



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 01:26 AM UTC

PDB ID : 8G31 / pdb_00008g31
EMDB ID : EMD-29687
Title : Time-resolved cryo-EM study of the 70S recycling by the HflX:2nd Intermediate
Authors : Bhattacharjee, S.; Brown, P.Z.; Frank, J.
Deposited on : 2023-02-06
Resolution : 3.20 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:

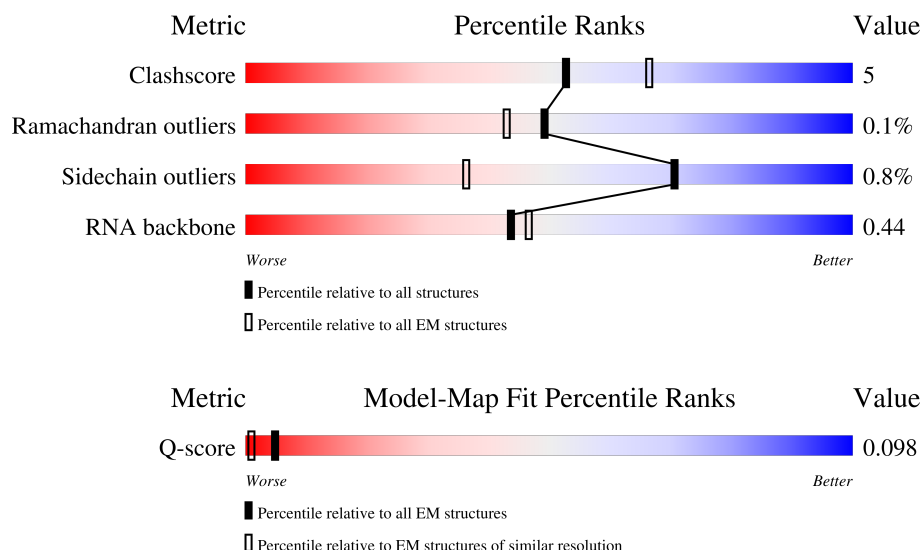
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.20 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	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	15020 (2.70 - 3.70)

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	0	56	64% 80% 20%
2	1	51	100% 78% 22%
3	2	46	70% 87% 13%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	3	64	78% 86% 14%
5	4	38	71% 66% 32% .
6	6	426	82% 82% 17% .
7	A	117	57% 62% 30% 9%
8	B	2903	56% 63% 32% 5%
9	C	272	65% 82% 18%
10	D	209	79% 91% 9%
11	E	201	79% 88% 12%
12	F	178	99% 81% 18% .
13	G	176	85% 83% 17%
14	J	142	68% 74% 26%
15	K	122	71% 78% 22%
16	L	143	69% 83% 17%
17	M	136	63% 80% 20%
18	N	121	72% 75% 25%
19	O	116	78% 83% 17%
20	P	114	74% 76% 24%
21	Q	117	74% 74% 24% ..
22	R	103	67% 85% 15%
23	S	110	70% 72% 27% .
24	T	94	79% 82% 17% .
25	U	103	77% 84% 16%
26	V	94	82% 86% 14%
27	W	79	70% 71% 28% .
28	X	77	60% 82% 18%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	Y	63	
30	Z	58	
31	c	205	
32	d	150	
33	e	100	
34	f	151	
35	g	129	
36	h	127	
37	i	98	
38	j	117	
39	k	123	
40	l	114	
41	m	100	
42	n	88	
43	o	82	
44	p	80	
45	q	55	
46	r	79	
47	s	85	
48	t	51	
49	u	59	
50	v	1539	
51	w	218	
52	x	206	

2 Entry composition

There are 52 unique types of molecules in this entry. The entry contains 144258 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 2 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	1	51	Total	C	N	O	0	1
			410	263	76	71		

- Molecule 3 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 4 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 5 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 6 is a protein called GTPase HflX.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	426	Total	C	N	O	S	0	0
			3403	2129	624	641	9		

- Molecule 7 is a RNA chain called 5S.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	117	Total	C	N	O	P	0	0
			2504	1116	459	813	116		

- Molecule 8 is a RNA chain called 23S.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	2903	Total	C	N	O	P	0	0
			62317	27801	11467	20147	2902		

- Molecule 9 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	272	Total	C	N	O	S	0	1
			2083	1288	424	364	7		

- Molecule 10 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 11 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 12 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	178	Total	C	N	O	S	0	0
			1420	905	251	258	6		

- Molecule 13 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 14 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	J	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 15 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	K	122	Total	C	N	O	S	0	1
			931	582	180	164	5		

- Molecule 16 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	L	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 17 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	M	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 18 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	N	121	Total	C	N	O	S	0	1
			961	593	197	166	5		

- Molecule 19 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	O	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 20 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	P	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 21 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	Q	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 22 is a protein called Ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	R	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 23 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	S	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 24 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	T	94	Total	C	N	O	S	0	1
			739	466	140	131	2		

- Molecule 25 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	U	103	Total	C	N	O	0	1
			780	492	147	141		

- Molecule 26 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	V	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 27 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	W	79	Total	C	N	O	S	0	0
			596	367	120	108	1		

- Molecule 28 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	X	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 29 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 30 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Z	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 31 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	c	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 32 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	d	150	Total	C	N	O	S	0	0
			1106	687	211	202	6		

- Molecule 33 is a protein called 30S ribosomal protein S6, non-modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	e	100	Total	C	N	O	S	0	0
			818	515	148	149	6		

- Molecule 34 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	f	151	Total	C	N	O	S	0	0
			1182	735	227	216	4		

- Molecule 35 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	g	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 36 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	h	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 37 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	i	98	Total	C	N	O	S	0	0
			787	493	150	143	1		

- Molecule 38 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	j	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 39 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	k	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 40 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	l	114	Total	C	N	O	S	0	0
			884	546	178	157	3		

- Molecule 41 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	m	96	Total	C	N	O	S	0	0
			774	483	160	128	3		

- Molecule 42 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	n	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 43 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	o	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 44 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	p	80	Total	C	N	O	S	0	0
			649	411	121	114	3		

- Molecule 45 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	q	55	Total	C	N	O	0	0
			456	288	86	82		

- Molecule 46 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	r	79	Total	C	N	O	S	0	0
			638	408	120	108	2		

- Molecule 47 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	s	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 48 is a protein called 30S ribosomal protein S21 (Fragment).

Mol	Chain	Residues	Atoms					AltConf	Trace
48	t	51	Total	C	N	O	S	0	0
			426	265	86	74	1		

- Molecule 49 is a protein called Transcription termination/antitermination protein NusG.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	u	59	Total	C	N	O	S	0	0
			468	297	78	92	1		

- Molecule 50 is a RNA chain called 16S.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	v	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 51 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	w	218	Total	C	N	O	S	0	0
			1705	1081	305	312	7		

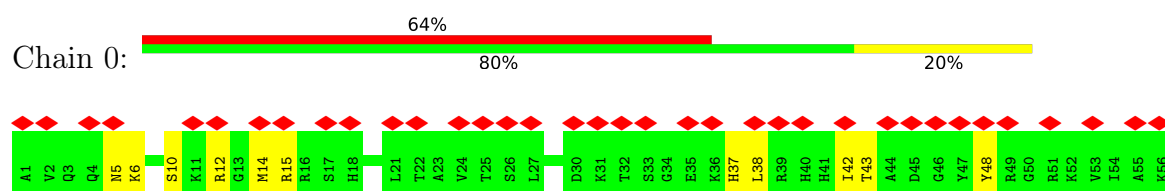
- Molecule 52 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	x	206	Total	C	N	O	S	0	0
			1625	1028	305	289	3		

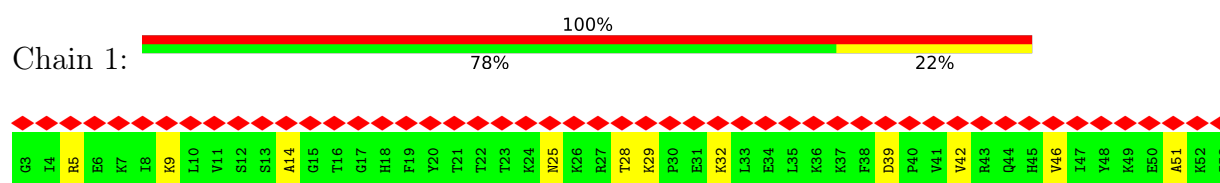
3 Residue-property plots [i](#)

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.

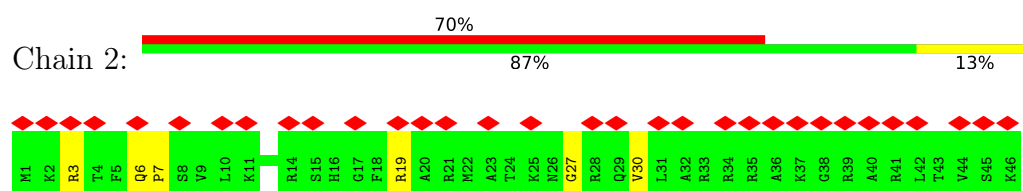
- Molecule 1: 50S ribosomal protein L32



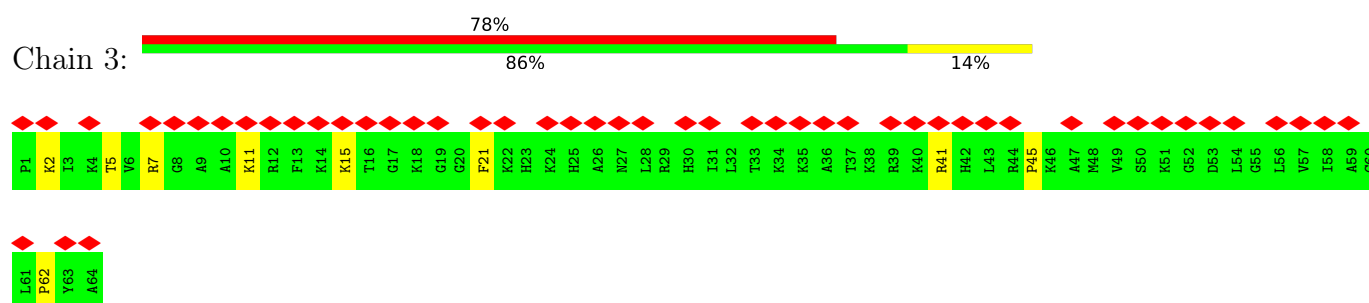
- Molecule 2: 50S ribosomal protein L33



- Molecule 3: 50S ribosomal protein L34

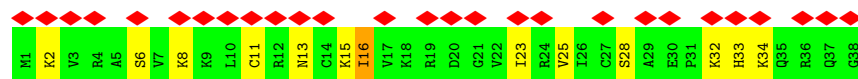


- Molecule 4: 50S ribosomal protein L35

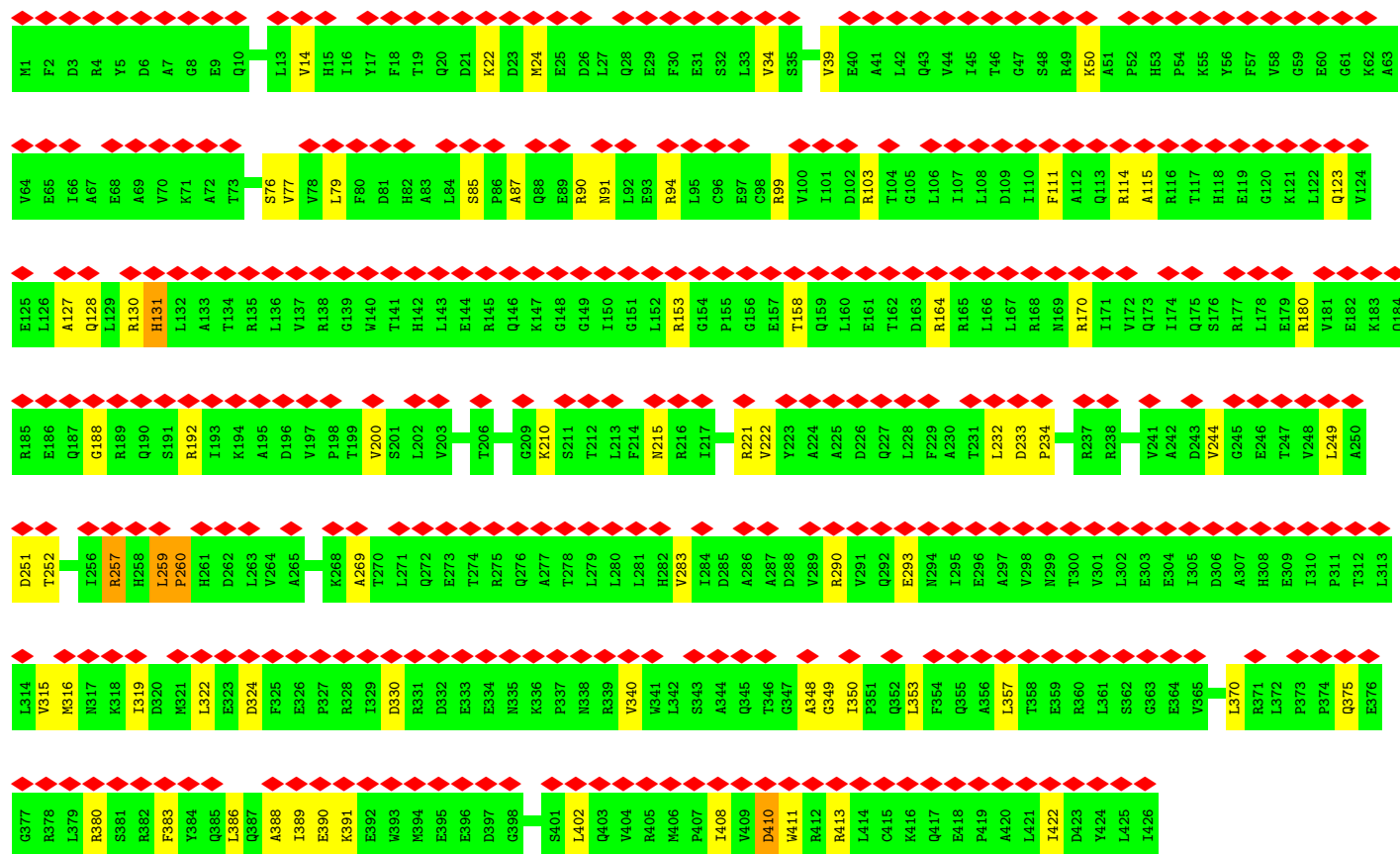
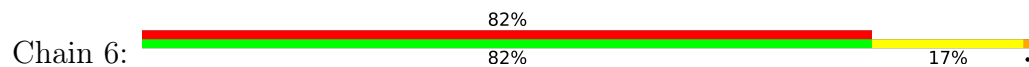


