



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 06:22 PM UTC

PDB ID : 6GZX / pdb_00006gzx
EMDB ID : EMD-0104
Title : T. thermophilus hibernating 100S ribosome (ice)
Authors : Flygaard, R.K.; Jenner, L.B.
Deposited on : 2018-07-05
Resolution : 4.57 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:

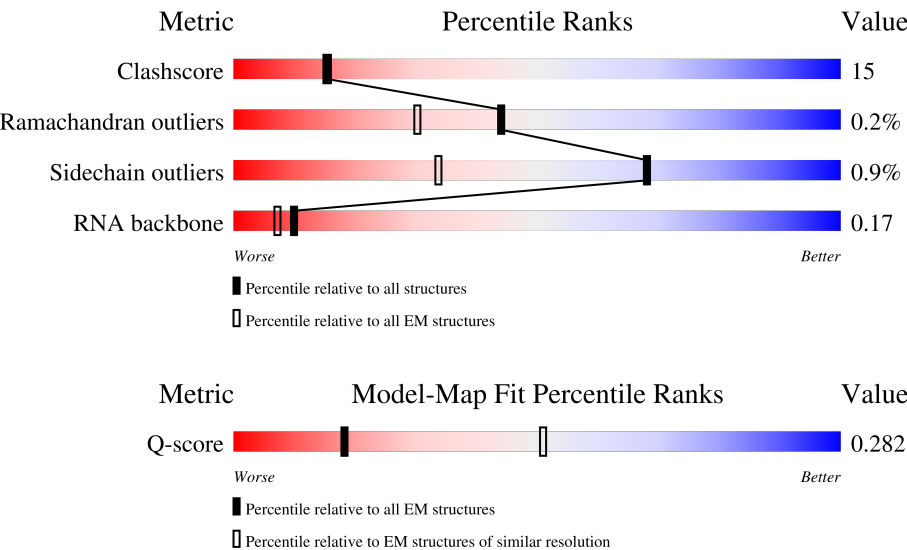
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 4.57 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	2418 (4.07 - 5.07)

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	C1	272	
1	C2	272	
2	D1	205	

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Mol	Chain	Length	Quality of chain
2	D2	205	
3	E1	208	
3	E2	208	
4	F1	181	
4	F2	181	
5	G1	170	
5	G2	170	
6	H1	50	
6	H2	50	
7	I1	138	
7	I2	138	
8	J1	122	
8	J2	122	
9	K1	150	
9	K2	150	
10	L1	141	
10	L2	141	
11	M1	117	
11	M2	117	
12	N1	111	
12	N2	111	
13	O1	137	
13	O2	137	
14	P1	117	
14	P2	117	

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Mol	Chain	Length	Quality of chain
15	Q1	101	50% 71% 29%
15	Q2	101	50% 65% 34%
16	R1	113	45% 68% 31%
16	R2	113	43% 62% 35%
17	S1	92	24% 73% 26%
17	S2	92	29% 62% 38%
18	T1	102	46% 65% 33%
18	T2	102	47% 67% 32%
19	U1	179	55% 68% 30%
19	U2	179	52% 72% 27%
20	V1	77	31% 57% 42%
20	V2	77	30% 69% 31%
21	W1	97	34% 51% 47%
21	W2	97	36% 66% 34%
22	X1	69	19% 59% 39%
22	X2	69	14% 67% 33%
23	Y1	59	56% 56% 44%
23	Y2	59	47% 68% 32%
24	Z1	63	17% 63% 27% 8%
24	Z2	63	21% 62% 35%
25	a1	59	29% 64% 36%
25	a2	59	32% 61% 39%
26	b1	45	9% 58% 40%
26	b2	45	13% 56% 42%
27	c1	49	35% 53% 47%

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Mol	Chain	Length	Quality of chain
27	c2	49	
28	d1	61	
28	d2	61	
29	A1	2912	
29	A2	2912	
30	B1	122	
30	B2	122	
31	e1	36	
31	e2	36	
32	B3	237	
32	B4	237	
33	C3	206	
33	C4	206	
34	D3	208	
34	D4	208	
35	E3	151	
35	E4	151	
36	F3	101	
36	F4	101	
37	G3	155	
37	G4	155	
38	H3	138	
38	H4	138	
39	I3	127	
39	I4	127	

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Mol	Chain	Length	Quality of chain
40	J3	99	
40	J4	99	
41	K3	118	
41	K4	118	
42	L3	125	
42	L4	125	
43	M3	117	
43	M4	117	
44	N3	60	
44	N4	60	
45	O3	88	
45	O4	88	
46	P3	84	
46	P4	84	
47	Q3	100	
47	Q4	100	
48	R3	62	
48	R4	62	
49	S3	78	
49	S4	78	
50	T3	99	
50	T4	99	
51	U3	25	
51	U4	25	
52	W4	57	

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Mol	Chain	Length	Quality of chain
52	X3	57	14% 61% 35%
53	A3	1506	24% 52% 25%
53	A4	1506	25% 48% 27%
54	V3	119	23% 67% 29%
54	V4	119	25% 61% 37%

2 Entry composition

There are 54 unique types of molecules in this entry. The entry contains 289188 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 L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C1	272	Total	C	N	O	S	0	0
			2116	1335	420	358	3		
1	C2	272	Total	C	N	O	S	0	0
			2116	1335	420	358	3		

- Molecule 2 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D1	205	Total	C	N	O	S	0	0
			1569	991	300	272	6		
2	D2	205	Total	C	N	O	S	0	0
			1569	991	300	272	6		

- Molecule 3 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E1	208	Total	C	N	O	S	0	0
			1628	1037	304	284	3		
3	E2	208	Total	C	N	O	S	0	0
			1628	1037	304	284	3		

- Molecule 4 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	F1	181	Total	C	N	O	S	0	0
			1474	942	268	260	4		
4	F2	181	Total	C	N	O	S	0	0
			1474	942	268	260	4		

- Molecule 5 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G1	170	Total	C	N	O	S	0	0
			1308	829	245	233	1		
5	G2	170	Total	C	N	O	S	0	0
			1308	829	245	233	1		

- Molecule 6 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	H1	50	Total	C	N	O	S	0	0
			383	245	66	71	1		
6	H2	50	Total	C	N	O	S	0	0
			383	245	66	71	1		

- Molecule 7 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	I1	138	Total	C	N	O	S	0	0
			1105	712	206	183	4		
7	I2	138	Total	C	N	O	S	0	0
			1105	712	206	183	4		

- Molecule 8 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	J1	122	Total	C	N	O	S	0	0
			933	588	171	170	4		
8	J2	122	Total	C	N	O	S	0	0
			933	588	171	170	4		

- Molecule 9 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	K1	150	Total	C	N	O	S	0	0
			1145	712	232	198	3		
9	K2	150	Total	C	N	O	S	0	0
			1145	712	232	198	3		

- Molecule 10 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L1	141	Total	C	N	O	S	0	0
			1122	715	212	188	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
10	L2	141	Total	C	N	O	S	0	0
			1122	715	212	188	7		

- Molecule 11 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	M1	117	Total	C	N	O		0	0
			960	599	202	159			
11	M2	117	Total	C	N	O		0	0
			960	599	202	159			

- Molecule 12 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	N1	111	Total	C	N	O		0	0
			882	556	176	150			
12	N2	111	Total	C	N	O		0	0
			882	556	176	150			

- Molecule 13 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	O1	137	Total	C	N	O	S	0	0
			1142	710	234	197	1		
13	O2	137	Total	C	N	O	S	0	0
			1142	710	234	197	1		

- Molecule 14 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	P1	117	Total	C	N	O	S	0	0
			964	610	202	151	1		
14	P2	117	Total	C	N	O	S	0	0
			964	610	202	151	1		

- Molecule 15 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Q1	101	Total	C	N	O	S	0	0
			779	501	142	135	1		
15	Q2	101	Total	C	N	O	S	0	0
			779	501	142	135	1		

- Molecule 16 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	R1	113	Total	C	N	O	S	0	0
			900	566	177	155	2		
16	R2	113	Total	C	N	O	S	0	0
			900	566	177	155	2		

- Molecule 17 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	S1	92	Total	C	N	O		0	0
			726	471	131	124			
17	S2	92	Total	C	N	O		0	0
			726	471	131	124			

- Molecule 18 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	T1	102	Total	C	N	O	S	0	0
			786	505	150	126	5		
18	T2	102	Total	C	N	O	S	0	0
			786	505	150	126	5		

- Molecule 19 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	U1	179	Total	C	N	O	S	0	0
			1429	911	255	260	3		
19	U2	179	Total	C	N	O	S	0	0
			1429	911	255	260	3		

- Molecule 20 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	V1	77	Total	C	N	O	S	0	0
			613	379	129	104	1		
20	V2	77	Total	C	N	O	S	0	0
			613	379	129	104	1		

- Molecule 21 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	W1	97	Total	C	N	O	S	0	0
			763	481	150	131	1		
21	W2	97	Total	C	N	O	S	0	0
			763	481	150	131	1		

- Molecule 22 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	X1	69	Total	C	N	O	S	0	0
			581	358	118	104	1		
22	X2	69	Total	C	N	O	S	0	0
			581	358	118	104	1		

- Molecule 23 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	Y1	59	Total	C	N	O	0	0
			469	298	90	81		
23	Y2	59	Total	C	N	O	0	0
			469	298	90	81		

- Molecule 24 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Z1	63	Total	C	N	O	S	0	0
			516	326	93	92	5		
24	Z2	63	Total	C	N	O	S	0	0
			516	326	93	92	5		

- Molecule 25 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	a1	59	Total	C	N	O	S	0	0
			459	288	90	76	5		
25	a2	59	Total	C	N	O	S	0	0
			459	288	90	76	5		

- Molecule 26 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	b1	45	Total	C	N	O	S	0	0
			390	241	79	66	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
26	b2	45	Total	C	N	O	S	0	0
			390	241	79	66	4		

- Molecule 27 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	c1	49	Total	C	N	O	S	0	0
			430	263	108	57	2		
27	c2	49	Total	C	N	O	S	0	0
			430	263	108	57	2		

- Molecule 28 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	d1	61	Total	C	N	O	S	0	0
			489	312	99	76	2		
28	d2	61	Total	C	N	O	S	0	0
			489	312	99	76	2		

- Molecule 29 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	A1	2912	Total	C	N	O	P	0	0
			62707	27911	11722	20163	2911		
29	A2	2912	Total	C	N	O	P	0	0
			62707	27911	11722	20163	2911		

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A1	156	U	UNK	conflict	GB 55771382
A1	682	A	G	conflict	GB 55771382
A1	686	C	G	conflict	GB 55771382
A1	697	G	C	conflict	GB 55771382
A1	701	A	C	conflict	GB 55771382
A1	1106	U	G	conflict	GB 55771382
A1	1128	A	C	conflict	GB 55771382
A2	156	U	UNK	conflict	GB 55771382
A2	682	A	G	conflict	GB 55771382
A2	686	C	G	conflict	GB 55771382
A2	697	G	C	conflict	GB 55771382
A2	701	A	C	conflict	GB 55771382

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Chain	Residue	Modelled	Actual	Comment	Reference
A2	1106	U	G	conflict	GB 55771382
A2	1128	A	C	conflict	GB 55771382

- Molecule 30 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	B1	122	Total	C	N	O	P	0	0
			2617	1166	486	844	121		
30	B2	122	Total	C	N	O	P	0	0
			2617	1166	486	844	121		

- Molecule 31 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	e1	36	Total	C	N	O	S	0	0
			299	183	67	46	3		
31	e2	36	Total	C	N	O	S	0	0
			299	183	67	46	3		

- Molecule 32 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	B3	237	Total	C	N	O	S	0	0
			1925	1228	344	348	5		
32	B4	237	Total	C	N	O	S	0	0
			1925	1228	344	348	5		

- Molecule 33 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	C3	206	Total	C	N	O	S	0	0
			1613	1016	314	282	1		
33	C4	206	Total	C	N	O	S	0	0
			1613	1016	314	282	1		

- Molecule 34 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	D3	208	Total	C	N	O	S	0	0
			1703	1066	339	291	7		
34	D4	208	Total	C	N	O	S	0	0
			1703	1066	339	291	7		

- Molecule 35 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	E3	151	Total	C	N	O	S	0	0
			1156	729	218	205	4		
35	E4	151	Total	C	N	O	S	0	0
			1156	729	218	205	4		

- Molecule 36 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	F3	101	Total	C	N	O	S	0	0
			843	531	155	154	3		
36	F4	101	Total	C	N	O	S	0	0
			843	531	155	154	3		

- Molecule 37 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	G3	155	Total	C	N	O	S	0	0
			1257	781	252	218	6		
37	G4	155	Total	C	N	O	S	0	0
			1257	781	252	218	6		

- Molecule 38 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	H3	138	Total	C	N	O	S	0	0
			1116	705	215	193	3		
38	H4	138	Total	C	N	O	S	0	0
			1116	705	215	193	3		

- Molecule 39 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	I3	127	Total	C	N	O	0	0
			1010	639	197	174		
39	I4	127	Total	C	N	O	0	0
			1010	639	197	174		

- Molecule 40 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	J3	99	Total	C	N	O	S	0	0
			802	504	157	140	1		
40	J4	99	Total	C	N	O	S	0	0
			802	504	157	140	1		

- Molecule 41 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	K3	118	Total	C	N	O	S	0	0
			879	546	167	163	3		
41	K4	118	Total	C	N	O	S	0	0
			879	546	167	163	3		

- Molecule 42 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	L3	125	Total	C	N	O	S	0	0
			976	614	196	165	1		
42	L4	125	Total	C	N	O	S	0	0
			976	614	196	165	1		

- Molecule 43 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	M3	117	Total	C	N	O	S	0	0
			934	577	192	163	2		
43	M4	117	Total	C	N	O	S	0	0
			934	577	192	163	2		

- Molecule 44 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	N3	60	Total	C	N	O	S	0	0
			492	312	104	72	4		
44	N4	60	Total	C	N	O	S	0	0
			492	312	104	72	4		

- Molecule 45 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	O3	88	Total	C	N	O	S	0	0
			734	459	147	126	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
45	O4	88	Total	C	N	O	S	0	0
			734	459	147	126	2		

- Molecule 46 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	P3	84	Total	C	N	O	S	0	0
			706	446	140	119	1		
46	P4	84	Total	C	N	O	S	0	0
			706	446	140	119	1		

- Molecule 47 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Q3	100	Total	C	N	O	S	0	0
			835	534	155	144	2		
47	Q4	100	Total	C	N	O	S	0	0
			835	534	155	144	2		

- Molecule 48 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	R3	62	Total	C	N	O	0	0
			515	328	101	86		
48	R4	62	Total	C	N	O	0	0
			515	328	101	86		

- Molecule 49 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	S3	78	Total	C	N	O	S	0	0
			625	398	115	110	2		
49	S4	78	Total	C	N	O	S	0	0
			625	398	115	110	2		

- Molecule 50 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	T3	99	Total	C	N	O	S	0	0
			763	470	162	129	2		
50	T4	99	Total	C	N	O	S	0	0
			763	470	162	129	2		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
51	U3	25	Total	C	N	O	0	0
			218	134	52	32		
51	U4	25	Total	C	N	O	0	0
			218	134	52	32		

- Molecule 52 is a protein called Ribosome hibernation promoting factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	X3	57	Total	C	N	O	S	0	0
			476	304	85	84	3		
52	W4	57	Total	C	N	O	S	0	0
			476	304	85	84	3		

- Molecule 53 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	A3	1506	Total	C	N	O	P	0	0
			32369	14408	5997	10459	1505		
53	A4	1506	Total	C	N	O	P	0	0
			32369	14408	5997	10459	1505		

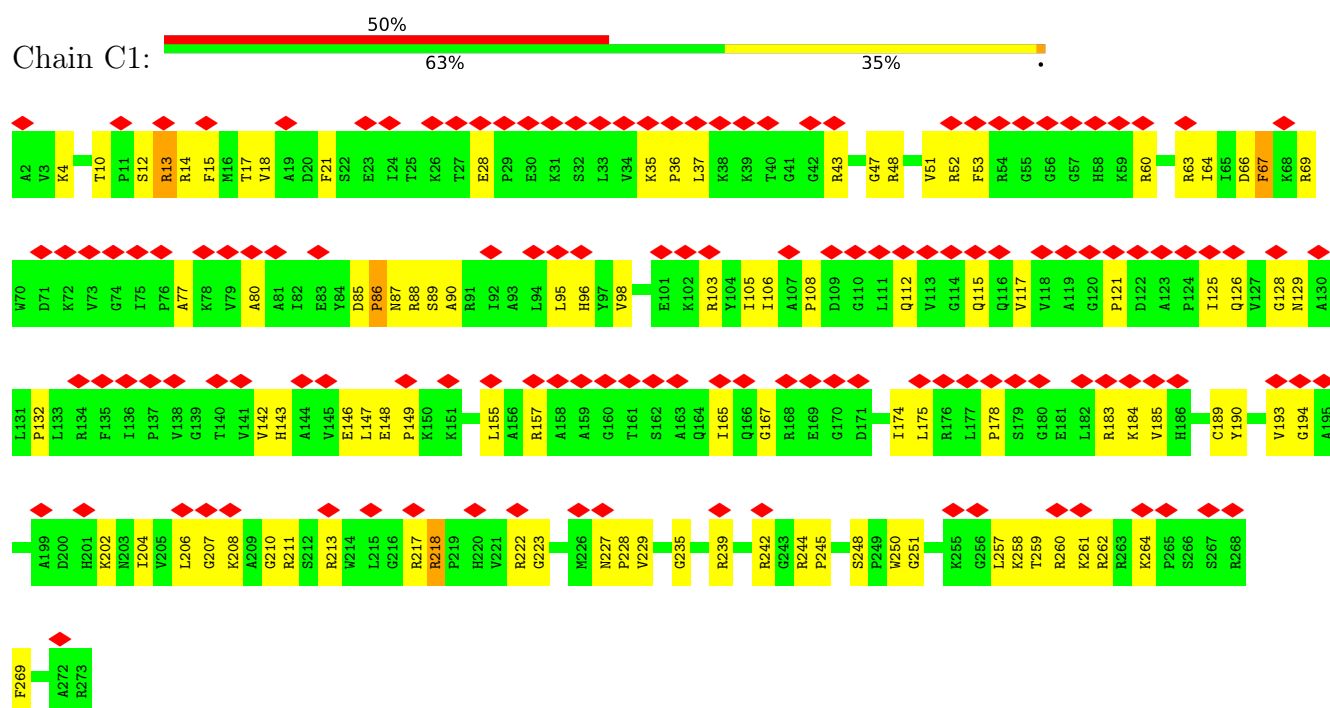
- Molecule 54 is a protein called Ribosome hibernation promoting factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	V3	119	Total	C	N	O	S	0	0
			963	603	179	180	1		
54	V4	119	Total	C	N	O	S	0	0
			963	603	179	180	1		

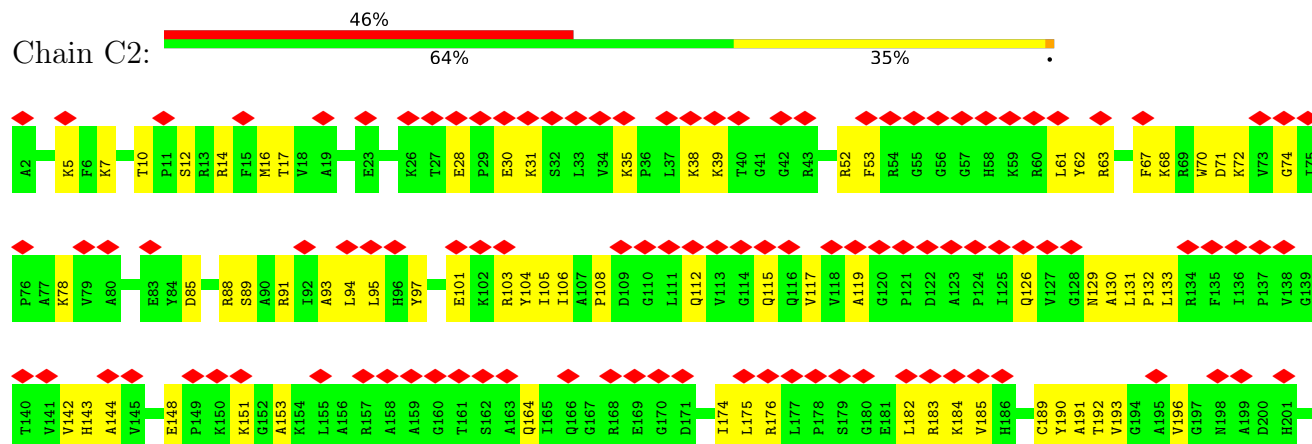
3 Residue-property plots

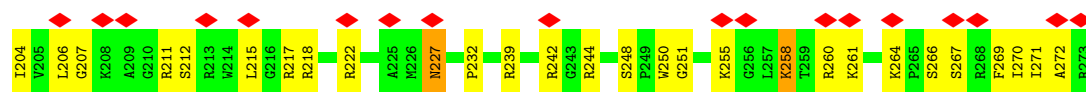
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 50S ribosomal protein L2

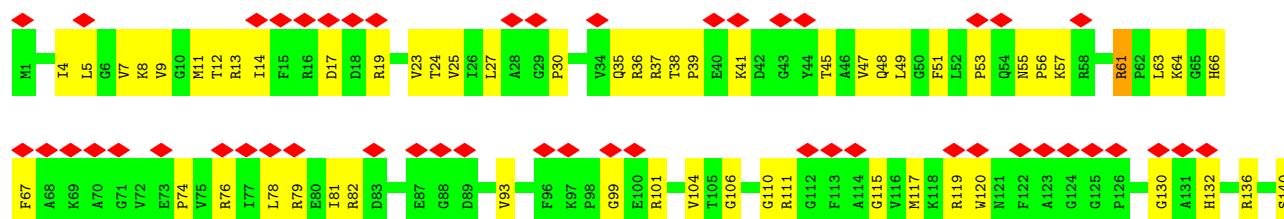
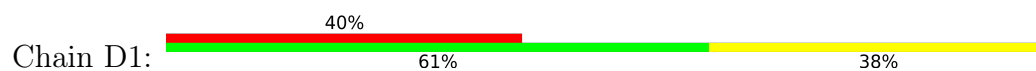


• Molecule 1: 50S ribosomal protein L2

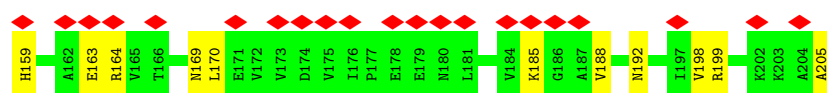
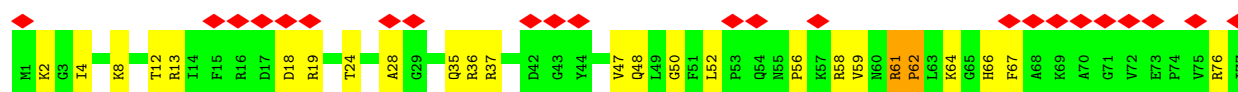
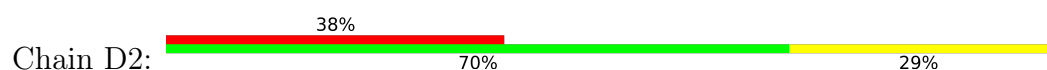




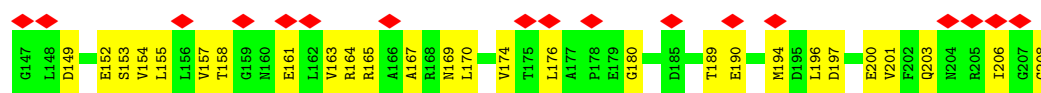
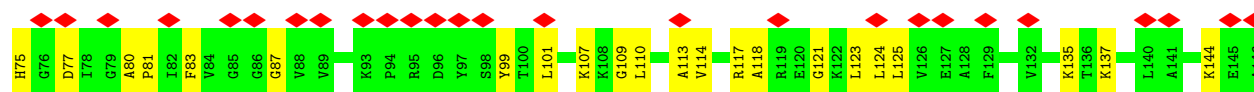
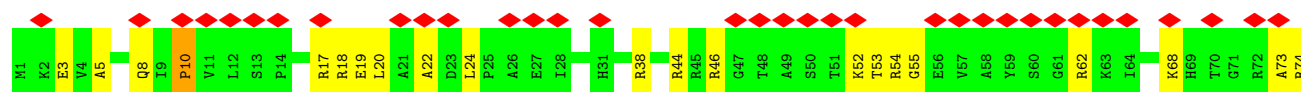
• Molecule 2: 50S ribosomal protein L3



