



## wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 12:27 AM UTC

PDB ID : 4V7E / pdb\_00004v7e  
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](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

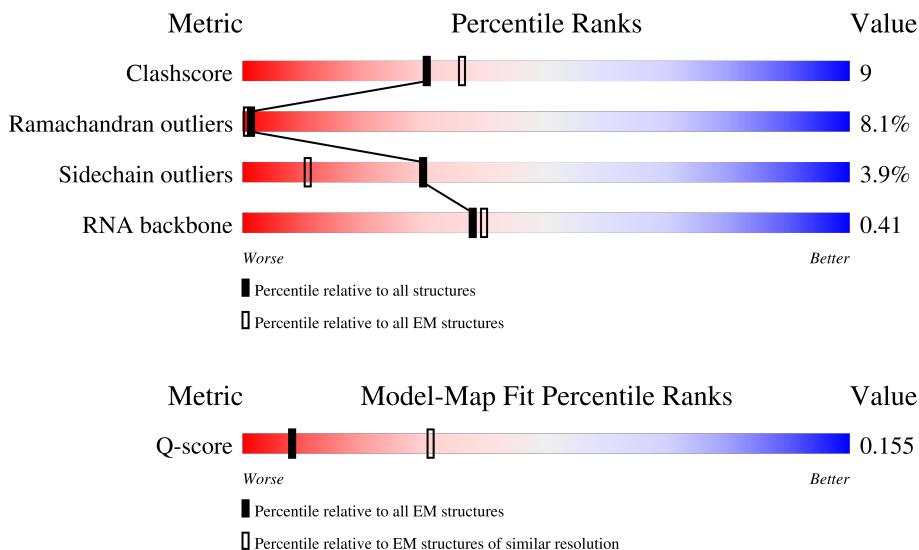
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	520 ( 5.00 - 6.00 )

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

Mol	Chain	Length	Quality of chain
1	Ad	1810	
2	Ae	75	
3	Af	11	

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Mol	Chain	Length	Quality of chain
4	BY	138	51% 67% 26% 7%
5	BI	220	14% 25% 5% 70%
6	BK	183	26% 43% 8% 48%
7	BM	171	47% 57% 13% 28%
8	Bf	155	25% 29% 11% 5% 54%
9	BX	142	48% 80% 17%
10	Bg	380	77% 90% 8%
11	BD	208	58% 67% 26% 5%
12	BE	265	32% 61% 12% 25%
13	BF	191	38% 86% 12%
14	BQ	149	40% 57% 19% 6% 15%
15	BU	128	59% 77% 19%
16	BO	151	41% 62% 12% 5% 21%
17	BS	152	48% 66% 23% 9%
18	BN	151	45% 49% 28% 20%
19	BL	160	31% 38% 12% 47%
20	BT	146	44% 76% 18%
21	BP	154	29% 47% 8% 41%
22	BZ	108	49% 64% 24% 7%
23	Bc	65	60% 66% 20% 11%
24	BW	130	56% 72% 24%
25	Bd	56	50% 43% 32% 11% 14%
26	Bb	86	49% 83% 13%
27	Be	62	58% 71% 26%
28	BA	260	42% 67% 8% 24%

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Mol	Chain	Length	Quality of chain
29	BR	141	50% 65% 16% .. 18%
30	BB	262	38% 63% 17% . 19%
31	BV	82	57% 84% 7% . 7%
32	Ba	133	26% 47% 15% 7% . 30%
33	BJ	195	31% 78% 14% . . .
34	BC	263	44% 72% 8% . 19%
35	BG	245	43% 65% 26% . 6%
36	BH	189	52% 79% 12% 5% . .
37	CG	257	38% 84% 7% . 8%
38	CT	164	47% 77% 18% . . .
39	CZ	136	33% 93% 7%
40	Cz	216	98% 85% 14% .
41	CA	261	54% 72% 23% . . .
42	CJ	180	34% 71% 19% . . 6%
43	CH	190	41% 91% 8% ..
44	CV	140	74% 89% 9% .
45	CN	200	35% 84% 12% . .
46	Ca	144	50% 69% 25% 5% .
47	CQ	188	39% 67% 16% .. 13%
48	CD	304	37% 65% 21% 11% .
49	CR	209	44% 64% 22% . . 10%
50	CP	171	42% 73% 23% .
51	CX	152	40% 66% 11% .. 20%
52	CW	162	31% 39% 7% . 54%
53	CY	150	21% 71% 13% . 13%

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Mol	Chain	Length	Quality of chain
54	Cr	147	18% 39% 8% 50%
55	Cc	112	45% 88% 9%
56	Cd	123	46% 77% 15% 5%
57	Ce	133	58% 82% 15%
58	Cj	94	39% 67% 28% 5%
59	Cl	51	47% 80% 18%
60	Co	105	48% 73% 22%
61	CM	134	35% 75% 19% 5%
62	CS	178	37% 68% 19% 7% 6%
63	CU	130	53% 60% 14% 6% 17%
64	Ci	112	31% 51% 13% 31%
65	CK	166	73% 62% 10% 23%
66	Cu	110	53% 51% 47%
66	Cv	110	53% 52% 47%
67	Cs	113	52% 50% 48%
67	Ct	113	52% 50% 48%
68	Ch	124	40% 80% 19%
69	CF	244	41% 83% 15%
70	Cq	319	76% 71% 9% 18%
71	CB	389	44% 76% 18% 5%
72	CC	405	45% 72% 15% 8%
73	CO	206	42% 81% 13%
74	Cp	92	50% 89% 11%
75	CI	224	36% 67% 12% 18%
76	Cn	25	72% 48% 44% 8%

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Mol	Chain	Length	Quality of chain
77	Cm	53	
78	CL	208	
79	CE	219	
80	Cf	111	
81	Ck	69	
82	Cb	60	
83	Cg	119	
84	Aa	3391	
85	Ac	160	
86	Ab	120	

## 2 Entry composition [i](#)

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
			Total	C	N	O	P		
1	Ad	1762	37584	16788	6708	12327	1761	0	0

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

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

- 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
			Total	C	N	O	P		
3	Af	11	232	106	45	71	10	0	0

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 10 is a protein called RACK1.

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

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

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

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

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

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

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

- 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
			Total	C	N	O	S		
28	BA	197	1537	969	280	278	10	0	0

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

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

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

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

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

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

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

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

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

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

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

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

- 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
			Total	C	N	O	S		
49	CR	189	1569	972	330	257	10	0	0

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

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

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

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

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

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

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

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

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

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

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

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

- 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
			Total	C	N	O	S		
63	CU	108	864	551	155	156	2	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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
			Total	C	N	O	P		
84	Aa	3391	72601	32373	13241	23598	3389	0	0

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

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

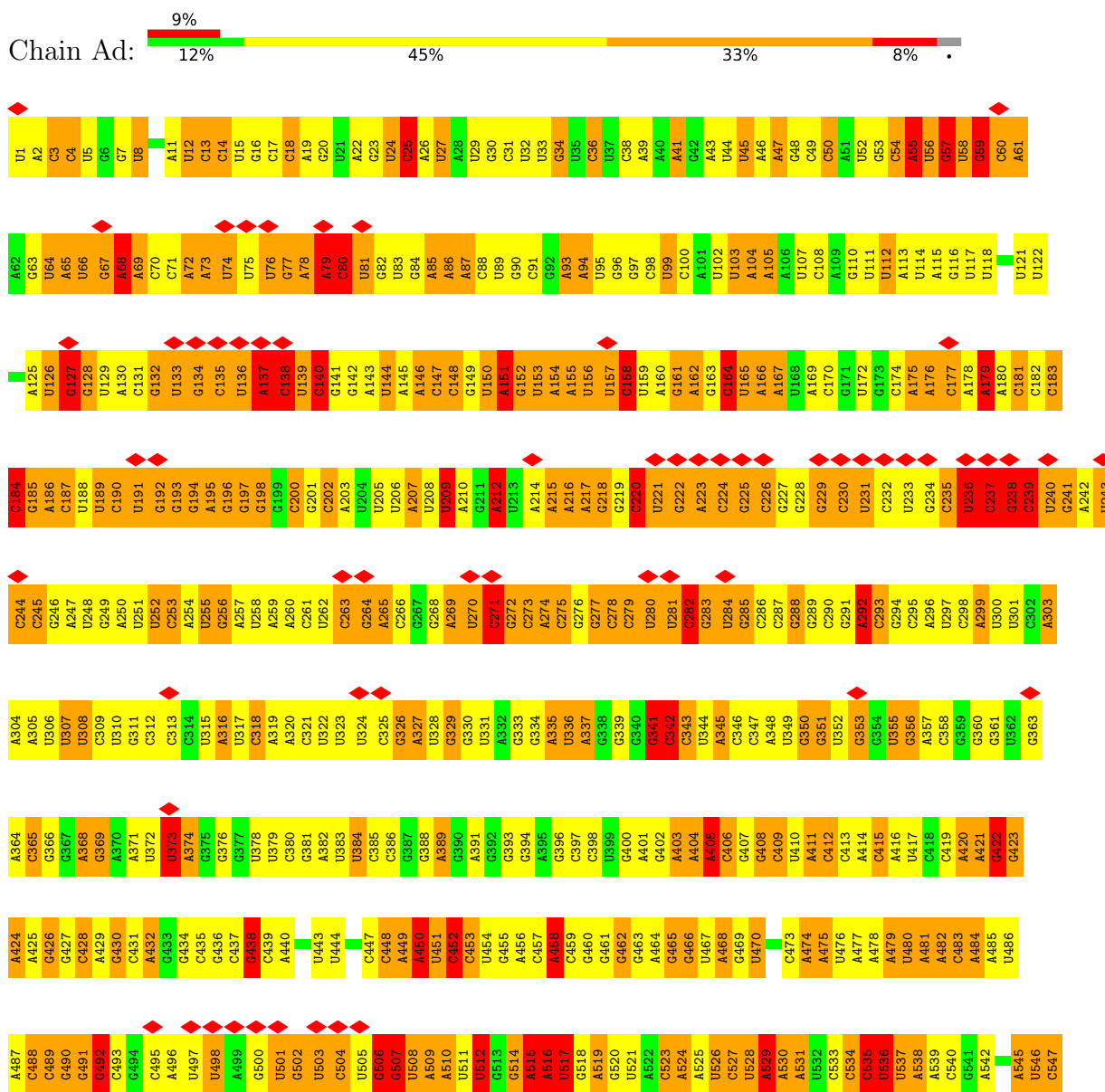
- Molecule 86 is a RNA chain called 5S ribosomal RNA.

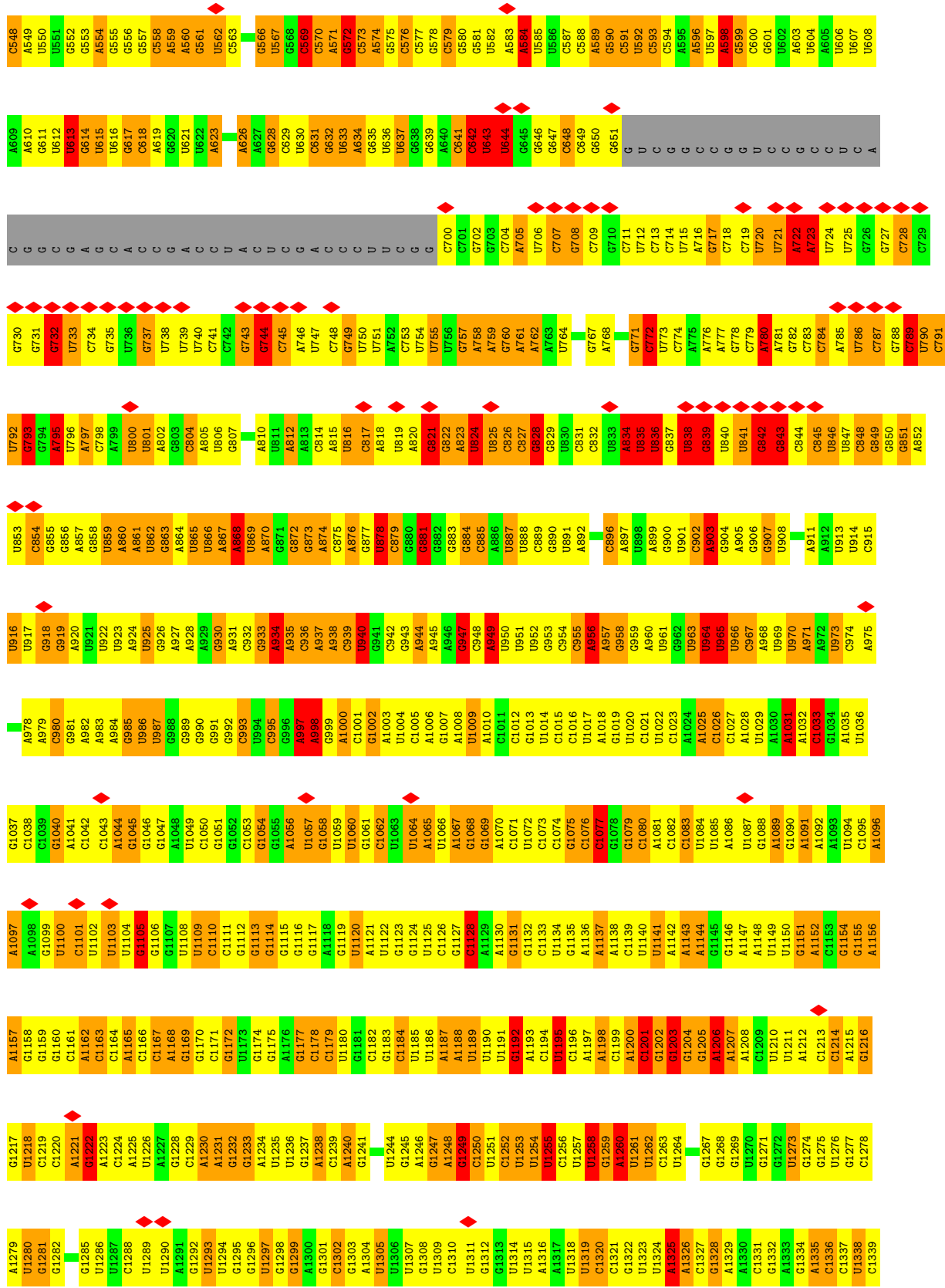
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
86	Ab	120	2561	1144	461	837	119	0	0

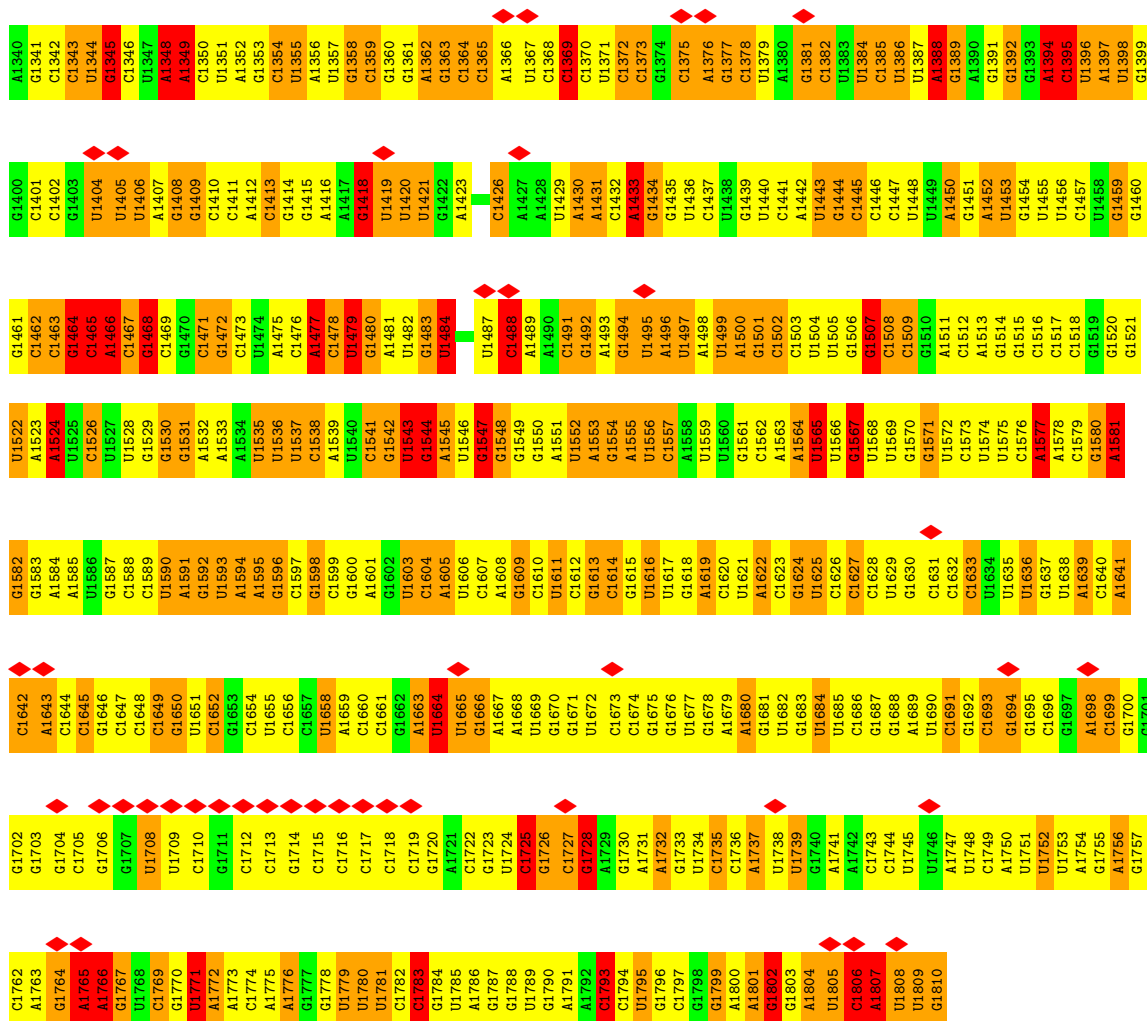
### 3 Residue-property plots

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

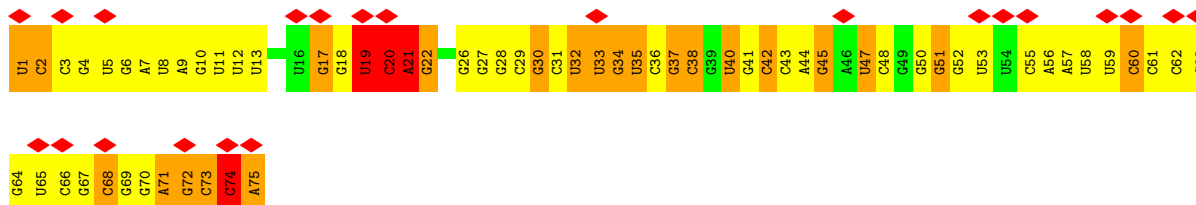
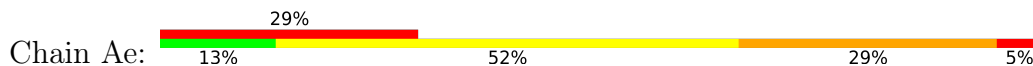
- Molecule 1: 18S ribosomal RNA



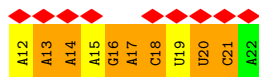
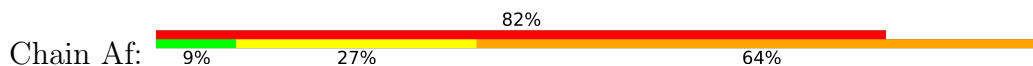




• Molecule 2: P-site tRNA



• Molecule 3: 5'-R(\*AP\*AP\*AP\*AP\*GP\*AP\*CP\*UP\*UP\*CP\*A)-3'

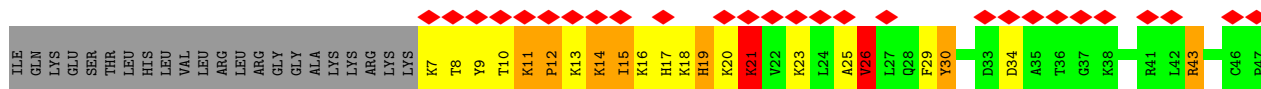
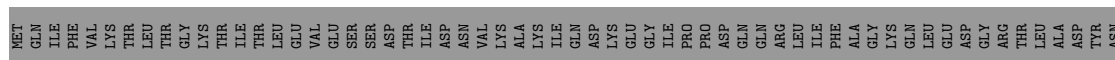
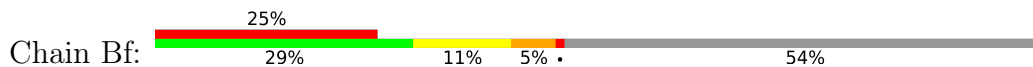


• Molecule 4: 40S ribosomal protein S24E

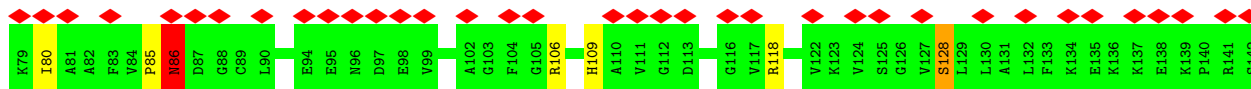
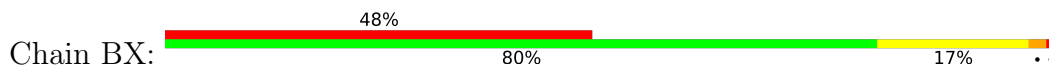




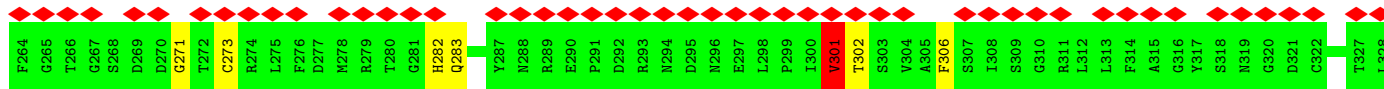
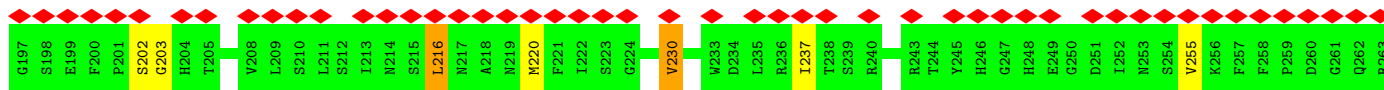
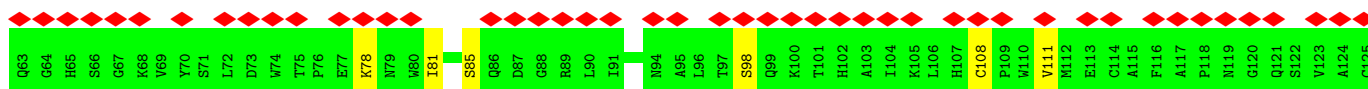
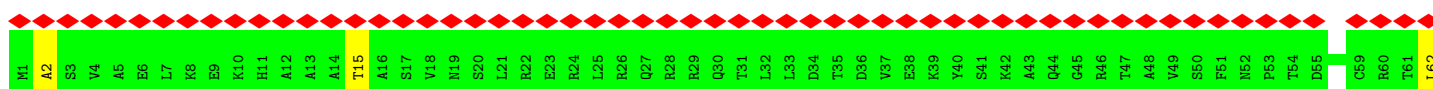
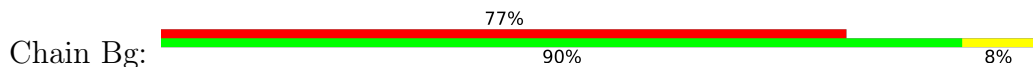
• Molecule 8: 40S ribosomal protein S31e

