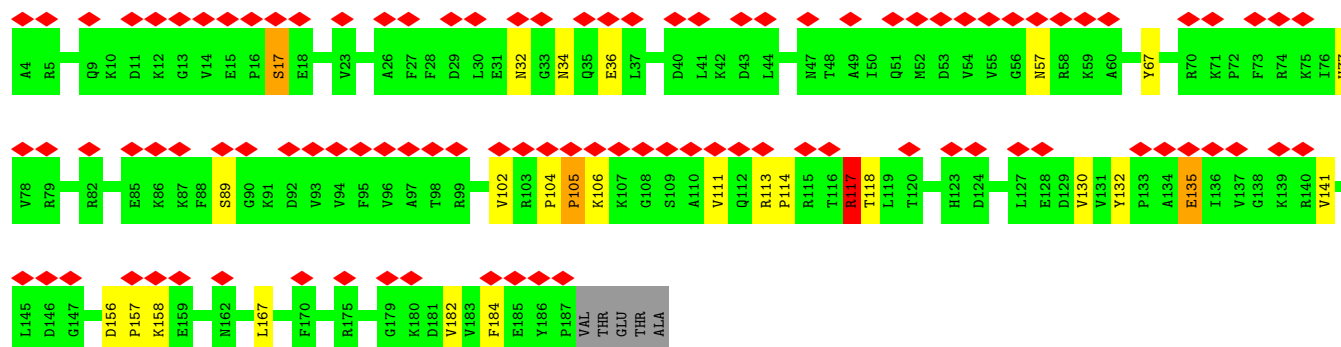
• Molecule 35: 40S ribosomal protein S6

Chain BG: 43% 88% 5% • 6%



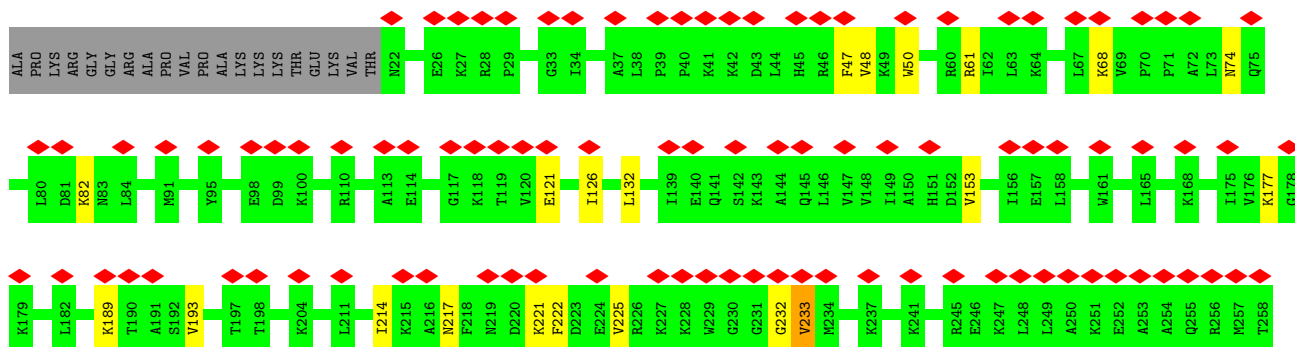
• Molecule 36: 40S ribosomal protein S7E

Chain BH: 52% 83% 12% ...

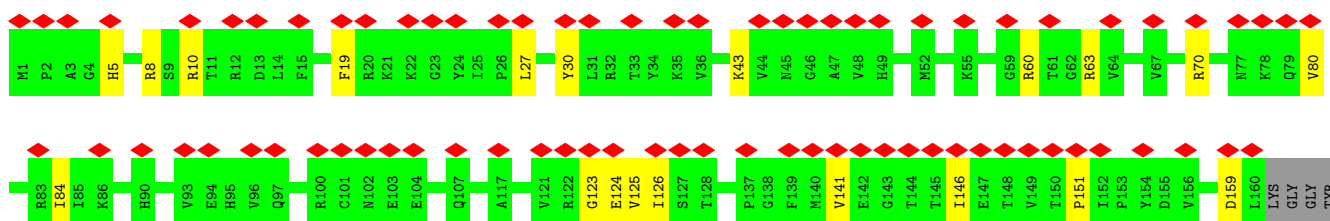
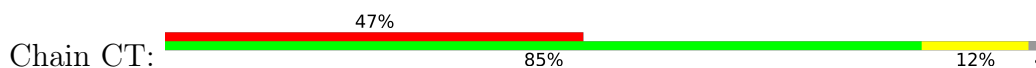


• Molecule 37: 60S ribosomal protein L8E

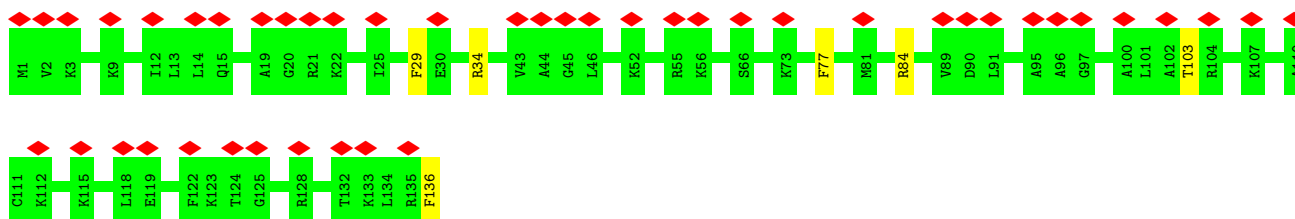
Chain CG: 38% 84% 8% 8%



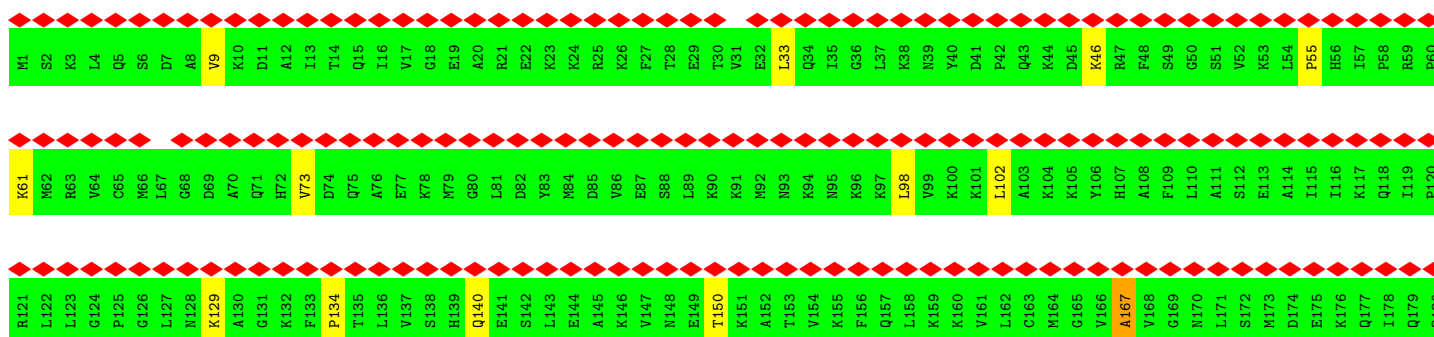
• Molecule 38: 60S ribosomal protein L21E



• Molecule 39: 60S ribosomal protein L27E

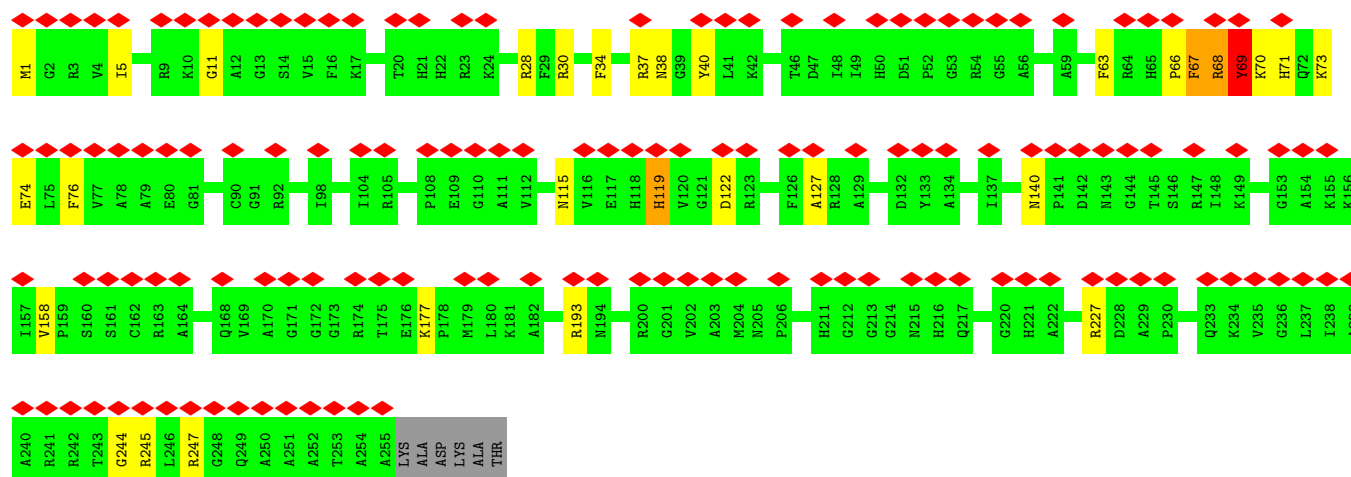


• Molecule 40: 60S ribosomal protein L1

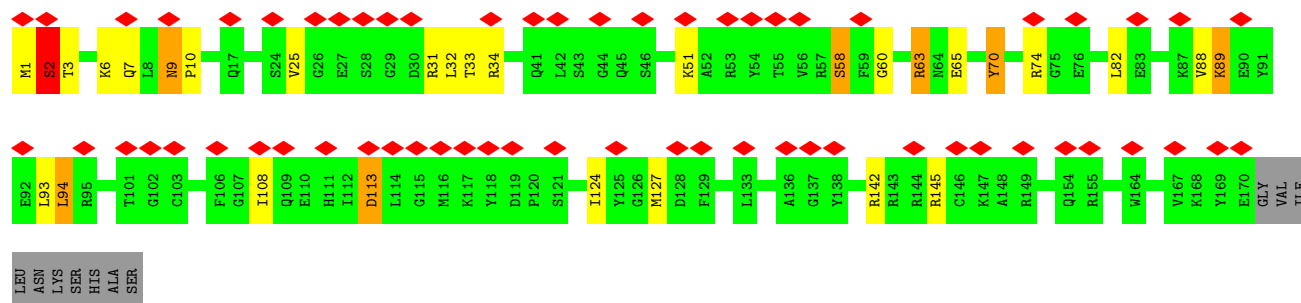
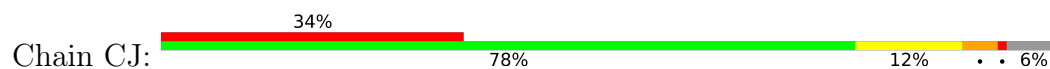




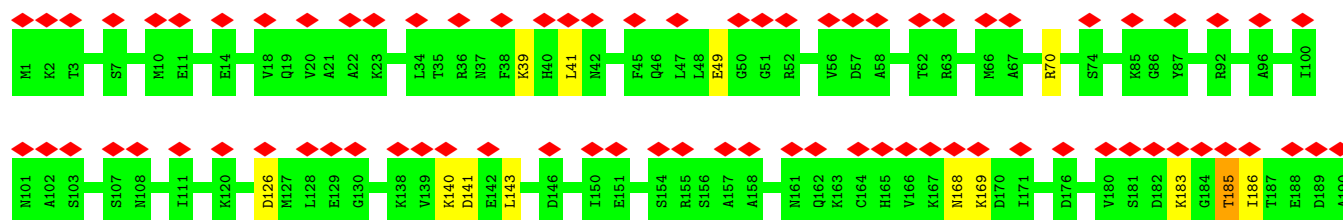
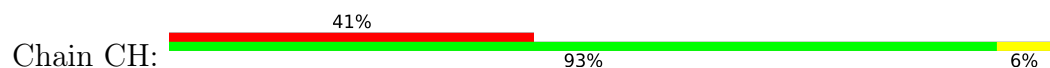
• Molecule 41: 60S ribosomal protein L2



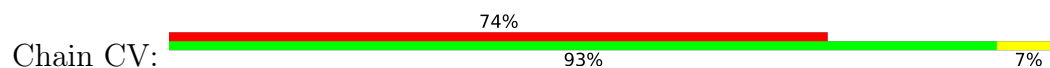
• Molecule 42: 60S ribosomal protein L5

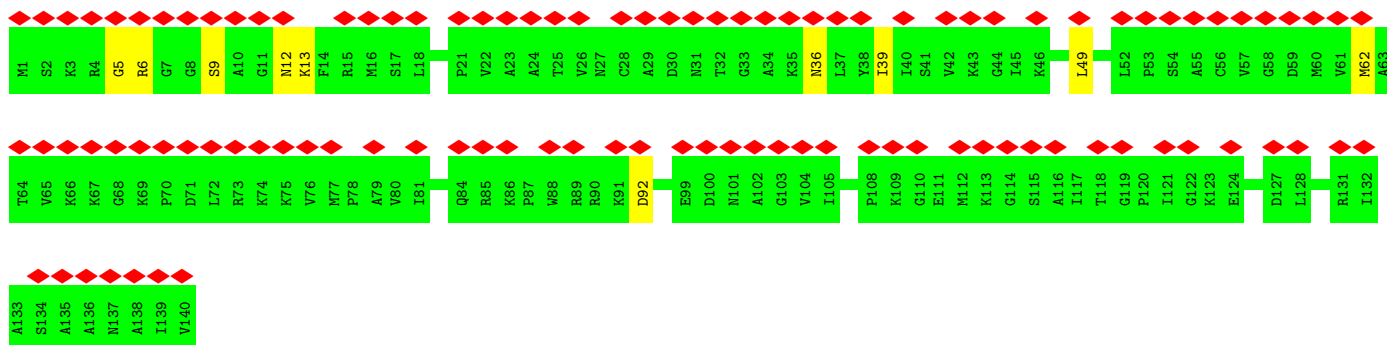


• Molecule 43: 60S ribosomal protein L6



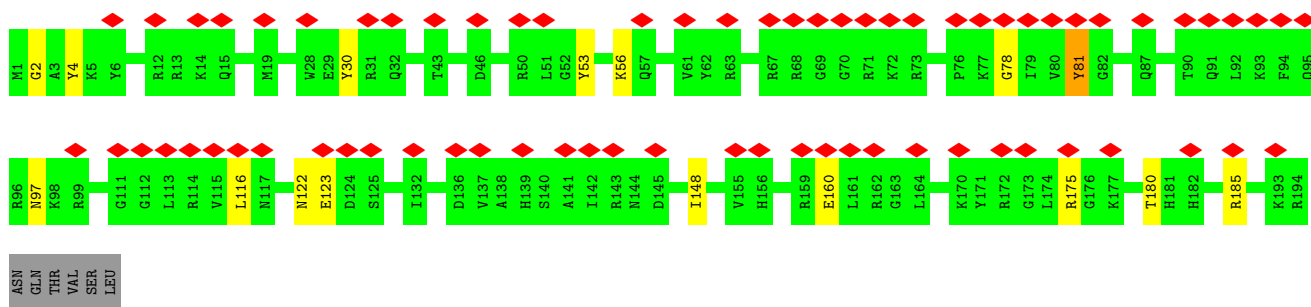
• Molecule 44: 60S ribosomal protein L14





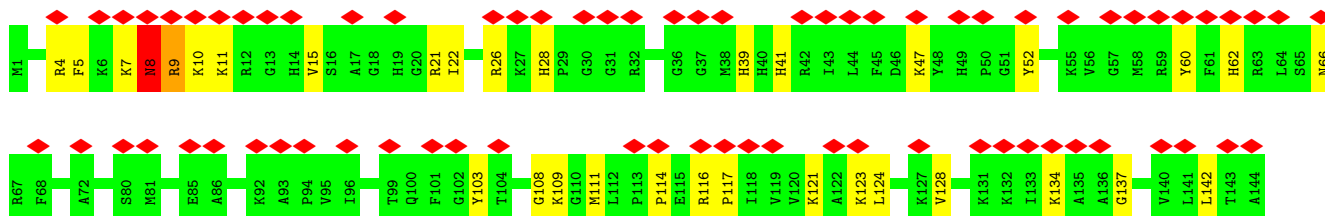
• Molecule 45: 60S ribosomal protein L15E

Chain CN: 35% 89% 8%



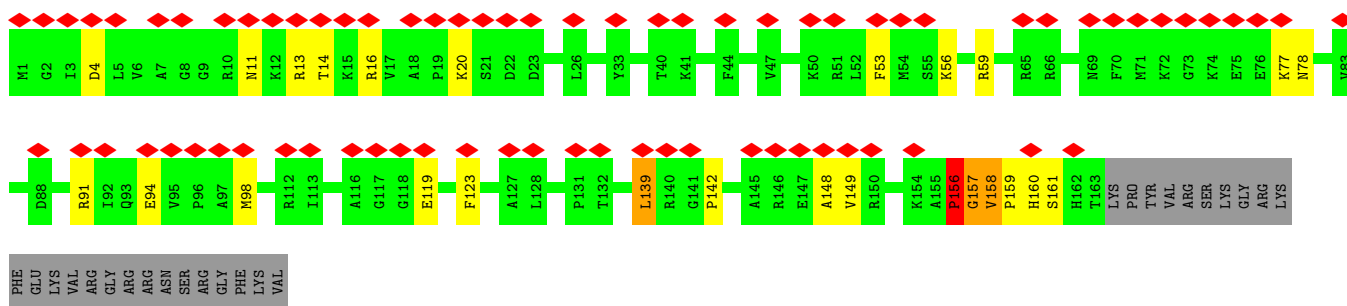
• Molecule 46: 60S ribosomal protein L15

