



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 05:00 PM UTC

PDB ID : 6GZZ / pdb_00006gzz
EMDB ID : EMD-0105
Title : T. thermophilus hibernating 100S ribosome (amc)
Authors : Flygaard, R.K.; Jenner, L.B.
Deposited on : 2018-07-05
Resolution : 4.13 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

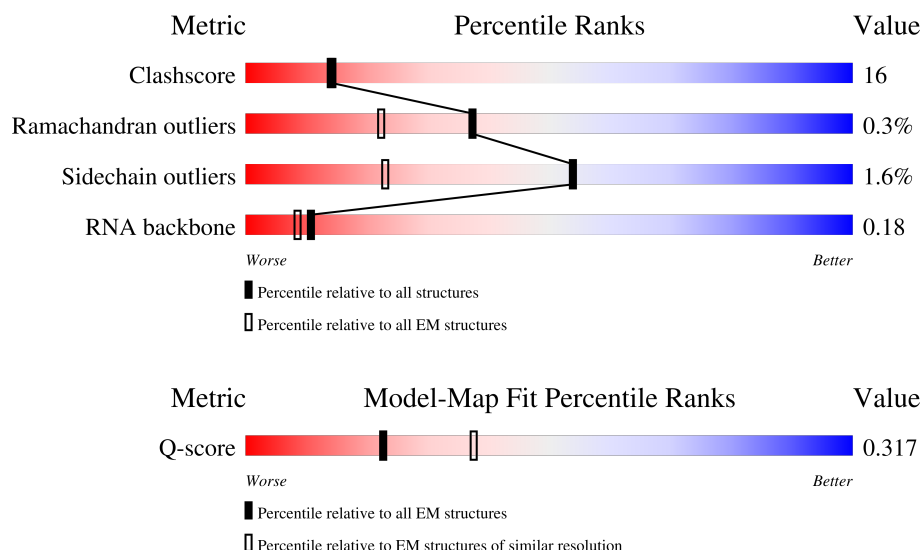
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.13 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	5607 (3.63 - 4.63)

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	22% 65% 34% .
1	C2	272	21% 58% 39% .
2	D1	205	15% 70% 30%

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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	29% 77% 23%
15	Q2	101	27% 76% 23%
16	R1	113	12% 60% 39%
16	R2	113	16% 68% 30%
17	S1	92	23% 67% 32%
17	S2	92	24% 65% 34%
18	T1	102	15% 64% 35%
18	T2	102	16% 72% 28%
19	U1	179	42% 69% 30%
19	U2	179	42% 63% 36%
20	V1	77	10% 60% 39%
20	V2	77	10% 61% 39%
21	W1	97	34% 73% 27%
21	W2	97	35% 65% 34%
22	X1	69	22% 59% 38%
22	X2	69	29% 71% 29%
23	Y1	59	12% 78% 22%
23	Y2	59	10% 64% 36%
24	Z1	63	84% 51% 41% 6%
24	Z2	63	79% 57% 37% 6%
25	a1	59	10% 76% 20%
25	a2	59	10% 71% 27%
26	b1	45	18% 58% 40%
26	b2	45	13% 51% 42% 7%
27	c1	49	12% 63% 37%

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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	26% 42% 28%
53	A3	1506	25% 49% 27%
53	A4	1506	24% 50% 26%
54	V3	119	10% 60% 33% 8%
54	V4	119	9% 59% 39%

2 Entry composition

There are 54 unique types of molecules in this entry. The entry contains 289175 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		

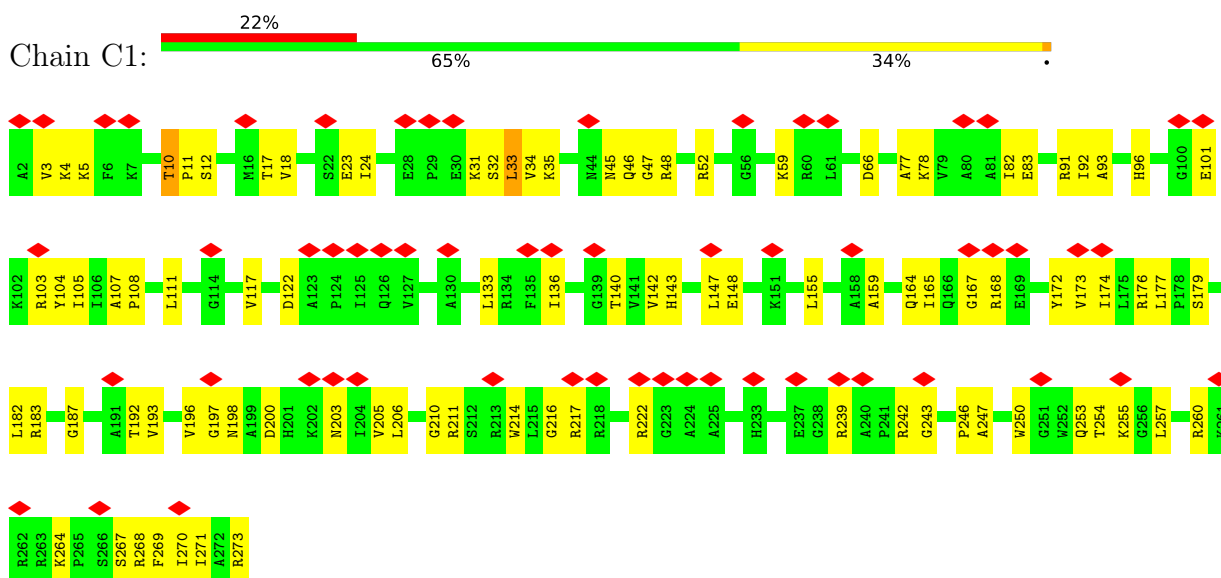
- Molecule 54 is a protein called Ribosome hibernation promoting factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	V3	119	Total	C	N	O	S	0	0
			963	603	179	180	1		
54	V4	117	Total	C	N	O	S	0	0
			950	594	177	178	1		

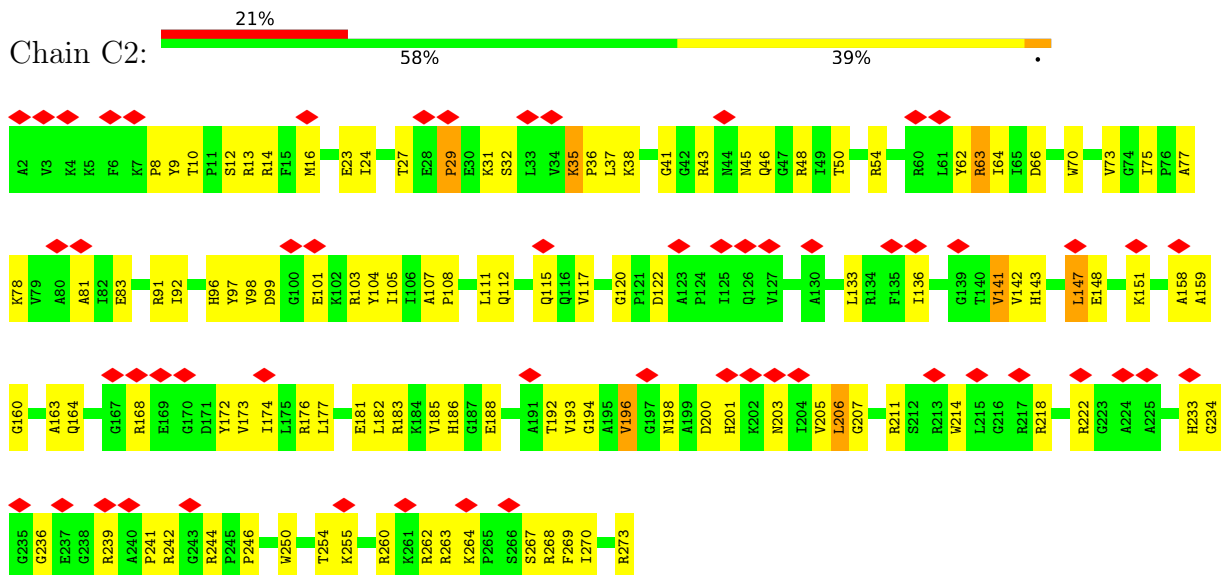
3 Residue-property plots

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.

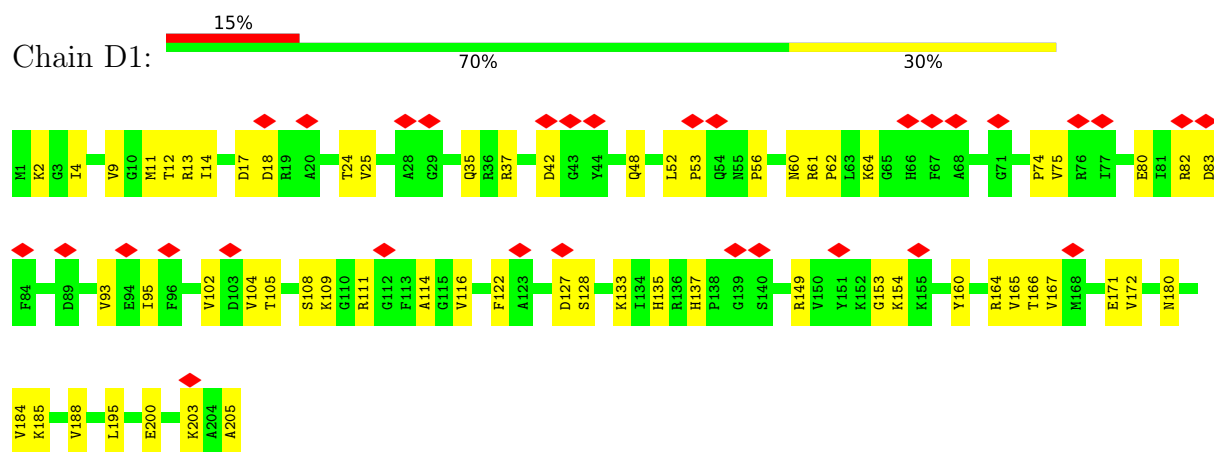
- Molecule 1: 50S ribosomal protein L2



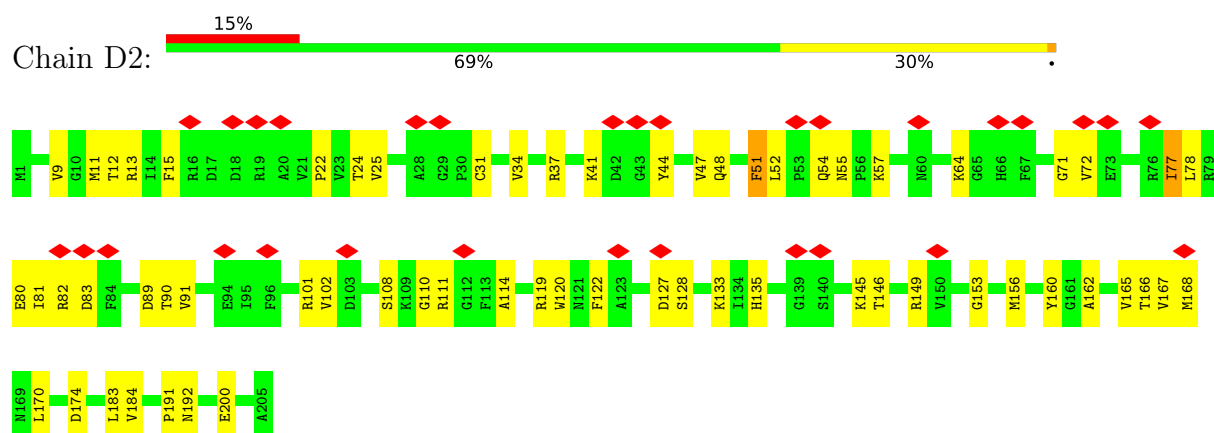
- Molecule 1: 50S ribosomal protein L2



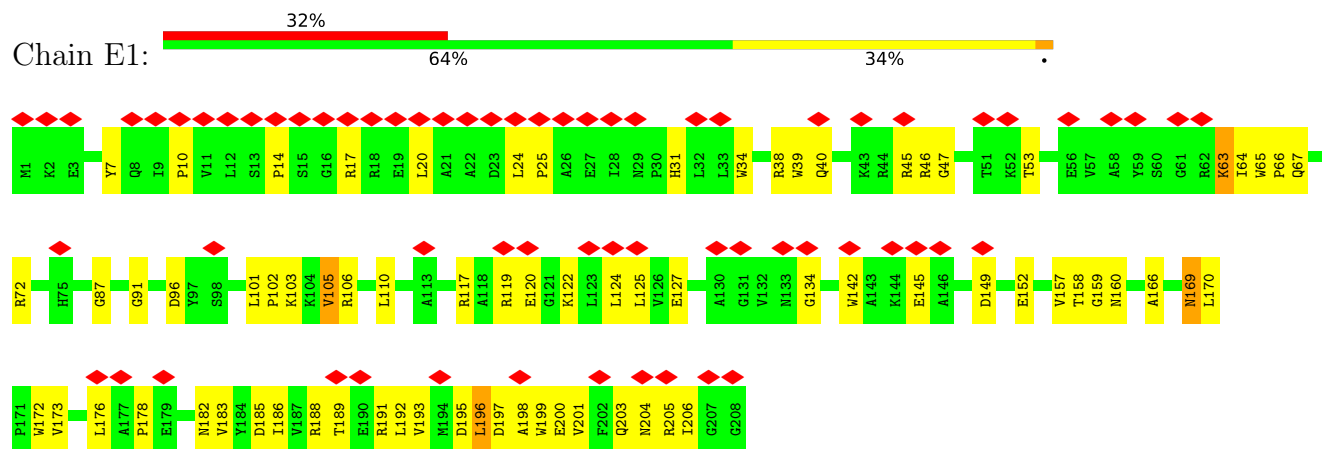
- Molecule 2: 50S ribosomal protein L3



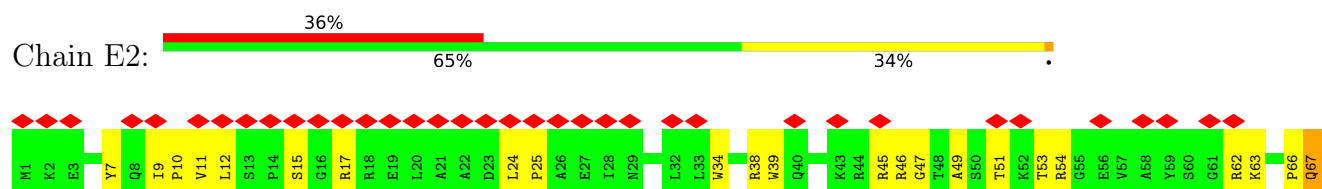
• Molecule 2: 50S ribosomal protein L3

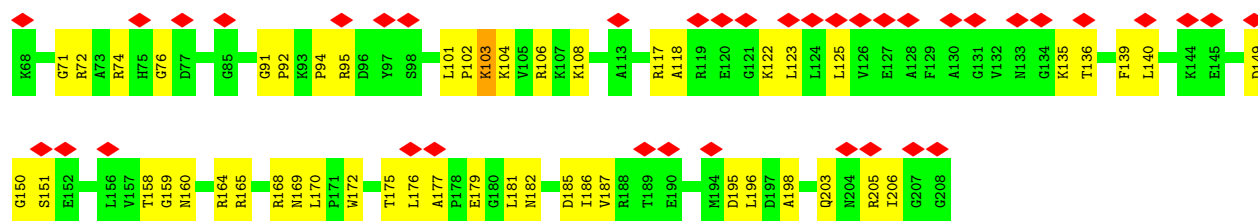


• Molecule 3: 50S ribosomal protein L4



• Molecule 3: 50S ribosomal protein L4

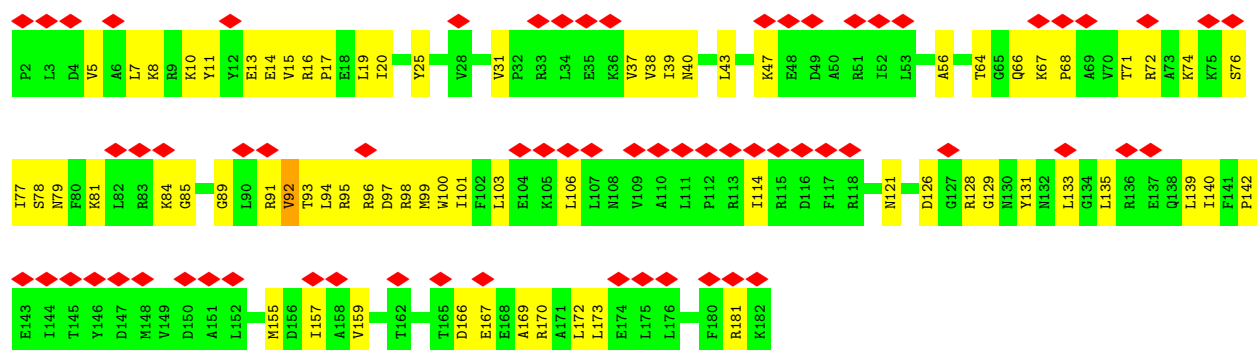




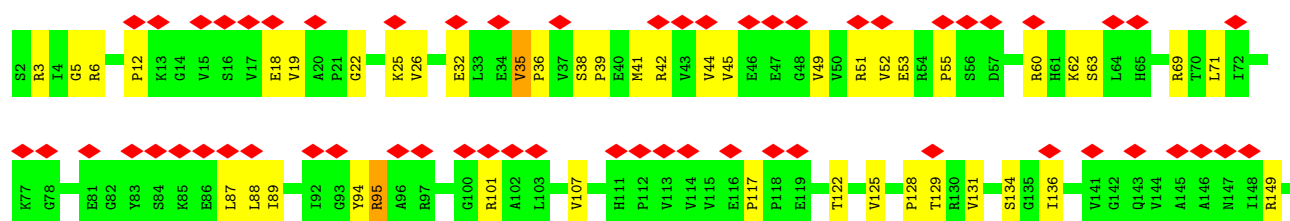
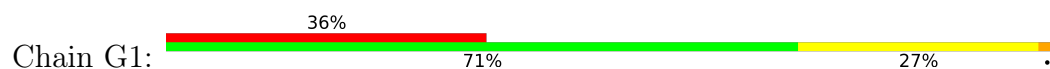
• Molecule 4: 50S ribosomal protein L5