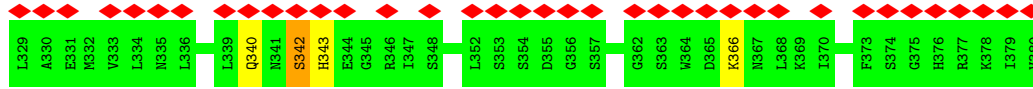


• Molecule 9: 40S ribosomal protein S12

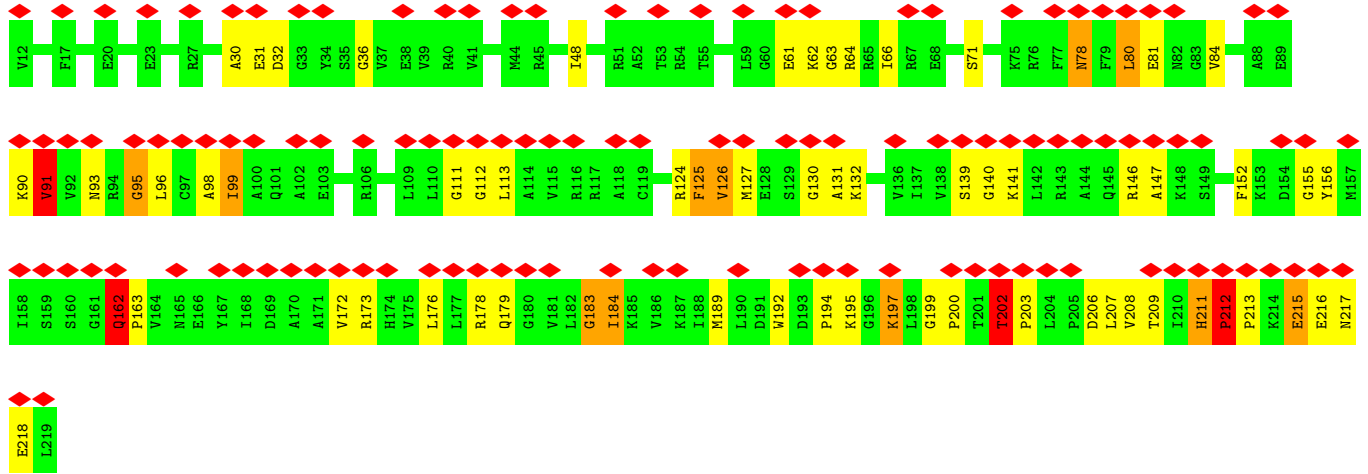


• Molecule 10: RACK1

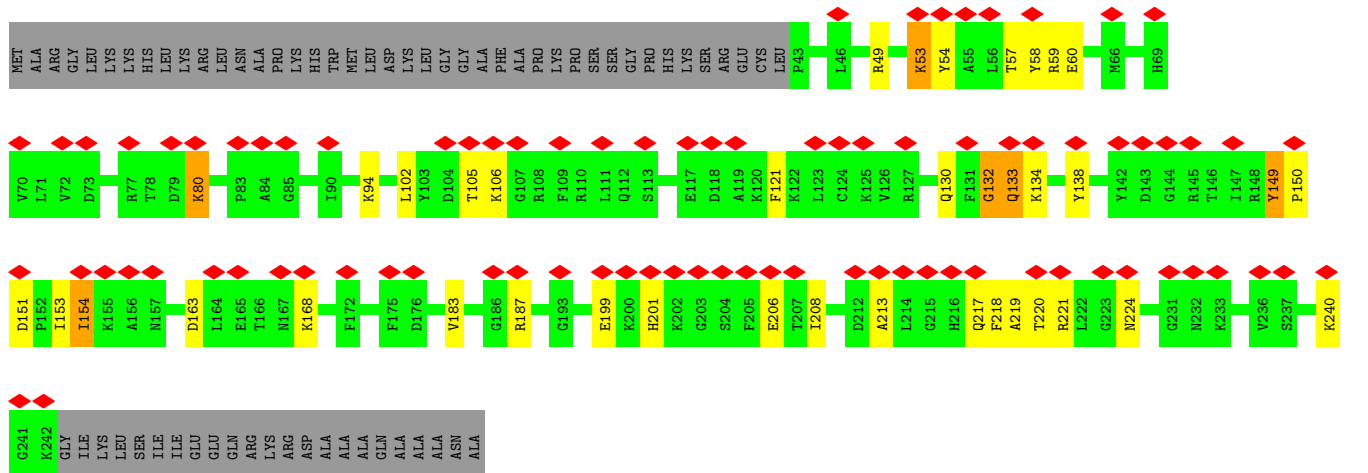




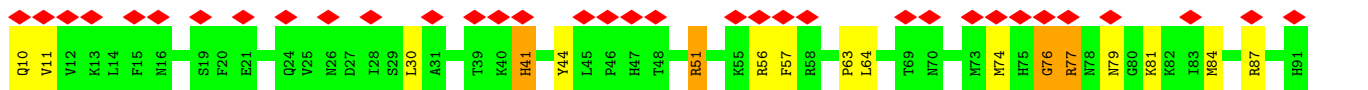
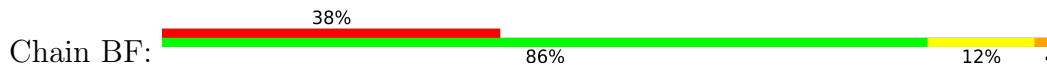
• Molecule 11: 40S ribosomal protein S3

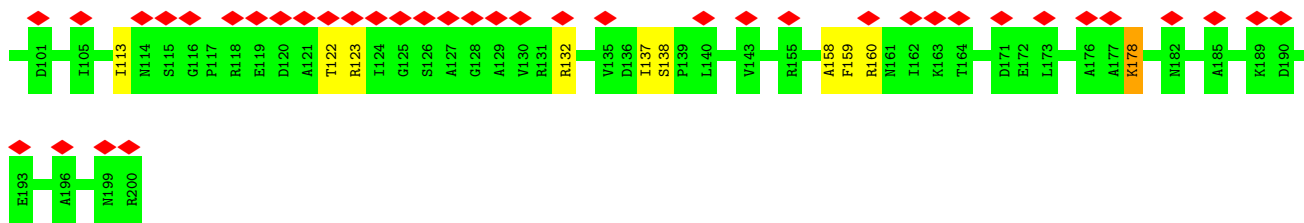


• Molecule 12: 40S ribosomal protein S4E

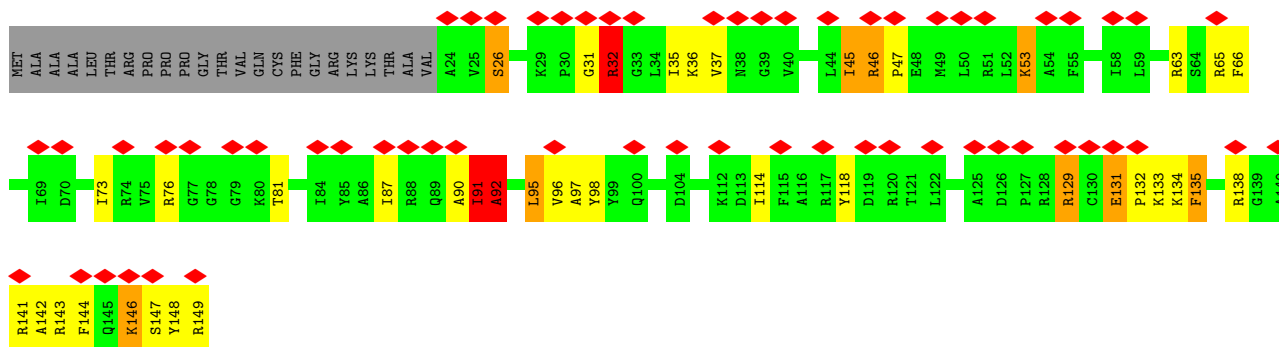
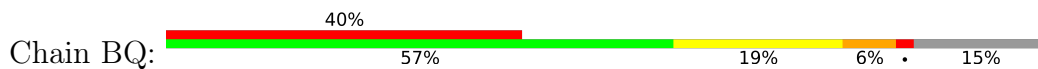


• Molecule 13: 40S ribosomal protein S7

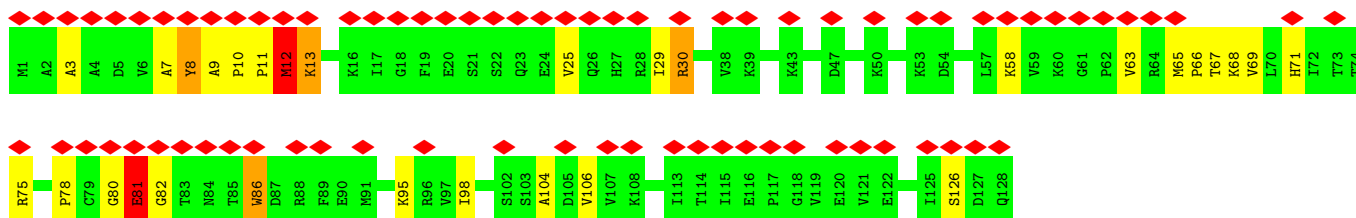
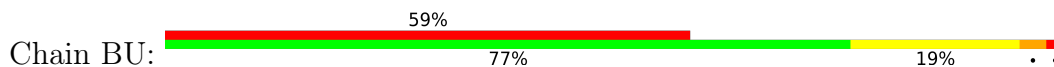




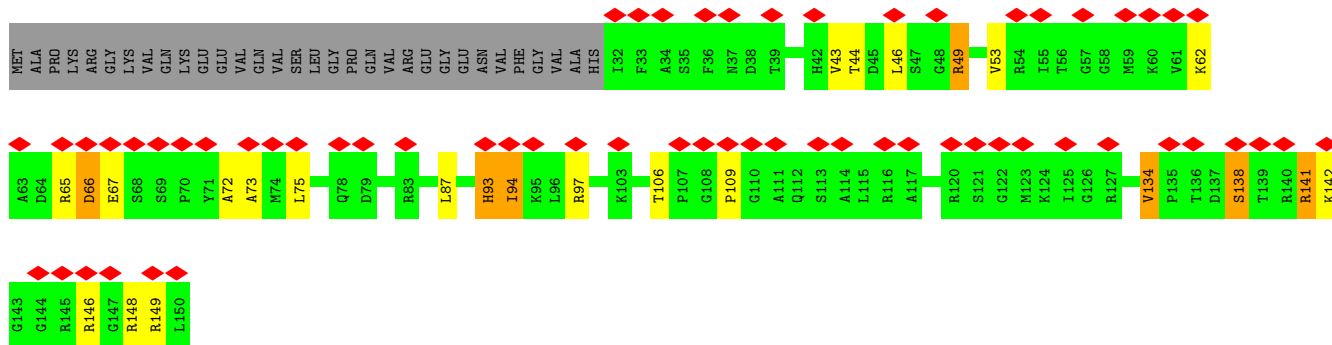
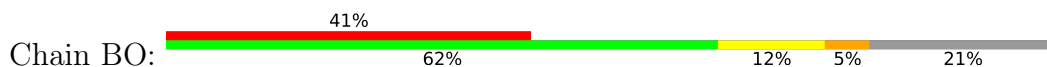
• Molecule 14: 40S ribosomal protein S9



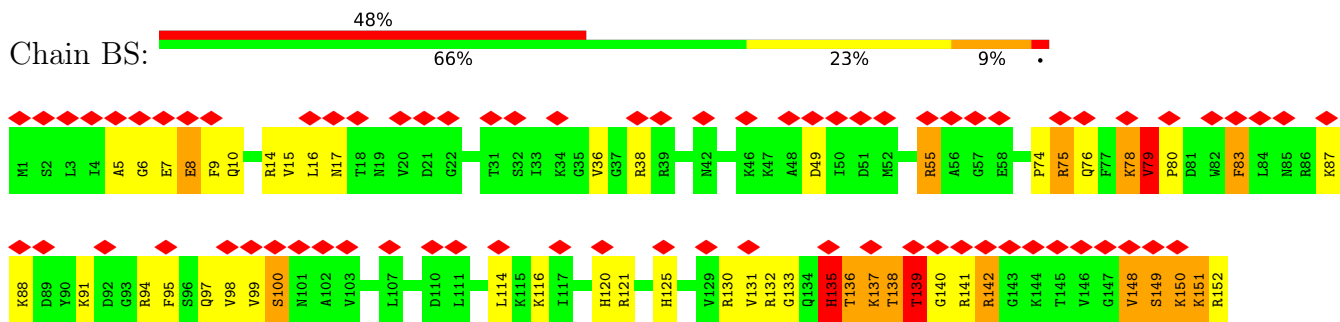
• Molecule 15: 40S ribosomal protein S10



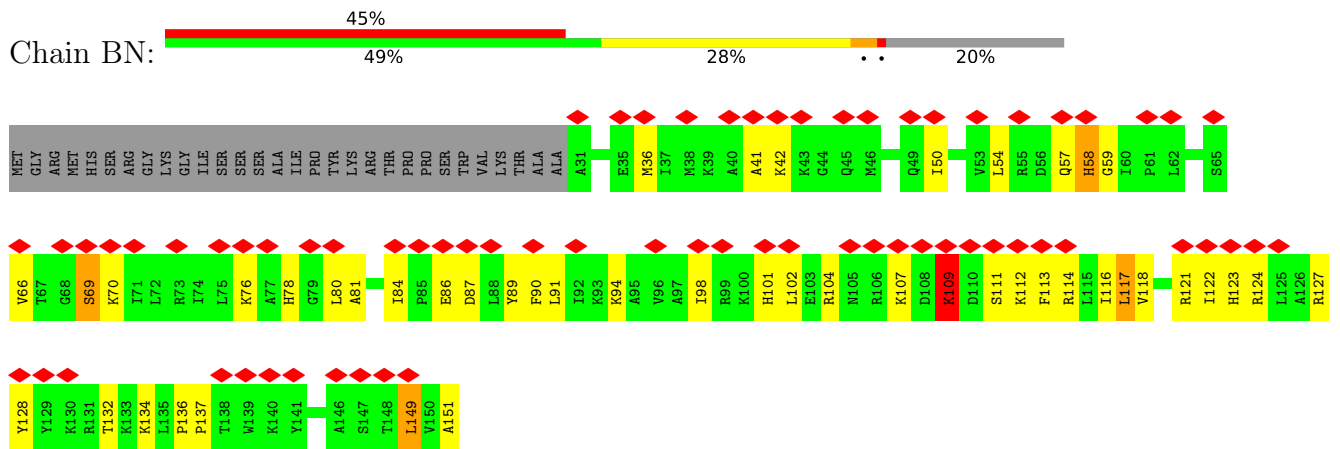
• Molecule 16: 40S ribosomal protein S11



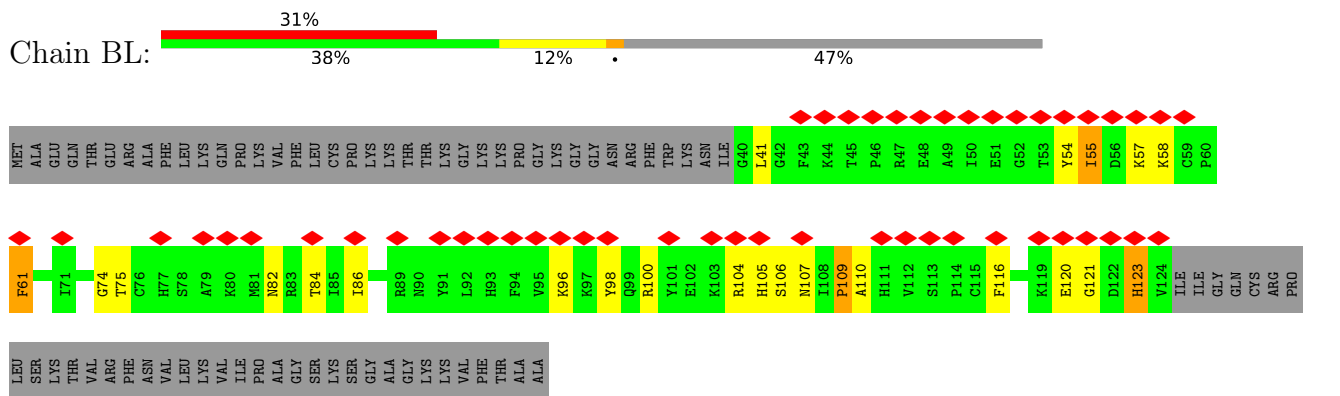
• Molecule 17: 40S ribosomal protein S13



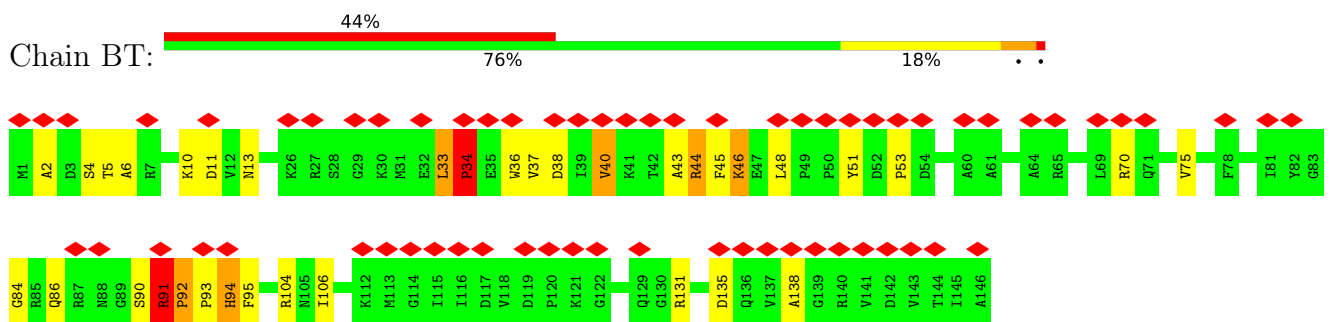
• Molecule 18: 40S ribosomal protein S15



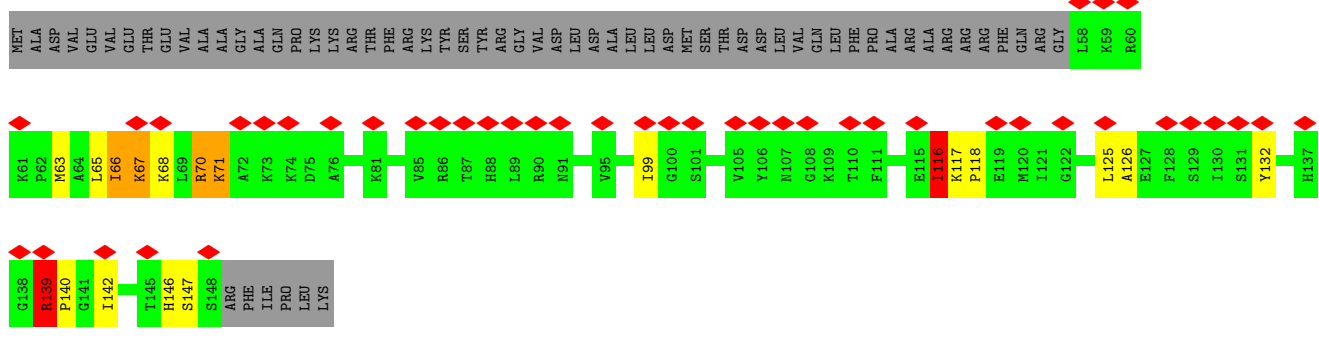
• Molecule 19: 40S ribosomal protein S17



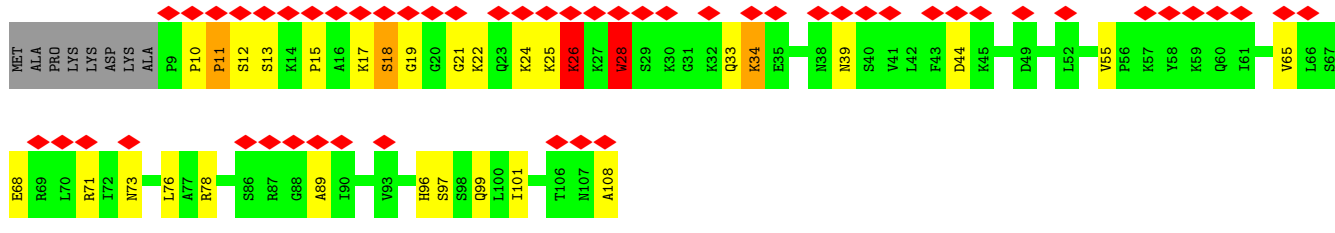
• Molecule 20: 40S ribosomal protein S19E



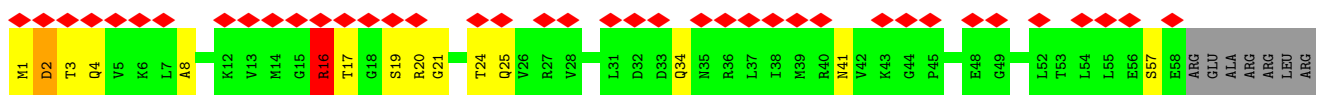
• Molecule 21: 40S ribosomal protein S19



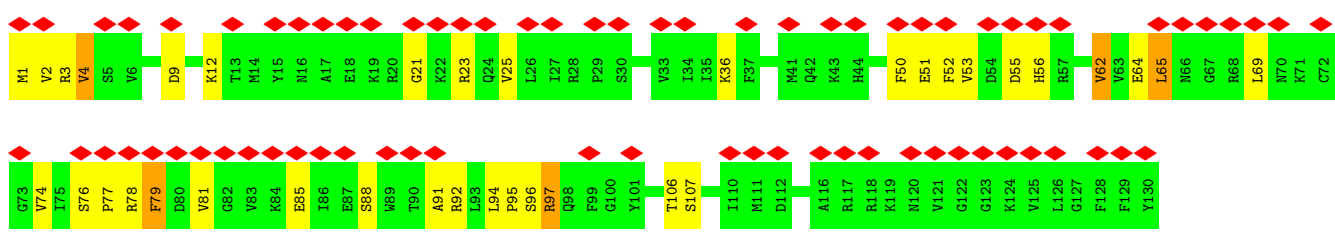
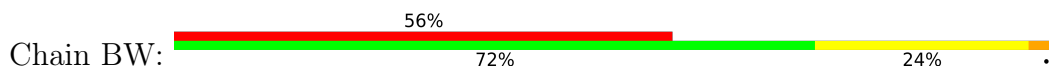
• Molecule 22: 40S ribosomal protein S25E



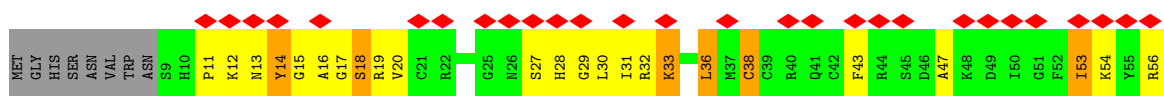
• Molecule 23: 40S ribosomal protein S28E



• Molecule 24: 40S ribosomal protein S8



• Molecule 25: 40S ribosomal protein S14




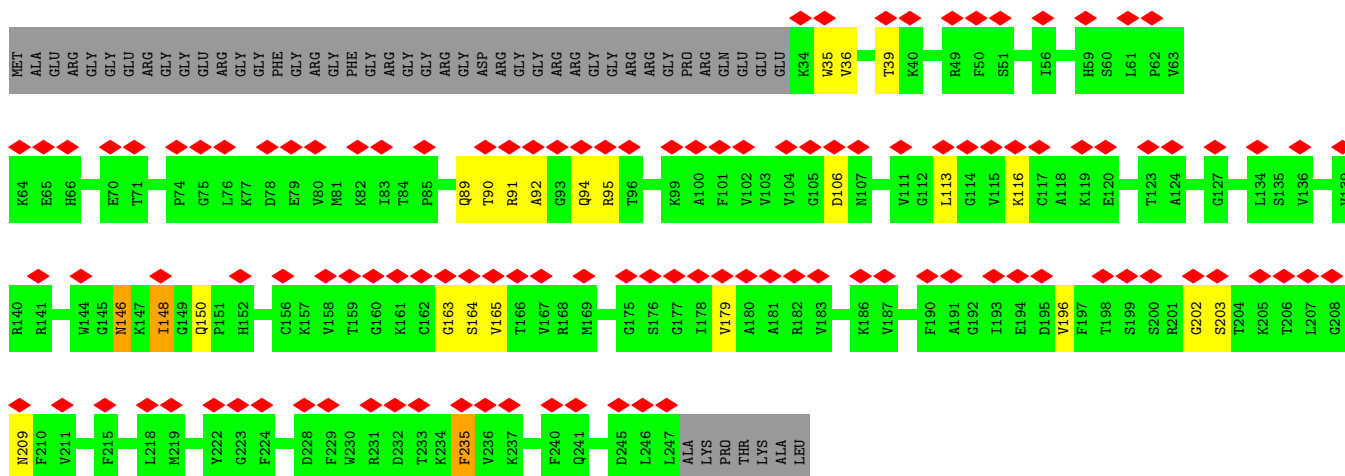





GLU  
GLU  
ASP  
GLU  
GLU

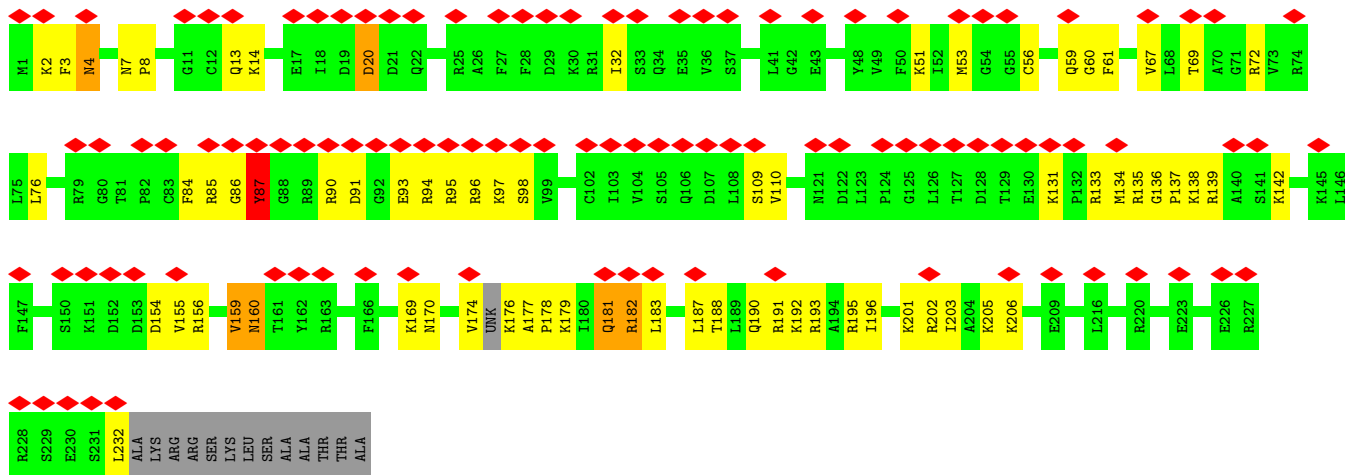
- Molecule 34: 40S ribosomal protein S5

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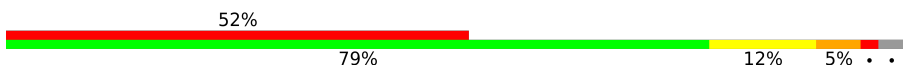