Chain Ca: 50% 77% 22%




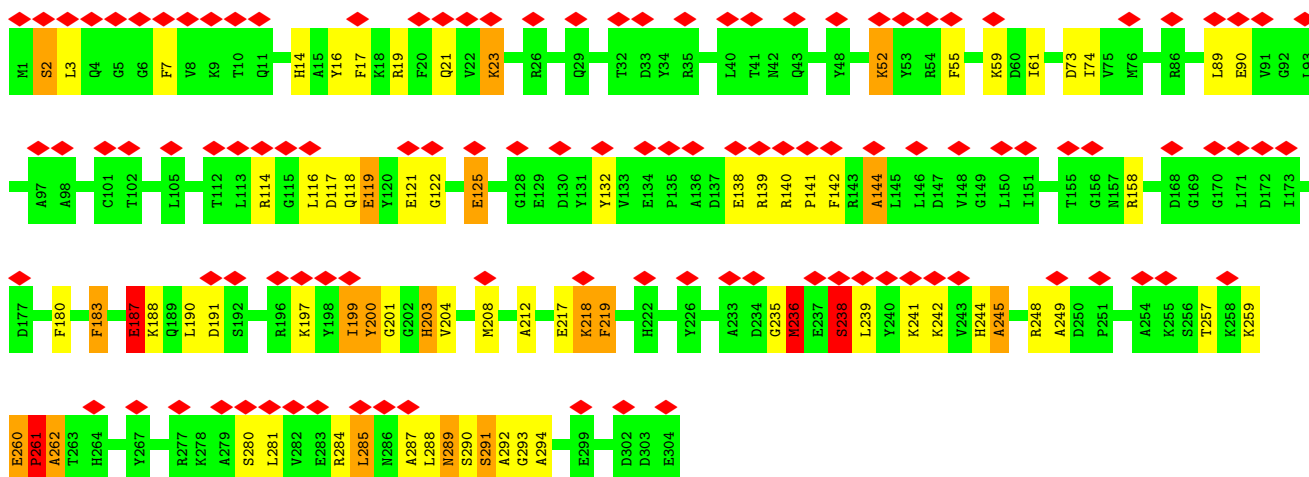
• Molecule 47: 60S ribosomal protein L18E

Chain CQ: 39% 73% 12% 13%




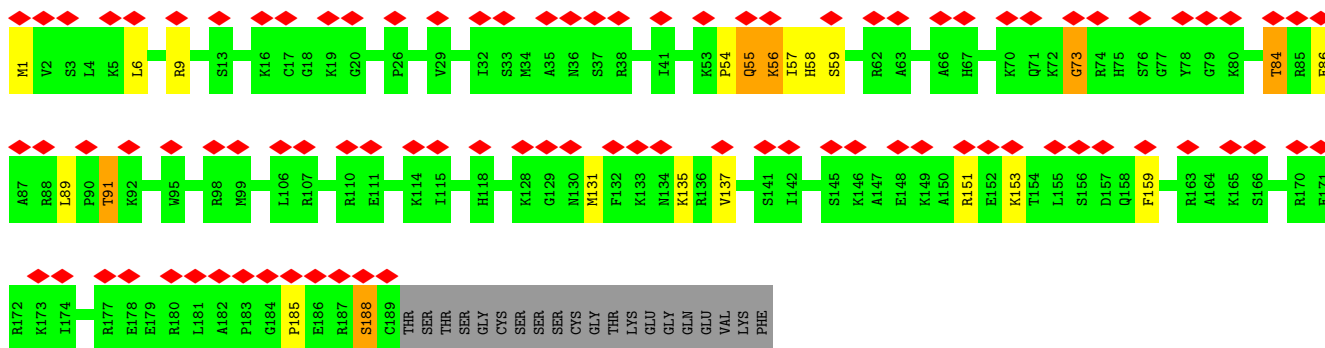
• Molecule 48: 60S ribosomal protein L18

Chain CD: 




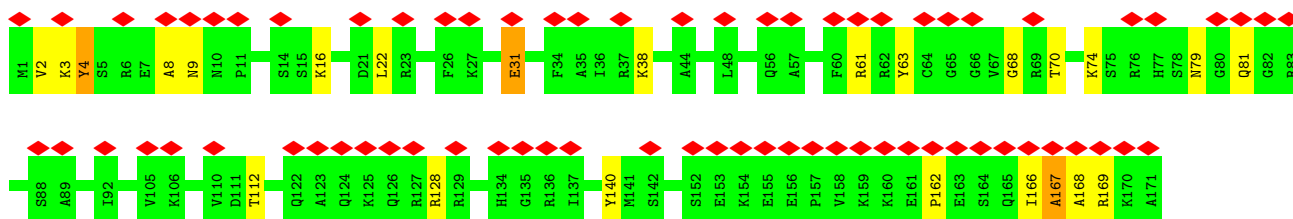
• Molecule 49: 60S ribosomal protein L19E

Chain CR: 




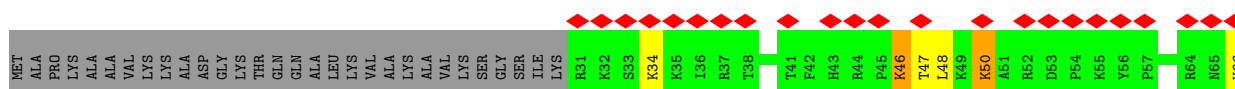
• Molecule 50: 60S ribosomal protein L22

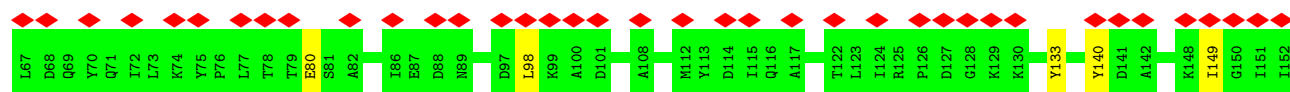
Chain CP: 



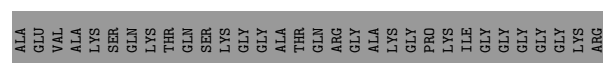
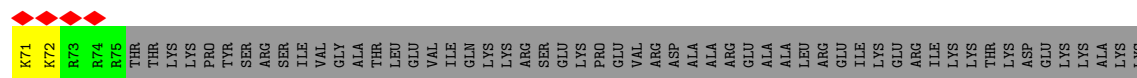
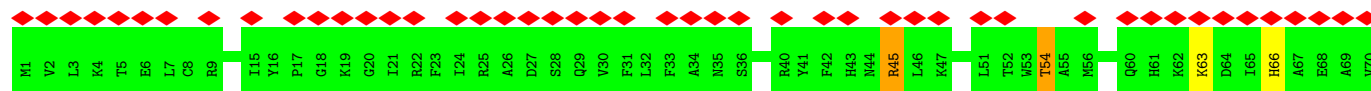
• Molecule 51: 60S ribosomal protein L23

Chain CX: 

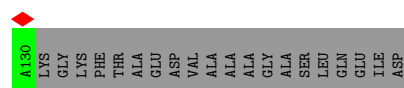
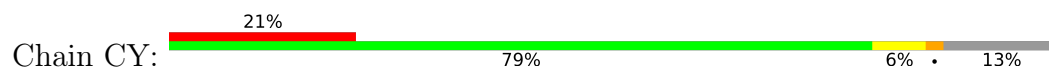




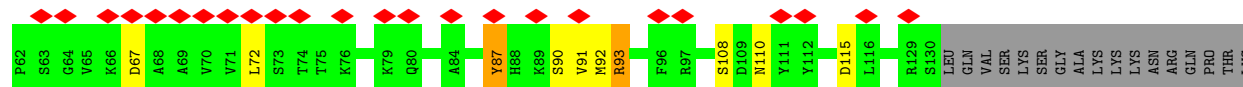
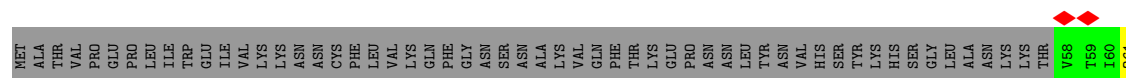
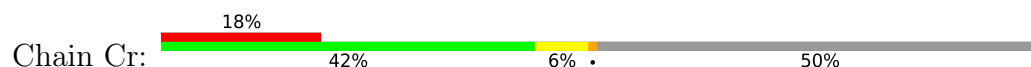
• Molecule 52: 60S ribosomal protein L24E



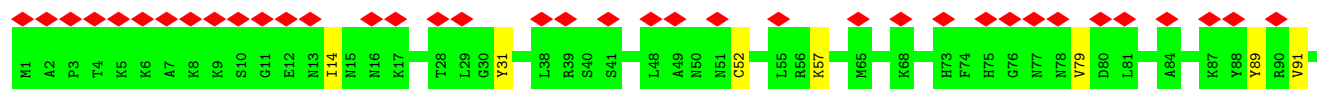
• Molecule 53: 60S ribosomal protein L24



• Molecule 54: 60S ribosomal protein L28E

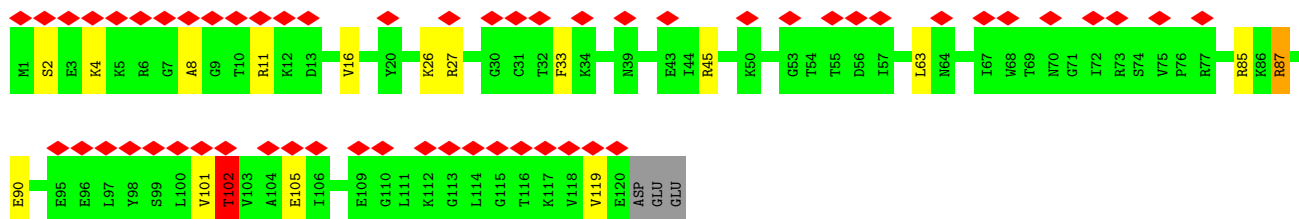
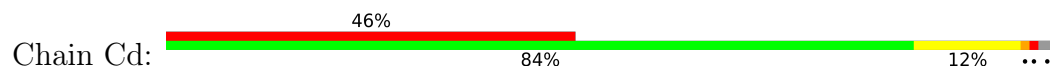


• Molecule 55: 60S ribosomal protein L30E

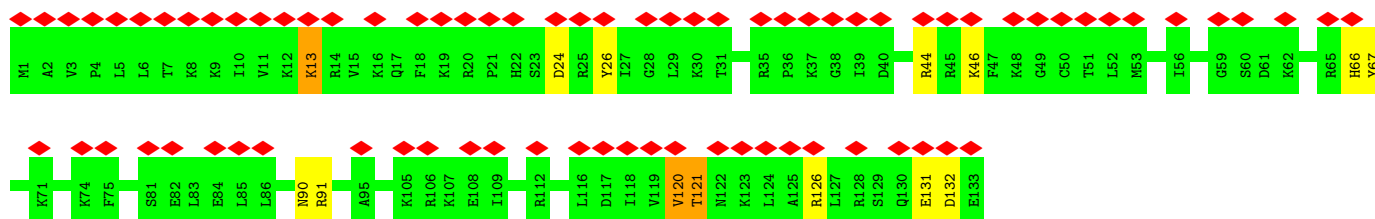
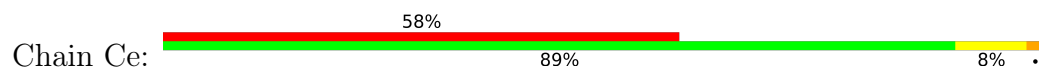




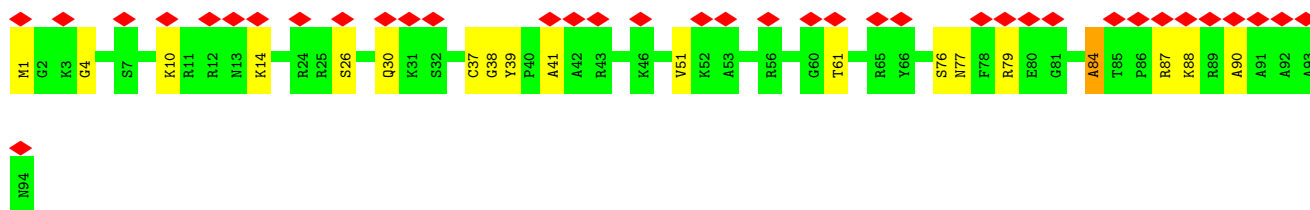
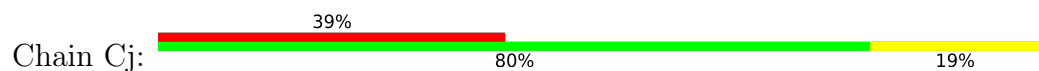
- Molecule 56: 60S ribosomal protein L31E



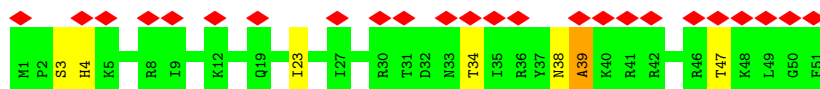
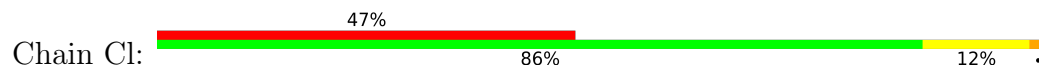
- Molecule 57: 60S ribosomal protein L32E



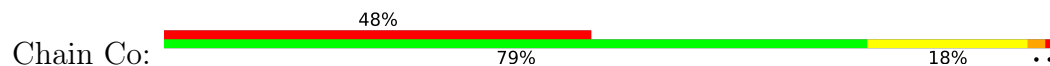
- Molecule 58: 60S ribosomal protein L37E

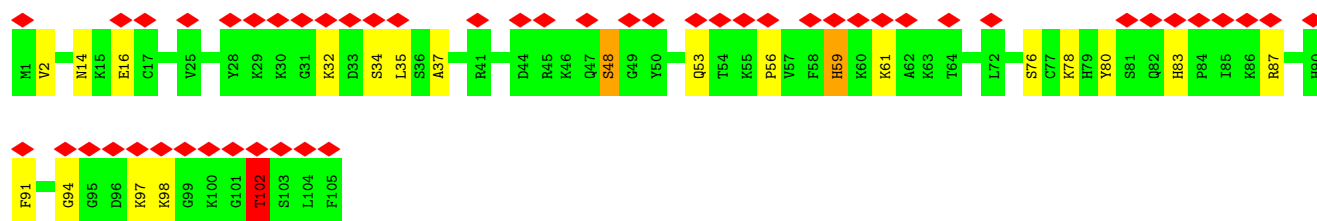


- Molecule 59: 60S ribosomal protein L39E



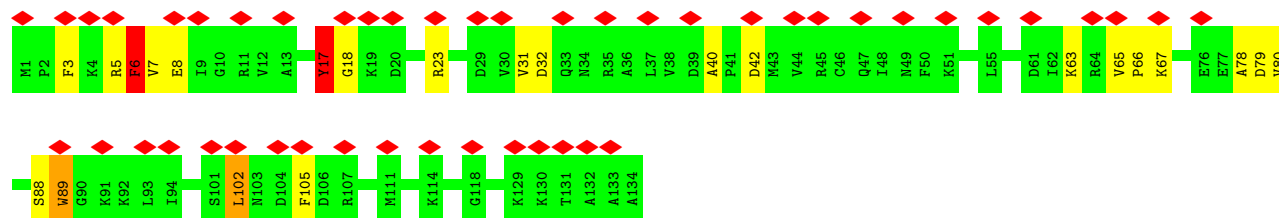
- Molecule 60: 60S ribosomal protein L44E





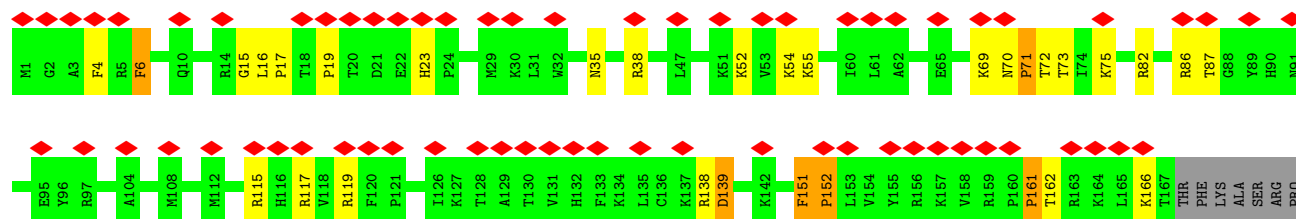
- Molecule 61: 60S ribosomal protein L14E

Chain CM: 35% 83% 14% ..