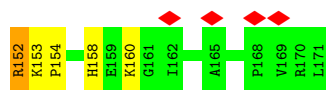


• Molecule 4: 50S ribosomal protein L5



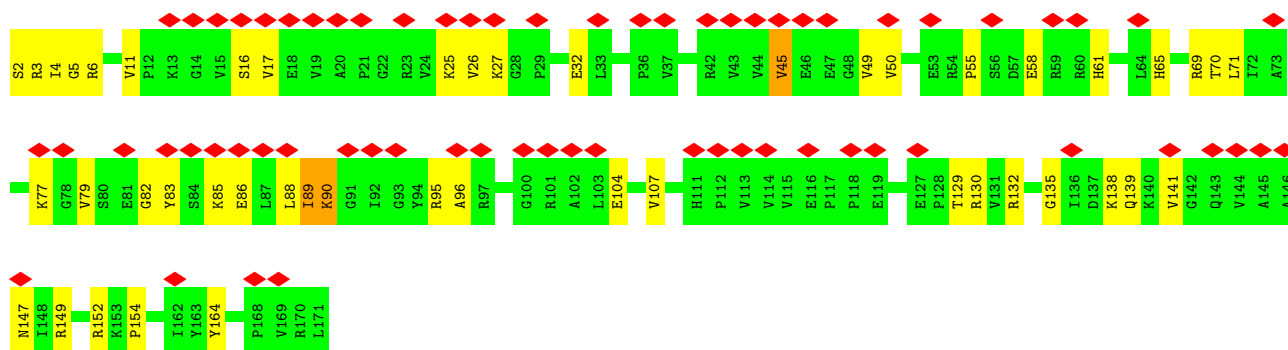
• Molecule 5: 50S ribosomal protein L6





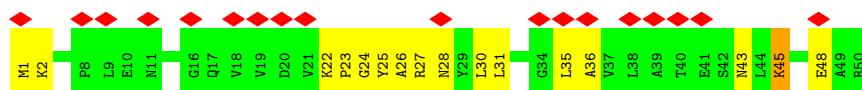
- Molecule 5: 50S ribosomal protein L6

Chain G2: 39% 72% 26%



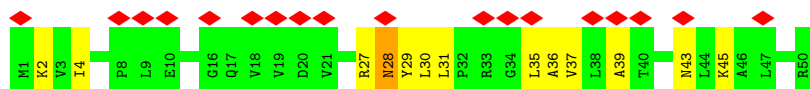
- Molecule 6: 50S ribosomal protein L9

Chain H1: 36% 68% 30%



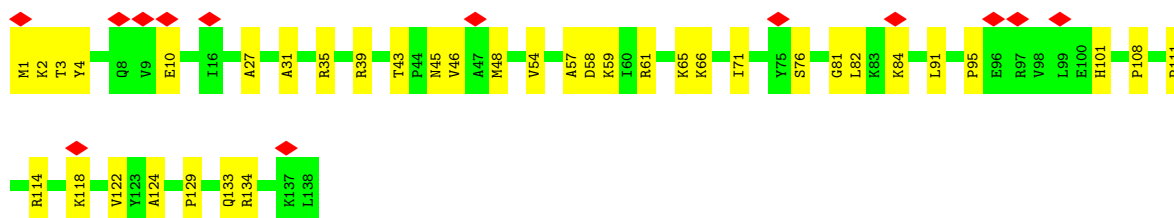
- Molecule 6: 50S ribosomal protein L9

Chain H2: 36% 74% 24%



- Molecule 7: 50S ribosomal protein L13

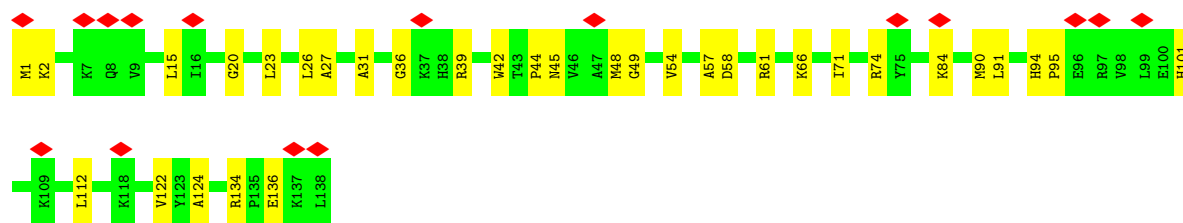
Chain I1: 9% 73% 27%



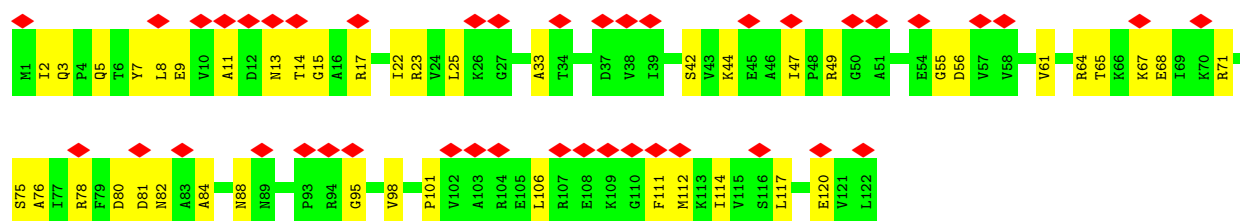
- Molecule 7: 50S ribosomal protein L13

Chain I2: 12% 76% 24%

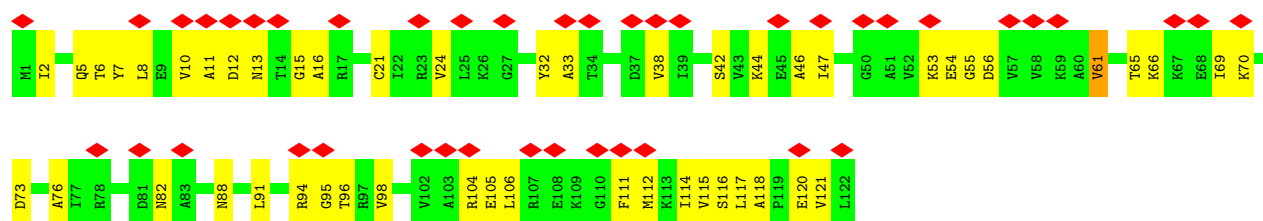




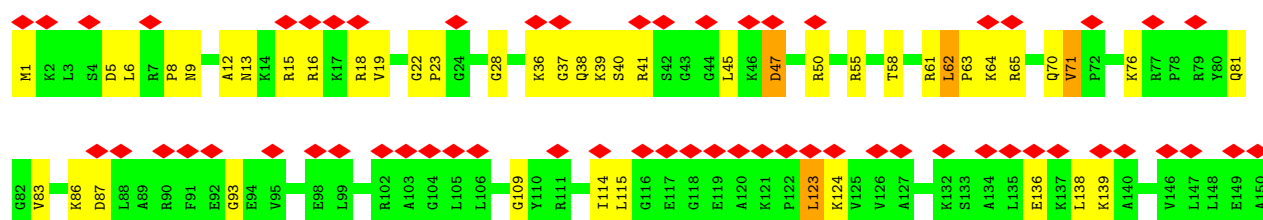
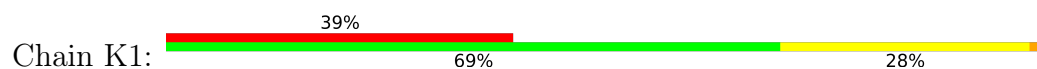
• Molecule 8: 50S ribosomal protein L14



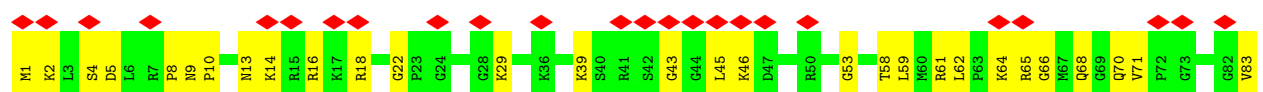
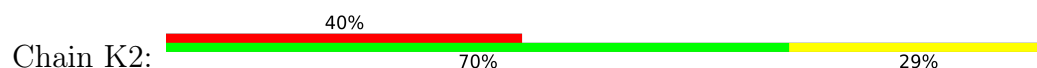
• Molecule 8: 50S ribosomal protein L14

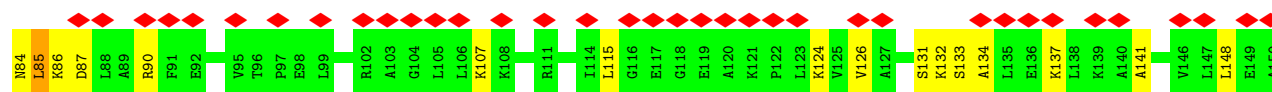


• Molecule 9: 50S ribosomal protein L15

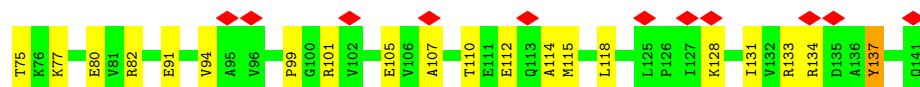
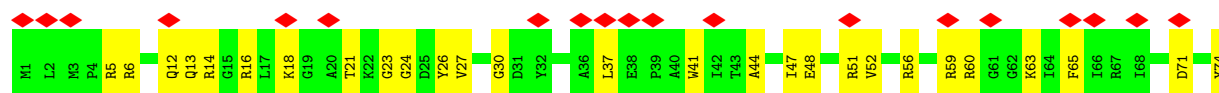


• Molecule 9: 50S ribosomal protein L15

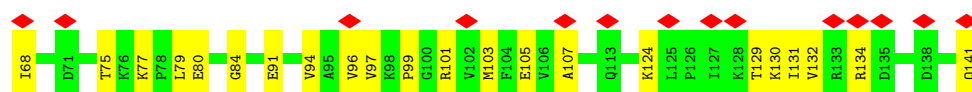
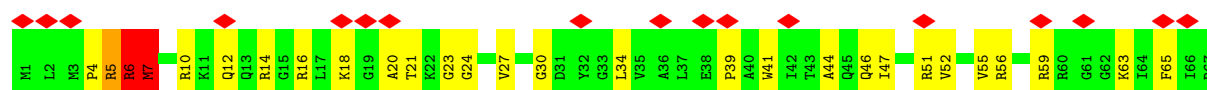




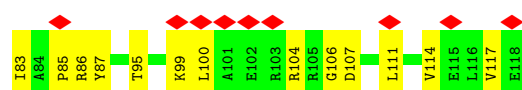
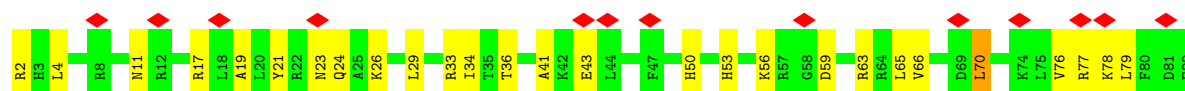
- Molecule 10: 50S ribosomal protein L16



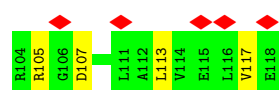
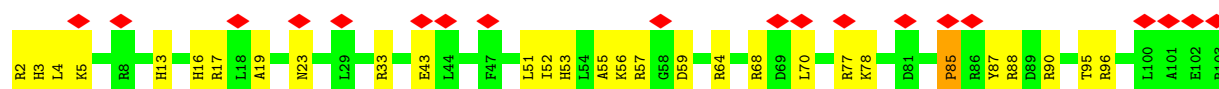
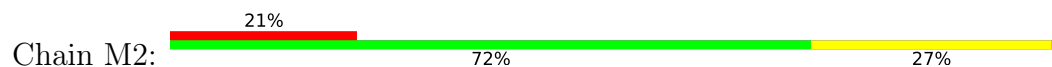
- Molecule 10: 50S ribosomal protein L16



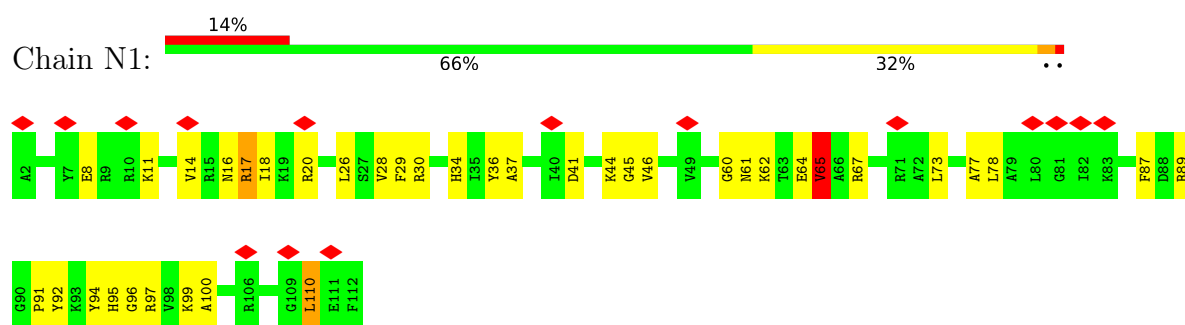
- Molecule 11: 50S ribosomal protein L17



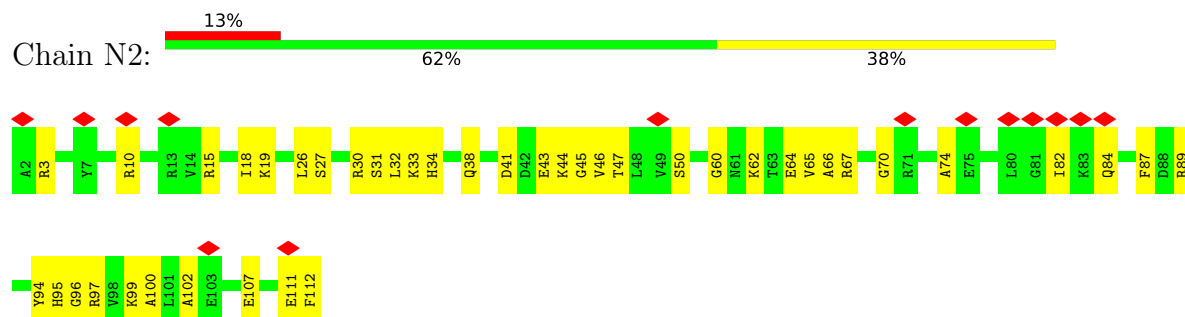
- Molecule 11: 50S ribosomal protein L17



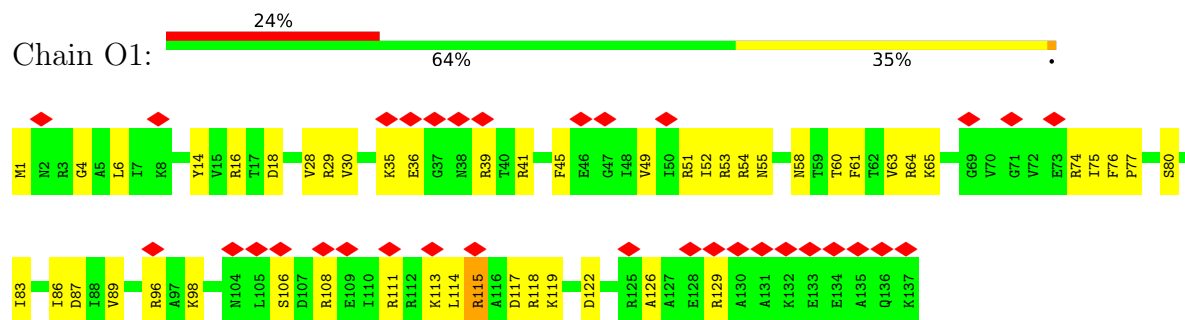
- Molecule 12: 50S ribosomal protein L18



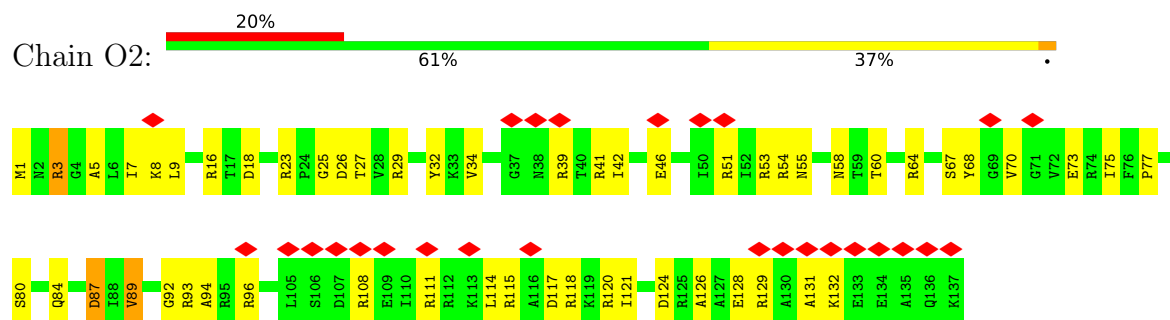
- Molecule 12: 50S ribosomal protein L18