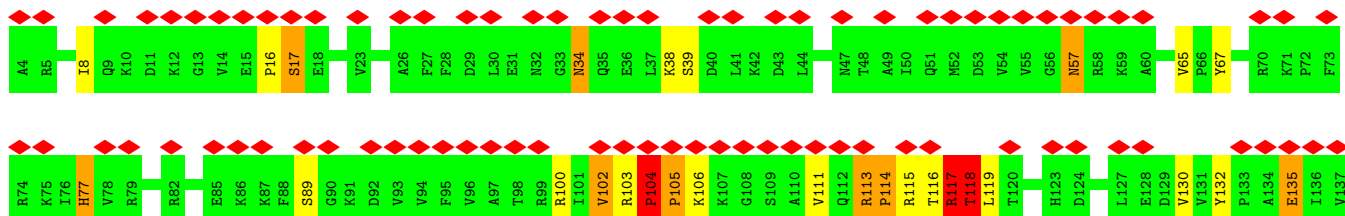
- Molecule 35: 40S ribosomal protein S6

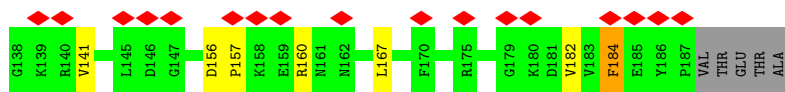
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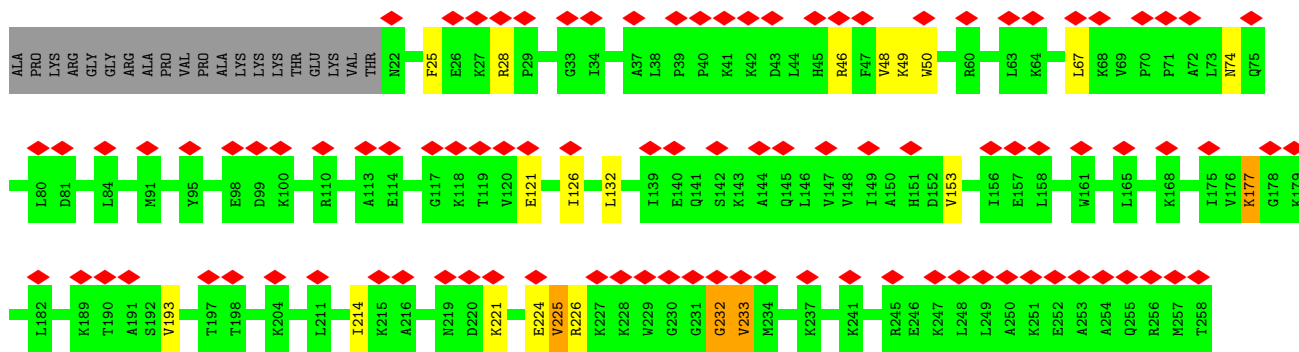
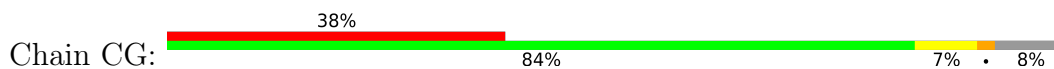
- Molecule 36: 40S ribosomal protein S7E

Chain BH: 

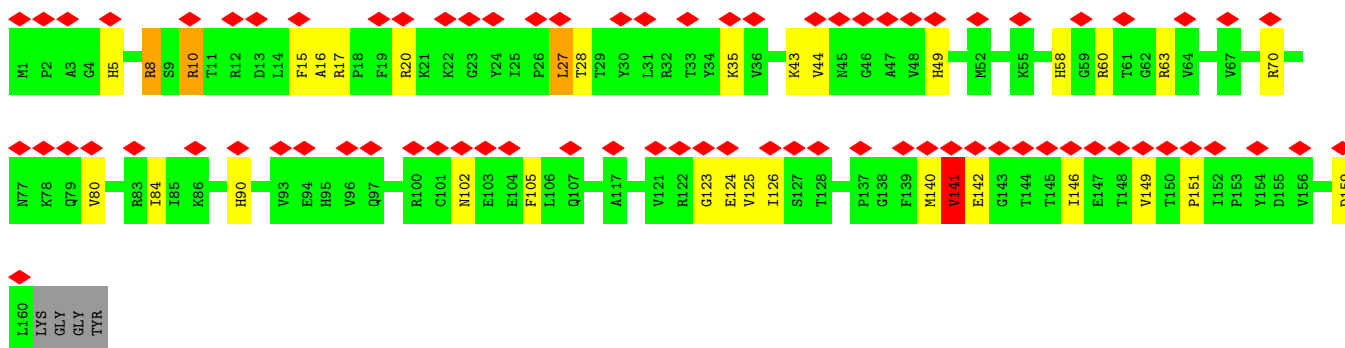
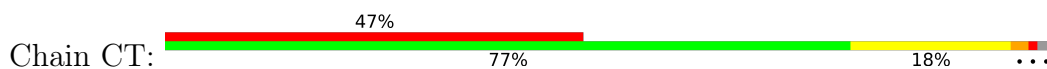




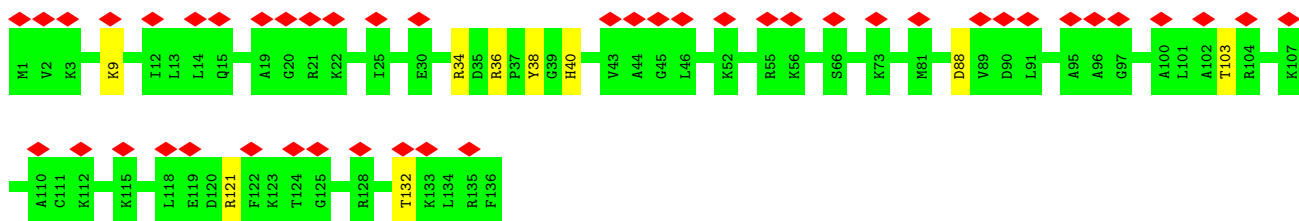
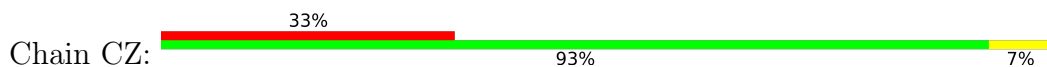
• Molecule 37: 60S ribosomal protein L8E



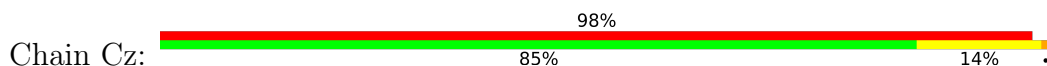
• Molecule 38: 60S ribosomal protein L21E

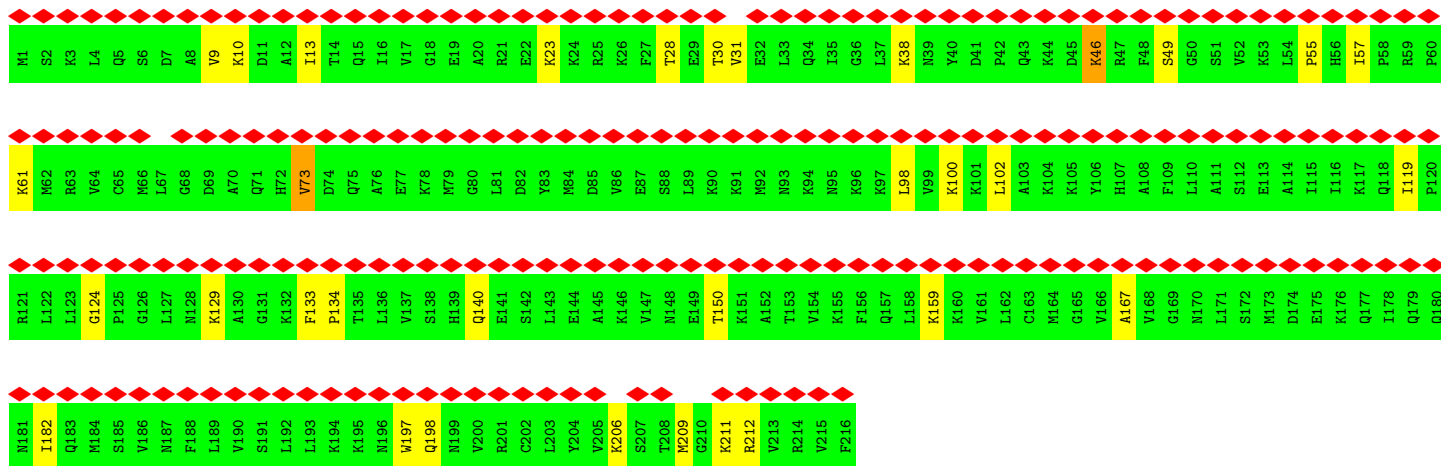


• Molecule 39: 60S ribosomal protein L27E

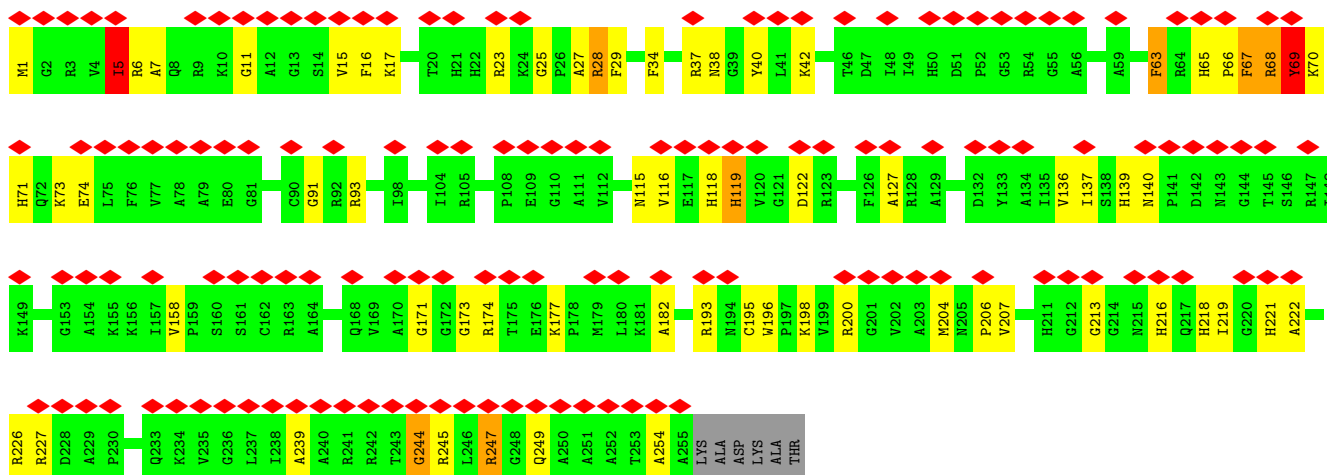
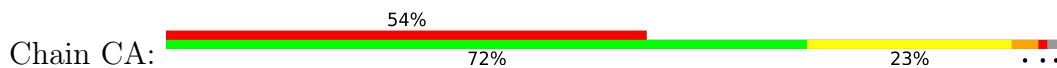


• Molecule 40: 60S ribosomal protein L1

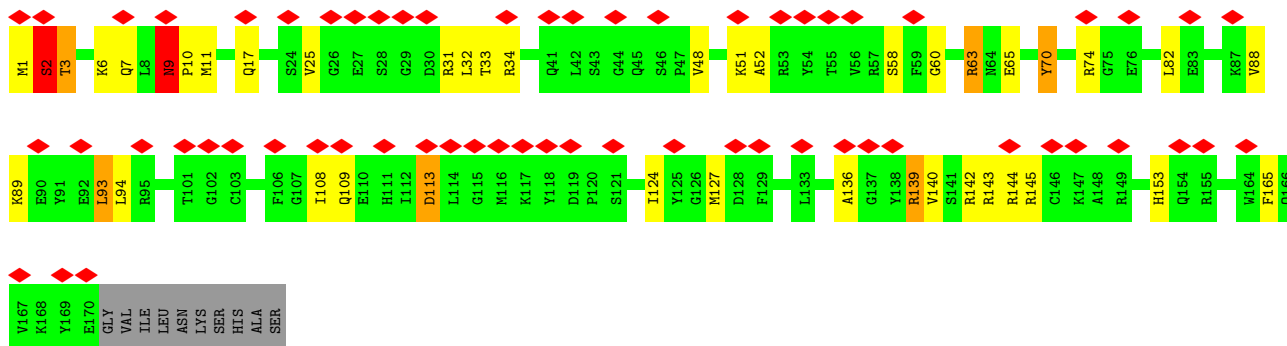
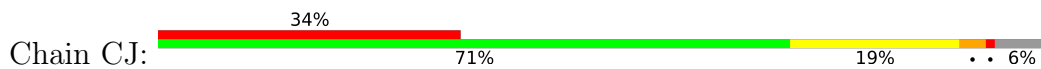




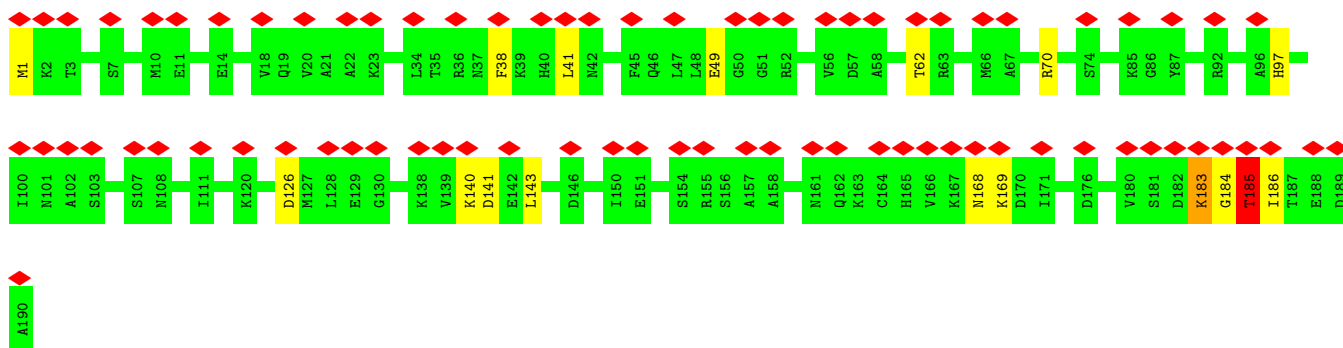
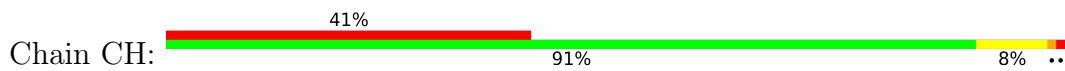
• Molecule 41: 60S ribosomal protein L2



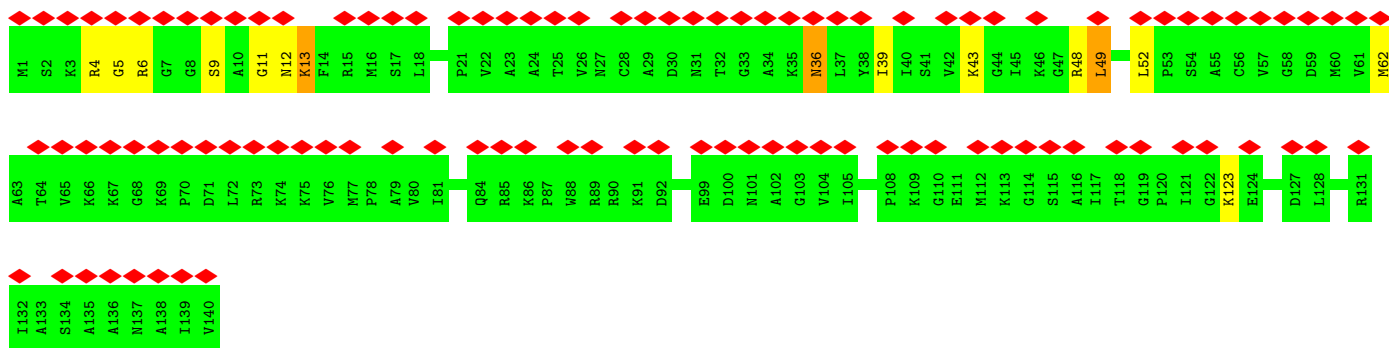
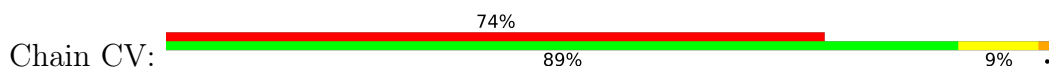
• Molecule 42: 60S ribosomal protein L5



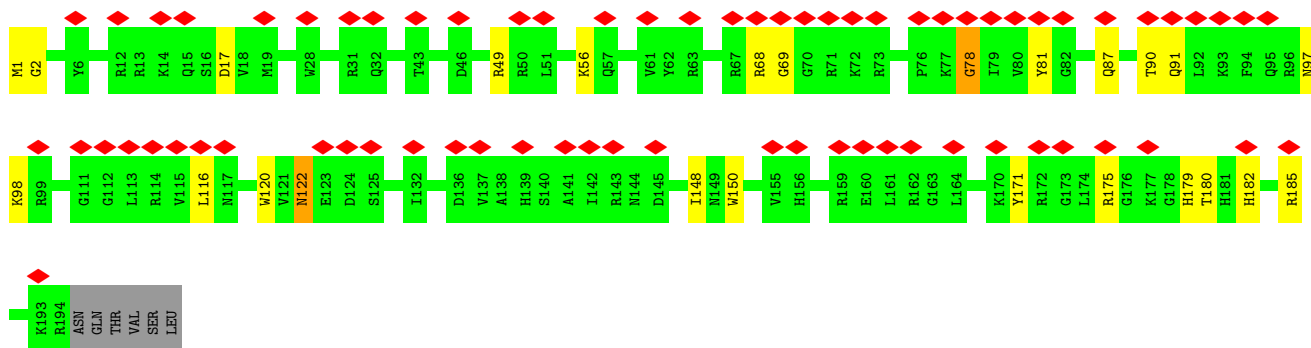
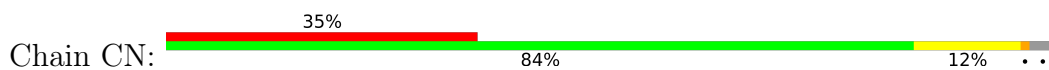
• Molecule 43: 60S ribosomal protein L6



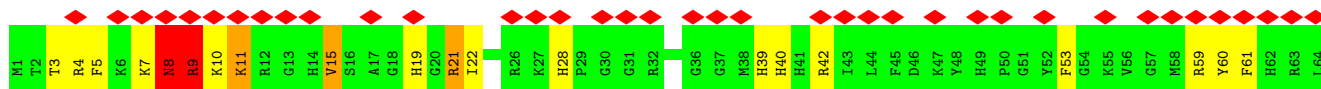
• Molecule 44: 60S ribosomal protein L14

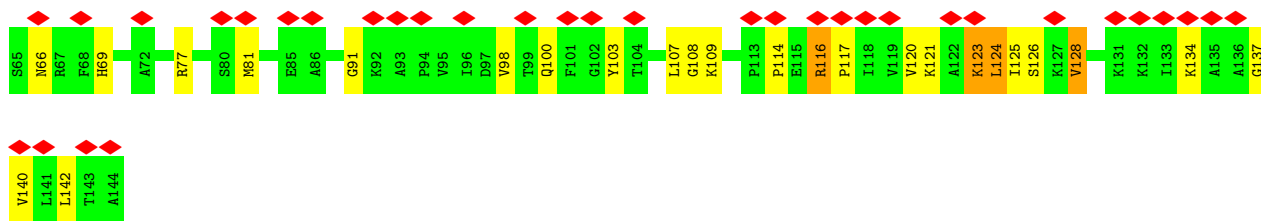


• Molecule 45: 60S ribosomal protein L15E

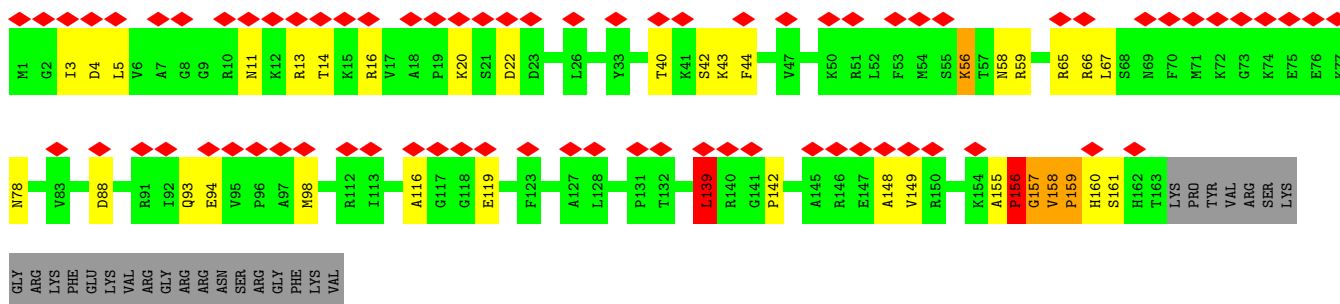
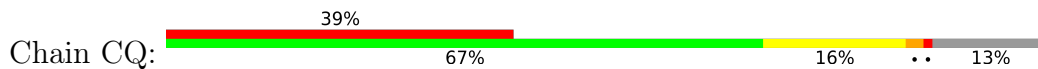


• Molecule 46: 60S ribosomal protein L15

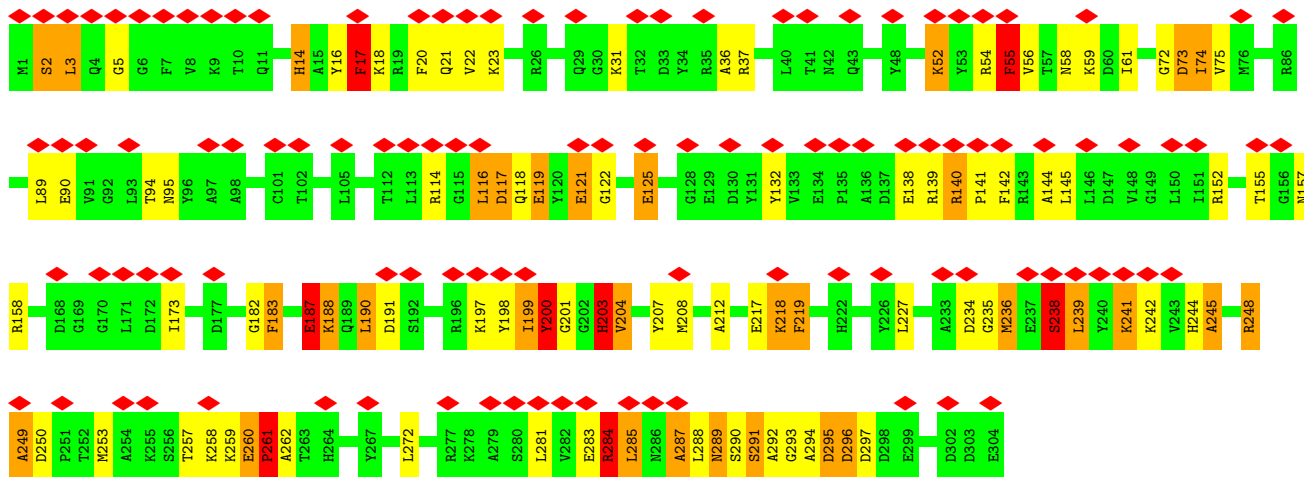




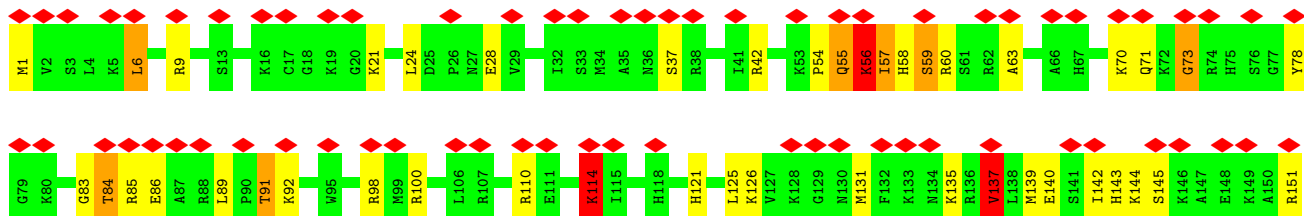
• Molecule 47: 60S ribosomal protein L18E