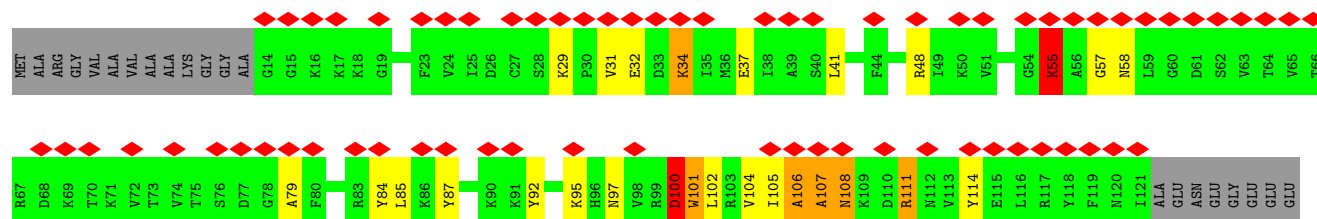
- Molecule 62: 60S ribosomal protein L20

Chain CS: 37% 76% 14% • 6%



- Molecule 63: 60S ribosomal protein L22E

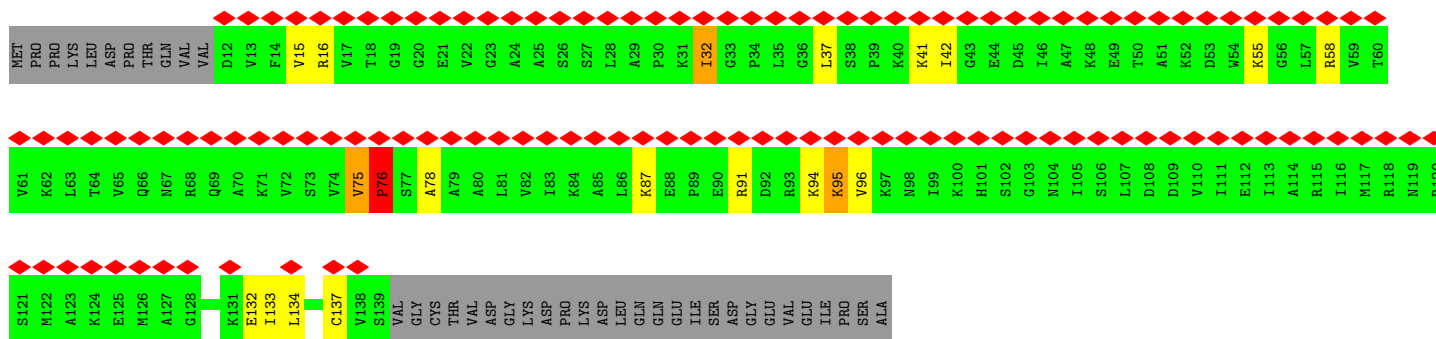
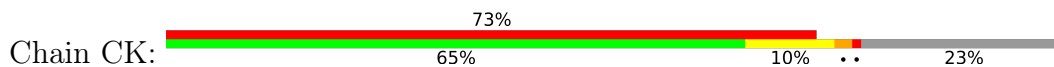
Chain CU: 53% 62% 15% 5% • 17%



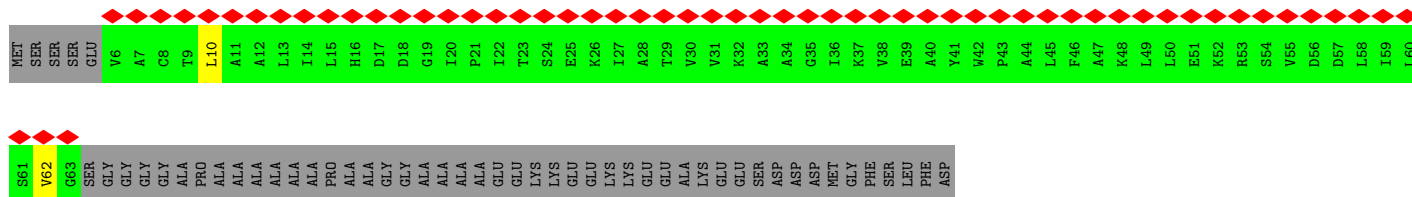
- Molecule 64: 60S ribosomal protein L36E

Chain Ci: 31% 55% 11% • 31%

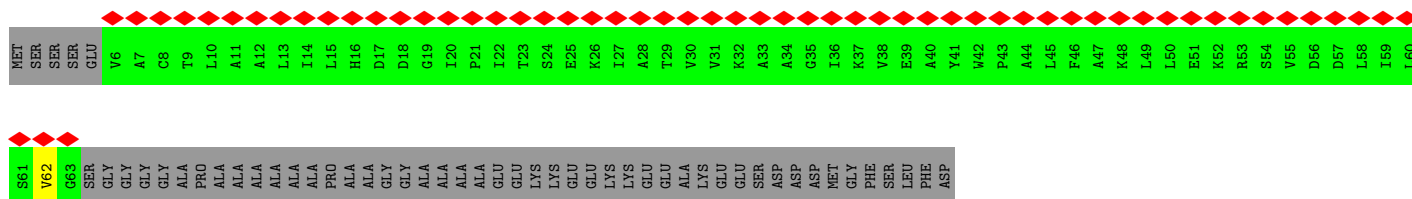
- Molecule 65: 60S ribosomal protein L11



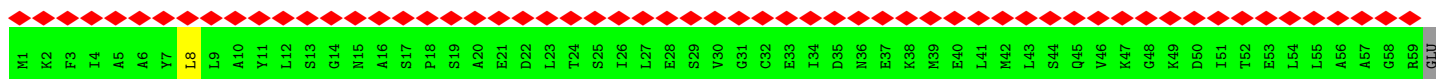
- Molecule 66: 60S ribosomal protein P1



- Molecule 66: 60S ribosomal protein P1

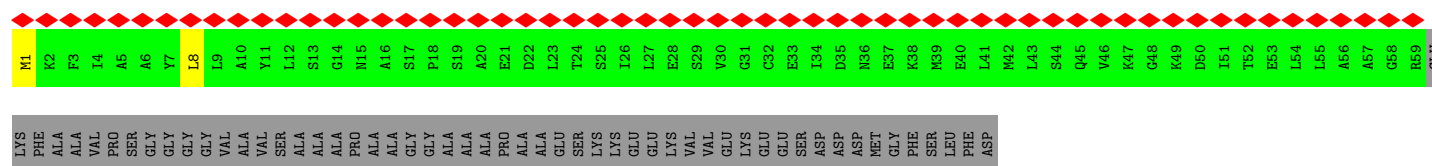


- Molecule 67: Acidic ribosomal protein P2

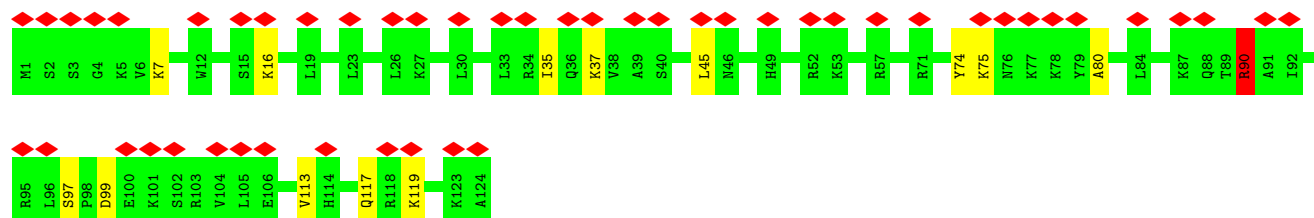
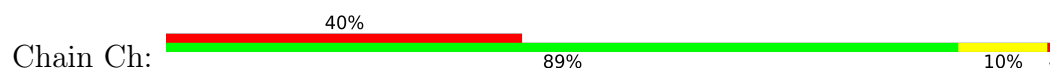


LYS PHE ALA ALA VAL PRO SER SER GLY GLY VAL VAL ALA VAL SER SER ALA ALA ALA PRO ALA ALA ALA PRO PRO GLU GLU LYS LYS LYS GLU GLU GLU LYS VAL VAL GLU LYS ASP ASP ASP ASP MET MET GLY PHE SER SER PHE LEU PHE ASP

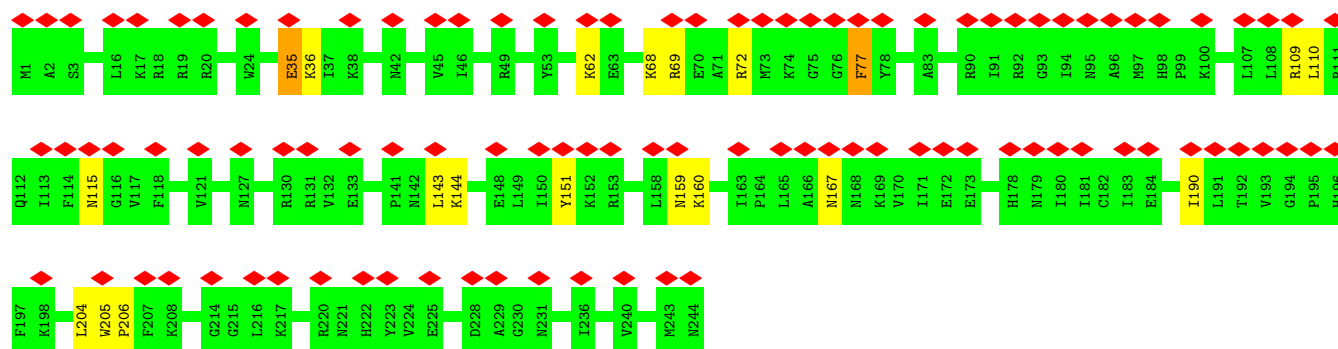
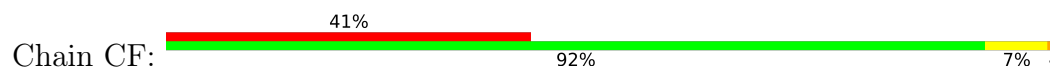
• Molecule 67: Acidic ribosomal protein P2



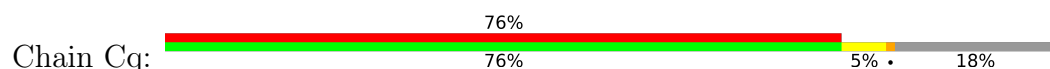
• Molecule 68: 60S ribosomal protein L29

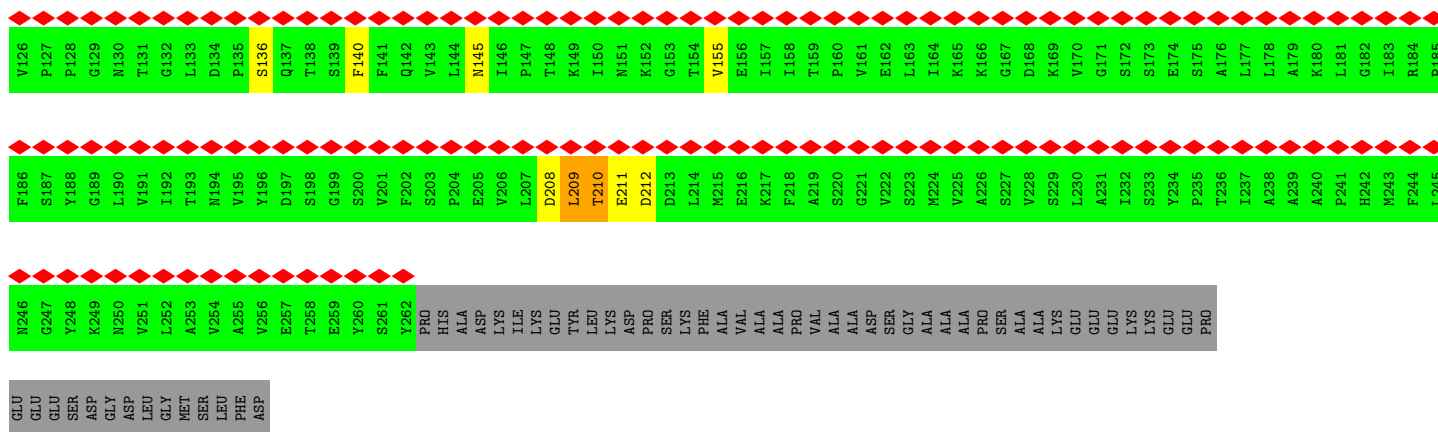


• Molecule 69: 60S ribosomal protein L30

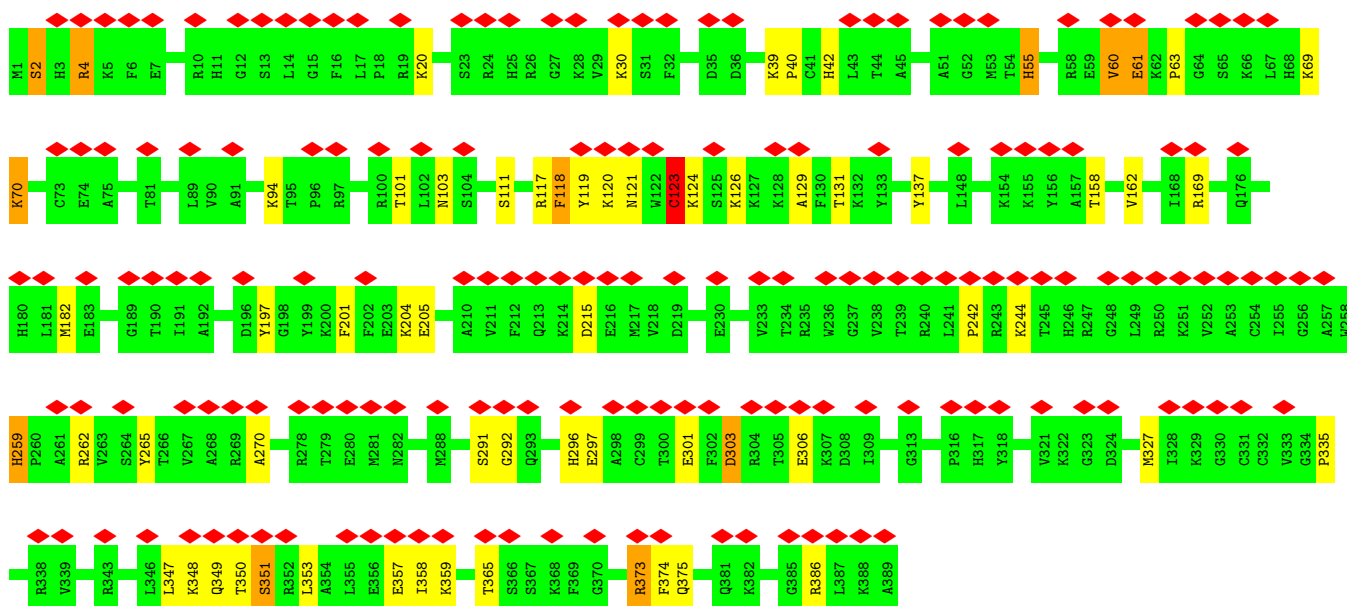
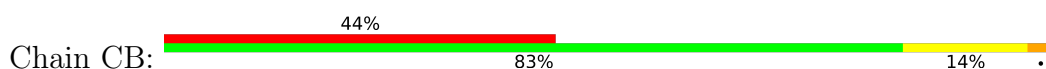


• Molecule 70: 60S acidic ribosomal protein P0

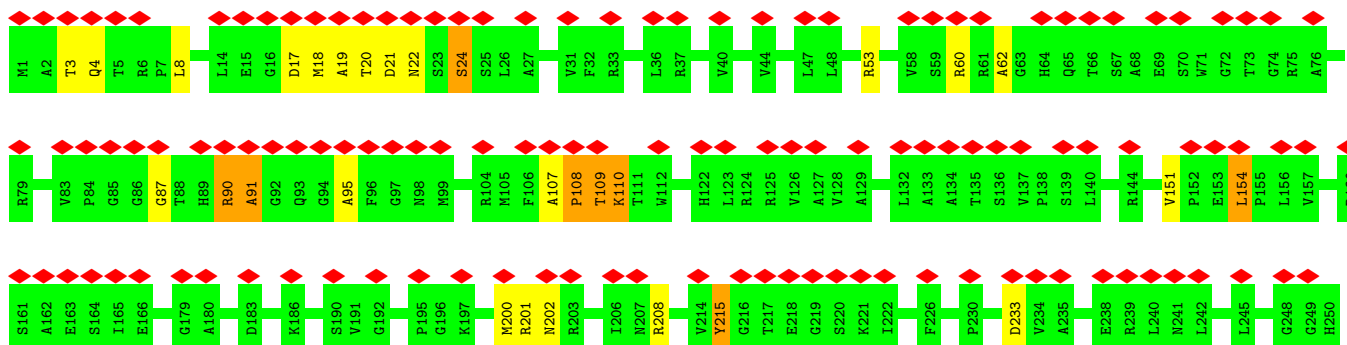
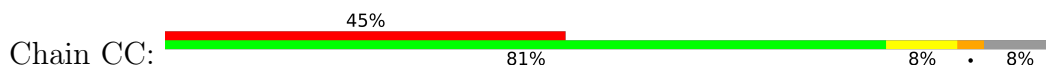