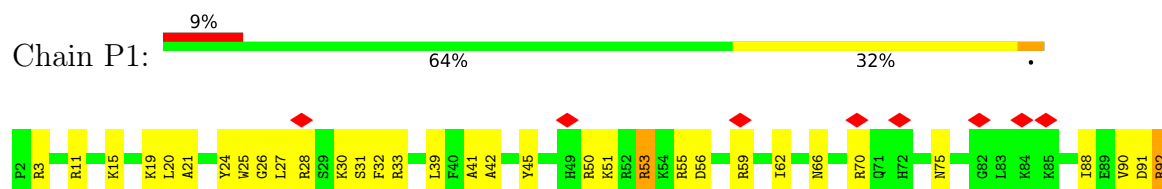
- Molecule 13: 50S ribosomal protein L19

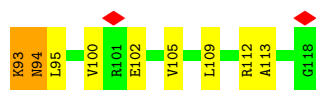


- Molecule 13: 50S ribosomal protein L19



- Molecule 14: 50S ribosomal protein L20

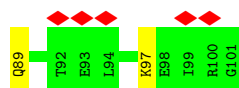
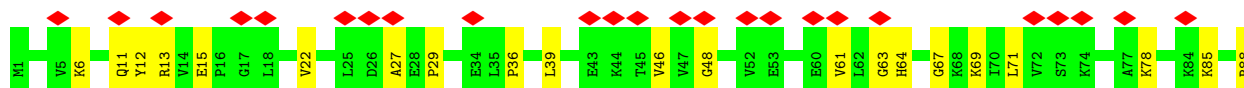
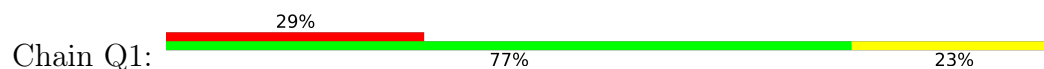




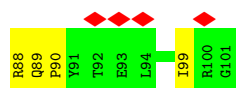
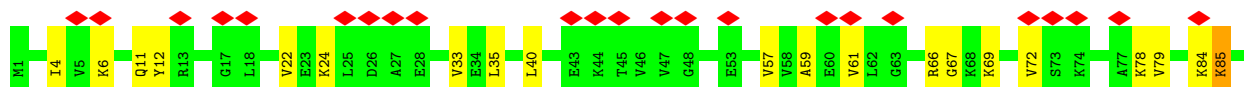
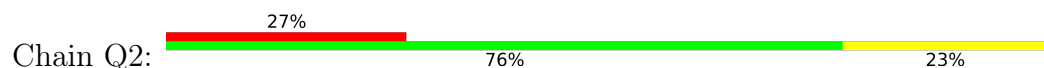
- Molecule 14: 50S ribosomal protein L20



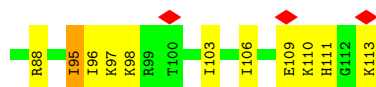
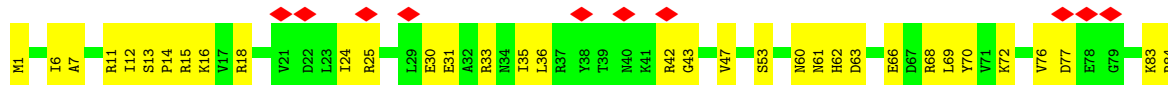
- Molecule 15: 50S ribosomal protein L21



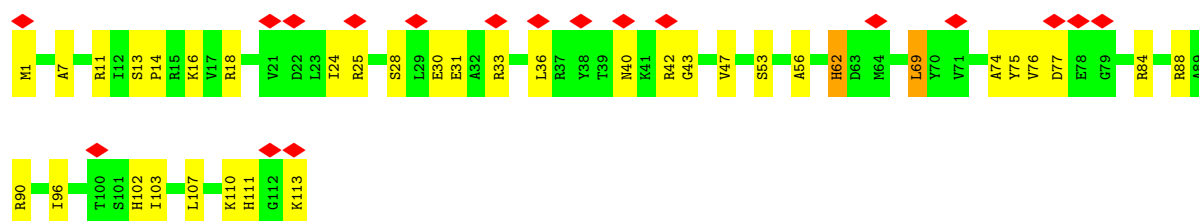
- Molecule 15: 50S ribosomal protein L21



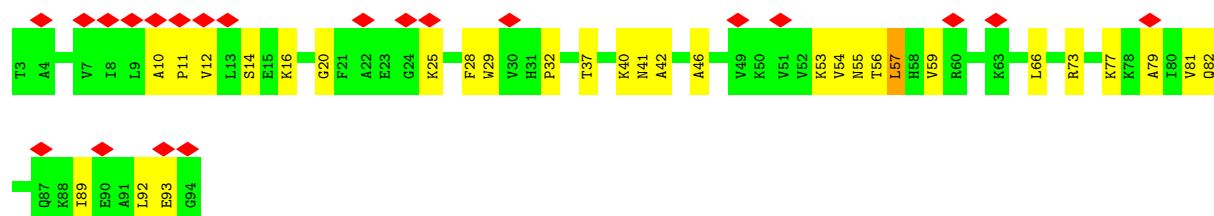
- Molecule 16: 50S ribosomal protein L22



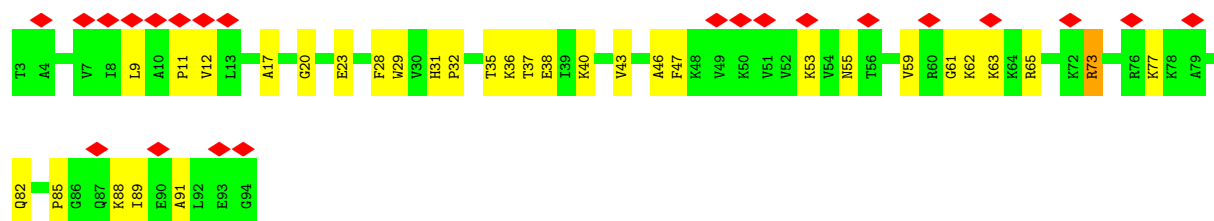
- Molecule 16: 50S ribosomal protein L22



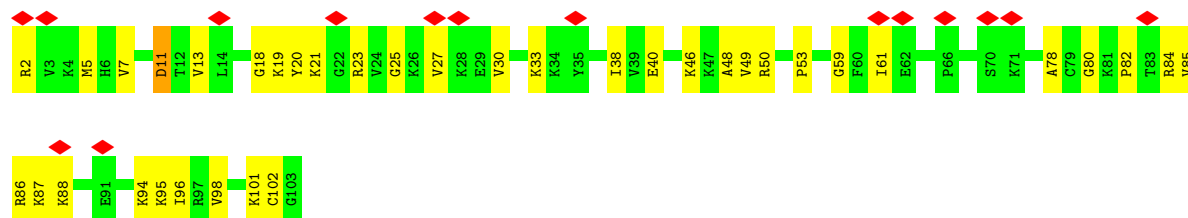
- Molecule 17: 50S ribosomal protein L23



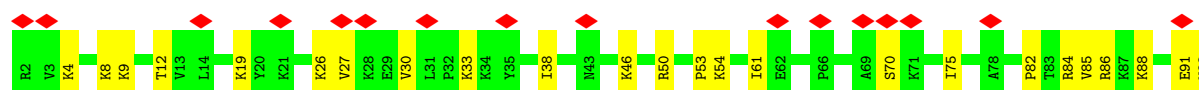
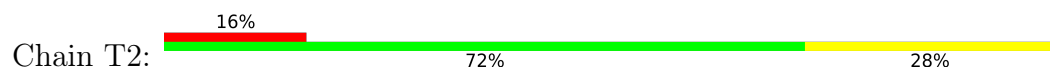
- Molecule 17: 50S ribosomal protein L23

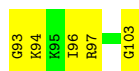


- Molecule 18: 50S ribosomal protein L24



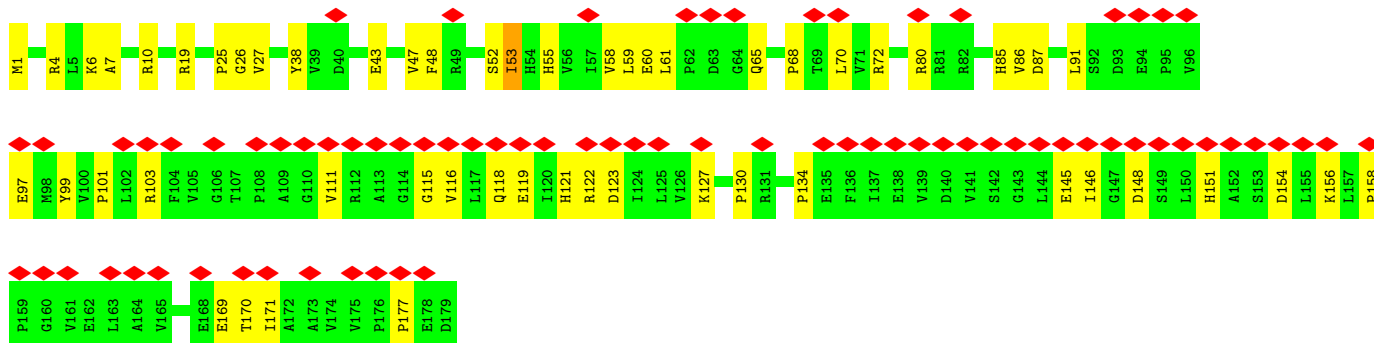
- Molecule 18: 50S ribosomal protein L24





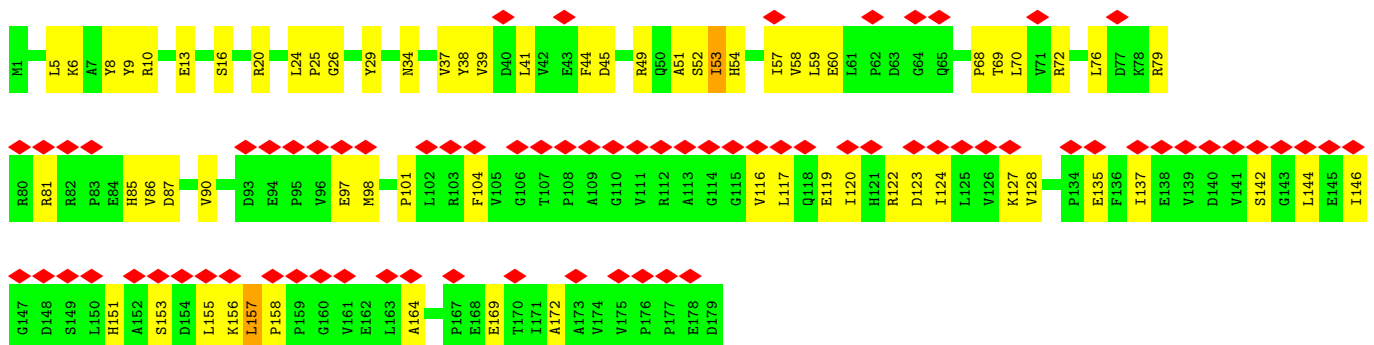
- Molecule 19: 50S ribosomal protein L25

Chain U1:



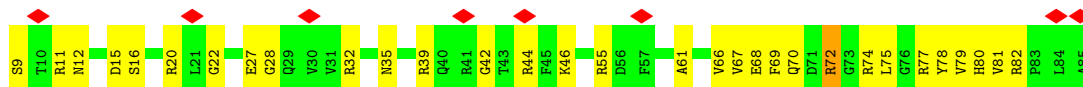
- Molecule 19: 50S ribosomal protein L25

Chain U2:



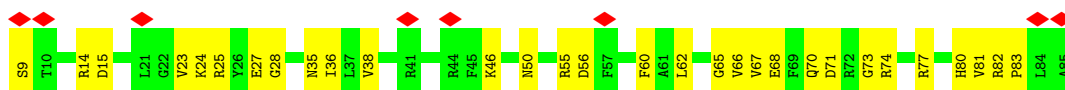
- Molecule 20: 50S ribosomal protein L27

Chain V1:

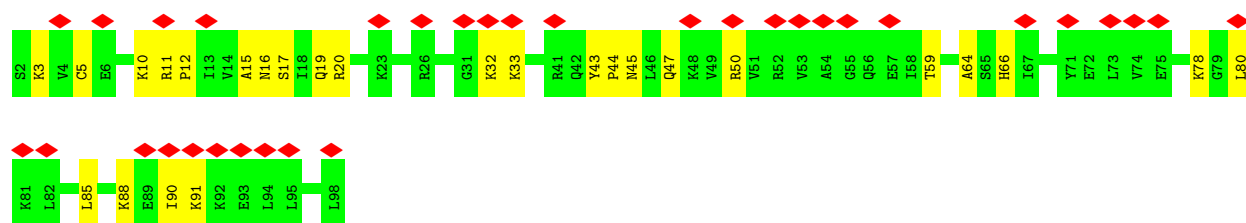
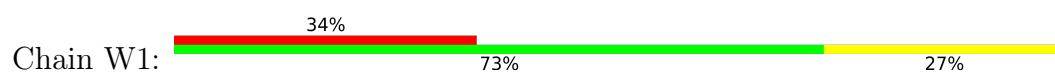


- Molecule 20: 50S ribosomal protein L27

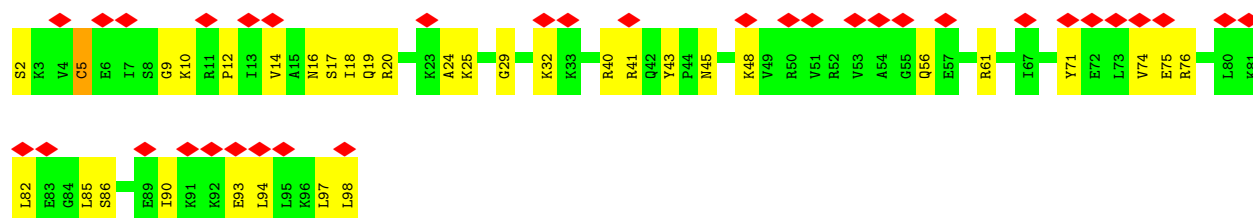
Chain V2:



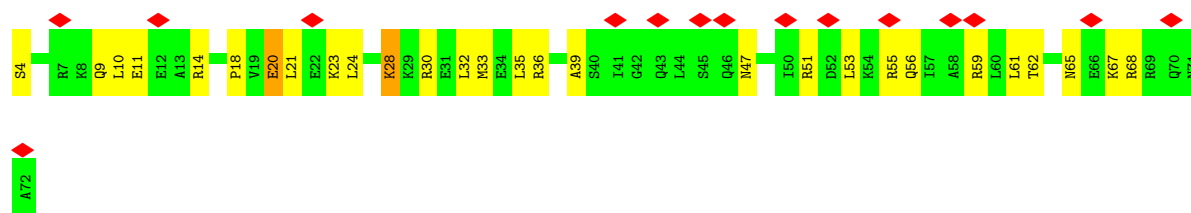
- Molecule 21: 50S ribosomal protein L28



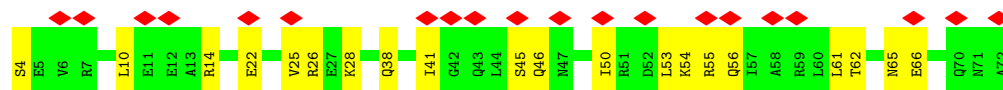
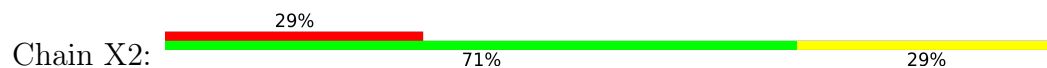
- Molecule 21: 50S ribosomal protein L28



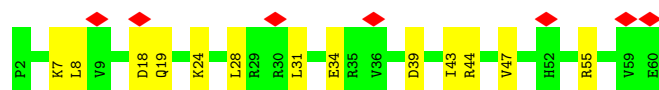
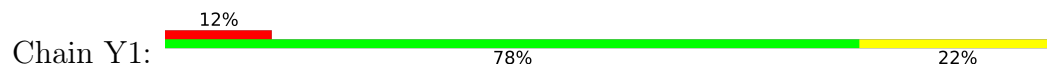
- Molecule 22: 50S ribosomal protein L29



- Molecule 22: 50S ribosomal protein L29

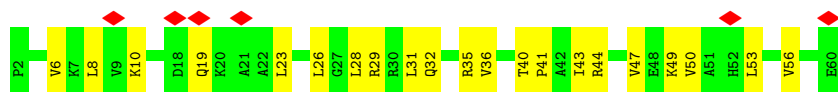


- Molecule 23: 50S ribosomal protein L30

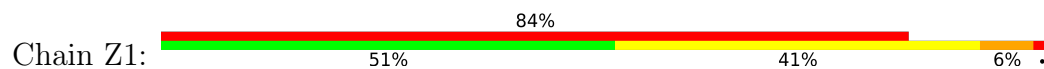


- Molecule 23: 50S ribosomal protein L30

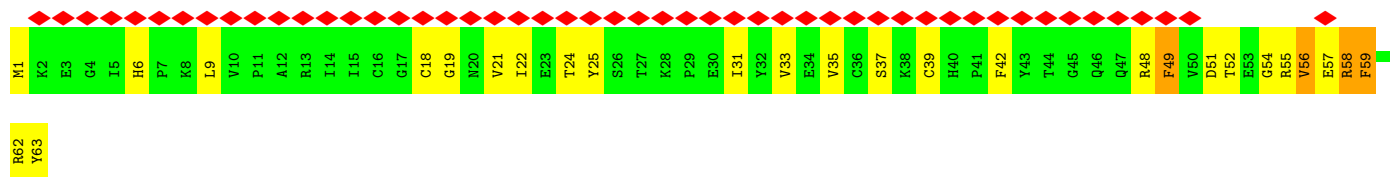
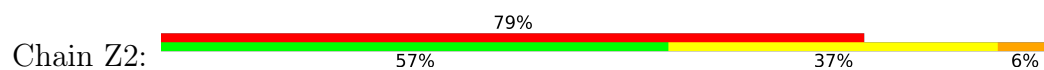