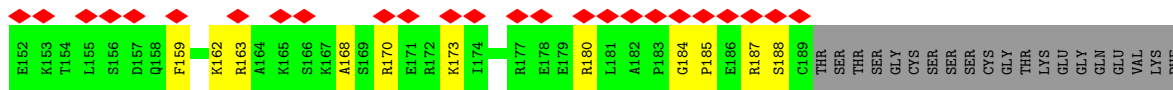


• Molecule 48: 60S ribosomal protein L18

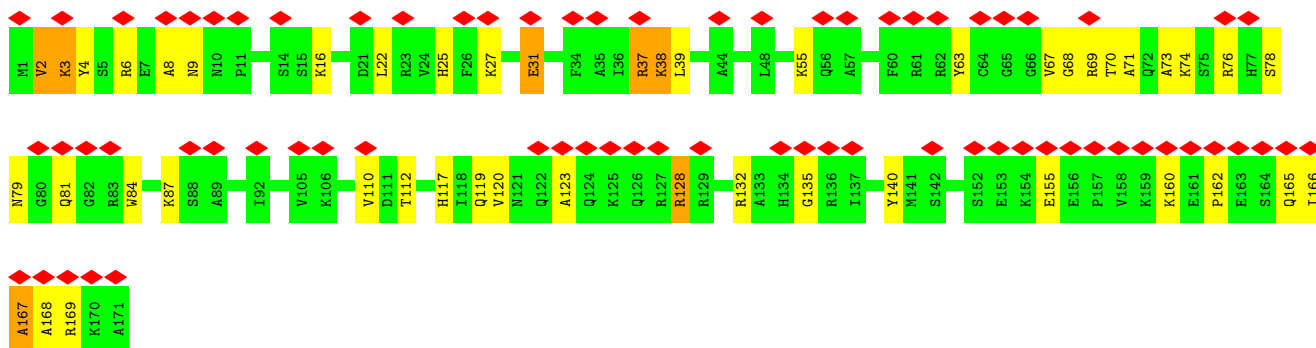
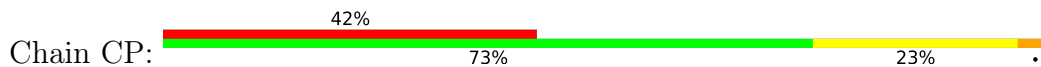


• Molecule 49: 60S ribosomal protein L19E

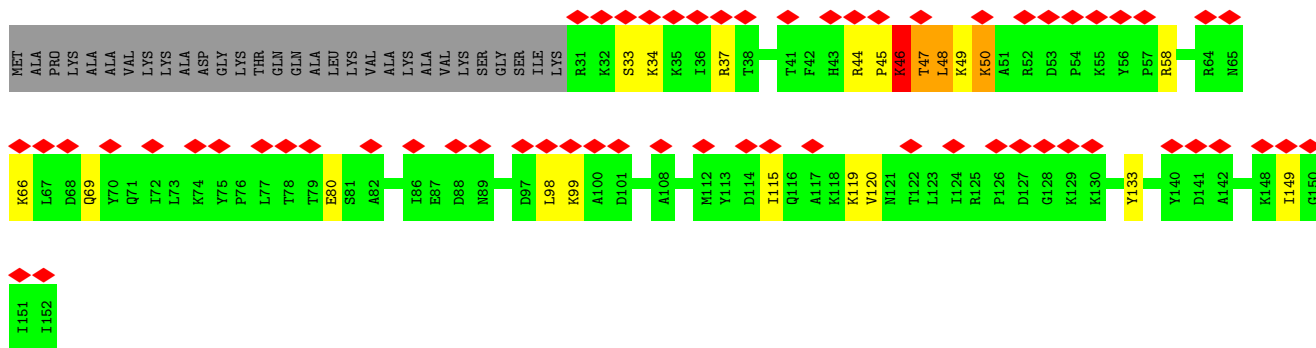
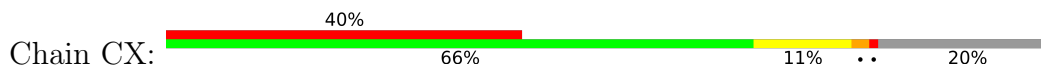




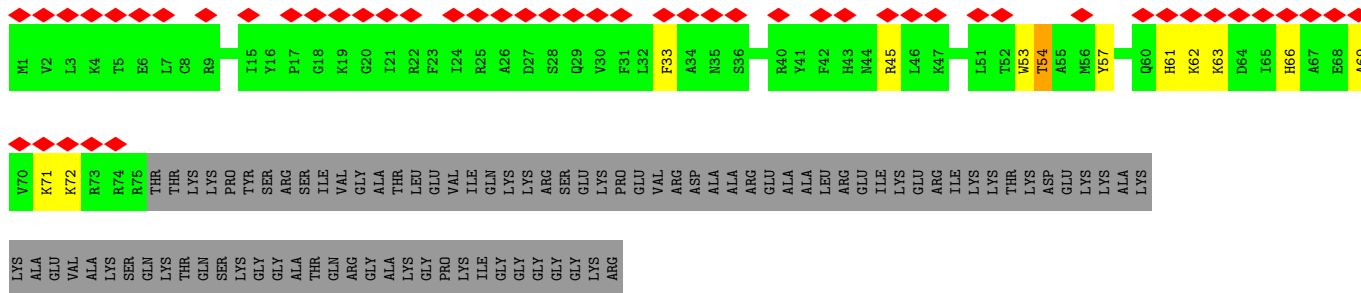
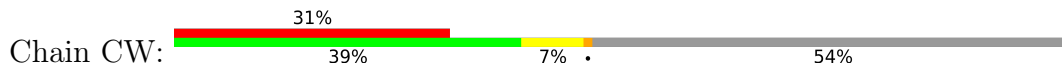
• Molecule 50: 60S ribosomal protein L22



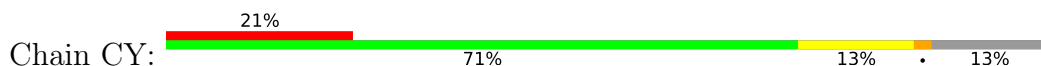
• Molecule 51: 60S ribosomal protein L23

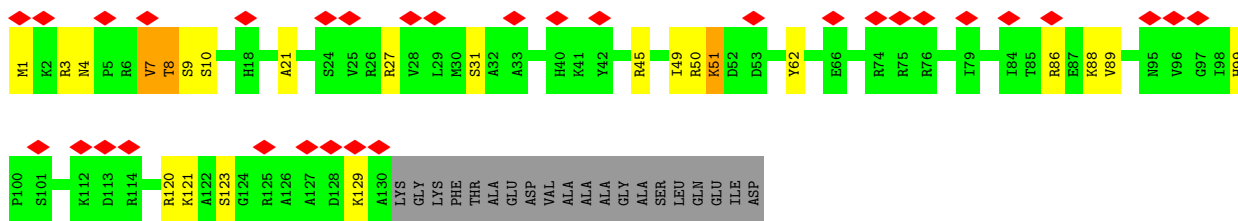


• Molecule 52: 60S ribosomal protein L24E

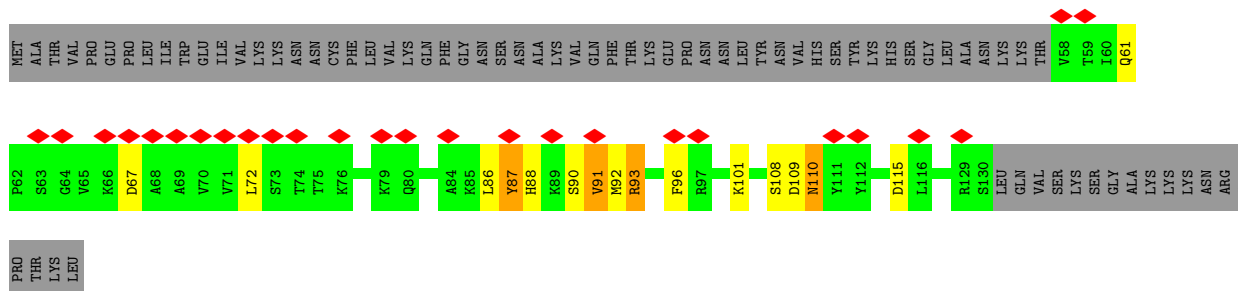
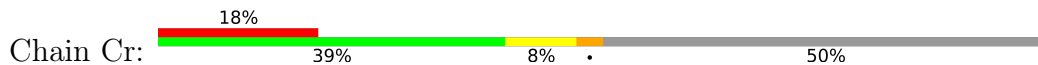


• Molecule 53: 60S ribosomal protein L24

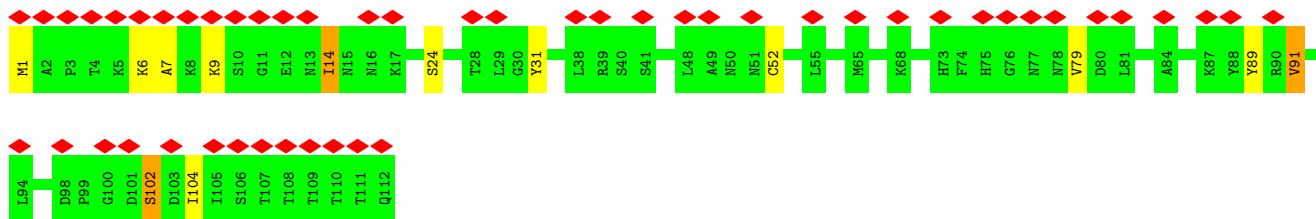
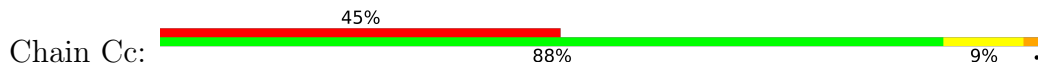




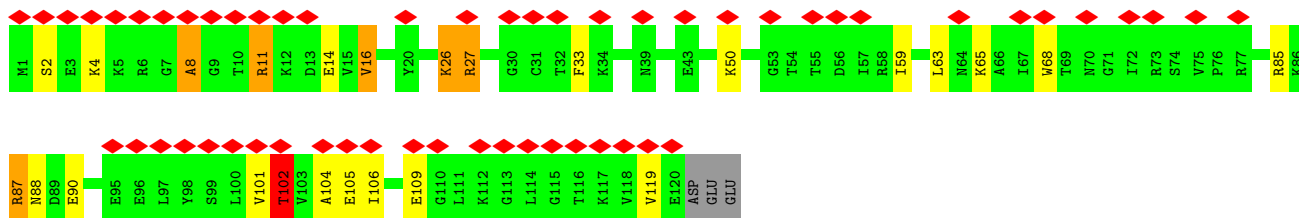
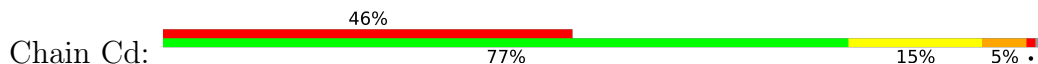
• Molecule 54: 60S ribosomal protein L28E



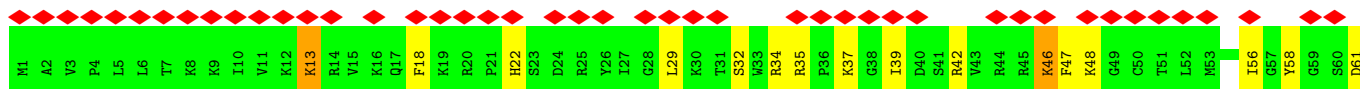
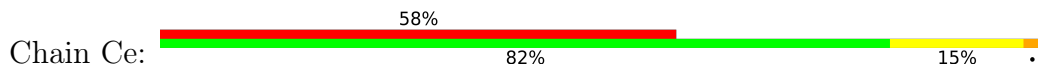
• Molecule 55: 60S ribosomal protein L30E

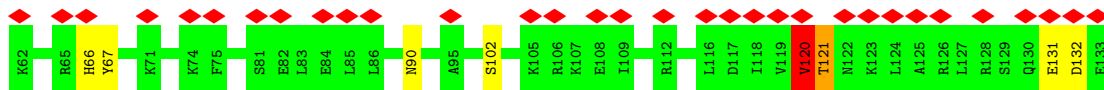


• Molecule 56: 60S ribosomal protein L31E

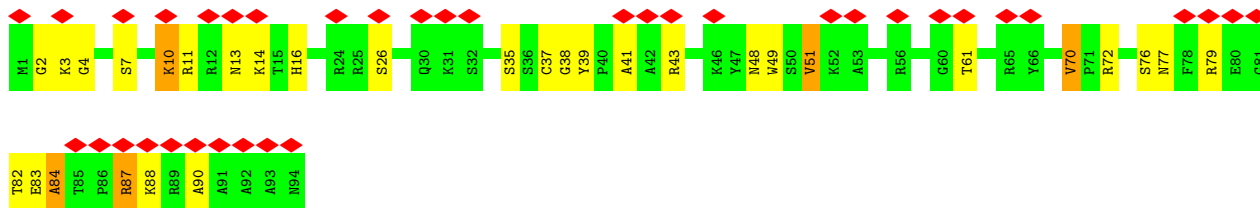
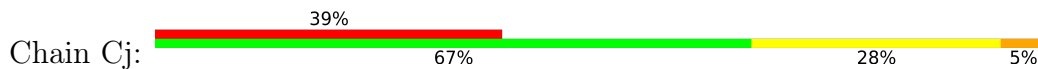


• Molecule 57: 60S ribosomal protein L32E

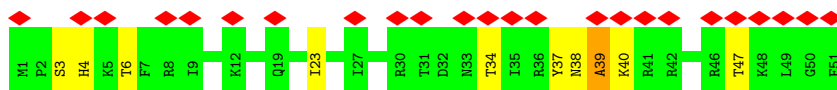
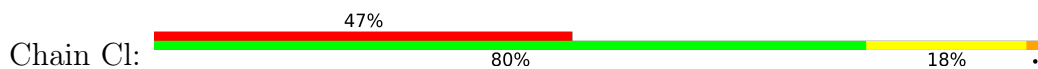




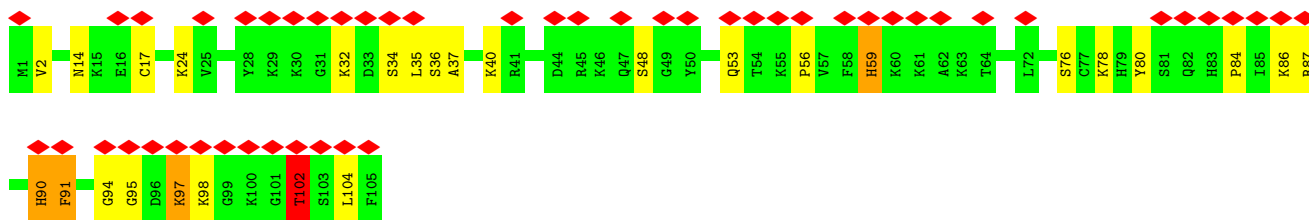
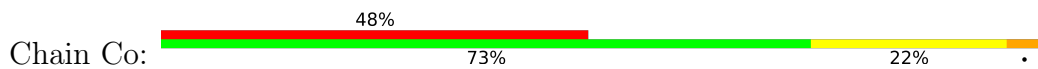
• Molecule 58: 60S ribosomal protein L37E



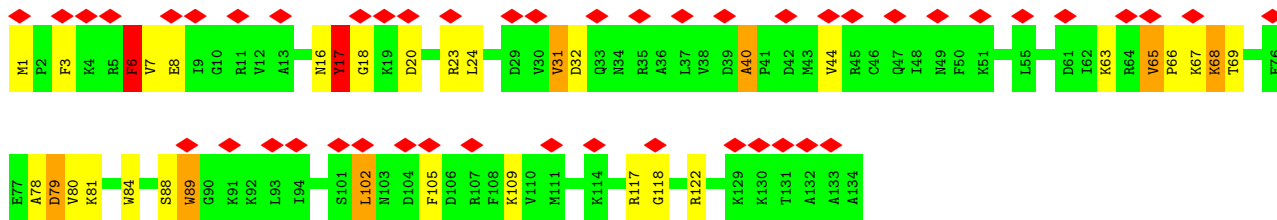
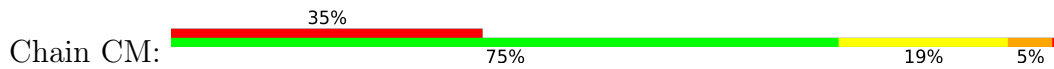
• Molecule 59: 60S ribosomal protein L39E



• Molecule 60: 60S ribosomal protein L44E

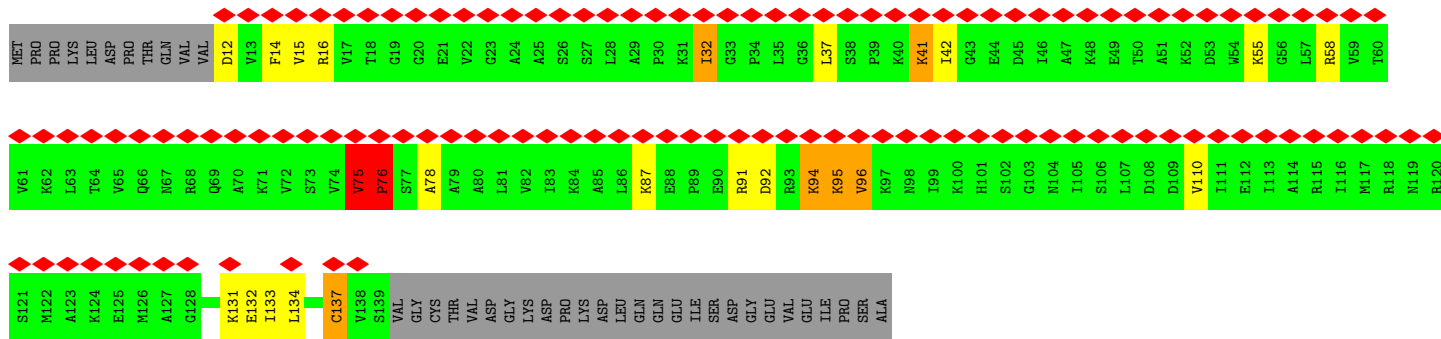
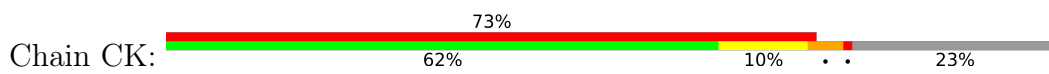
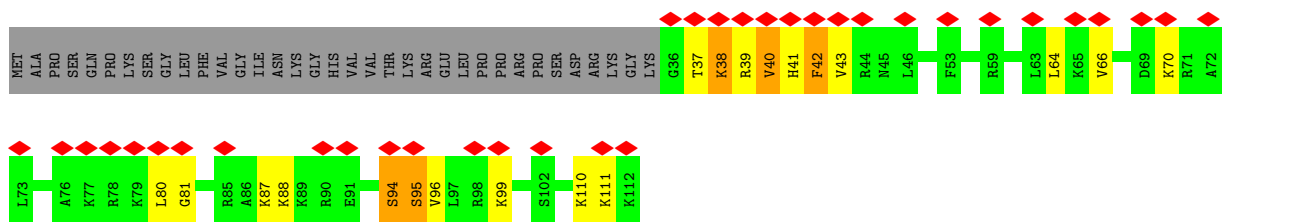
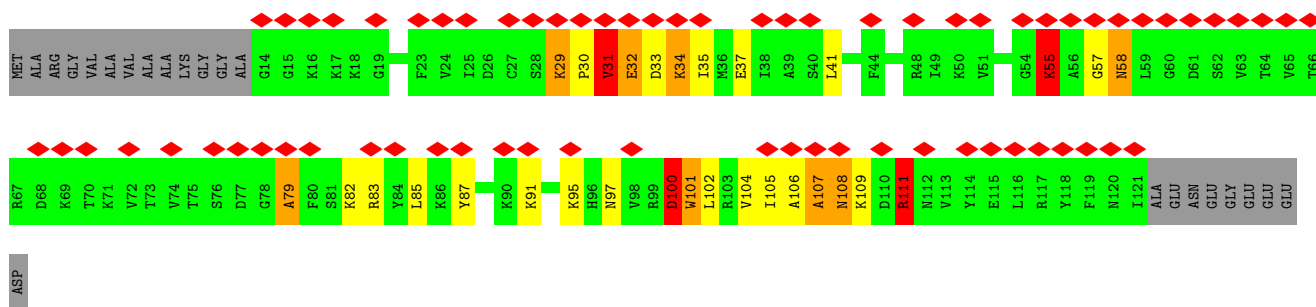
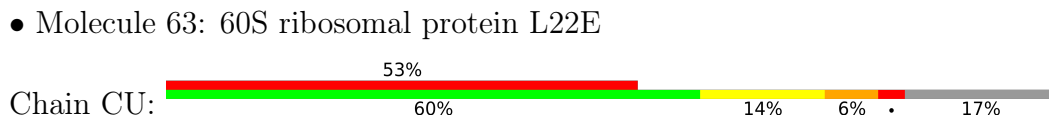
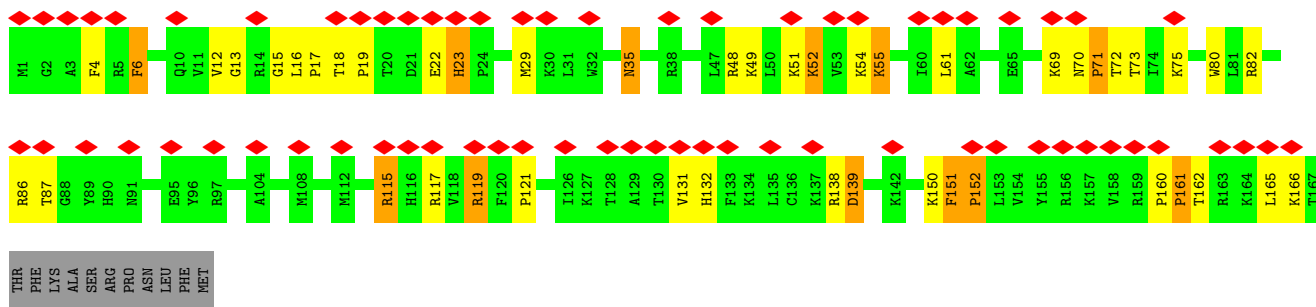


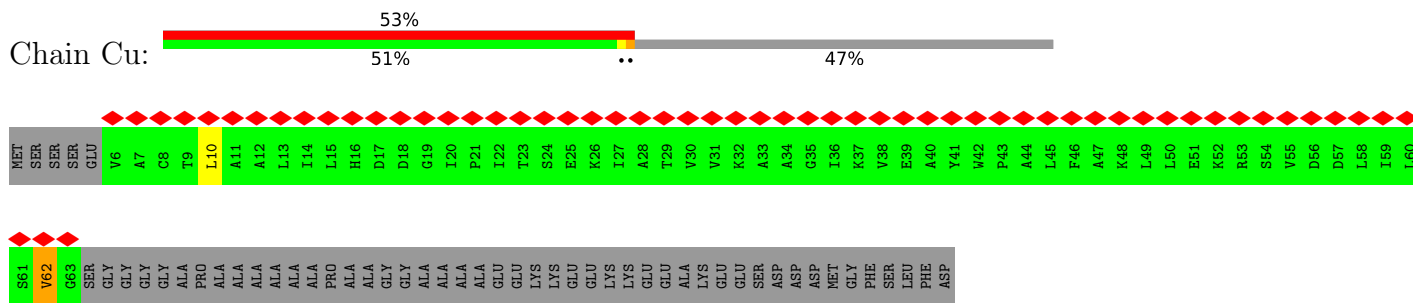
• Molecule 61: 60S ribosomal protein L14E