- Molecule 5: 50S ribosomal protein L36

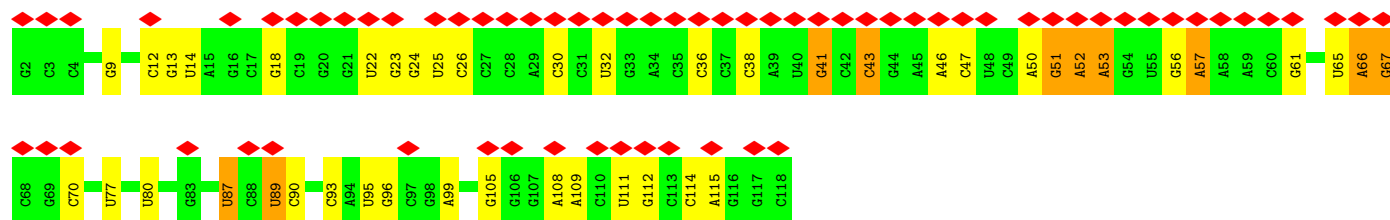




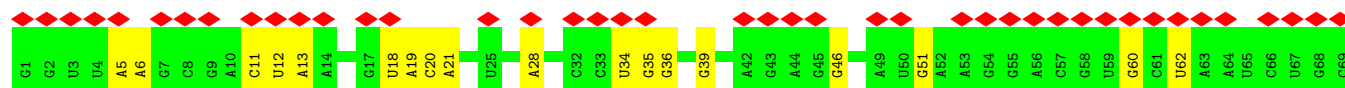
• Molecule 6: GTPase HfX

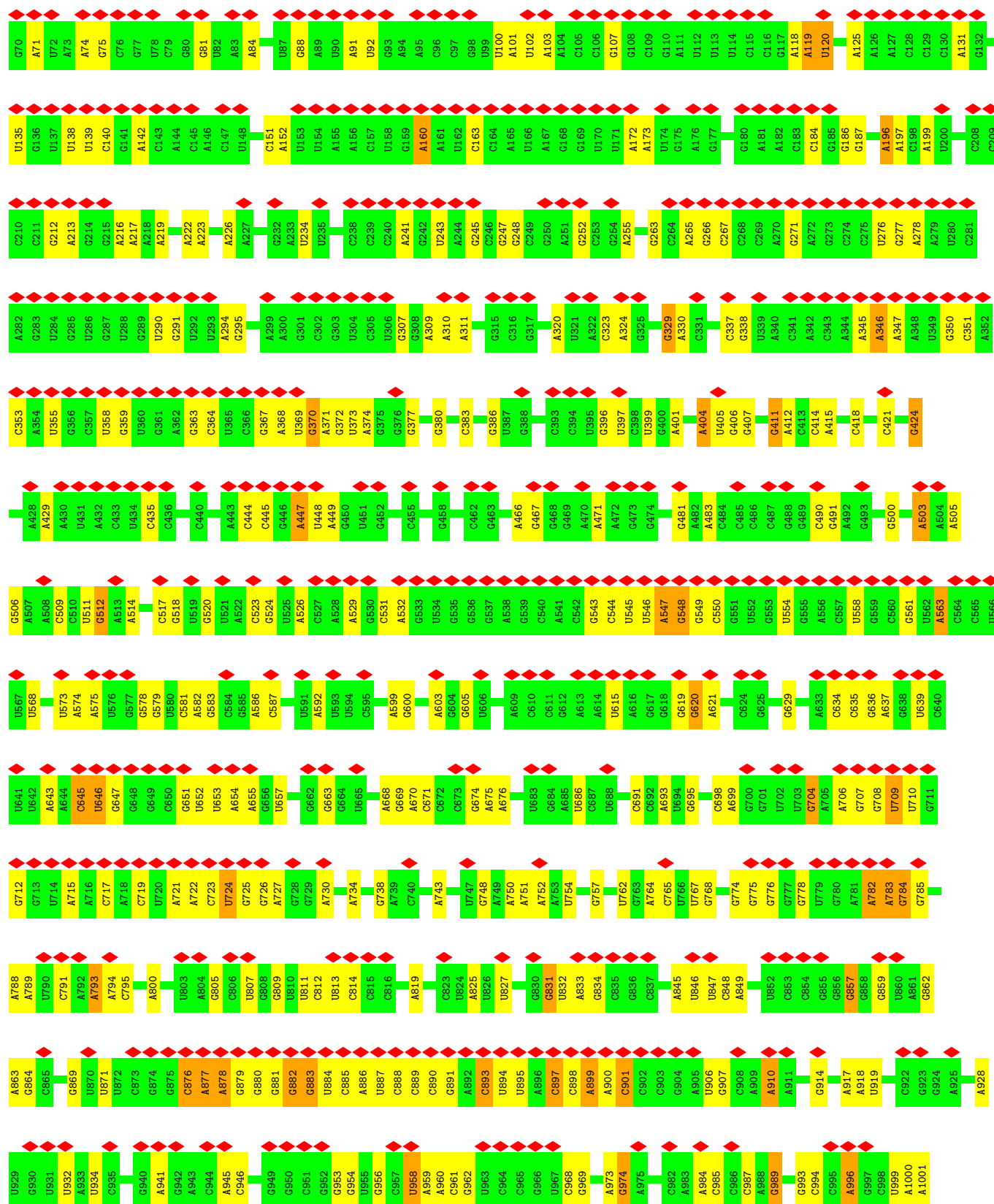


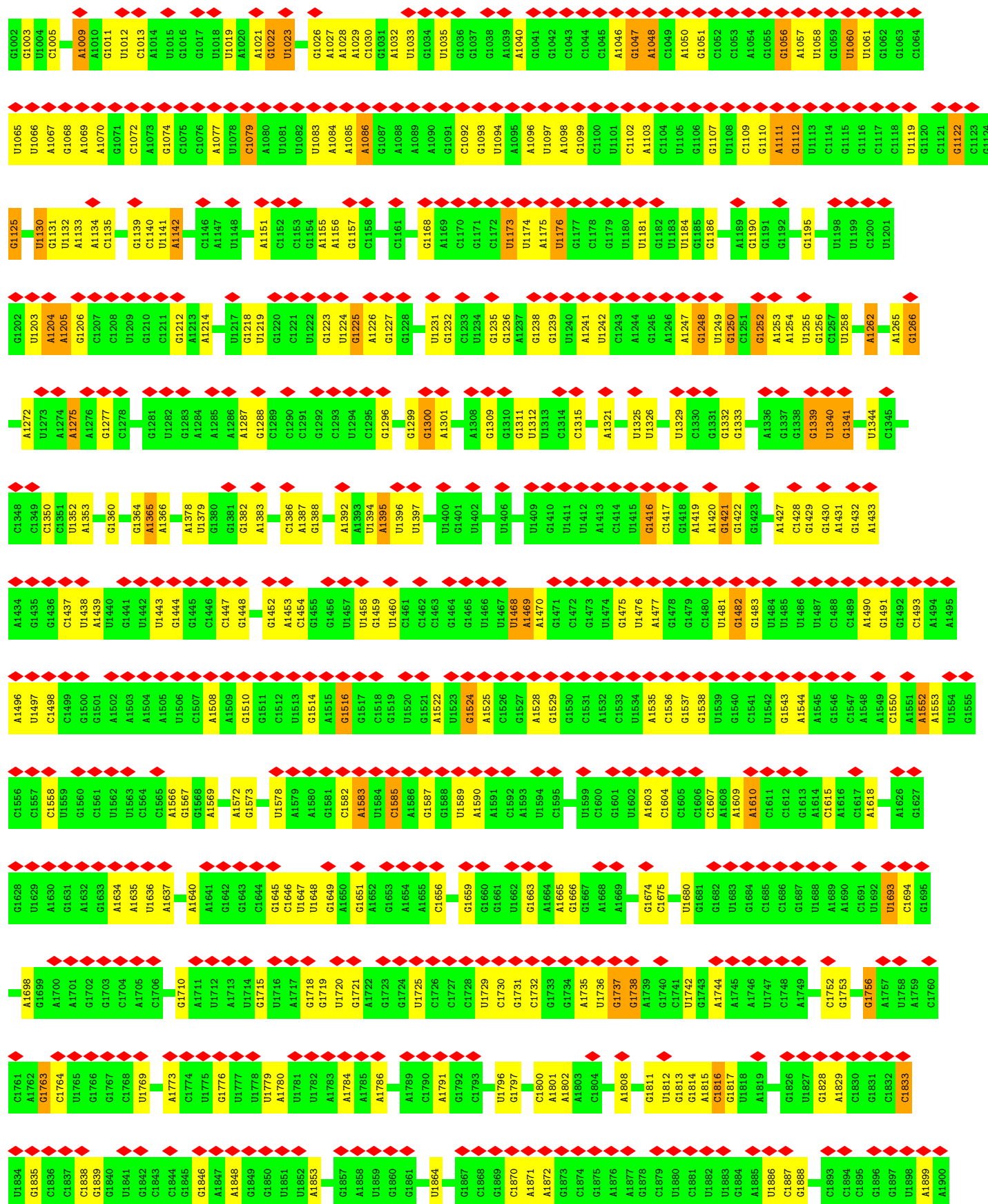
• Molecule 7: 5S

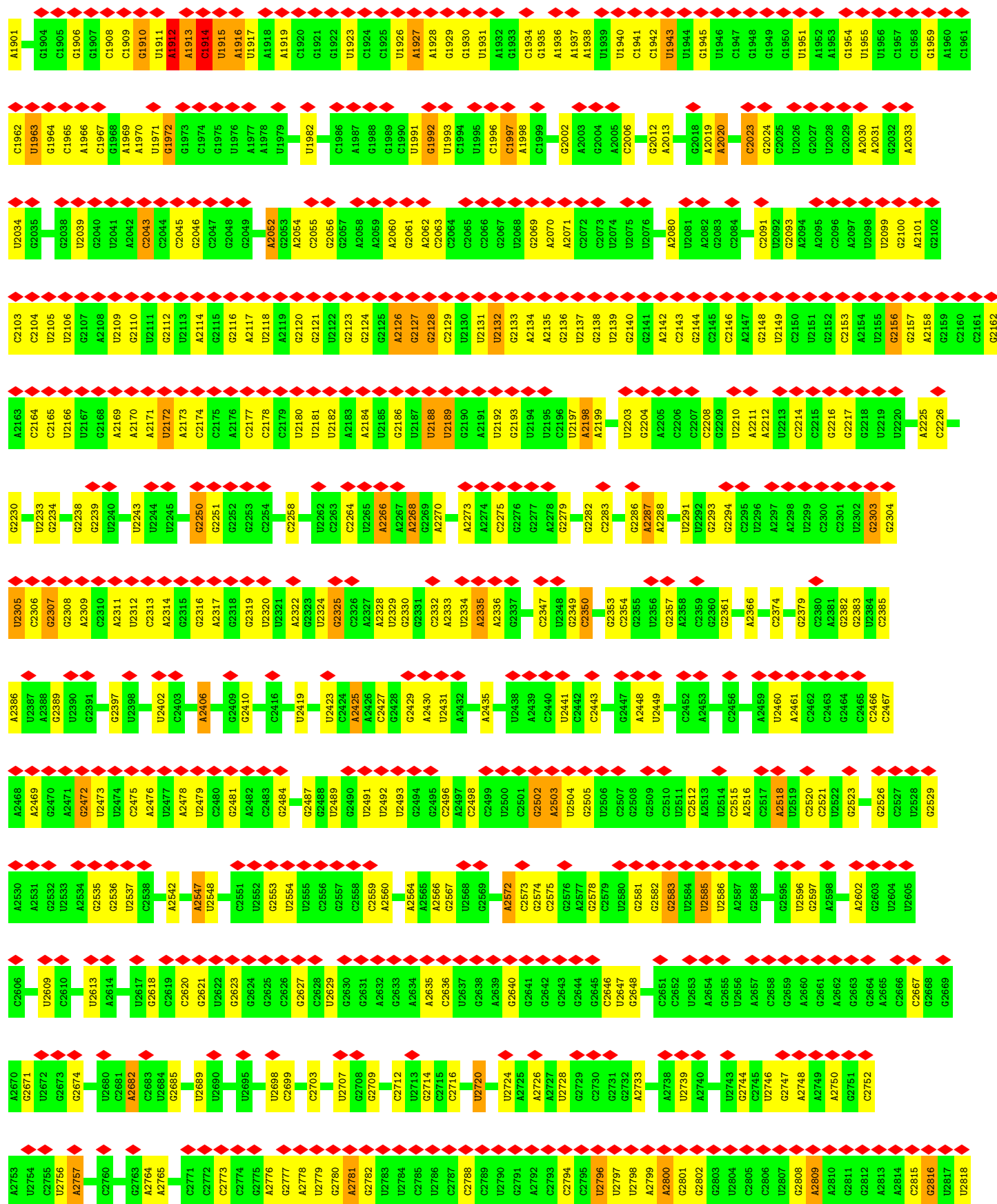


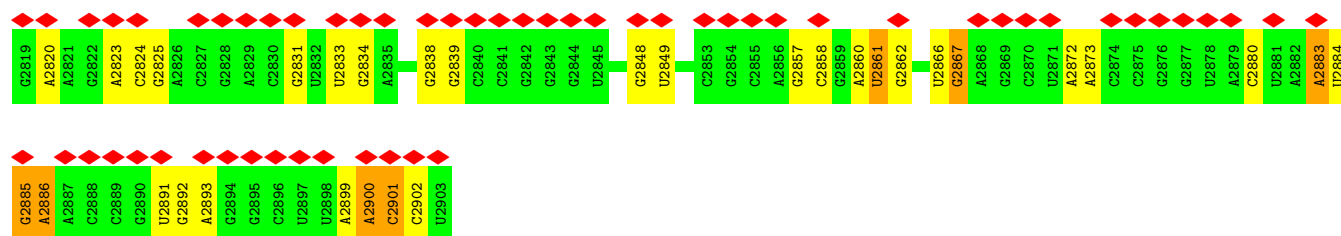
• Molecule 8: 23S



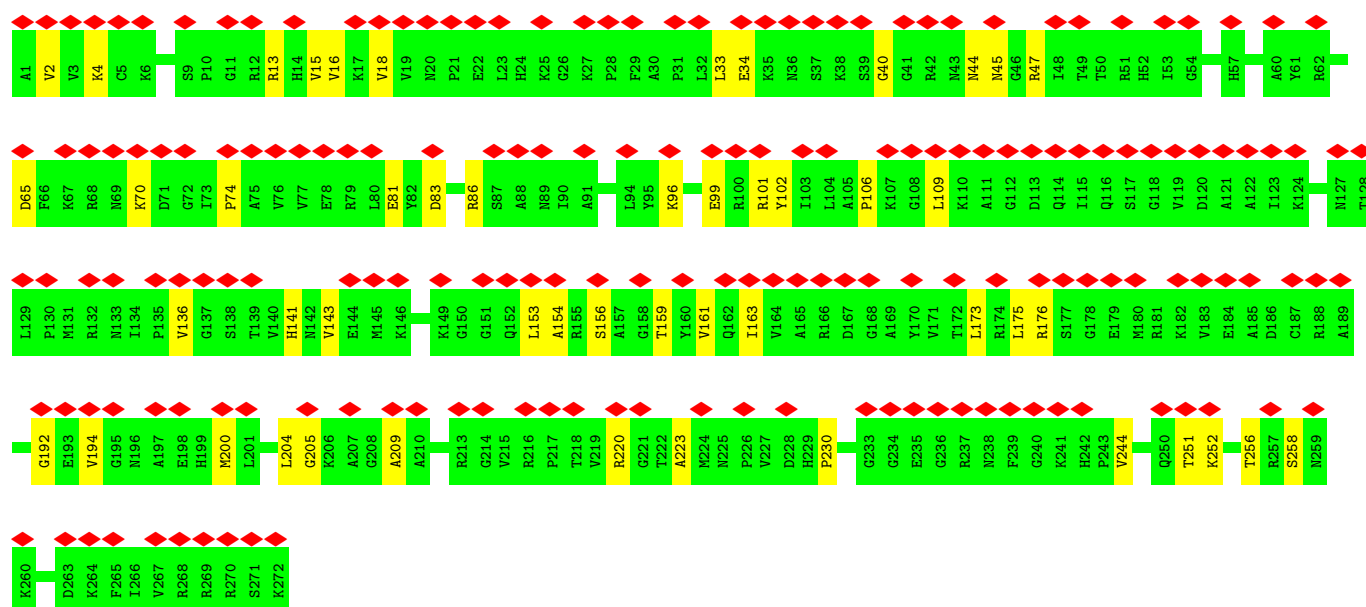
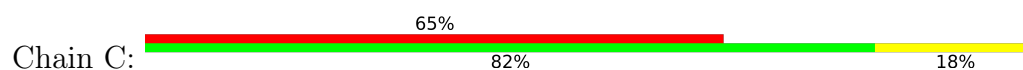