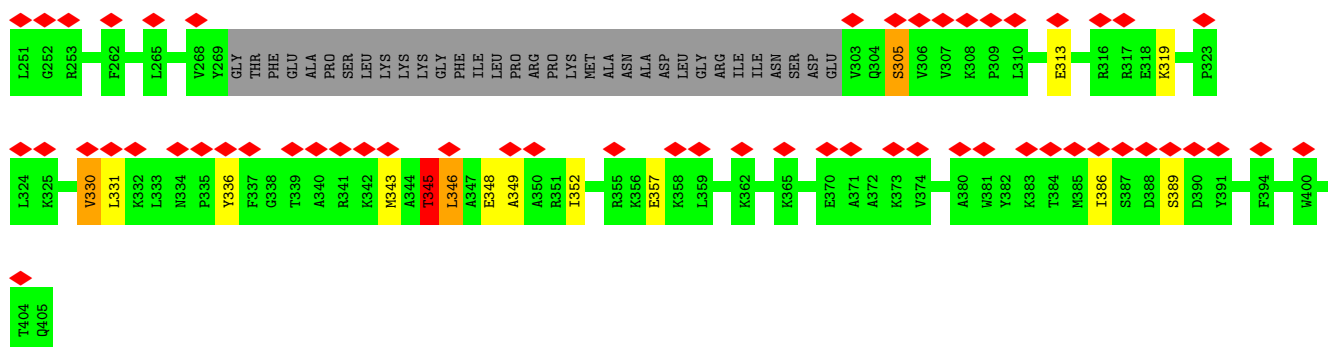


• Molecule 71: 60S ribosomal protein L3

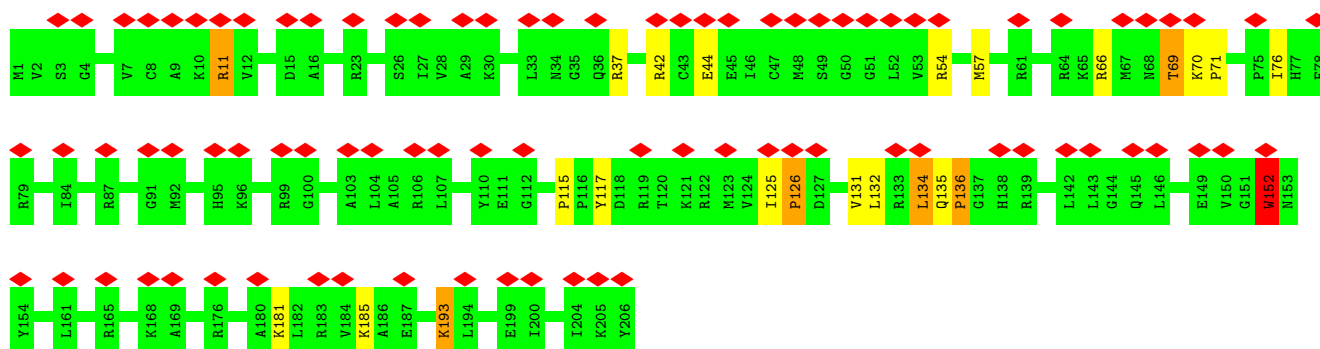
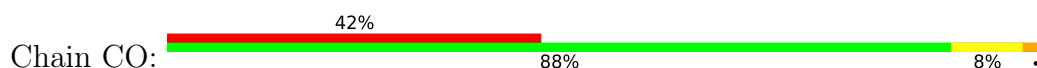


• Molecule 72: 60S ribosomal protein L4

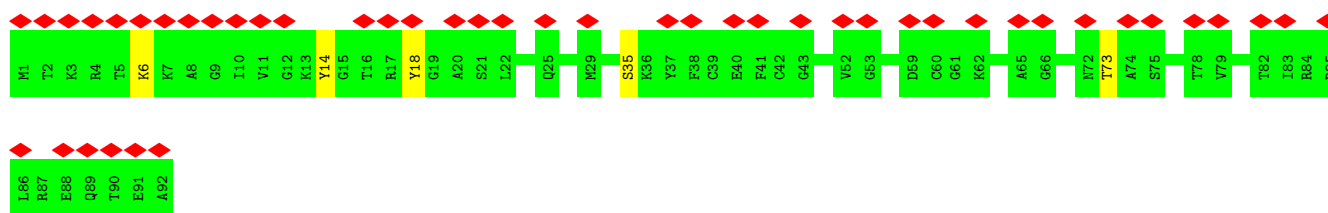




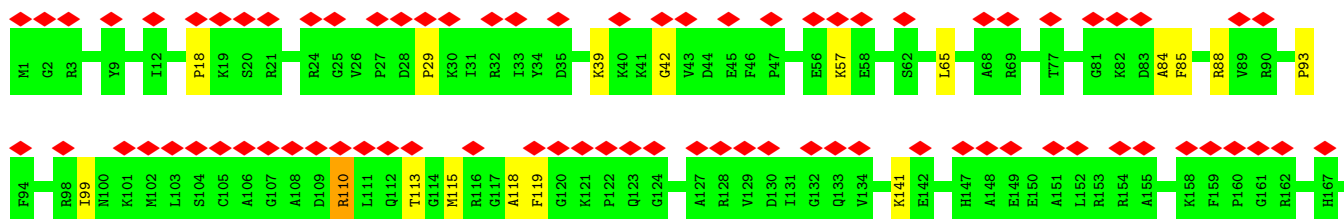
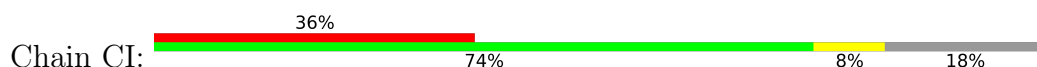
• Molecule 73: 60S ribosomal protein L13

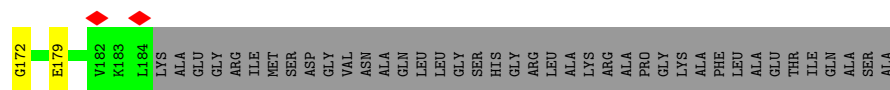


• Molecule 74: 60S ribosomal protein L43E

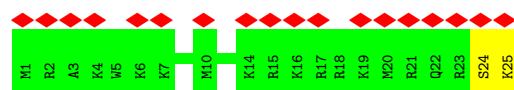
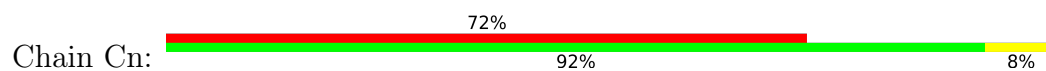


• Molecule 75: 60S ribosomal protein L16

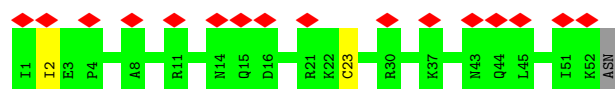




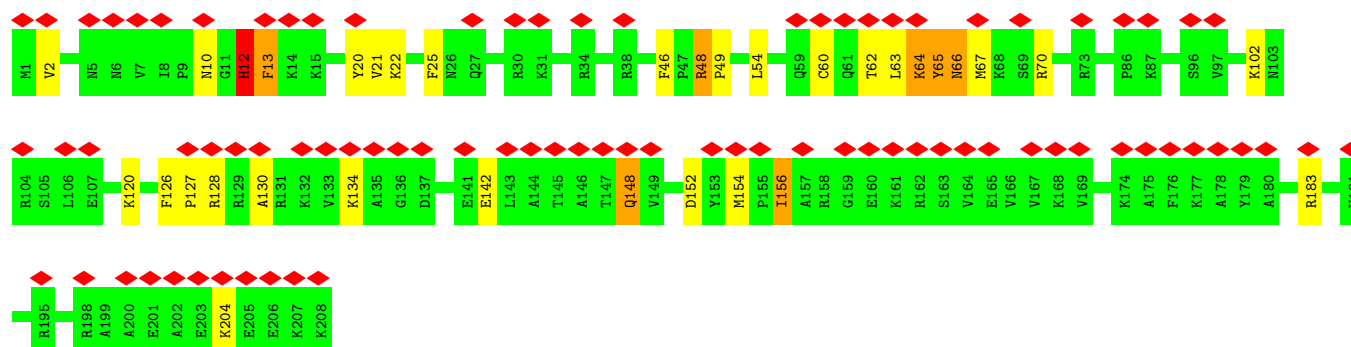
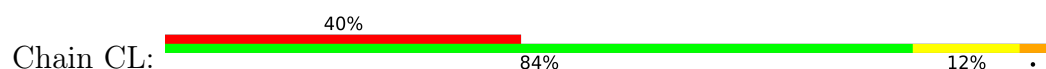
- Molecule 76: 60S ribosomal protein L41E



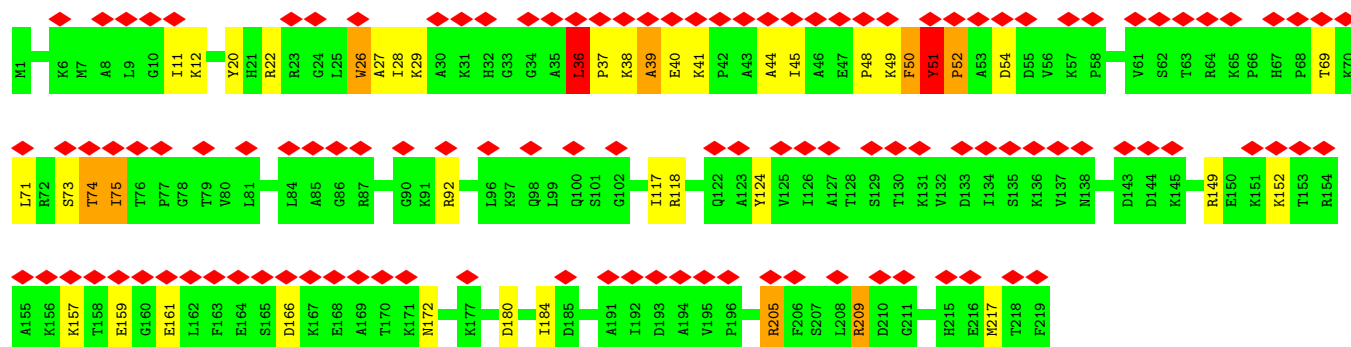
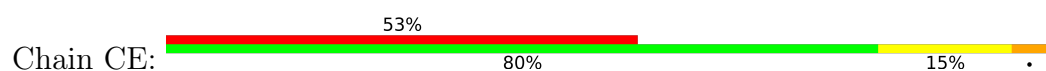
- Molecule 77: 60S ribosomal protein L40E



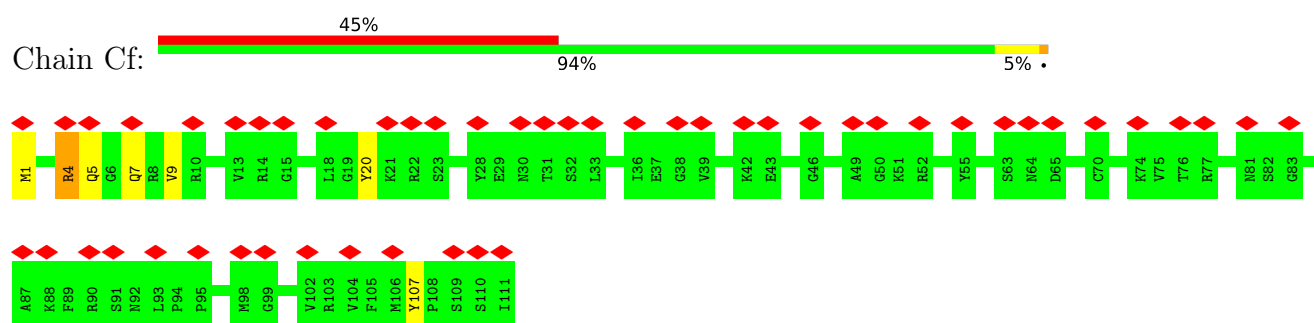
- Molecule 78: 60S ribosomal protein L13E



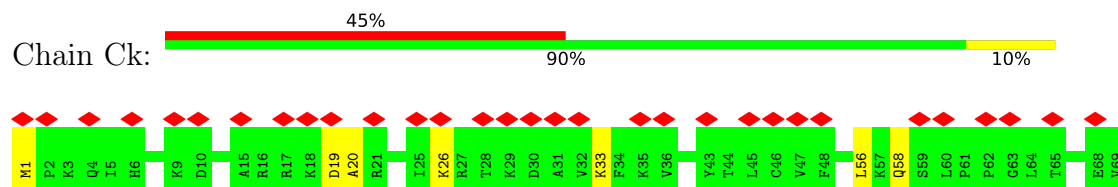
- Molecule 79: 60S ribosomal protein L6E



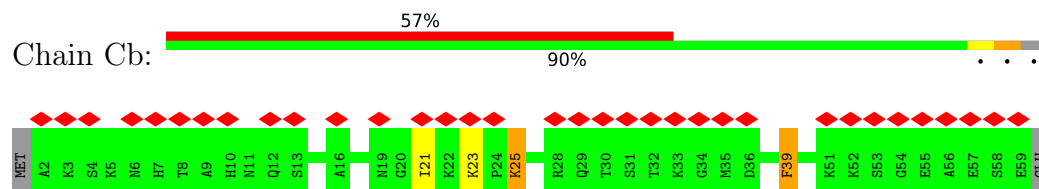
- Molecule 80: 60S ribosomal protein L33E



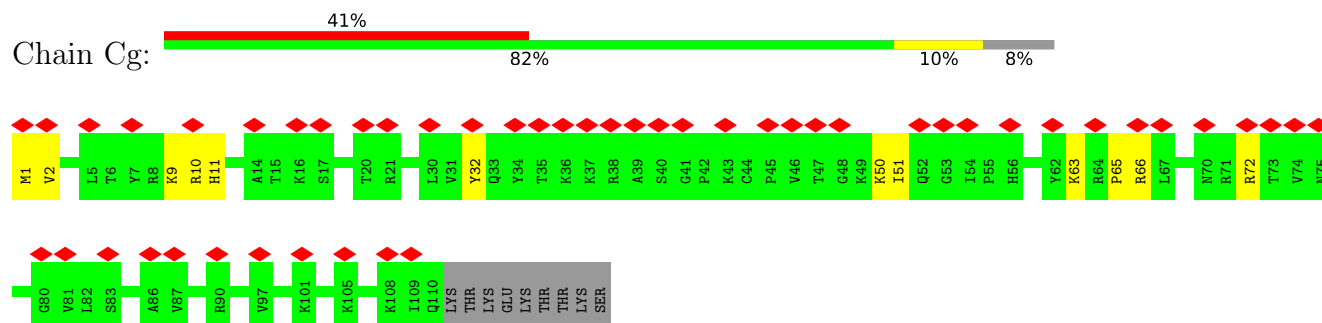
- Molecule 81: 60S ribosomal protein L38E



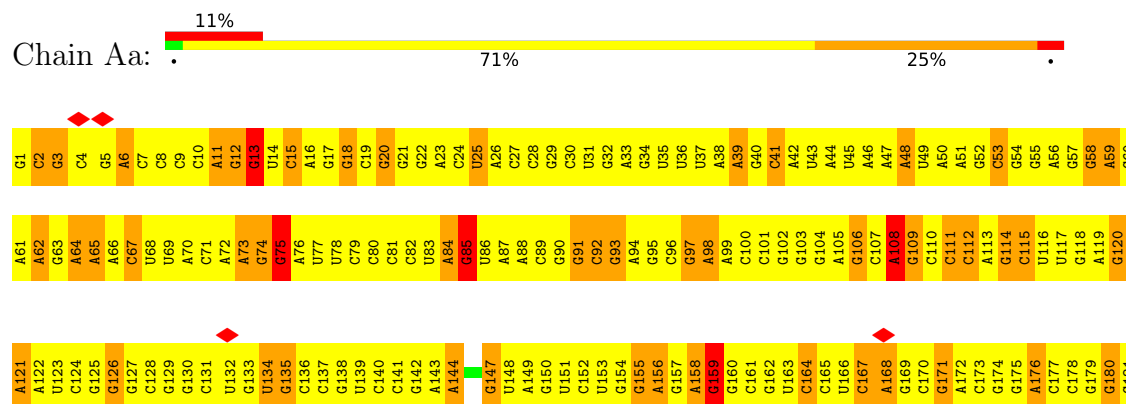
- Molecule 82: 60S ribosomal protein L29E