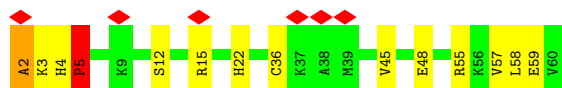
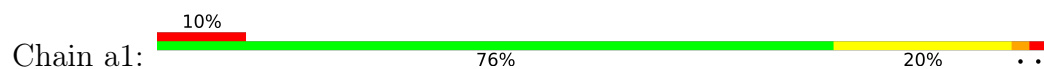
- Molecule 24: 50S ribosomal protein L31



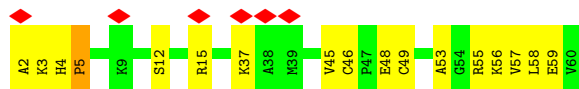
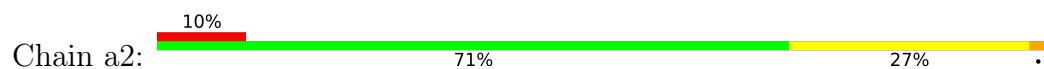
- Molecule 24: 50S ribosomal protein L31



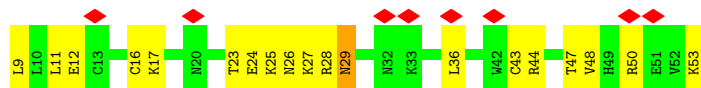
- Molecule 25: 50S ribosomal protein L32



- Molecule 25: 50S ribosomal protein L32

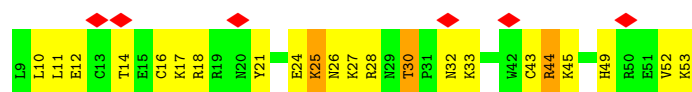


- Molecule 26: 50S ribosomal protein L33



- Molecule 26: 50S ribosomal protein L33

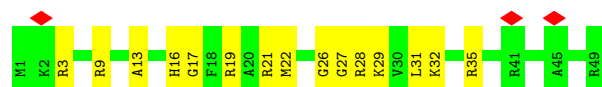




- Molecule 27: 50S ribosomal protein L34



- Molecule 27: 50S ribosomal protein L34



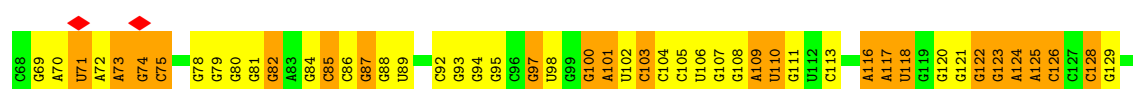
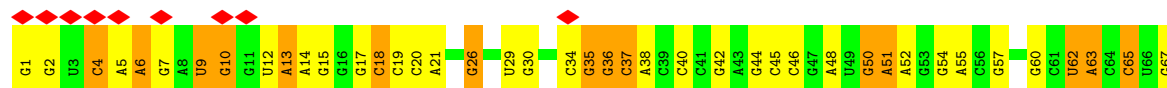
- Molecule 28: 50S ribosomal protein L35



- Molecule 28: 50S ribosomal protein L35

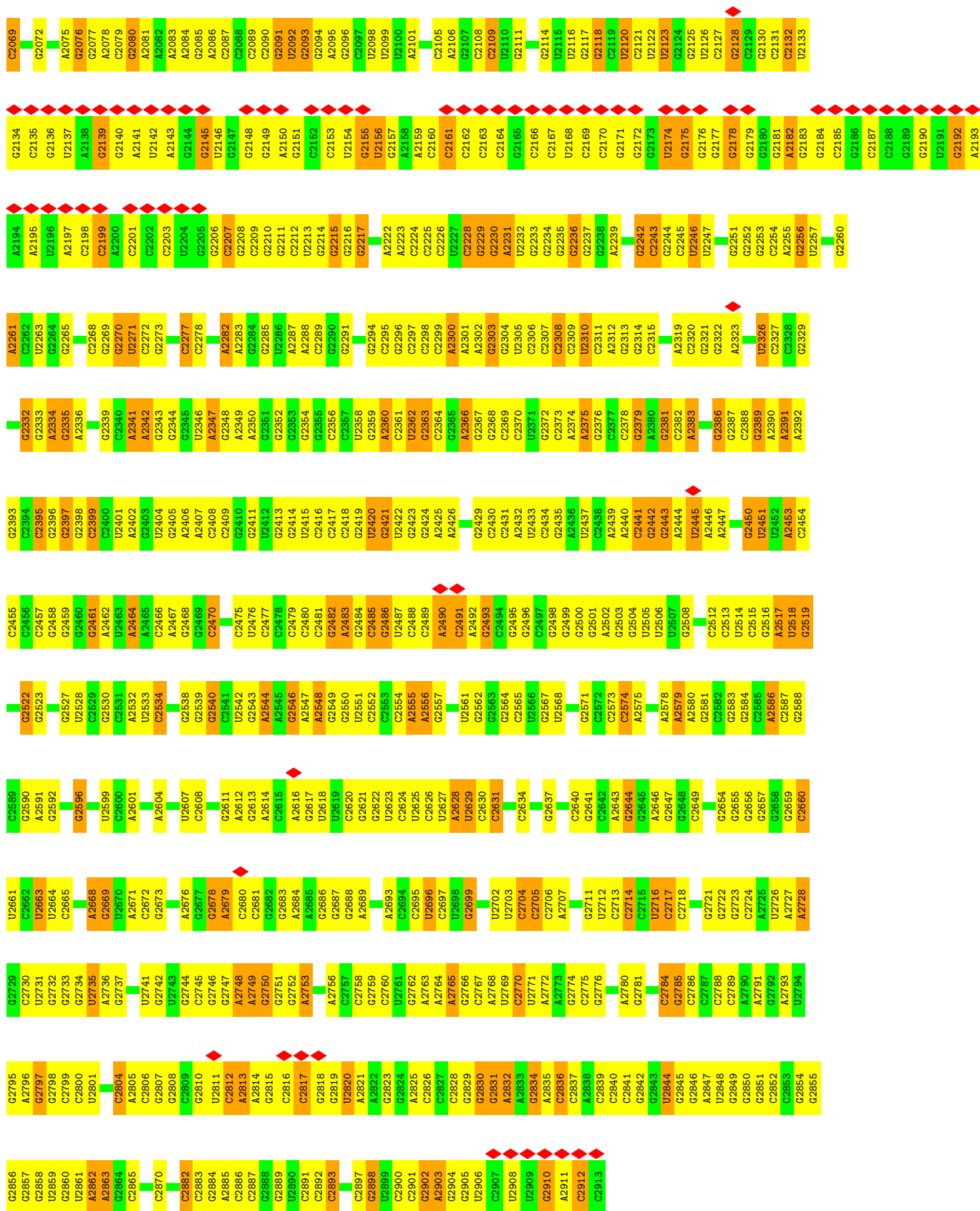


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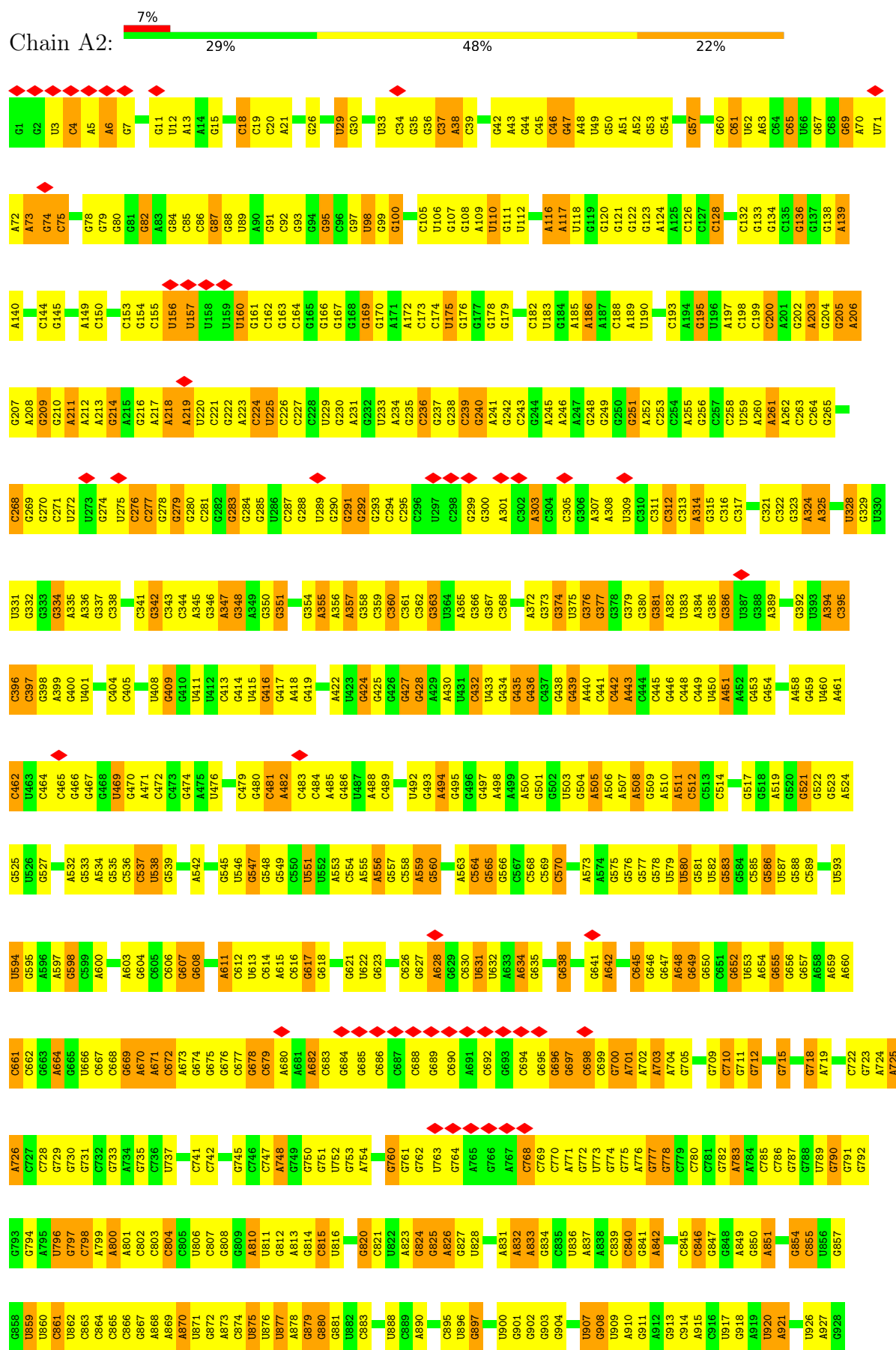




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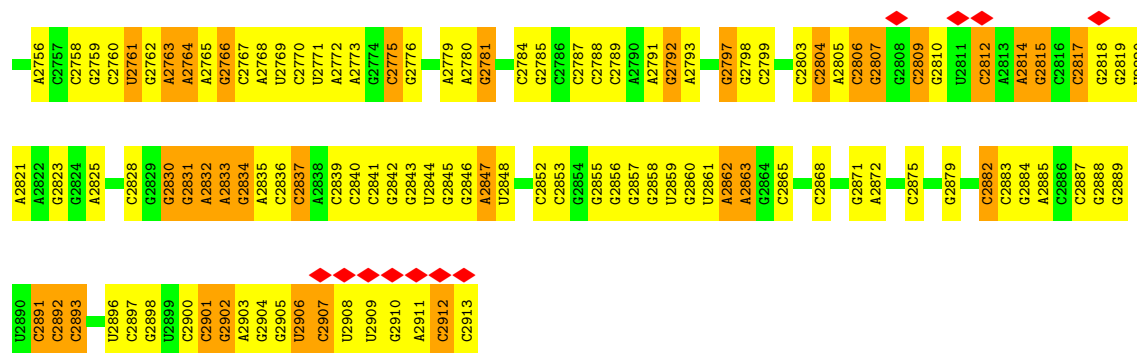


- Molecule 29: 23S ribosomal RNA

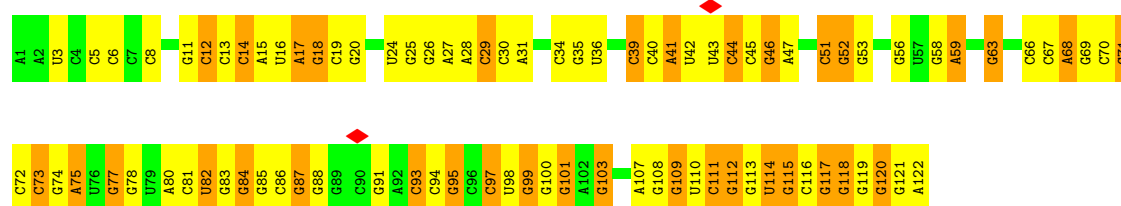
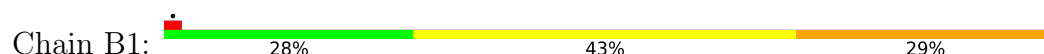


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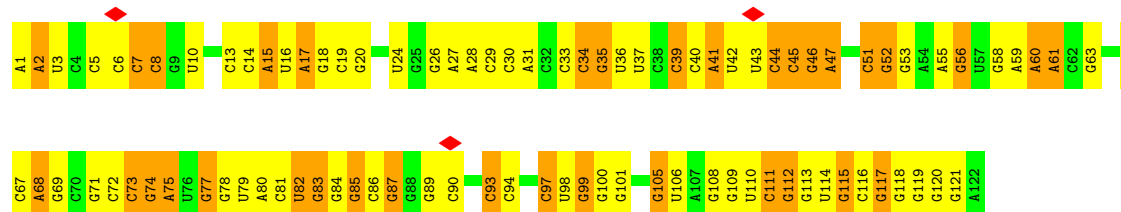
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A2083	A2084	C2085	A2086	C2087	C2088	C2089	C2090	C2091	C2092	U2093	C2094	A2095	C2096	U2099	U2100	A2101	C2105	A2106	C2107	C2108	C2109	U2110	C2111	C2114	U2115	U2116	C2117	U2120	C2121	U2122	C2123	C2124	C2125	U2126	C2127	C2128	C2129	C2130	C2131	C2132	C2133	U2134	C2135	C2136	U2137	A2138	C2139	C2140	A2141	U2142	A2143	C2144	G2145	U2146	C2147			
U2017	C2018	U2019	C2020	C2021	C2022	C2023	C2024	A2025	C2026	C2027	C2028	A2029	C2032	C2033	C2034	U2035	C2036	A2037	C2038	C2039	U2040	U2041	C2042	A2043	A2044	C2045	C2046	C2047	C2048	C2049	C2050	C2051	C2052	C2053	A2054	C2055	C2056	A2057	C2058	C2059	C2063	C2064	U2065	A2066	C2067	C2068	C2072	A2075	C2076	C2077	C2078	C2079	C2080	A2081	C2082			
U1917	A1942	A1943	C1944	C1945	U1946	U1947	C1948	G1953	C1954	C1955	A1956	C1958	G1959	A1960	A1961	U1962	U1963	U1964	C1965	C1966	G1969	U1970	C1971	C1972	C1973	C1974	U1975	A1976	A1977	C1978	U1979	U1980	C1981	C1985	C1986	U1987	C1988	C1989	C1990	C1991	C1992	A1993	A1994	A1995	A1996	G2004	A2005	C2006	G2009	C2013	C2014	U2015	C2016					
C1877	C1878	G1879	A1880	A1881	C1885	A1886	A1887	G1888	C1889	G1890	G1891	A1892	G1893	G1894	G1895	G1896	U1897	C1898	C1899	A1900	A1901	C1902	C1903	C1904	C1905	C1906	G1907	A1908	C1909	C1910	C1911	G1912	A1913	C1916	C1917	C1918	C1919	G1920	C1921	U1922	G1923	A1924	A1925	C1926	G1927	G1930	C1931	C1932	C1933	G1934	U1935	A1936	C1937	C1938	U1939	A1940		



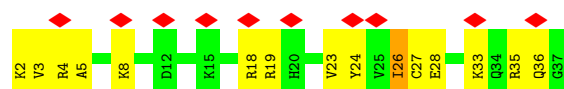
• Molecule 30: 5S ribosomal RNA



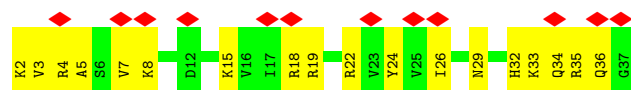
• Molecule 30: 5S ribosomal RNA



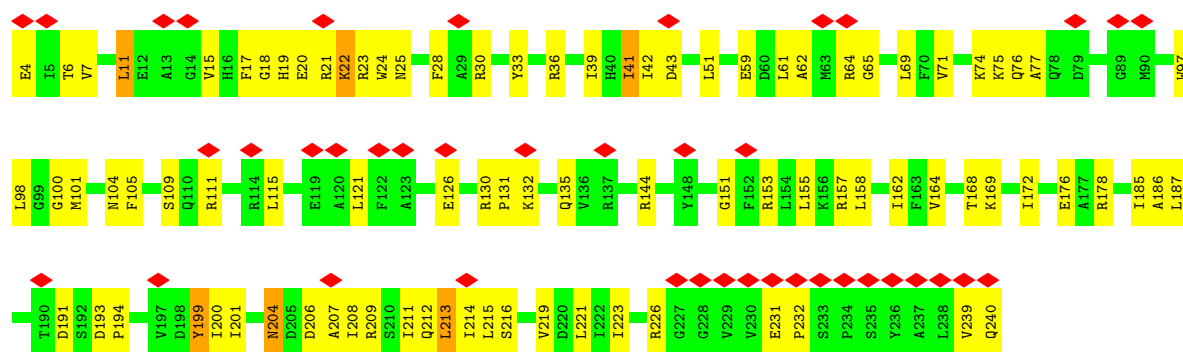
• Molecule 31: 50S ribosomal protein L36