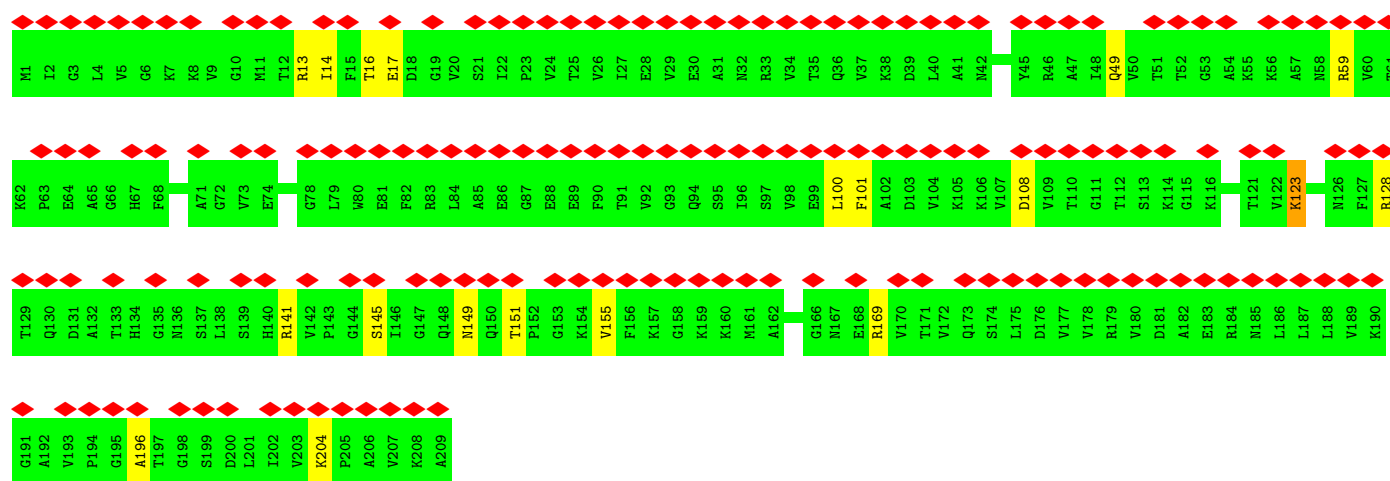
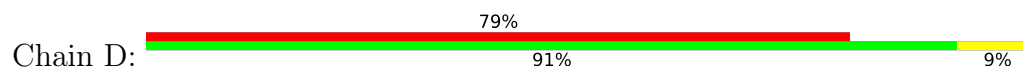




• Molecule 9: 50S ribosomal protein L2

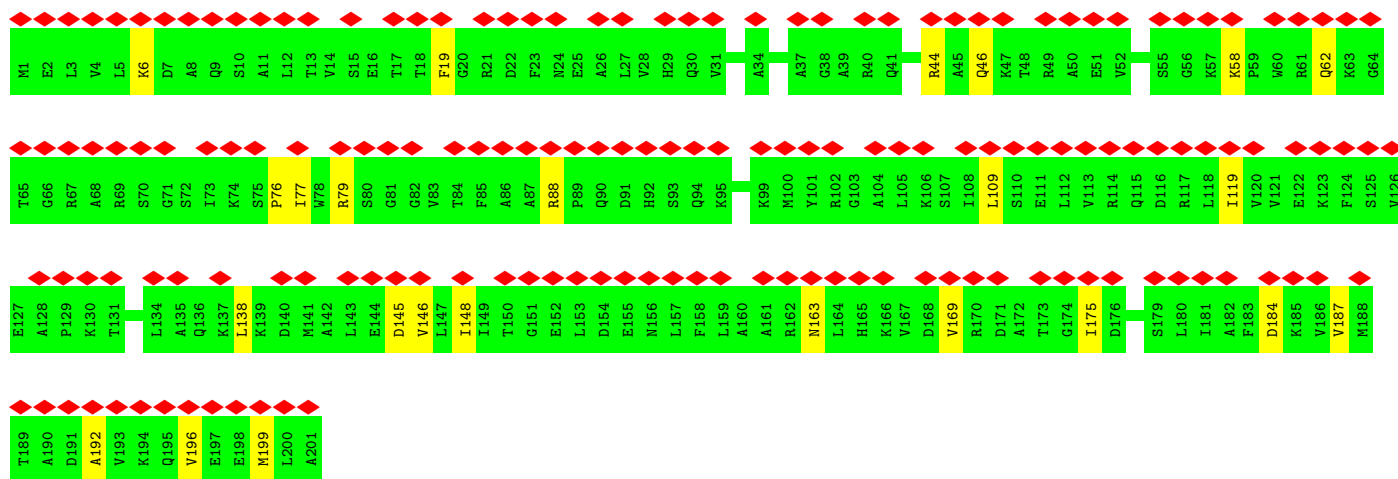


• Molecule 10: 50S ribosomal protein L3



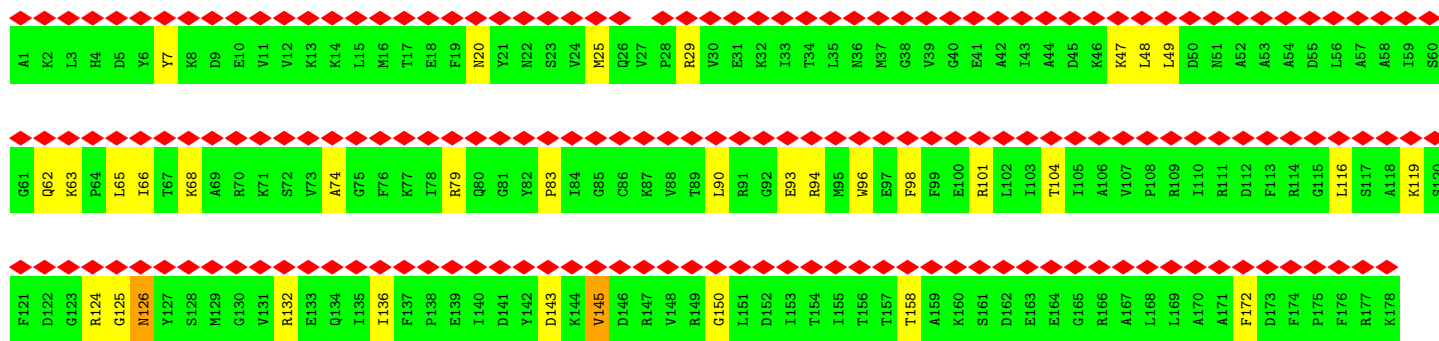
• Molecule 11: 50S ribosomal protein L4

Chain E:



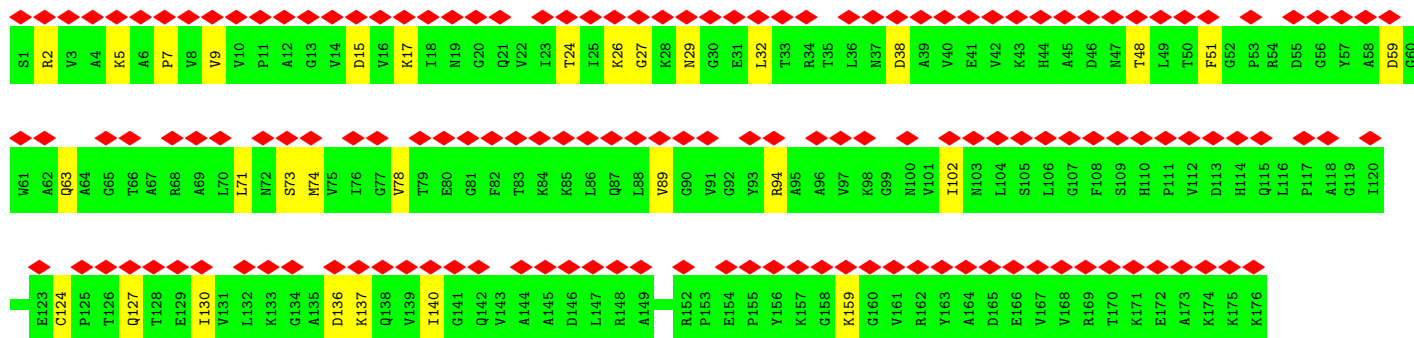
- Molecule 12: 50S ribosomal protein L5

Chain F:



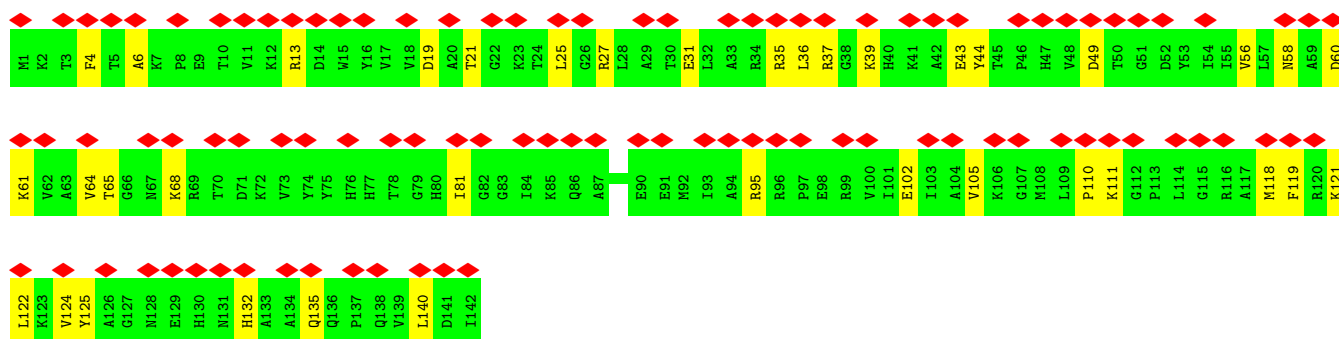
- Molecule 13: 50S ribosomal protein L6

Chain G:

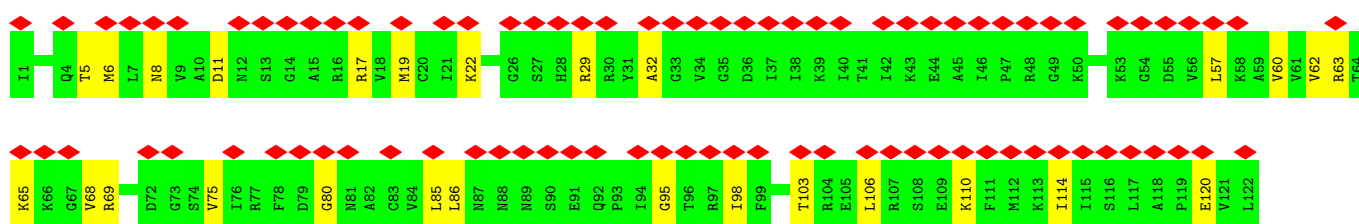
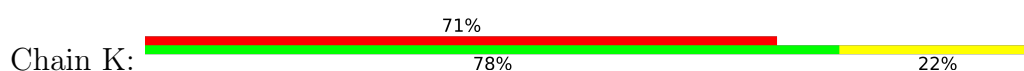


- Molecule 14: 50S ribosomal protein L13

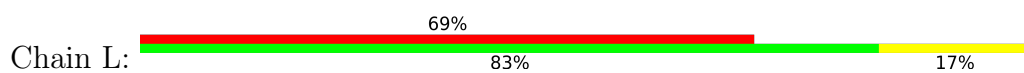
Chain J:



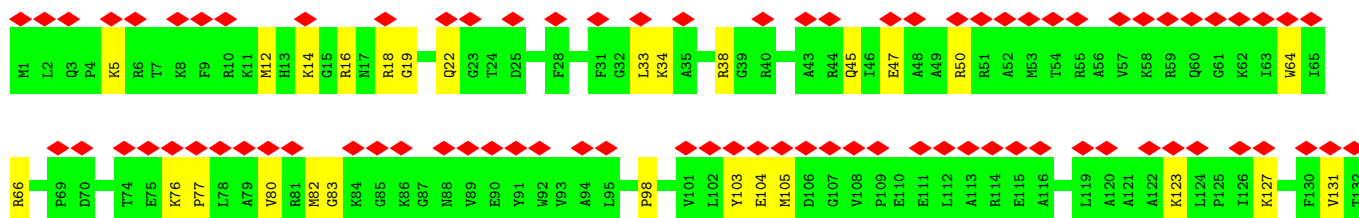
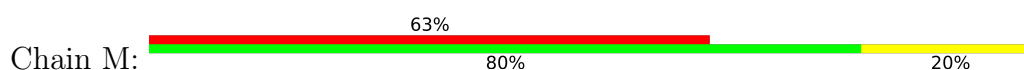
• Molecule 15: 50S ribosomal protein L14

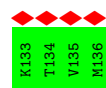


• Molecule 16: 50S ribosomal protein L15

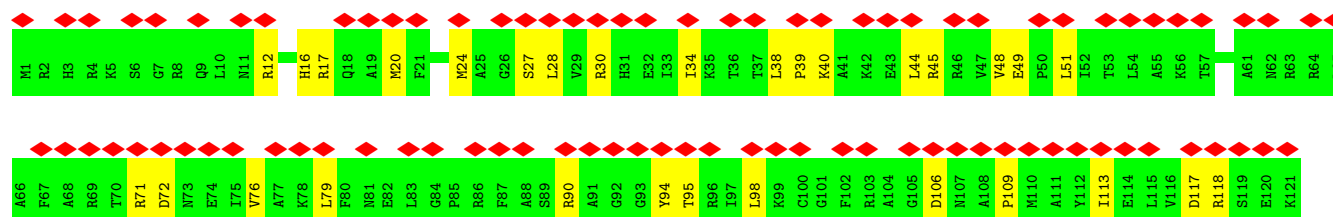
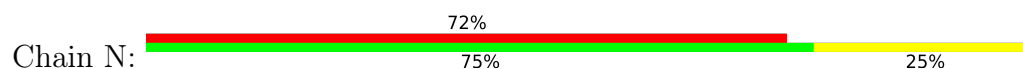


• Molecule 17: 50S ribosomal protein L16

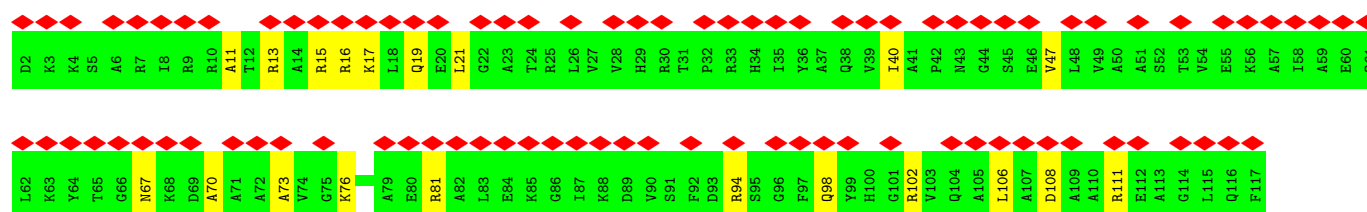
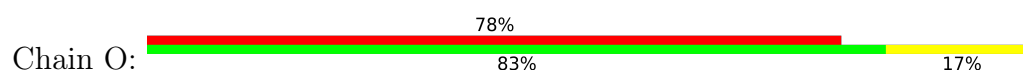




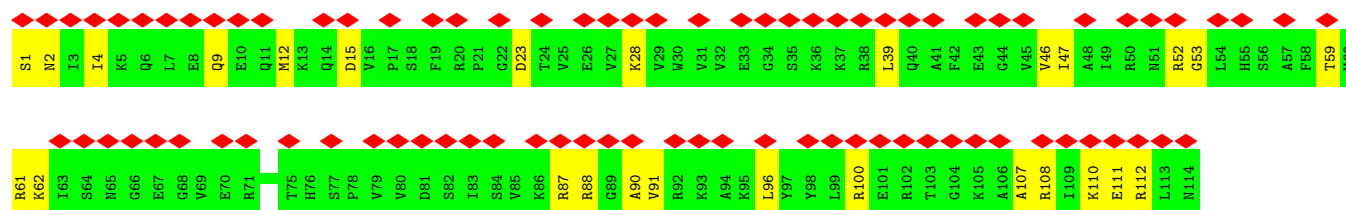
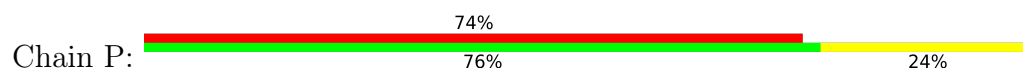
• Molecule 18: 50S ribosomal protein L17