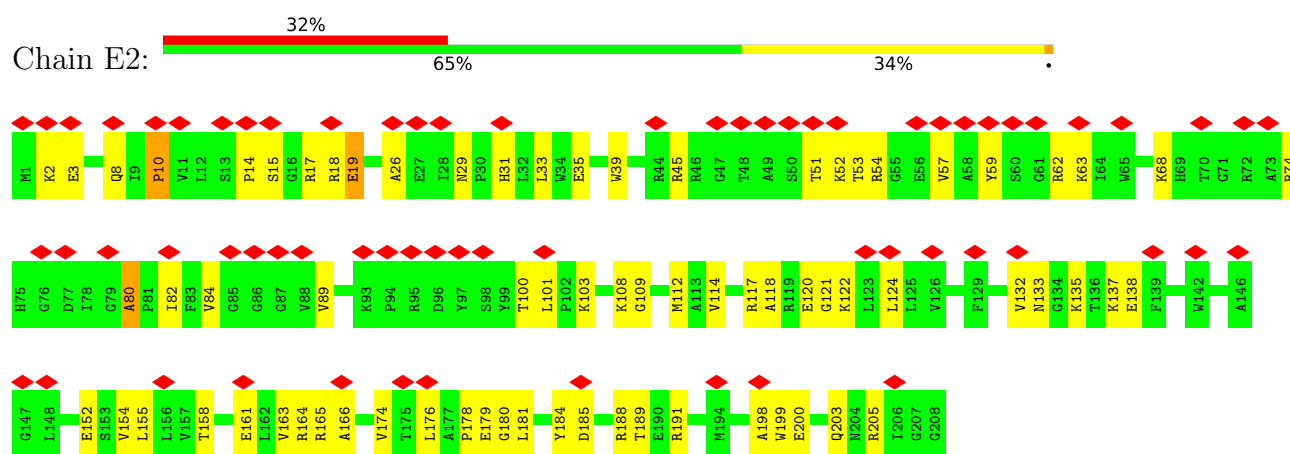
• Molecule 2: 50S ribosomal protein L3



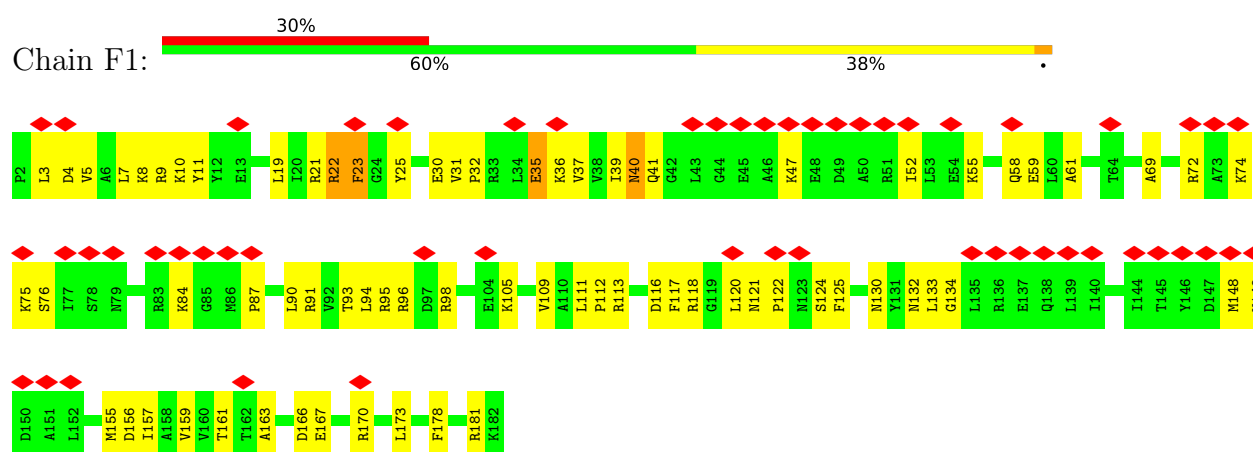
• Molecule 3: 50S ribosomal protein L4



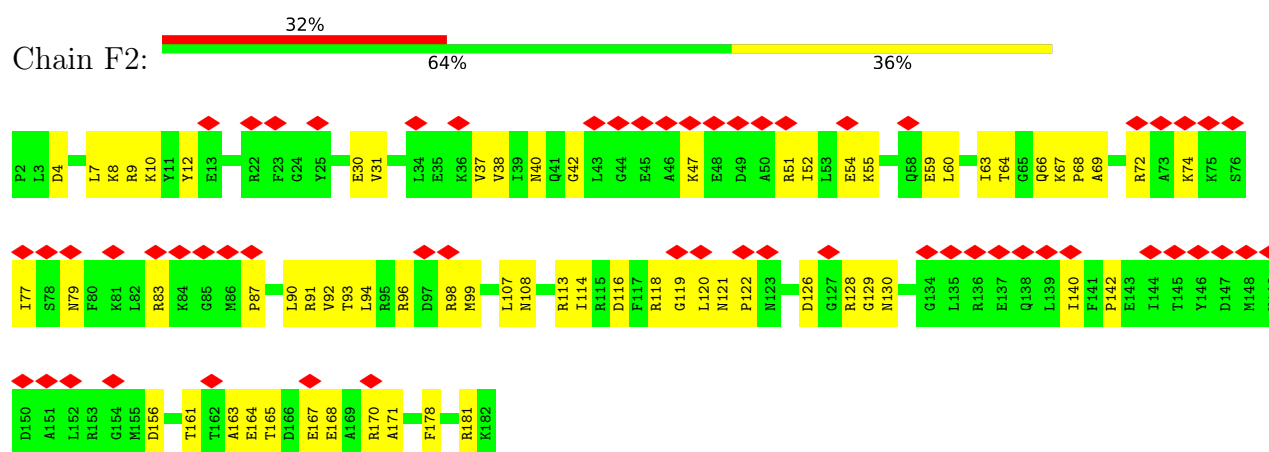
• Molecule 3: 50S ribosomal protein L4



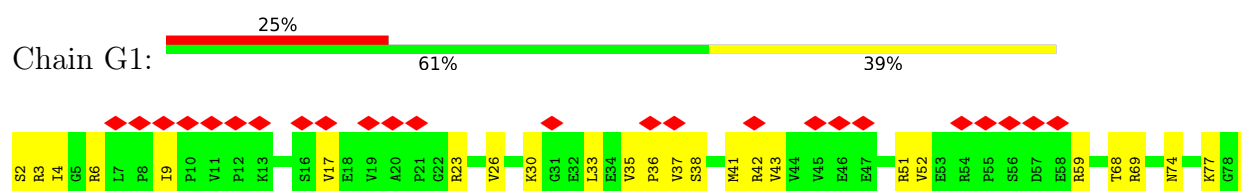
• Molecule 4: 50S ribosomal protein L5

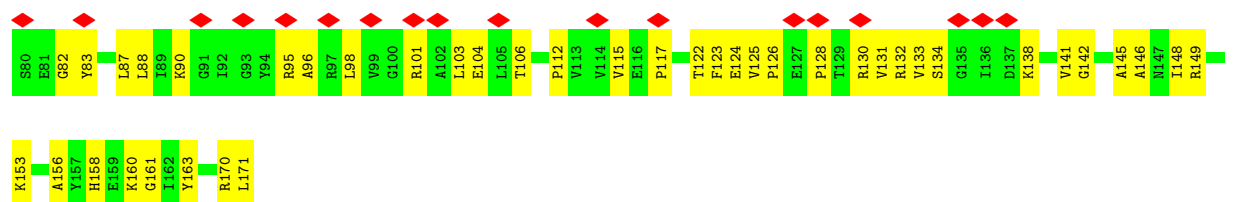


• Molecule 4: 50S ribosomal protein L5

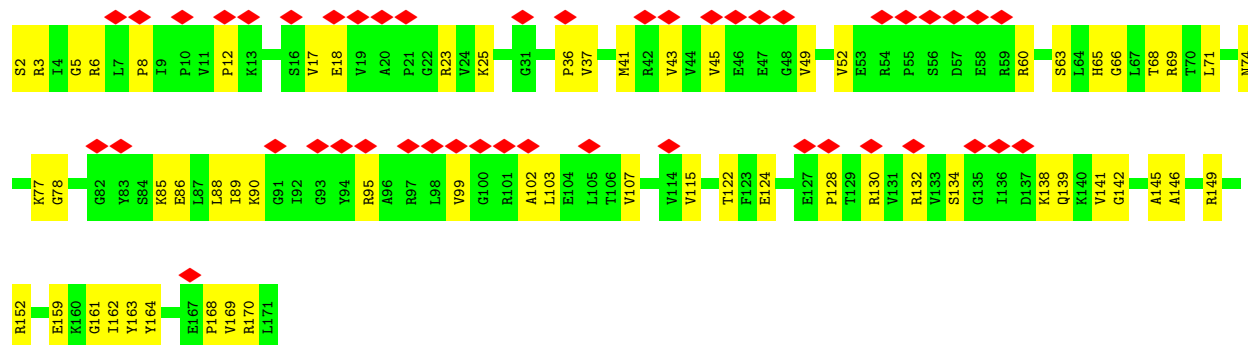


• Molecule 5: 50S ribosomal protein L6

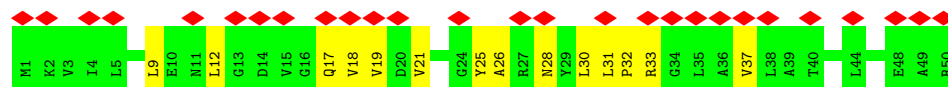




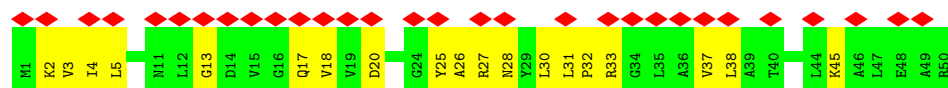
• Molecule 5: 50S ribosomal protein L6



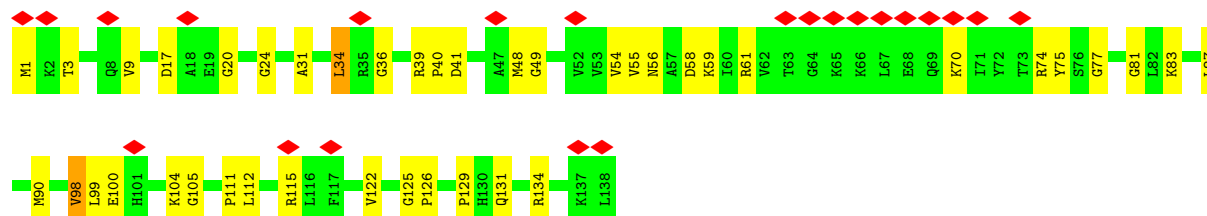
• Molecule 6: 50S ribosomal protein L9



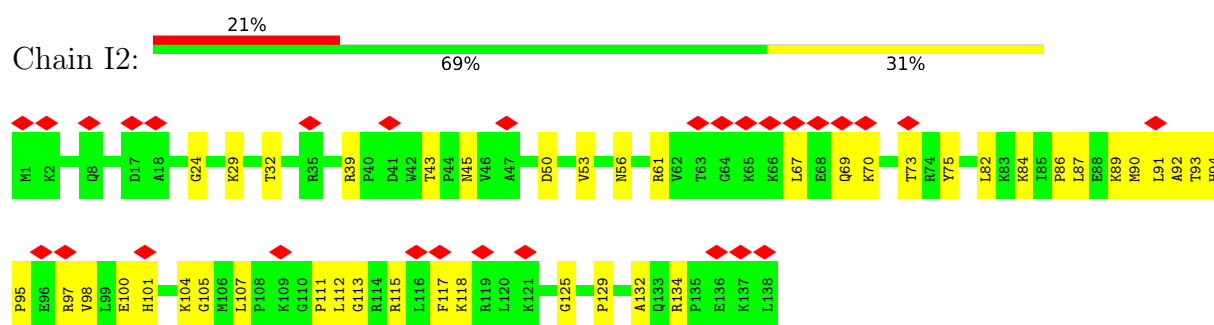
• Molecule 6: 50S ribosomal protein L9



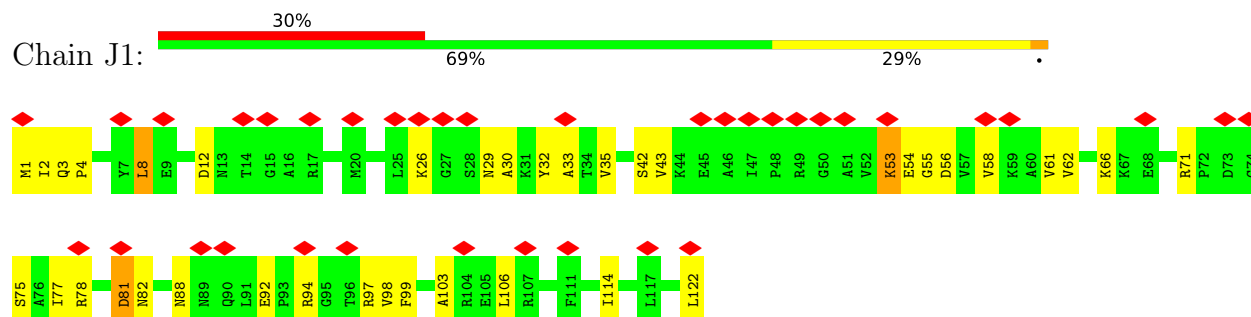
• Molecule 7: 50S ribosomal protein L13



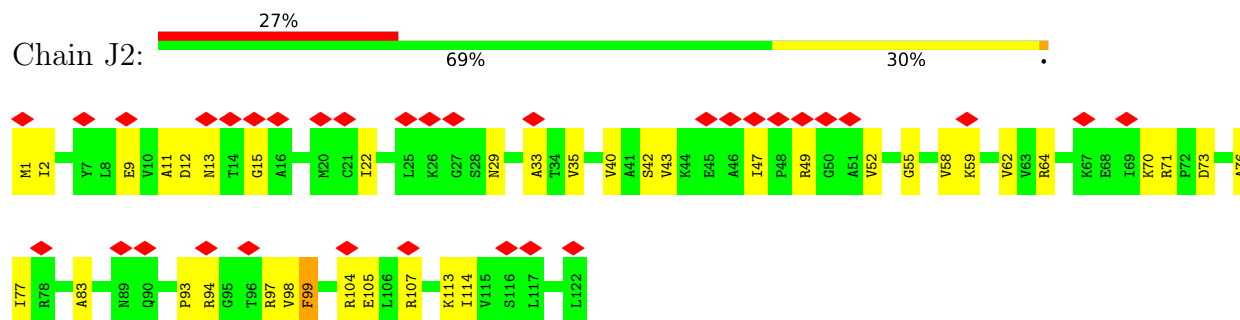
• Molecule 7: 50S ribosomal protein L13



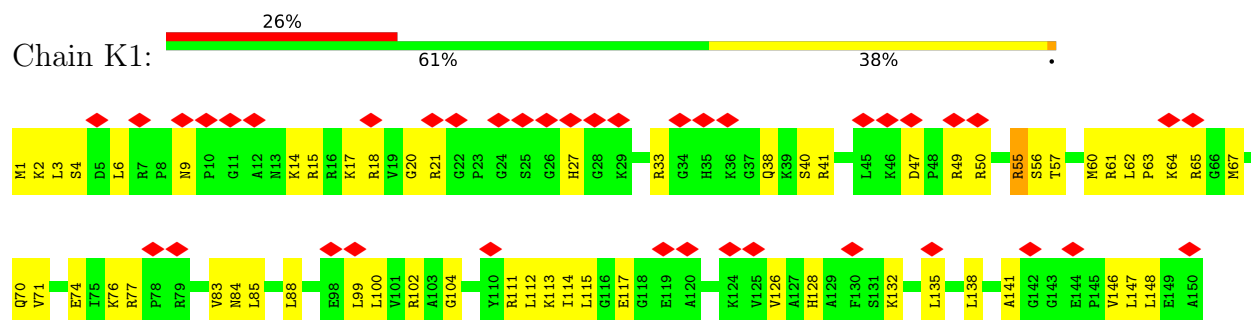
• Molecule 8: 50S ribosomal protein L14



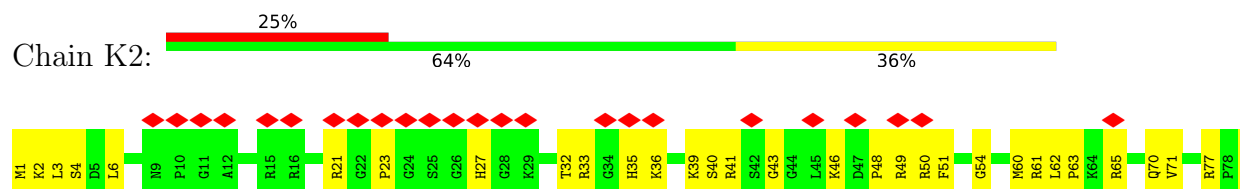
• Molecule 8: 50S ribosomal protein L14

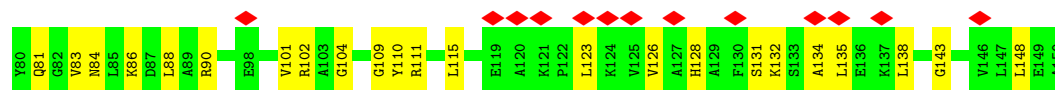


• Molecule 9: 50S ribosomal protein L15

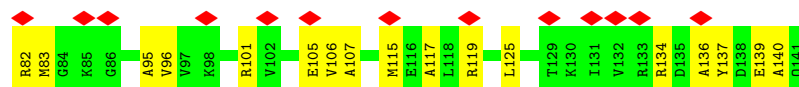
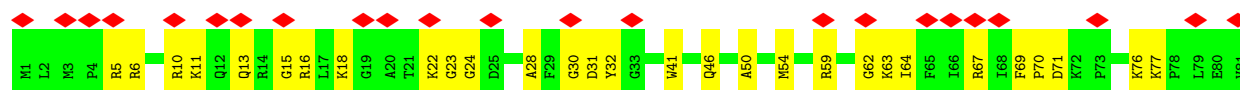


• Molecule 9: 50S ribosomal protein L15

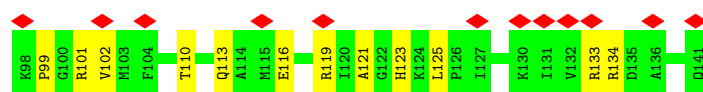
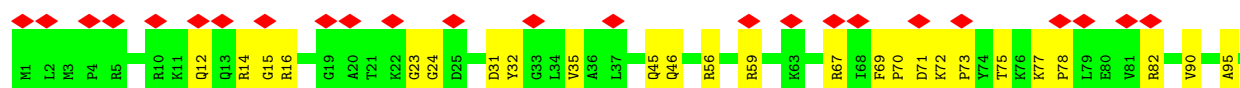
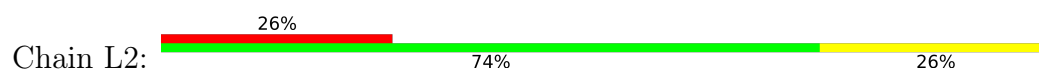




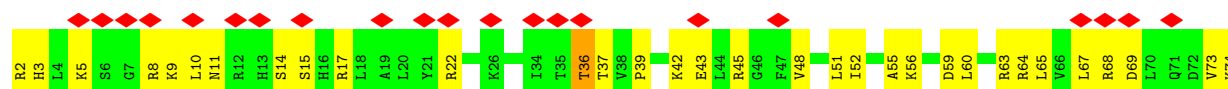
• Molecule 10: 50S ribosomal protein L16



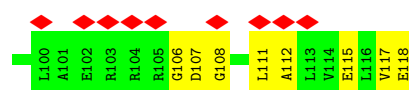
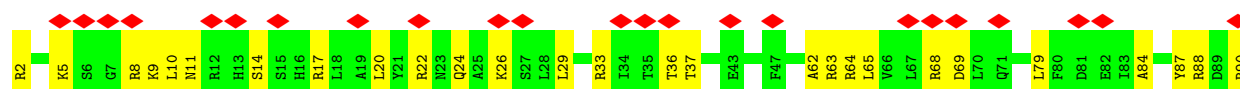
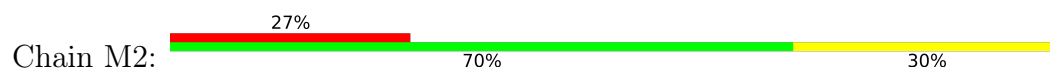
• Molecule 10: 50S ribosomal protein L16



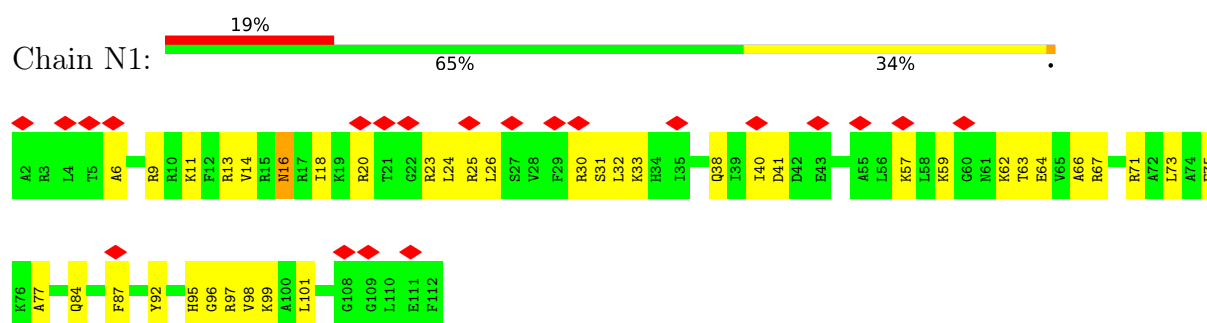
• Molecule 11: 50S ribosomal protein L17



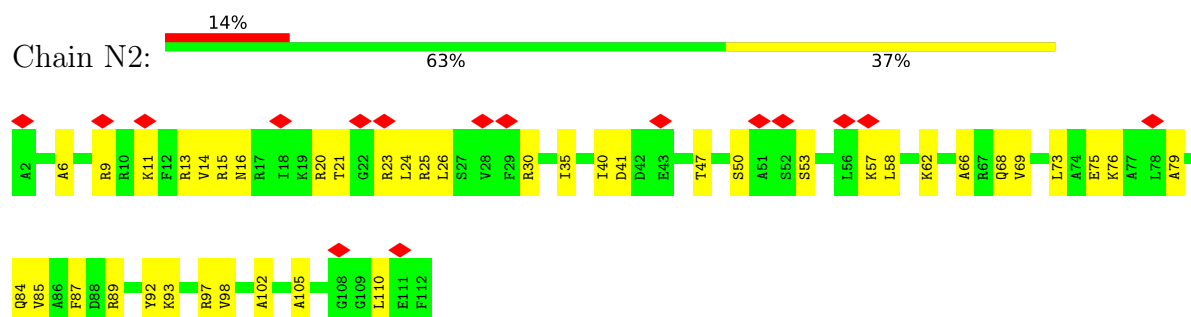
• Molecule 11: 50S ribosomal protein L17



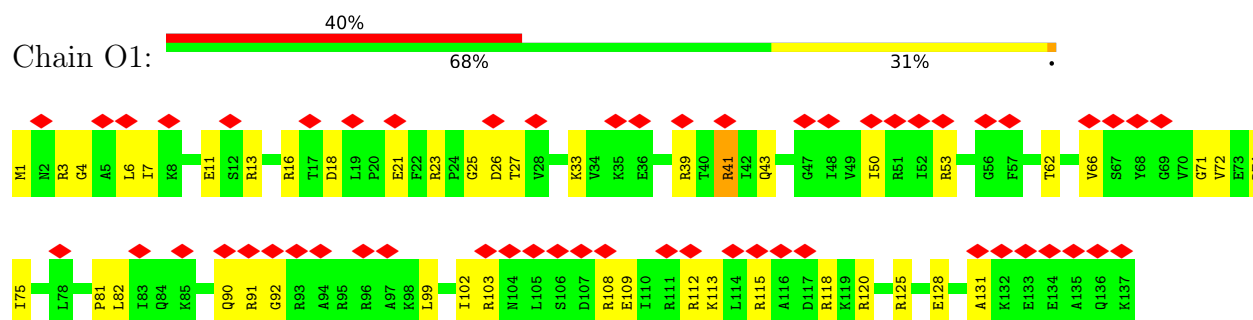
• Molecule 12: 50S ribosomal protein L18



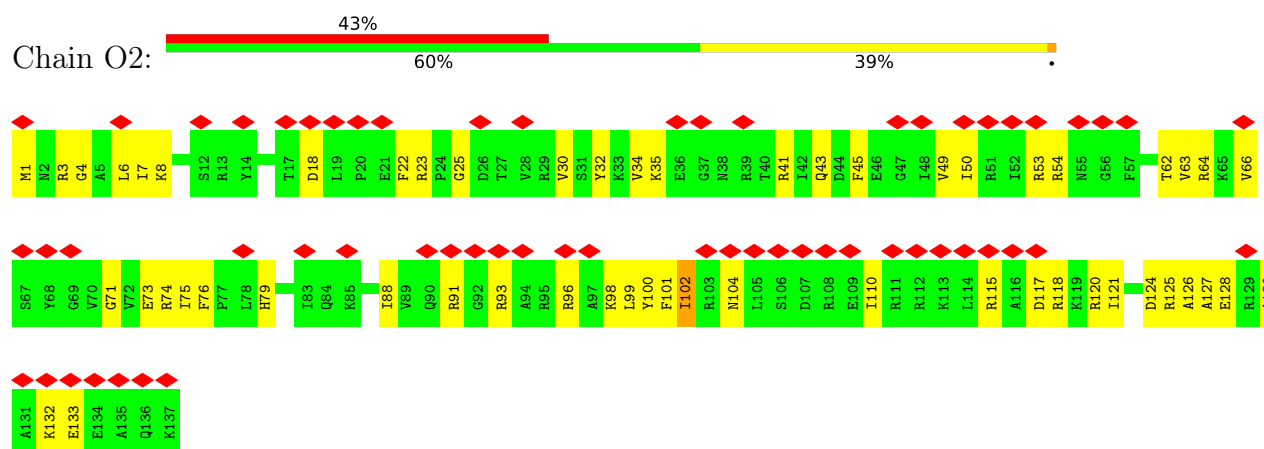
- Molecule 12: 50S ribosomal protein L18



- Molecule 13: 50S ribosomal protein L19

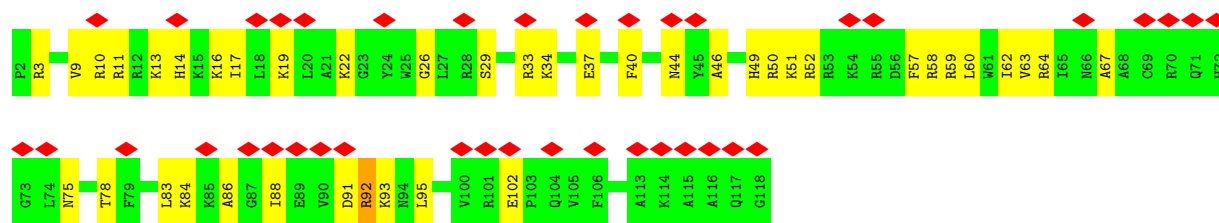


- Molecule 13: 50S ribosomal protein L19

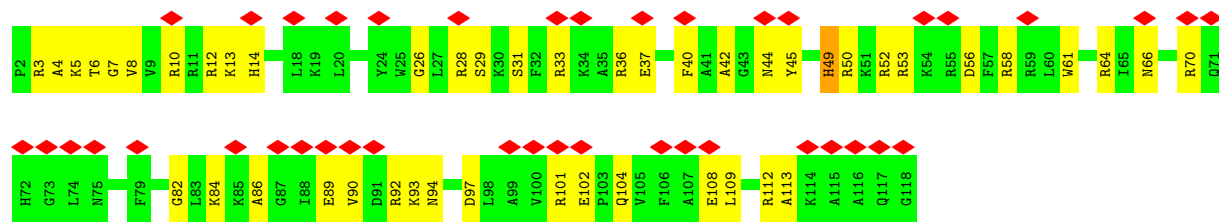


- Molecule 14: 50S ribosomal protein L20

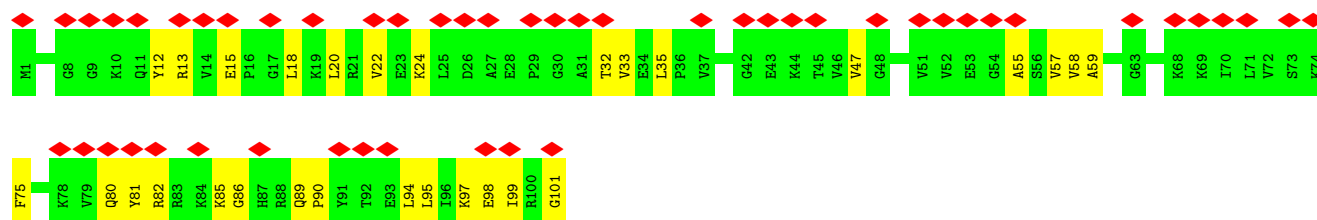
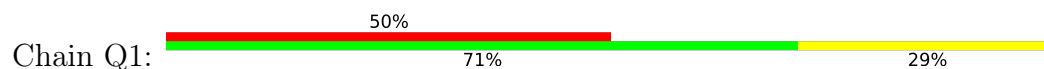