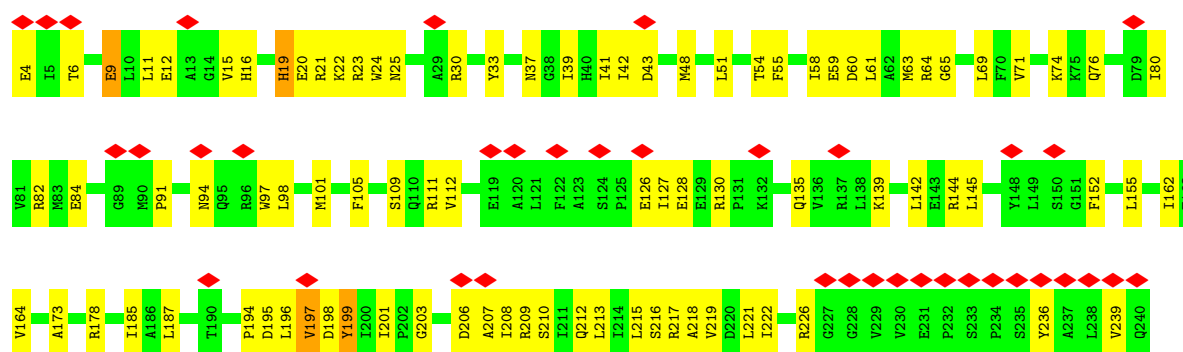
• Molecule 31: 50S ribosomal protein L36



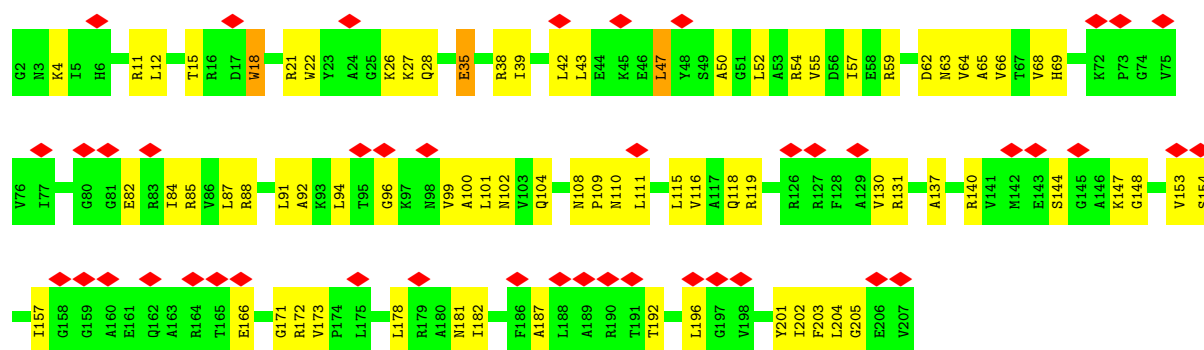
• Molecule 32: 30S ribosomal protein S2



• Molecule 32: 30S ribosomal protein S2

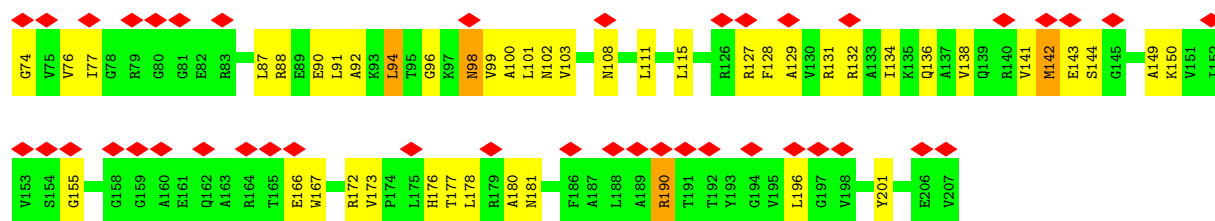


• Molecule 33: 30S ribosomal protein S3

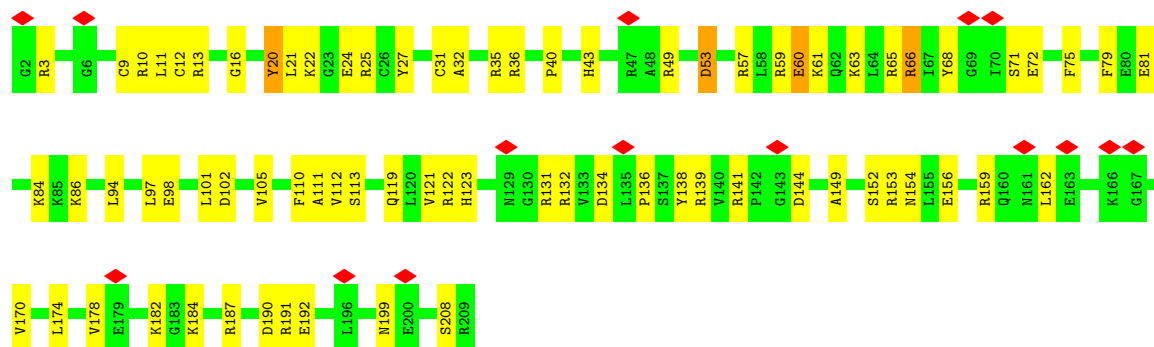


• Molecule 33: 30S ribosomal protein S3

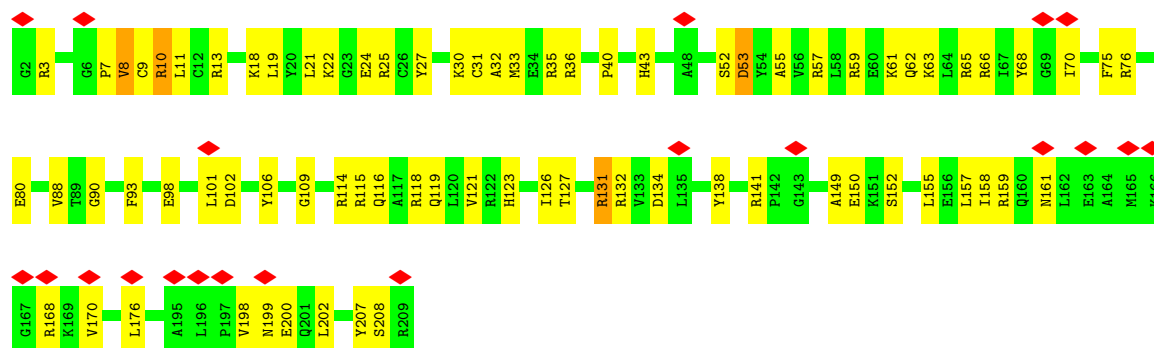




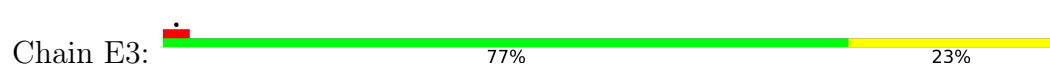
• Molecule 34: 30S ribosomal protein S4



• Molecule 34: 30S ribosomal protein S4

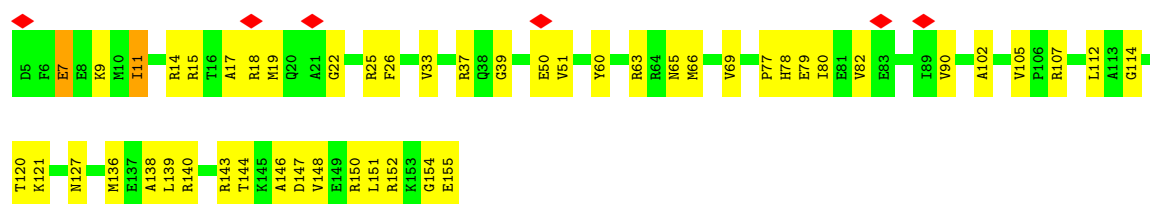


• Molecule 35: 30S ribosomal protein S5



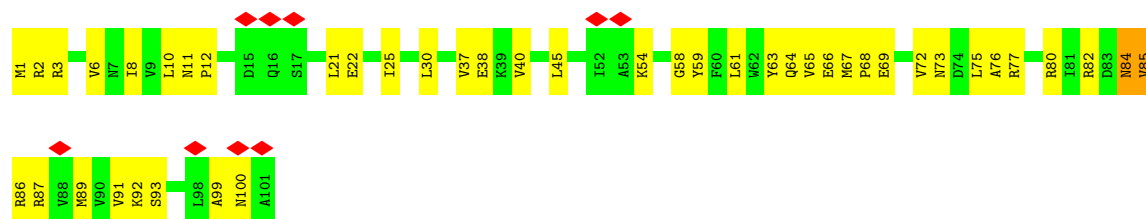
• Molecule 35: 30S ribosomal protein S5

Chain E4:  68% 31%

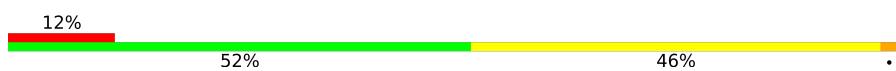


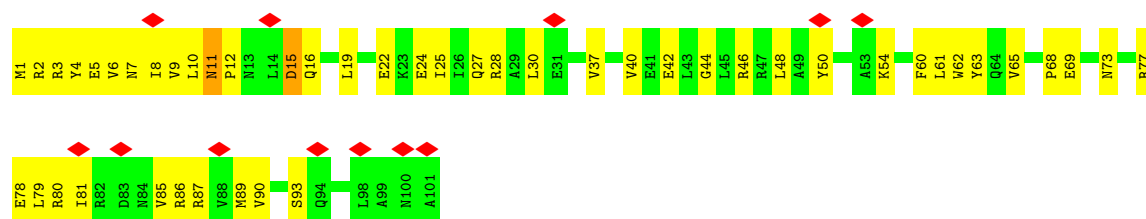
• Molecule 36: 30S ribosomal protein S6

Chain F3:  9% 56% 42%



• Molecule 36: 30S ribosomal protein S6

Chain F4:  12% 52% 46%



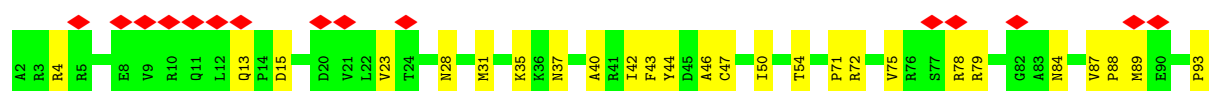
• Molecule 37: 30S ribosomal protein S7

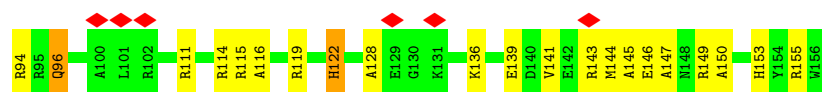
Chain G3:  14% 68% 32%



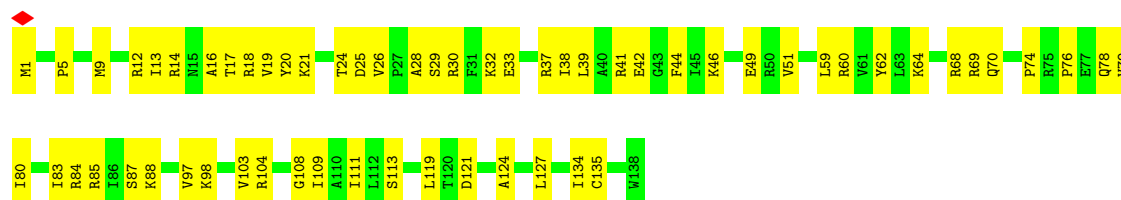
• Molecule 37: 30S ribosomal protein S7

Chain G4:  14% 70% 29%

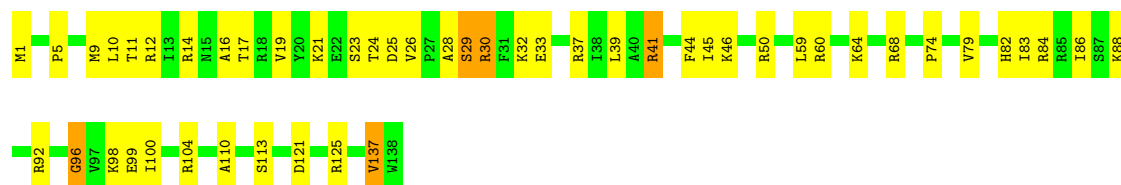




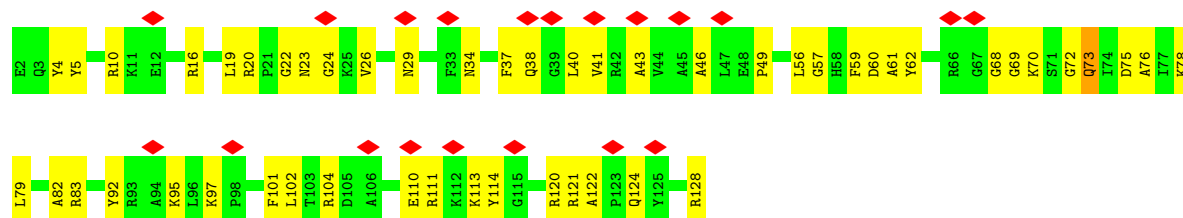
- Molecule 38: 30S ribosomal protein S8



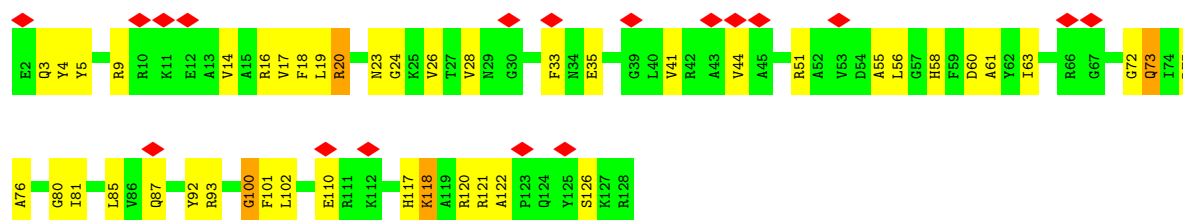
- Molecule 38: 30S ribosomal protein S8



- Molecule 39: 30S ribosomal protein S9

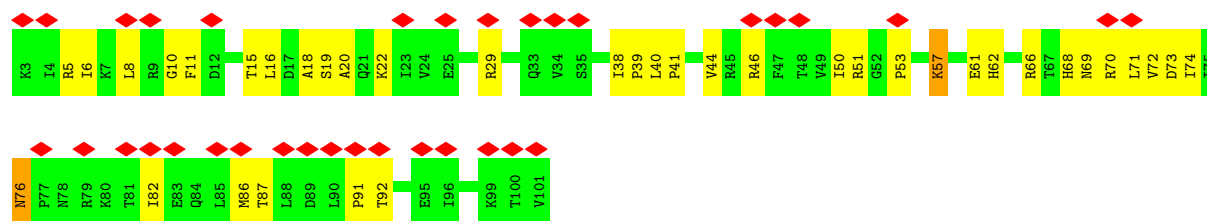


- Molecule 39: 30S ribosomal protein S9

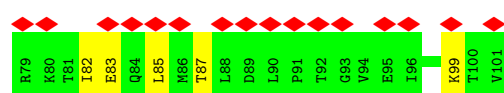
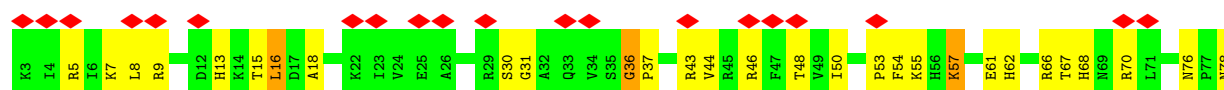


- Molecule 40: 30S ribosomal protein S10

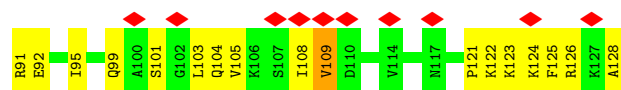




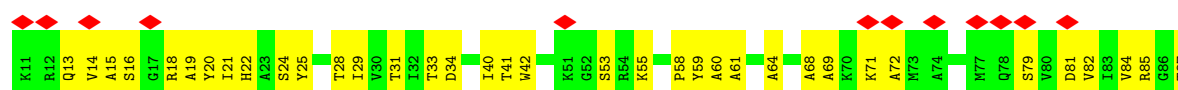
- Molecule 40: 30S ribosomal protein S10