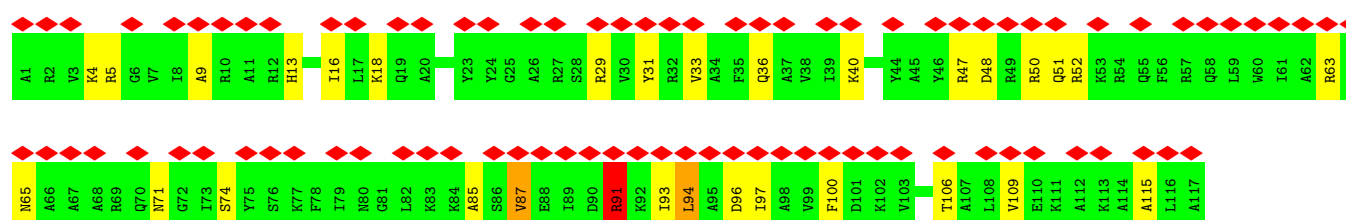
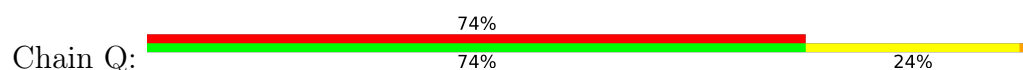
• Molecule 19: 50S ribosomal protein L18



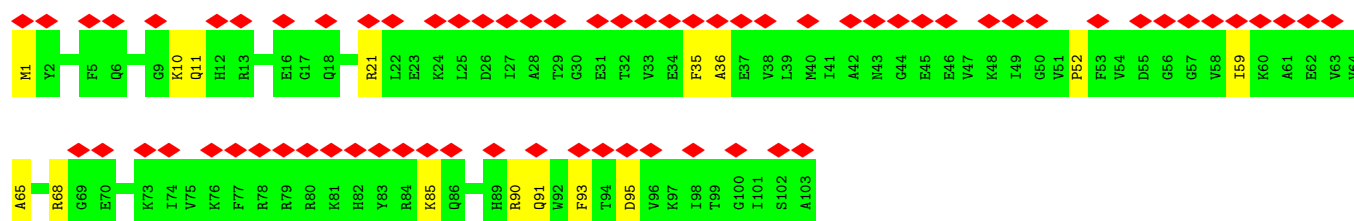
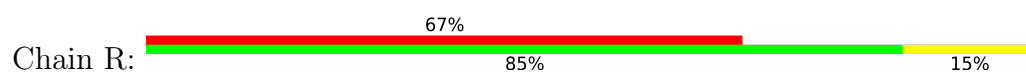
• Molecule 20: 50S ribosomal protein L19



• Molecule 21: 50S ribosomal protein L20



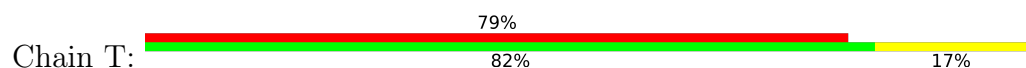
• Molecule 22: Ribosomal protein L21



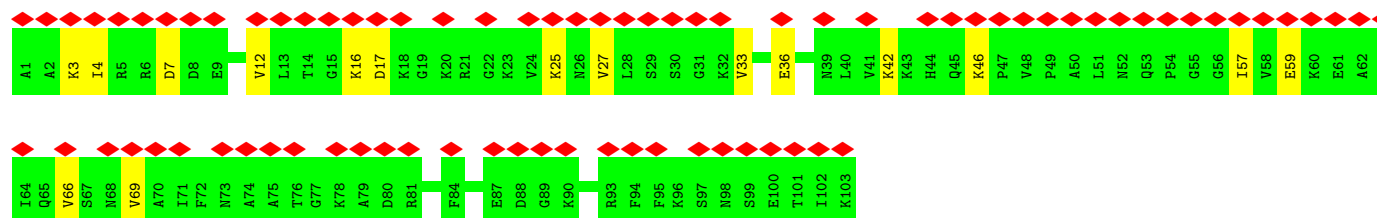
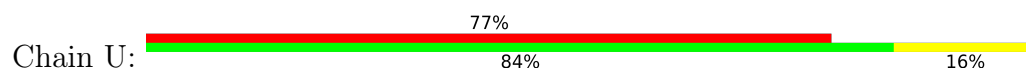
• Molecule 23: 50S ribosomal protein L22



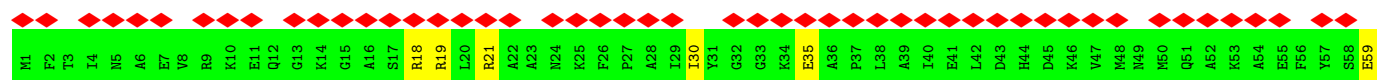
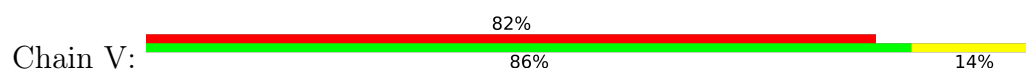
• Molecule 24: 50S ribosomal protein L23

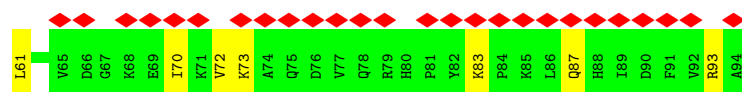


• Molecule 25: 50S ribosomal protein L24

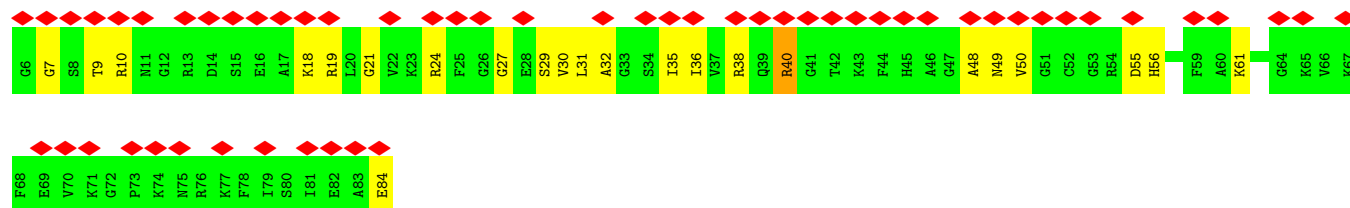


• Molecule 26: 50S ribosomal protein L25

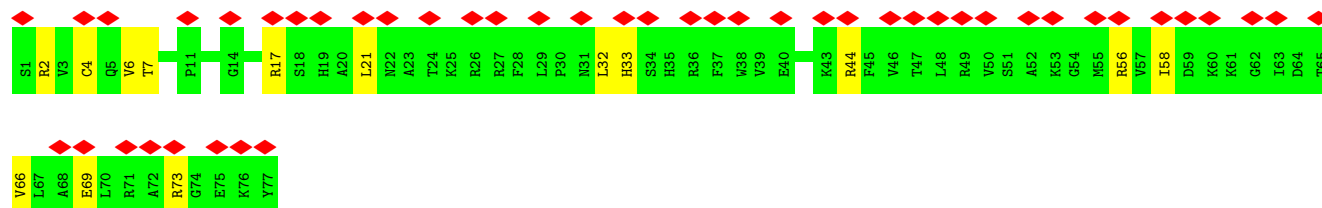
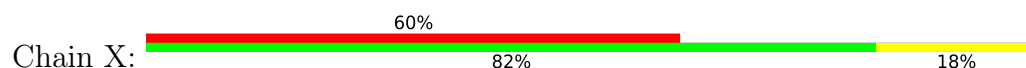




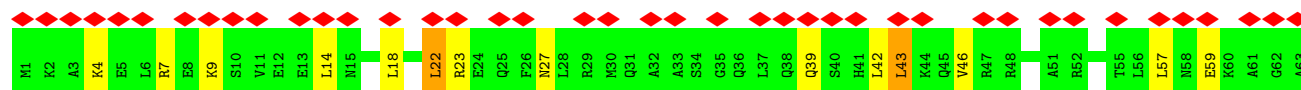
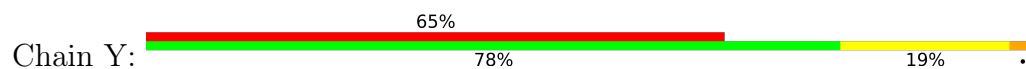
- Molecule 27: 50S ribosomal protein L27



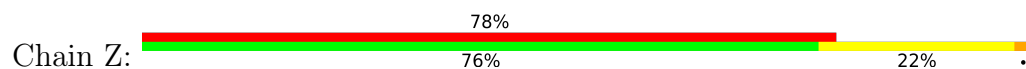
- Molecule 28: 50S ribosomal protein L28



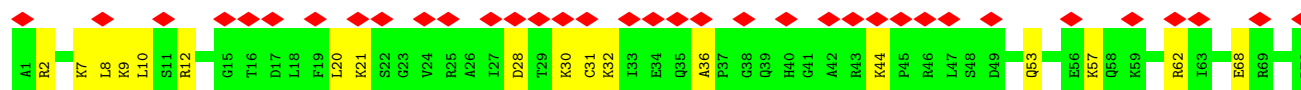
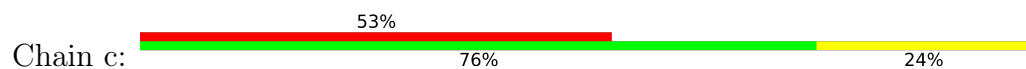
- Molecule 29: 50S ribosomal protein L29

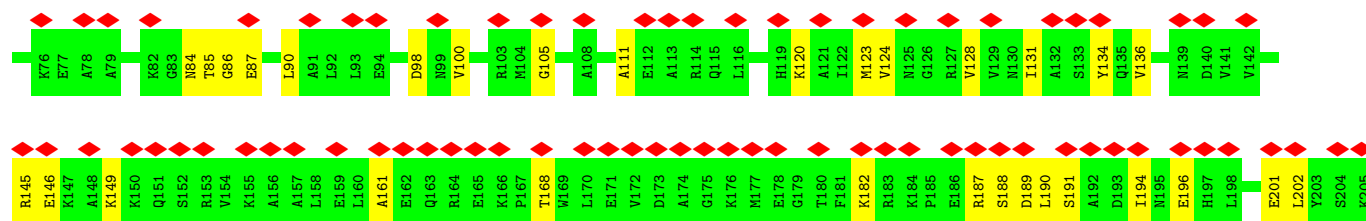


- Molecule 30: 50S ribosomal protein L30

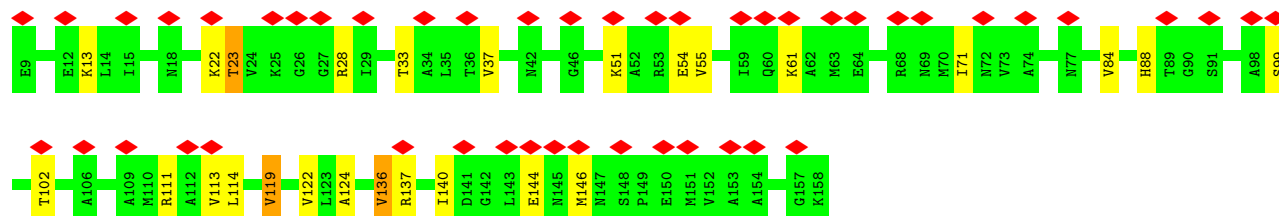
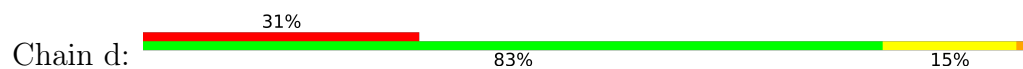


- Molecule 31: 30S ribosomal protein S4

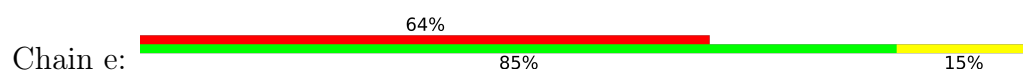




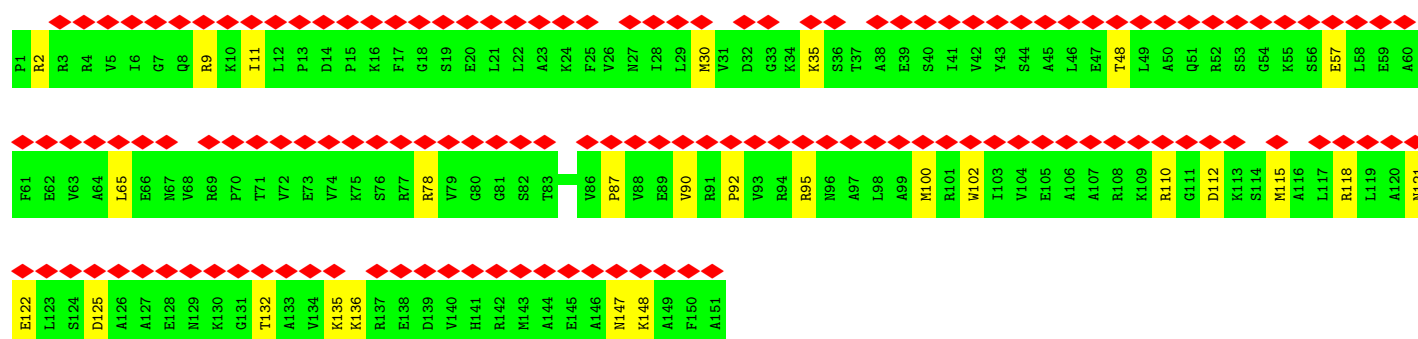
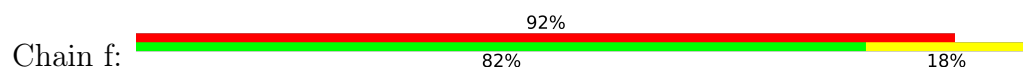
• Molecule 32: 30S ribosomal protein S5



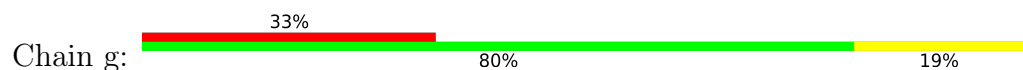
• Molecule 33: 30S ribosomal protein S6, non-modified isoform

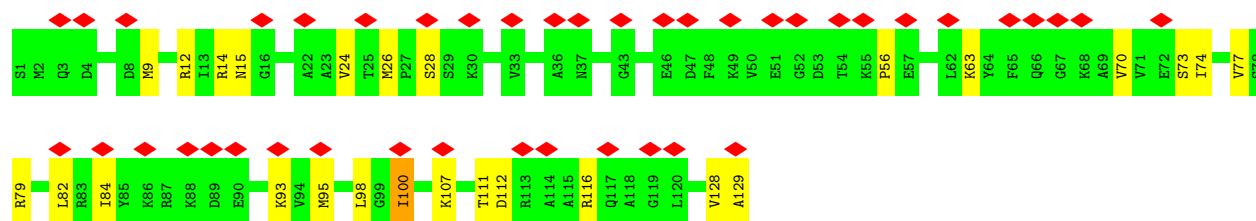


• Molecule 34: 30S ribosomal protein S7

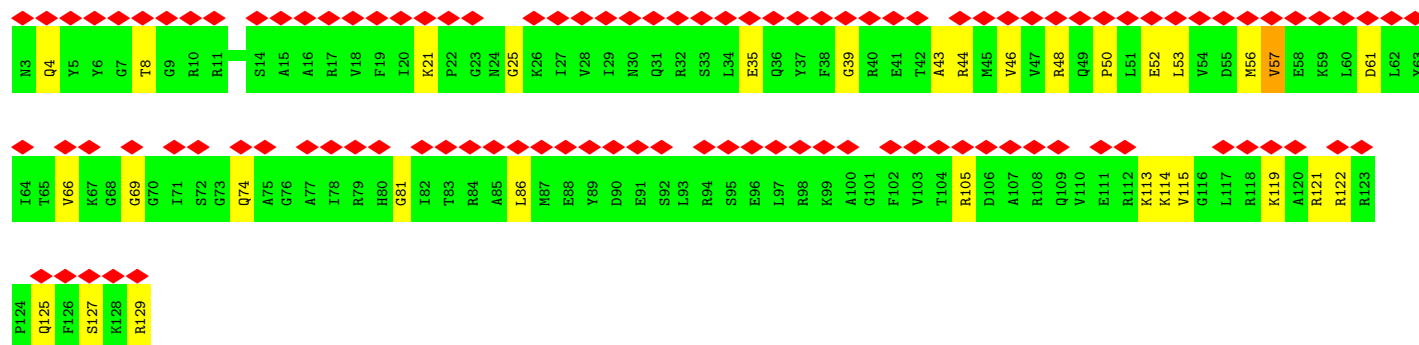
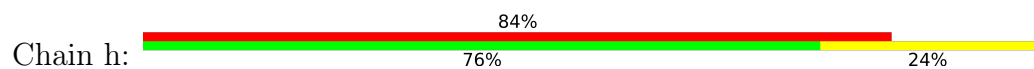