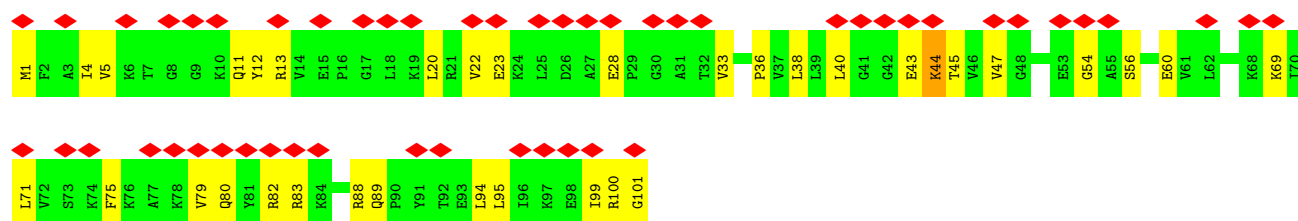
• Molecule 14: 50S ribosomal protein L20



• Molecule 15: 50S ribosomal protein L21

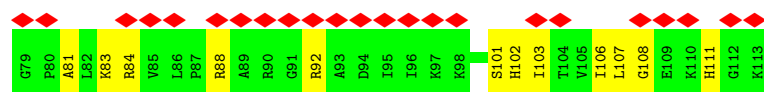


• Molecule 15: 50S ribosomal protein L21

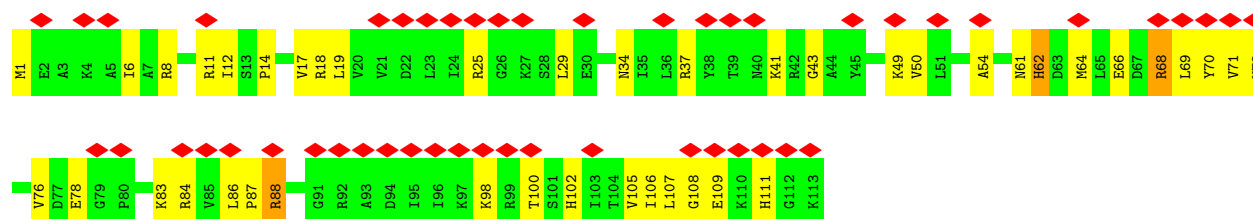


• Molecule 16: 50S ribosomal protein L22

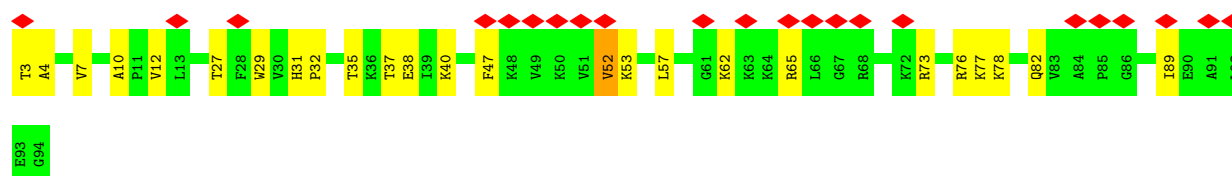
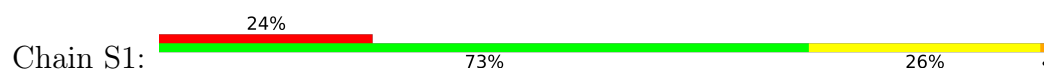




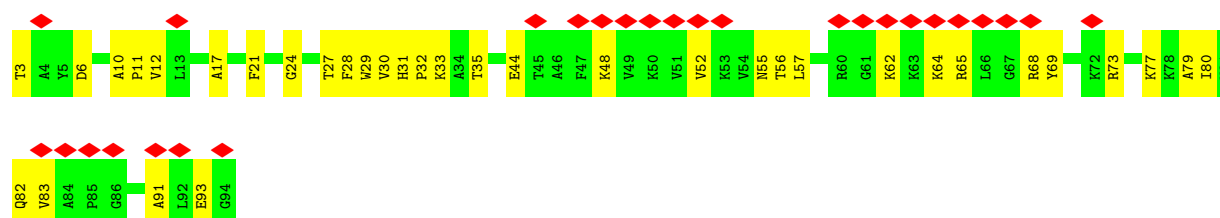
• Molecule 16: 50S ribosomal protein L22



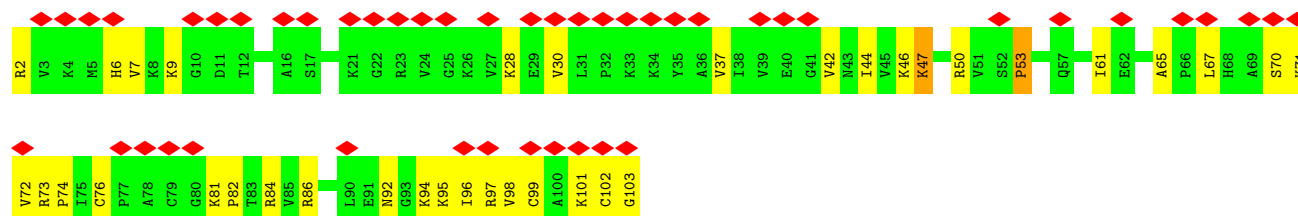
• Molecule 17: 50S ribosomal protein L23



• Molecule 17: 50S ribosomal protein L23

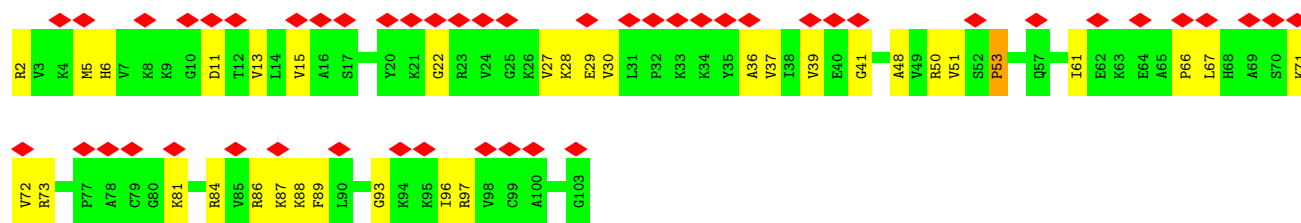


• Molecule 18: 50S ribosomal protein L24

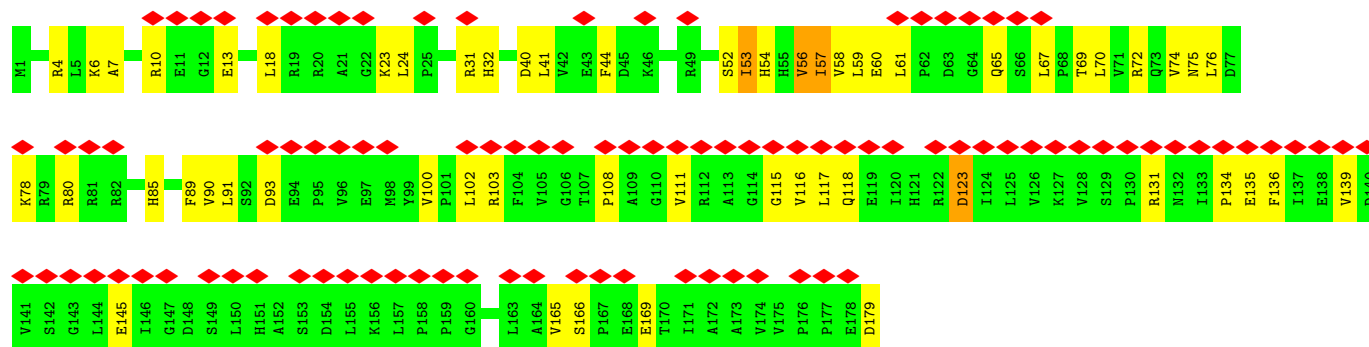


• Molecule 18: 50S ribosomal protein L24

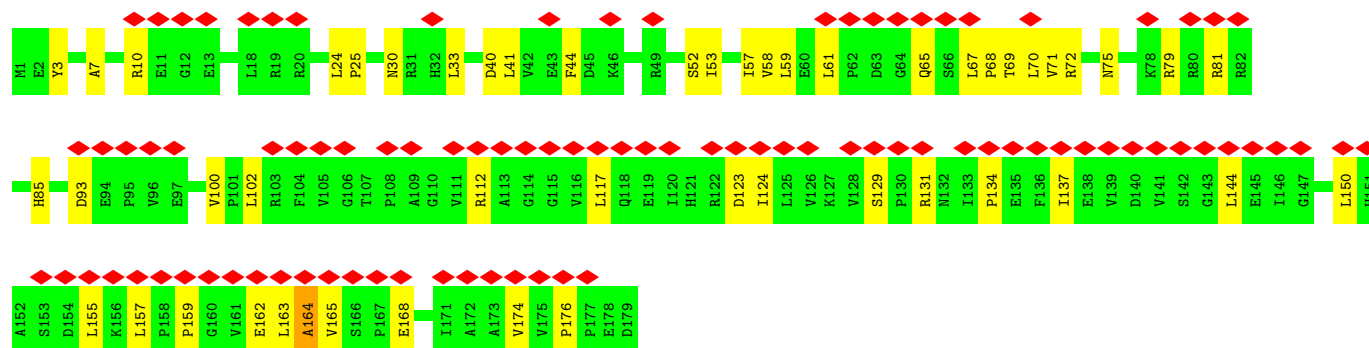
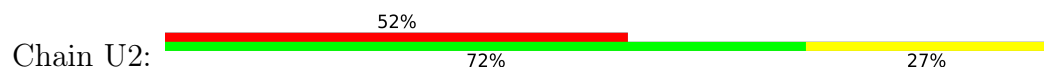




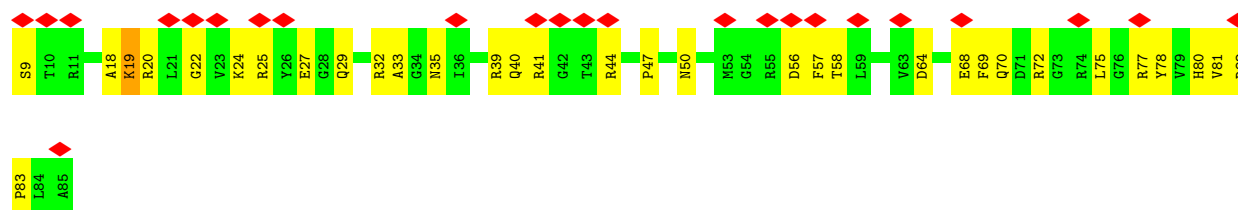
• Molecule 19: 50S ribosomal protein L25



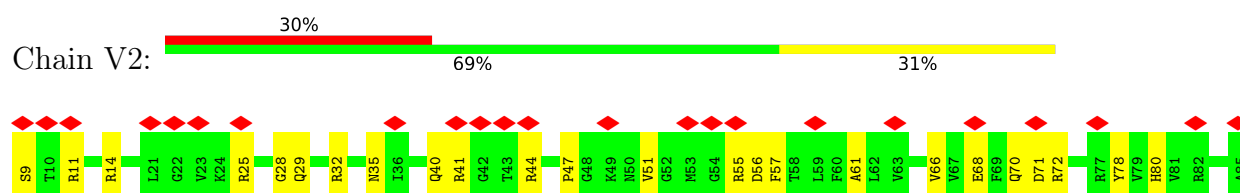
• Molecule 19: 50S ribosomal protein L25



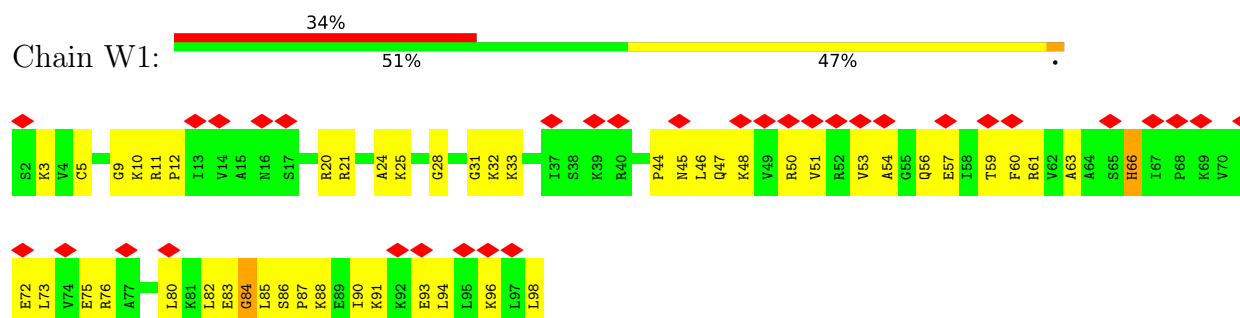
• Molecule 20: 50S ribosomal protein L27



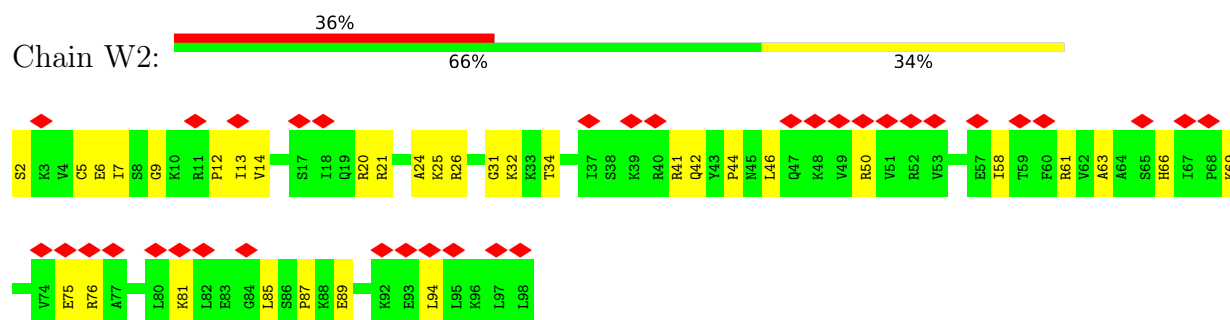
• Molecule 20: 50S ribosomal protein L27



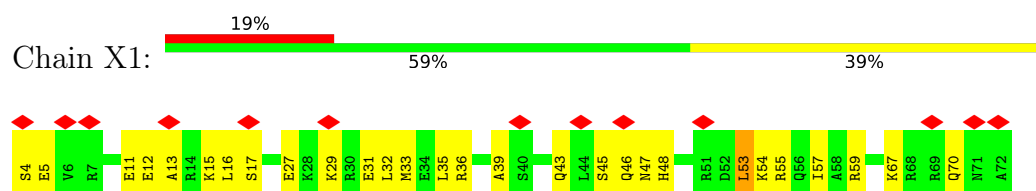
- Molecule 21: 50S ribosomal protein L28



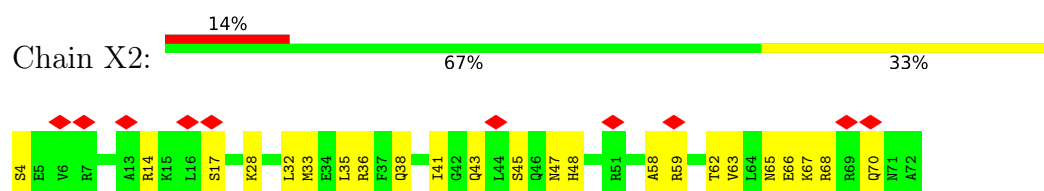
- Molecule 21: 50S ribosomal protein L28



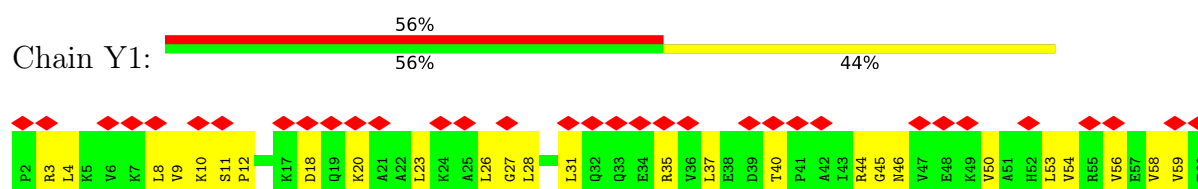
- Molecule 22: 50S ribosomal protein L29



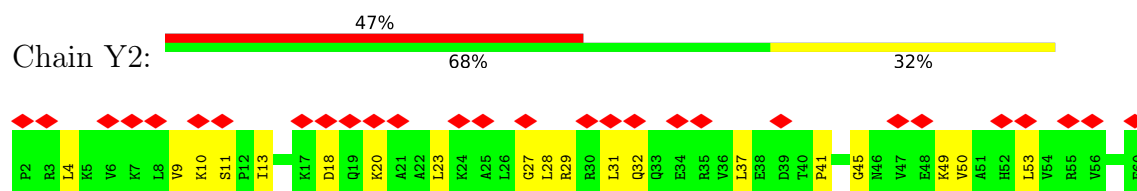
- Molecule 22: 50S ribosomal protein L29



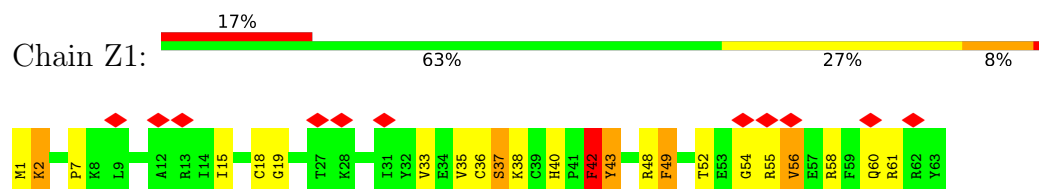
- Molecule 23: 50S ribosomal protein L30



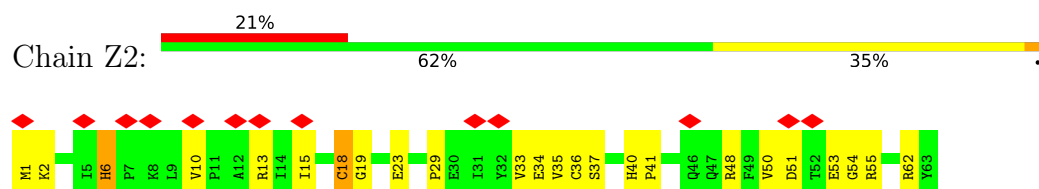
- Molecule 23: 50S ribosomal protein L30



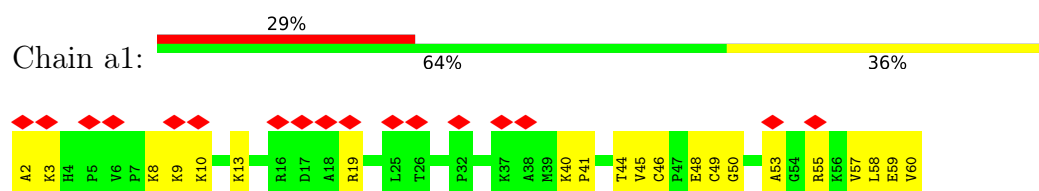
- Molecule 24: 50S ribosomal protein L31



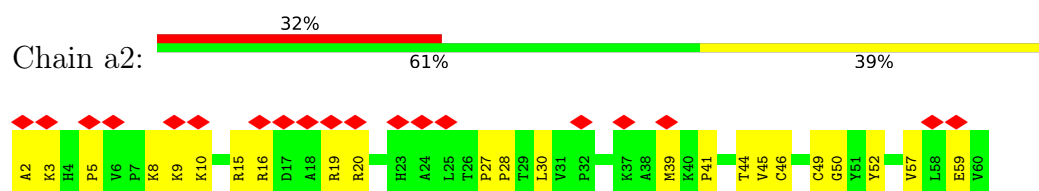
- Molecule 24: 50S ribosomal protein L31



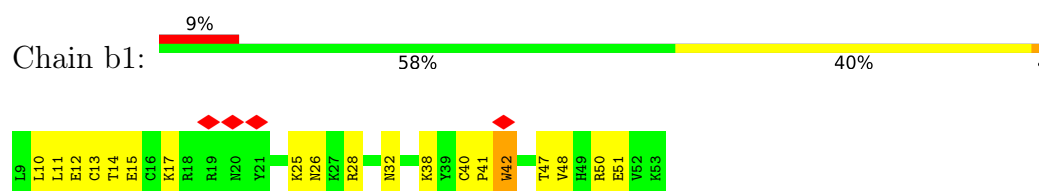
- Molecule 25: 50S ribosomal protein L32



- Molecule 25: 50S ribosomal protein L32

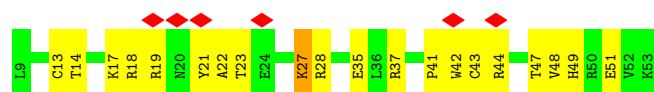


- Molecule 26: 50S ribosomal protein L33

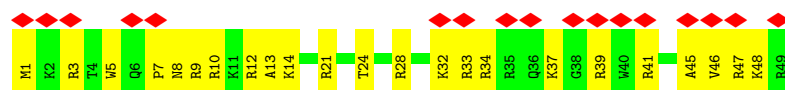


- Molecule 26: 50S ribosomal protein L33

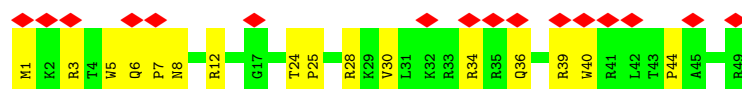




- Molecule 27: 50S ribosomal protein L34



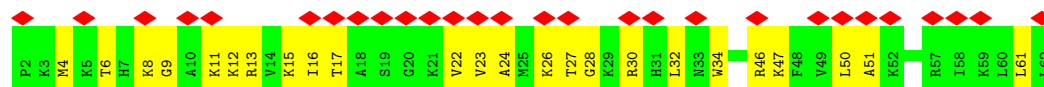
- Molecule 27: 50S ribosomal protein L34



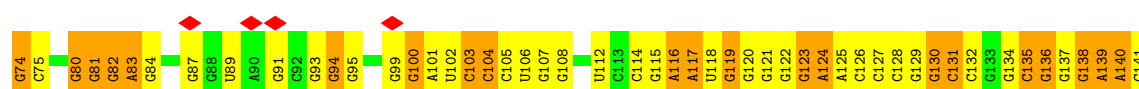
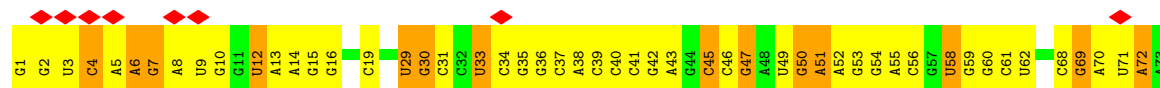
- Molecule 28: 50S ribosomal protein L35