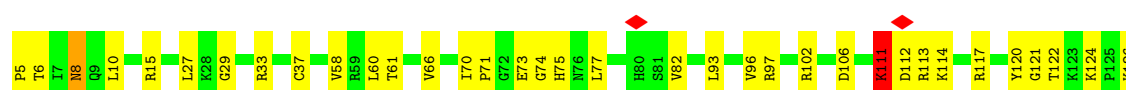
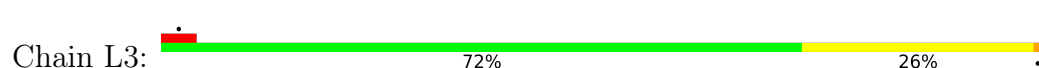
- Molecule 41: 30S ribosomal protein S11



- Molecule 41: 30S ribosomal protein S11



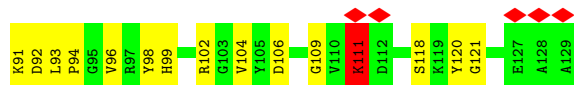
- Molecule 42: 30S ribosomal protein S12





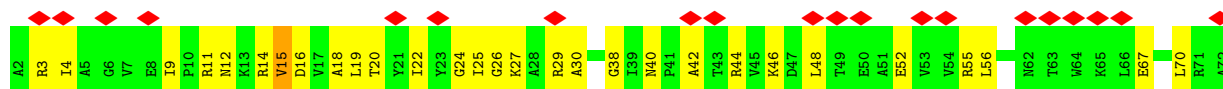
- Molecule 42: 30S ribosomal protein S12

Chain L4: 59% 40%



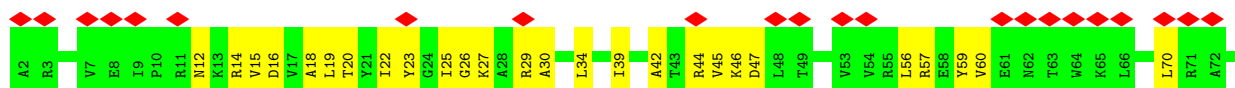
- Molecule 43: 30S ribosomal protein S13

Chain M3: 20% 56% 43%



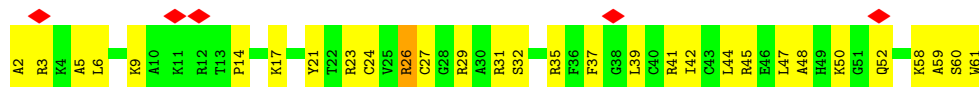
- Molecule 43: 30S ribosomal protein S13

Chain M4: 22% 61% 39%



- Molecule 44: 30S ribosomal protein S14 type Z

Chain N3: 8% 50% 48%



- Molecule 44: 30S ribosomal protein S14 type Z

Chain N4: 8% 57% 43%



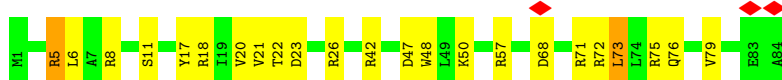
- Molecule 45: 30S ribosomal protein S15



- Molecule 45: 30S ribosomal protein S15



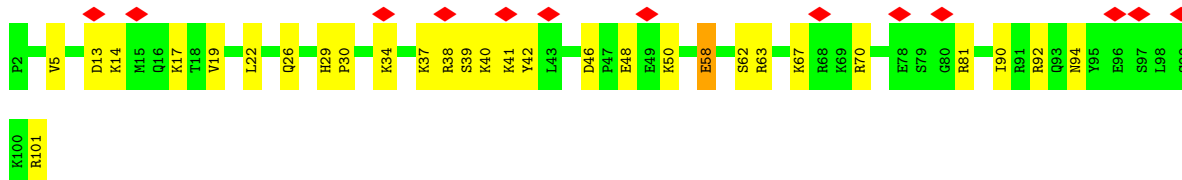
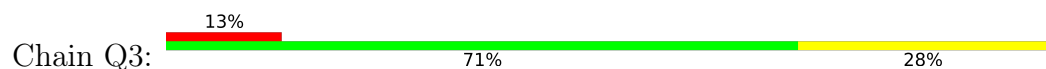
- Molecule 46: 30S ribosomal protein S16



- Molecule 46: 30S ribosomal protein S16

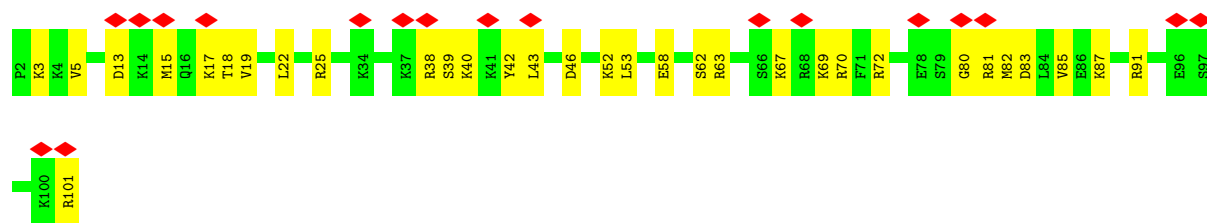


- Molecule 47: 30S ribosomal protein S17

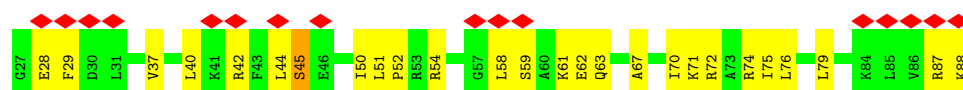


- Molecule 47: 30S ribosomal protein S17

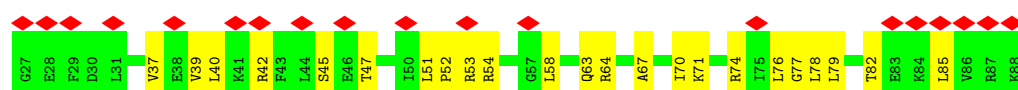




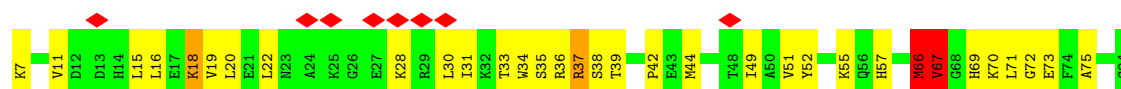
- Molecule 48: 30S ribosomal protein S18



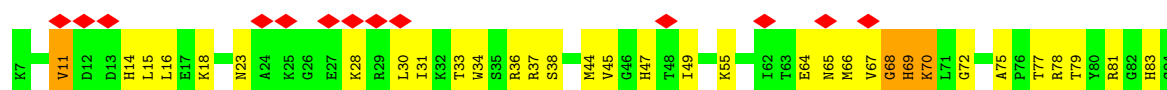
- Molecule 48: 30S ribosomal protein S18



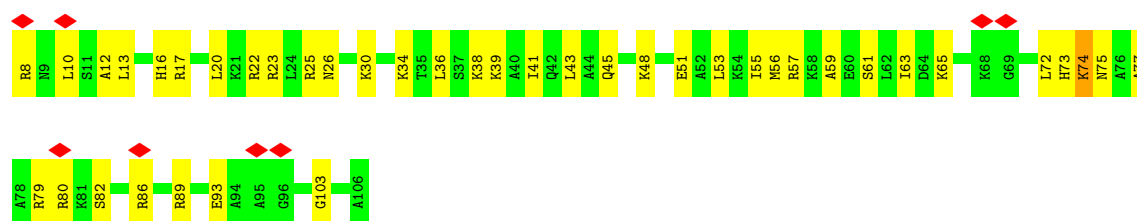
- Molecule 49: 30S ribosomal protein S19



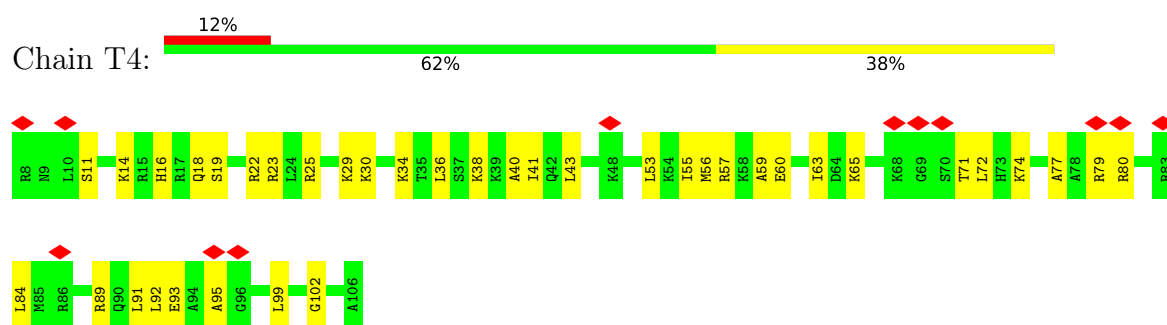
- Molecule 49: 30S ribosomal protein S19



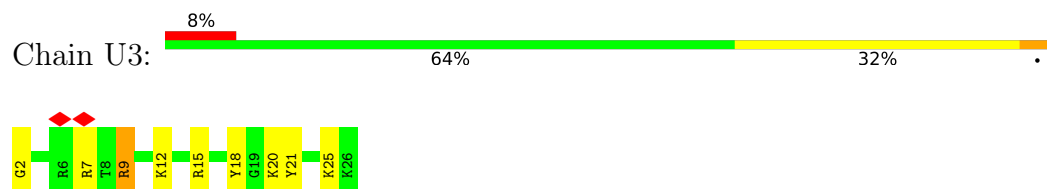
- Molecule 50: 30S ribosomal protein S20



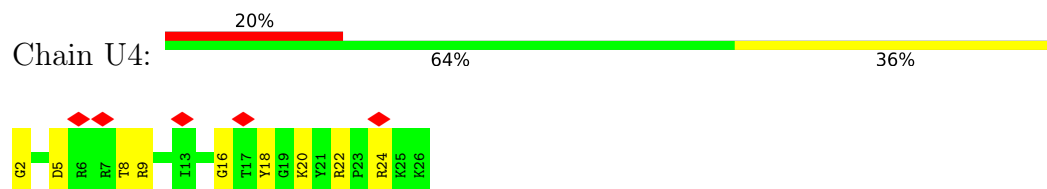
- Molecule 50: 30S ribosomal protein S20



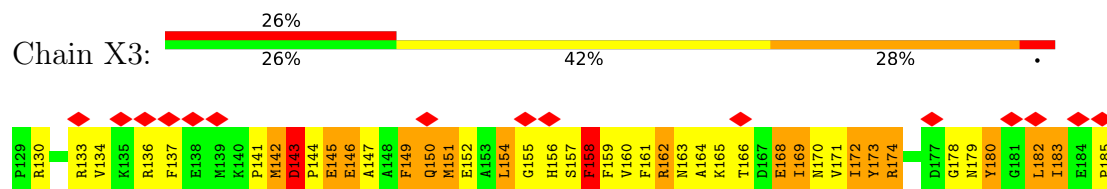
- Molecule 51: 30S ribosomal protein Thx



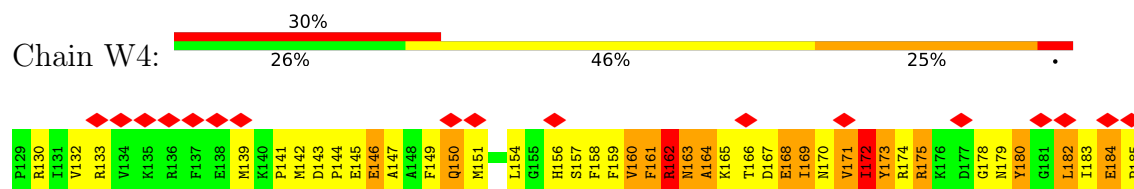
- Molecule 51: 30S ribosomal protein Thx



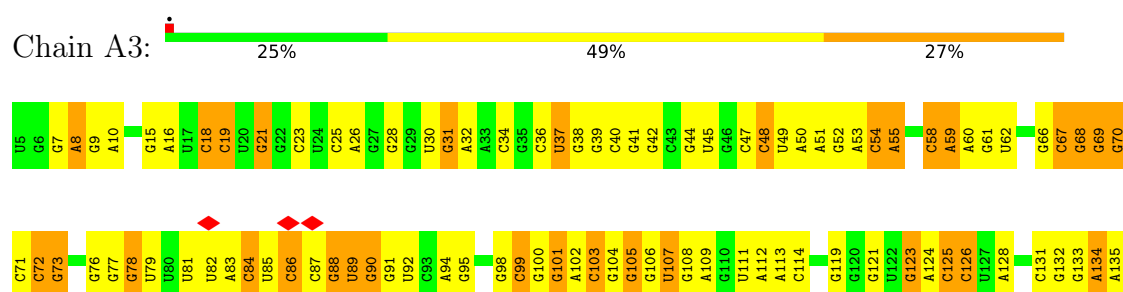
- Molecule 52: Ribosome hibernation promoting factor



- Molecule 52: Ribosome hibernation promoting factor



- Molecule 53: 16S ribosomal RNA



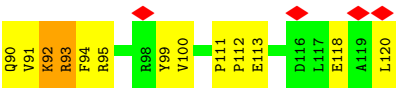
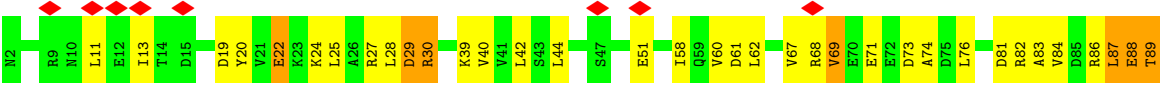
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U675	G676	A677	A678	A679	U680	G681	G682	U683	G684	A685	G686	A687	U688	A689	C690	G691	G692	G693	G694	G697	A698	A699	C700	G701	A631	C632	G633	A634	U635	G636	G637	G638	G639	G640	G641	A646	G647	G650	G651	G652	G653	G654	G655	G656	G657	G658	U659	U660	C661	C662	C663	C664	G665	G666	C730	C731	C732	G733	U734	C735	A736																																												
G801	A802	U803	U804	C805	G806	C807	C808	C809	U810	A811	G812	G813	U814	C815	U816	C817	U818	G819	G820	G821	U822	C823	U824	C825	G829	G830	G831	G835	A836	A837	G838	C839	U840	A841	A842	G846	U847	U848	A849	A850	G851	C852	G853	C854	G855	C856	C857	U858	C859	U860	C861	U862	U863	U864	A866	G867																																																	
U868	A869	C870	G871	C872	C873	C874	C875	C876	A877	A878	G879	G880	C881	A884	A885	A886	C887	U888	C889	A890	A891	A892	G893	G894	A895	A896	U897	U898	G899	A900	C901	G902	G903	G904	C907	C908	C909	G910	C911	A912	C913	A914	A915	G916	G919	U920	G921	G922	A923	G924	C925	A926	U927	G928	G931																																																		
U932	U933	U934	A935	U936	U937	U938	C939	G940	A941	A942	G943	A946	C947	G948	C949	G950	A951	A952	G953	A954	A955	C956	C957	U958	U959	A960	C961	C962	A963	C966	C967	U968	U969	G970	A971	C972	A973	U974	U975	C976	A977	U978	G979	G980	G981	A982	A983	C984	C985	C986	G987	G988	G989	U990	G991	U1052	C1053	U1054	U1055	G1056	G1057																																												
A994	G995	C996	C997	U998	G999	G1000	G1001	G1002	U1003	U1004	C1005	C1006	C1007	C1008	G1009	C1010	G1011	G1012	G1013	G1014	G1015	G1016	A1017	A1018	C1019	C1020	C1021	C1022	A1023	C966	C967	U968	U969	G970	A971	C972	A973	U974	U975	C976	A977	U978	G979	G980	G981	A982	A983	C984	C985	C986	G987	G988	G989	U990	G991	U1052	C1053	U1054	U1055	G1056	G1057																																												
A137	G138	G139	G140	G141	G142	A143	C144	C145	A146	C147	C148	C149	G150	G151	G152	G153	A154	A155	A156	C157	U158	C159	U164	A165	A166	U167	C168	C169	C170	C171	C172	A173	U174	G175	U176	G177	G178	C181	C186	G187	U188	U189	G190	G191	G192	G193	U194	G195	U196	G197	U198	C199	C200	A201	A202																																																		
A203	G204	G205	C206	C207	G208	U209	U210	G211	C212	C213	C214	G215	C216	U217	U218	G222	A223	U224	G225	G226	G227	C228	C229	C230	C231	C232	C235	C236	C237	A238	U239	C240	A241	G242	G243	G246	U247	U248	G249	U251	G252	G253	G254	G255	U256	U259	G260	G261	C262	C263	C264	A265	A268																																																				
A269	G270	G271	C272	G273	A274	C275	G276	G279	U416	G280	C281	U282	A283	C284	C285	C286	C287	G288	U289	G292	A293	G294	A298	U299	G300	G301	G304	C305	C306	C307	A308	C309	A310	G311	G312	G313	G314	C315	A316	C317	U318	G319	G321	A322	C323	A324	C325	G326	G327	G328	C329	C330	C331	G332	A333																																																		
C334	U335	C336	C337	U338	A339	C340	C341	G342	G343	A344	G345	G346	C347	A348	C349	C350	A351	G352	U353	U354	A355	G356	G357	U362	U363	G371	G372	G373	C376	G379	C380	C381	U382	G383	A384	C385	G386	G391	A392	C393	C396	G401	G402	C403	G404	G405	C406	A407	G408	A409	A410	C411	C412	C413	C414	U415	A416	C417	G418	G419	G420	G421	U422	U423	A424	A425	A426	A427	C428	U429	U432	A433	A434	A435	C436	G439	G440	G441	A442	C443	G444	A445	A446	A447	C448	C449	C450	C451	C452	G453	A454	C455	A456	A457	G458	G459	G460	G461	A462	C463	U464	G465	A466	A467	G468
G469	U470	A471	C472	C473	G474	G475	A479	A480	U481	A482	G483	C484	G485	G488	G489	C490	A491	A492	A493	C494	U495	A496	C497	G498	U499	A500	C501	C502	A503	G504	C505	A506	G507	C508	C509	G510	C511	G512	G513	U514	A515	A516	U517	A518	C519	G520	G521	G524	G525	C526	G527	C528	G529	A530	G531	C532																																																	
G533	A536	C537	C538	C539	C540	G541	G542	U543	U544	A545	A546	C547	U548	G549	G553	U554	A555	A556	A557	G558	G559	G560	C561	G562	U563	G564	U565	U566	G567	G568	C569	G570	C573	U574	G575	G576	G577	G578	C579	G580	U581	C582	U586	G587	U588	G589	A590	A591	A592	G593	A594	C595	G596	A597																																																			
C601	U602	A603	A604	C605	G606	G607	G608	U609	G610	G611	G612	G613	G614	A615	U619	G620	G621	G622	A625	C626	G627	G628	C629	C630	A631	C632	G633	A634	U635	G636	G637	G638	G639	G640	G641	A646	G647	G650	G651	G652	G653	G654	G655	G656	G657	G658	U659	U660	C661	C662	C663	C664	G665	G666	C730	C731	C732	G733	U734	C735	A736																																												
U675	G676	A677	A678	A679	U680	G681	G682	U683	G684	A685	G686	A687	U688	A689	C690	G691	G692	G693	G694	G697	A698	A699	C700	G701	A631	C632	G633	A634	U635	G636	G637	G638	G639	G640	G641	A646	G647	G650	G651	G652	G653	G654	G655	G656	G657	G658	U659	U660	C661	C662	C663	C664	G665	G666	C730	C731	C732	G733	U734	C735	A736																																												
G737	G738	G739	U740	A741	U742	G743	G744	G745	U746	A747	G748	A749	U750	A751	G752	C753	G754	G757	G758	G759	A760	G761	C762	G763	A764	A765	G766	C767	G768	G769	A770	U771	U772	U773	A774	G775	U776	U777	C778	C779	U780	G781	G782	G783	U784	U785	U787	C788	C789	A790	C791	C794	C795	U796	C800																																																		
G801	A802	U803	U804	C805	G806	C807	C808	C809	U810	A811	G812	G813	U814	C815	U816	C817	U818	G819	G820	G821	U822	C823	U824	C825	G829	G830	G831	G835	A836	A837	G838	C839	U840	A841	A842	G846	U847	U848	A849	A850	G851	C852	G853	C854	G855	C856	C857	U858	C859	U860	C861	U862	U863	U864	A866	G867																																																	
U868	A869	C870	G871	C872	C873	C874	C875	C876	A877	A878	G879	G880	C881	A884	A885	A886	C887	U888	C889	A890	A891	A892	G893	G894	A895	A896	U897	U898	G899	A900	C901	G902	G903	G904	C907	C908	C909	G910	C911	A912	C913	A914	A915	G916	G919	U920	G921	G922	A923	G924	C925	A926	U927	G928	G931																																																		
U932	U933	U934	A935	U936	U937	U938	C939	G940	A941	A942	G943	A946	C947	G948	C949	G950	A951	A952																																																																																							