• Molecule 35: 30S ribosomal protein S8

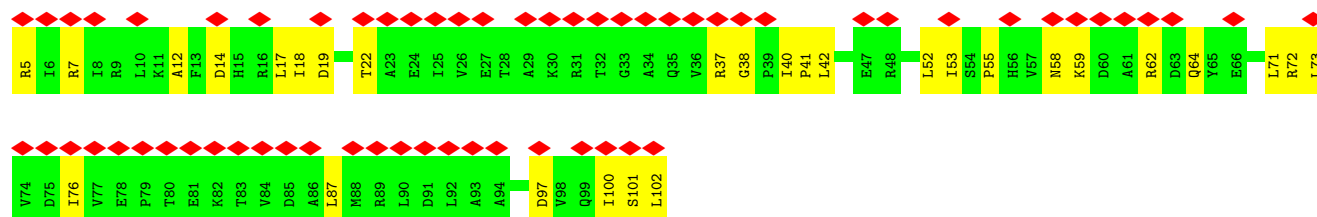




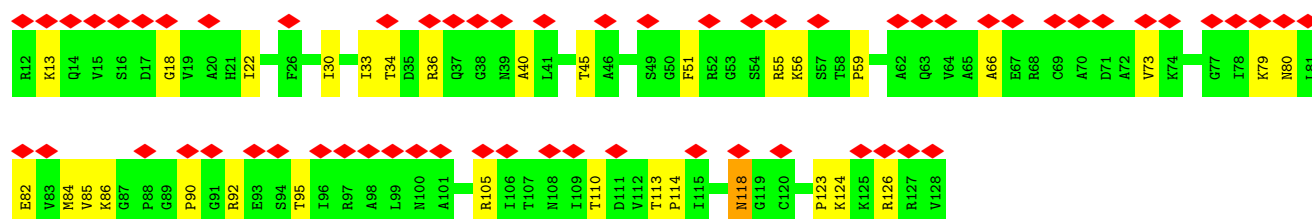
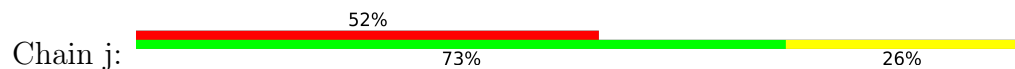
• Molecule 36: 30S ribosomal protein S9



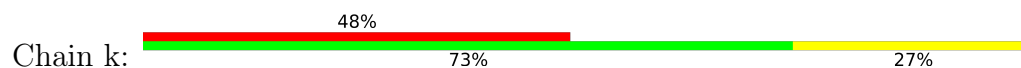
• Molecule 37: 30S ribosomal protein S10

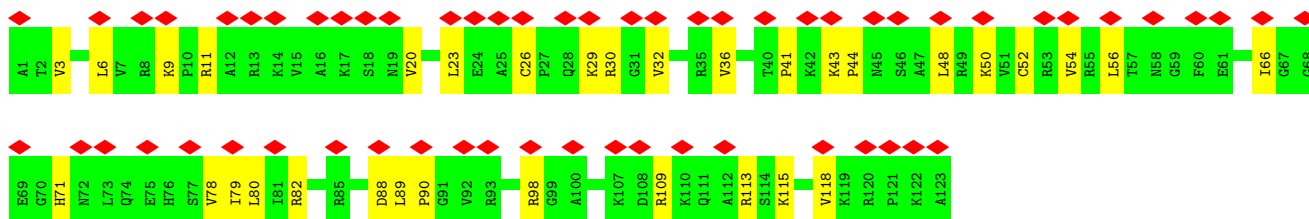


• Molecule 38: 30S ribosomal protein S11

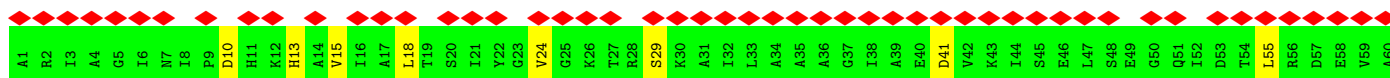
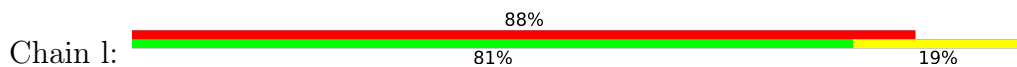


• Molecule 39: 30S ribosomal protein S12

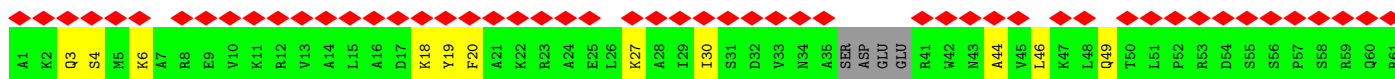
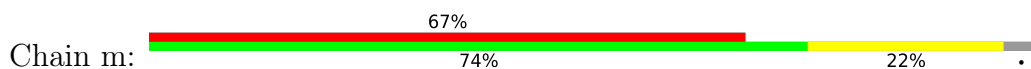




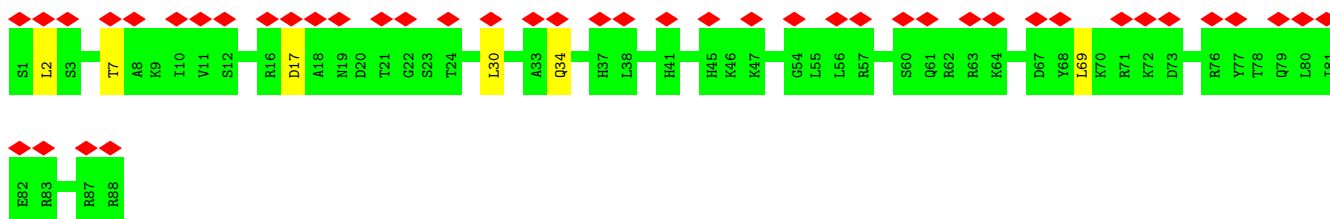
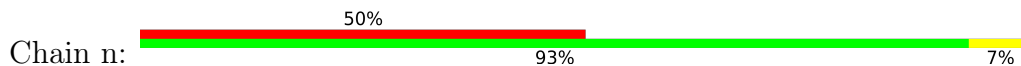
• Molecule 40: 30S ribosomal protein S13



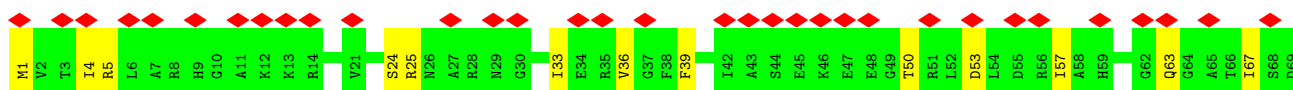
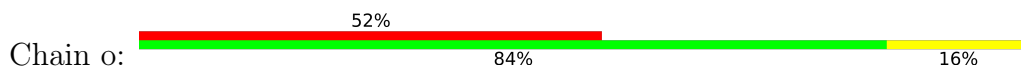
• Molecule 41: 30S ribosomal protein S14

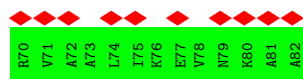


• Molecule 42: 30S ribosomal protein S15

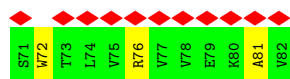
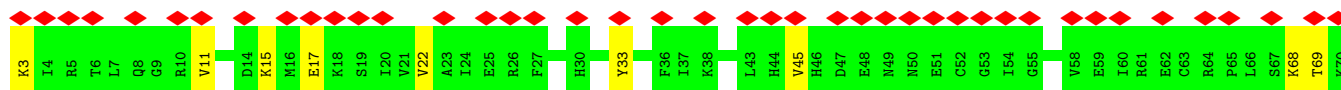
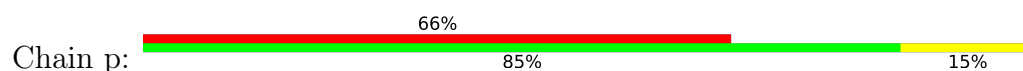


• Molecule 43: 30S ribosomal protein S16

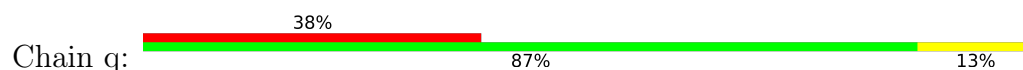




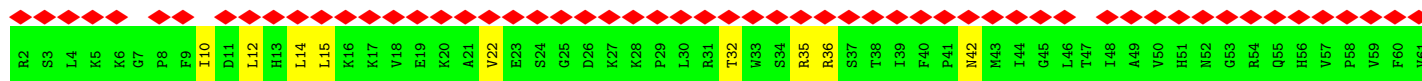
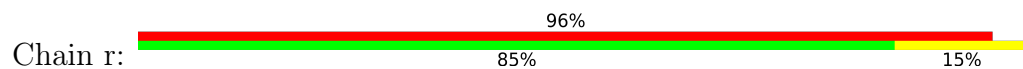
- Molecule 44: 30S ribosomal protein S17



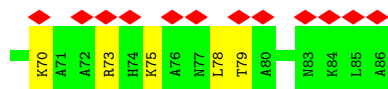
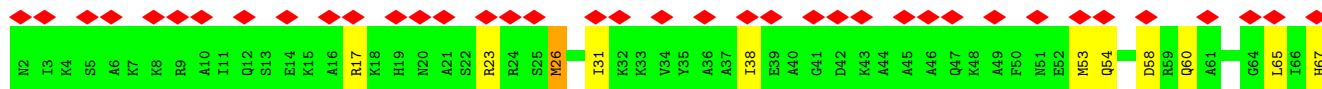
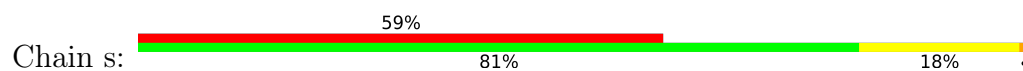
- Molecule 45: 30S ribosomal protein S18



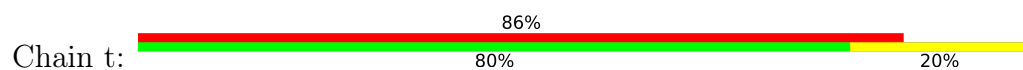
- Molecule 46: 30S ribosomal protein S19

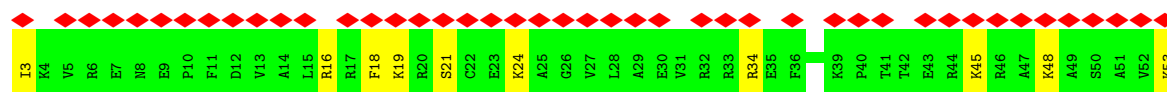


- Molecule 47: 30S ribosomal protein S20

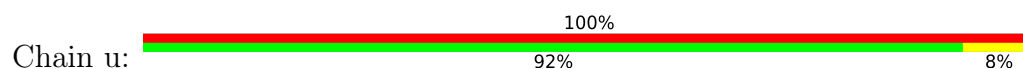


- Molecule 48: 30S ribosomal protein S21 (Fragment)

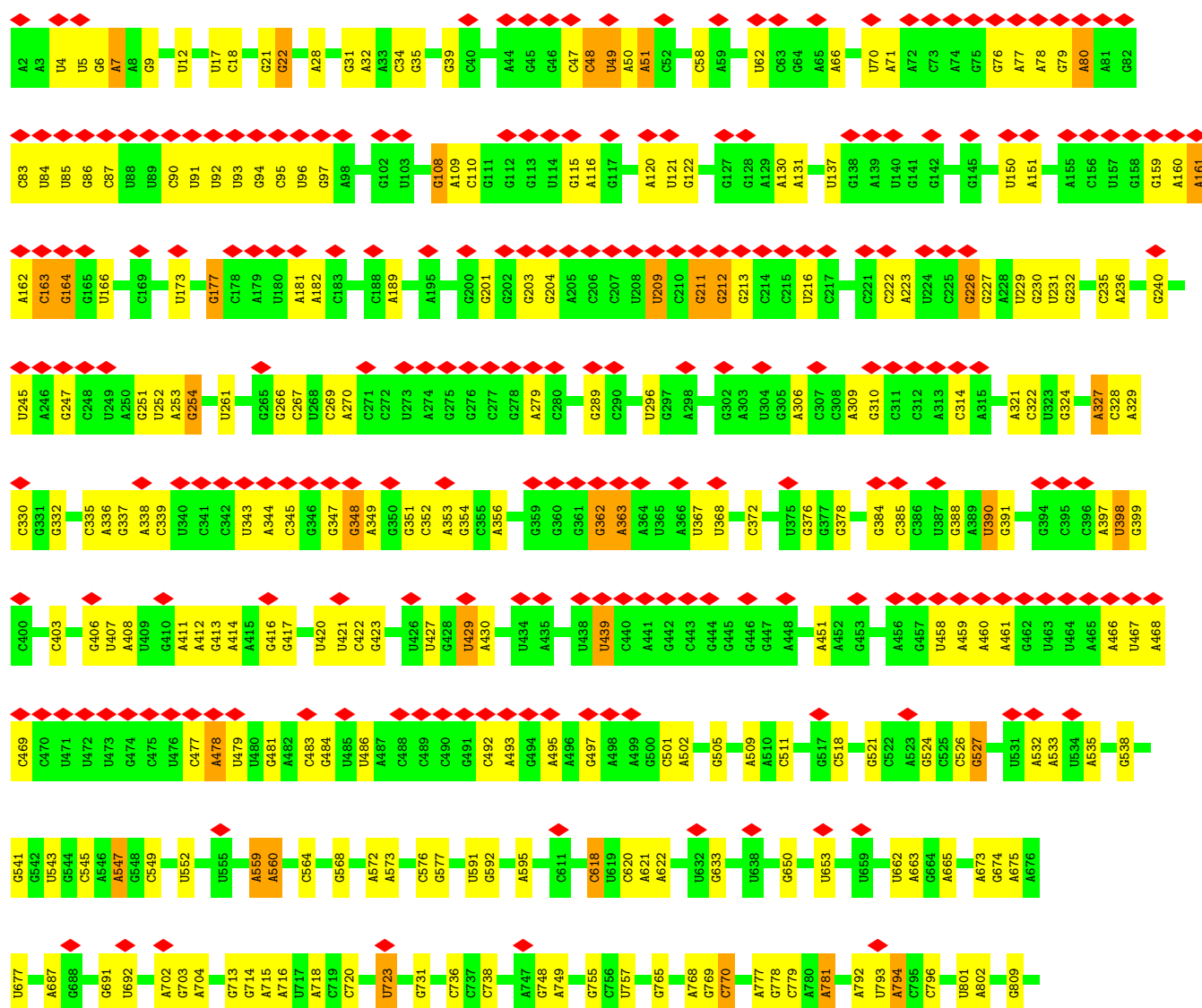
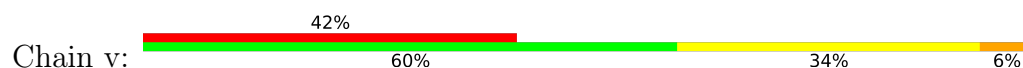