- Molecule 28: 50S ribosomal protein L35



- Molecule 29: 23S ribosomal RNA



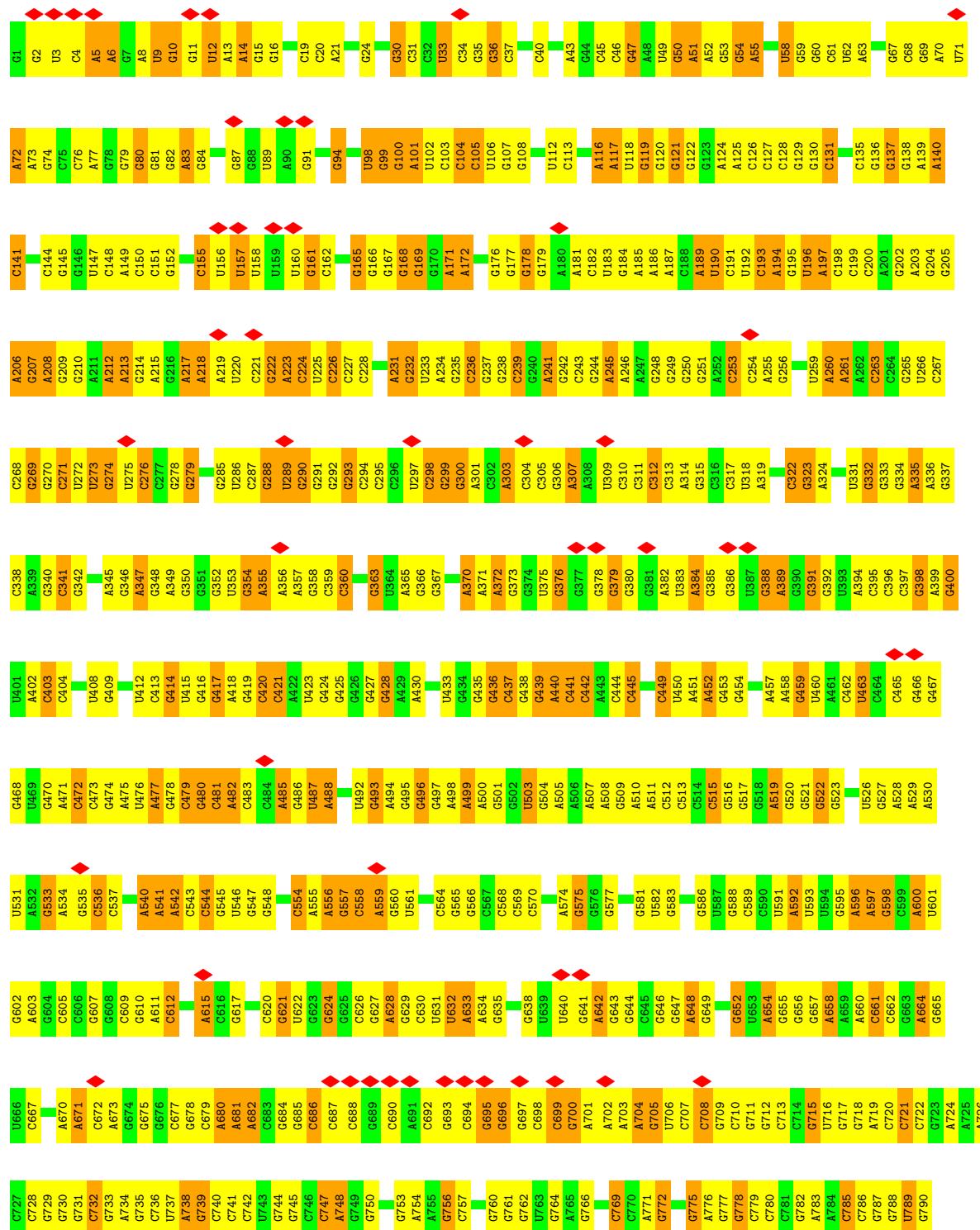
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A1043	G981	G850	G850	C785	G717	G657	U593	G528	A462	C396	A335	U272	A208
A1044	C982	G786	A658	G786	G718	A659	U594	A528	U463	C397	A336	U273	G209
G1045	C983	G787	A659	G787	A719	A660	G595	A529	A464	G398	A337	G274	G210
G1046	U984	A921	G854	G788	C720	G660	A596	A530	C465	A399	C338	U275	A211
U1047	C985	G922	C855	G789	C721	C661	A597	U531	G466	G400	A339	C276	A212
A1048	U856	G923	U856	G790	C722	C662	G596	A532	G467	U401	G340	C277	A213
A1049	G987	G924	G857	G791	G723	G663	C599	G533	G468	A402	G341	C278	G214
G1050	A988	C925	C858	G792	A725	A664	A600	A534	U469	C403	G342	G279	A215
G1051	G989	U926	U859	G792	C727	G665	U601	G535	G470	C404	G343		G216
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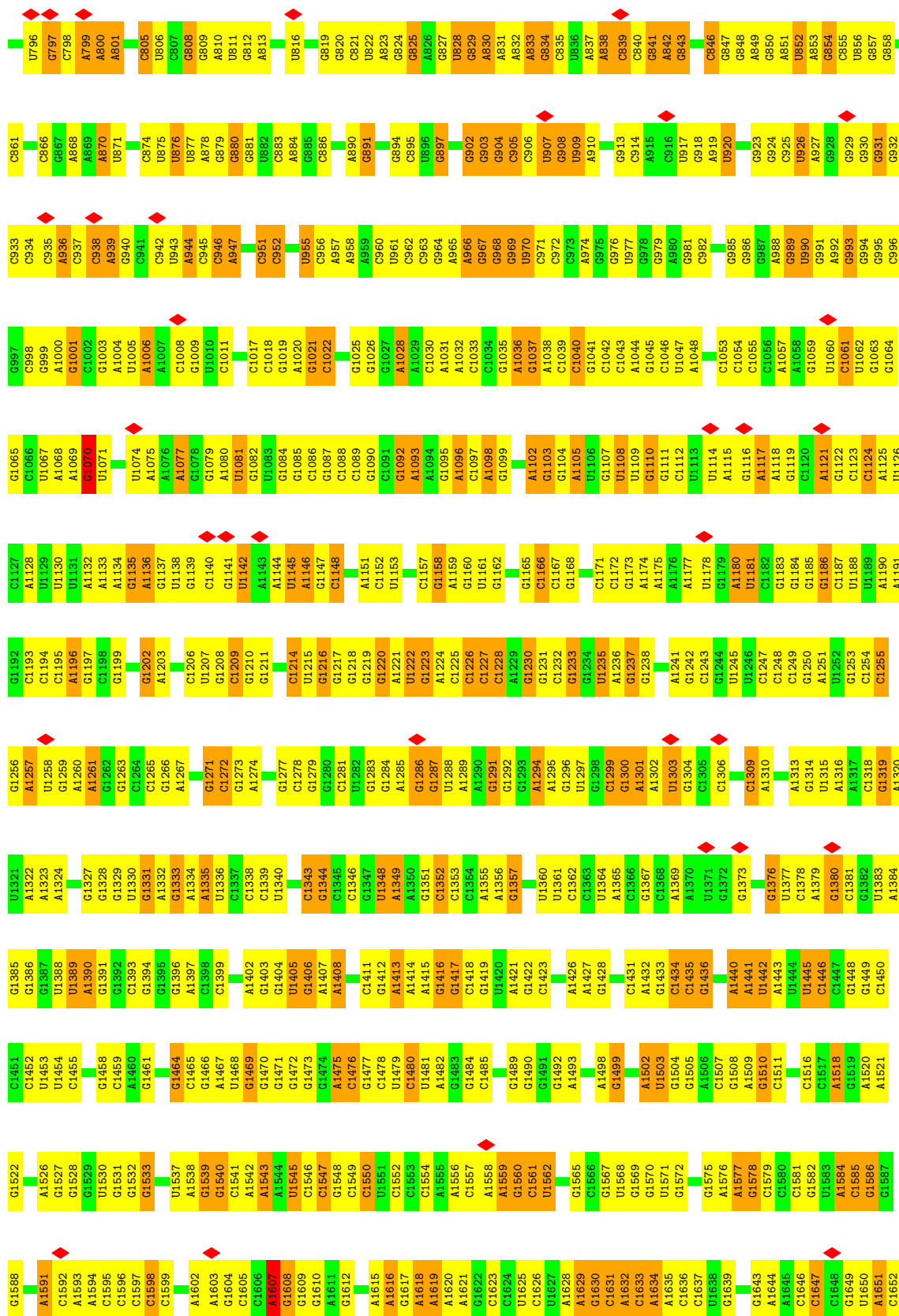
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G2820	U2759	C2560	C2631	G2628	G2500	G2501	G2436	G2365	G2306	U2231			
A2821	G2760	G2561	G2632							U2232			
A2822										U2233			
G2823										U2234			

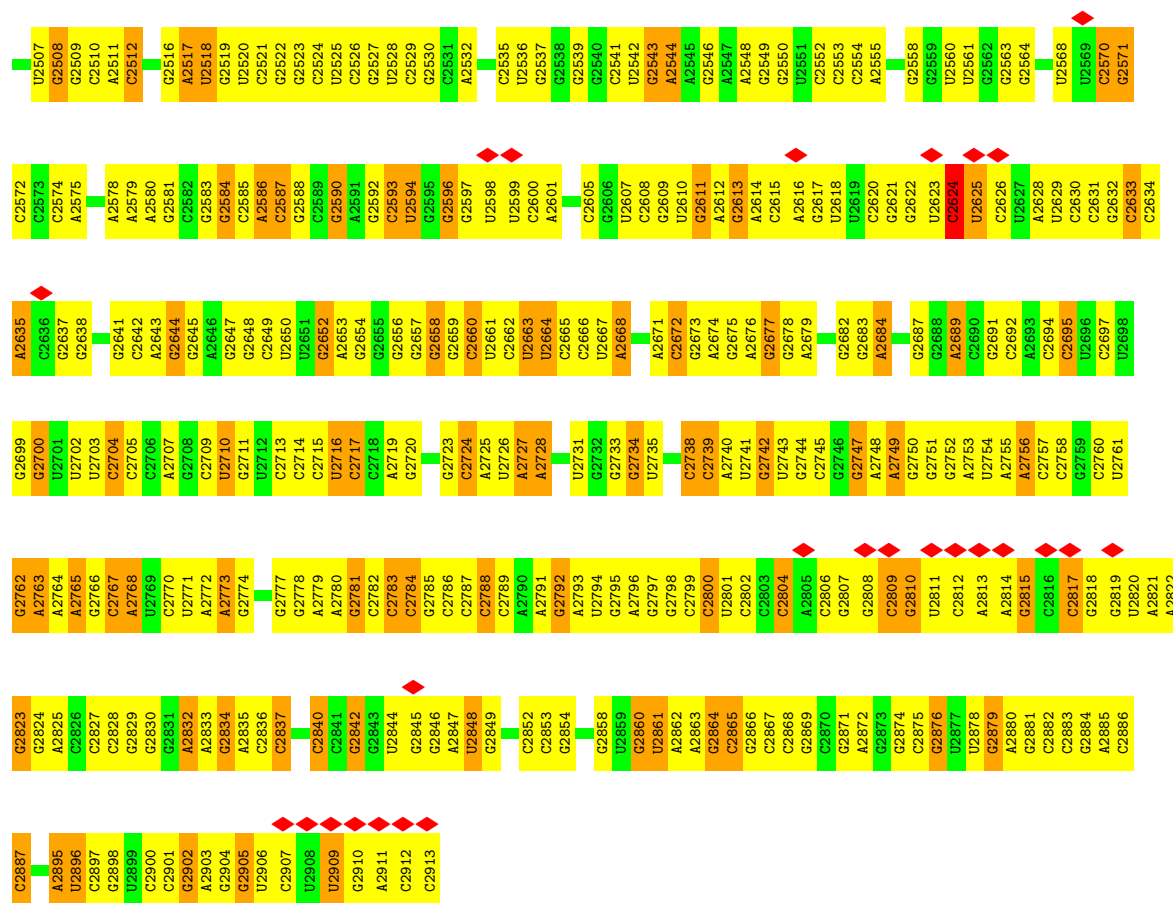


● Molecule 29: 23S ribosomal RNA

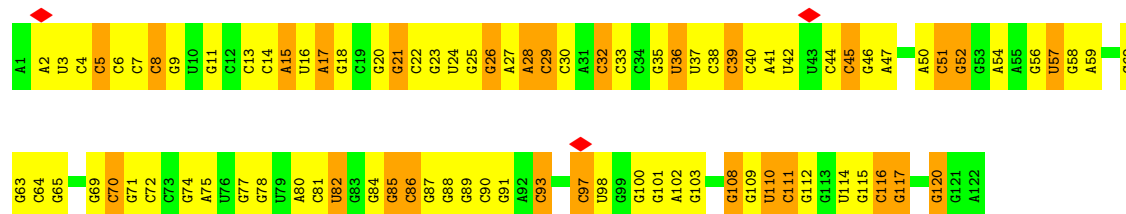




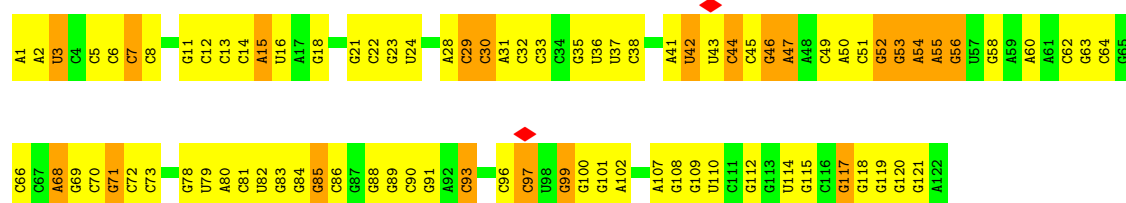
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A2440	C2377	G2376	C2311	G2183	U2123	A2055	G1988	U1924	G1789	C1724	G1654
G2442	G2378	G2377	G2312	C2184	G2124	A2056	C1989	A1925	U1790	A1725	C1655
G2443	G2379	G2379	G2313	C2185	G2125	A2057	A1990	G1926	G1791	A1726	A1656
A2444	A2380	G2379	G2314	G2186	U2126	G2059	C1991	G1927	A1792		A1657
U2445	G2381	A2354	G2315	C2187	C2127	G2058	G1992	G1928			A1658
U2446	G2382	A2255	G2316	C2188	C2127	G2059	G1992	G1929	A1795	G1730	A1659
A2447	G2383	A2256	G2317	C2189	C2128	G2060	G1993	G1930	G1796	G1731	A1660
	G2384	U2257	A2318	G2190	C2129	G2061	A1994	G1931	G1797	C1732	G1661
	G2385	U2258	C2320	G2062	C2130	G2062	A1995	C1932	U1798	C1733	A1662
U2451	G2386	U2259	G2321	C2064	C2131	C2064	A1996		C1799	C1734	A1663
A2452	G2386	U2260	G2322	C2067	C2132		G1997	U1935	C1735	G1735	A1664
A2453	G2387	U2261	A2323	C2068	U2133		C1998	U1936	U1737	U1737	A1665
C2454	G2388	A2261	A2324	C2068	G2134		U1999	A1937	A1738	A1738	C1666
C2455	A2324	A2262	A2325	C2069	U2134		U2000	A1938	A1739	A1739	A1667
C2456	U2326	U2263	A2326	G2070	C2135		A2001	C1870	G1804	G1740	G1668
C2457	U2327	U2264	U2327	U2071	G2136		C2003	C1871	G1805	C1741	U1669
G2458	C2328	G2265	C2328	G2072	U2137		G2004	C1872	A1806	U1741	G1670
G2459	G2329	G2266	C2329	G2073	A2138		A2005	C1873	C1807	U1742	G1671
G2460	C2330	C2267	A2200	G2074	G2139		C2006	C1877	U1808	G1744	C1672
G2461	G2331	C2268	C2201	A2075	G2140		C2007	G1877	U1809	G1745	G1673
A2462	C2332	G2269	C2202	G2076	A2141		G2008	G1878	U1810	G1746	
U2463	G2332	G2270	C2203	G2077	U2142		G2009	G1879	U1811	A1747	G1674
G2464	G2333	U2271	U2204	A2078	A2143			A1880	U1812	G1747	
A2465	A2334	C2272	G2205	G2079	G2144		C2013	A1881	A1813	G1748	G1675
A2466	G2335	G2273	G2206	C2080	G2145		C2014		C1814	A1749	A1680
A2467	A2336	C2274	G2207	A2081	U2146		U2015	U1884	C1815	A1750	A1681
G2468	C2337	C2275	C2207		G2147		G2016	C1885	A1816	G1751	G1682
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G2470	G2405		C2209	A2085	G2149		U2018	A1887	A1818	G1753	G1684
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G2482	C2416	C2288	C2220	U2099	G2158		G2027	G1896	U1827	U1762	C1695
A2483	C2417	G2290	U2221	A2100	A2159			C1897	G1763	G1696	
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G2485	G2419	C2292	A2223	C2102	C2161		G2033	C1899	G1765	G1698	
G2486	U2420	G2293	C2224	G2103	C2162			C1900	G1766	G1699	
U2487		G2294	C2225	G2104	C2163		G2036	A1901	U1767	G1700	
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C2489	G2424	G2296	U2227	G2106	G2165		A2038	C1903	A1769	G1702	
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G2498	U2433	U2305	G2236	G2173	G2173		G2047	C1912	G1777	G1778	
G2499	G2434	C2306	G2237	U2114	C1981		C2048	G1913	G1844		
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G2504	G2504	C2308	A2239	G2116	G1983		C2050	A1914	G1849	C1784	
		C2309	C2240	G2117	G1984			C1919	G1850	C1785	
			C2243	G2118	C1985			G1920	U1851	G1786	
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				G2178							
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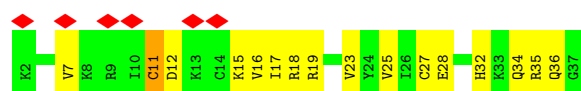
• Molecule 30: 5S ribosomal RNA



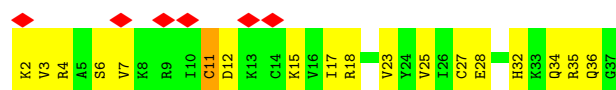
• Molecule 30: 5S ribosomal RNA



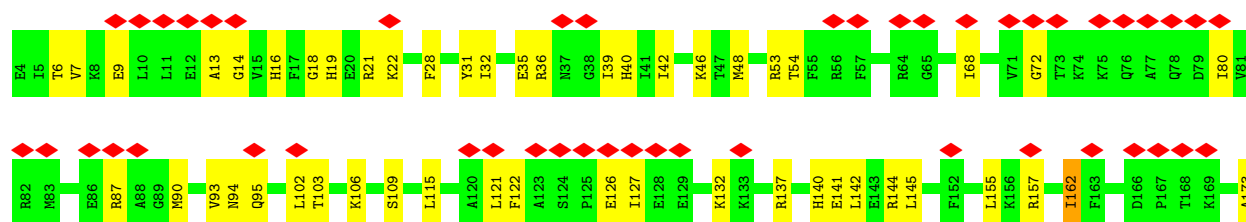
• Molecule 31: 50S ribosomal protein L36



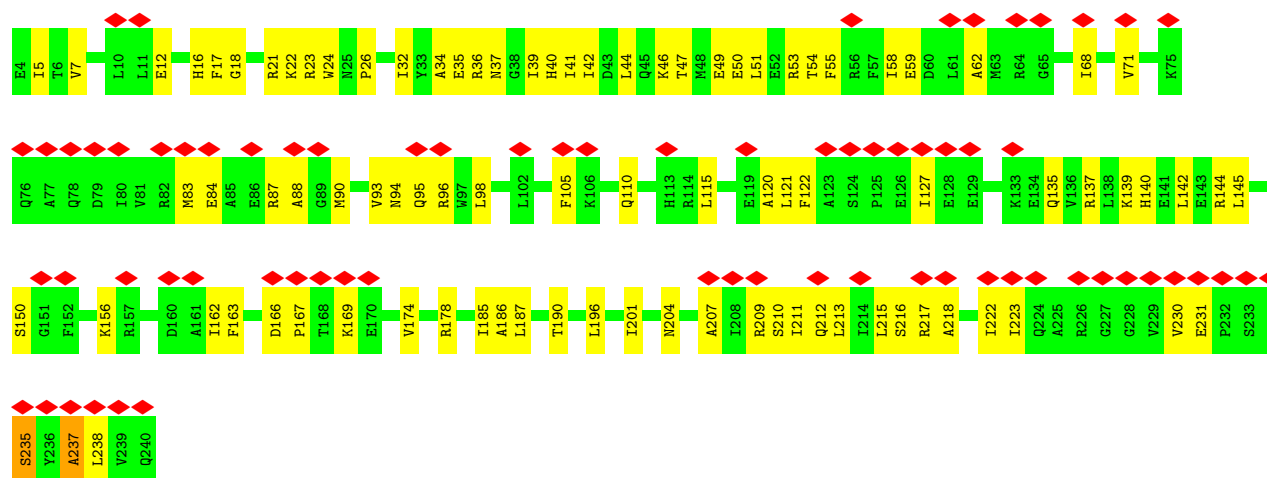
- Molecule 31: 50S ribosomal protein L36



- Molecule 32: 30S ribosomal protein S2

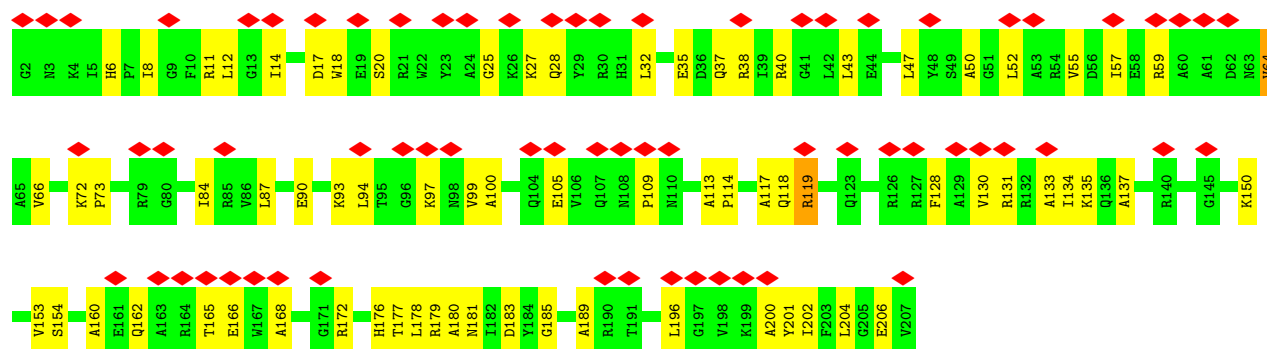


- Molecule 32: 30S ribosomal protein S2



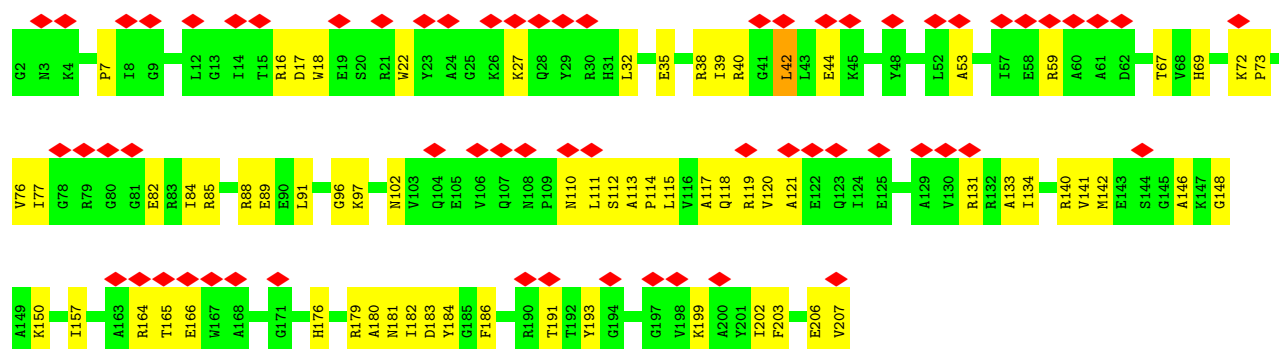
- Molecule 33: 30S ribosomal protein S3





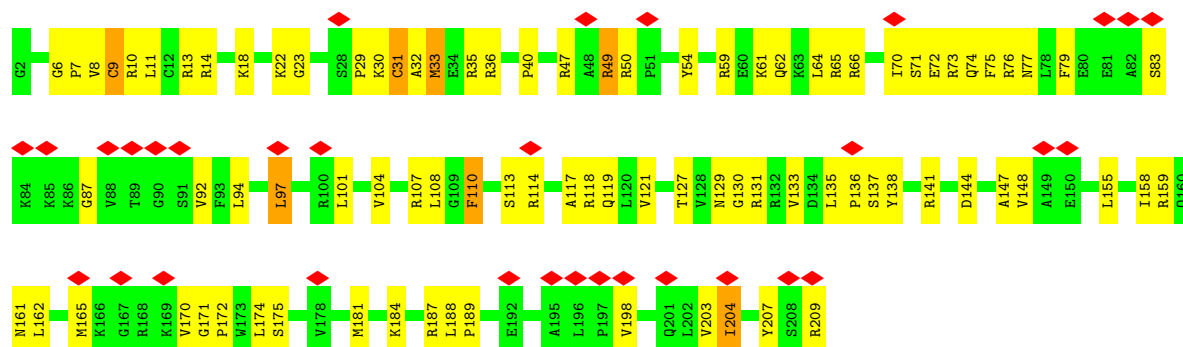
• Molecule 33: 30S ribosomal protein S3

Chain C4: 31% 67% 33%



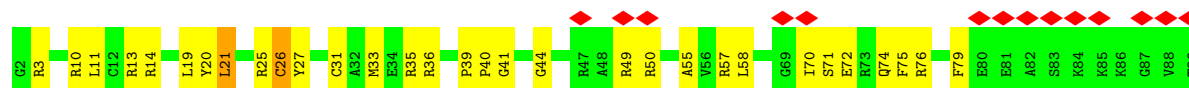
• Molecule 34: 30S ribosomal protein S4

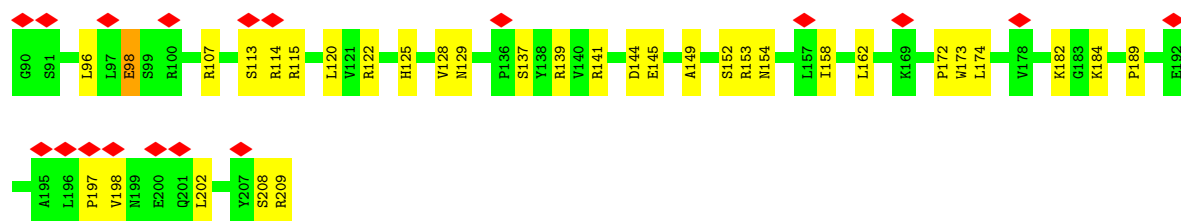
Chain D3: 15% 58% 39%



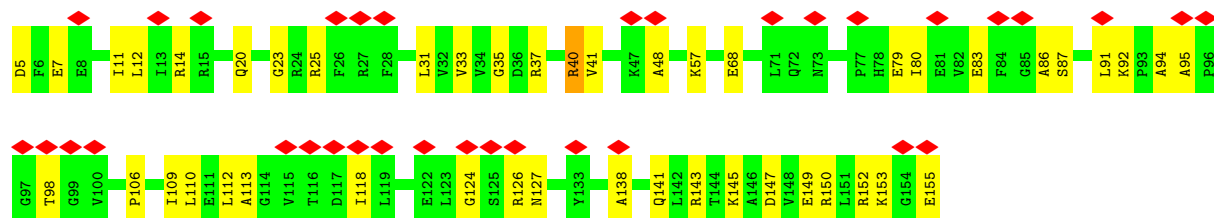
• Molecule 34: 30S ribosomal protein S4

Chain D4: 15% 69% 29%

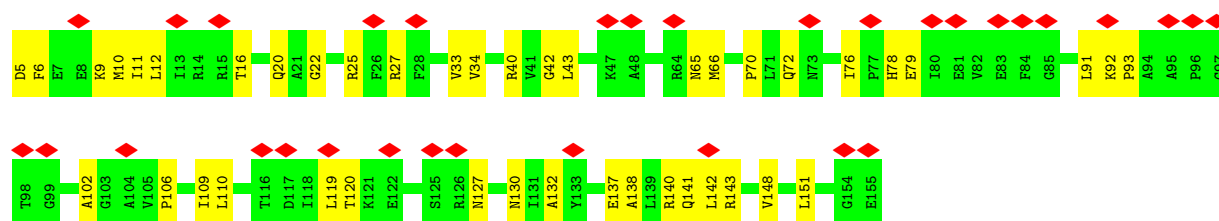
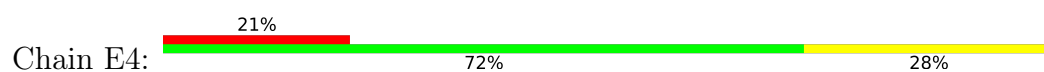




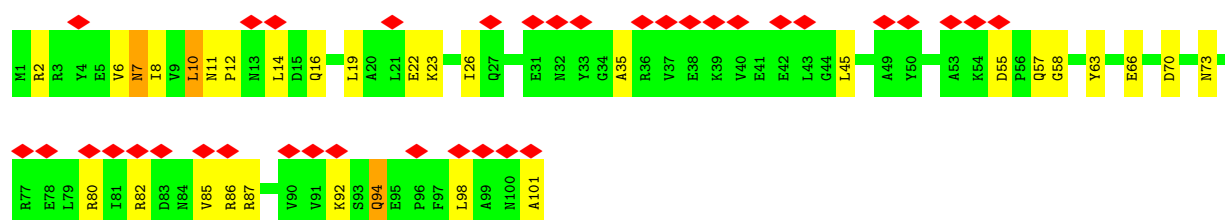
• Molecule 35: 30S ribosomal protein S5



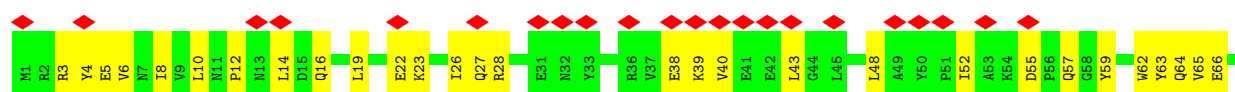
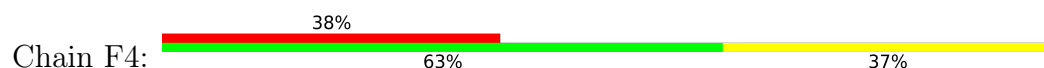
• Molecule 35: 30S ribosomal protein S5