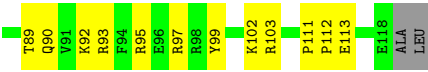
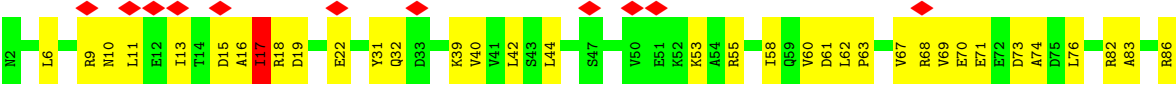
G1368	G1369	G1370	G1371	G1372	G1373	G1374	G1375	G1376	G1377	G1378	G1379	G1380	G1381	G1382	G1383	G1384	G1385	G1386	G1387	G1388	G1389	G1390	G1391	G1392	G1393	G1394	G1395	G1396	G1397	G1398	G1399	G1400	G1401	G1402	G1403	G1404	G1405	G1406	G1407	G1410	G1411	G1412	G1413	G1414	G1415	G1416	G1417	G1418	G1419	G1420	G1421	G1422	G1423	G1424	G1425	G1426	G1427	G1430		
C1303	C1304	C1308	C1309	C1310	C1311	C1312	C1313	C1314	C1315	C1316	C1317	C1318	C1319	C1320	C1321	C1322	C1323	C1324	C1325	C1326	C1327	C1328	C1329	C1332	C1333	C1336	C1337	C1338	C1340	C1341	C1342	C1343	C1344	C1345	C1346	C1347	C1348	C1349	C1350	C1351	C1352	C1353	C1354	C1355	C1356	C1359	C1360	C1361	C1362	C1363	C1364	C1365	C1366	C1367						
U1181	U1182	U1183	U1184	U1185	U1186	U1187	U1190	U1191	U1192	U1193	U1194	U1195	U1196	U1197	U1198	U1199	U1200	U1201	U1202	U1203	U1204	U1205	U1206	U1207	U1208	U1209	U1210	U1211	U1212	U1213	U1214	U1215	U1216	U1217	U1218	U1219	U1220	U1221	U1222	U1223	U1224	U1225	U1226	U1227	U1228	U1229	U1230	U1231	U1232	U1233	U1234	U1235	U1236	U1237	U1238	U1239	U1240	U1241		
U1118	U1119	U1120	U1121	U1122	U1123	U1124	U1125	U1126	U1127	U1128	U1129	U1130	U1131	U1132	U1133	U1134	U1135	U1136	U1137	U1138	U1139	U1140	U1141	U1142	U1143	U1144	U1145	U1146	U1147	U1148	U1149	U1152	U1153	U1154	U1155	U1156	U1159	U1160	U1161	U1162	U1163	U1164	U1165	U1166	U1167	U1168	U1169	U1170	U1171	U1172	U1173	U1174	U1177	U1178	U1179	U1180				
C1053	C1054	C1057	C1058	C1059	C1060	C1061	C1062	C1063	C1064	C1065	C1066	C1067	C1068	C1069	C1070	C1071	C1072	C1076	C1077	C1078	C1079	C1080	C1081	C1082	C1083	C1084	C1085	C1086	C1087	C1088	C1089	C1090	C1091	C1092	C1093	C1094	C1095	C1096	C1100	C1101	C1102	C1103	C1104	C1105	C1106	C1107	C1108	C1109	C1110	C1111	C1112	C1113	C1114	C1115	C1116	C1117				
G991	G992	G993	G994	G995	G996	G997	G998	G999	G1000	G1001	G1002	U1003	G1004	G1005	C1006	C1007	C1008	C1009	C1010	C1011	C1012	C1013	C1014	C1015	C1016	U1017	C1018	C1019	C1020	C1021	C1022	C1023	C1024	C1025	C1026	C1027	C1028	C1029	C1030	C1031	C1032	C1033	C1034	C1035	C1036	C1037	C1038	C1039	C1040	C1041	U1044	C1045	C1046	U1047	C1048	C1049	U1052			
A926	U927	G928	U929	G930	U931	U932	U933	U934	U935	A936	U937	U938	A941	A942	G943	A946	G947	G948	G949	G950	G951	A952	G953	A954	A955	C956	C957	G958	A959	A960	C961	C962	A963	G964	G965	C966	C967	U968	U969	G970	A971	C972	A973	U974	G975	C976	U977	A978	G979	G980	C981	A982	A983	C984	C985	U990				
G854	G855	A856	G857	U858	U859	U860	C870	C871	C872	C873	C874	C875	C876	A877	A878	A879	C881	A884	A885	C886	C887	U888	C889	A890	A891	A892	C893	C894	C895	C896	C897	C898	C899	C900	C901	C902	C903	C904	C905	C906	C907	C908	C909	C910	C911	C912	C913	C914	C915	C916	C917	C918	C919	C920	C921	C922	C923	C924	C925	
U796	C800	G801	A802	U803	U804	C807	C808	C809	U810	A811	C812	U816	A817	A818	A819	A820	A821	U822	C823	U824	C825	C826	G829	C830	C831	G835	A836	A837	G838	C839	U840	C841	C842	C843	C844	C845	U846	U847	U848	A849	C851	C852	C853	C854	C855	C856	C857	C858	C859	U861	C862	C863	C864	C865						
G733	U734	G735	A736	C737	G738	U739	U740	G741	A742	G743	G744	C747	A748	A749	A750	A751	C752	C753	G754	U755	C756	C757	C758	C759	C760	C761	C762	C763	C764	C765	C766	C767	C768	C769	C770	C771	C772	C773	C774	C775	C776	C777	C778	C779	C780	C781	C782	C783	C784	C785	C786	C787	C788	C789	C790	C791	C792	C793	C794	C795
G459	G465	A466	C467	G468	C469	U470	A471	C472	G475	C476	G477	A478	A479	A480	U481	A482	C483	C484	C485	G488	C489	C490	C491	A492	A493	C494	C497	G498	U499	G500	C501	C502	A503	G504	C505	A506	C507	C508	C509	G510	C511	G512	G513	U514	A515	A516	A517	A518	C519	A522	G523	G524	G525	C526						



● 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	12126	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	16.115	Depositor
Minimum map value	-7.302	Depositor
Average map value	0.038	Depositor
Map value standard deviation	0.495	Depositor
Recommended contour level	3.1	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	0.61	0/2166	0.94	2/2919 (0.1%)
1	C2	0.60	0/2166	0.92	0/2919
2	D1	0.63	1/1602 (0.1%)	0.90	0/2160
2	D2	0.61	0/1602	0.98	4/2160 (0.2%)
3	E1	0.56	0/1663	0.89	0/2249
3	E2	0.56	0/1663	0.89	1/2249 (0.0%)
4	F1	0.47	0/1499	0.84	1/2016 (0.0%)
4	F2	0.48	0/1499	0.84	0/2016
5	G1	0.44	0/1333	0.84	2/1802 (0.1%)
5	G2	0.43	0/1333	0.85	2/1802 (0.1%)
6	H1	0.53	0/387	0.89	0/523
6	H2	0.47	0/387	0.92	1/523 (0.2%)
7	I1	0.53	0/1132	0.81	0/1525
7	I2	0.54	0/1132	0.83	0/1525
8	J1	0.64	0/943	0.86	0/1269
8	J2	0.62	0/943	0.85	0/1269
9	K1	0.54	0/1162	0.99	5/1544 (0.3%)
9	K2	0.57	0/1162	0.95	0/1544
10	L1	0.54	0/1143	0.89	0/1527
10	L2	0.53	0/1143	0.96	3/1527 (0.2%)
11	M1	0.52	0/974	0.87	0/1302
11	M2	0.54	0/974	0.87	0/1302
12	N1	0.46	0/892	0.84	0/1187
12	N2	0.49	0/892	0.85	0/1187
13	O1	0.61	0/1156	0.88	0/1542
13	O2	0.58	0/1156	0.92	1/1542 (0.1%)
14	P1	0.57	0/982	0.86	1/1306 (0.1%)
14	P2	0.57	0/982	0.84	0/1306
15	Q1	0.46	0/790	0.83	2/1057 (0.2%)
15	Q2	0.47	0/790	0.84	1/1057 (0.1%)
16	R1	0.56	0/911	0.80	0/1220
16	R2	0.53	0/911	0.83	2/1220 (0.2%)
17	S1	0.49	0/740	0.86	1/993 (0.1%)
17	S2	0.48	0/740	0.88	0/993

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
18	T1	0.42	0/799	0.86	0/1064
18	T2	0.44	0/799	0.90	2/1064 (0.2%)
19	U1	0.45	0/1461	0.87	1/1982 (0.1%)
19	U2	0.46	0/1461	0.81	1/1982 (0.1%)
20	V1	0.52	0/621	0.87	0/827
20	V2	0.50	0/621	0.87	0/827
21	W1	0.54	0/770	0.88	0/1022
21	W2	0.60	0/770	0.93	0/1022
22	X1	0.43	0/583	0.80	0/771
22	X2	0.45	0/583	0.85	0/771
23	Y1	0.54	0/474	0.87	0/635
23	Y2	0.54	0/474	0.82	0/635
24	Z1	0.48	0/528	1.05	2/709 (0.3%)
24	Z2	0.49	0/528	1.10	2/709 (0.3%)
25	a1	0.66	0/473	0.98	1/639 (0.2%)
25	a2	0.60	0/473	0.87	0/639
26	b1	0.53	0/397	1.15	0/529
26	b2	0.57	0/397	1.17	2/529 (0.4%)
27	c1	0.61	0/438	0.84	0/575
27	c2	0.57	0/438	0.86	0/575
28	d1	0.54	0/495	1.04	2/649 (0.3%)
28	d2	0.57	0/495	0.99	1/649 (0.2%)
29	A1	0.62	0/70233	0.71	11/109643 (0.0%)
29	A2	0.62	0/70233	0.71	8/109643 (0.0%)
30	B1	0.49	0/2928	0.64	0/4568
30	B2	0.48	0/2928	0.63	0/4568
31	e1	0.49	0/302	1.01	0/397
31	e2	0.45	0/302	0.91	0/397
32	B3	0.60	0/1960	1.11	6/2642 (0.2%)
32	B4	0.58	0/1960	0.90	1/2642 (0.0%)
33	C3	0.47	0/1637	0.92	0/2205
33	C4	0.49	0/1637	0.89	1/2205 (0.0%)
34	D3	0.52	0/1733	0.91	0/2318
34	D4	0.55	0/1733	0.96	2/2318 (0.1%)
35	E3	0.57	0/1172	0.88	0/1576
35	E4	0.58	0/1172	0.93	0/1576
36	F3	0.51	0/856	0.86	1/1154 (0.1%)
36	F4	0.49	0/856	0.82	0/1154
37	G3	0.56	0/1276	0.89	0/1709
37	G4	0.57	0/1276	0.91	0/1709
38	H3	0.68	0/1136	0.92	0/1527
38	H4	0.66	0/1136	0.92	1/1527 (0.1%)
39	I3	0.53	0/1029	0.93	0/1379

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
39	I4	0.56	0/1029	0.96	4/1379 (0.3%)
40	J3	0.46	0/815	0.88	0/1095
40	J4	0.50	0/815	0.95	4/1095 (0.4%)
41	K3	0.53	0/894	0.86	0/1205
41	K4	0.52	0/894	0.80	1/1205 (0.1%)
42	L3	0.58	0/992	0.96	0/1327
42	L4	0.59	0/992	0.96	0/1327
43	M3	0.47	0/944	0.86	0/1265
43	M4	0.46	0/944	0.90	0/1265
44	N3	0.51	0/501	0.91	0/664
44	N4	0.53	0/501	0.89	0/664
45	O3	0.56	0/745	0.92	1/992 (0.1%)
45	O4	0.56	0/745	0.89	0/992
46	P3	0.57	0/722	0.89	0/970
46	P4	0.57	0/722	0.95	0/970
47	Q3	0.56	0/848	0.96	2/1131 (0.2%)
47	Q4	0.56	0/848	0.85	2/1131 (0.2%)
48	R3	0.58	1/520 (0.2%)	0.89	0/690
48	R4	0.57	0/520	0.89	0/690
49	S3	0.49	0/639	0.90	0/860
49	S4	0.48	0/639	0.88	1/860 (0.1%)
50	T3	0.56	0/765	0.87	0/1007
50	T4	0.53	0/765	0.86	0/1007
51	U3	0.44	0/222	0.75	0/288
51	U4	0.45	0/222	0.74	0/288
52	W4	0.74	0/487	1.30	8/650 (1.2%)
52	X3	0.53	0/487	1.05	4/650 (0.6%)
53	A3	0.64	0/36234	0.74	5/56554 (0.0%)
53	A4	0.64	0/36234	0.75	6/56554 (0.0%)
54	V3	0.56	0/977	1.08	2/1316 (0.2%)
54	V4	0.55	0/964	1.11	0/1298
All	All	0.60	2/314149 (0.0%)	0.78	114/469332 (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	10
2	D1	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	D2	0	4
3	E1	0	4
3	E2	0	6
4	F1	0	2
4	F2	0	2
5	G1	0	6
5	G2	0	3
6	H1	0	2
6	H2	0	2
7	I1	0	1
8	J1	0	3
8	J2	0	2
9	K1	0	5
9	K2	0	1
10	L1	0	3
10	L2	0	6
11	M1	0	4
11	M2	0	2
12	N1	0	3
12	N2	0	2
13	O1	0	4
13	O2	0	3
14	P1	0	3
14	P2	0	1
15	Q2	0	1
16	R2	0	1
18	T1	0	3
18	T2	0	1
19	U2	0	3
20	V1	0	1
21	W1	0	2
21	W2	0	2
22	X1	0	2
22	X2	0	1
23	Y2	0	1
24	Z1	0	9
24	Z2	0	5
25	a1	0	2
26	b2	0	1
27	c2	0	1
28	d1	0	2
28	d2	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
32	B3	0	9
32	B4	0	7
33	C3	0	4
33	C4	0	6
34	D3	0	5
34	D4	0	7
35	E3	0	3
35	E4	0	3
36	F3	0	1
36	F4	0	1
37	G3	0	1
37	G4	0	4
38	H4	0	3
39	I3	0	3
39	I4	0	3
40	J3	0	4
40	J4	0	5
41	K3	0	2
42	L3	0	3
42	L4	0	4
43	M3	0	2
44	N3	0	1
44	N4	0	3
45	O3	0	3
45	O4	0	3
46	P3	0	2
46	P4	0	3
47	Q3	0	1
47	Q4	0	1
48	R3	0	2
48	R4	0	1
49	S3	0	2
49	S4	0	2
54	V3	0	2
54	V4	0	2
All	All	0	241

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D1	52	LEU	C-O	6.35	1.26	1.23
48	R3	50	ILE	C-N	-5.00	1.25	1.33

The worst 5 of 114 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	B3	232	PRO	CA-C-N	23.05	157.78	121.83
32	B3	232	PRO	C-N-CA	23.05	157.78	121.83
13	O2	7	ILE	N-CA-C	-9.58	103.79	113.47
52	W4	162	ARG	N-CA-C	7.87	121.22	108.63
39	I4	100	GLY	CA-C-N	7.76	135.67	121.70

There are no chirality outliers.