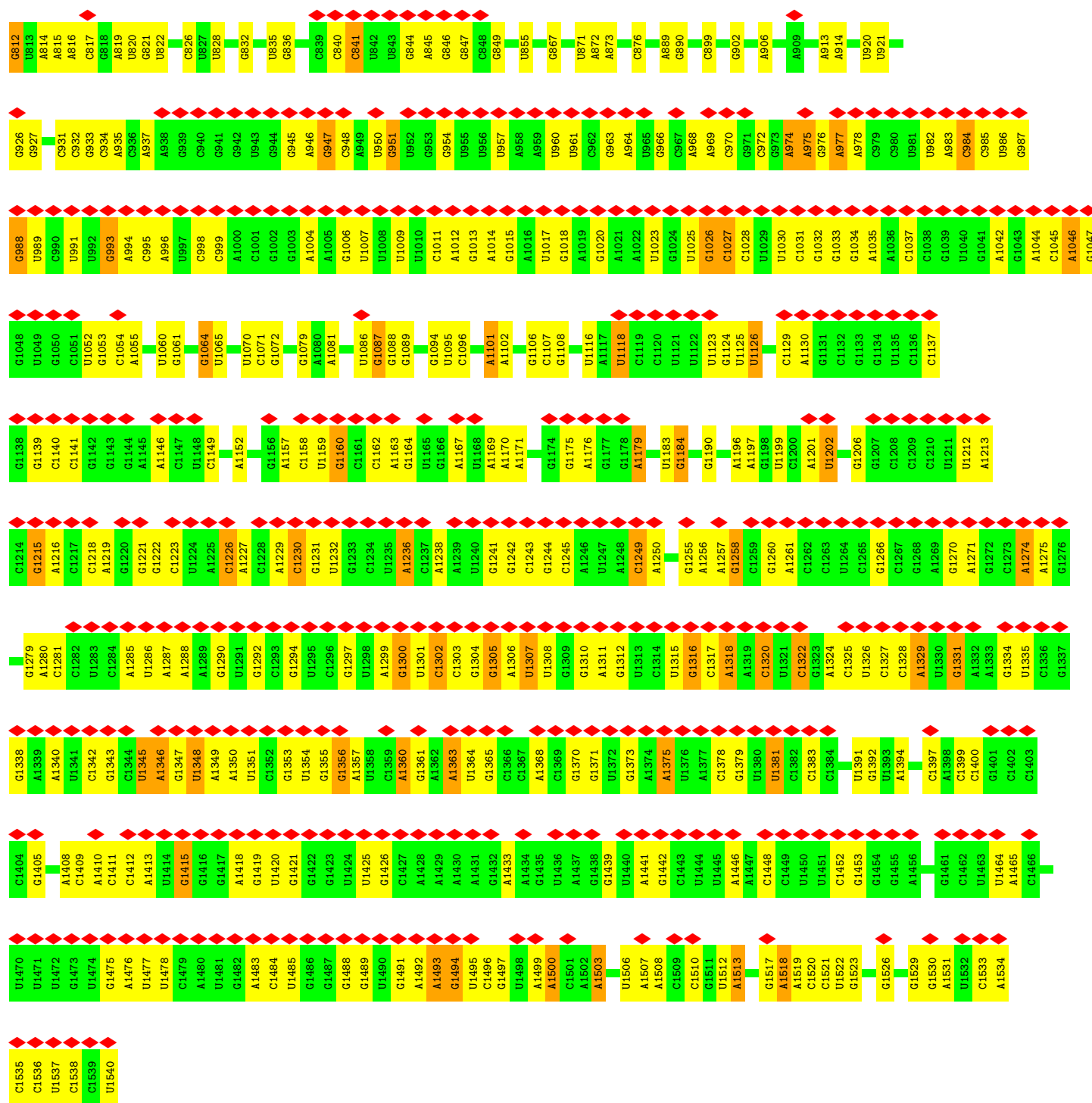


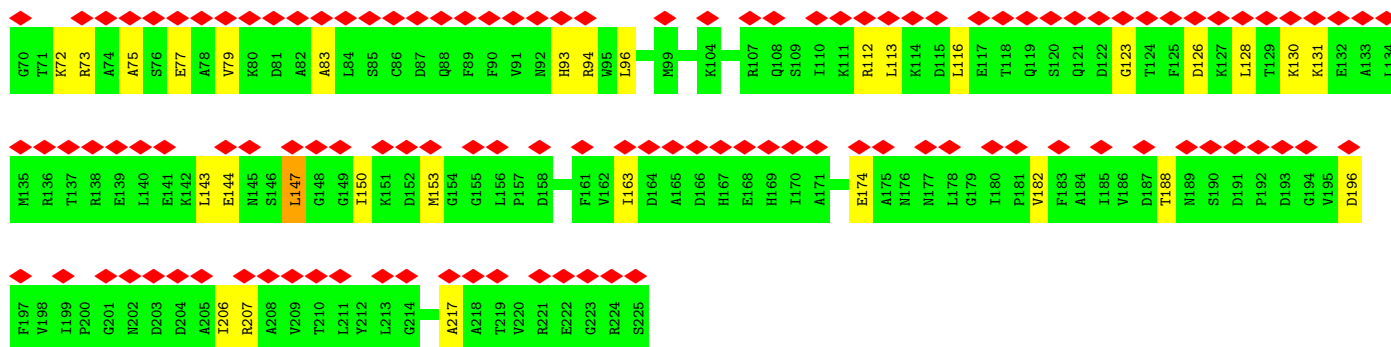
• Molecule 49: Transcription termination/antitermination protein NusG



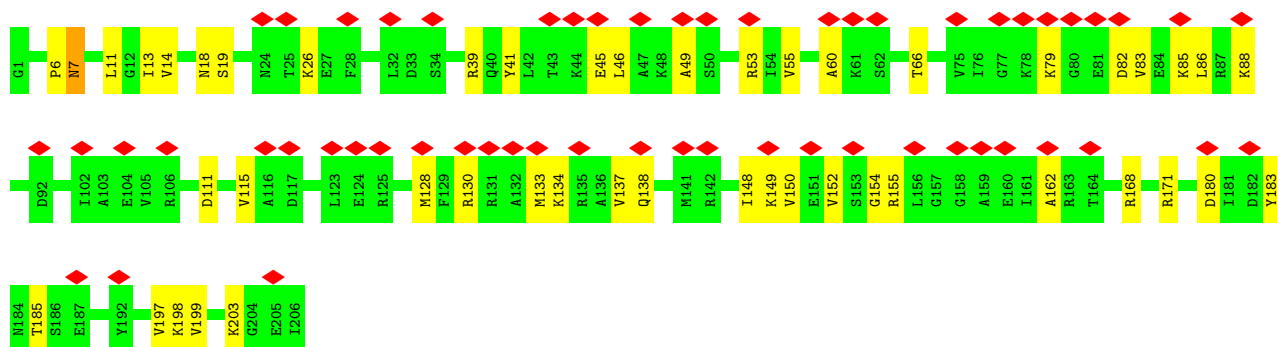
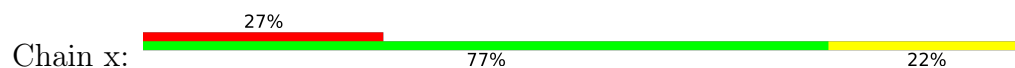
• Molecule 50: 16S







• Molecule 52: 30S ribosomal protein S3



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	140682	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	58	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.382	Depositor
Minimum map value	-0.072	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.054	Depositor
Recommended contour level	0.182	Depositor
Map size ($\text{\AA}$)	350.19998, 350.19998, 350.19998	wwPDB
Map dimensions	340, 340, 340	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.03, 1.03, 1.03	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	0	0.34	0/450	0.61	0/599
2	1	0.13	0/417	0.35	0/556
3	2	0.38	0/380	0.51	0/498
4	3	0.35	0/513	0.73	1/676 (0.1%)
5	4	0.32	0/303	0.59	0/397
6	6	0.27	0/3456	0.67	3/4675 (0.1%)
7	A	0.24	0/2800	0.37	0/4367
8	B	0.32	0/69796	0.40	5/108888 (0.0%)
9	C	0.30	0/2122	0.54	0/2854
10	D	0.35	0/1586	0.65	0/2134
11	E	0.41	1/1571 (0.1%)	0.69	3/2113 (0.1%)
12	F	0.19	0/1444	0.49	0/1937
13	G	0.25	0/1343	0.58	1/1816 (0.1%)
14	J	0.35	0/1152	0.64	0/1551
15	K	0.36	0/940	0.62	0/1260
16	L	0.34	0/1054	0.69	1/1403 (0.1%)
17	M	0.31	0/1093	0.57	0/1460
18	N	0.37	0/974	0.65	0/1303
19	O	0.32	0/902	0.70	1/1209 (0.1%)
20	P	0.34	0/929	0.63	2/1242 (0.2%)
21	Q	0.39	0/960	0.69	0/1278
22	R	0.35	0/829	0.65	0/1107
23	S	0.39	0/864	0.75	0/1156
24	T	0.35	0/745	0.75	1/996 (0.1%)
25	U	0.31	0/788	0.64	0/1053
26	V	0.30	0/766	0.58	0/1025
27	W	0.36	0/603	0.76	0/797
28	X	0.35	0/635	0.59	0/848
29	Y	0.34	0/510	0.83	3/677 (0.4%)
30	Z	0.31	0/453	0.53	0/605
31	c	0.32	0/1665	0.62	0/2227
32	d	0.49	1/1119 (0.1%)	0.80	3/1504 (0.2%)
33	e	0.33	0/836	0.74	0/1128
34	f	0.41	0/1196	0.67	2/1602 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	g	0.34	0/989	0.57	0/1326
36	h	0.32	0/1034	0.81	1/1375 (0.1%)
37	i	0.33	0/797	0.65	0/1077
38	j	0.31	0/893	0.60	0/1205
39	k	0.32	0/969	0.61	0/1300
40	l	0.34	0/893	0.69	0/1193
41	m	0.41	0/785	0.75	0/1043
42	n	0.32	0/722	0.60	0/964
43	o	0.32	0/659	0.48	0/884
44	p	0.29	0/658	0.61	0/881
45	q	0.33	0/463	0.59	0/621
46	r	0.26	0/653	0.55	0/877
47	s	0.35	0/671	0.68	0/888
48	t	0.31	0/431	0.71	0/570
49	u	0.16	0/477	0.44	0/642
50	v	0.34	0/36963	0.44	0/57662
51	w	0.31	0/1736	0.66	0/2338
52	x	0.36	0/1652	0.63	0/2225
All	All	0.33	2/156639 (0.0%)	0.49	27/234012 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
6	6	0	3
21	Q	0	2
23	S	0	1
27	W	0	1
38	j	0	1
39	k	0	1
All	All	0	9

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	E	76	PRO	CG-CD	-8.61	1.21	1.50
32	d	55	VAL	CA-CB	-8.56	1.48	1.53

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	E	76	PRO	N-CD-CG	-12.02	85.17	103.20
36	h	57	VAL	N-CA-C	-9.43	103.94	113.47
4	3	45	PRO	CA-N-CD	-8.92	99.52	112.00
8	B	1914	C	P-O3'-C3'	-7.68	108.68	120.20
11	E	76	PRO	CA-N-CD	-7.66	101.28	112.00

There are no chirality outliers.

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	6	257	ARG	Peptide
6	6	259	LEU	Peptide
6	6	260	PRO	Peptide
21	Q	91	ARG	Sidechain
21	Q	94	LEU	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	0	444	0	461	13	0
2	1	410	0	440	6	0
3	2	377	0	418	5	0
4	3	504	0	574	9	0
5	4	302	0	343	10	0
6	6	3403	0	3434	48	0
7	A	2504	0	1271	23	0
8	B	62317	0	31345	387	0
9	C	2083	0	2157	37	0
10	D	1565	0	1616	16	0
11	E	1552	0	1619	16	0
12	F	1420	0	1460	24	0
13	G	1323	0	1374	17	0
14	J	1129	0	1162	27	0
15	K	931	0	1003	19	0
16	L	1045	0	1117	19	0
17	M	1074	0	1157	21	0
18	N	961	0	1000	22	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	O	892	0	923	15	0
20	P	917	0	965	16	0
21	Q	947	0	1022	27	0
22	R	816	0	839	10	0
23	S	857	0	922	18	0
24	T	739	0	807	10	0
25	U	780	0	834	10	0
26	V	753	0	780	10	0
27	W	596	0	610	18	0
28	X	625	0	655	11	0
29	Y	509	0	543	8	0
30	Z	449	0	491	11	0
31	c	1643	0	1710	36	0
32	d	1106	0	1148	19	0
33	e	818	0	808	9	0
34	f	1182	0	1240	17	0
35	g	979	0	1034	18	0
36	h	1022	0	1070	24	0
37	i	787	0	828	25	0
38	j	877	0	887	23	0
39	k	955	0	1019	21	0
40	l	884	0	944	16	0
41	m	774	0	827	18	0
42	n	714	0	737	4	0
43	o	649	0	666	9	0
44	p	649	0	691	7	0
45	q	456	0	478	6	0
46	r	638	0	665	9	0
47	s	665	0	714	13	0
48	t	426	0	449	8	0
49	u	468	0	458	6	0
50	v	33012	0	16618	237	0
51	w	1705	0	1732	26	0
52	x	1625	0	1699	30	0
All	All	144258	0	97764	1231	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 5.

The worst 5 of 1231 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)
8:B:1311:G:N2	8:B:1603:A:H62	1.59	1.00
8:B:1168:G:H1	8:B:1181:U:H3	1.07	0.94
8:B:1913:A:H61	50:v:1493:A:H2'	1.31	0.93
8:B:1913:A:N6	50:v:1493:A:H2'	1.87	0.90
8:B:1311:G:H21	8:B:1603:A:H62	0.91	0.89

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	54/56 (96%)	48 (89%)	6 (11%)	0	100	100
2	1	49/51 (96%)	49 (100%)	0	0	100	100
3	2	44/46 (96%)	44 (100%)	0	0	100	100
4	3	62/64 (97%)	58 (94%)	4 (6%)	0	100	100
5	4	36/38 (95%)	32 (89%)	4 (11%)	0	100	100
6	6	424/426 (100%)	382 (90%)	42 (10%)	0	100	100
9	C	270/272 (99%)	260 (96%)	10 (4%)	0	100	100
10	D	207/209 (99%)	176 (85%)	31 (15%)	0	100	100
11	E	199/201 (99%)	188 (94%)	11 (6%)	0	100	100
12	F	176/178 (99%)	162 (92%)	14 (8%)	0	100	100
13	G	174/176 (99%)	166 (95%)	8 (5%)	0	100	100
14	J	140/142 (99%)	128 (91%)	12 (9%)	0	100	100
15	K	120/122 (98%)	110 (92%)	10 (8%)	0	100	100
16	L	141/143 (99%)	136 (96%)	5 (4%)	0	100	100
17	M	134/136 (98%)	128 (96%)	6 (4%)	0	100	100
18	N	119/121 (98%)	110 (92%)	9 (8%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	O	114/116 (98%)	112 (98%)	2 (2%)	0	100	100
20	P	112/114 (98%)	101 (90%)	11 (10%)	0	100	100
21	Q	115/117 (98%)	110 (96%)	4 (4%)	1 (1%)	14	47
22	R	101/103 (98%)	94 (93%)	6 (6%)	1 (1%)	12	45
23	S	108/110 (98%)	99 (92%)	9 (8%)	0	100	100
24	T	92/94 (98%)	84 (91%)	7 (8%)	1 (1%)	11	43
25	U	101/103 (98%)	90 (89%)	11 (11%)	0	100	100
26	V	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
27	W	77/79 (98%)	65 (84%)	12 (16%)	0	100	100
28	X	75/77 (97%)	73 (97%)	2 (3%)	0	100	100
29	Y	61/63 (97%)	57 (93%)	4 (7%)	0	100	100
30	Z	56/58 (97%)	54 (96%)	2 (4%)	0	100	100
31	c	203/205 (99%)	192 (95%)	11 (5%)	0	100	100
32	d	148/150 (99%)	136 (92%)	12 (8%)	0	100	100
33	e	98/100 (98%)	91 (93%)	7 (7%)	0	100	100
34	f	149/151 (99%)	144 (97%)	5 (3%)	0	100	100
35	g	127/129 (98%)	126 (99%)	1 (1%)	0	100	100
36	h	125/127 (98%)	116 (93%)	9 (7%)	0	100	100
37	i	96/98 (98%)	91 (95%)	5 (5%)	0	100	100
38	j	115/117 (98%)	111 (96%)	4 (4%)	0	100	100
39	k	121/123 (98%)	113 (93%)	8 (7%)	0	100	100
40	l	112/114 (98%)	107 (96%)	5 (4%)	0	100	100
41	m	92/100 (92%)	89 (97%)	3 (3%)	0	100	100
42	n	86/88 (98%)	84 (98%)	2 (2%)	0	100	100
43	o	80/82 (98%)	78 (98%)	2 (2%)	0	100	100
44	p	78/80 (98%)	72 (92%)	6 (8%)	0	100	100
45	q	53/55 (96%)	53 (100%)	0	0	100	100
46	r	77/79 (98%)	72 (94%)	5 (6%)	0	100	100
47	s	83/85 (98%)	81 (98%)	2 (2%)	0	100	100
48	t	49/51 (96%)	45 (92%)	4 (8%)	0	100	100
49	u	57/59 (97%)	56 (98%)	1 (2%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	w	216/218 (99%)	202 (94%)	14 (6%)	0	100	100
52	x	204/206 (99%)	196 (96%)	8 (4%)	0	100	100
All	All	5822/5926 (98%)	5460 (94%)	359 (6%)	3 (0%)	49	79