- Molecule 83: 60S ribosomal protein L34E



- Molecule 84: 60S ribosomal RNA



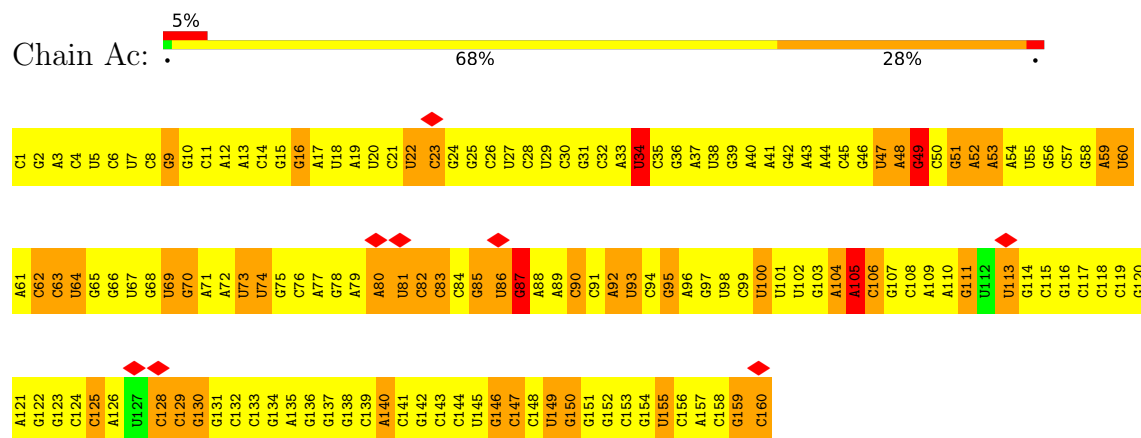
A965	A966	G905	G906	G845	G846	G785	G786	G725	G726	G665	G666	C604	C544	G485	G486	G422	G423	G362	G363	G302	G303	U242	U243	C182
G967	G968	U906	U907	A846	A847	G787	G788	G727	G728	U607	U608	U609	C545	G487	G488	G424	G425	A363	A364	U303	U304	C242	C243	C183
U969	U970	A848	A849	G848	G849	U687	U688	G608	G609	G609	G610	G611	C546	U488	U489	G426	G427	A365	A366	G304	G305	C244	C245	A185
A970	A971	A850	A851	A852	A853	A670	A671	G610	G611	G612	G613	G614	C547	G490	G491	A428	A429	A367	A368	A306	A307	C246	C247	A186
G971	G972	G852	G853	G854	G855	G672	G673	G612	G613	G614	G615	G616	C548	G492	G493	U427	U428	U369	U370	C308	C309	C248	C249	U188
G973	G974	U853	U854	U855	U856	A673	A674	U613	U614	U615	U616	U617	C549	G494	G495	G429	G430	A371	A372	C310	C311	C250	C251	C190
G975	G976	G856	G857	G858	G859	G674	G675	A615	A616	A617	A618	A619	C550	C496	C497	G431	G432	A373	A374	C312	C313	C252	C253	C191
G977	G978	U857	U858	U859	U860	U676	U677	G617	G618	G619	G620	G621	C551	C498	C499	C433	C434	G374	G375	C314	C315	C254	C255	U193
C978	C979	A917	A918	A919	A920	G678	G679	G618	G619	G620	G621	G622	C552	C499	C500	G435	G436	A376	A377	C316	C317	C256	C257	U195
C980	C981	A921	A922	A923	A924	G680	G681	G620	G621	G622	G623	G624	C553	C501	C502	G437	G438	U378	U379	C318	C319	C258	C259	A196
A981	A982	U922	U923	U924	U925	G802	G803	G622	G623	G624	G625	G626	C554	C503	C504	C437	C438	U380	U381	C320	C321	C260	C261	G201
U983	U984	A926	A927	A928	A929	G804	G805	G623	G624	G625	G626	G627	C555	C505	C506	G441	G442	A382	A383	A322	A323	C262	C263	G202
C985	C986	U926	U927	U928	U929	G806	G807	G624	G625	G626	G627	G628	C556	C507	C508	G443	G444	A384	A385	U324	U325	C264	C265	G203
A987	A988	G927	G928	G929	G930	C806	C807	G625	G626	G627	G628	G629	C557	C509	C510	G445	G446	A386	A387	A326	A327	C266	C267	U207
C988	C989	A928	A929	A930	A931	G808	G809	G626	G627	G628	G629	G630	C558	C511	C512	G447	G448	U268	U269	A327	A328	C267	C268	G207
U989	U990	U931	U932	U933	U934	A810	A811	G627	G628	G629	G630	G631	C559	C513	C514	G449	G450	C269	C270	A329	A330	C269	C270	G208
C991	C992	A932	A933	A934	A935	G812	G813	G628	G629	G630	G631	G632	C560	C515	C516	G451	G452	C271	C272	U331	U332	C271	C272	G210
U993	U994	U935	U936	U937	U938	U814	U815	G629	G630	G631	G632	G633	C561	C517	C518	C451	C452	G391	G392	A332	A333	C272	C273	G211
C995	C996	A936	A937	A938	A939	G816	G817	G630	G631	G632	G633	G634	C562	C519	C520	C453	C454	U273	U274	A334	A335	C273	C274	G212
A996	A997	G937	G938	G939	G940	U817	U818	G631	G632	G633	G634	G635	C563	C521	C522	C455	C456	U275	U276	U335	U336	C274	C275	G213
C998	C999	U938	U939	U940	U941	G818	G819	G632	G633	G634	G635	G636	C564	C523	C524	C457	C458	A395	A396	A336	A337	C275	C276	G214
U999	U1000	A939	A940	A941	A942	A819	A820	G633	G634	G635	G636	G637	C565	C525	C526	C459	C460	U277	U278	A337	A338	C276	C277	A217
A1001	A1002	G942	G943	G944	G945	U821	U822	G634	G635	G636	G637	G638	C566	C527	C528	C461	C462	U279	U280	U339	U340	C277	C278	A219
C1003	C1004	U946	U947	U948	U949	G823	G824	G635	G636	G637	G638	G639	C567	C529	C530	C463	C464	G281	G282	A341	A342	C278	C279	G220
U1005	U1006	A946	A947	A948	A949	G825	G826	G636	G637	G638	G639	G640	C568	C531	C532	G465	G466	A283	A284	U343	U344	C279	C280	G221
A1007	A1008	C947	C948	C949	C950	C827	C828	G637	G638	G639	G640	G641	C569	C533	C534	C467	C468	U285	U286	A345	A346	C280	C281	G222
U1009	U1010	U948	U949	U950	U951	U828	U829	G638	G639	G640	G641	G642	C570	C535	C536	C469	C470	G285	G286	A347	A348	C281	C282	G223
C1011	C1012	A950	A951	A952	A953	A830	A831	G639	G640	G641	G642	G643	C571	C537	C538	C471	C472	U287	U288	U349	U350	C282	C283	G224
U1013	U1014	U954	U955	U956	U957	G832	G833	G640	G641	G642	G643	G644	C572	C539	C540	C473	C474	G287	G288	A351	A352	C283	C284	G225
A1015	A1016	A954	A955	A956	A957	G834	G835	G641	G642	G643	G644	G645	C573	C541	C542	C475	C476	U289	U290	U353	U354	C284	C285	G226
G1017	G1018	U958	U959	U960	U961	G836	G837	G642	G643	G644	G645	G646	C574	C543	C544	C477	C478	G290	G291	A355	A356	C285	C286	G227
C1018	C1019	U959	U960	U961	U962	U837	U838	G643	G644	G645	G646	G647	C575	C545	C546	C479	C480	U291	U292	U357	U358	C286	C287	G228
A1019	A1020	A960	A961	A962	A963	A839	A840	G644	G645	G646	G647	G648	C576	C547	C548	C481	C482	G292	G293	A357	A358	C287	C288	G229
C1021	C1022	U963	U964	U965	U966	U841	U842	G645	G646	G647	G648	G649	C577	C549	C550	C483	C484	U293	U294	A359	A360	C288	C289	G230
G1023	G1024	G964	G965	G966	G967	C843	C844	G646	G647	G648	G649	G650	C578	C551	C552	C485	C486	G294	G295	U361	U362	C289	C290	G231
						G723	G724	G647	G648	G649	G650	G651	C579	C553	C554	C487	C488	A405	A406	U363	U364	C290	C291	G232
						A724	A725	G648	G649	G650	G651	G652	C580	C555	C556	C489	C490	G405	G406	A407	A408	C291	C292	G233
								G649	G650	G651	G652	G653	C581	C557	C558	C491	C492	U405	U406	U409	U410	C292	C293	G234
								G650	G651	G652	G653	G654	C582	C559	C560	C493	C494	G407	G408	U411	U412	C293	C294	G235
								G651	G652	G653	G654	G655	C583	C561	C562	C495	C496	U409	U410	U411	U412	C294	C295	G236
								G652	G653	G654	G655	G656	C584	C563	C564	C497	C498	G413	G414	U413	U414	C295	C296	G237
								G653	G654	G655	G656	G657	C585	C565	C566	C499	C500	U415	U416	U415	U416	C296	C297	G238
								G654	G655	G656	G657	G658	C586	C567	C568	C501	C502	G417	G418	U417	U418	C297	C298	G239
								G655	G656	G657	G658	G659	C587	C569	C570	C503	C504	G419	G420	U419	U420	C298	C299	G240
								G656	G657	G658	G659	G660	C588	C571	C572	C505	C506	G421	G422	U421	U422	C299	C300	G241
								G657	G658	G659	G660	G661	C589	C573	C574	C507	C508	A421	A422	U423	U424	C300	C301	G242

A1747	A1748	G1749	G1750	G1751	G1752	A1753	C1754	C1755	C1756	C1757	C1758	C1759	G1760	G1761	C1762	C1763	A1764	C1765	C1766	C1767	C1768	C1769	C1770	C1771	A1772	A1773	C1774	C1775	C1776	C1777	C1778	C1779	C1780	C1781	C1782	C1783	C1784	C1785	C1786	C1787	C1788	C1789	A1790	C1791	C1792	A1793	A1794	A1795	A1796	C1797	C1798	C1799	G1800	C1801	A1802	C1803	G1804	A1805	C1806		
C1687	U1688	G1689	C1690	U1691	G1692	A1693	A1694	C1695	G1696	C1697	C1698	C1699	U1700	G1701	C1702	C1703	A1704	A1705	C1706	C1707	C1708	U1709	G1710	G1711	A1712	A1713	A1714	C1715	C1716	C1717	U1718	U1719	C1720	A1721	G1722	C1723	C1724	G1725	C1726	C1727	C1728	G1729	U1730	A1731	C1732	G1733	C1734	U1735	C1736	C1737	A1738	C1739	U1740	G1741	C1742	C1743	G1744	C1745	G1746		
U1627	G1628	A1629	C1630	G1631	G1632	C1633	G1634	A1635	C1636	G1637	U1638	U1639	A1640	G1641	G1642	A1643	A1644	G1645	U1646	C1647	C1648	G1649	G1650	A1651	G1652	C1653	C1654	G1655	C1656	C1657	G1658	C1659	C1660	G1661	G1662	G1663	G1664	C1665	C1666	C1667	U1668	C1669	G1670	G1671	G1672	A1673	A1674	G1675	A1676	C1677	U1678	C1679	A1680	U1681	C1682	U1683	C1684	U1685	U1686		
G1567	A1568	U1569	C1570	G1571	C1572	G1573	C1574	G1575	C1576	A1577	U1578	C1579	C1580	C1581	C1582	A1583	A1584	A1585	A1586	G1587	G1588	U1589	A1590	A1591	U1592	C1593	G1594	G1595	C1596	U1597	U1598	A1599	A1600	G1601	G1602	U1603	U1604	U1605	C1606	C1607	C1608	C1609	A1610	G1611	C1612	G1613	G1614	G1615	G1616	A1617	U1618	G1619	U1620	G1621	C1622	C1623	U1624	G1625	U1626		
A1506	A1507	C1508	G1509	G1510	C1511	A1512	A1513	U1514	U1515	U1516	U1517	A1518	C1519	A1520	U1521	G1522	G1523	U1524	U1525	A1526	A1527	G1528	C1529	G1530	U1531	U1532	U1533	U1534	C1535	U1536	A1537	U1538	G1539	G1540	G1541	A1542	G1543	G1544	G1545	G1546	G1547	U1548	A1549	A1550	C1551	C1552	C1553	C1554	G1555	U1556	G1559	A1560	U1561	U1562	U1563	G1564	U1565	C1566			
U1445	G1446	G1447	C1448	A1449	G1450	U1451	A1452	G1453	A1454	C1455	A1456	A1457	U1458	A1459	U1460	U1461	C1462	G1463	A1464	A1465	U1466	G1467	A1468	G1469	A1470	A1471	C1472	U1473	U1474	U1475	G1476	A1477	A1478	G1479	G1480	G1481	C1482	G1483	A1484	A1485	G1486	A1487	G1488	G1489	A1490	G1491	A1492	A1493	A1494	G1495	G1496	G1499	C1500	A1501	U1502	U1503	U1504	G1505			
C1385	G1386	G1387	C1388	C1389	G1390	A1391	U1392	G1393	C1394	A1395	A1396	A1397	A1398	C1399	C1400	C1401	G1402	G1403	G1404	G1405	U1406	G1407	C1408	G1409	A1410	C1411	C1412	C1413	C1414	G1415	G1416	G1417	C1418	G1419	G1420	A1421	G1422	C1423	G1424	G1425	C1426	C1427	G1428	U1429	C1430	G1431	G1432	U1433	G1434	C1435	A1436	A1437	A1438	U1439	C1440	U1441	U1442	G1443	G1444		
G1325	C1326	G1327	C1328	G1329	A1330	C1331	C1332	C1333	A1334	C1335	A1336	C1337	C1338	C1339	G1340	G1341	C1342	C1343	A1344	U1345	U1346	U1347	G1348	G1349	G1350	C1351	G1352	A1353	G1354	U1355	G1356	C1357	C1358	A1359	U1360	G1361	C1362	C1363	C1364	C1365	G1366	A1367	U1368	G1369	A1370	G1371	U1372	A1373	G1374	G1375	A1376	G1377	G1378	G1379	C1380	C1381	C1382	G1383	G1384		
G1265	G1266	A1267	G1268	U1269	G1270	U1271	G1272	U1273	A1274	A1275	C1276	A1277	C1278	C1279	U1280	C1281	C1282	A1282	C1283	C1284	U1285	G1286	C1287	C1288	G1289	A1290	A1291	U1292	C1293	C1294	A1295	C1296	G1297	U1298	A1298	G1299	C1300	C1301	C1302	C1303	G1304	A1305	A1306	A1307	A1308	U1309	G1310	G1311	U1312	U1313	G1314	C1315	G1316	G1317	C1318	U1319	C1320	A1321	G1322	C1323	C1324
C1205	A1206	U1207	A1208	G1209	G1210	G1211	U1212	G1213	U1214	U1215	G1216	U1217	U1218	C1219	G1220	A1221	U1222	U1223	A1224	C1225	G1226	C1227	G1228	A1229	G1230	C1231	A1232	C1233	G1234	A1235	C1236	G1237	G1238	U1239	G1240	G1241	U1242	C1243	A1244	U1245	U1246	G1247	A1248	A1249	G1250	U1251	C1252	G1253	A1254	A1255	A1256	U1257	C1258	C1259	G1260	U1261	U1262	A1263	A1264		
G1086	U1087	A1088	G1089	C1090	C1091	G1092	U1093	C1094	C1095	C1096	A1097	C1098	U1099	G1100	A1101	A1102	U1103	C1104	G1105	G1106	G1107	U1108	G1109	C1110	U1111	C1112	C1113	G1114	A1115	U1116	U1117	U1118	C1119	G1120	C1121	C1122	A1123	U1124	U1125	U1126	U1127	U1128	G1129	U1130	U1131	A1132	A1133	G1134	C1135	U1136	G1137	A1138	A1139	C1140	U1141	G1142	C1143	C1144			
G1025	A1026	C1027	U1028	C1029	A1030	A1031	C1032	U1033	C1034	C1035	C1036	C1037	U1038	C1039	G1100	A1101	A1102	U1103	C1104	G1105	G1106	G1107	U1108	G1109	C1110	U1111	C1112	C1113	G1114	A1115	U1116	U1117	U1118	C1119	G1120	C1121	C1122	A1123	U1124	U1125	U1126	U1127	U1128	G1129	U1130	U1131	A1132	A1133	G1134	C1135	U1136	G1137	A1138	A1139	C1140	U1141	G1142	C1143	C1144		