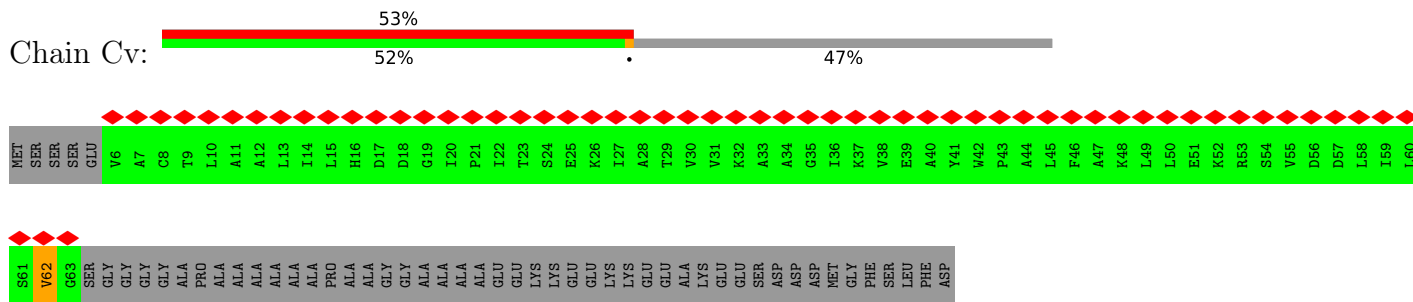
• Molecule 62: 60S ribosomal protein L20



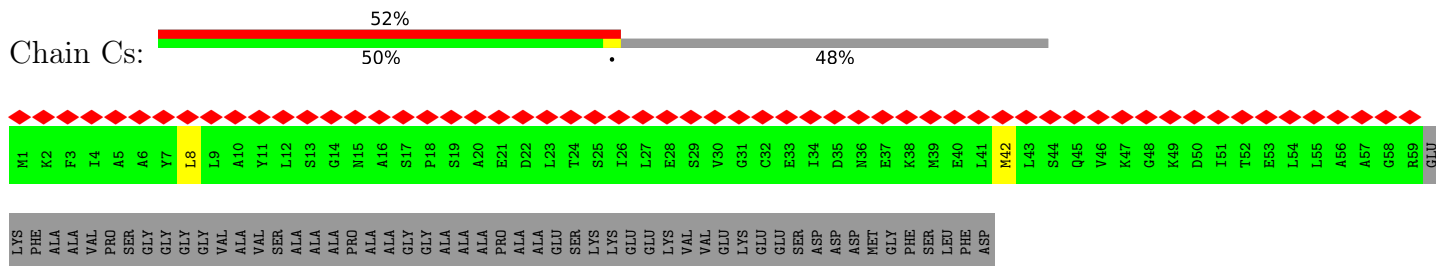




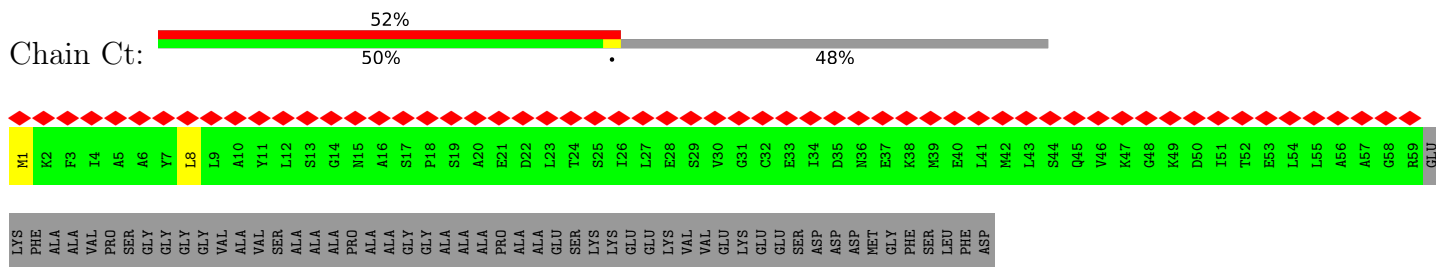
• Molecule 66: 60S ribosomal protein P1



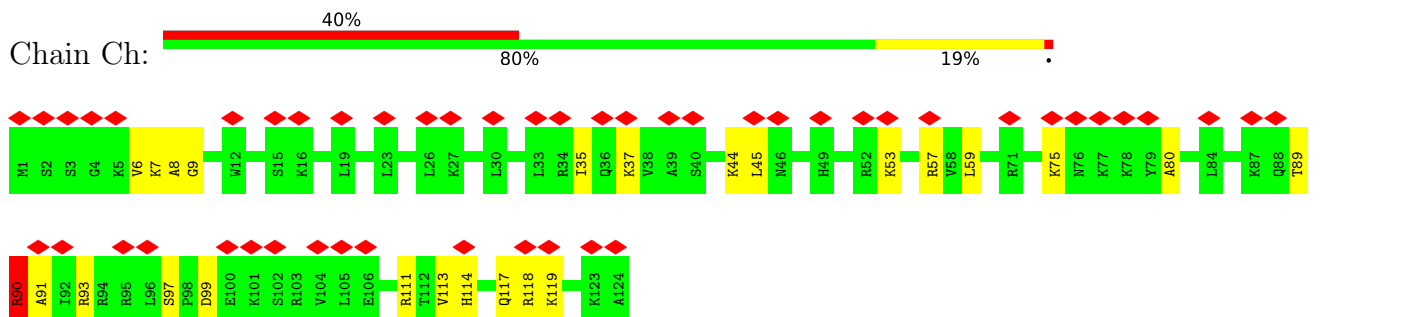
• Molecule 67: Acidic ribosomal protein P2



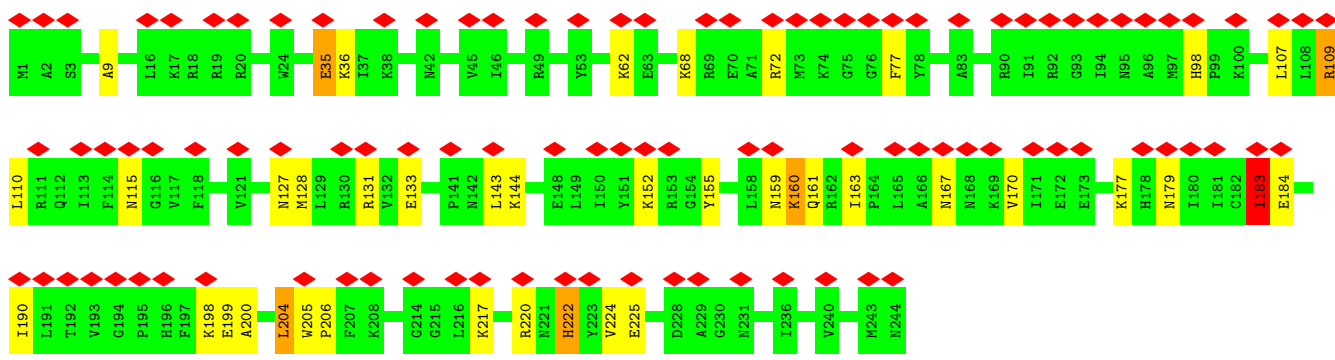
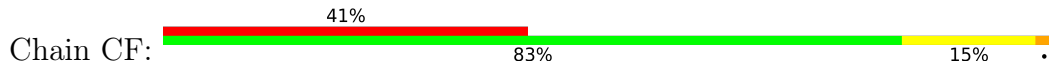
• Molecule 67: Acidic ribosomal protein P2



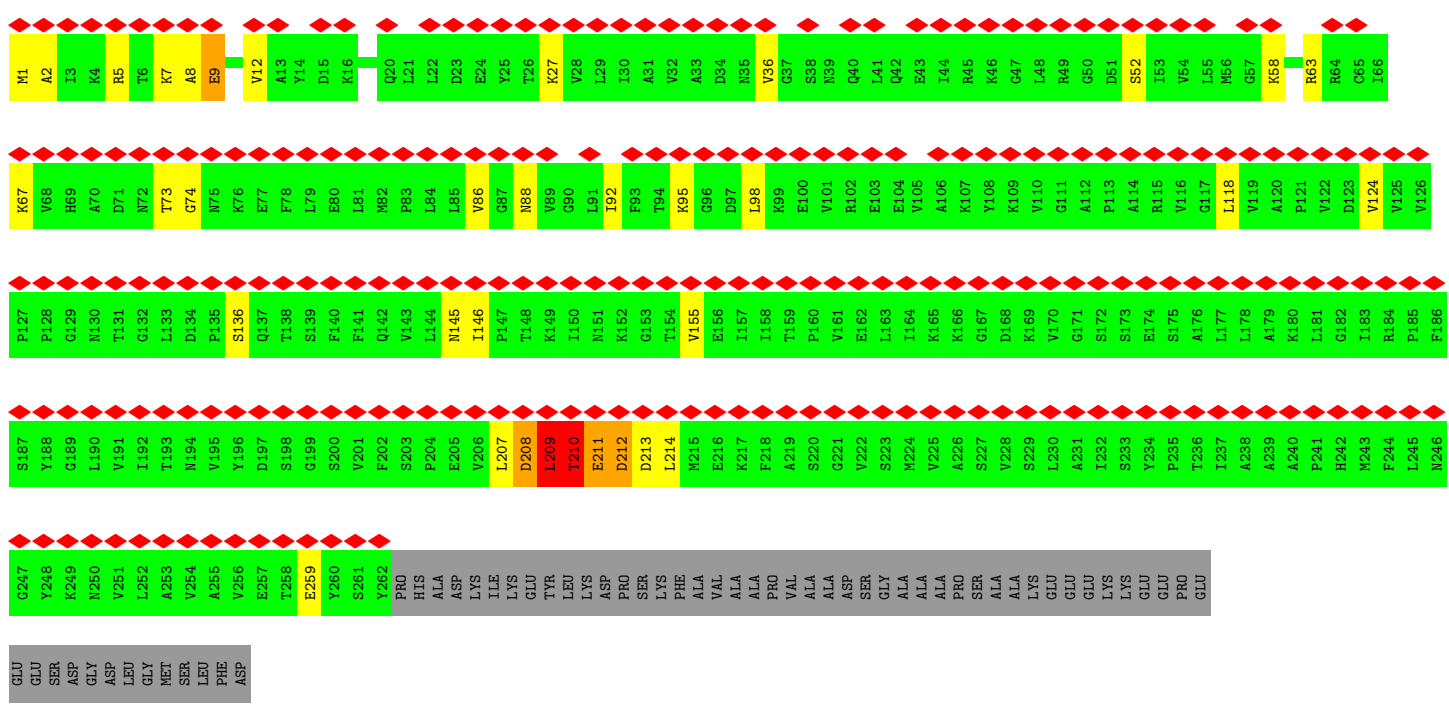
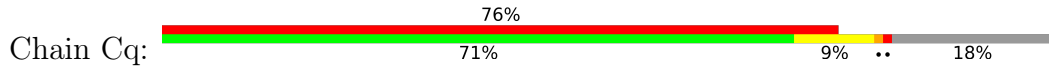
• Molecule 68: 60S ribosomal protein L29



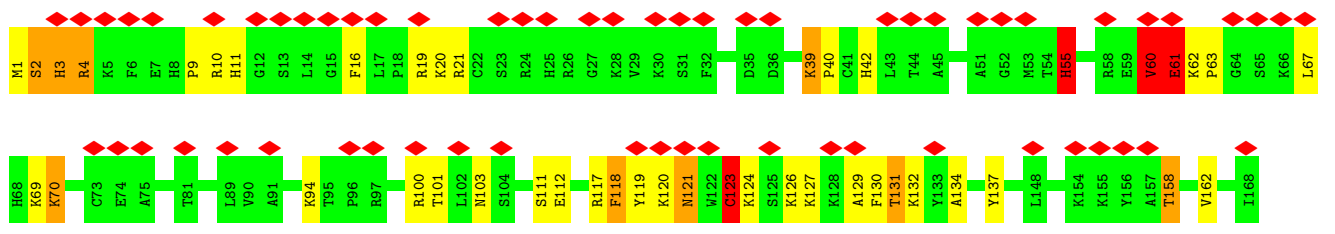
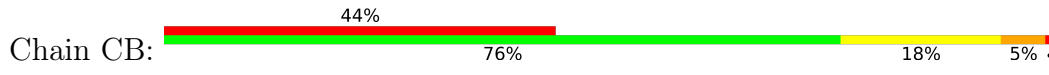
• Molecule 69: 60S ribosomal protein L30

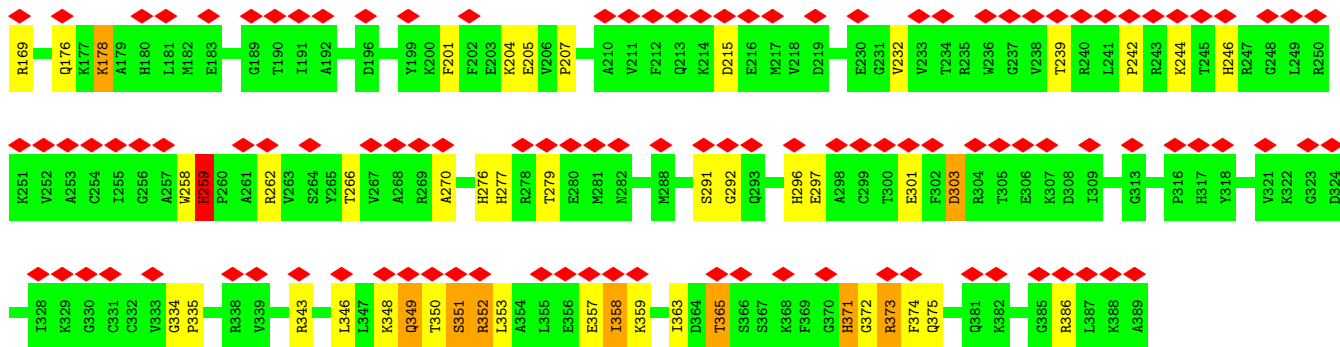


• Molecule 70: 60S acidic ribosomal protein P0

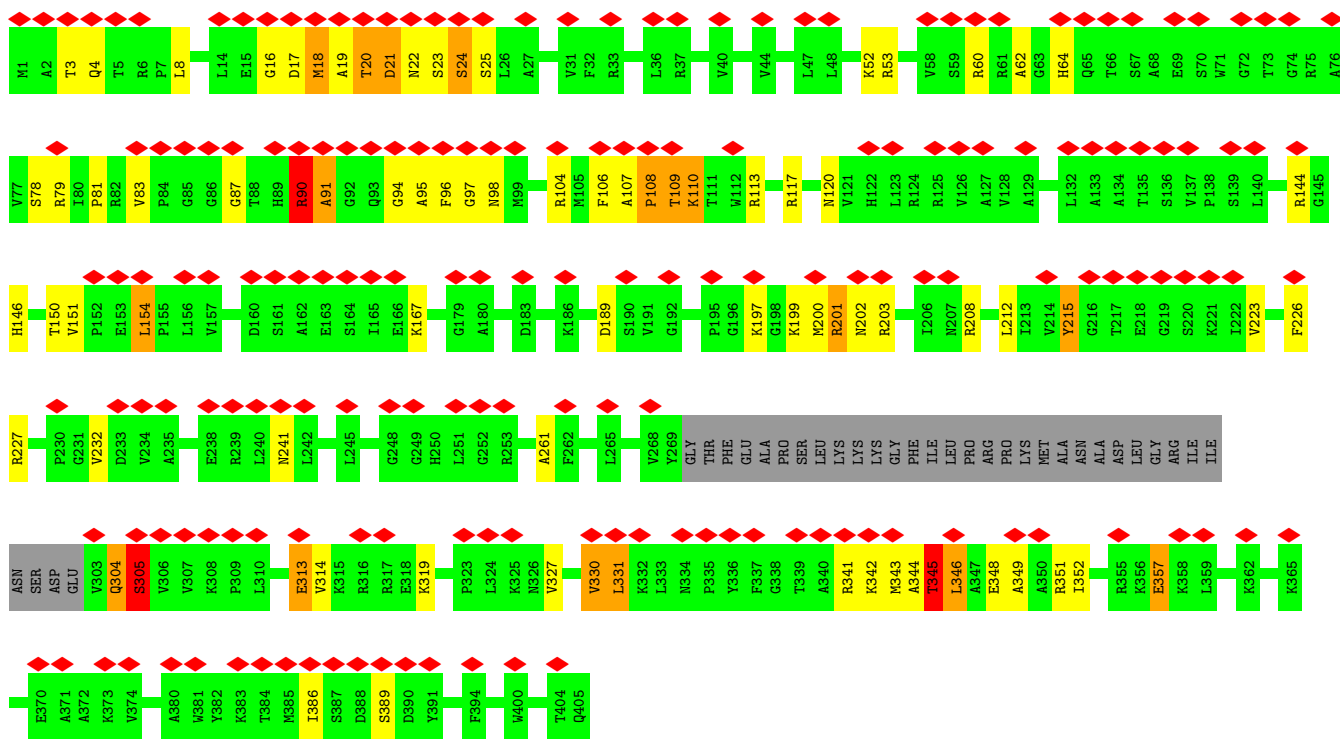
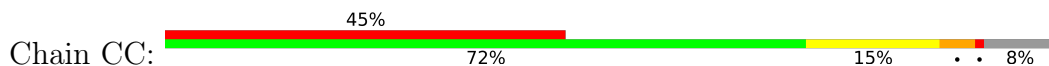


• Molecule 71: 60S ribosomal protein L3

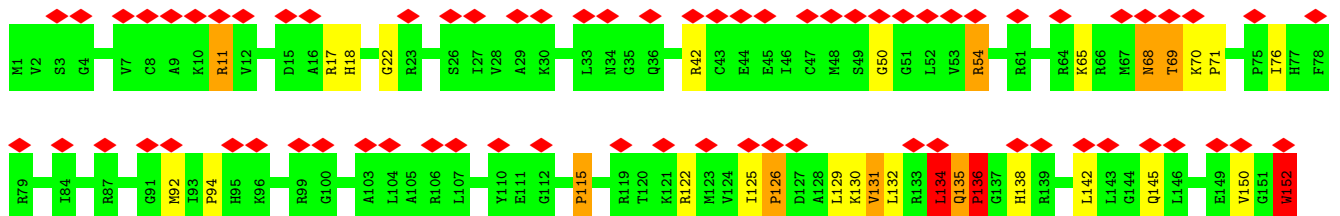
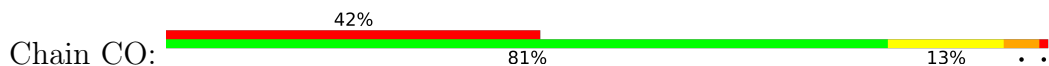


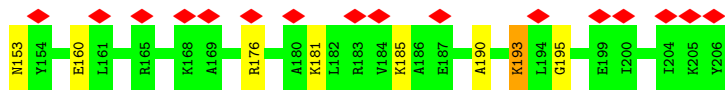


• Molecule 72: 60S ribosomal protein L4

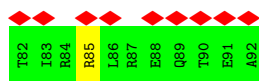
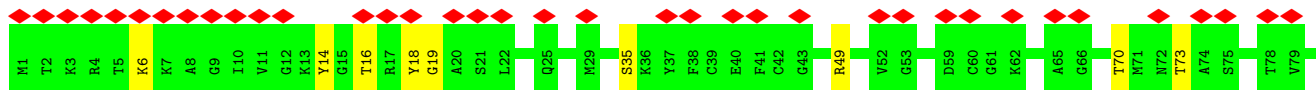
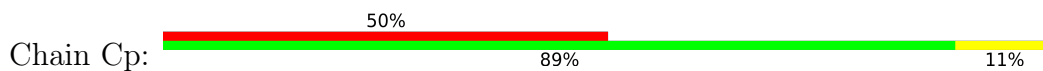


• Molecule 73: 60S ribosomal protein L13

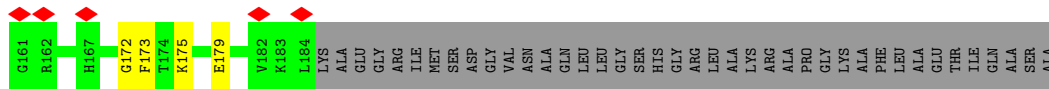
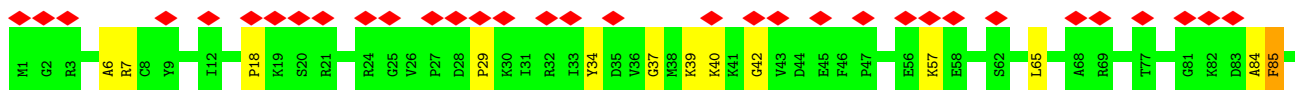




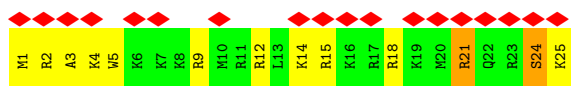
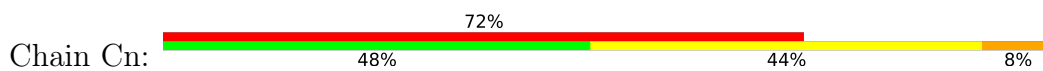
• Molecule 74: 60S ribosomal protein L43E



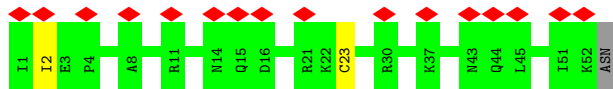
• Molecule 75: 60S ribosomal protein L16



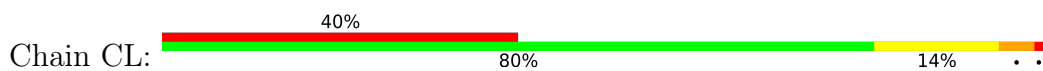
• Molecule 76: 60S ribosomal protein L41E

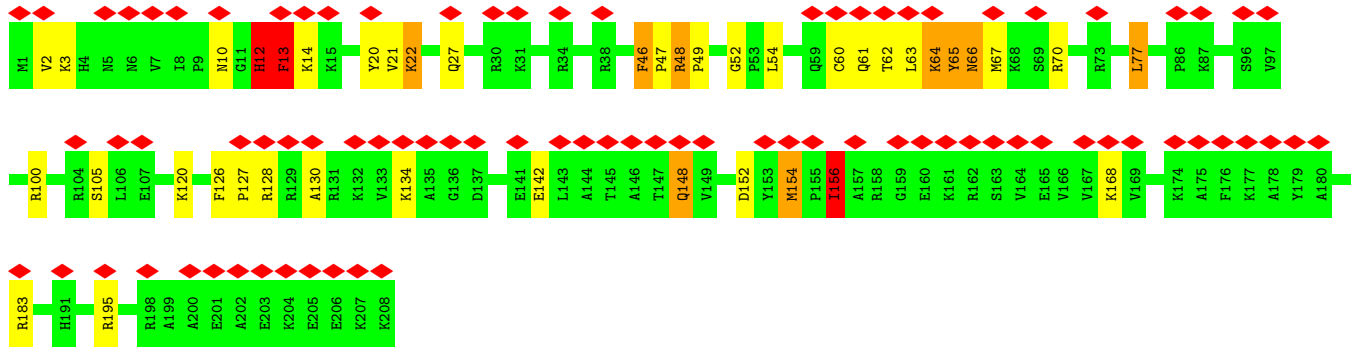


• Molecule 77: 60S ribosomal protein L40E

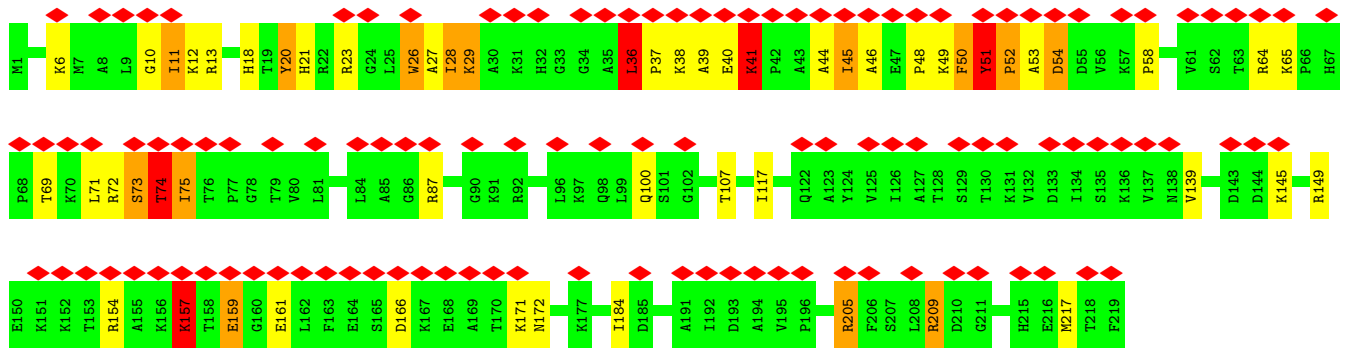
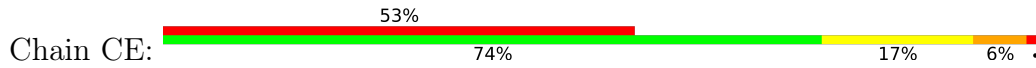