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
22	R	36	ALA
24	T	14	PRO
21	Q	87	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	47/47 (100%)	47 (100%)	0	100	100
2	1	45/46 (98%)	45 (100%)	0	100	100
3	2	38/38 (100%)	38 (100%)	0	100	100
4	3	51/51 (100%)	51 (100%)	0	100	100
5	4	34/34 (100%)	33 (97%)	1 (3%)	37	67
6	6	364/364 (100%)	362 (100%)	2 (0%)	81	85
9	C	216/217 (100%)	215 (100%)	1 (0%)	81	85
10	D	164/164 (100%)	162 (99%)	2 (1%)	63	79
11	E	165/165 (100%)	164 (99%)	1 (1%)	78	84
12	F	149/149 (100%)	147 (99%)	2 (1%)	61	78
13	G	137/137 (100%)	136 (99%)	1 (1%)	76	83
14	J	116/116 (100%)	115 (99%)	1 (1%)	70	81
15	K	102/103 (99%)	102 (100%)	0	100	100
16	L	102/102 (100%)	101 (99%)	1 (1%)	68	80
17	M	109/109 (100%)	108 (99%)	1 (1%)	70	81

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	N	100/101 (99%)	100 (100%)	0	100	100
19	O	86/86 (100%)	86 (100%)	0	100	100
20	P	99/99 (100%)	99 (100%)	0	100	100
21	Q	89/89 (100%)	88 (99%)	1 (1%)	65	79
22	R	84/84 (100%)	82 (98%)	2 (2%)	43	70
23	S	93/93 (100%)	92 (99%)	1 (1%)	65	79
24	T	80/81 (99%)	79 (99%)	1 (1%)	61	78
25	U	83/84 (99%)	81 (98%)	2 (2%)	43	70
26	V	78/78 (100%)	76 (97%)	2 (3%)	40	69
27	W	59/59 (100%)	59 (100%)	0	100	100
28	X	67/67 (100%)	67 (100%)	0	100	100
29	Y	55/55 (100%)	55 (100%)	0	100	100
30	Z	48/48 (100%)	47 (98%)	1 (2%)	47	71
31	c	172/172 (100%)	171 (99%)	1 (1%)	78	84
32	d	113/113 (100%)	111 (98%)	2 (2%)	51	74
33	e	87/87 (100%)	87 (100%)	0	100	100
34	f	124/124 (100%)	122 (98%)	2 (2%)	55	75
35	g	104/104 (100%)	103 (99%)	1 (1%)	68	80
36	h	105/105 (100%)	105 (100%)	0	100	100
37	i	86/86 (100%)	86 (100%)	0	100	100
38	j	90/90 (100%)	89 (99%)	1 (1%)	65	79
39	k	103/103 (100%)	103 (100%)	0	100	100
40	l	92/92 (100%)	92 (100%)	0	100	100
41	m	79/83 (95%)	79 (100%)	0	100	100
42	n	76/76 (100%)	76 (100%)	0	100	100
43	o	65/65 (100%)	65 (100%)	0	100	100
44	p	74/74 (100%)	73 (99%)	1 (1%)	59	77
45	q	48/48 (100%)	48 (100%)	0	100	100
46	r	70/70 (100%)	69 (99%)	1 (1%)	59	77
47	s	65/65 (100%)	64 (98%)	1 (2%)	57	76
48	t	44/44 (100%)	44 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
49	u	52/52 (100%)	52 (100%)	0	100	100
51	w	180/180 (100%)	178 (99%)	2 (1%)	65	79
52	x	170/170 (100%)	168 (99%)	2 (1%)	63	79
All	All	4859/4869 (100%)	4822 (99%)	37 (1%)	70	82

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
35	g	100	ILE
52	x	7	ASN
38	j	22	ILE
47	s	26	MET
17	M	105	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 60 such sidechains are listed below:

Mol	Chain	Res	Type
26	V	87	GLN
47	s	19	HIS
31	c	119	HIS
46	r	56	HIS
52	x	101	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
50	v	1538/1539 (99%)	395 (25%)	0
7	A	116/117 (99%)	25 (21%)	0
8	B	2902/2903 (99%)	697 (24%)	9 (0%)
All	All	4556/4559 (99%)	1117 (24%)	9 (0%)

5 of 1117 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	A	9	G
7	A	12	C
7	A	13	G
7	A	23	G
7	A	24	G

5 of 9 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
8	B	1963	U
8	B	2756	U
8	B	1339	G
8	B	1364	G
8	B	1912	A

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.

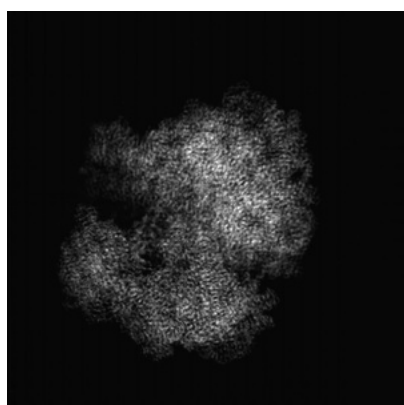
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-29687. These allow visual inspection of the internal detail of the map and identification of artifacts.

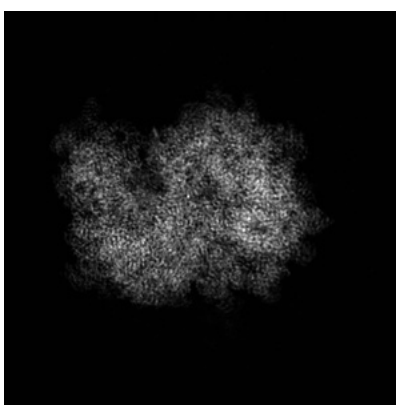
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

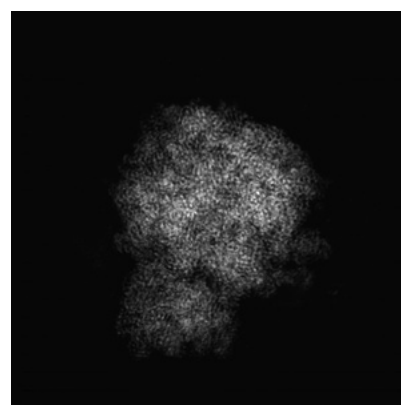
6.1.1 Primary map



X



Y



Z

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

6.2 Central slices [i](#)

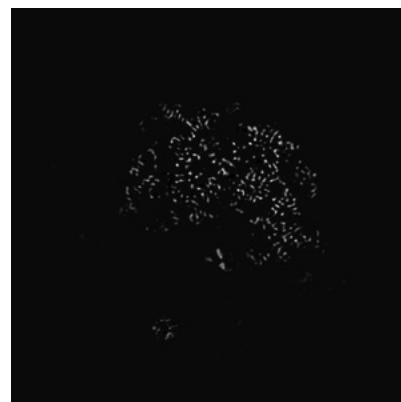
6.2.1 Primary map



X Index: 170



Y Index: 170



Z Index: 170

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: 146



Y Index: 178

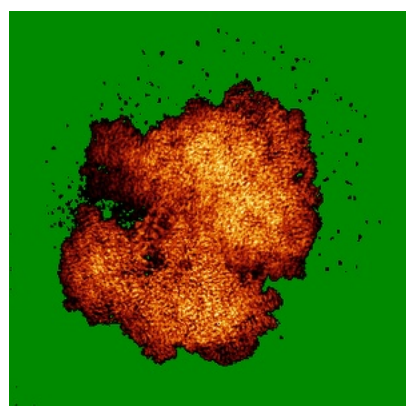


Z Index: 220

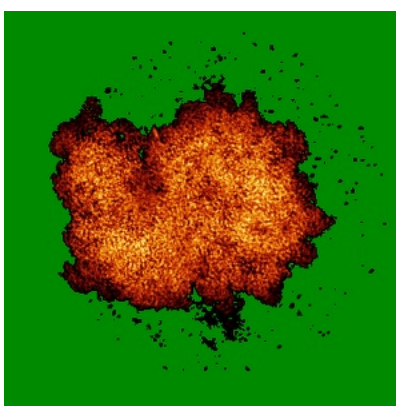
The images above show the largest variance slices of the map in three orthogonal directions.

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

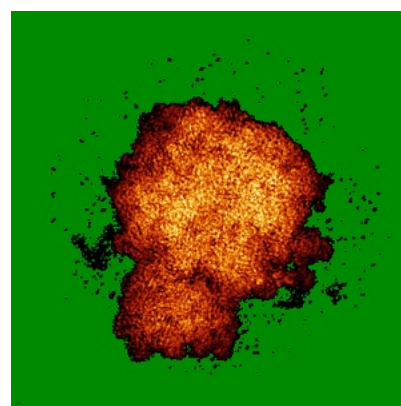
6.4.1 Primary map



X



Y



Z

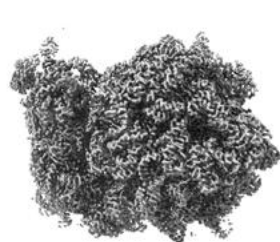
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.182. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

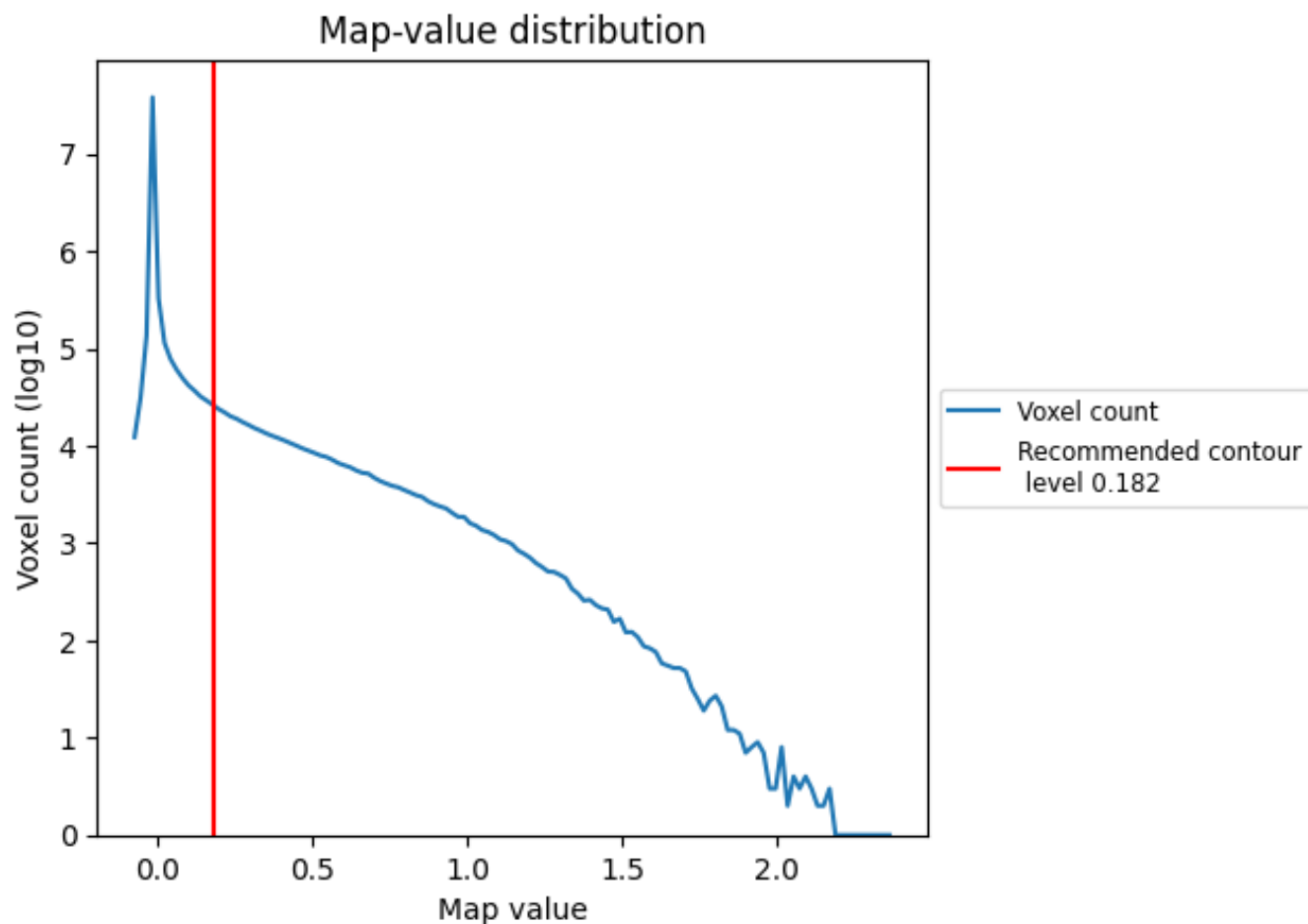
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

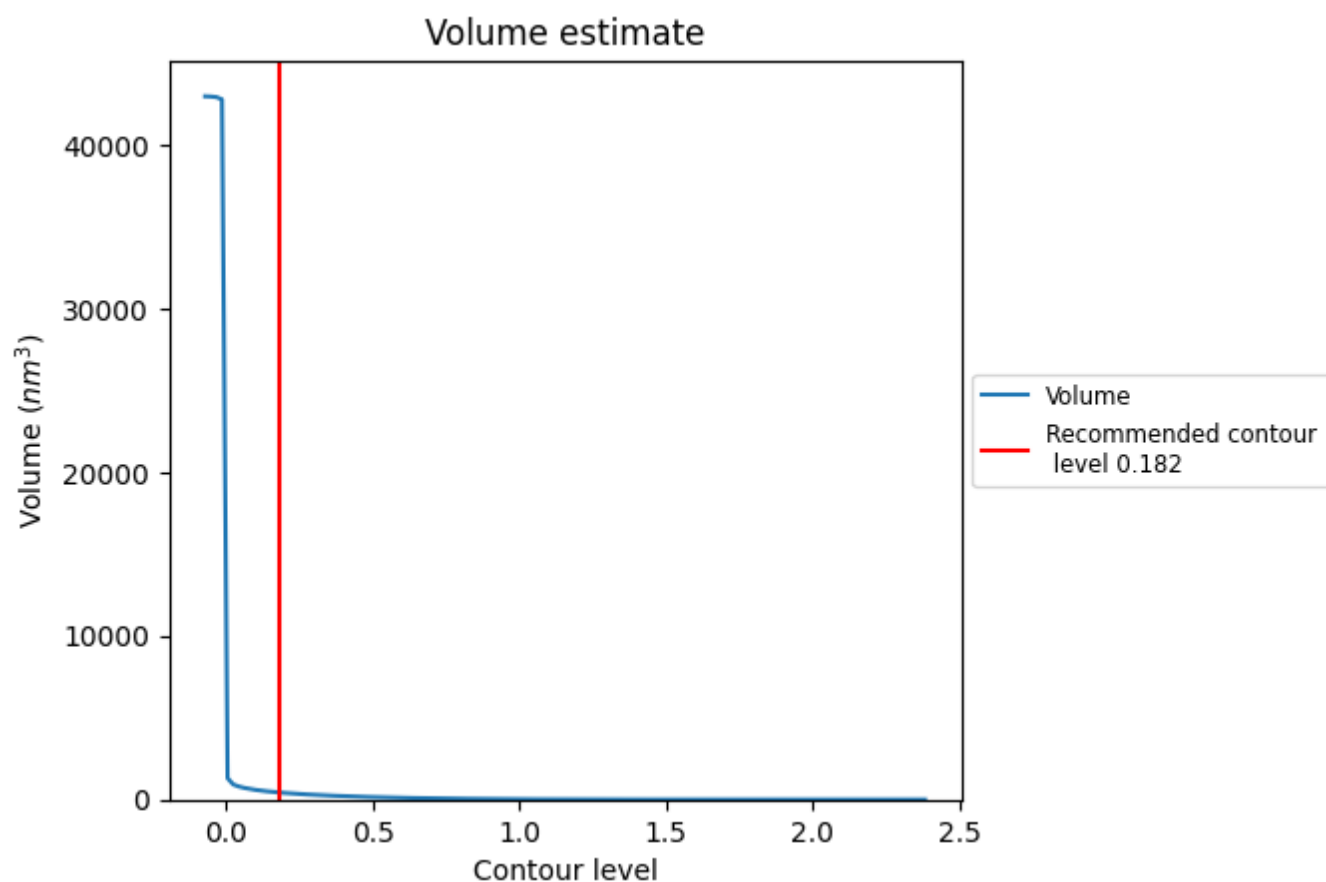
This section contains the results of statistical analysis of the map.