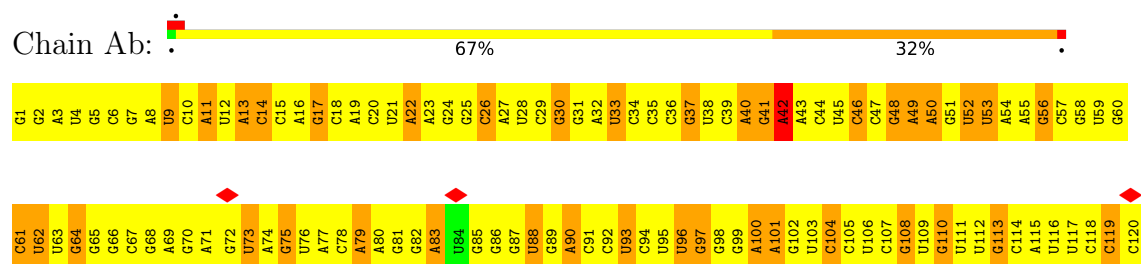




● Molecule 85: 5.8S ribosomal RNA



● Molecule 86: 5S ribosomal RNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	2108230	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Wiener Filter on 3D volumes (SPIDER)	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	4500	Depositor
Magnification	38900	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	0.454	Depositor
Minimum map value	-0.200	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.027	Depositor
Recommended contour level	0.11	Depositor
Map size (\AA)	455.4, 455.4, 455.4	wwPDB
Map dimensions	368, 368, 368	wwPDB
Map angles ($^\circ$)	90, 90, 90	wwPDB
Pixel spacing (\AA)	1.2375, 1.2375, 1.2375	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	Ad	2.49	2030/42036 (4.8%)	2.11	2382/65520 (3.6%)
2	Ae	2.62	95/1781 (5.3%)	2.13	105/2775 (3.8%)
3	Af	2.45	12/260 (4.6%)	2.06	16/403 (4.0%)
4	BY	0.99	0/1123	1.10	1/1487 (0.1%)
5	BI	1.05	0/539	0.95	0/712
6	BK	0.93	0/840	1.21	6/1135 (0.5%)
7	BM	0.82	0/936	1.11	2/1260 (0.2%)
8	Bf	0.93	0/590	1.17	1/788 (0.1%)
9	BX	0.96	0/1122	1.05	4/1492 (0.3%)
10	Bg	0.97	0/2988	1.06	3/4049 (0.1%)
11	BD	1.01	0/1652	1.20	4/2222 (0.2%)
12	BE	0.99	0/1637	1.07	0/2202
13	BF	0.98	0/1509	1.00	3/2034 (0.1%)
14	BQ	1.11	0/1034	1.19	6/1379 (0.4%)
15	BU	0.93	0/995	1.14	3/1338 (0.2%)
16	BO	1.05	0/909	1.11	2/1217 (0.2%)
17	BS	1.04	0/1258	1.15	5/1674 (0.3%)
18	BN	0.96	0/994	1.13	5/1332 (0.4%)
19	BL	1.04	0/704	1.15	3/944 (0.3%)
20	BT	1.01	0/1179	1.08	3/1586 (0.2%)
21	BP	0.91	0/727	1.11	2/975 (0.2%)
22	BZ	0.94	0/791	1.18	7/1057 (0.7%)
23	Bc	1.04	0/455	1.26	2/609 (0.3%)
24	BW	1.02	0/1060	1.16	6/1419 (0.4%)
25	Bd	1.11	0/386	1.25	4/510 (0.8%)
26	Bb	0.92	0/674	1.04	0/905
27	Be	1.07	0/476	1.01	0/627
28	BA	0.96	0/1567	1.06	4/2121 (0.2%)
29	BR	1.03	0/955	1.03	1/1273 (0.1%)
30	BB	0.96	0/1736	1.12	4/2329 (0.2%)
31	BV	1.00	0/610	1.07	0/820
32	Ba	1.07	0/766	1.13	0/1023
33	BJ	1.09	0/1553	1.05	4/2079 (0.2%)
34	BC	0.93	0/1701	1.05	3/2298 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	BG	1.06	0/1888	1.05	4/2507 (0.2%)
36	BH	3.40	1/1535 (0.1%)	1.14	4/2065 (0.2%)
37	CG	0.94	0/1939	1.01	5/2598 (0.2%)
38	CT	0.99	0/1316	1.11	2/1772 (0.1%)
39	CZ	1.00	0/1110	1.02	2/1480 (0.1%)
40	Cz	0.89	0/1741	1.00	1/2323 (0.0%)
41	CA	1.05	0/1992	1.15	10/2681 (0.4%)
42	CJ	1.06	0/1401	1.14	7/1869 (0.4%)
43	CH	0.96	0/1519	1.03	0/2042
44	CV	0.99	0/1064	1.07	0/1425
45	CN	1.12	0/1669	1.07	6/2235 (0.3%)
46	Ca	0.98	0/1143	1.17	4/1527 (0.3%)
47	CQ	1.04	0/1303	1.11	5/1748 (0.3%)
48	CD	1.00	0/2489	1.23	22/3342 (0.7%)
49	CR	1.09	0/1590	1.06	4/2100 (0.2%)
50	CP	1.03	0/1397	1.14	6/1871 (0.3%)
51	CX	0.90	0/1002	1.03	3/1340 (0.2%)
52	CW	1.04	0/649	1.07	1/861 (0.1%)
53	CY	1.10	0/1061	1.08	4/1418 (0.3%)
54	Cr	0.98	0/585	1.16	1/786 (0.1%)
55	Cc	0.86	0/869	0.98	1/1169 (0.1%)
56	Cd	1.01	0/970	1.10	4/1295 (0.3%)
57	Ce	1.01	0/1122	1.06	4/1497 (0.3%)
58	Cj	1.17	0/769	1.16	1/1019 (0.1%)
59	Cl	1.14	0/472	1.12	1/627 (0.2%)
60	Co	0.93	0/867	1.12	3/1144 (0.3%)
61	CM	0.99	0/1094	1.10	4/1461 (0.3%)
62	CS	1.01	0/1457	1.16	3/1957 (0.2%)
63	CU	0.98	0/876	1.27	12/1170 (1.0%)
64	Ci	1.07	0/618	1.16	5/809 (0.6%)
65	CK	0.92	0/968	1.11	1/1299 (0.1%)
66	Cu	0.78	0/438	0.91	0/596
66	Cv	0.79	0/438	0.90	0/596
67	Cs	0.83	0/444	0.82	0/596
67	Ct	0.84	0/444	0.81	0/596
68	Ch	1.02	0/1023	1.05	2/1359 (0.1%)
69	CF	0.98	0/2020	1.00	4/2708 (0.1%)
70	Cq	0.87	0/2023	0.96	5/2739 (0.2%)
71	CB	0.97	0/3207	1.14	16/4289 (0.4%)
72	CC	1.01	0/2951	1.11	8/3972 (0.2%)
73	CO	1.03	0/1678	1.07	6/2246 (0.3%)
74	Cp	1.00	0/724	1.02	1/958 (0.1%)
75	CI	1.01	0/1523	1.00	1/2036 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Cn	1.34	0/239	1.04	0/302
77	Cm	1.01	0/434	0.95	0/574
78	CL	1.03	0/1721	1.13	6/2299 (0.3%)
79	CE	0.95	0/1766	1.16	8/2374 (0.3%)
80	Cf	1.05	0/908	1.13	3/1215 (0.2%)
81	Ck	0.98	0/572	1.09	0/763
82	Cb	0.98	0/486	1.06	2/641 (0.3%)
83	Cg	1.07	0/913	1.02	0/1223
84	Aa	1.61	170/81235 (0.2%)	2.52	9121/126706 (7.2%)
85	Ac	1.61	7/3809 (0.2%)	2.48	426/5936 (7.2%)
86	Ab	2.31	125/2864 (4.4%)	2.91	380/4464 (8.5%)
All	All	1.65	2440/227878 (1.1%)	2.00	12710/334219 (3.8%)

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
4	BY	0	1
6	BK	0	4
7	BM	0	1
8	Bf	0	1
10	Bg	0	1
11	BD	0	3
12	BE	0	2
13	BF	0	2
14	BQ	0	1
15	BU	0	2
17	BS	0	1
19	BL	0	1
20	BT	0	4
23	Bc	0	1
24	BW	0	1
25	Bd	0	1
26	Bb	0	2
29	BR	0	1
30	BB	0	1
32	Ba	0	1
35	BG	0	1
36	BH	0	4
37	CG	0	2

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
41	CA	0	4
42	CJ	0	2
43	CH	0	3
45	CN	0	1
46	Ca	0	7
47	CQ	0	6
48	CD	0	13
49	CR	0	3
50	CP	0	1
51	CX	0	1
55	Cc	0	1
57	Ce	0	1
58	Cj	0	1
59	Cl	0	1
60	Co	0	2
61	CM	0	4
62	CS	0	3
63	CU	0	2
65	CK	0	2
68	Ch	0	1
69	CF	0	3
70	Cq	0	2
71	CB	0	9
72	CC	0	4
73	CO	0	4
74	Cp	0	1
75	CI	0	4
78	CL	0	5
79	CE	0	7
80	Cf	0	2
83	Cg	0	1
84	Aa	0	309
85	Ac	0	18
86	Ab	0	19
All	All	0	486

The worst 5 of 2440 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	BH	117	ARG	CZ-NH2	127.06	2.98	1.33
1	Ad	1203	G	C2'-C1'	23.55	1.79	1.53
2	Ae	28	G	C2'-C1'	-23.31	1.27	1.53

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Ad	218	G	C2'-C1'	-23.01	1.28	1.53
1	Ad	999	G	C2'-C1'	-22.88	1.28	1.53

The worst 5 of 12710 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Ad	1005	C	O4'-C1'-N1	31.46	133.37	108.20
1	Ad	1462	C	O4'-C1'-N1	29.23	131.58	108.20
1	Ad	547	C	O4'-C1'-N1	28.96	131.37	108.20
1	Ad	1765	A	O4'-C1'-N9	28.77	131.22	108.20
84	Aa	2162	C	P-O3'-C3'	27.64	152.86	119.70

There are no chirality outliers.

5 of 486 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	BK	22	TYR	Sidechain
6	BK	83	PRO	Peptide
6	BK	86	ILE	Peptide
6	BK	87	VAL	Peptide
4	BY	48	LYS	Peptide

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	BY	136/138 (99%)	118 (87%)	8 (6%)	10 (7%)	1	13
5	BI	64/220 (29%)	61 (95%)	2 (3%)	1 (2%)	9	43

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	BK	94/183 (51%)	66 (70%)	17 (18%)	11 (12%)	0	6
7	BM	121/171 (71%)	84 (69%)	20 (16%)	17 (14%)	0	4
8	Bf	69/155 (44%)	46 (67%)	10 (14%)	13 (19%)	0	2
9	BX	140/142 (99%)	124 (89%)	11 (8%)	5 (4%)	3	25
10	Bg	378/380 (100%)	334 (88%)	26 (7%)	18 (5%)	2	21
11	BD	206/208 (99%)	125 (61%)	34 (16%)	47 (23%)	0	1
12	BE	198/265 (75%)	173 (87%)	16 (8%)	9 (4%)	2	22
13	BF	189/191 (99%)	162 (86%)	20 (11%)	7 (4%)	3	25
14	BQ	124/149 (83%)	93 (75%)	15 (12%)	16 (13%)	0	5
15	BU	126/128 (98%)	102 (81%)	14 (11%)	10 (8%)	1	12
16	BO	117/151 (78%)	91 (78%)	12 (10%)	14 (12%)	0	6
17	BS	150/152 (99%)	109 (73%)	16 (11%)	25 (17%)	0	3
18	BN	119/151 (79%)	92 (77%)	14 (12%)	13 (11%)	0	8
19	BL	83/160 (52%)	61 (74%)	16 (19%)	6 (7%)	1	14
20	BT	144/146 (99%)	123 (85%)	13 (9%)	8 (6%)	2	18
21	BP	89/154 (58%)	69 (78%)	12 (14%)	8 (9%)	1	11
22	BZ	98/108 (91%)	75 (76%)	10 (10%)	13 (13%)	0	4
23	Bc	56/65 (86%)	40 (71%)	5 (9%)	11 (20%)	0	2
24	BW	128/130 (98%)	101 (79%)	16 (12%)	11 (9%)	1	11
25	Bd	46/56 (82%)	29 (63%)	6 (13%)	11 (24%)	0	1
26	Bb	84/86 (98%)	75 (89%)	6 (7%)	3 (4%)	3	25
27	Be	58/62 (94%)	49 (84%)	5 (9%)	4 (7%)	1	14
28	BA	195/260 (75%)	176 (90%)	10 (5%)	9 (5%)	2	21
29	BR	114/141 (81%)	89 (78%)	15 (13%)	10 (9%)	1	11
30	BB	209/262 (80%)	153 (73%)	31 (15%)	25 (12%)	0	6
31	BV	74/82 (90%)	62 (84%)	9 (12%)	3 (4%)	3	22
32	Ba	91/133 (68%)	65 (71%)	13 (14%)	13 (14%)	0	4
33	BJ	185/195 (95%)	162 (88%)	16 (9%)	7 (4%)	3	24
34	BC	212/263 (81%)	189 (89%)	16 (8%)	7 (3%)	4	26
35	BG	227/245 (93%)	211 (93%)	10 (4%)	6 (3%)	5	31
36	BH	182/189 (96%)	154 (85%)	10 (6%)	18 (10%)	0	9

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	CG	235/257 (91%)	205 (87%)	24 (10%)	6 (3%)	5	31
38	CT	158/164 (96%)	137 (87%)	6 (4%)	15 (10%)	0	10
39	CZ	134/136 (98%)	123 (92%)	10 (8%)	1 (1%)	22	62
40	Cz	214/216 (99%)	197 (92%)	9 (4%)	8 (4%)	3	25
41	CA	253/261 (97%)	219 (87%)	19 (8%)	15 (6%)	1	17
42	CJ	168/180 (93%)	132 (79%)	14 (8%)	22 (13%)	0	4
43	CH	188/190 (99%)	167 (89%)	16 (8%)	5 (3%)	5	31
44	CV	138/140 (99%)	124 (90%)	7 (5%)	7 (5%)	2	19
45	CN	192/200 (96%)	168 (88%)	18 (9%)	6 (3%)	4	27
46	Ca	142/144 (99%)	101 (71%)	24 (17%)	17 (12%)	0	6
47	CQ	161/188 (86%)	127 (79%)	18 (11%)	16 (10%)	0	9
48	CD	302/304 (99%)	213 (70%)	35 (12%)	54 (18%)	0	3
49	CR	187/209 (90%)	163 (87%)	14 (8%)	10 (5%)	2	19
50	CP	169/171 (99%)	140 (83%)	12 (7%)	17 (10%)	0	9
51	CX	120/152 (79%)	100 (83%)	17 (14%)	3 (2%)	5	32
52	CW	73/162 (45%)	55 (75%)	12 (16%)	6 (8%)	1	12
53	CY	128/150 (85%)	114 (89%)	8 (6%)	6 (5%)	2	21
54	Cr	71/147 (48%)	49 (69%)	13 (18%)	9 (13%)	0	5
55	Cc	110/112 (98%)	96 (87%)	10 (9%)	4 (4%)	3	25
56	Cd	118/123 (96%)	98 (83%)	8 (7%)	12 (10%)	0	8
57	Ce	131/133 (98%)	113 (86%)	10 (8%)	8 (6%)	1	16
58	Cj	92/94 (98%)	58 (63%)	19 (21%)	15 (16%)	0	3
59	Cl	49/51 (96%)	36 (74%)	8 (16%)	5 (10%)	0	8
60	Co	103/105 (98%)	76 (74%)	13 (13%)	14 (14%)	0	4
61	CM	132/134 (98%)	101 (76%)	14 (11%)	17 (13%)	0	5
62	CS	165/178 (93%)	122 (74%)	20 (12%)	23 (14%)	0	4
63	CU	106/130 (82%)	76 (72%)	13 (12%)	17 (16%)	0	3
64	Ci	75/112 (67%)	59 (79%)	5 (7%)	11 (15%)	0	4
65	CK	126/166 (76%)	94 (75%)	17 (14%)	15 (12%)	0	6
66	Cu	56/110 (51%)	54 (96%)	1 (2%)	1 (2%)	8	40
66	Cv	56/110 (51%)	53 (95%)	2 (4%)	1 (2%)	8	40

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
67	Cs	57/113 (50%)	54 (95%)	3 (5%)	0	100	100
67	Ct	57/113 (50%)	54 (95%)	3 (5%)	0	100	100
68	Ch	122/124 (98%)	103 (84%)	11 (9%)	8 (7%)	1	15
69	CF	242/244 (99%)	217 (90%)	16 (7%)	9 (4%)	3	25
70	Cq	260/319 (82%)	233 (90%)	15 (6%)	12 (5%)	2	21
71	CB	387/389 (100%)	307 (79%)	43 (11%)	37 (10%)	0	9
72	CC	368/405 (91%)	311 (84%)	27 (7%)	30 (8%)	1	12
73	CO	204/206 (99%)	179 (88%)	14 (7%)	11 (5%)	2	19
74	Cp	90/92 (98%)	81 (90%)	7 (8%)	2 (2%)	6	35
75	CI	182/224 (81%)	147 (81%)	24 (13%)	11 (6%)	1	16
76	Cn	23/25 (92%)	21 (91%)	1 (4%)	1 (4%)	2	22
77	Cm	50/53 (94%)	46 (92%)	3 (6%)	1 (2%)	7	37
78	CL	206/208 (99%)	168 (82%)	13 (6%)	25 (12%)	0	5
79	CE	217/219 (99%)	177 (82%)	14 (6%)	26 (12%)	0	6
80	Cf	109/111 (98%)	103 (94%)	5 (5%)	1 (1%)	17	56
81	Ck	67/69 (97%)	63 (94%)	2 (3%)	2 (3%)	4	28
82	Cb	56/60 (93%)	48 (86%)	4 (7%)	4 (7%)	1	14
83	Cg	108/119 (91%)	96 (89%)	8 (7%)	4 (4%)	3	25
All	All	11663/13543 (86%)	9641 (83%)	1083 (9%)	939 (8%)	2	12

5 of 939 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	BY	2	ALA
4	BY	39	ASN
4	BY	41	SER
4	BY	46	LYS
4	BY	49	LEU

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	
4	BY	116/116 (100%)	110 (95%)	6 (5%)	23	49
5	BI	56/179 (31%)	53 (95%)	3 (5%)	22	49
6	BK	90/146 (62%)	88 (98%)	2 (2%)	52	71
7	BM	101/142 (71%)	101 (100%)	0	100	100
8	Bf	62/135 (46%)	60 (97%)	2 (3%)	39	61
9	BX	113/113 (100%)	111 (98%)	2 (2%)	59	77
10	Bg	323/323 (100%)	310 (96%)	13 (4%)	31	56
11	BD	175/175 (100%)	170 (97%)	5 (3%)	42	64
12	BE	176/225 (78%)	172 (98%)	4 (2%)	50	70
13	BF	159/159 (100%)	153 (96%)	6 (4%)	33	57
14	BQ	103/120 (86%)	97 (94%)	6 (6%)	20	46
15	BU	113/113 (100%)	107 (95%)	6 (5%)	22	49
16	BO	94/120 (78%)	90 (96%)	4 (4%)	29	54
17	BS	133/133 (100%)	125 (94%)	8 (6%)	19	46
18	BN	106/130 (82%)	101 (95%)	5 (5%)	26	52
19	BL	74/135 (55%)	70 (95%)	4 (5%)	22	49
20	BT	121/121 (100%)	115 (95%)	6 (5%)	24	50
21	BP	77/130 (59%)	71 (92%)	6 (8%)	12	38
22	BZ	87/93 (94%)	84 (97%)	3 (3%)	37	60
23	Bc	52/58 (90%)	48 (92%)	4 (8%)	13	39
24	BW	113/113 (100%)	109 (96%)	4 (4%)	36	60
25	Bd	40/47 (85%)	39 (98%)	1 (2%)	47	68
26	Bb	78/78 (100%)	78 (100%)	0	100	100
27	Be	47/49 (96%)	46 (98%)	1 (2%)	53	72
28	BA	161/204 (79%)	153 (95%)	8 (5%)	24	50
29	BR	105/127 (83%)	103 (98%)	2 (2%)	57	75
30	BB	188/226 (83%)	186 (99%)	2 (1%)	73	84
31	BV	63/68 (93%)	59 (94%)	4 (6%)	18	44
32	Ba	80/107 (75%)	78 (98%)	2 (2%)	47	68
33	BJ	160/167 (96%)	157 (98%)	3 (2%)	57	75
34	BC	182/211 (86%)	177 (97%)	5 (3%)	44	65