• Molecule 78: 60S ribosomal protein L13E

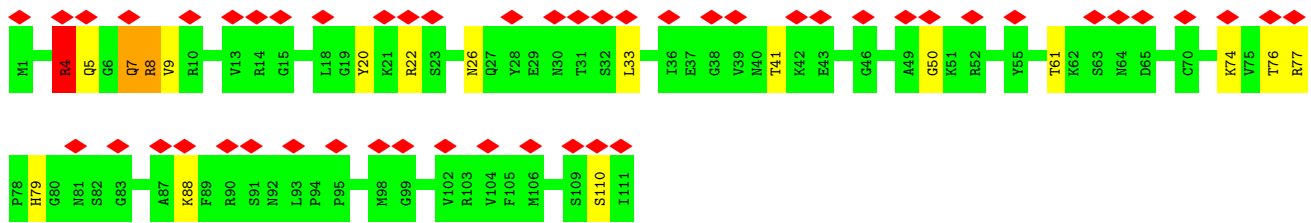
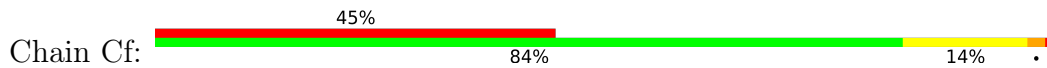




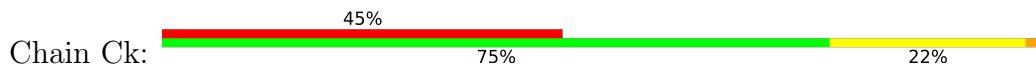
- Molecule 79: 60S ribosomal protein L6E



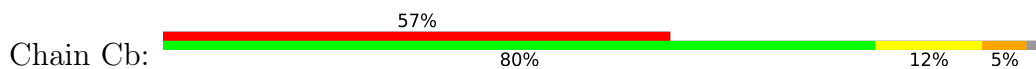
- Molecule 80: 60S ribosomal protein L33E

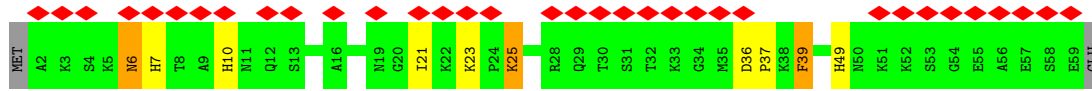


- Molecule 81: 60S ribosomal protein L38E

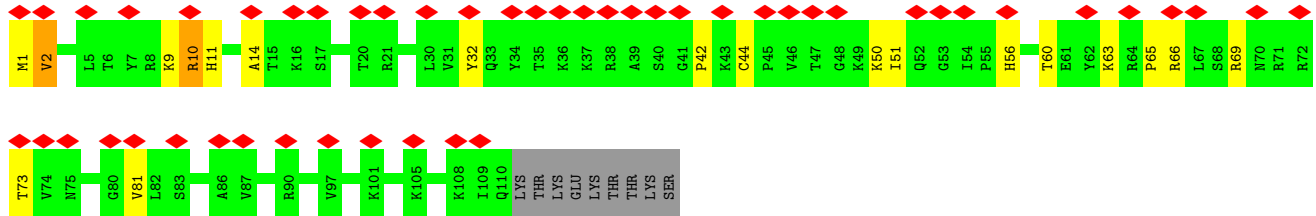
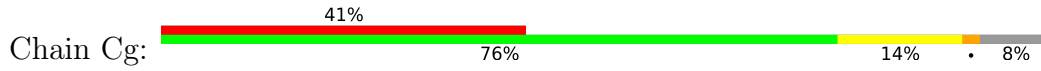


- Molecule 82: 60S ribosomal protein L29E

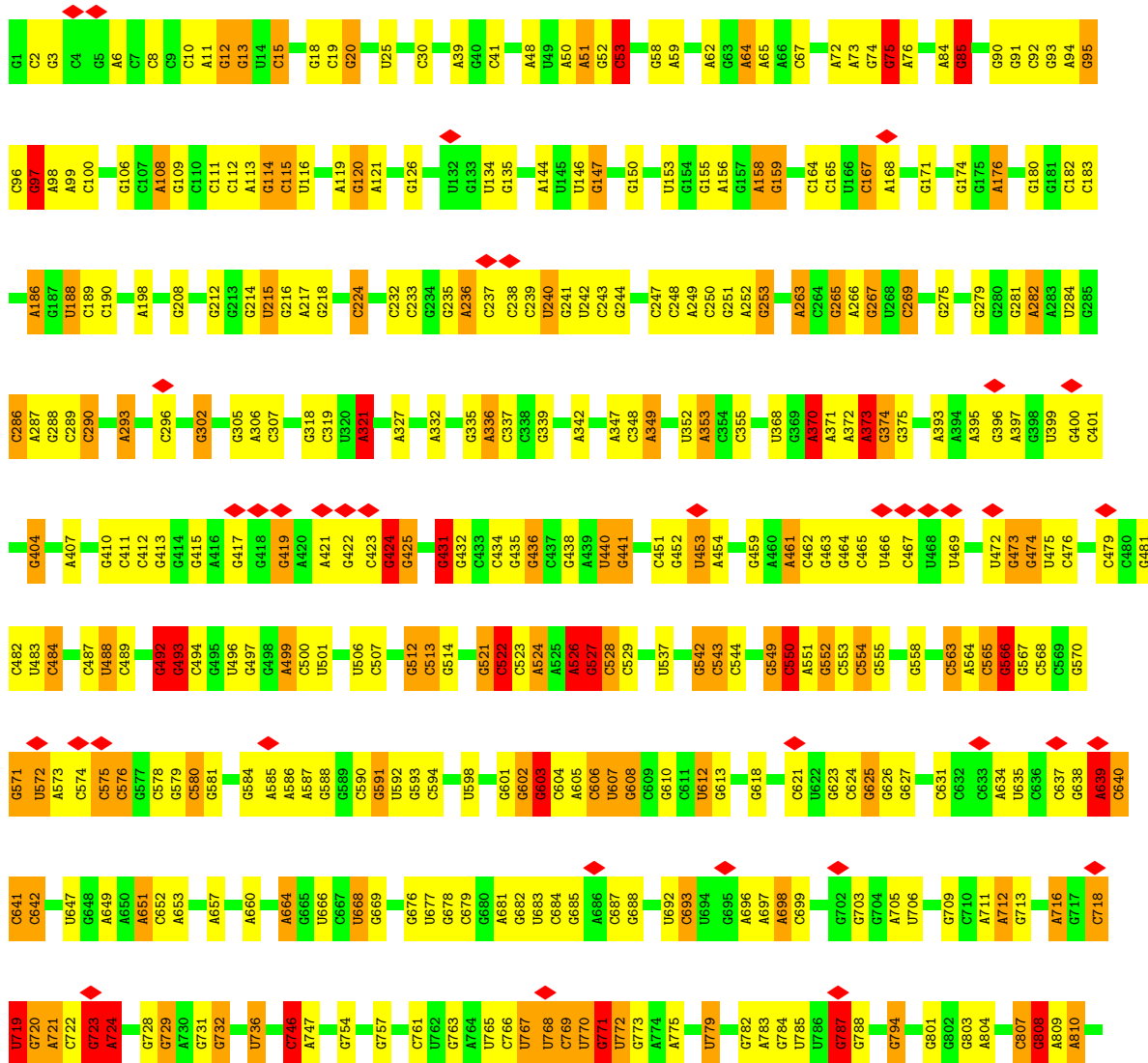


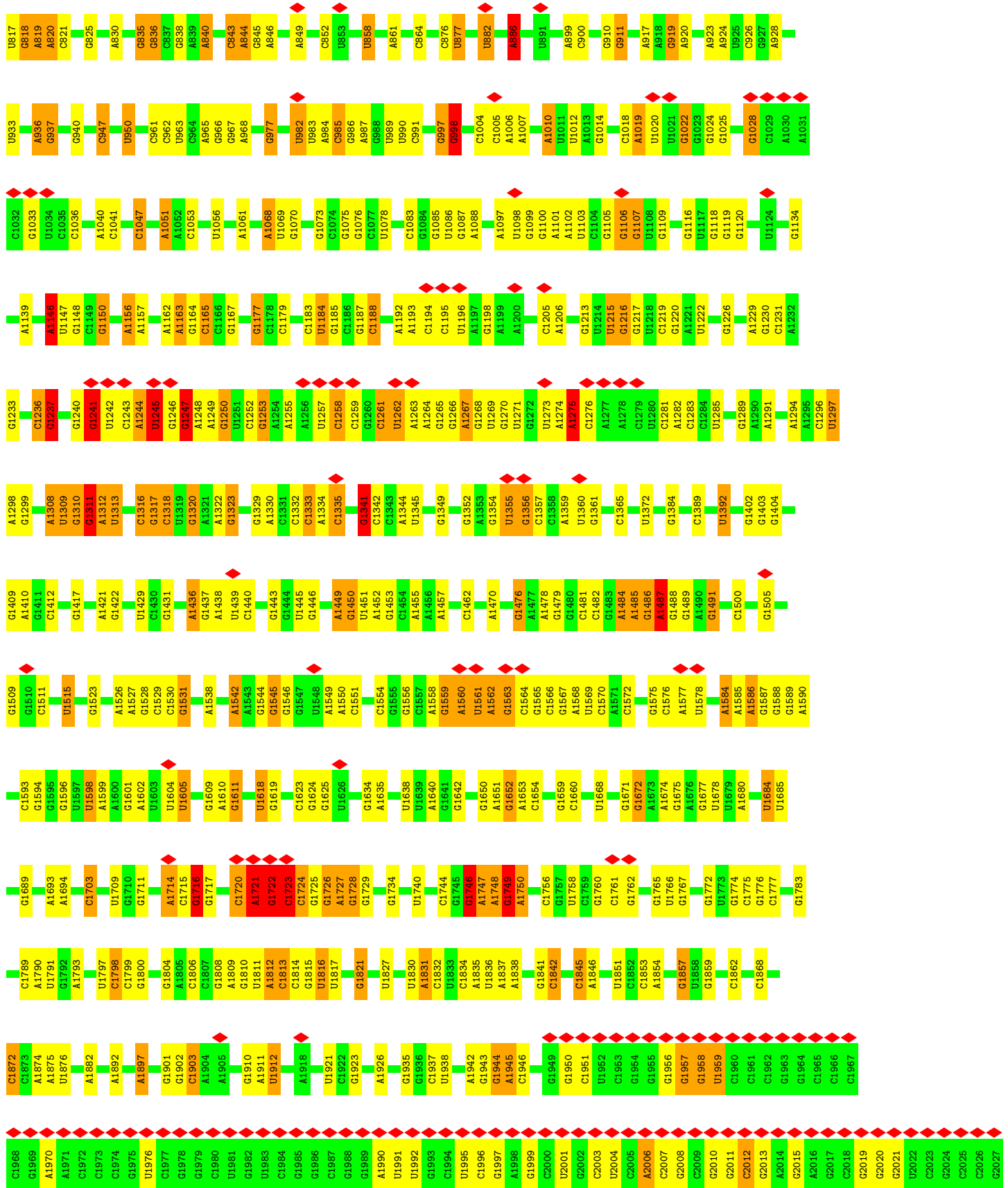


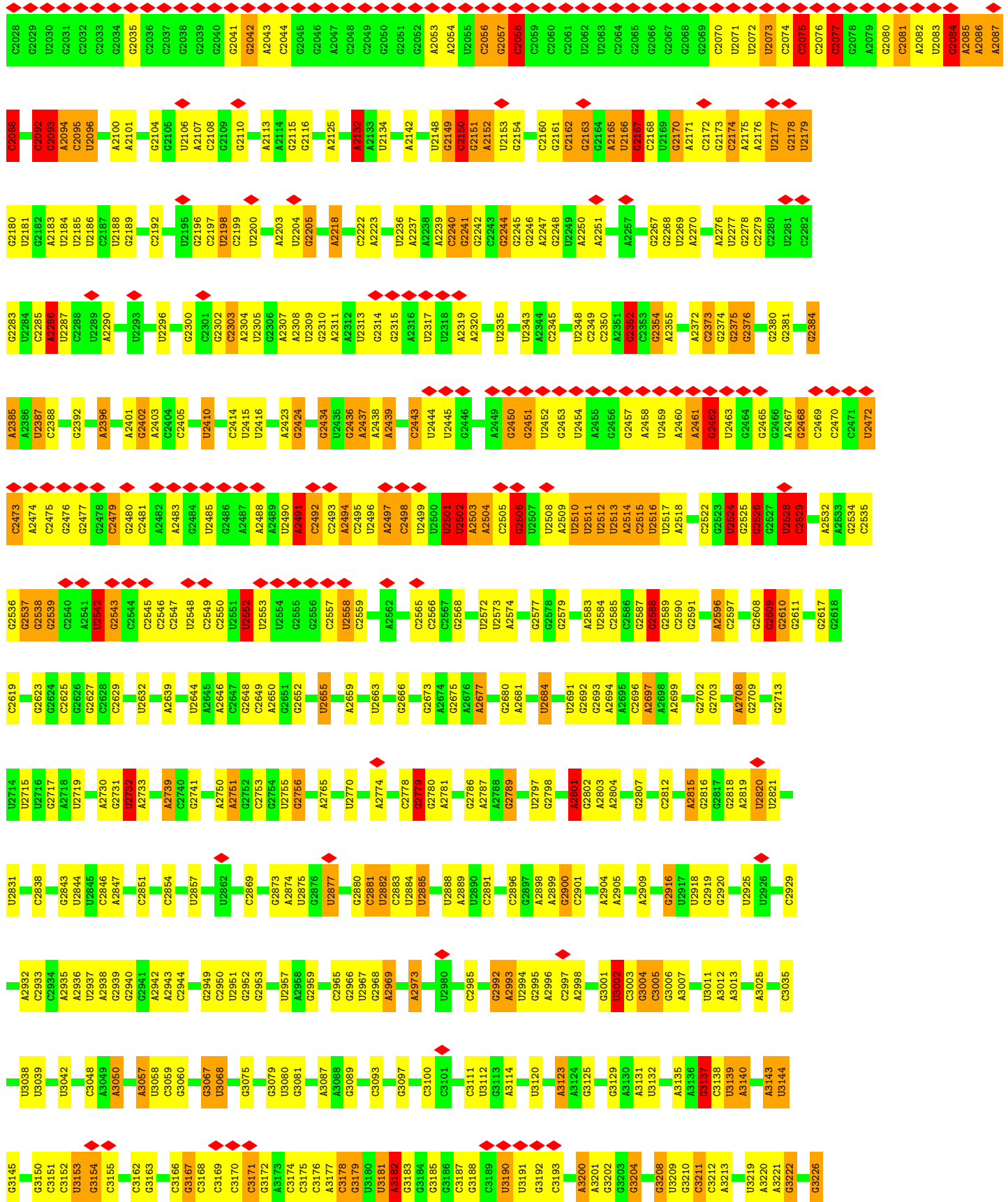
• Molecule 83: 60S ribosomal protein L34E

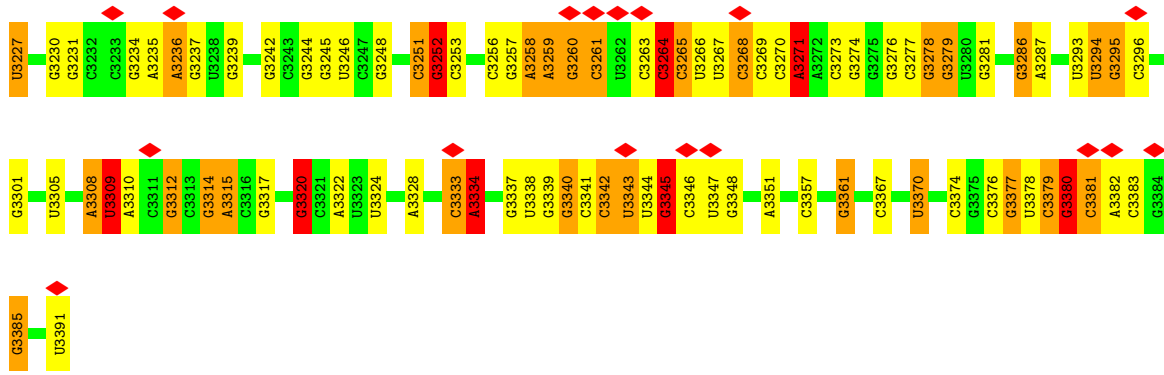


• Molecule 84: 60S ribosomal RNA

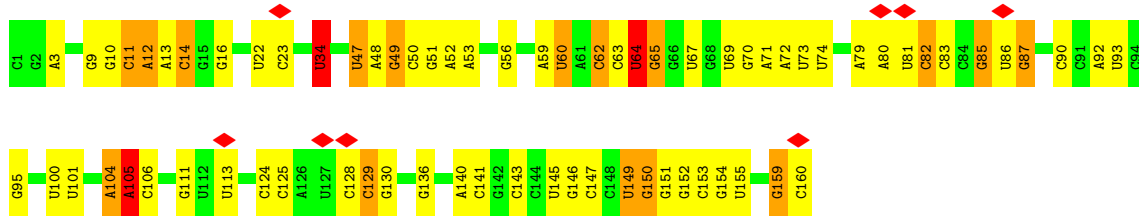




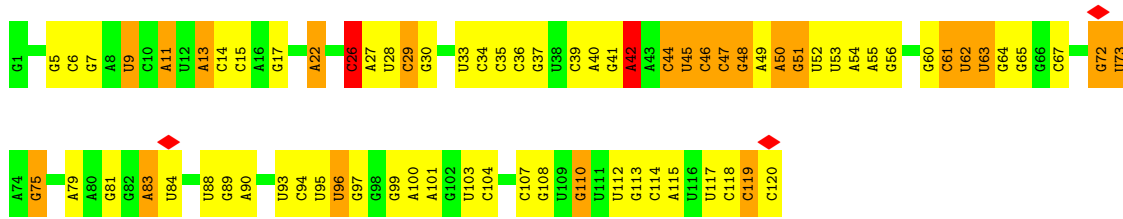




• Molecule 85: 5.8S ribosomal RNA



• 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 ( $\text{\AA}$ )	455.4, 455.4, 455.4	wwPDB
Map dimensions	368, 368, 368	wwPDB
Map angles ( $^\circ$ )	90, 90, 90	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.2375, 1.2375, 1.2375	Depositor

## 5 Model quality i

### 5.1 Standard geometry i

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	Ad	1.98	1479/42036 (3.5%)	1.78	1718/65520 (2.6%)
2	Ae	2.08	74/1781 (4.2%)	1.86	83/2775 (3.0%)
3	Af	1.99	10/260 (3.8%)	1.78	11/403 (2.7%)
4	BY	1.24	0/1123	1.64	18/1487 (1.2%)
5	BI	1.30	0/539	1.52	2/712 (0.3%)
6	BK	1.16	0/840	1.63	14/1135 (1.2%)
7	BM	1.14	0/936	1.68	9/1260 (0.7%)
8	Bf	1.23	0/590	1.63	6/788 (0.8%)
9	BX	1.25	0/1122	1.54	5/1492 (0.3%)
10	Bg	1.26	0/2988	1.50	14/4049 (0.3%)
11	BD	1.26	0/1652	1.69	29/2222 (1.3%)
12	BE	1.25	0/1637	1.46	12/2202 (0.5%)
13	BF	1.27	0/1509	1.60	6/2034 (0.3%)
14	BQ	1.35	0/1034	1.61	16/1379 (1.2%)
15	BU	1.26	0/995	1.63	12/1338 (0.9%)
16	BO	1.32	0/909	1.67	7/1217 (0.6%)
17	BS	1.31	0/1258	1.73	23/1674 (1.4%)
18	BN	1.22	0/994	1.73	15/1332 (1.1%)
19	BL	1.34	0/704	1.52	6/944 (0.6%)
20	BT	1.25	0/1179	1.71	21/1586 (1.3%)
21	BP	1.22	0/727	1.63	5/975 (0.5%)
22	BZ	1.20	0/791	1.72	11/1057 (1.0%)
23	Bc	1.34	0/455	1.58	2/609 (0.3%)
24	BW	1.28	0/1060	1.60	13/1419 (0.9%)
25	Bd	1.34	0/386	1.81	11/510 (2.2%)
26	Bb	1.22	0/674	1.54	4/905 (0.4%)
27	Be	1.31	0/476	1.53	2/627 (0.3%)
28	BA	1.24	0/1567	1.59	7/2121 (0.3%)
29	BR	1.30	0/955	1.64	8/1273 (0.6%)
30	BB	1.24	0/1736	1.65	23/2329 (1.0%)
31	BV	1.29	0/610	1.54	6/820 (0.7%)
32	Ba	1.38	0/766	1.69	8/1023 (0.8%)
33	BJ	1.33	0/1553	1.61	11/2079 (0.5%)
34	BC	1.20	0/1701	1.51	5/2298 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
35	BG	1.31	0/1888	1.48	10/2507 (0.4%)
36	BH	3.48	2/1535 (0.1%)	1.56	20/2065 (1.0%)
37	CG	1.22	0/1939	1.61	5/2598 (0.2%)
38	CT	1.25	0/1316	1.59	9/1772 (0.5%)
39	CZ	1.26	0/1110	1.50	2/1480 (0.1%)
40	Cz	1.18	0/1741	1.57	12/2323 (0.5%)
41	CA	1.34	0/1992	1.64	24/2681 (0.9%)
42	CJ	1.30	0/1401	1.65	14/1869 (0.7%)
43	CH	1.27	0/1519	1.43	8/2042 (0.4%)
44	CV	1.27	0/1064	1.50	8/1425 (0.6%)
45	CN	1.36	0/1669	1.49	5/2235 (0.2%)
46	Ca	1.27	0/1143	1.72	17/1527 (1.1%)
47	CQ	1.32	0/1303	1.59	16/1748 (0.9%)
48	CD	1.26	0/2489	1.74	61/3342 (1.8%)
49	CR	1.35	0/1590	1.67	15/2100 (0.7%)
50	CP	1.32	0/1397	1.58	12/1871 (0.6%)
51	CX	1.16	0/1002	1.48	4/1340 (0.3%)
52	CW	1.31	0/649	1.51	7/861 (0.8%)
53	CY	1.38	0/1061	1.54	6/1418 (0.4%)
54	Cr	1.21	0/585	1.56	6/786 (0.8%)
55	Cc	1.13	0/869	1.59	6/1169 (0.5%)
56	Cd	1.28	0/970	1.60	9/1295 (0.7%)
57	Ce	1.28	0/1122	1.67	8/1497 (0.5%)
58	Cj	1.41	0/769	1.64	8/1019 (0.8%)
59	Cl	1.38	0/472	1.63	3/627 (0.5%)
60	Co	1.25	0/867	1.63	7/1144 (0.6%)
61	CM	1.26	0/1094	1.65	20/1461 (1.4%)
62	CS	1.27	0/1457	1.63	17/1957 (0.9%)
63	CU	1.25	0/876	1.61	10/1170 (0.9%)
64	Ci	1.33	0/618	1.79	11/809 (1.4%)
65	CK	1.20	0/968	1.71	13/1299 (1.0%)
66	Cu	1.07	0/438	1.62	1/596 (0.2%)
66	Cv	1.10	0/438	1.64	1/596 (0.2%)
67	Cs	1.08	0/444	1.50	2/596 (0.3%)
67	Ct	1.08	0/444	1.55	0/596
68	Ch	1.27	0/1023	1.62	9/1359 (0.7%)
69	CF	1.24	1/2020 (0.0%)	1.58	18/2708 (0.7%)
70	Cq	1.14	0/2023	1.54	10/2739 (0.4%)
71	CB	1.27	1/3207 (0.0%)	1.62	39/4289 (0.9%)
72	CC	1.27	0/2951	1.64	34/3972 (0.9%)
73	CO	1.30	0/1678	1.66	22/2246 (1.0%)
74	Cp	1.25	0/724	1.48	3/958 (0.3%)
75	CI	1.27	0/1523	1.50	12/2036 (0.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
76	Cn	1.57	0/239	1.34	1/302 (0.3%)
77	Cm	1.30	0/434	1.45	0/574
78	CL	1.30	0/1721	1.68	16/2299 (0.7%)
79	CE	1.21	0/1766	1.69	27/2374 (1.1%)
80	Cf	1.28	0/908	1.36	4/1215 (0.3%)
81	Ck	1.26	0/572	1.63	8/763 (1.0%)
82	Cb	1.27	0/486	1.73	5/641 (0.8%)
83	Cg	1.30	0/913	1.45	2/1223 (0.2%)
84	Aa	0.93	7/81235 (0.0%)	1.30	599/126706 (0.5%)
85	Ac	0.93	0/3809	1.21	14/5936 (0.2%)
86	Ab	1.37	1/2864 (0.0%)	1.38	16/4464 (0.4%)
All	All	1.36	1575/227878 (0.7%)	1.53	3359/334219 (1.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
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

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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 1575 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	BH	117	ARG	CZ-NH2	126.76	2.98	1.33
1	Ad	843	G	O4'-C1'	18.72	1.69	1.41
1	Ad	1810	G	O4'-C1'	18.20	1.69	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Ad	1080	C	O4'-C1'	17.82	1.68	1.41
1	Ad	1203	G	C2'-C1'	17.27	1.79	1.53

The worst 5 of 3359 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
84	Aa	1957	G	C4'-C3'-O3'	27.86	154.79	113.00
84	Aa	2084	G	C4'-C3'-O3'	27.56	154.34	113.00
84	Aa	2178	G	C4'-C3'-O3'	-23.61	77.58	113.00
1	Ad	67	G	N9-C1'-C2'	21.91	146.87	114.00
84	Aa	2162	C	P-O3'-C3'	21.77	152.86	120.20