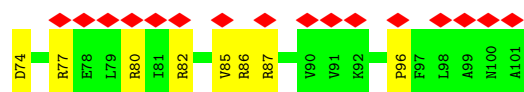


• Molecule 36: 30S ribosomal protein S6

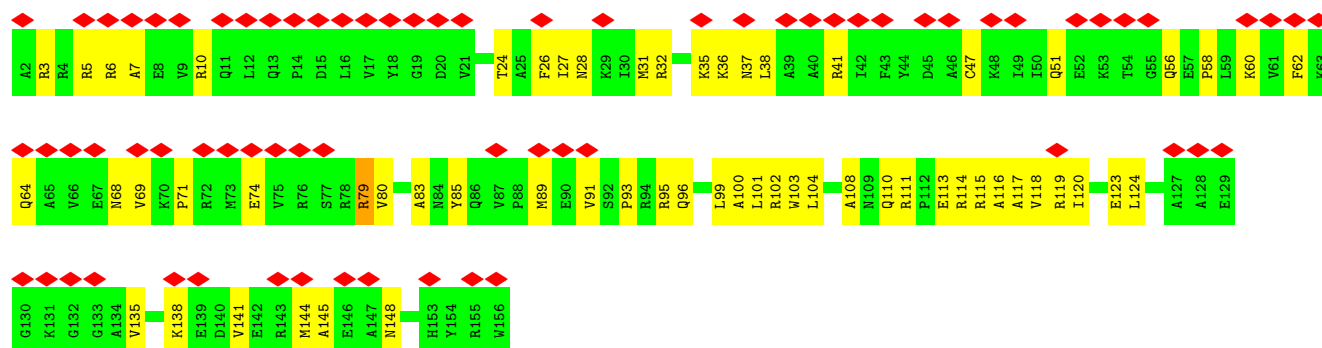


• Molecule 36: 30S ribosomal protein S6

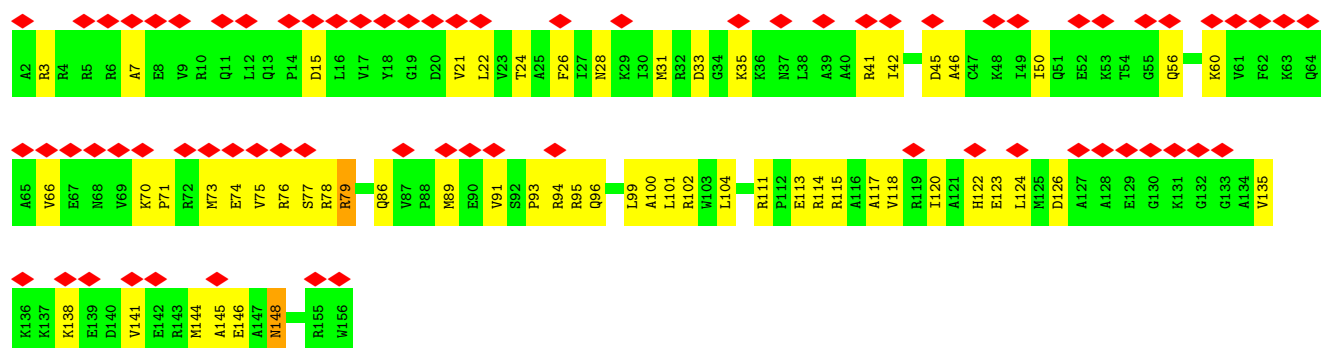




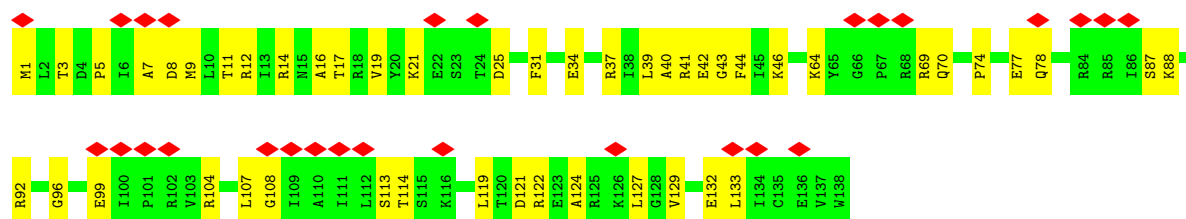
• Molecule 37: 30S ribosomal protein S7



• Molecule 37: 30S ribosomal protein S7

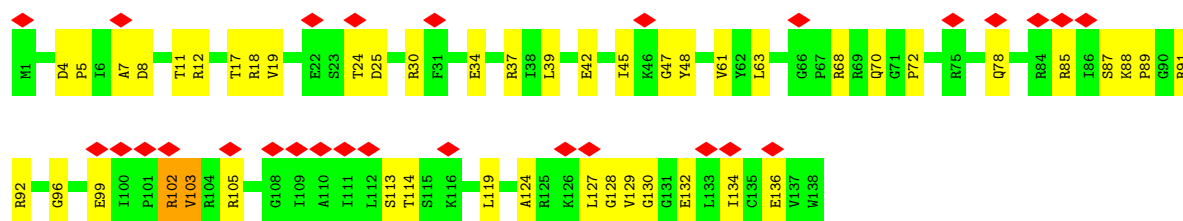


• Molecule 38: 30S ribosomal protein S8

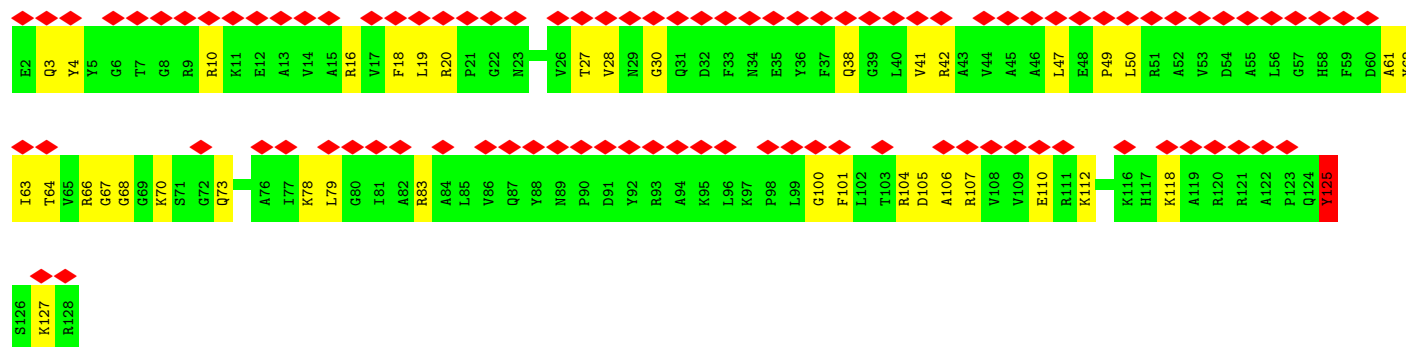
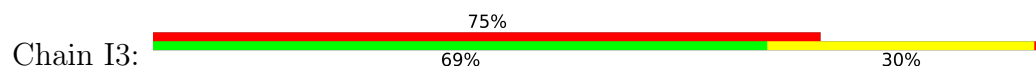


• Molecule 38: 30S ribosomal protein S8

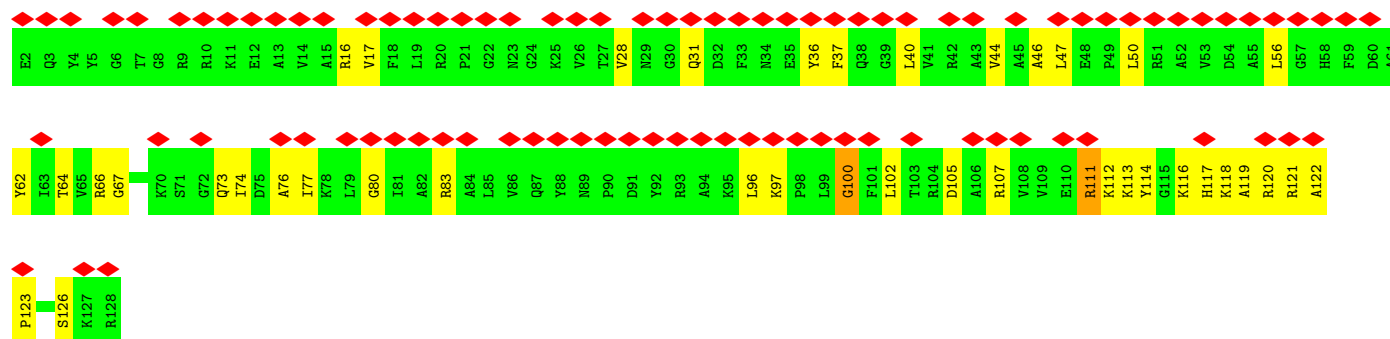
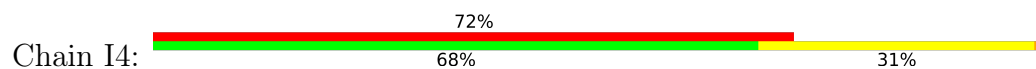




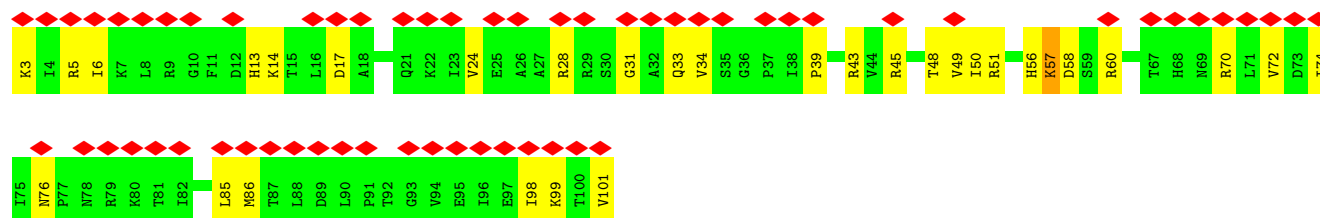
- Molecule 39: 30S ribosomal protein S9



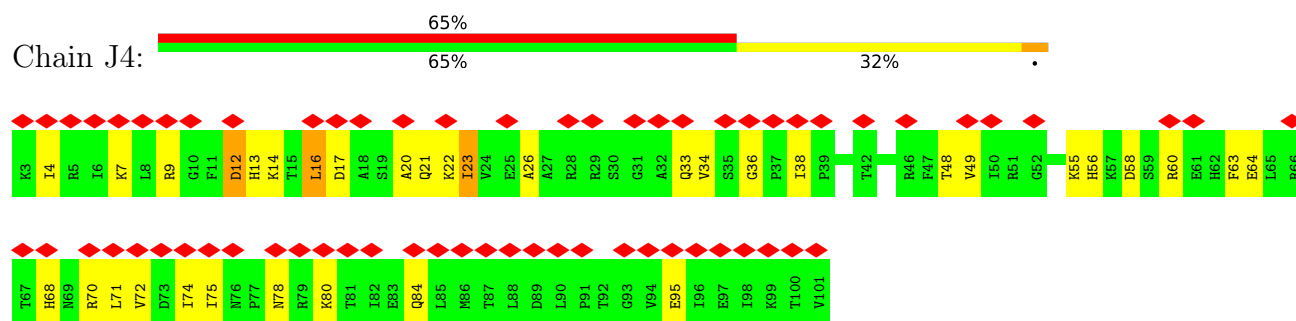
- Molecule 39: 30S ribosomal protein S9



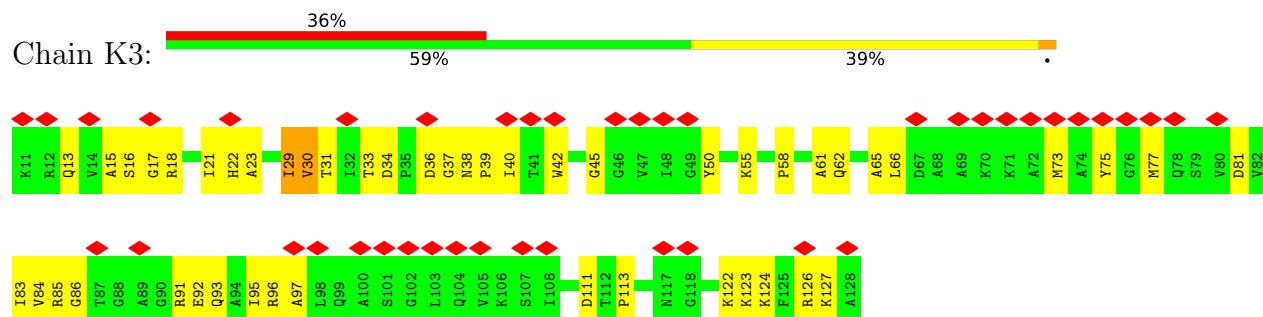
- Molecule 40: 30S ribosomal protein S10



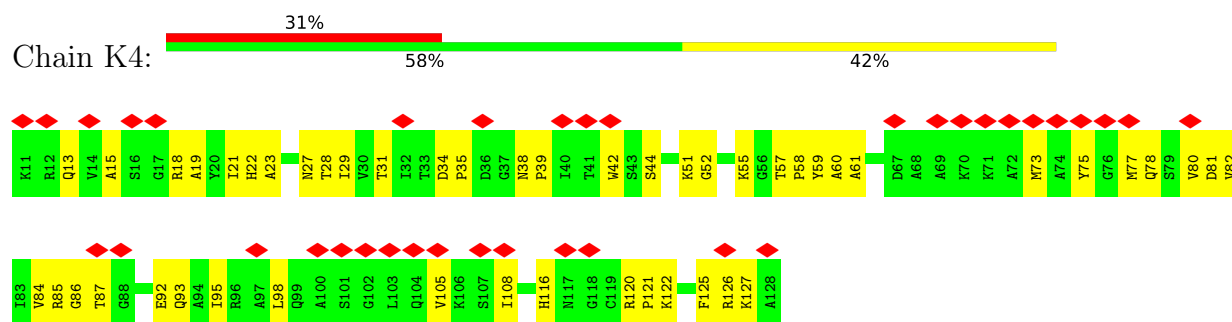
- Molecule 40: 30S ribosomal protein S10



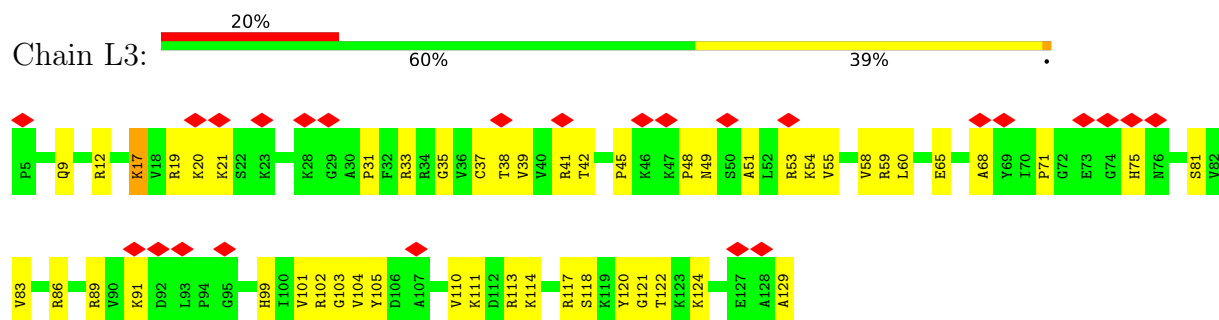
- Molecule 41: 30S ribosomal protein S11



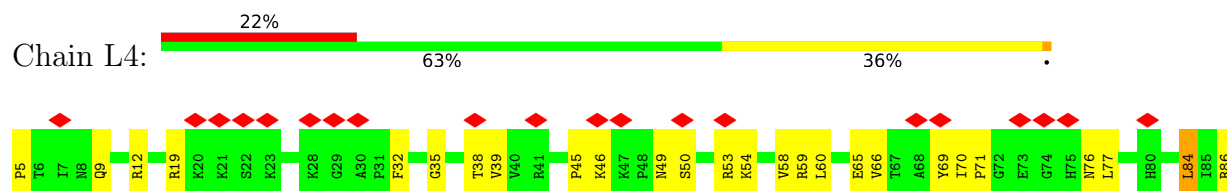
- Molecule 41: 30S ribosomal protein S11

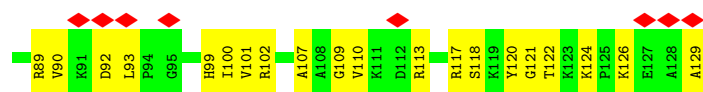


- Molecule 42: 30S ribosomal protein S12

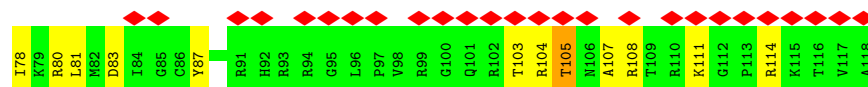
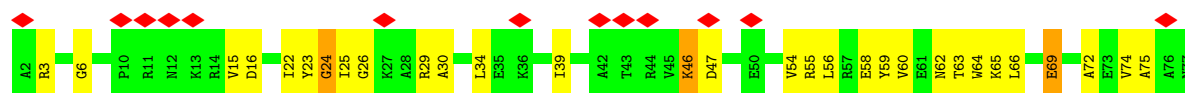


- Molecule 42: 30S ribosomal protein S12





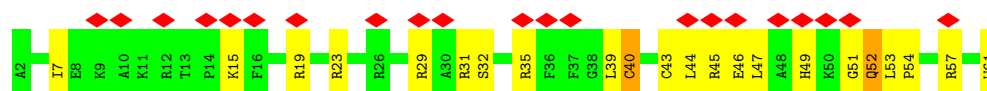
- Molecule 43: 30S ribosomal protein S13



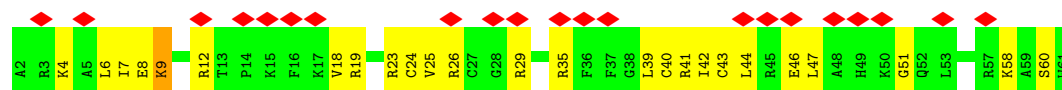
- Molecule 43: 30S ribosomal protein S13



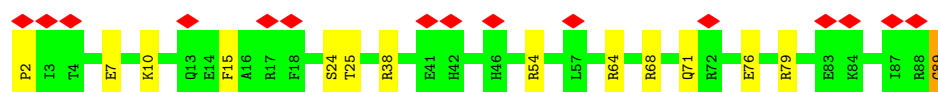
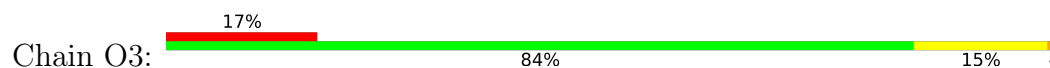
- Molecule 44: 30S ribosomal protein S14 type Z



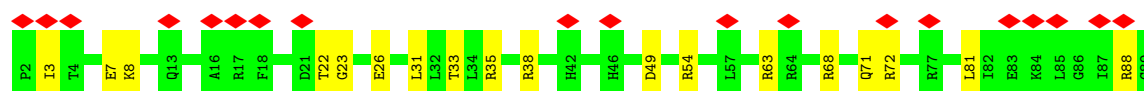
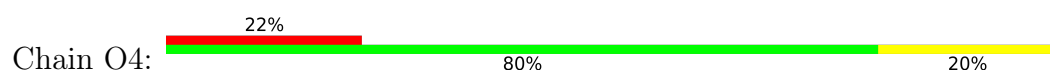
- Molecule 44: 30S ribosomal protein S14 type Z



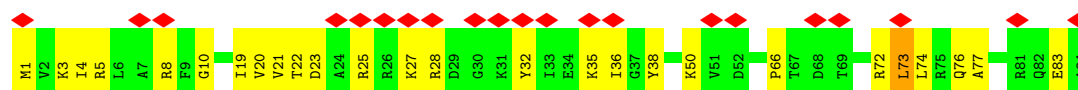
- Molecule 45: 30S ribosomal protein S15



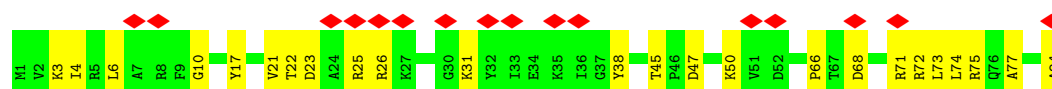
- Molecule 45: 30S ribosomal protein S15



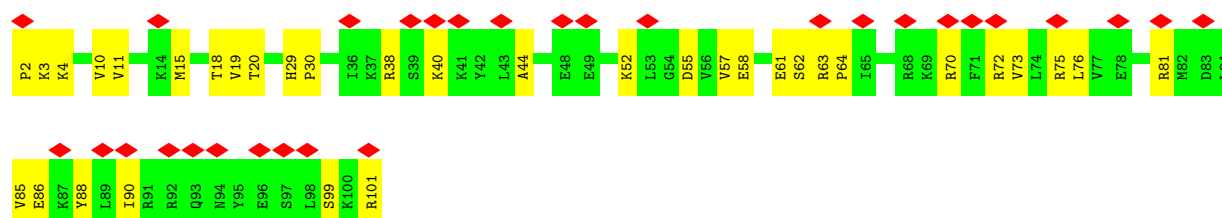
- Molecule 46: 30S ribosomal protein S16



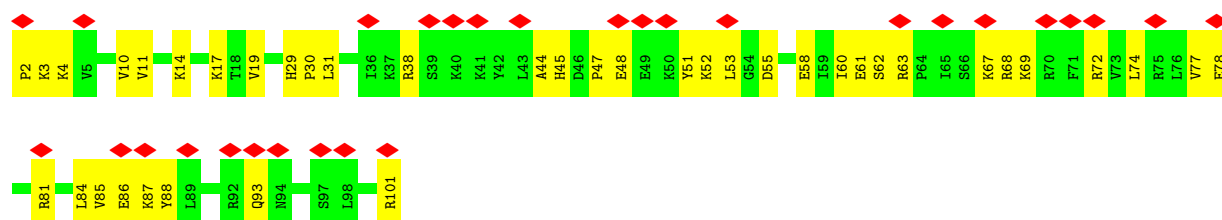
- Molecule 46: 30S ribosomal protein S16



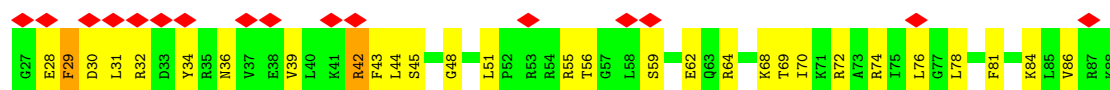
- Molecule 47: 30S ribosomal protein S17



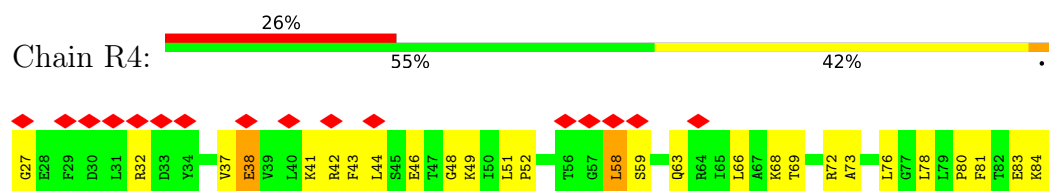
- Molecule 47: 30S ribosomal protein S17



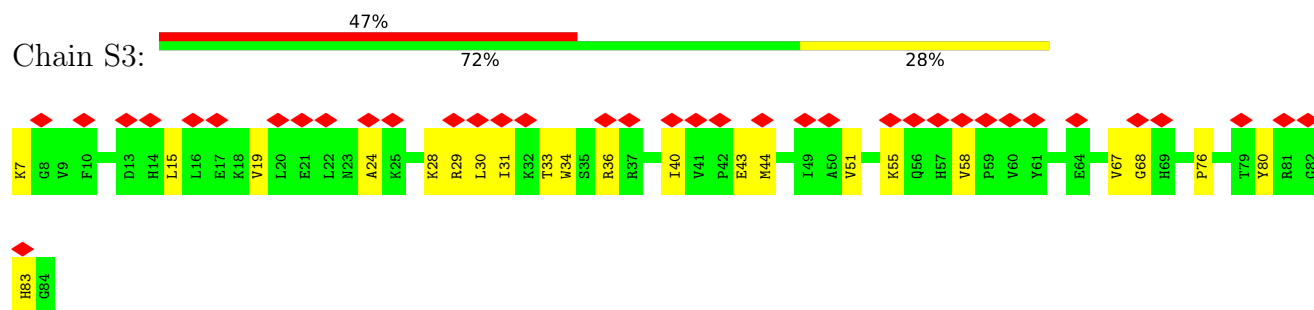
- Molecule 48: 30S ribosomal protein S18



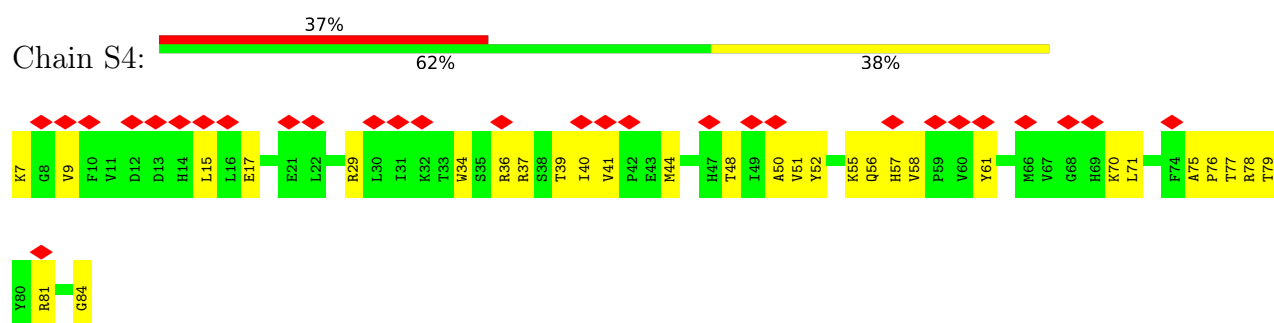
- Molecule 48: 30S ribosomal protein S18



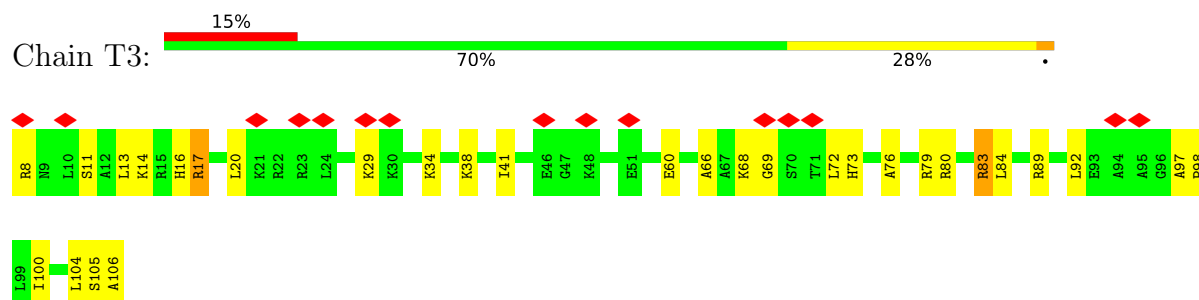
- Molecule 49: 30S ribosomal protein S19