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	BG	201/210 (96%)	192 (96%)	9 (4%)	27	53
36	BH	164/168 (98%)	157 (96%)	7 (4%)	29	54
37	CG	205/220 (93%)	194 (95%)	11 (5%)	22	49
38	CT	139/141 (99%)	135 (97%)	4 (3%)	42	64
39	CZ	113/113 (100%)	109 (96%)	4 (4%)	36	60
40	Cz	192/192 (100%)	182 (95%)	10 (5%)	23	49
41	CA	195/199 (98%)	184 (94%)	11 (6%)	21	47
42	CJ	149/157 (95%)	139 (93%)	10 (7%)	16	42
43	CH	164/164 (100%)	158 (96%)	6 (4%)	34	58
44	CV	109/109 (100%)	106 (97%)	3 (3%)	43	65
45	CN	167/173 (96%)	161 (96%)	6 (4%)	35	59
46	Ca	110/110 (100%)	101 (92%)	9 (8%)	11	36
47	CQ	138/160 (86%)	132 (96%)	6 (4%)	29	54
48	CD	251/251 (100%)	234 (93%)	17 (7%)	16	42
49	CR	166/183 (91%)	154 (93%)	12 (7%)	14	41
50	CP	144/144 (100%)	139 (96%)	5 (4%)	36	60
51	CX	109/130 (84%)	102 (94%)	7 (6%)	17	44
52	CW	66/133 (50%)	65 (98%)	1 (2%)	65	80
53	CY	115/128 (90%)	110 (96%)	5 (4%)	29	54
54	Cr	64/131 (49%)	61 (95%)	3 (5%)	26	52
55	Cc	98/98 (100%)	94 (96%)	4 (4%)	30	55
56	Cd	103/106 (97%)	98 (95%)	5 (5%)	25	51
57	Ce	122/122 (100%)	116 (95%)	6 (5%)	25	51
58	Cj	77/77 (100%)	74 (96%)	3 (4%)	32	57
59	Cl	48/48 (100%)	47 (98%)	1 (2%)	53	72
60	Co	94/94 (100%)	87 (93%)	7 (7%)	13	40
61	CM	116/116 (100%)	110 (95%)	6 (5%)	23	49
62	CS	153/163 (94%)	145 (95%)	8 (5%)	23	49
63	CU	94/106 (89%)	86 (92%)	8 (8%)	10	35
64	Ci	62/92 (67%)	59 (95%)	3 (5%)	25	52
65	CK	105/139 (76%)	98 (93%)	7 (7%)	16	42

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
66	Cu	46/77 (60%)	45 (98%)	1 (2%)	52	71
66	Cv	46/77 (60%)	46 (100%)	0	100	100
67	Cs	48/82 (58%)	47 (98%)	1 (2%)	53	72
67	Ct	48/82 (58%)	46 (96%)	2 (4%)	30	54
68	Ch	109/109 (100%)	103 (94%)	6 (6%)	21	48
69	CF	206/206 (100%)	199 (97%)	7 (3%)	37	60
70	Cq	222/265 (84%)	216 (97%)	6 (3%)	44	65
71	CB	335/335 (100%)	315 (94%)	20 (6%)	19	46
72	CC	302/329 (92%)	286 (95%)	16 (5%)	22	49
73	CO	173/173 (100%)	160 (92%)	13 (8%)	13	39
74	Cp	73/73 (100%)	72 (99%)	1 (1%)	67	80
75	CI	156/183 (85%)	152 (97%)	4 (3%)	46	67
76	Cn	24/24 (100%)	23 (96%)	1 (4%)	30	54
77	Cm	47/48 (98%)	46 (98%)	1 (2%)	53	72
78	CL	175/175 (100%)	166 (95%)	9 (5%)	24	50
79	CE	185/185 (100%)	169 (91%)	16 (9%)	10	34
80	Cf	96/96 (100%)	93 (97%)	3 (3%)	40	62
81	Ck	63/63 (100%)	58 (92%)	5 (8%)	12	38
82	Cb	51/53 (96%)	51 (100%)	0	100	100
83	Cg	98/107 (92%)	91 (93%)	7 (7%)	14	41
All	All	10084/11382 (89%)	9634 (96%)	450 (4%)	31	53

5 of 450 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
48	CD	203	HIS
83	Cg	9	LYS
57	Ce	121	THR
81	Ck	1	MET
73	CO	152	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 129 such sidechains are listed below:

Mol	Chain	Res	Type
75	CI	14	ASN
79	CE	67	HIS
35	BG	160	ASN
35	BG	59	GLN
80	Cf	26	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	Ad	1760/1810 (97%)	458 (26%)	0
2	Ae	74/75 (98%)	19 (25%)	0
3	Af	10/11 (90%)	2 (20%)	0
84	Aa	3389/3391 (99%)	748 (22%)	0
85	Ac	159/160 (99%)	35 (22%)	0
86	Ab	119/120 (99%)	23 (19%)	0
All	All	5511/5567 (98%)	1285 (23%)	0

5 of 1285 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	Ad	4	C
1	Ad	8	U
1	Ad	16	G
1	Ad	25	C
1	Ad	26	A

There are no RNA pucker outliers to report.

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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

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.

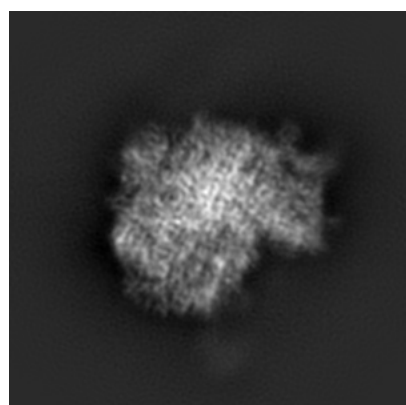
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1780. These allow visual inspection of the internal detail of the map and identification of artifacts.

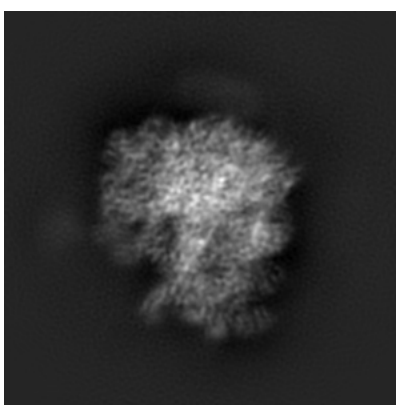
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

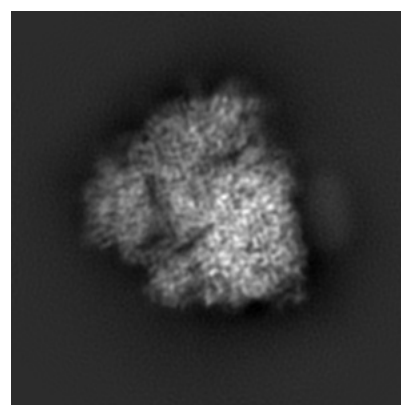
6.1.1 Primary map



X



Y

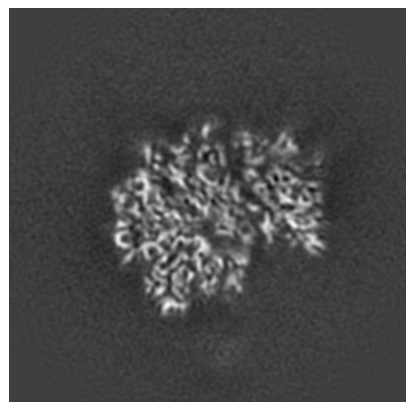


Z

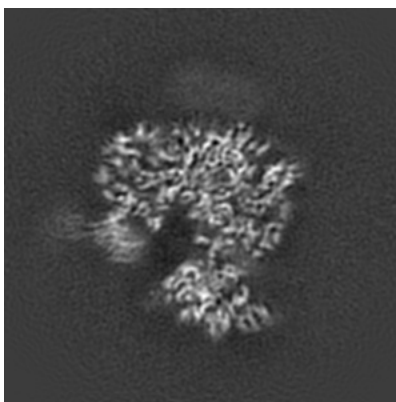
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

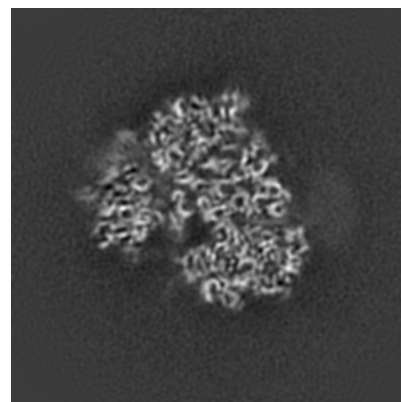
6.2.1 Primary map



X Index: 184



Y Index: 184

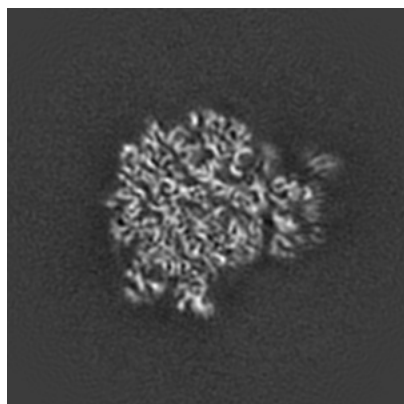


Z Index: 184

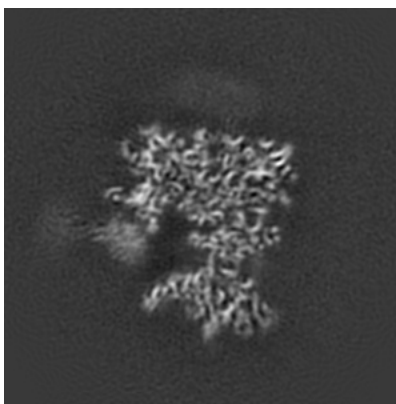
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

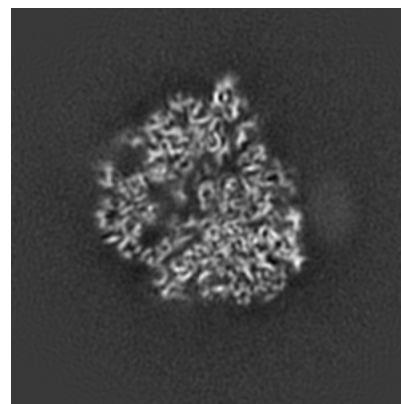
6.3.1 Primary map



X Index: 213



Y Index: 193

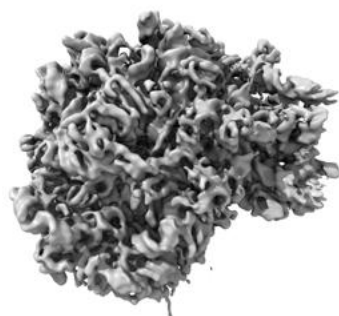


Z Index: 173

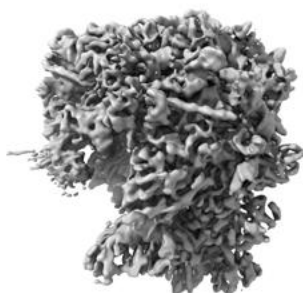
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.11. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

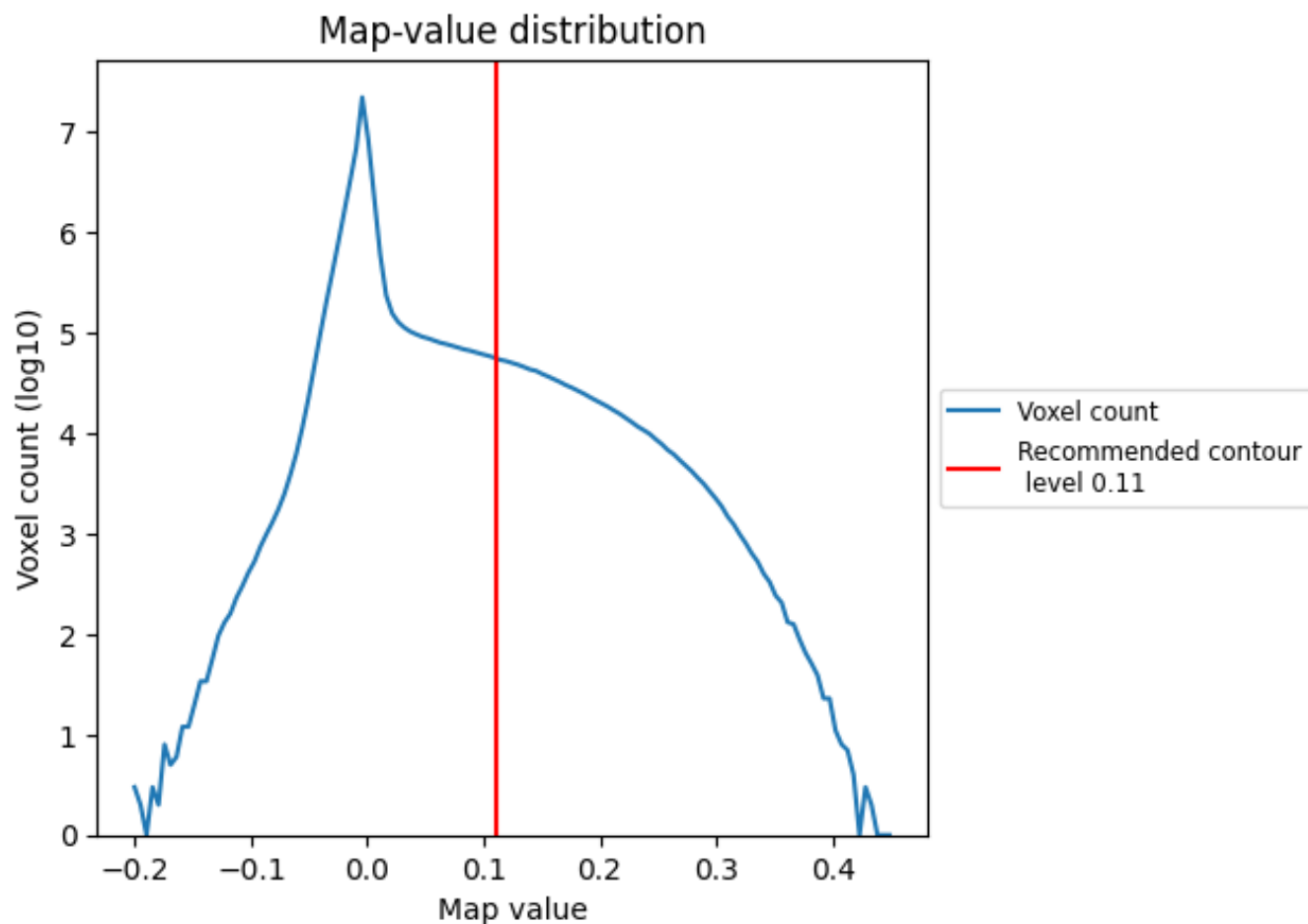
6.5 Mask visualisation

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

7 Map analysis [i](#)

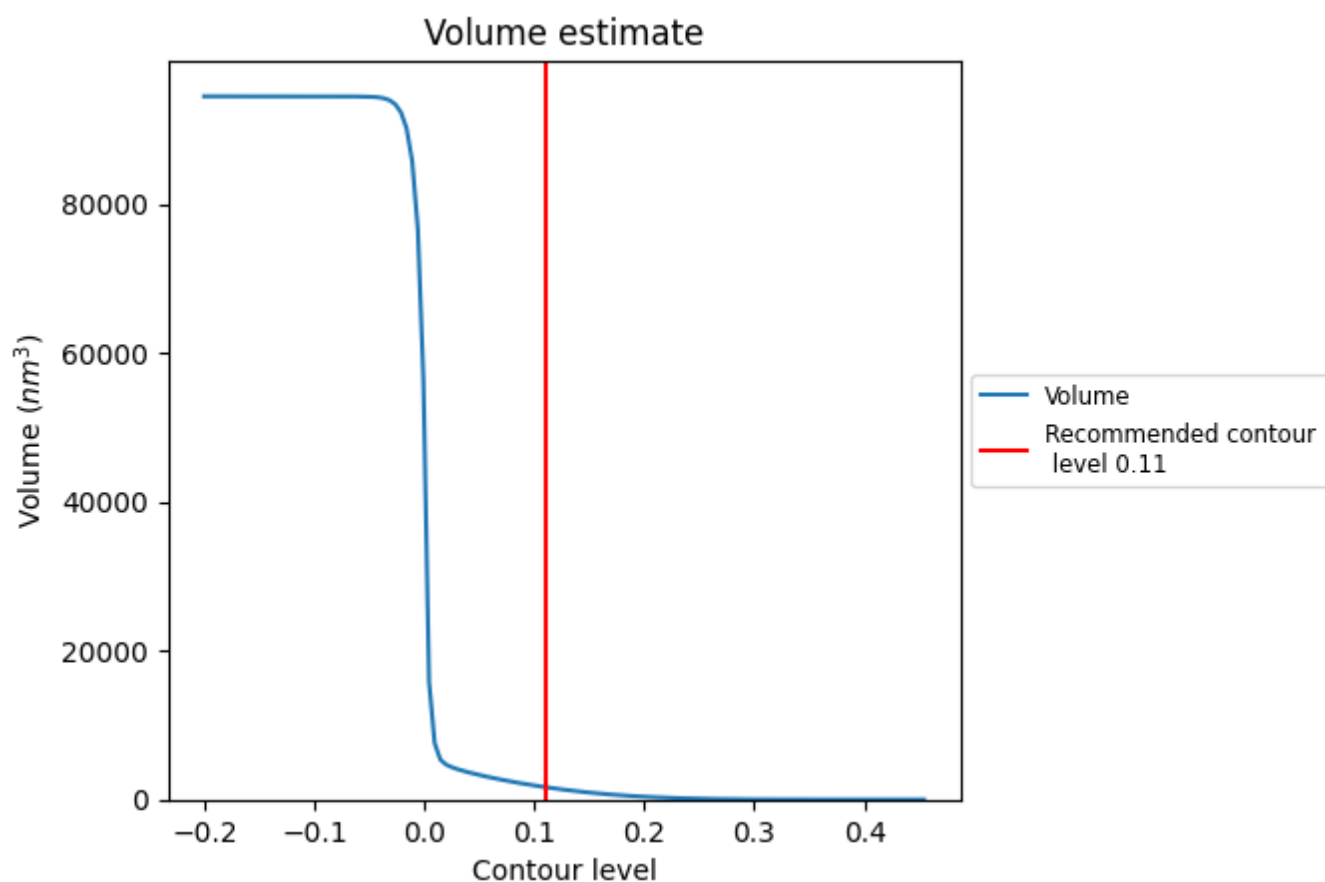
This section contains the results of statistical analysis of the map.