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](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Ad	37584	0	18947	2056	0
2	Ae	1595	0	808	33	0
3	Af	232	0	121	22	0
4	BY	1108	0	1200	99	0
5	BI	533	0	551	27	0
6	BK	818	0	831	1	0
7	BM	924	0	939	15	0
8	Bf	577	0	589	84	0
9	BX	1103	0	1170	114	0
10	Bg	2929	0	2843	4	0
11	BD	1629	0	1694	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	BE	1607	0	1678	99	0
13	BF	1489	0	1537	43	0
14	BQ	1017	0	1080	65	0
15	BU	982	0	1032	38	0
16	BO	899	0	936	16	0
17	BS	1240	0	1293	108	0
18	BN	977	0	1057	113	0
19	BL	688	0	704	66	0
20	BT	1155	0	1175	33	0
21	BP	711	0	759	40	0
22	BZ	779	0	833	47	0
23	Bc	454	0	489	9	0
24	BW	1042	0	1086	43	0
25	Bd	379	0	378	24	0
26	Bb	663	0	680	61	0
27	Be	469	0	506	29	0
28	BA	1537	0	1557	15	0
29	BR	945	0	1002	38	0
30	BB	1707	0	1783	6	0
31	BV	601	0	588	0	0
32	Ba	753	0	769	105	0
33	BJ	1525	0	1600	88	0
34	BC	1665	0	1751	31	0
35	BG	1867	0	1990	252	0
36	BH	1508	0	1572	63	0
37	CG	1906	0	2064	10	0
38	CT	1288	0	1341	17	0
39	CZ	1090	0	1183	5	0
40	Cz	1718	0	1841	20	0
41	CA	1946	0	1974	86	0
42	CJ	1380	0	1422	66	0
43	CH	1500	0	1564	3	0
44	CV	1048	0	1116	4	0
45	CN	1630	0	1704	16	0
46	Ca	1114	0	1166	19	0
47	CQ	1284	0	1376	9	0
48	CD	2444	0	2418	102	0
49	CR	1569	0	1695	72	0
50	CP	1372	0	1410	23	0
51	CX	987	0	1082	57	0
52	CW	635	0	677	3	0
53	CY	1048	0	1130	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
54	Cr	576	0	616	6	0
55	Cc	857	0	904	11	0
56	Cd	960	0	1025	14	0
57	Ce	1103	0	1177	23	0
58	Cj	755	0	782	14	0
59	Cl	460	0	490	2	0
60	Co	851	0	909	7	0
61	CM	1081	0	1171	29	0
62	CS	1419	0	1466	34	0
63	CU	864	0	910	30	0
64	Ci	613	0	684	4	0
65	CK	960	0	1042	2	0
66	Cu	432	0	463	0	0
66	Cv	432	0	463	0	0
67	Cs	441	0	453	0	0
67	Ct	441	0	453	0	0
68	Ch	1012	0	1112	10	0
69	CF	1984	0	2092	26	0
70	Cq	1993	0	2086	19	0
71	CB	3139	0	3258	32	0
72	CC	2898	0	3023	32	0
73	CO	1650	0	1770	32	0
74	Cp	715	0	758	9	0
75	CI	1490	0	1539	50	0
76	Cn	238	0	289	34	0
77	Cm	428	0	470	0	0
78	CL	1691	0	1788	9	0
79	CE	1731	0	1825	39	0
80	Cf	891	0	928	18	0
81	Ck	564	0	612	7	0
82	Cb	477	0	483	6	0
83	Cg	897	0	983	11	0
84	Aa	72601	0	36663	796	0
85	Ac	3408	0	1732	35	0
86	Ab	2561	0	1295	219	0
All	All	212263	0	158405	3313	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

The worst 5 of 3313 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ad:1203:G:C1'	1:Ad:1203:G:C2'	1.79	1.54
1:Ad:707:C:C1'	1:Ad:707:C:C2'	1.78	1.53
1:Ad:1580:G:C1'	1:Ad:1580:G:C2'	1.77	1.48
1:Ad:944:A:C6	18:BN:117:LEU:HG	1.48	1.47
73:CO:17:ARG:NH1	84:Aa:3181:U:C5	1.87	1.41

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	BY	136/138 (99%)	118 (87%)	8 (6%)	10 (7%)	1	10
5	BI	64/220 (29%)	61 (95%)	2 (3%)	1 (2%)	7	37
6	BK	94/183 (51%)	66 (70%)	17 (18%)	11 (12%)	0	4
7	BM	121/171 (71%)	84 (69%)	20 (16%)	17 (14%)	0	3
8	Bf	69/155 (44%)	46 (67%)	10 (14%)	13 (19%)	0	2
9	BX	140/142 (99%)	124 (89%)	11 (8%)	5 (4%)	2	20
10	Bg	378/380 (100%)	334 (88%)	26 (7%)	18 (5%)	2	16
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	16
13	BF	189/191 (99%)	162 (86%)	20 (11%)	7 (4%)	2	19
14	BQ	124/149 (83%)	93 (75%)	15 (12%)	16 (13%)	0	4
15	BU	126/128 (98%)	102 (81%)	14 (11%)	10 (8%)	1	9
16	BO	117/151 (78%)	91 (78%)	12 (10%)	14 (12%)	0	4
17	BS	150/152 (99%)	109 (73%)	16 (11%)	25 (17%)	0	2
18	BN	119/151 (79%)	92 (77%)	14 (12%)	13 (11%)	0	6
19	BL	83/160 (52%)	61 (74%)	16 (19%)	6 (7%)	1	10

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	BT	144/146 (99%)	123 (85%)	13 (9%)	8 (6%)	1	14
21	BP	89/154 (58%)	69 (78%)	12 (14%)	8 (9%)	0	8
22	BZ	98/108 (91%)	75 (76%)	10 (10%)	13 (13%)	0	3
23	Bc	56/65 (86%)	40 (71%)	5 (9%)	11 (20%)	0	2
24	BW	128/130 (98%)	101 (79%)	16 (12%)	11 (9%)	0	8
25	Bd	46/56 (82%)	29 (63%)	6 (13%)	11 (24%)	0	1
26	Bb	84/86 (98%)	75 (89%)	6 (7%)	3 (4%)	2	20
27	Be	58/62 (94%)	49 (84%)	5 (9%)	4 (7%)	1	11
28	BA	195/260 (75%)	176 (90%)	10 (5%)	9 (5%)	2	16
29	BR	114/141 (81%)	89 (78%)	15 (13%)	10 (9%)	0	8
30	BB	209/262 (80%)	153 (73%)	31 (15%)	25 (12%)	0	4
31	BV	74/82 (90%)	62 (84%)	9 (12%)	3 (4%)	2	17
32	Ba	91/133 (68%)	65 (71%)	13 (14%)	13 (14%)	0	3
33	BJ	185/195 (95%)	162 (88%)	16 (9%)	7 (4%)	2	19
34	BC	212/263 (81%)	189 (89%)	16 (8%)	7 (3%)	3	20
35	BG	227/245 (93%)	211 (93%)	10 (4%)	6 (3%)	4	25
36	BH	182/189 (96%)	154 (85%)	10 (6%)	18 (10%)	0	7
37	CG	235/257 (91%)	205 (87%)	24 (10%)	6 (3%)	4	25
38	CT	158/164 (96%)	137 (87%)	6 (4%)	15 (10%)	0	8
39	CZ	134/136 (98%)	123 (92%)	10 (8%)	1 (1%)	18	56
40	Cz	214/216 (99%)	197 (92%)	9 (4%)	8 (4%)	2	19
41	CA	253/261 (97%)	219 (87%)	19 (8%)	15 (6%)	1	12
42	CJ	168/180 (93%)	132 (79%)	14 (8%)	22 (13%)	0	3
43	CH	188/190 (99%)	167 (89%)	16 (8%)	5 (3%)	4	25
44	CV	138/140 (99%)	124 (90%)	7 (5%)	7 (5%)	1	14
45	CN	192/200 (96%)	168 (88%)	18 (9%)	6 (3%)	3	21
46	Ca	142/144 (99%)	101 (71%)	24 (17%)	17 (12%)	0	4
47	CQ	161/188 (86%)	127 (79%)	18 (11%)	16 (10%)	0	7
48	CD	302/304 (99%)	213 (70%)	35 (12%)	54 (18%)	0	2
49	CR	187/209 (90%)	163 (87%)	14 (8%)	10 (5%)	1	14
50	CP	169/171 (99%)	140 (83%)	12 (7%)	17 (10%)	0	7

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	CX	120/152 (79%)	100 (83%)	17 (14%)	3 (2%)	4	25
52	CW	73/162 (45%)	55 (75%)	12 (16%)	6 (8%)	0	9
53	CY	128/150 (85%)	114 (89%)	8 (6%)	6 (5%)	2	16
54	Cr	71/147 (48%)	49 (69%)	13 (18%)	9 (13%)	0	4
55	Cc	110/112 (98%)	96 (87%)	10 (9%)	4 (4%)	2	20
56	Cd	118/123 (96%)	98 (83%)	8 (7%)	12 (10%)	0	6
57	Ce	131/133 (98%)	113 (86%)	10 (8%)	8 (6%)	1	12
58	Cj	92/94 (98%)	58 (63%)	19 (21%)	15 (16%)	0	2
59	Cl	49/51 (96%)	36 (74%)	8 (16%)	5 (10%)	0	6
60	Co	103/105 (98%)	76 (74%)	13 (13%)	14 (14%)	0	3
61	CM	132/134 (98%)	101 (76%)	14 (11%)	17 (13%)	0	4
62	CS	165/178 (93%)	122 (74%)	20 (12%)	23 (14%)	0	3
63	CU	106/130 (82%)	76 (72%)	13 (12%)	17 (16%)	0	2
64	Ci	75/112 (67%)	59 (79%)	5 (7%)	11 (15%)	0	3
65	CK	126/166 (76%)	94 (75%)	17 (14%)	15 (12%)	0	4
66	Cu	56/110 (51%)	54 (96%)	1 (2%)	1 (2%)	6	33
66	Cv	56/110 (51%)	53 (95%)	2 (4%)	1 (2%)	6	33
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	11
69	CF	242/244 (99%)	217 (90%)	16 (7%)	9 (4%)	2	19
70	Cq	260/319 (82%)	233 (90%)	15 (6%)	12 (5%)	2	16
71	CB	387/389 (100%)	307 (79%)	43 (11%)	37 (10%)	0	7
72	CC	368/405 (91%)	311 (84%)	27 (7%)	30 (8%)	0	9
73	CO	204/206 (99%)	179 (88%)	14 (7%)	11 (5%)	1	14
74	Cp	90/92 (98%)	81 (90%)	7 (8%)	2 (2%)	5	28
75	CI	182/224 (81%)	147 (81%)	24 (13%)	11 (6%)	1	12
76	Cn	23/25 (92%)	21 (91%)	1 (4%)	1 (4%)	2	17
77	Cm	50/53 (94%)	46 (92%)	3 (6%)	1 (2%)	6	30
78	CL	206/208 (99%)	168 (82%)	13 (6%)	25 (12%)	0	4
79	CE	217/219 (99%)	177 (82%)	14 (6%)	26 (12%)	0	4

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
80	Cf	109/111 (98%)	103 (94%)	5 (5%)	1 (1%)	14	50
81	Ck	67/69 (97%)	63 (94%)	2 (3%)	2 (3%)	3	22
82	Cb	56/60 (93%)	48 (86%)	4 (7%)	4 (7%)	1	10
83	Cg	108/119 (91%)	96 (89%)	8 (7%)	4 (4%)	2	19
All	All	11663/13543 (86%)	9641 (83%)	1083 (9%)	939 (8%)	1	9

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 [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	BY	116/116 (100%)	110 (95%)	6 (5%)	21	42
5	BI	56/179 (31%)	53 (95%)	3 (5%)	20	41
6	BK	90/146 (62%)	89 (99%)	1 (1%)	65	75
7	BM	101/142 (71%)	101 (100%)	0	100	100
8	Bf	62/135 (46%)	61 (98%)	1 (2%)	55	69
9	BX	113/113 (100%)	110 (97%)	3 (3%)	39	60
10	Bg	323/323 (100%)	313 (97%)	10 (3%)	35	56
11	BD	175/175 (100%)	170 (97%)	5 (3%)	37	57
12	BE	176/225 (78%)	171 (97%)	5 (3%)	38	59
13	BF	159/159 (100%)	153 (96%)	6 (4%)	29	50
14	BQ	103/120 (86%)	101 (98%)	2 (2%)	50	66
15	BU	113/113 (100%)	109 (96%)	4 (4%)	32	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	BO	94/120 (78%)	90 (96%)	4 (4%)	26	47
17	BS	133/133 (100%)	125 (94%)	8 (6%)	17	39
18	BN	106/130 (82%)	103 (97%)	3 (3%)	38	59
19	BL	74/135 (55%)	71 (96%)	3 (4%)	27	48
20	BT	121/121 (100%)	115 (95%)	6 (5%)	22	43
21	BP	77/130 (59%)	73 (95%)	4 (5%)	21	42
22	BZ	87/93 (94%)	84 (97%)	3 (3%)	32	54
23	Bc	52/58 (90%)	49 (94%)	3 (6%)	18	39
24	BW	113/113 (100%)	109 (96%)	4 (4%)	32	53
25	Bd	40/47 (85%)	39 (98%)	1 (2%)	42	62
26	Bb	78/78 (100%)	78 (100%)	0	100	100
27	Be	47/49 (96%)	47 (100%)	0	100	100
28	BA	161/204 (79%)	153 (95%)	8 (5%)	22	43
29	BR	105/127 (83%)	103 (98%)	2 (2%)	50	66
30	BB	188/226 (83%)	186 (99%)	2 (1%)	65	75
31	BV	63/68 (93%)	62 (98%)	1 (2%)	55	69
32	Ba	80/107 (75%)	78 (98%)	2 (2%)	42	62
33	BJ	160/167 (96%)	155 (97%)	5 (3%)	35	56
34	BC	182/211 (86%)	178 (98%)	4 (2%)	45	64
35	BG	201/210 (96%)	194 (96%)	7 (4%)	32	53
36	BH	164/168 (98%)	160 (98%)	4 (2%)	43	63
37	CG	205/220 (93%)	199 (97%)	6 (3%)	37	57
38	CT	139/141 (99%)	134 (96%)	5 (4%)	31	52
39	CZ	113/113 (100%)	111 (98%)	2 (2%)	51	67
40	Cz	192/192 (100%)	179 (93%)	13 (7%)	14	36
41	CA	195/199 (98%)	185 (95%)	10 (5%)	21	42
42	CJ	149/157 (95%)	141 (95%)	8 (5%)	20	41
43	CH	164/164 (100%)	159 (97%)	5 (3%)	36	57
44	CV	109/109 (100%)	106 (97%)	3 (3%)	38	59
45	CN	167/173 (96%)	164 (98%)	3 (2%)	51	67
46	Ca	110/110 (100%)	106 (96%)	4 (4%)	31	52

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
47	CQ	138/160 (86%)	133 (96%)	5 (4%)	31	52
48	CD	251/251 (100%)	237 (94%)	14 (6%)	19	40
49	CR	166/183 (91%)	155 (93%)	11 (7%)	15	37
50	CP	144/144 (100%)	140 (97%)	4 (3%)	38	59
51	CX	109/130 (84%)	102 (94%)	7 (6%)	16	37
52	CW	66/133 (50%)	66 (100%)	0	100	100
53	CY	115/128 (90%)	111 (96%)	4 (4%)	32	53
54	Cr	64/131 (49%)	61 (95%)	3 (5%)	23	45
55	Cc	98/98 (100%)	95 (97%)	3 (3%)	35	56
56	Cd	103/106 (97%)	98 (95%)	5 (5%)	22	43
57	Ce	122/122 (100%)	120 (98%)	2 (2%)	55	69
58	Cj	77/77 (100%)	75 (97%)	2 (3%)	40	61
59	Cl	48/48 (100%)	47 (98%)	1 (2%)	47	65
60	Co	94/94 (100%)	89 (95%)	5 (5%)	20	41
61	CM	116/116 (100%)	110 (95%)	6 (5%)	21	42
62	CS	153/163 (94%)	145 (95%)	8 (5%)	21	42
63	CU	94/106 (89%)	87 (93%)	7 (7%)	13	33
64	Ci	62/92 (67%)	58 (94%)	4 (6%)	15	37
65	CK	105/139 (76%)	97 (92%)	8 (8%)	12	33
66	Cu	46/77 (60%)	45 (98%)	1 (2%)	45	64
66	Cv	46/77 (60%)	46 (100%)	0	100	100
67	Cs	48/82 (58%)	47 (98%)	1 (2%)	47	65
67	Ct	48/82 (58%)	46 (96%)	2 (4%)	26	48
68	Ch	109/109 (100%)	104 (95%)	5 (5%)	24	45
69	CF	206/206 (100%)	198 (96%)	8 (4%)	28	49
70	Cq	222/265 (84%)	213 (96%)	9 (4%)	27	48
71	CB	335/335 (100%)	315 (94%)	20 (6%)	17	39
72	CC	302/329 (92%)	285 (94%)	17 (6%)	19	40
73	CO	173/173 (100%)	163 (94%)	10 (6%)	18	39
74	Cp	73/73 (100%)	72 (99%)	1 (1%)	59	72
75	CI	156/183 (85%)	152 (97%)	4 (3%)	40	61

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
76	Cn	24/24 (100%)	24 (100%)	0	100	100
77	Cm	47/48 (98%)	46 (98%)	1 (2%)	47	65
78	CL	175/175 (100%)	166 (95%)	9 (5%)	21	42
79	CE	185/185 (100%)	171 (92%)	14 (8%)	12	33
80	Cf	96/96 (100%)	92 (96%)	4 (4%)	26	48
81	Ck	63/63 (100%)	58 (92%)	5 (8%)	11	32
82	Cb	51/53 (96%)	51 (100%)	0	100	100
83	Cg	98/107 (92%)	93 (95%)	5 (5%)	21	42
All	All	10084/11382 (89%)	9690 (96%)	394 (4%)	30	49

5 of 394 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
56	Cd	63	LEU
68	Ch	90	ARG
58	Cj	70	VAL
63	CU	35	ILE
70	Cq	124	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 293 such sidechains are listed below:

Mol	Chain	Res	Type
69	CF	231	ASN
82	Cb	17	HIS
71	CB	121	ASN
72	CC	334	ASN
33	BJ	93	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	Ad	1760/1810 (97%)	463 (26%)	0
2	Ae	74/75 (98%)	20 (27%)	0
3	Af	10/11 (90%)	2 (20%)	0
84	Aa	3389/3391 (99%)	762 (22%)	0
85	Ac	159/160 (99%)	35 (22%)	0
86	Ab	119/120 (99%)	23 (19%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	5511/5567 (98%)	1305 (23%)	0

5 of 1305 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 [i](#)

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

#### 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

#### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

#### 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

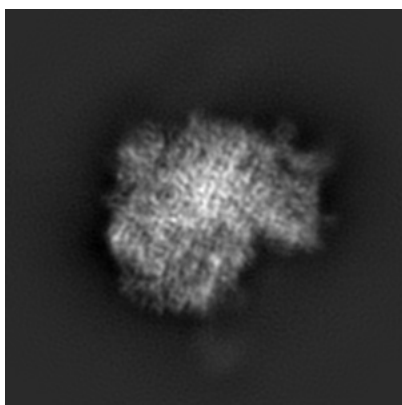
## 6 Map visualisation [i](#)

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

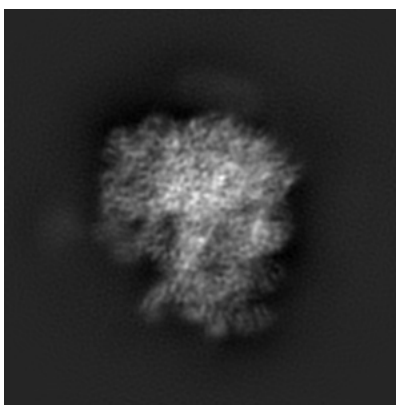
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

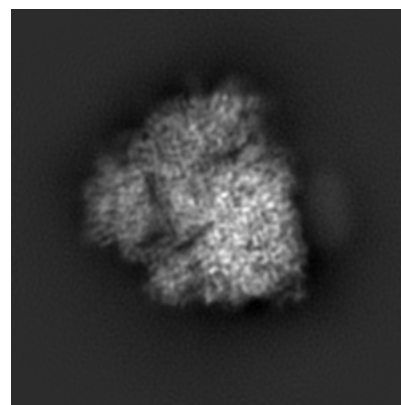
#### 6.1.1 Primary map



X



Y

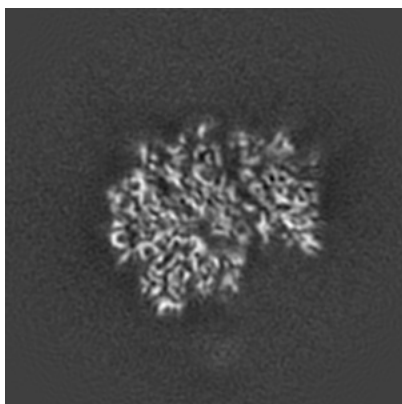


Z

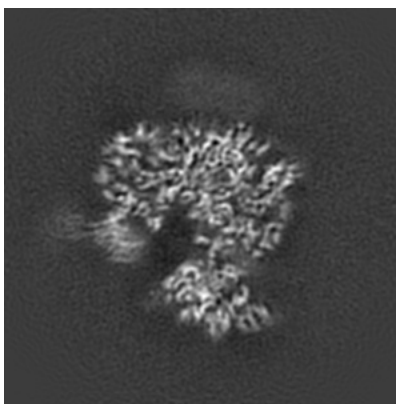
The images above show the map projected in three orthogonal directions.

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

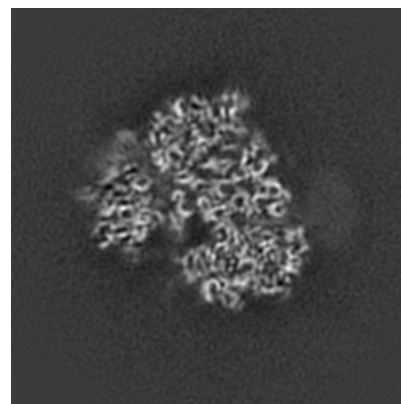
#### 6.2.1 Primary map



X Index: 184



Y Index: 184

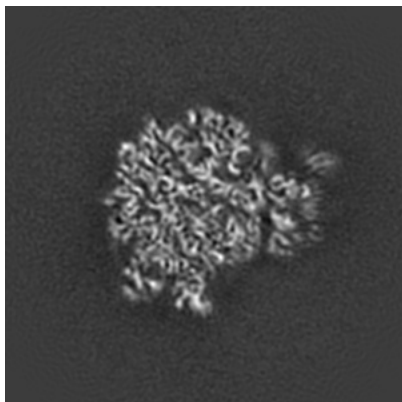


Z Index: 184

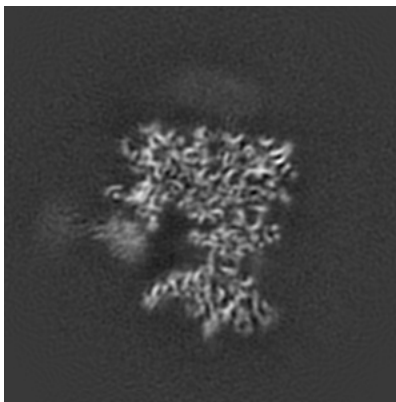
The images above show central slices of the map in three orthogonal directions.

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

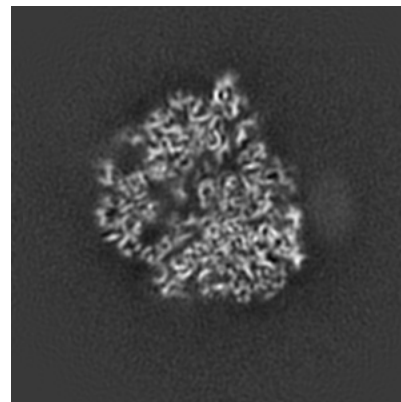
### 6.3.1 Primary map



X Index: 213



Y Index: 193

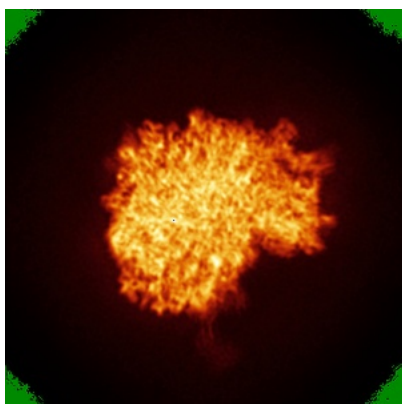


Z Index: 173

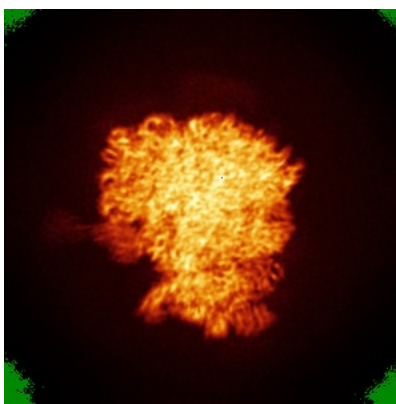
The images above show the largest variance slices of the map in three orthogonal directions.