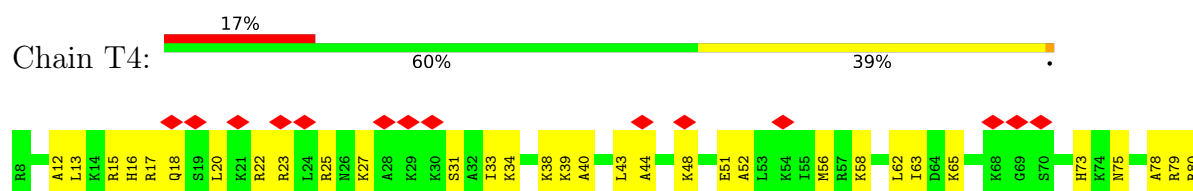
- Molecule 49: 30S ribosomal protein S19

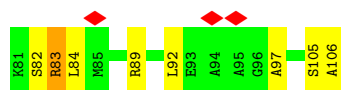


- Molecule 50: 30S ribosomal protein S20

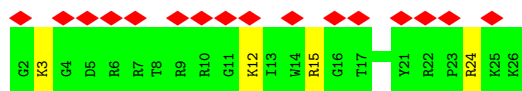
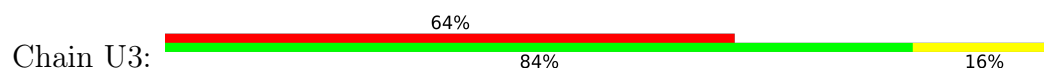


- Molecule 50: 30S ribosomal protein S20

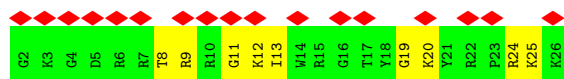




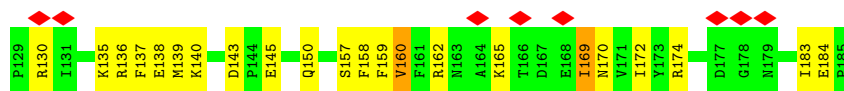
- Molecule 51: 30S ribosomal protein Thx



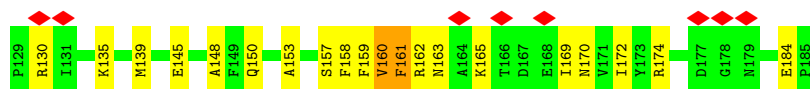
- Molecule 51: 30S ribosomal protein Thx



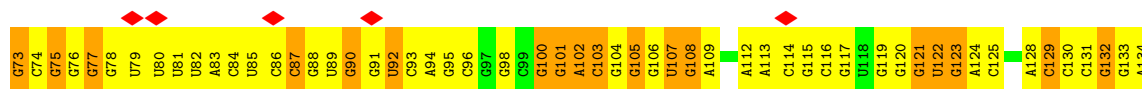
- Molecule 52: Ribosome hibernation promoting factor

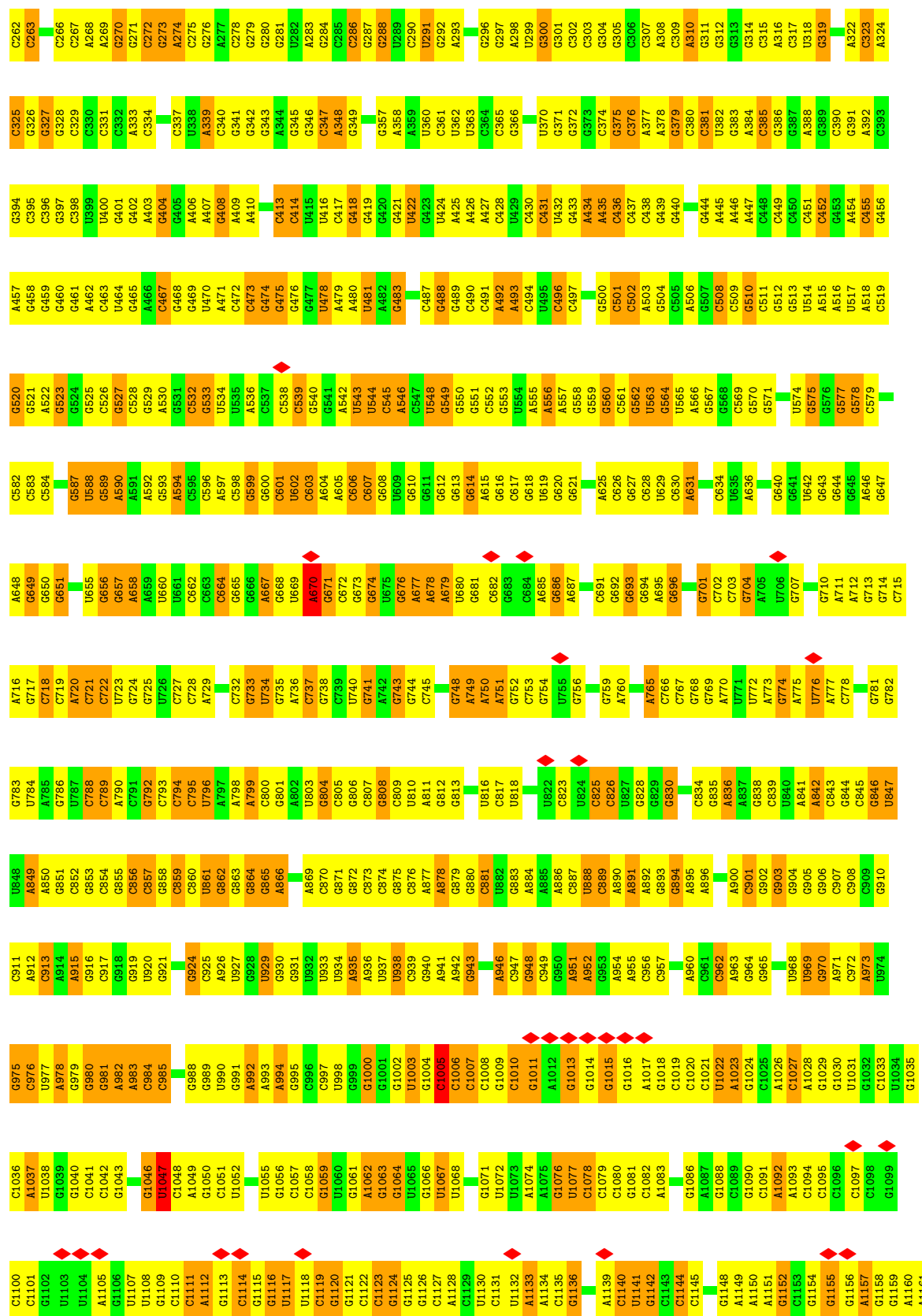


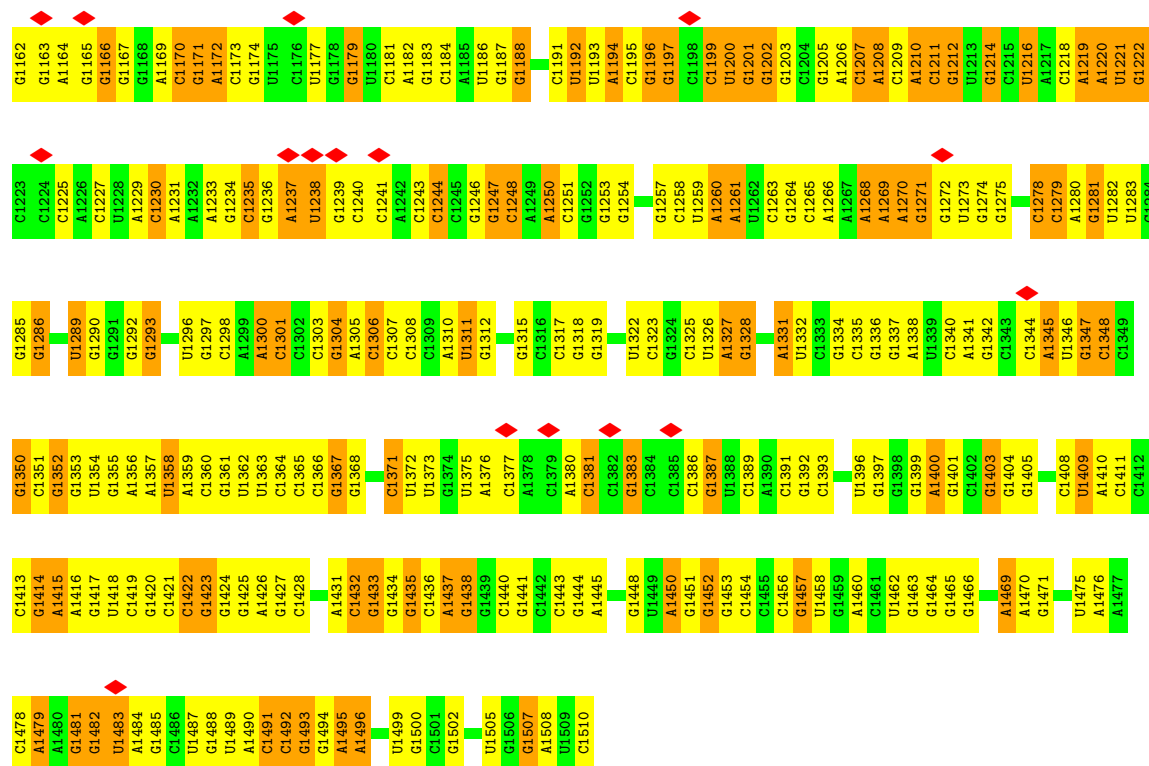
- Molecule 52: Ribosome hibernation promoting factor



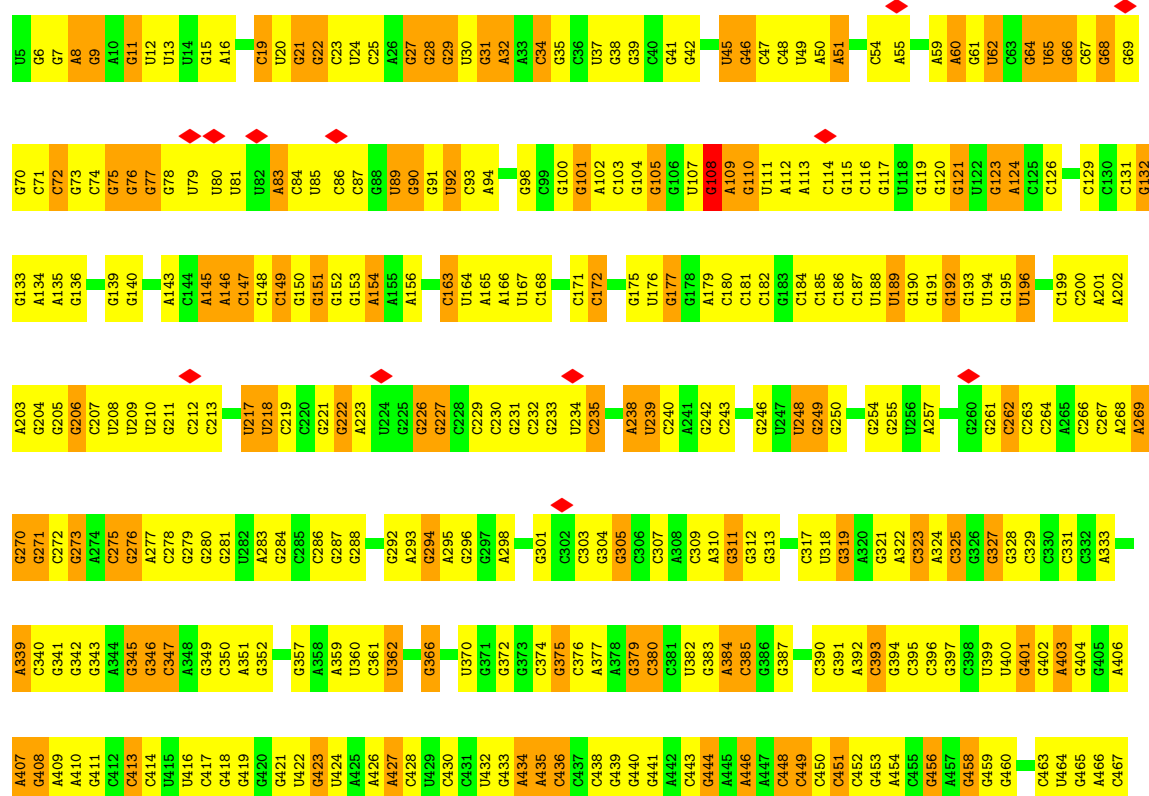
- Molecule 53: 16S ribosomal RNA







• Molecule 53: 16S ribosomal RNA



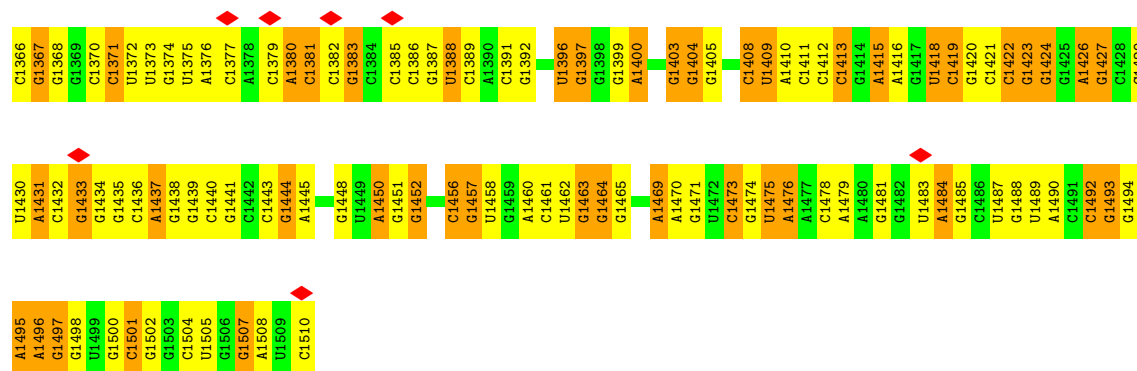
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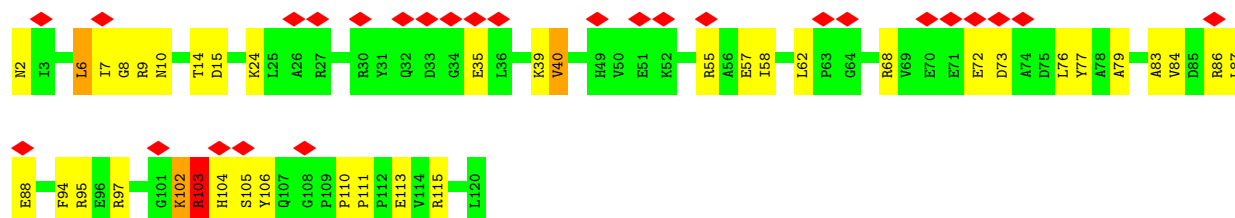
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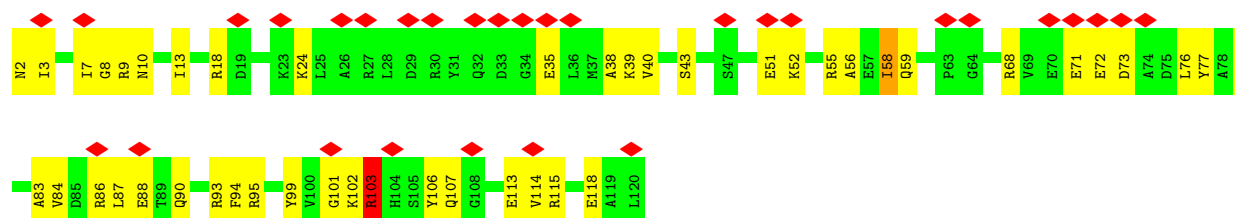
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U1118	C1119	G1120	G1121	C1122	G1123	G1124	G1125	G1126	G1127	A1128	C1129	U1130	C1131	A1132	A1133	A1134	C1135	G1136	G1137	G1138	A1139	U1140	U1141	C1142	G1143	C1144	G1145	G1146	C1147	G1148	A1149	A1150	A1151	G1152	C1153	G1154	G1155	G1156	A1157	G1158	G1159	A1160	A1161	G1162	G1163	A1164	G1165	G1166	G1167	G1168	A1169	C1170	G1171	A1172	C1173	G1174	U1175	C1176



- Molecule 54: Ribosome hibernation promoting factor



- Molecule 54: Ribosome hibernation promoting factor



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	25368	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 ($e^-/\text{\AA}^2$)	1.06	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	11.760	Depositor
Minimum map value	-5.930	Depositor
Average map value	0.024	Depositor
Map value standard deviation	0.355	Depositor
Recommended contour level	2.3	Depositor
Map size ($\text{\AA}$)	770.0, 770.0, 770.0	wwPDB
Map dimensions	700, 700, 700	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.1, 1.1, 1.1	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	C1	0.56	1/2166 (0.0%)	0.86	1/2919 (0.0%)
1	C2	0.51	0/2166	0.83	0/2919
2	D1	0.46	0/1602	0.82	0/2160
2	D2	0.46	0/1602	0.79	0/2160
3	E1	0.47	0/1663	0.81	0/2249
3	E2	0.46	0/1663	0.79	0/2249
4	F1	0.42	0/1499	0.80	0/2016
4	F2	0.42	0/1499	0.84	2/2016 (0.1%)
5	G1	0.39	0/1333	0.78	0/1802
5	G2	0.40	0/1333	0.80	0/1802
6	H1	0.41	0/387	0.84	0/523
6	H2	0.39	0/387	0.85	0/523
7	I1	0.39	0/1132	0.74	1/1525 (0.1%)
7	I2	0.41	0/1132	0.80	0/1525
8	J1	0.52	0/943	0.78	0/1269
8	J2	0.52	0/943	0.75	0/1269
9	K1	0.45	0/1162	0.89	0/1544
9	K2	0.44	0/1162	0.86	0/1544
10	L1	0.45	0/1143	0.84	0/1527
10	L2	0.45	0/1143	0.75	0/1527
11	M1	0.42	0/974	0.84	0/1302
11	M2	0.41	0/974	0.79	0/1302
12	N1	0.42	0/892	0.86	0/1187
12	N2	0.40	0/892	0.81	0/1187
13	O1	0.46	0/1156	0.80	0/1542
13	O2	0.46	0/1156	0.80	0/1542
14	P1	0.42	0/982	0.78	1/1306 (0.1%)
14	P2	0.43	0/982	0.81	1/1306 (0.1%)
15	Q1	0.39	0/790	0.82	0/1057
15	Q2	0.38	0/790	0.79	0/1057
16	R1	0.41	0/911	0.73	0/1220
16	R2	0.41	0/911	0.79	2/1220 (0.2%)
17	S1	0.44	0/740	0.80	0/993
17	S2	0.43	0/740	0.80	0/993

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
18	T1	0.36	0/799	0.81	0/1064
18	T2	0.35	0/799	0.78	1/1064 (0.1%)
19	U1	0.39	0/1461	0.79	1/1982 (0.1%)
19	U2	0.39	0/1461	0.73	0/1982
20	V1	0.45	0/621	0.81	0/827
20	V2	0.46	0/621	0.77	0/827
21	W1	0.47	0/770	0.86	1/1022 (0.1%)
21	W2	0.43	0/770	0.81	0/1022
22	X1	0.41	0/583	0.79	0/771
22	X2	0.43	0/583	0.82	0/771
23	Y1	0.40	0/474	0.79	0/635
23	Y2	0.40	0/474	0.76	0/635
24	Z1	0.43	0/528	0.94	4/709 (0.6%)
24	Z2	0.45	0/528	1.04	2/709 (0.3%)
25	a1	0.45	0/473	0.78	0/639
25	a2	0.43	0/473	0.80	0/639
26	b1	0.44	0/397	0.84	0/529
26	b2	0.47	0/397	1.04	0/529
27	c1	0.55	0/438	0.77	0/575
27	c2	0.52	0/438	0.79	0/575
28	d1	0.47	0/495	0.96	0/649
28	d2	0.54	0/495	0.93	0/649
29	A1	0.59	5/70233 (0.0%)	0.64	6/109643 (0.0%)
29	A2	0.50	0/70233	0.65	8/109643 (0.0%)
30	B1	0.41	0/2928	0.57	0/4568
30	B2	0.42	0/2928	0.59	0/4568
31	e1	0.42	0/302	0.71	0/397
31	e2	0.43	0/302	0.72	0/397
32	B3	0.43	0/1960	0.87	1/2642 (0.0%)
32	B4	0.43	0/1960	0.82	5/2642 (0.2%)
33	C3	0.43	0/1637	0.85	1/2205 (0.0%)
33	C4	0.42	0/1637	0.83	1/2205 (0.0%)
34	D3	0.44	0/1731	0.88	4/2312 (0.2%)
34	D4	0.42	0/1733	0.85	0/2318
35	E3	0.44	0/1172	0.82	0/1576
35	E4	0.43	0/1172	0.80	0/1576
36	F3	0.46	0/856	0.82	2/1154 (0.2%)
36	F4	0.48	0/856	0.79	2/1154 (0.2%)
37	G3	0.42	0/1276	0.81	0/1709
37	G4	0.41	0/1276	0.74	0/1709
38	H3	0.43	0/1136	0.77	0/1527
38	H4	0.41	0/1136	0.83	3/1527 (0.2%)
39	I3	0.43	0/1029	0.92	4/1379 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
39	I4	0.41	0/1029	0.85	2/1379 (0.1%)
40	J3	0.40	0/815	0.78	0/1095
40	J4	0.40	0/815	0.80	0/1095
41	K3	0.45	0/894	0.76	0/1205
41	K4	0.44	0/894	0.82	0/1205
42	L3	0.45	0/992	0.85	0/1327
42	L4	0.46	0/992	0.87	0/1327
43	M3	0.38	0/944	0.87	5/1265 (0.4%)
43	M4	0.43	0/944	1.00	4/1265 (0.3%)
44	N3	0.39	0/501	0.77	0/664
44	N4	0.41	0/501	0.84	0/664
45	O3	3.69	1/745 (0.1%)	0.77	1/992 (0.1%)
45	O4	0.43	0/745	0.78	0/992
46	P3	0.40	0/722	0.82	0/970
46	P4	0.37	0/722	0.76	0/970
47	Q3	0.43	0/848	0.79	0/1131
47	Q4	0.47	0/848	0.91	1/1131 (0.1%)
48	R3	0.46	0/520	0.86	0/690
48	R4	0.46	0/520	0.85	0/690
49	S3	0.43	0/639	0.80	0/860
49	S4	0.39	0/639	0.82	0/860
50	T3	0.46	0/765	0.79	0/1007
50	T4	0.42	0/765	0.76	0/1007
51	U3	0.37	0/222	0.91	0/288
51	U4	0.40	0/222	1.07	1/288 (0.3%)
52	W4	0.45	0/487	0.89	0/650
52	X3	0.44	0/487	0.98	1/650 (0.2%)
53	A3	0.49	0/36234	0.66	8/56554 (0.0%)
53	A4	0.49	0/36234	0.67	7/56554 (0.0%)
54	V3	0.49	0/977	0.97	3/1316 (0.2%)
54	V4	0.49	0/977	0.97	0/1316
All	All	0.53	7/314160 (0.0%)	0.70	87/469344 (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
1	C1	0	6
1	C2	0	6
2	D1	0	4

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	D2	0	2
3	E1	0	1
3	E2	0	2
4	F1	0	6
4	F2	0	4
5	G2	0	1
6	H1	0	1
7	I1	0	2
7	I2	0	2
8	J1	0	2
8	J2	0	2
9	K1	0	2
9	K2	0	1
11	M2	0	1
12	N1	0	2
12	N2	0	1
13	O1	0	2
13	O2	0	3
14	P1	0	1
14	P2	0	3
15	Q2	0	2
16	R1	0	1
16	R2	0	5
17	S2	0	1
18	T1	0	1
18	T2	0	1
19	U1	0	1
19	U2	0	4
20	V1	0	1
20	V2	0	1
21	W1	0	3
21	W2	0	1
22	X1	0	1
22	X2	0	2
24	Z1	0	8
24	Z2	0	1
25	a2	0	1
26	b1	0	2
26	b2	0	2
27	c1	0	1
28	d1	0	2
28	d2	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
31	e1	0	1
31	e2	0	1
32	B3	0	7
32	B4	0	6
33	C3	0	1
33	C4	0	1
34	D3	0	8
34	D4	0	5
35	E3	0	1
35	E4	0	1
36	F3	0	2
36	F4	0	1
37	G3	0	3
37	G4	0	3
38	H3	0	1
38	H4	0	4
39	I3	0	2
40	J3	0	1
40	J4	0	3
41	K3	0	2
42	L3	0	3
42	L4	0	3
43	M3	0	4
43	M4	0	2
44	N3	0	2
44	N4	0	2
45	O3	0	1
46	P3	0	2
47	Q4	0	5
48	R3	0	2
48	R4	0	3
49	S3	0	1
50	T3	0	2
50	T4	0	2
51	U3	0	1
51	U4	0	1
52	W4	0	1
54	V3	0	2
54	V4	0	1
All	All	0	194

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
45	O3	89	GLY	C-OXT	100.10	3.23	1.23
29	A1	764	G	N9-C8	39.24	2.16	1.37
29	A1	764	G	C8-N7	38.63	2.08	1.30
29	A1	764	G	N9-C4	38.17	2.14	1.38
29	A1	764	G	N7-C5	37.62	2.14	1.39

The worst 5 of 87 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	Q4	31	LEU	N-CA-C	-10.07	103.14	114.62
32	B4	5	ILE	N-CA-C	-9.42	104.15	113.20
51	U4	13	ILE	N-CA-C	-9.41	103.53	111.91
33	C3	8	ILE	N-CA-C	-9.40	104.78	113.71
45	O3	89	GLY	CA-C-O	-9.02	93.94	121.00

There are no chirality outliers.