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.

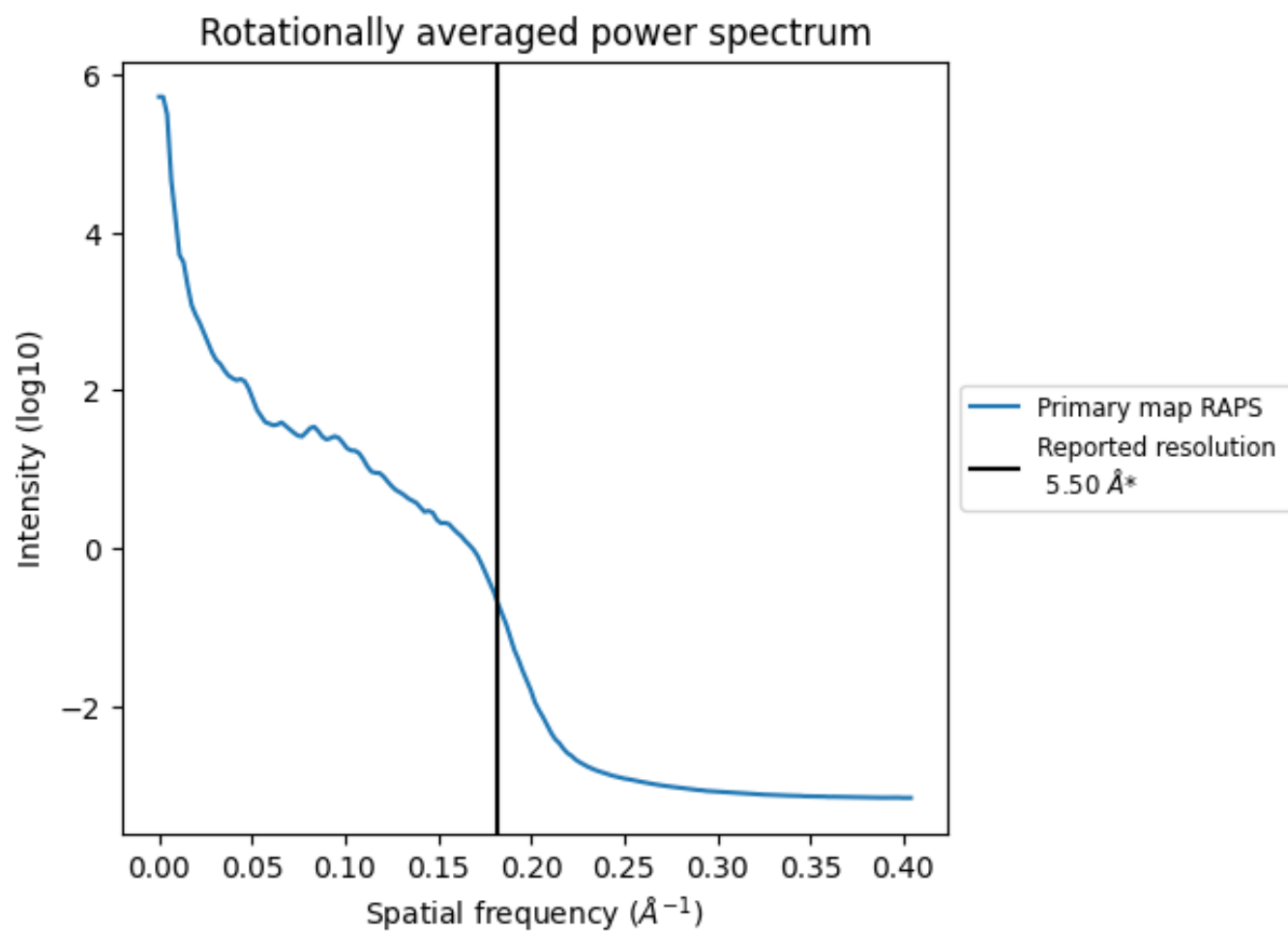
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1668 nm³; this corresponds to an approximate mass of 1506 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 0.182 Å⁻¹

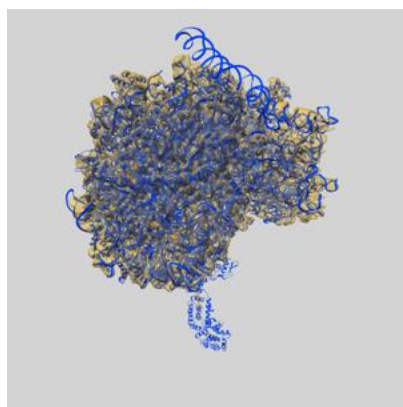
8 Fourier-Shell correlation

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

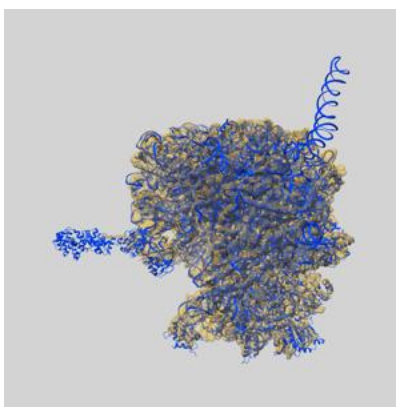
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-1780 and PDB model 4V7E. Per-residue inclusion information can be found in section [3](#) on page [20](#).

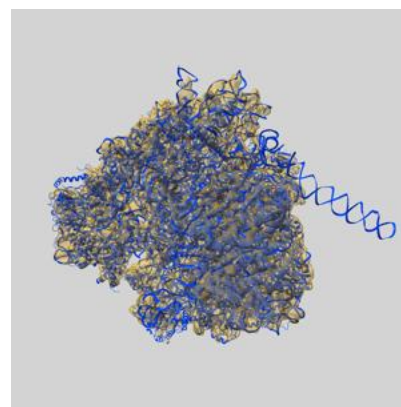
9.1 Map-model overlay [i](#)



X



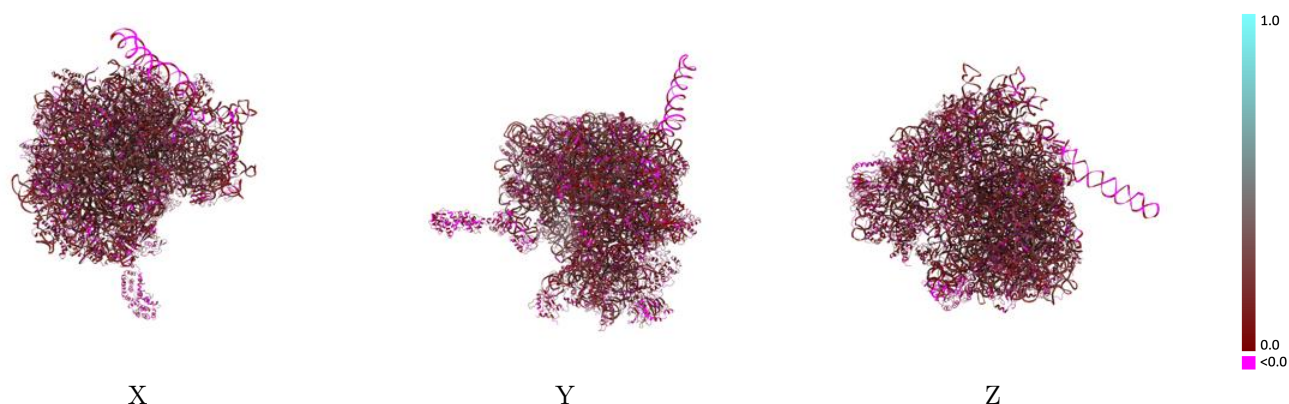
Y



Z

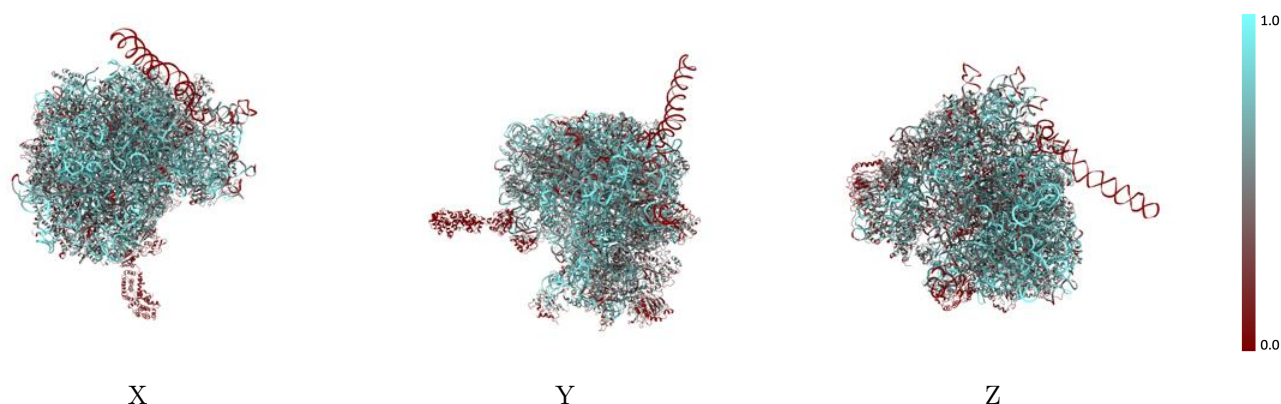
The images above show the 3D surface view of the map at the recommended contour level 0.11 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



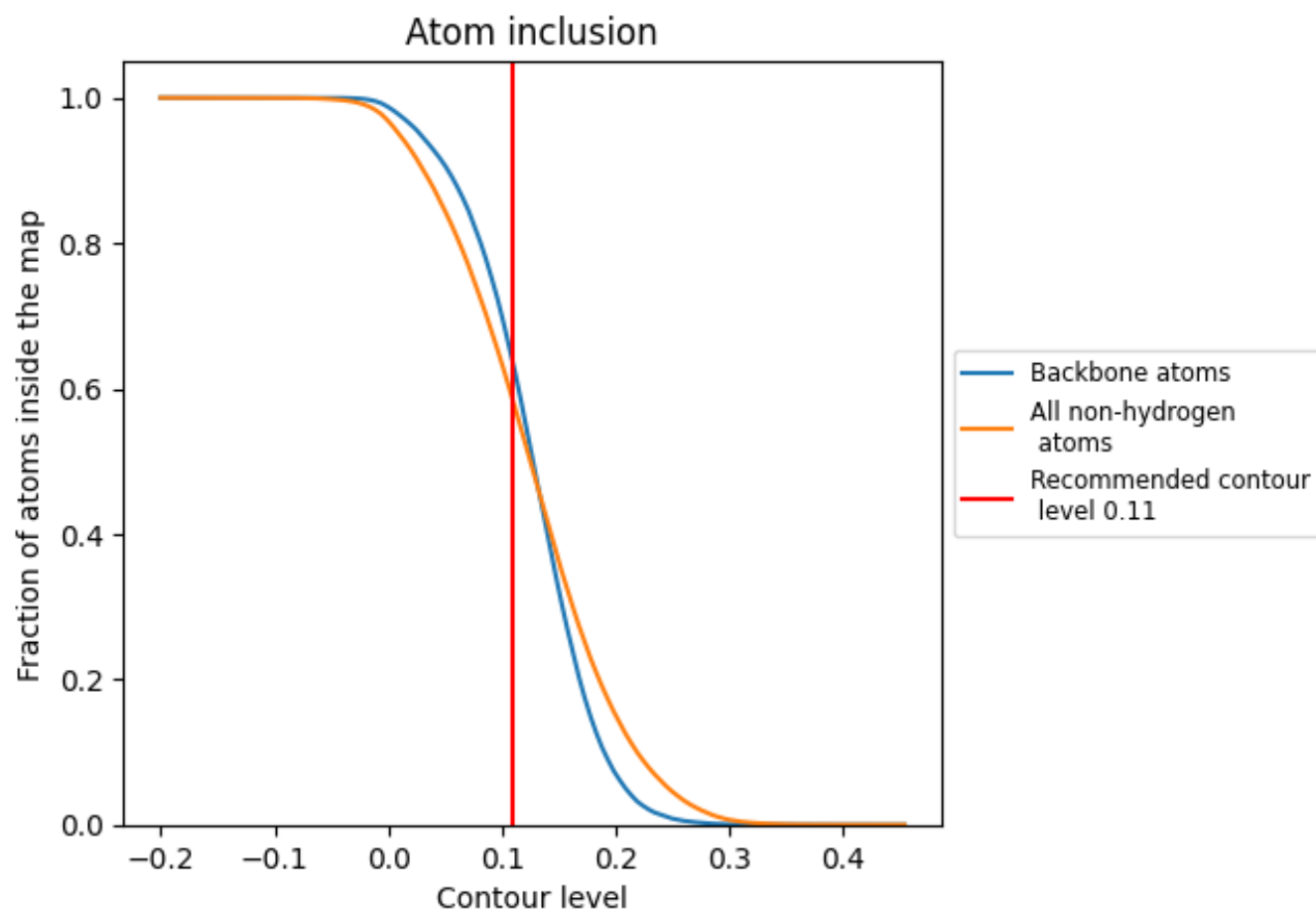
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.11).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 63% of all backbone atoms, 58% 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 (0.11) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5826	 0.1550
Aa	 0.7377	 0.1940
Ab	 0.8528	 0.2080
Ac	 0.7934	 0.2070
Ad	 0.7396	 0.1960
Ae	 0.4915	 0.1860
Af	 0.1293	 0.0800
BA	 0.3804	 0.1240
BB	 0.4210	 0.1260
BC	 0.3646	 0.1210
BD	 0.3293	 0.1190
BE	 0.4311	 0.1040
BF	 0.4542	 0.1280
BG	 0.4302	 0.1120
BH	 0.3666	 0.1230
BI	 0.4139	 0.1110
BJ	 0.4894	 0.1170
BK	 0.4180	 0.0950
BL	 0.3153	 0.1070
BM	 0.2871	 0.0870
BN	 0.3866	 0.0980
BO	 0.3839	 0.1130
BP	 0.4370	 0.1110
BQ	 0.3975	 0.0950
BR	 0.3454	 0.1130
BS	 0.4000	 0.1130
BT	 0.4459	 0.1070
BU	 0.3075	 0.0920
BV	 0.3601	 0.1050
BW	 0.3448	 0.0840
BX	 0.4157	 0.1190
BY	 0.4148	 0.0740
BZ	 0.3447	 0.0990
Ba	 0.4599	 0.1350
Bb	 0.4000	 0.1200



























Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Bc	 0.3077	 0.0630
Bd	 0.3736	 0.0680
Be	 0.3031	 0.0730
Bf	 0.3569	 0.0730
Bg	 0.2151	 0.0850
CA	 0.3965	 0.1150
CB	 0.4292	 0.1080
CC	 0.4029	 0.1160
CD	 0.4762	 0.1050
CE	 0.3678	 0.0960
CF	 0.4640	 0.1200
CG	 0.4751	 0.1180
CH	 0.4758	 0.1140
CI	 0.4448	 0.1210
CJ	 0.4656	 0.1300
CK	 0.0583	 0.0530
CL	 0.4417	 0.1020
CM	 0.4739	 0.1230
CN	 0.4819	 0.1090
CO	 0.4495	 0.1070
CP	 0.4274	 0.1150
CQ	 0.4246	 0.1150
CR	 0.4299	 0.1140
CS	 0.4637	 0.1040
CT	 0.3952	 0.1130
CU	 0.3175	 0.0650
CV	 0.2652	 0.1300
CW	 0.2757	 0.1230
CX	 0.3930	 0.1120
CY	 0.5448	 0.1270
CZ	 0.5066	 0.1270
Ca	 0.4074	 0.0920
Cb	 0.3613	 0.0940
Cc	 0.4303	 0.1090
Cd	 0.4082	 0.0930
Ce	 0.3661	 0.1060
Cf	 0.4198	 0.0960
Cg	 0.4448	 0.1210
Ch	 0.4536	 0.0910
Ci	 0.4105	 0.0870
Cj	 0.4672	 0.1040
Ck	 0.4709	 0.1140

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Cl	 0.4312	 0.1180
Cm	 0.5290	 0.1580
Cn	 0.2831	 -0.0170
Co	 0.3911	 0.0940
Cp	 0.3991	 0.1240
Cq	 0.0737	 0.0580
Cr	 0.4893	 0.1140
Cs	 0.0137	 0.0590
Ct	 0.0000	 0.0300
Cu	 0.0000	 0.0430
Cv	 0.0000	 0.0280
Cz	 0.0260	 0.0410