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

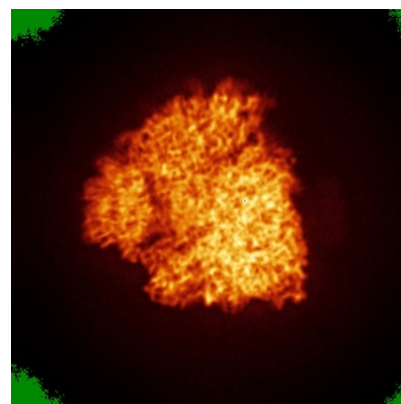
### 6.4.1 Primary map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

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

### 6.5.1 Primary map



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

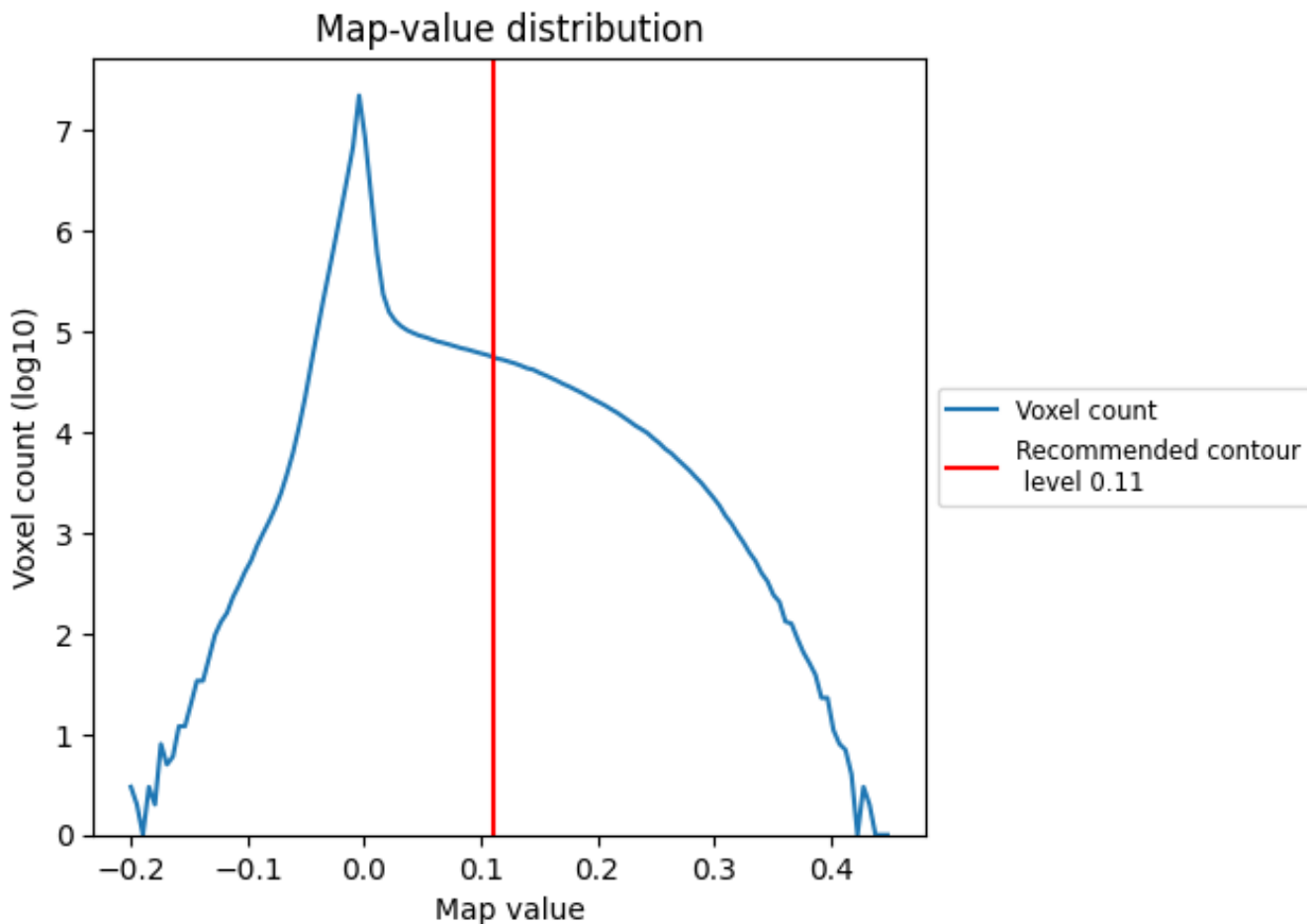
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

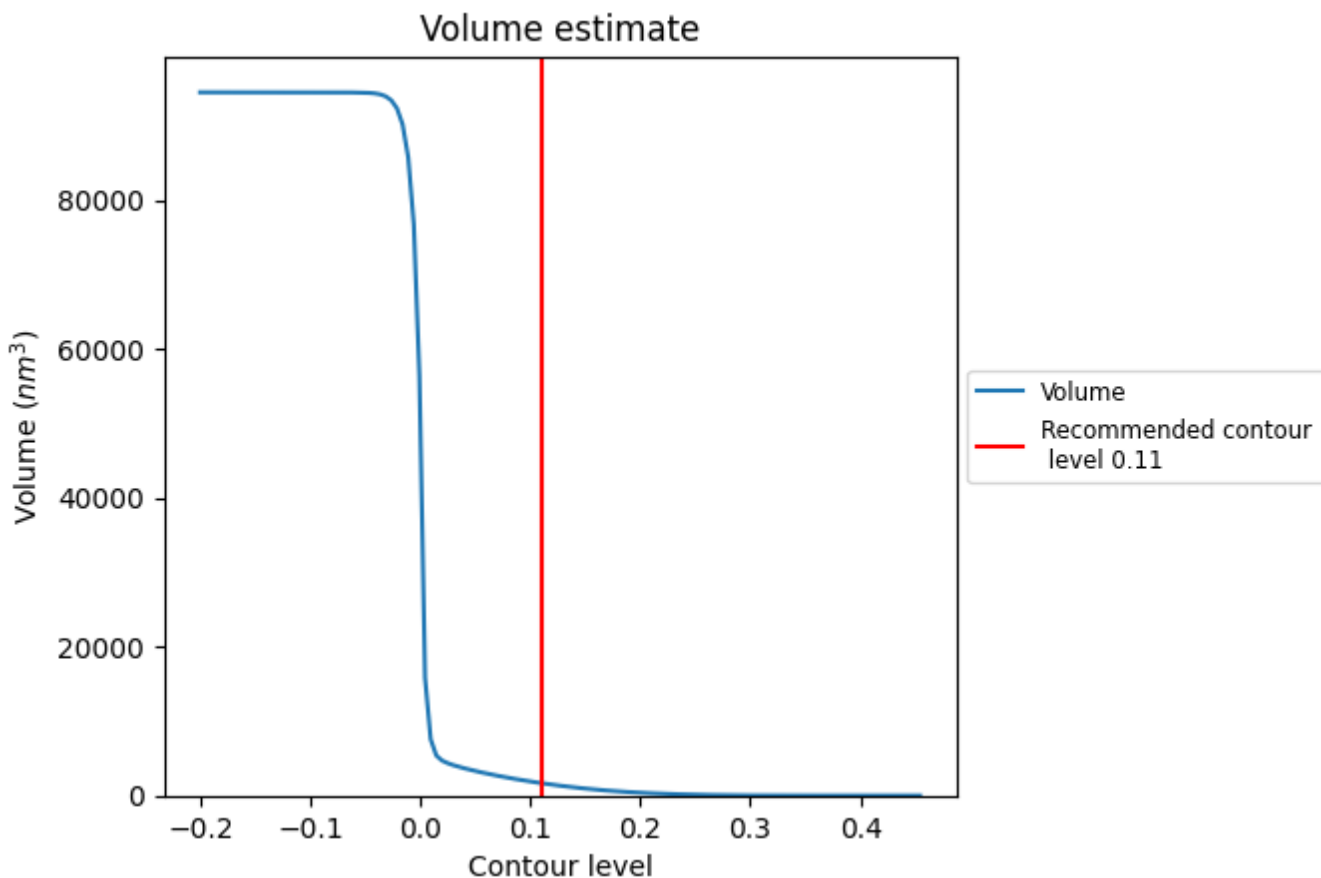
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

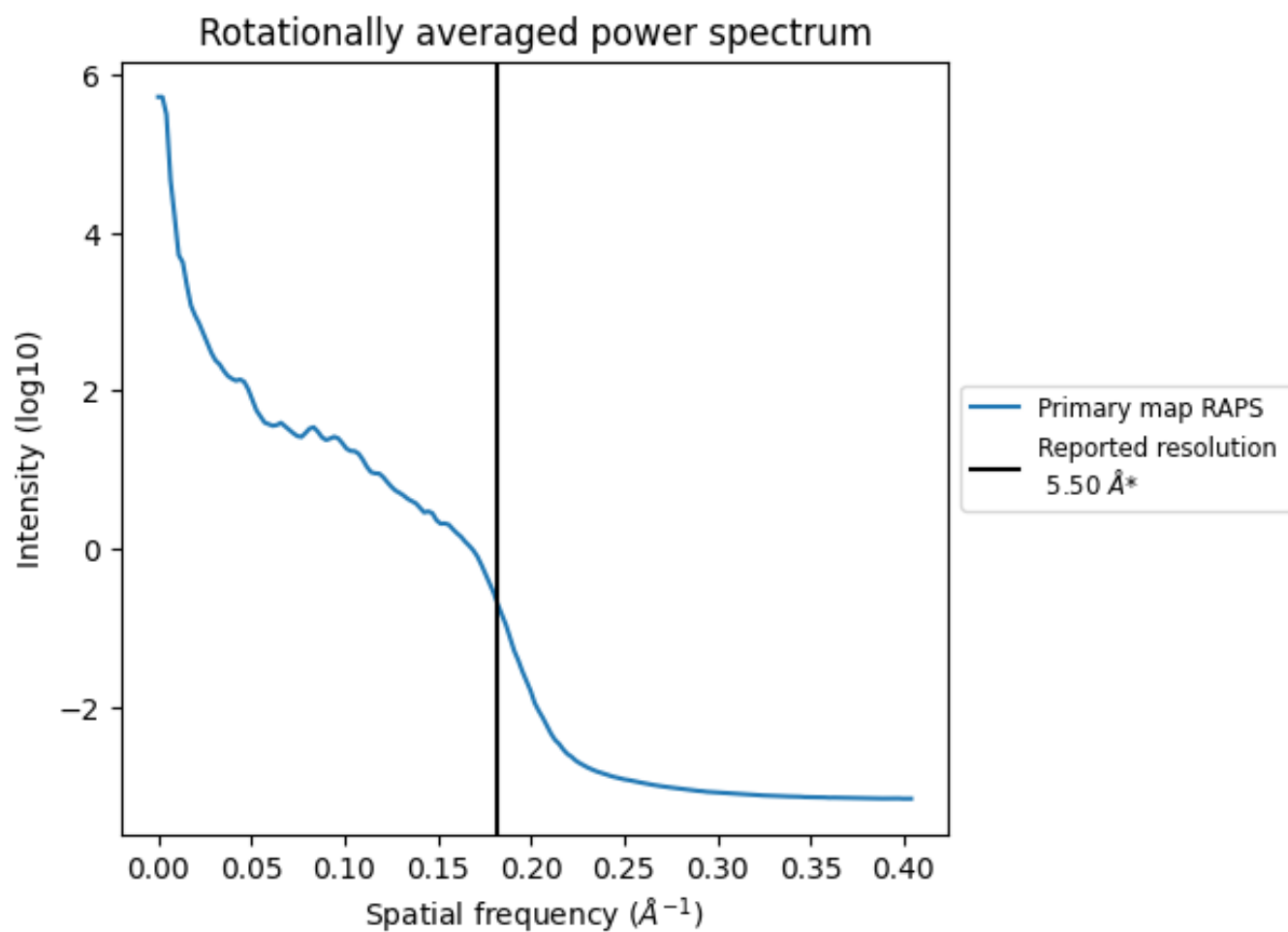
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1668 nm<sup>3</sup>; 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 [i](#)



\*Reported resolution corresponds to spatial frequency of  $0.182 \text{\AA}^{-1}$

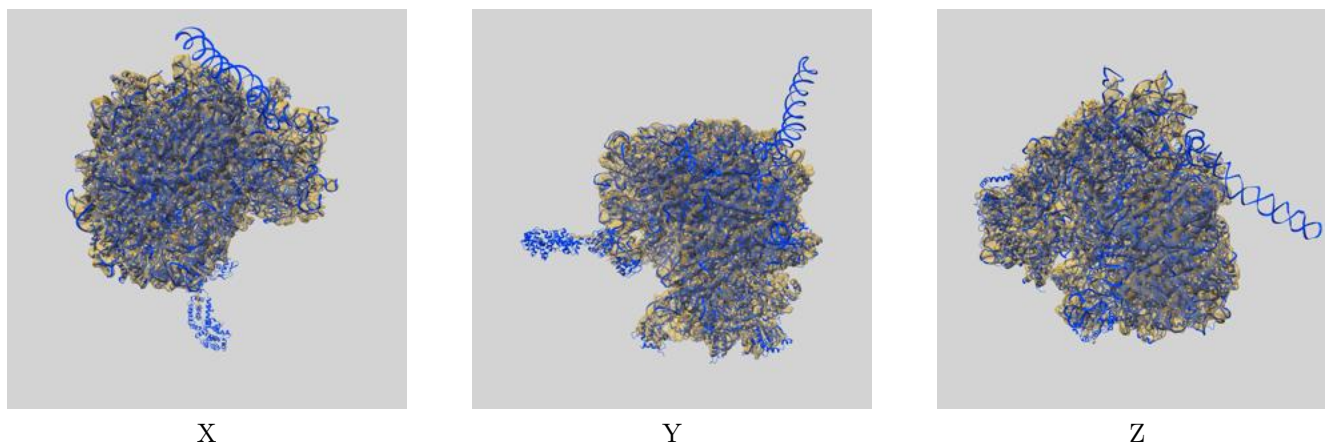
## 8 Fourier-Shell correlation

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

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

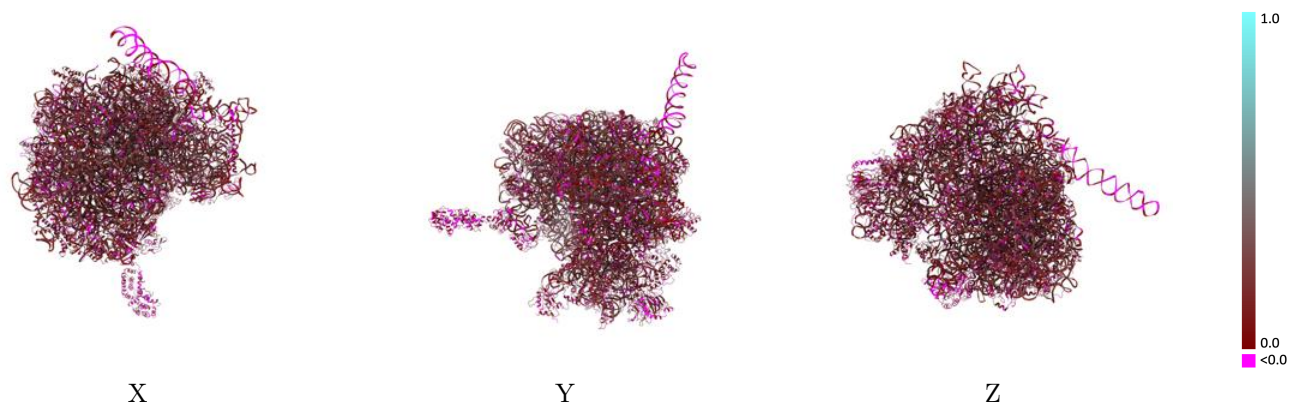
This section contains information regarding the fit between EMDB map EMD-1780 and PDB model 4V7E. Per-residue inclusion information can be found in section 3 on page 20.

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



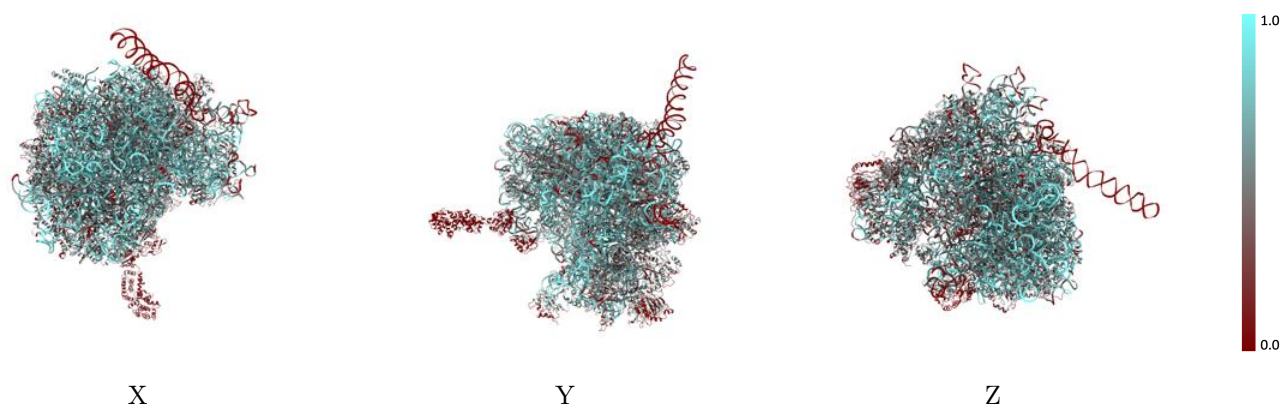
The images above show the 3D surface view of the map at the recommended contour level 0.11 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



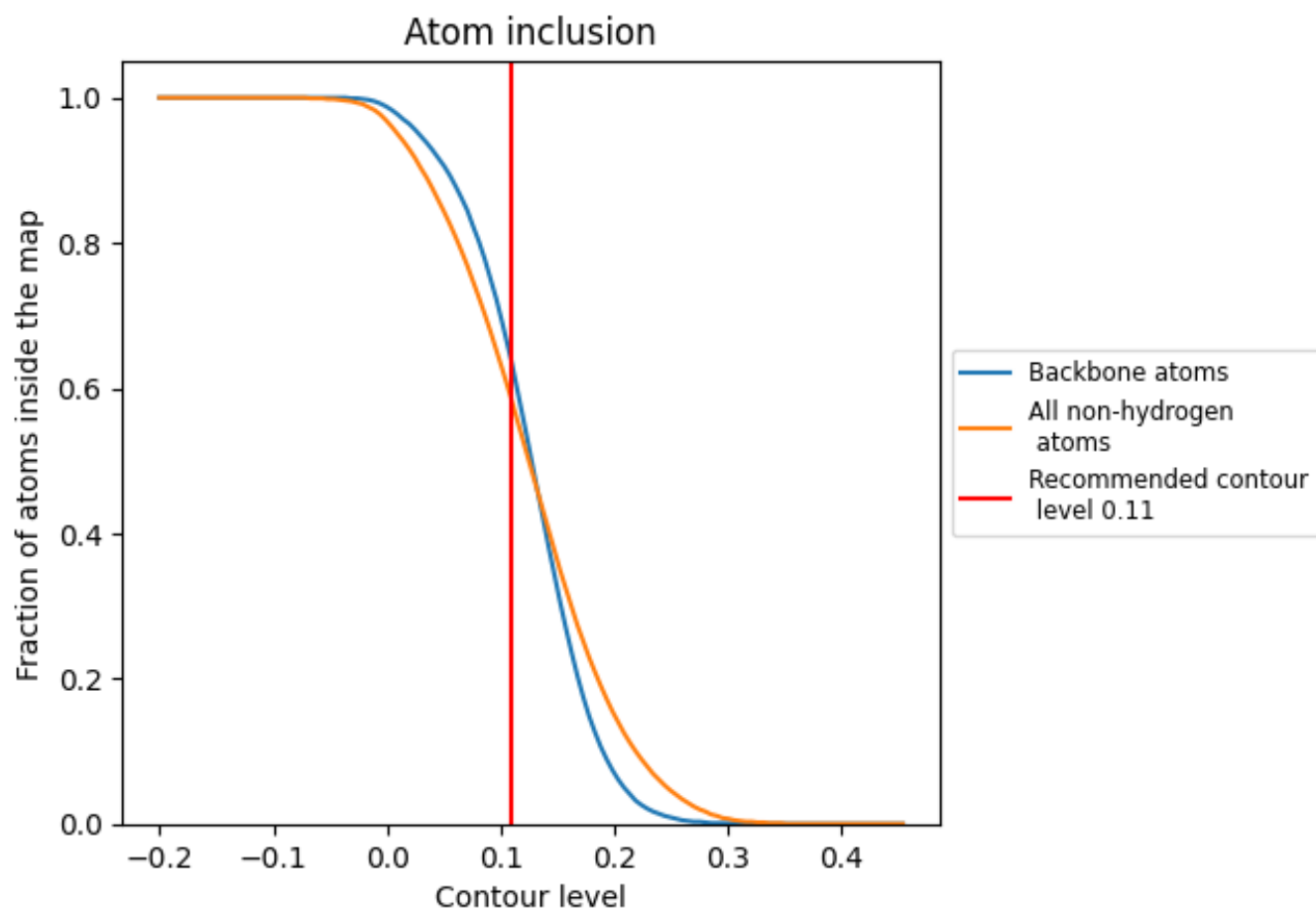
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.11).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 64% 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	 0.5830	 0.1550
Aa	 0.7380	 0.1940
Ab	 0.8530	 0.2080
Ac	 0.7930	 0.2070
Ad	 0.7400	 0.1960
Ae	 0.4910	 0.1860
Af	 0.1290	 0.0800
BA	 0.3800	 0.1240
BB	 0.4210	 0.1260
BC	 0.3650	 0.1210
BD	 0.3290	 0.1190
BE	 0.4310	 0.1040
BF	 0.4540	 0.1280
BG	 0.4300	 0.1120
BH	 0.3670	 0.1230
BI	 0.4140	 0.1110
BJ	 0.4890	 0.1170
BK	 0.4180	 0.0950
BL	 0.3150	 0.1070
BM	 0.2870	 0.0870
BN	 0.3870	 0.0980
BO	 0.3840	 0.1130
BP	 0.4370	 0.1110
BQ	 0.3980	 0.0950
BR	 0.3450	 0.1130
BS	 0.4000	 0.1130
BT	 0.4460	 0.1070
BU	 0.3070	 0.0920
BV	 0.3600	 0.1050
BW	 0.3450	 0.0840
BX	 0.4160	 0.1190
BY	 0.4150	 0.0740
BZ	 0.3450	 0.0990
Ba	 0.4600	 0.1350
Bb	 0.4000	 0.1200



























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Chain	Atom inclusion	Q-score
Bc	0.3080	0.0630
Bd	0.3740	0.0680
Be	0.3030	0.0730
Bf	0.3570	0.0730
Bg	0.2150	0.0850
CA	0.3970	0.1150
CB	0.4290	0.1080
CC	0.4030	0.1160
CD	0.4760	0.1050
CE	0.3680	0.0960
CF	0.4640	0.1200
CG	0.4750	0.1180
CH	0.4760	0.1140
CI	0.4450	0.1210
CJ	0.4660	0.1300
CK	0.0580	0.0530
CL	0.4420	0.1020
CM	0.4740	0.1230
CN	0.4820	0.1090
CO	0.4500	0.1070
CP	0.4270	0.1150
CQ	0.4250	0.1150
CR	0.4300	0.1140
CS	0.4640	0.1040
CT	0.3950	0.1130
CU	0.3180	0.0650
CV	0.2650	0.1300
CW	0.2760	0.1230
CX	0.3930	0.1120
CY	0.5450	0.1270
CZ	0.5070	0.1270
Ca	0.4070	0.0920
Cb	0.3610	0.0940
Cc	0.4300	0.1090
Cd	0.4080	0.0930
Ce	0.3660	0.1060
Cf	0.4200	0.0960
Cg	0.4450	0.1210
Ch	0.4540	0.0910
Ci	0.4100	0.0870
Cj	0.4670	0.1040
Ck	0.4710	0.1140

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Chain	Atom inclusion	Q-score
Cl	 0.4310	 0.1180
Cm	 0.5290	 0.1580
Cn	 0.2830	 -0.0170
Co	 0.3910	 0.0940
Cp	 0.3990	 0.1240
Cq	 0.0740	 0.0580
Cr	 0.4890	 0.1140
Cs	 0.0140	 0.0590
Ct	 0.0000	 0.0300
Cu	 0.0000	 0.0430
Cv	 0.0000	 0.0280
Cz	 0.0260	 0.0410