5 of 194 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C1	13	ARG	Peptide
1	C1	178	PRO	Peptide
1	C1	51	VAL	Peptide
1	C1	67	PHE	Peptide
1	C1	86	PRO	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	C1	2116	0	2195	79	0
1	C2	2116	0	2195	77	0
2	D1	1569	0	1634	55	0
2	D2	1569	0	1634	49	0
3	E1	1628	0	1680	53	0
3	E2	1628	0	1680	58	0
4	F1	1474	0	1535	49	0
4	F2	1474	0	1535	47	0
5	G1	1308	0	1382	47	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	G2	1308	0	1382	43	0
6	H1	383	0	410	8	0
6	H2	383	0	410	11	0
7	I1	1105	0	1180	31	0
7	I2	1105	0	1180	29	0
8	J1	933	0	996	29	0
8	J2	933	0	996	29	0
9	K1	1145	0	1228	56	0
9	K2	1145	0	1228	49	0
10	L1	1122	0	1179	41	0
10	L2	1122	0	1179	27	0
11	M1	960	0	1021	47	0
11	M2	960	0	1021	29	0
12	N1	882	0	943	27	0
12	N2	882	0	943	26	0
13	O1	1142	0	1202	34	0
13	O2	1142	0	1202	50	0
14	P1	964	0	1022	36	0
14	P2	964	0	1022	36	0
15	Q1	779	0	852	24	0
15	Q2	779	0	852	26	0
16	R1	900	0	964	27	0
16	R2	900	0	964	29	0
17	S1	726	0	778	17	0
17	S2	726	0	778	24	0
18	T1	786	0	878	29	0
18	T2	786	0	878	21	0
19	U1	1429	0	1454	40	0
19	U2	1429	0	1454	36	0
20	V1	613	0	633	27	0
20	V2	613	0	633	19	0
21	W1	763	0	848	32	0
21	W2	763	0	848	28	0
22	X1	581	0	629	20	0
22	X2	581	0	629	20	0
23	Y1	469	0	518	19	0
23	Y2	469	0	518	12	0
24	Z1	516	0	514	18	0
24	Z2	516	0	514	17	0
25	a1	459	0	480	20	0
25	a2	459	0	480	17	0
26	b1	390	0	404	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	b2	390	0	404	16	0
27	c1	430	0	480	22	0
27	c2	430	0	480	16	0
28	d1	489	0	560	17	0
28	d2	489	0	560	19	0
29	A1	62707	0	31614	1057	0
29	A2	62707	0	31614	1035	0
30	B1	2617	0	1328	40	0
30	B2	2617	0	1328	35	0
31	e1	299	0	326	13	0
31	e2	299	0	326	13	0
32	B3	1925	0	1975	49	0
32	B4	1925	0	1975	62	0
33	C3	1613	0	1677	48	0
33	C4	1613	0	1677	43	0
34	D3	1703	0	1765	60	0
34	D4	1703	0	1765	46	0
35	E3	1156	0	1213	36	0
35	E4	1156	0	1213	31	0
36	F3	843	0	857	25	0
36	F4	843	0	857	22	0
37	G3	1257	0	1296	49	0
37	G4	1257	0	1296	49	0
38	H3	1116	0	1177	34	0
38	H4	1116	0	1177	30	0
39	I3	1010	0	1037	30	0
39	I4	1010	0	1037	30	0
40	J3	802	0	849	22	0
40	J4	802	0	849	28	0
41	K3	879	0	899	37	0
41	K4	879	0	899	35	0
42	L3	976	0	1062	38	0
42	L4	976	0	1062	30	0
43	M3	934	0	992	29	0
43	M4	934	0	992	38	0
44	N3	492	0	533	20	0
44	N4	492	0	533	19	0
45	O3	734	0	771	19	0
45	O4	734	0	771	14	0
46	P3	706	0	725	21	0
46	P4	706	0	725	18	0
47	Q3	835	0	904	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
47	Q4	835	0	904	35	0
48	R3	515	0	568	29	0
48	R4	515	0	568	17	0
49	S3	625	0	636	17	0
49	S4	625	0	636	26	0
50	T3	763	0	861	26	0
50	T4	763	0	861	33	0
51	U3	218	0	234	3	0
51	U4	218	0	234	6	0
52	W4	476	0	472	28	0
52	X3	476	0	472	29	0
53	A3	32369	0	16339	629	0
53	A4	32369	0	16339	622	0
54	V3	963	0	982	36	0
54	V4	963	0	982	38	0
All	All	289188	0	197382	5661	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 15.

The worst 5 of 5661 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)
29:A1:764:G:C5	29:A1:764:G:C4	2.02	1.46
29:A1:764:G:C8	29:A1:764:G:N7	2.08	1.22
29:A1:764:G:C4	29:A1:764:G:N9	2.14	1.15
29:A1:764:G:C5	29:A1:764:G:N7	2.14	1.14
29:A1:764:G:C8	29:A1:764:G:N9	2.16	1.12

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	
1	C1	270/272 (99%)	208 (77%)	62 (23%)	0	100	100
1	C2	270/272 (99%)	214 (79%)	56 (21%)	0	100	100
2	D1	203/205 (99%)	159 (78%)	44 (22%)	0	100	100
2	D2	203/205 (99%)	153 (75%)	48 (24%)	2 (1%)	12	47
3	E1	206/208 (99%)	157 (76%)	48 (23%)	1 (0%)	24	63
3	E2	206/208 (99%)	148 (72%)	57 (28%)	1 (0%)	24	63
4	F1	179/181 (99%)	141 (79%)	38 (21%)	0	100	100
4	F2	179/181 (99%)	139 (78%)	40 (22%)	0	100	100
5	G1	168/170 (99%)	126 (75%)	42 (25%)	0	100	100
5	G2	168/170 (99%)	130 (77%)	38 (23%)	0	100	100
6	H1	48/50 (96%)	37 (77%)	11 (23%)	0	100	100
6	H2	48/50 (96%)	36 (75%)	12 (25%)	0	100	100
7	I1	136/138 (99%)	113 (83%)	22 (16%)	1 (1%)	18	55
7	I2	136/138 (99%)	112 (82%)	24 (18%)	0	100	100
8	J1	120/122 (98%)	98 (82%)	22 (18%)	0	100	100
8	J2	120/122 (98%)	93 (78%)	27 (22%)	0	100	100
9	K1	148/150 (99%)	119 (80%)	29 (20%)	0	100	100
9	K2	148/150 (99%)	106 (72%)	42 (28%)	0	100	100
10	L1	139/141 (99%)	107 (77%)	32 (23%)	0	100	100
10	L2	139/141 (99%)	104 (75%)	35 (25%)	0	100	100
11	M1	115/117 (98%)	100 (87%)	15 (13%)	0	100	100
11	M2	115/117 (98%)	100 (87%)	15 (13%)	0	100	100
12	N1	109/111 (98%)	87 (80%)	22 (20%)	0	100	100
12	N2	109/111 (98%)	86 (79%)	23 (21%)	0	100	100
13	O1	135/137 (98%)	105 (78%)	30 (22%)	0	100	100
13	O2	135/137 (98%)	96 (71%)	39 (29%)	0	100	100
14	P1	115/117 (98%)	96 (84%)	19 (16%)	0	100	100
14	P2	115/117 (98%)	102 (89%)	13 (11%)	0	100	100
15	Q1	99/101 (98%)	79 (80%)	20 (20%)	0	100	100
15	Q2	99/101 (98%)	72 (73%)	27 (27%)	0	100	100
16	R1	111/113 (98%)	96 (86%)	15 (14%)	0	100	100
16	R2	111/113 (98%)	91 (82%)	20 (18%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	S1	90/92 (98%)	73 (81%)	17 (19%)	0	100	100
17	S2	90/92 (98%)	74 (82%)	16 (18%)	0	100	100
18	T1	100/102 (98%)	76 (76%)	23 (23%)	1 (1%)	12	47
18	T2	100/102 (98%)	80 (80%)	19 (19%)	1 (1%)	12	47
19	U1	177/179 (99%)	140 (79%)	37 (21%)	0	100	100
19	U2	177/179 (99%)	141 (80%)	36 (20%)	0	100	100
20	V1	75/77 (97%)	63 (84%)	12 (16%)	0	100	100
20	V2	75/77 (97%)	61 (81%)	14 (19%)	0	100	100
21	W1	95/97 (98%)	73 (77%)	22 (23%)	0	100	100
21	W2	95/97 (98%)	69 (73%)	26 (27%)	0	100	100
22	X1	67/69 (97%)	53 (79%)	14 (21%)	0	100	100
22	X2	67/69 (97%)	55 (82%)	12 (18%)	0	100	100
23	Y1	57/59 (97%)	46 (81%)	11 (19%)	0	100	100
23	Y2	57/59 (97%)	50 (88%)	7 (12%)	0	100	100
24	Z1	61/63 (97%)	31 (51%)	28 (46%)	2 (3%)	3	21
24	Z2	61/63 (97%)	36 (59%)	23 (38%)	2 (3%)	3	21
25	a1	57/59 (97%)	45 (79%)	12 (21%)	0	100	100
25	a2	57/59 (97%)	46 (81%)	11 (19%)	0	100	100
26	b1	43/45 (96%)	30 (70%)	13 (30%)	0	100	100
26	b2	43/45 (96%)	29 (67%)	14 (33%)	0	100	100
27	c1	47/49 (96%)	39 (83%)	8 (17%)	0	100	100
27	c2	47/49 (96%)	38 (81%)	9 (19%)	0	100	100
28	d1	59/61 (97%)	38 (64%)	21 (36%)	0	100	100
28	d2	59/61 (97%)	41 (70%)	18 (30%)	0	100	100
31	e1	34/36 (94%)	27 (79%)	7 (21%)	0	100	100
31	e2	34/36 (94%)	28 (82%)	6 (18%)	0	100	100
32	B3	235/237 (99%)	170 (72%)	65 (28%)	0	100	100
32	B4	235/237 (99%)	186 (79%)	49 (21%)	0	100	100
33	C3	204/206 (99%)	158 (78%)	46 (22%)	0	100	100
33	C4	204/206 (99%)	153 (75%)	51 (25%)	0	100	100
34	D3	202/208 (97%)	171 (85%)	30 (15%)	1 (0%)	24	63

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	D4	206/208 (99%)	156 (76%)	50 (24%)	0	100	100
35	E3	149/151 (99%)	117 (78%)	32 (22%)	0	100	100
35	E4	149/151 (99%)	122 (82%)	27 (18%)	0	100	100
36	F3	99/101 (98%)	82 (83%)	17 (17%)	0	100	100
36	F4	99/101 (98%)	84 (85%)	15 (15%)	0	100	100
37	G3	153/155 (99%)	125 (82%)	28 (18%)	0	100	100
37	G4	153/155 (99%)	130 (85%)	23 (15%)	0	100	100
38	H3	136/138 (99%)	115 (85%)	21 (15%)	0	100	100
38	H4	136/138 (99%)	110 (81%)	25 (18%)	1 (1%)	18	55
39	I3	125/127 (98%)	96 (77%)	29 (23%)	0	100	100
39	I4	125/127 (98%)	101 (81%)	24 (19%)	0	100	100
40	J3	97/99 (98%)	74 (76%)	23 (24%)	0	100	100
40	J4	97/99 (98%)	79 (81%)	18 (19%)	0	100	100
41	K3	116/118 (98%)	90 (78%)	26 (22%)	0	100	100
41	K4	116/118 (98%)	88 (76%)	28 (24%)	0	100	100
42	L3	123/125 (98%)	93 (76%)	29 (24%)	1 (1%)	16	53
42	L4	123/125 (98%)	96 (78%)	26 (21%)	1 (1%)	16	53
43	M3	115/117 (98%)	85 (74%)	30 (26%)	0	100	100
43	M4	115/117 (98%)	91 (79%)	24 (21%)	0	100	100
44	N3	58/60 (97%)	46 (79%)	12 (21%)	0	100	100
44	N4	58/60 (97%)	45 (78%)	13 (22%)	0	100	100
45	O3	86/88 (98%)	67 (78%)	19 (22%)	0	100	100
45	O4	86/88 (98%)	71 (83%)	15 (17%)	0	100	100
46	P3	82/84 (98%)	64 (78%)	18 (22%)	0	100	100
46	P4	82/84 (98%)	68 (83%)	14 (17%)	0	100	100
47	Q3	98/100 (98%)	80 (82%)	18 (18%)	0	100	100
47	Q4	98/100 (98%)	74 (76%)	24 (24%)	0	100	100
48	R3	60/62 (97%)	45 (75%)	15 (25%)	0	100	100
48	R4	60/62 (97%)	47 (78%)	13 (22%)	0	100	100
49	S3	76/78 (97%)	53 (70%)	23 (30%)	0	100	100
49	S4	76/78 (97%)	59 (78%)	17 (22%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
50	T3	97/99 (98%)	83 (86%)	14 (14%)	0	100	100
50	T4	97/99 (98%)	83 (86%)	14 (14%)	0	100	100
51	U3	23/25 (92%)	15 (65%)	8 (35%)	0	100	100
51	U4	23/25 (92%)	16 (70%)	7 (30%)	0	100	100
52	W4	55/57 (96%)	39 (71%)	16 (29%)	0	100	100
52	X3	55/57 (96%)	39 (71%)	16 (29%)	0	100	100
54	V3	117/119 (98%)	89 (76%)	26 (22%)	2 (2%)	7	35
54	V4	117/119 (98%)	89 (76%)	26 (22%)	2 (2%)	7	35
All	All	11542/11750 (98%)	9036 (78%)	2487 (22%)	19 (0%)	44	77

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
54	V3	103	ARG
54	V3	104	HIS
38	H4	103	VAL
3	E1	10	PRO
24	Z1	43	TYR

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C1	214/214 (100%)	212 (99%)	2 (1%)	70	76
1	C2	214/214 (100%)	212 (99%)	2 (1%)	70	76
2	D1	165/165 (100%)	164 (99%)	1 (1%)	78	80
2	D2	165/165 (100%)	165 (100%)	0	100	100
3	E1	165/165 (100%)	164 (99%)	1 (1%)	78	80
3	E2	165/165 (100%)	163 (99%)	2 (1%)	63	73
4	F1	155/155 (100%)	153 (99%)	2 (1%)	61	72
4	F2	155/155 (100%)	154 (99%)	1 (1%)	78	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	G1	142/142 (100%)	141 (99%)	1 (1%)	76	79
5	G2	142/142 (100%)	142 (100%)	0	100	100
6	H1	41/41 (100%)	41 (100%)	0	100	100
6	H2	41/41 (100%)	41 (100%)	0	100	100
7	I1	117/117 (100%)	117 (100%)	0	100	100
7	I2	117/117 (100%)	115 (98%)	2 (2%)	53	67
8	J1	100/100 (100%)	98 (98%)	2 (2%)	48	65
8	J2	100/100 (100%)	100 (100%)	0	100	100
9	K1	116/116 (100%)	116 (100%)	0	100	100
9	K2	116/116 (100%)	116 (100%)	0	100	100
10	L1	111/111 (100%)	111 (100%)	0	100	100
10	L2	111/111 (100%)	111 (100%)	0	100	100
11	M1	100/100 (100%)	99 (99%)	1 (1%)	68	76
11	M2	100/100 (100%)	98 (98%)	2 (2%)	48	65
12	N1	87/87 (100%)	87 (100%)	0	100	100
12	N2	87/87 (100%)	86 (99%)	1 (1%)	65	74
13	O1	120/120 (100%)	118 (98%)	2 (2%)	53	67
13	O2	120/120 (100%)	119 (99%)	1 (1%)	73	77
14	P1	93/93 (100%)	93 (100%)	0	100	100
14	P2	93/93 (100%)	92 (99%)	1 (1%)	65	74
15	Q1	82/82 (100%)	82 (100%)	0	100	100
15	Q2	82/82 (100%)	81 (99%)	1 (1%)	63	73
16	R1	92/92 (100%)	91 (99%)	1 (1%)	65	74
16	R2	92/92 (100%)	92 (100%)	0	100	100
17	S1	74/74 (100%)	73 (99%)	1 (1%)	59	71
17	S2	74/74 (100%)	74 (100%)	0	100	100
18	T1	85/85 (100%)	83 (98%)	2 (2%)	43	63
18	T2	85/85 (100%)	85 (100%)	0	100	100
19	U1	158/158 (100%)	154 (98%)	4 (2%)	42	62
19	U2	158/158 (100%)	158 (100%)	0	100	100
20	V1	62/62 (100%)	62 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	V2	62/62 (100%)	62 (100%)	0	100	100
21	W1	82/82 (100%)	82 (100%)	0	100	100
21	W2	82/82 (100%)	82 (100%)	0	100	100
22	X1	64/64 (100%)	62 (97%)	2 (3%)	35	56
22	X2	64/64 (100%)	64 (100%)	0	100	100
23	Y1	51/51 (100%)	50 (98%)	1 (2%)	48	65
23	Y2	51/51 (100%)	51 (100%)	0	100	100
24	Z1	57/57 (100%)	56 (98%)	1 (2%)	51	66
24	Z2	57/57 (100%)	54 (95%)	3 (5%)	20	42
25	a1	51/51 (100%)	51 (100%)	0	100	100
25	a2	51/51 (100%)	50 (98%)	1 (2%)	48	65
26	b1	44/44 (100%)	44 (100%)	0	100	100
26	b2	44/44 (100%)	44 (100%)	0	100	100
27	c1	42/42 (100%)	42 (100%)	0	100	100
27	c2	42/42 (100%)	42 (100%)	0	100	100
28	d1	51/51 (100%)	51 (100%)	0	100	100
28	d2	51/51 (100%)	51 (100%)	0	100	100
31	e1	33/33 (100%)	33 (100%)	0	100	100
31	e2	33/33 (100%)	33 (100%)	0	100	100
32	B3	205/205 (100%)	203 (99%)	2 (1%)	68	76
32	B4	205/205 (100%)	204 (100%)	1 (0%)	81	81
33	C3	160/160 (100%)	157 (98%)	3 (2%)	50	66
33	C4	160/160 (100%)	157 (98%)	3 (2%)	50	66
34	D3	180/180 (100%)	179 (99%)	1 (1%)	78	80
34	D4	180/180 (100%)	180 (100%)	0	100	100
35	E3	116/116 (100%)	115 (99%)	1 (1%)	70	76
35	E4	116/116 (100%)	116 (100%)	0	100	100
36	F3	90/90 (100%)	89 (99%)	1 (1%)	65	74
36	F4	90/90 (100%)	90 (100%)	0	100	100
37	G3	126/126 (100%)	125 (99%)	1 (1%)	73	77
37	G4	126/126 (100%)	126 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	H3	119/119 (100%)	119 (100%)	0	100	100
38	H4	119/119 (100%)	118 (99%)	1 (1%)	73	77
39	I3	98/98 (100%)	98 (100%)	0	100	100
39	I4	98/98 (100%)	97 (99%)	1 (1%)	68	76
40	J3	89/89 (100%)	89 (100%)	0	100	100
40	J4	89/89 (100%)	89 (100%)	0	100	100
41	K3	89/89 (100%)	87 (98%)	2 (2%)	45	64
41	K4	89/89 (100%)	89 (100%)	0	100	100
42	L3	104/104 (100%)	104 (100%)	0	100	100
42	L4	104/104 (100%)	103 (99%)	1 (1%)	68	76
43	M3	94/94 (100%)	92 (98%)	2 (2%)	47	65
43	M4	94/94 (100%)	92 (98%)	2 (2%)	47	65
44	N3	49/49 (100%)	48 (98%)	1 (2%)	48	65
44	N4	49/49 (100%)	48 (98%)	1 (2%)	48	65
45	O3	79/79 (100%)	79 (100%)	0	100	100
45	O4	79/79 (100%)	78 (99%)	1 (1%)	61	72
46	P3	72/72 (100%)	71 (99%)	1 (1%)	59	71
46	P4	72/72 (100%)	72 (100%)	0	100	100
47	Q3	95/95 (100%)	95 (100%)	0	100	100
47	Q4	95/95 (100%)	95 (100%)	0	100	100
48	R3	55/55 (100%)	54 (98%)	1 (2%)	51	66
48	R4	55/55 (100%)	53 (96%)	2 (4%)	31	52
49	S3	67/67 (100%)	67 (100%)	0	100	100
49	S4	67/67 (100%)	66 (98%)	1 (2%)	57	70
50	T3	76/76 (100%)	76 (100%)	0	100	100
50	T4	76/76 (100%)	76 (100%)	0	100	100
51	U3	20/20 (100%)	20 (100%)	0	100	100
51	U4	20/20 (100%)	20 (100%)	0	100	100
52	W4	50/50 (100%)	49 (98%)	1 (2%)	48	65
52	X3	50/50 (100%)	48 (96%)	2 (4%)	28	49
54	V3	101/101 (100%)	93 (92%)	8 (8%)	11	32

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
54	V4	101/101 (100%)	96 (95%)	5 (5%)	22	43
All	All	9776/9776 (100%)	9689 (99%)	87 (1%)	68	76

5 of 87 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
52	X3	160	VAL
38	H4	129	VAL
54	V3	6	LEU
54	V3	103	ARG
43	M4	115	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 166 such sidechains are listed below:

Mol	Chain	Res	Type
36	F3	57	GLN
36	F4	57	GLN
37	G3	148	ASN
45	O3	62	GLN
39	I4	89	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
29	A1	2911/2912 (99%)	1510 (51%)	28 (0%)
29	A2	2911/2912 (99%)	1484 (50%)	30 (1%)
30	B1	121/122 (99%)	62 (51%)	0
30	B2	121/122 (99%)	58 (47%)	1 (0%)
53	A3	1505/1506 (99%)	789 (52%)	26 (1%)
53	A4	1505/1506 (99%)	795 (52%)	16 (1%)
All	All	9074/9080 (99%)	4698 (51%)	101 (1%)

5 of 4698 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
29	A1	3	U
29	A1	4	C
29	A1	5	A
29	A1	6	A
29	A1	7	G

5 of 101 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
29	A2	2792	G
53	A3	670	A
53	A4	1305	A
53	A3	133	G
53	A3	382	U

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

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

5.5 Carbohydrates [i](#)

There are no 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
34	D3	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D3	10:ARG	C	11:LEU	N	4.44
1	D3	8:VAL	C	9:CYS	N	3.57

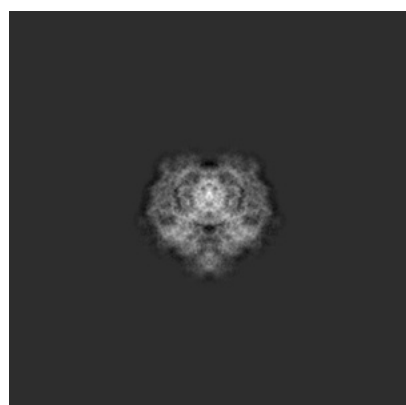
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0104. These allow visual inspection of the internal detail of the map and identification of artifacts.

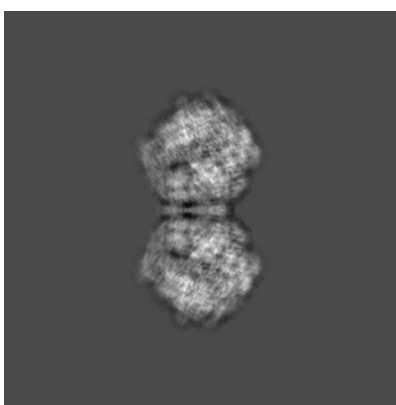
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

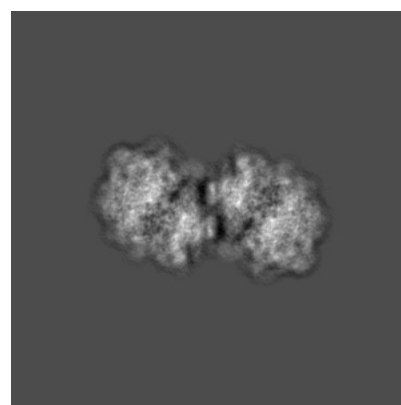
6.1.1 Primary map



X



Y

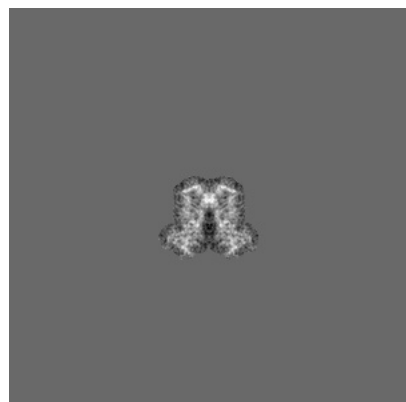


Z

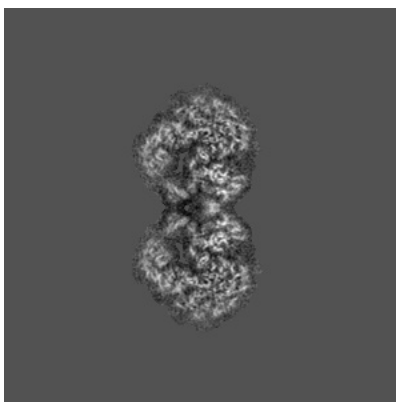
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

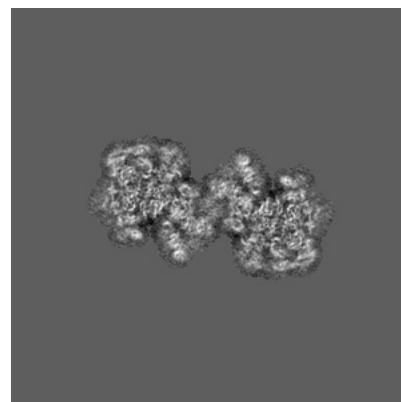
6.2.1 Primary map



X Index: 350



Y Index: 350

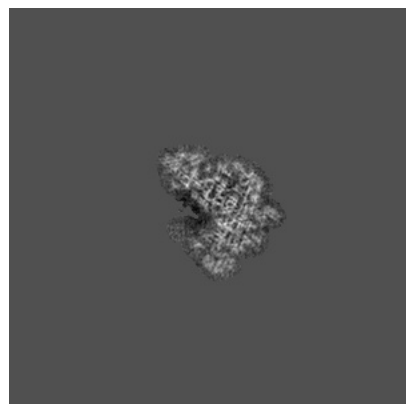


Z Index: 350

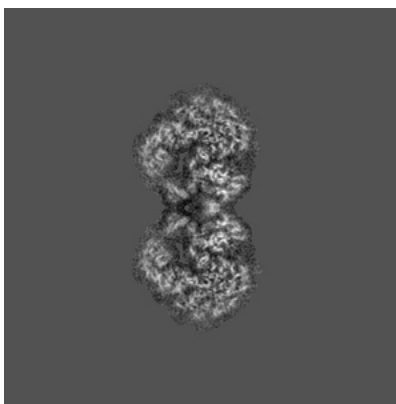
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

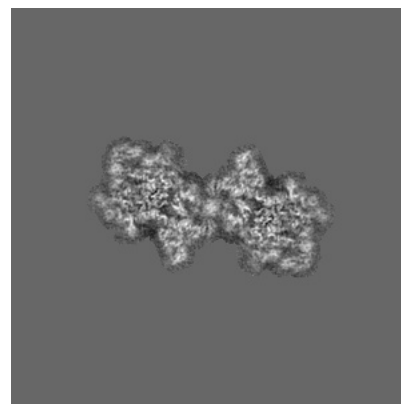
6.3.1 Primary map



X Index: 242



Y Index: 350

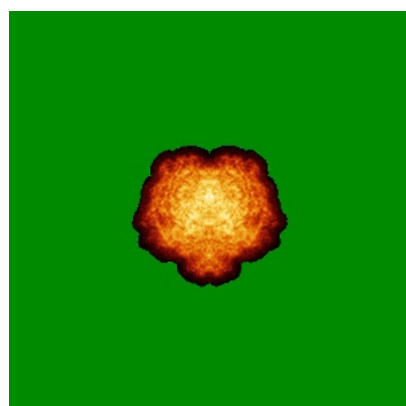


Z Index: 362

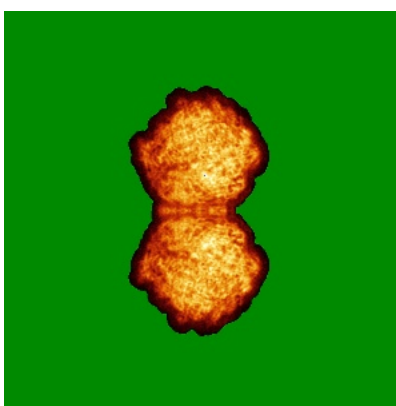
The images above show the largest variance slices of the map in three orthogonal directions.