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.

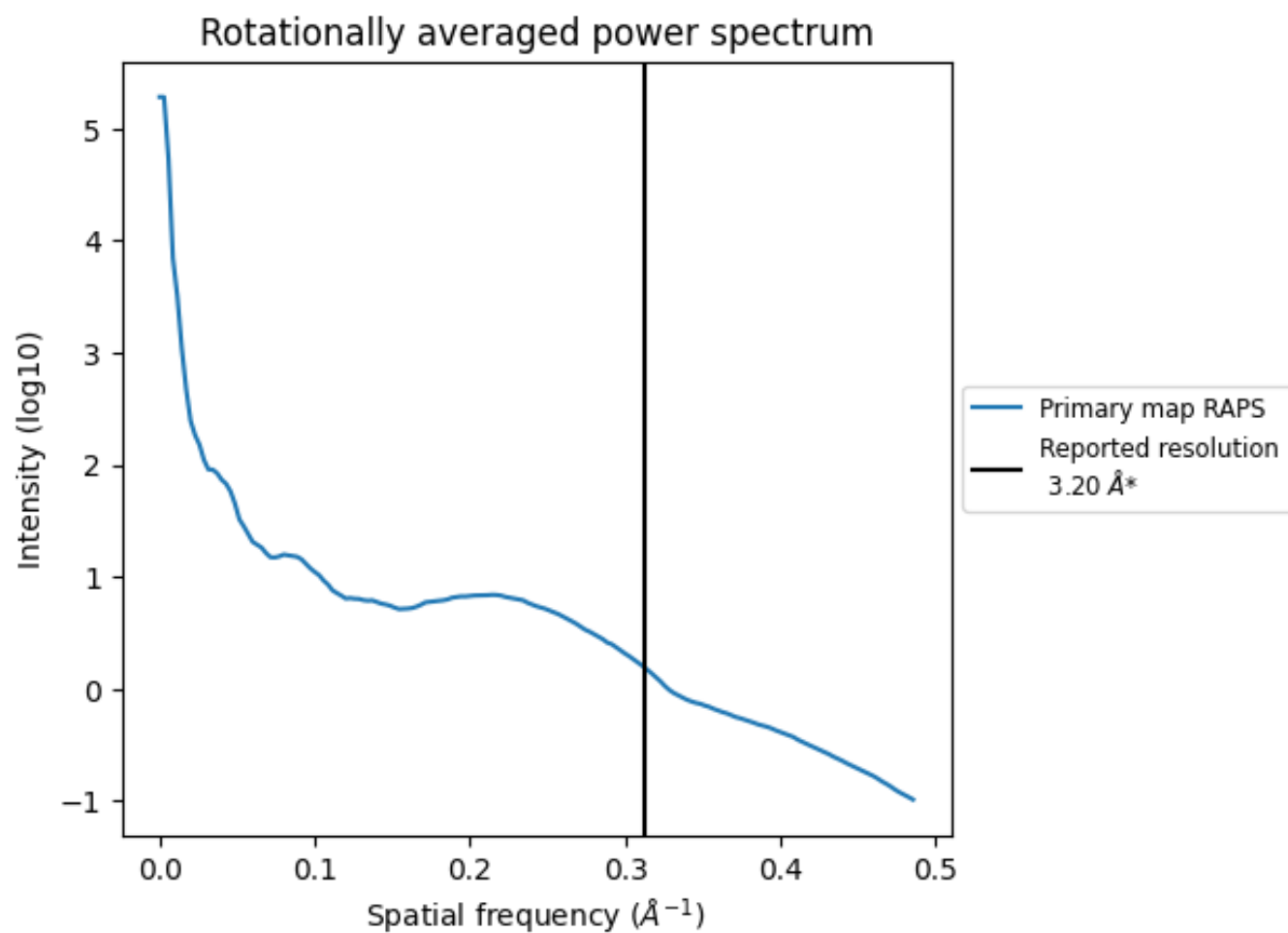
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 430 nm³; this corresponds to an approximate mass of 389 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 0.312 Å⁻¹

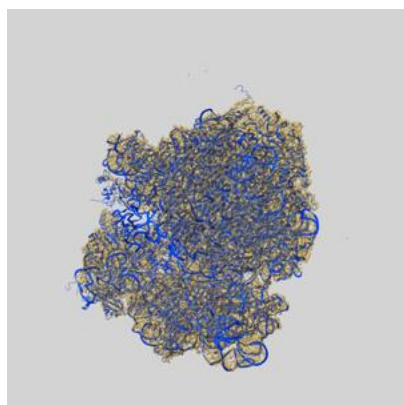
8 Fourier-Shell correlation

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

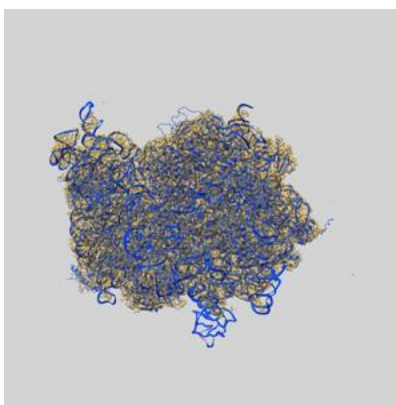
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-29687 and PDB model 8G31. Per-residue inclusion information can be found in section [3](#) on page [13](#).

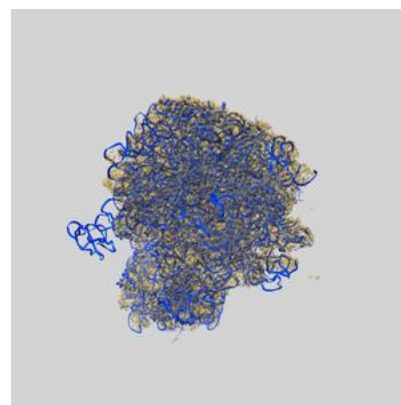
9.1 Map-model overlay [i](#)



X



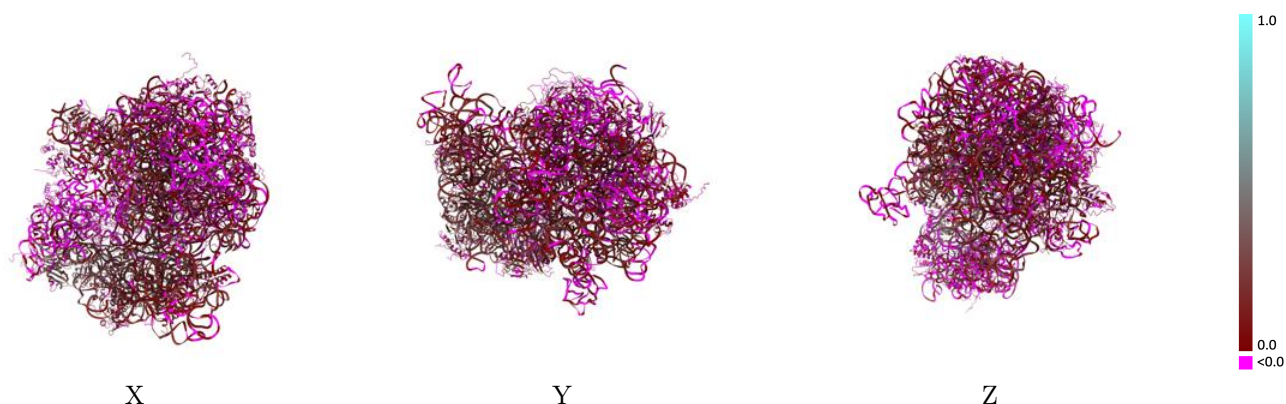
Y



Z

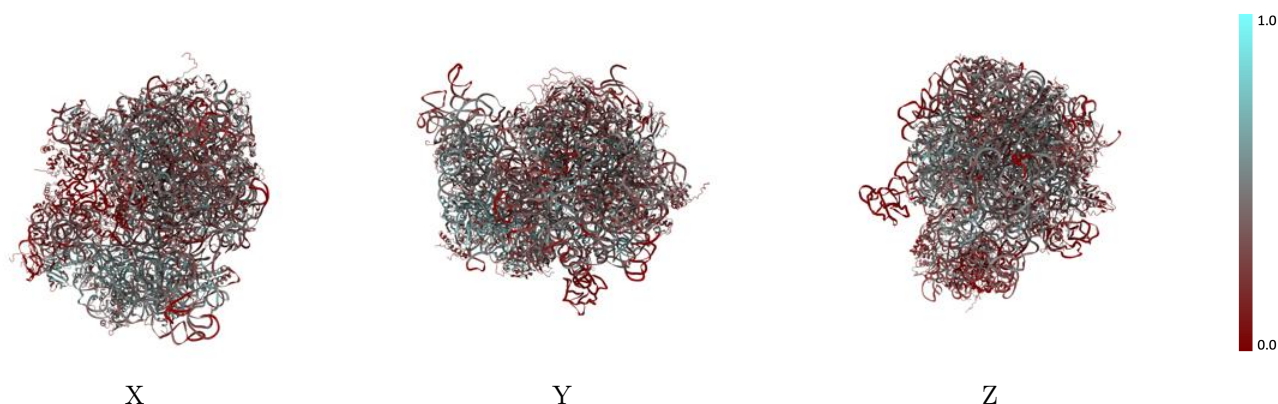
The images above show the 3D surface view of the map at the recommended contour level 0.182 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



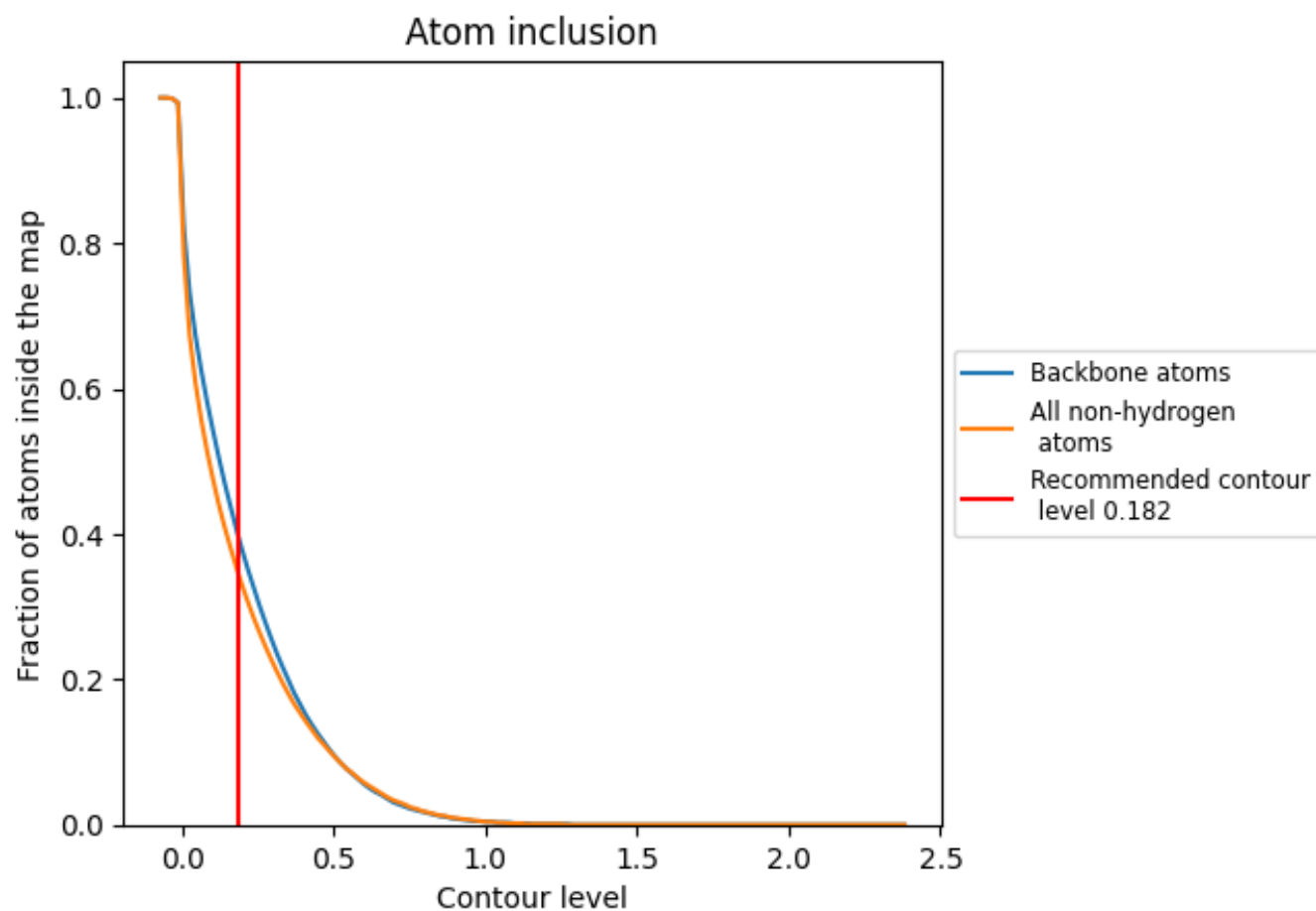
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.182).

9.4 Atom inclusion ⓘ



At the recommended contour level, 40% of all backbone atoms, 35% 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 (0.182) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3490	 0.0980
0	 0.2970	 0.0420
1	 0.0000	 0.0150
2	 0.3520	 0.0850
3	 0.2730	 0.1190
4	 0.3150	 0.0840
6	 0.1530	 -0.0030
A	 0.3450	 0.1450
B	 0.3580	 0.0820
C	 0.3310	 0.1350
D	 0.2210	 0.0170
E	 0.2520	 0.0290
F	 0.0330	 -0.0000
G	 0.1770	 0.0520
J	 0.3320	 0.0540
K	 0.2830	 0.0750
L	 0.3150	 0.0850
M	 0.3020	 0.0900
N	 0.3240	 0.0410
O	 0.2580	 0.1250
P	 0.2610	 0.0690
Q	 0.3210	 0.0190
R	 0.3060	 0.0510
S	 0.3280	 0.0500
T	 0.2560	 0.0040
U	 0.2600	 0.0480
V	 0.2720	 0.0890
W	 0.3090	 0.0770
X	 0.3860	 0.1240
Y	 0.2860	 0.0440
Z	 0.2400	 0.0260
c	 0.4040	 0.1730
d	 0.5100	 0.2370
e	 0.3380	 0.1270
f	 0.1380	 -0.0360



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
g	 0.5040	 0.2280
h	 0.2120	 -0.0100
i	 0.3190	 0.1370
j	 0.3990	 0.1690
k	 0.4040	 0.1750
l	 0.1750	 -0.0220
m	 0.2870	 0.0600
n	 0.4270	 0.1940
o	 0.4150	 0.1540
p	 0.3180	 0.1330
q	 0.4760	 0.1870
r	 0.1110	 -0.0630
s	 0.3860	 0.1080
t	 0.1600	 0.0880
u	 0.0000	 -0.0130
v	 0.4180	 0.1430
w	 0.2360	 0.1070
x	 0.5220	 0.3140