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

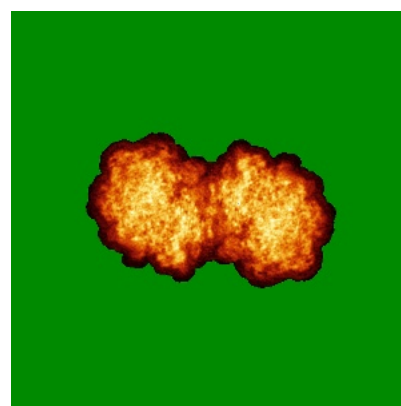
6.4.1 Primary map



X



Y

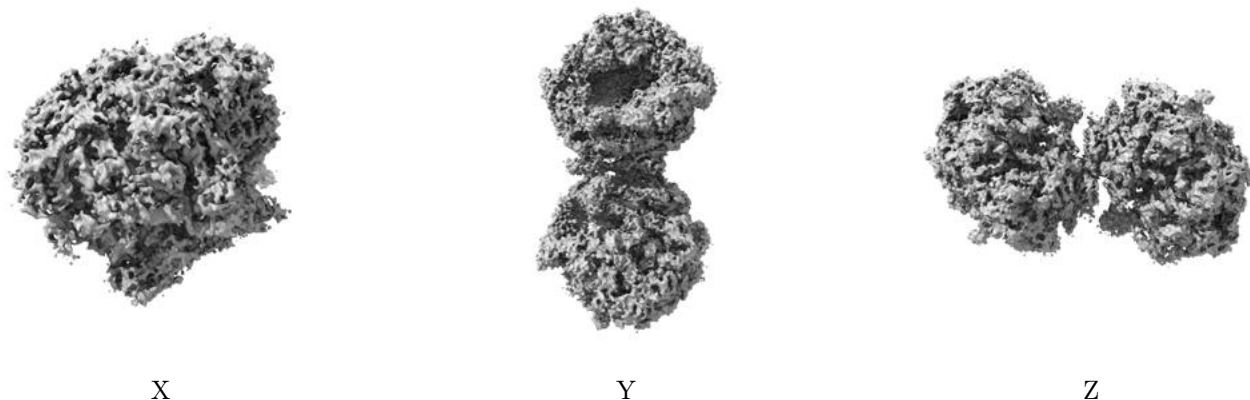


Z

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

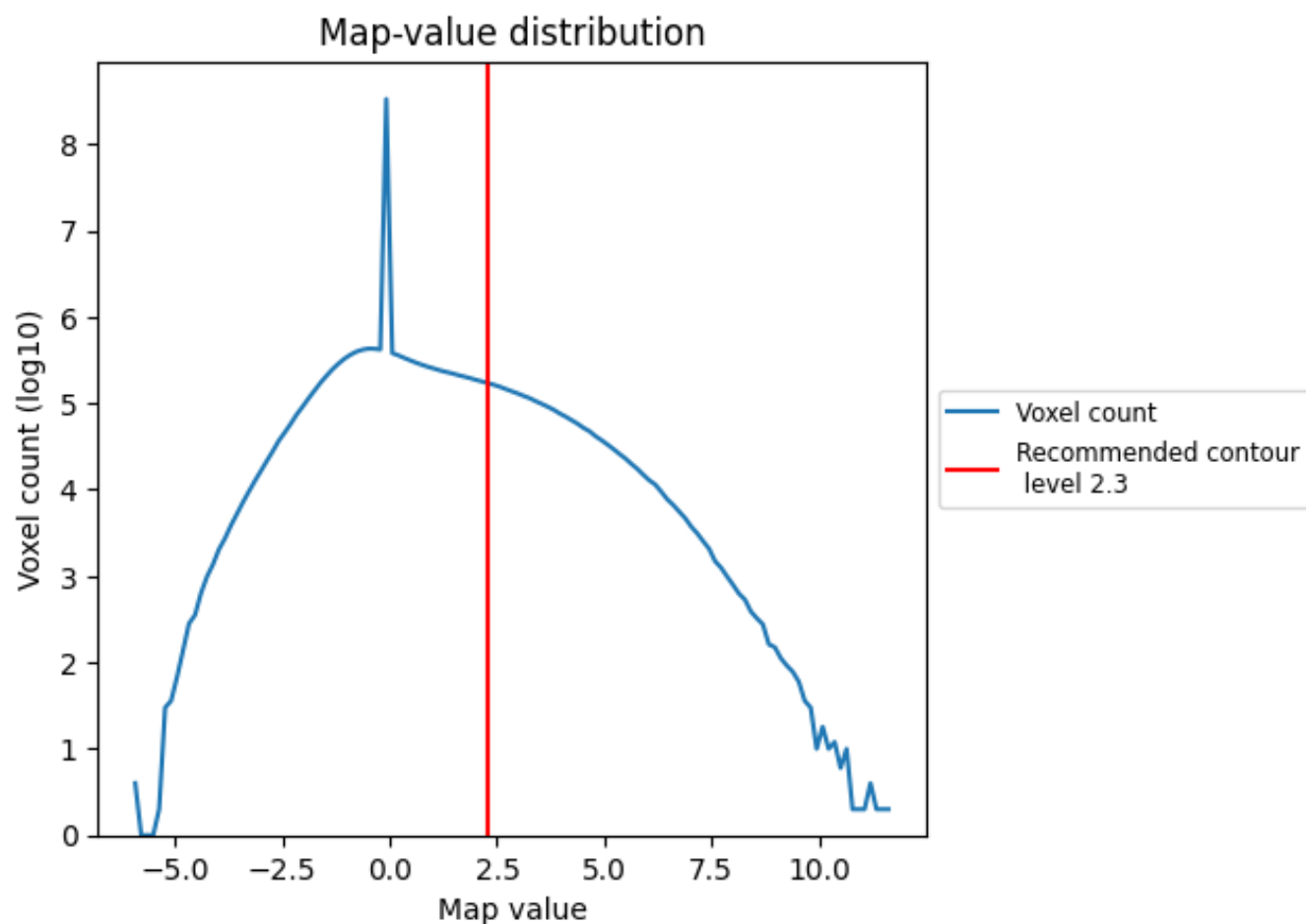
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

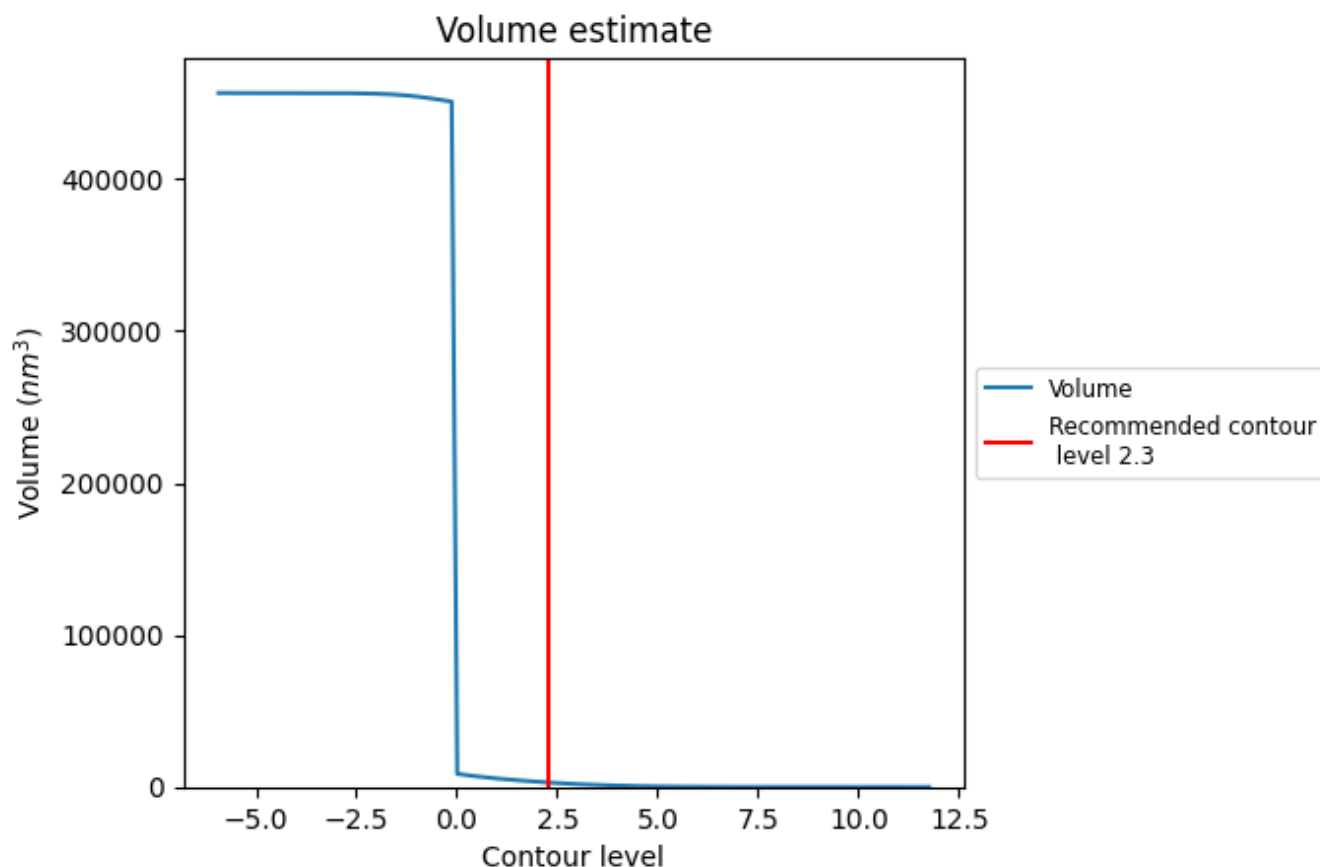
This section contains the results of statistical analysis of the map.

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.

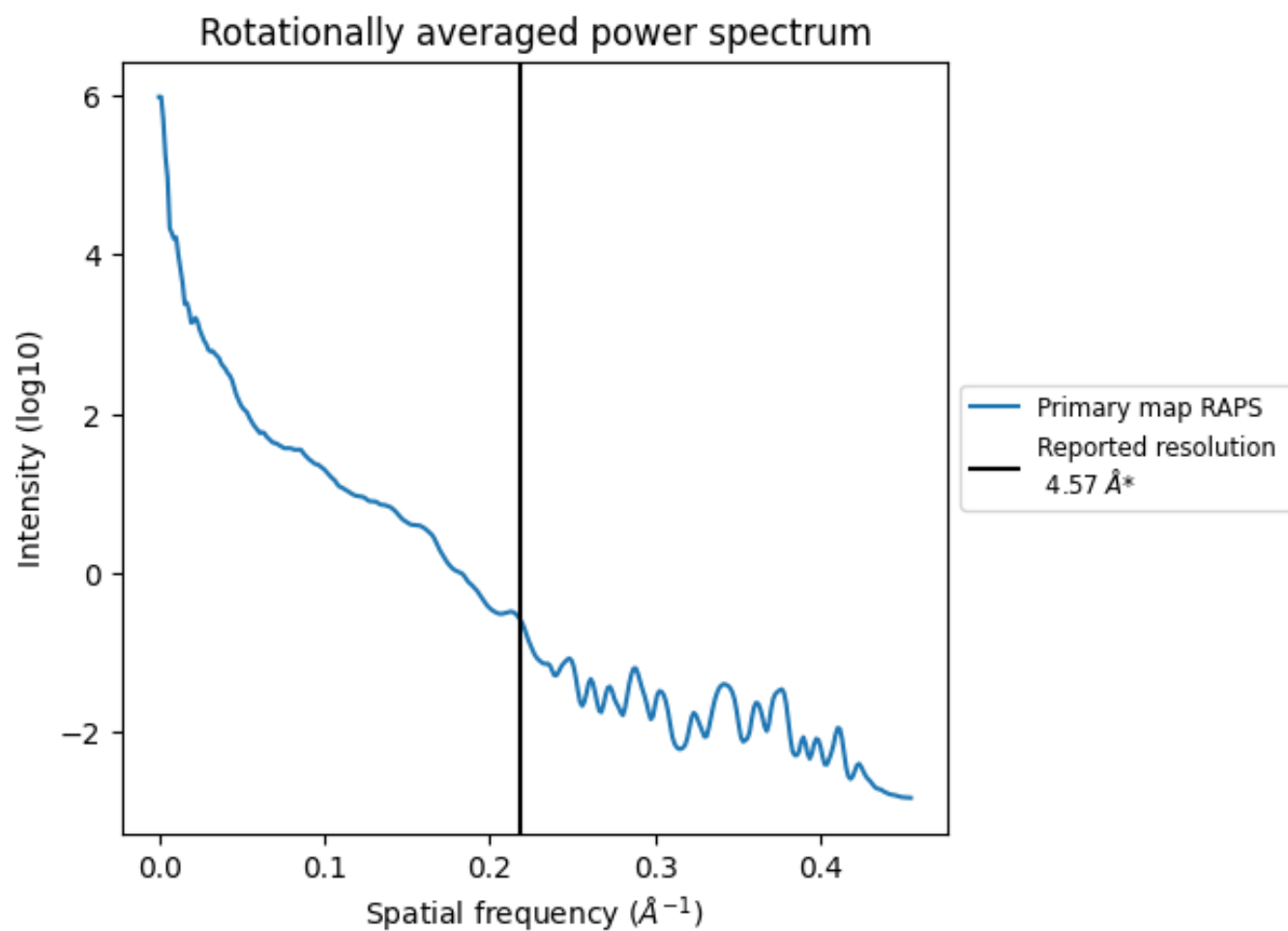
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2918 nm³; this corresponds to an approximate mass of 2636 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 0.219 Å⁻¹

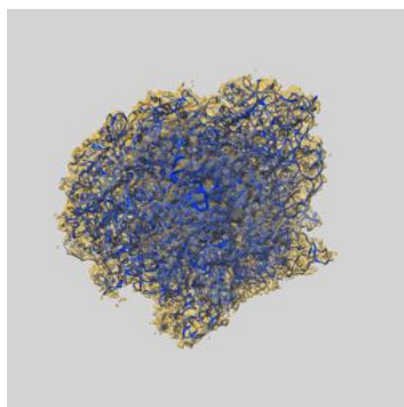
8 Fourier-Shell correlation

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

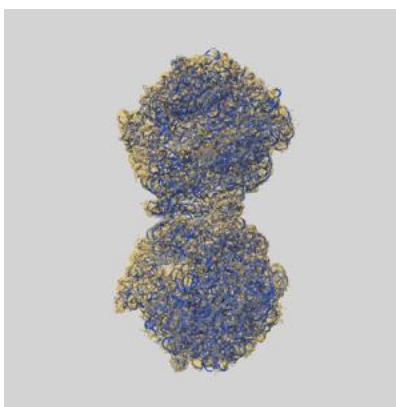
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0104 and PDB model 6GZX. Per-residue inclusion information can be found in section 3 on page 19.

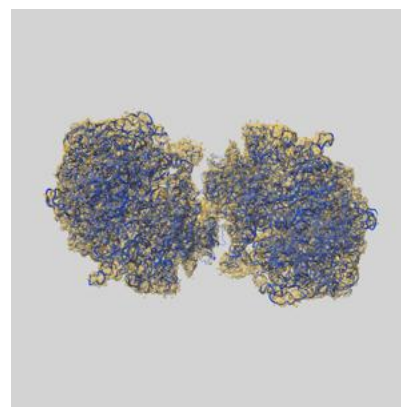
9.1 Map-model overlay [i](#)



X



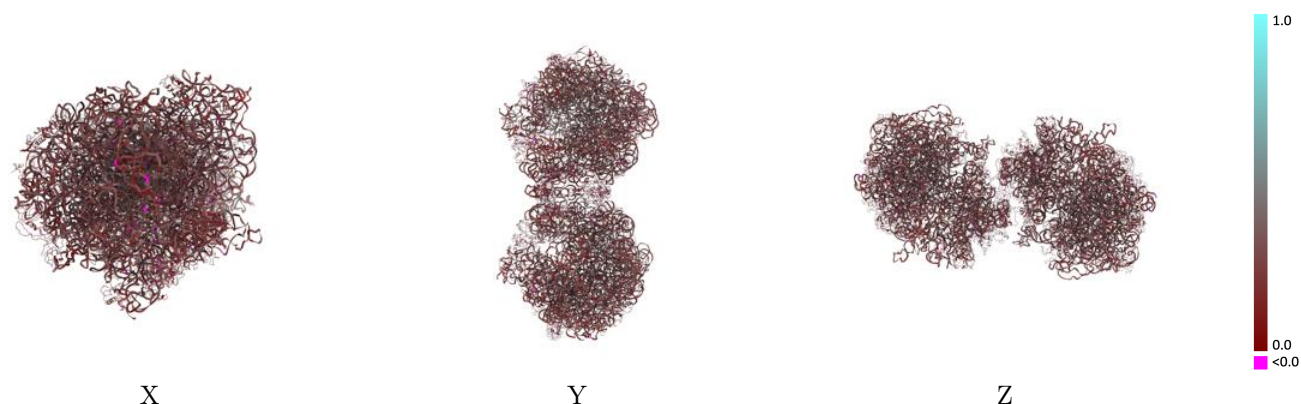
Y



Z

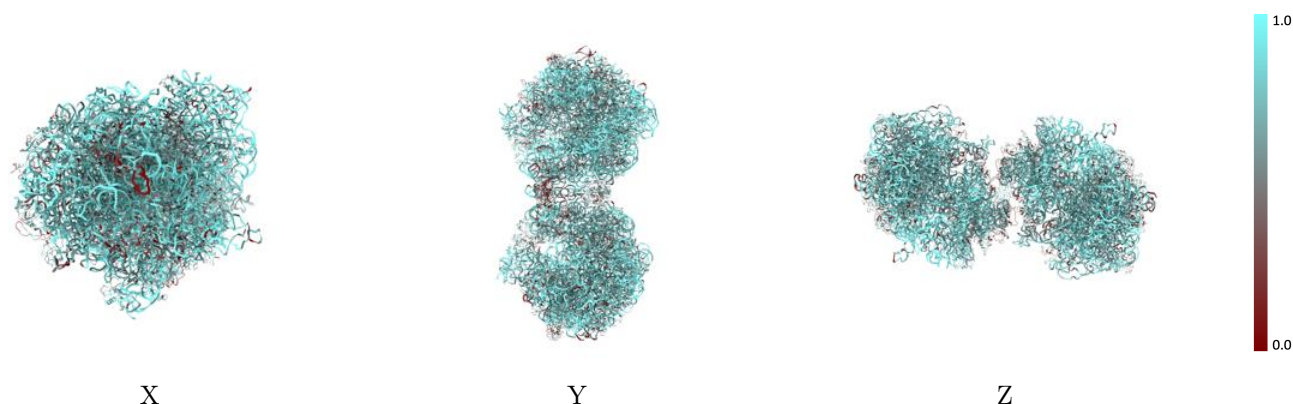
The images above show the 3D surface view of the map at the recommended contour level 2.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



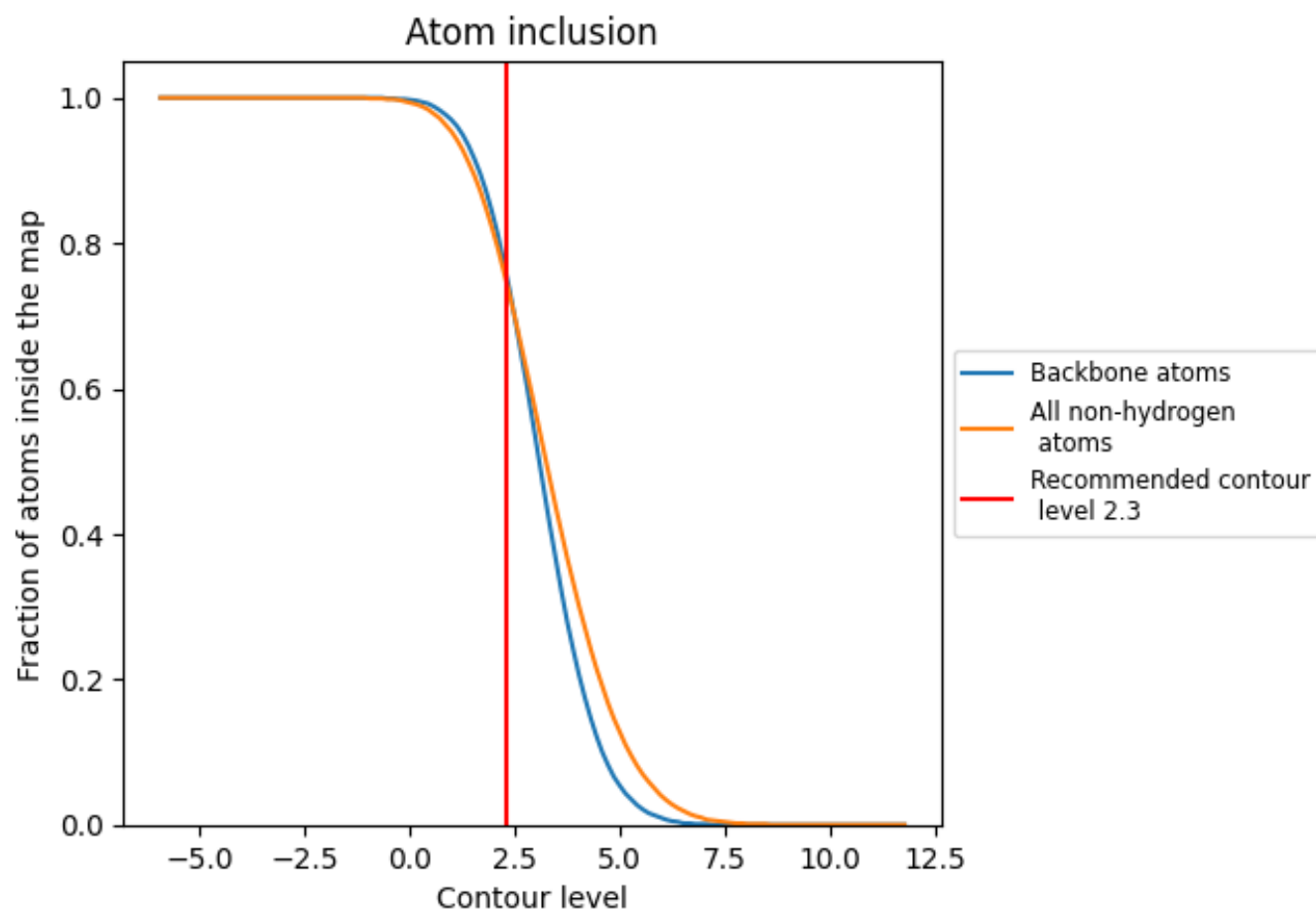
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 75% 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 (2.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7460	 0.2820
A1	 0.8230	 0.2990
A2	 0.8250	 0.2990
A3	 0.8550	 0.2850
A4	 0.8540	 0.2860
B1	 0.8790	 0.2750
B2	 0.8750	 0.2760
B3	 0.5860	 0.2420
B4	 0.5830	 0.2420
C1	 0.4360	 0.2870
C2	 0.4380	 0.2860
C3	 0.5890	 0.2660
C4	 0.5830	 0.2630
D1	 0.5050	 0.2730
D2	 0.5040	 0.2750
D3	 0.6900	 0.2630
D4	 0.7070	 0.2690
E1	 0.5560	 0.2520
E2	 0.5580	 0.2580
E3	 0.6330	 0.2680
E4	 0.6500	 0.2620
F1	 0.5790	 0.2320
F2	 0.5890	 0.2290
F3	 0.5300	 0.2490
F4	 0.5210	 0.2570
G1	 0.6190	 0.2530
G2	 0.5910	 0.2480
G3	 0.4570	 0.2270
G4	 0.4590	 0.2270
H1	 0.3490	 0.2650
H2	 0.3650	 0.2590
H3	 0.6330	 0.2460
H4	 0.6290	 0.2450
I1	 0.6230	 0.2690
I2	 0.6200	 0.2780



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Chain	Atom inclusion	Q-score
I3	 0.2530	 0.2330
I4	 0.2600	 0.2390
J1	 0.5510	 0.2980
J2	 0.5530	 0.2920
J3	 0.3690	 0.2480
J4	 0.3620	 0.2500
K1	 0.6190	 0.2640
K2	 0.6280	 0.2620
K3	 0.5670	 0.2410
K4	 0.5800	 0.2380
L1	 0.5800	 0.2770
L2	 0.5530	 0.2670
L3	 0.6270	 0.2870
L4	 0.6240	 0.2910
M1	 0.5900	 0.2560
M2	 0.5960	 0.2510
M3	 0.5770	 0.2410
M4	 0.5750	 0.2180
N1	 0.7050	 0.2510
N2	 0.7210	 0.2280
N3	 0.5550	 0.2620
N4	 0.5370	 0.2520
O1	 0.4980	 0.2610
O2	 0.5050	 0.2590
O3	 0.6410	 0.2460
O4	 0.6310	 0.2580
P1	 0.5440	 0.2360
P2	 0.5370	 0.2490
P3	 0.6170	 0.2640
P4	 0.6310	 0.2500
Q1	 0.4030	 0.2710
Q2	 0.3920	 0.2880
Q3	 0.5430	 0.2730
Q4	 0.5300	 0.2810
R1	 0.4910	 0.2620
R2	 0.4970	 0.2530
R3	 0.5910	 0.2450
R4	 0.5970	 0.2440
S1	 0.5540	 0.2700
S2	 0.5440	 0.2660
S3	 0.4440	 0.2380
S4	 0.5020	 0.2200

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Chain	Atom inclusion	Q-score
T1	 0.4300	 0.2670
T2	 0.4430	 0.2660
T3	 0.6560	 0.2670
T4	 0.6600	 0.2630
U1	 0.4160	 0.2300
U2	 0.4210	 0.2370
U3	 0.3580	 0.2330
U4	 0.3780	 0.2370
V1	 0.5680	 0.2580
V2	 0.5570	 0.2580
V3	 0.5830	 0.2360
V4	 0.5870	 0.2420
W1	 0.5360	 0.2550
W2	 0.5180	 0.2580
W4	 0.8070	 0.2120
X1	 0.6380	 0.2670
X2	 0.6680	 0.2580
X3	 0.7990	 0.2120
Y1	 0.3930	 0.2650
Y2	 0.3930	 0.2680
Z1	 0.6860	 0.2450
Z2	 0.6940	 0.2510
a1	 0.5710	 0.2730
a2	 0.5610	 0.2640
b1	 0.7730	 0.2610
b2	 0.7790	 0.2590
c1	 0.5400	 0.2870
c2	 0.5480	 0.2890
d1	 0.4640	 0.2500
d2	 0.4640	 0.2400
e1	 0.6400	 0.2860
e2	 0.6360	 0.2770