5 of 241 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C1	10	THR	Peptide
1	C1	148	GLU	Peptide
1	C1	242	ARG	Peptide
1	C1	246	PRO	Peptide
1	C1	33	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	C1	2116	0	2195	72	0
1	C2	2116	0	2195	86	0
2	D1	1569	0	1634	44	0
2	D2	1569	0	1634	42	0
3	E1	1628	0	1680	54	0
3	E2	1628	0	1680	45	0
4	F1	1474	0	1535	65	0
4	F2	1474	0	1535	53	0
5	G1	1308	0	1382	31	0
5	G2	1308	0	1382	34	0
6	H1	383	0	410	15	0
6	H2	383	0	410	8	0
7	I1	1105	0	1180	26	0
7	I2	1105	0	1180	23	0
8	J1	933	0	996	26	0
8	J2	933	0	996	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	K1	1145	0	1228	39	0
9	K2	1145	0	1228	38	0
10	L1	1122	0	1179	34	0
10	L2	1122	0	1179	35	0
11	M1	960	0	1021	29	0
11	M2	960	0	1021	26	0
12	N1	882	0	943	28	0
12	N2	882	0	943	32	0
13	O1	1142	0	1202	43	0
13	O2	1142	0	1202	43	0
14	P1	964	0	1022	33	0
14	P2	964	0	1022	33	0
15	Q1	779	0	852	15	0
15	Q2	779	0	852	19	0
16	R1	900	0	964	32	0
16	R2	900	0	964	30	0
17	S1	726	0	778	20	0
17	S2	726	0	778	23	0
18	T1	786	0	878	27	0
18	T2	786	0	878	22	0
19	U1	1429	0	1454	38	0
19	U2	1429	0	1454	49	0
20	V1	613	0	633	32	0
20	V2	613	0	633	22	0
21	W1	763	0	848	19	0
21	W2	763	0	848	24	0
22	X1	581	0	629	27	0
22	X2	581	0	629	15	0
23	Y1	469	0	518	12	0
23	Y2	469	0	518	12	0
24	Z1	516	0	514	29	0
24	Z2	516	0	514	27	0
25	a1	459	0	480	11	0
25	a2	459	0	480	13	0
26	b1	390	0	404	22	0
26	b2	390	0	404	20	0
27	c1	430	0	480	14	0
27	c2	430	0	480	14	0
28	d1	489	0	560	15	0
28	d2	489	0	560	17	0
29	A1	62707	0	31614	1069	0
29	A2	62707	0	31614	1099	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	B1	2617	0	1328	60	0
30	B2	2617	0	1328	66	0
31	e1	299	0	326	15	0
31	e2	299	0	326	15	0
32	B3	1925	0	1975	70	0
32	B4	1925	0	1975	59	0
33	C3	1613	0	1677	59	0
33	C4	1613	0	1677	59	0
34	D3	1703	0	1767	59	0
34	D4	1703	0	1766	54	0
35	E3	1156	0	1213	23	0
35	E4	1156	0	1213	36	0
36	F3	843	0	857	33	0
36	F4	843	0	857	33	0
37	G3	1257	0	1295	46	0
37	G4	1257	0	1296	38	0
38	H3	1116	0	1177	42	0
38	H4	1116	0	1177	40	0
39	I3	1010	0	1037	39	0
39	I4	1010	0	1037	38	0
40	J3	802	0	849	33	0
40	J4	802	0	849	22	0
41	K3	879	0	899	39	0
41	K4	879	0	899	41	0
42	L3	976	0	1062	27	0
42	L4	976	0	1062	33	0
43	M3	934	0	992	47	0
43	M4	934	0	992	41	0
44	N3	492	0	533	32	0
44	N4	492	0	533	22	0
45	O3	734	0	771	24	0
45	O4	734	0	771	21	0
46	P3	706	0	725	19	0
46	P4	706	0	725	17	0
47	Q3	835	0	904	24	0
47	Q4	835	0	904	24	0
48	R3	515	0	568	21	0
48	R4	515	0	568	17	0
49	S3	625	0	636	40	0
49	S4	625	0	636	42	0
50	T3	763	0	861	28	0
50	T4	763	0	861	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
51	U3	218	0	234	8	0
51	U4	218	0	234	8	0
52	W4	476	0	470	237	0
52	X3	476	0	470	201	0
53	A3	32369	0	16337	652	0
53	A4	32369	0	16338	675	0
54	V3	963	0	982	53	0
54	V4	950	0	966	34	0
All	All	289175	0	197361	6224	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 16.

The worst 5 of 6224 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)
52:X3:154:LEU:HD12	52:W4:173:TYR:CE2	1.11	1.63
52:X3:147:ALA:HB2	52:X3:161:PHE:CD2	1.23	1.63
52:X3:173:TYR:CE2	52:W4:158:PHE:CB	1.77	1.60
52:X3:147:ALA:HB1	52:X3:161:PHE:CE2	1.37	1.56
52:W4:160:VAL:CG1	52:W4:169:ILE:HG22	1.35	1.54

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%)	205 (76%)	65 (24%)	0	100	100
1	C2	270/272 (99%)	210 (78%)	59 (22%)	1 (0%)	30	65
2	D1	203/205 (99%)	152 (75%)	49 (24%)	2 (1%)	12	46

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	D2	203/205 (99%)	144 (71%)	57 (28%)	2 (1%)	12	46
3	E1	206/208 (99%)	163 (79%)	43 (21%)	0	100	100
3	E2	206/208 (99%)	160 (78%)	45 (22%)	1 (0%)	24	61
4	F1	179/181 (99%)	146 (82%)	33 (18%)	0	100	100
4	F2	179/181 (99%)	142 (79%)	37 (21%)	0	100	100
5	G1	168/170 (99%)	127 (76%)	41 (24%)	0	100	100
5	G2	168/170 (99%)	124 (74%)	43 (26%)	1 (1%)	21	58
6	H1	48/50 (96%)	38 (79%)	10 (21%)	0	100	100
6	H2	48/50 (96%)	35 (73%)	13 (27%)	0	100	100
7	I1	136/138 (99%)	110 (81%)	26 (19%)	0	100	100
7	I2	136/138 (99%)	108 (79%)	28 (21%)	0	100	100
8	J1	120/122 (98%)	95 (79%)	25 (21%)	0	100	100
8	J2	120/122 (98%)	103 (86%)	17 (14%)	0	100	100
9	K1	148/150 (99%)	102 (69%)	46 (31%)	0	100	100
9	K2	148/150 (99%)	105 (71%)	42 (28%)	1 (1%)	18	54
10	L1	139/141 (99%)	112 (81%)	27 (19%)	0	100	100
10	L2	139/141 (99%)	106 (76%)	31 (22%)	2 (1%)	9	39
11	M1	115/117 (98%)	97 (84%)	18 (16%)	0	100	100
11	M2	115/117 (98%)	94 (82%)	21 (18%)	0	100	100
12	N1	109/111 (98%)	89 (82%)	20 (18%)	0	100	100
12	N2	109/111 (98%)	88 (81%)	21 (19%)	0	100	100
13	O1	135/137 (98%)	105 (78%)	30 (22%)	0	100	100
13	O2	135/137 (98%)	107 (79%)	28 (21%)	0	100	100
14	P1	115/117 (98%)	100 (87%)	15 (13%)	0	100	100
14	P2	115/117 (98%)	99 (86%)	16 (14%)	0	100	100
15	Q1	99/101 (98%)	75 (76%)	24 (24%)	0	100	100
15	Q2	99/101 (98%)	80 (81%)	19 (19%)	0	100	100
16	R1	111/113 (98%)	92 (83%)	19 (17%)	0	100	100
16	R2	111/113 (98%)	83 (75%)	28 (25%)	0	100	100
17	S1	90/92 (98%)	71 (79%)	19 (21%)	0	100	100
17	S2	90/92 (98%)	71 (79%)	19 (21%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	T1	100/102 (98%)	72 (72%)	27 (27%)	1 (1%)	12	46
18	T2	100/102 (98%)	67 (67%)	32 (32%)	1 (1%)	12	46
19	U1	177/179 (99%)	129 (73%)	48 (27%)	0	100	100
19	U2	177/179 (99%)	129 (73%)	47 (27%)	1 (1%)	21	58
20	V1	75/77 (97%)	59 (79%)	16 (21%)	0	100	100
20	V2	75/77 (97%)	55 (73%)	20 (27%)	0	100	100
21	W1	95/97 (98%)	71 (75%)	24 (25%)	0	100	100
21	W2	95/97 (98%)	81 (85%)	14 (15%)	0	100	100
22	X1	67/69 (97%)	56 (84%)	11 (16%)	0	100	100
22	X2	67/69 (97%)	54 (81%)	13 (19%)	0	100	100
23	Y1	57/59 (97%)	46 (81%)	11 (19%)	0	100	100
23	Y2	57/59 (97%)	45 (79%)	12 (21%)	0	100	100
24	Z1	61/63 (97%)	42 (69%)	18 (30%)	1 (2%)	7	37
24	Z2	61/63 (97%)	39 (64%)	21 (34%)	1 (2%)	7	37
25	a1	57/59 (97%)	38 (67%)	19 (33%)	0	100	100
25	a2	57/59 (97%)	42 (74%)	15 (26%)	0	100	100
26	b1	43/45 (96%)	28 (65%)	15 (35%)	0	100	100
26	b2	43/45 (96%)	33 (77%)	10 (23%)	0	100	100
27	c1	47/49 (96%)	42 (89%)	5 (11%)	0	100	100
27	c2	47/49 (96%)	41 (87%)	6 (13%)	0	100	100
28	d1	59/61 (97%)	47 (80%)	12 (20%)	0	100	100
28	d2	59/61 (97%)	44 (75%)	15 (25%)	0	100	100
31	e1	34/36 (94%)	27 (79%)	7 (21%)	0	100	100
31	e2	34/36 (94%)	26 (76%)	8 (24%)	0	100	100
32	B3	235/237 (99%)	184 (78%)	51 (22%)	0	100	100
32	B4	235/237 (99%)	190 (81%)	45 (19%)	0	100	100
33	C3	204/206 (99%)	158 (78%)	46 (22%)	0	100	100
33	C4	204/206 (99%)	162 (79%)	42 (21%)	0	100	100
34	D3	206/208 (99%)	159 (77%)	47 (23%)	0	100	100
34	D4	206/208 (99%)	161 (78%)	44 (21%)	1 (0%)	24	61
35	E3	149/151 (99%)	121 (81%)	28 (19%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	E4	149/151 (99%)	119 (80%)	30 (20%)	0	100	100
36	F3	99/101 (98%)	84 (85%)	15 (15%)	0	100	100
36	F4	99/101 (98%)	86 (87%)	13 (13%)	0	100	100
37	G3	153/155 (99%)	129 (84%)	24 (16%)	0	100	100
37	G4	153/155 (99%)	120 (78%)	33 (22%)	0	100	100
38	H3	136/138 (99%)	112 (82%)	24 (18%)	0	100	100
38	H4	136/138 (99%)	113 (83%)	23 (17%)	0	100	100
39	I3	125/127 (98%)	89 (71%)	36 (29%)	0	100	100
39	I4	125/127 (98%)	92 (74%)	33 (26%)	0	100	100
40	J3	97/99 (98%)	74 (76%)	23 (24%)	0	100	100
40	J4	97/99 (98%)	72 (74%)	25 (26%)	0	100	100
41	K3	116/118 (98%)	91 (78%)	25 (22%)	0	100	100
41	K4	116/118 (98%)	97 (84%)	19 (16%)	0	100	100
42	L3	123/125 (98%)	102 (83%)	21 (17%)	0	100	100
42	L4	123/125 (98%)	95 (77%)	28 (23%)	0	100	100
43	M3	115/117 (98%)	99 (86%)	16 (14%)	0	100	100
43	M4	115/117 (98%)	87 (76%)	28 (24%)	0	100	100
44	N3	58/60 (97%)	45 (78%)	13 (22%)	0	100	100
44	N4	58/60 (97%)	46 (79%)	12 (21%)	0	100	100
45	O3	86/88 (98%)	72 (84%)	14 (16%)	0	100	100
45	O4	86/88 (98%)	74 (86%)	12 (14%)	0	100	100
46	P3	82/84 (98%)	69 (84%)	13 (16%)	0	100	100
46	P4	82/84 (98%)	64 (78%)	18 (22%)	0	100	100
47	Q3	98/100 (98%)	78 (80%)	20 (20%)	0	100	100
47	Q4	98/100 (98%)	78 (80%)	20 (20%)	0	100	100
48	R3	60/62 (97%)	50 (83%)	10 (17%)	0	100	100
48	R4	60/62 (97%)	50 (83%)	10 (17%)	0	100	100
49	S3	76/78 (97%)	68 (90%)	6 (8%)	2 (3%)	4	28
49	S4	76/78 (97%)	57 (75%)	18 (24%)	1 (1%)	9	41
50	T3	97/99 (98%)	82 (84%)	14 (14%)	1 (1%)	12	46
50	T4	97/99 (98%)	80 (82%)	16 (16%)	1 (1%)	12	46

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	U3	23/25 (92%)	18 (78%)	5 (22%)	0	100	100
51	U4	23/25 (92%)	19 (83%)	4 (17%)	0	100	100
52	W4	55/57 (96%)	40 (73%)	12 (22%)	3 (6%)	1	17
52	X3	55/57 (96%)	39 (71%)	14 (26%)	2 (4%)	2	22
54	V3	117/119 (98%)	90 (77%)	25 (21%)	2 (2%)	7	36
54	V4	115/119 (97%)	90 (78%)	23 (20%)	2 (2%)	7	36
All	All	11544/11750 (98%)	9056 (78%)	2458 (21%)	30 (0%)	37	70

5 of 30 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
50	T3	74	LYS
52	X3	143	ASP
52	X3	164	ALA
54	V3	93	ARG
50	T4	74	LYS

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%)	209 (98%)	5 (2%)	44	63
2	D1	165/165 (100%)	162 (98%)	3 (2%)	51	67
2	D2	165/165 (100%)	162 (98%)	3 (2%)	51	67
3	E1	165/165 (100%)	160 (97%)	5 (3%)	36	57
3	E2	165/165 (100%)	161 (98%)	4 (2%)	43	63
4	F1	155/155 (100%)	155 (100%)	0	100	100
4	F2	155/155 (100%)	153 (99%)	2 (1%)	61	72
5	G1	142/142 (100%)	140 (99%)	2 (1%)	59	71
5	G2	142/142 (100%)	140 (99%)	2 (1%)	59	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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%)	117 (100%)	0	100	100
8	J1	100/100 (100%)	98 (98%)	2 (2%)	48	66
8	J2	100/100 (100%)	98 (98%)	2 (2%)	48	66
9	K1	116/116 (100%)	113 (97%)	3 (3%)	40	60
9	K2	116/116 (100%)	115 (99%)	1 (1%)	70	76
10	L1	111/111 (100%)	109 (98%)	2 (2%)	51	67
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%)	100 (100%)	0	100	100
12	N1	87/87 (100%)	85 (98%)	2 (2%)	44	63
12	N2	87/87 (100%)	87 (100%)	0	100	100
13	O1	120/120 (100%)	119 (99%)	1 (1%)	73	77
13	O2	120/120 (100%)	119 (99%)	1 (1%)	73	77
14	P1	93/93 (100%)	92 (99%)	1 (1%)	65	74
14	P2	93/93 (100%)	92 (99%)	1 (1%)	65	74
15	Q1	82/82 (100%)	80 (98%)	2 (2%)	43	63
15	Q2	82/82 (100%)	81 (99%)	1 (1%)	63	73
16	R1	92/92 (100%)	90 (98%)	2 (2%)	45	64
16	R2	92/92 (100%)	91 (99%)	1 (1%)	65	74
17	S1	74/74 (100%)	72 (97%)	2 (3%)	39	60
17	S2	74/74 (100%)	72 (97%)	2 (3%)	39	60
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%)	155 (98%)	3 (2%)	50	66
19	U2	158/158 (100%)	158 (100%)	0	100	100
20	V1	62/62 (100%)	62 (100%)	0	100	100
20	V2	62/62 (100%)	62 (100%)	0	100	100
21	W1	82/82 (100%)	82 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	W2	82/82 (100%)	82 (100%)	0	100	100
22	X1	64/64 (100%)	64 (100%)	0	100	100
22	X2	64/64 (100%)	63 (98%)	1 (2%)	55	69
23	Y1	51/51 (100%)	51 (100%)	0	100	100
23	Y2	51/51 (100%)	49 (96%)	2 (4%)	28	50
24	Z1	57/57 (100%)	56 (98%)	1 (2%)	51	67
24	Z2	57/57 (100%)	55 (96%)	2 (4%)	32	54
25	a1	51/51 (100%)	50 (98%)	1 (2%)	48	66
25	a2	51/51 (100%)	50 (98%)	1 (2%)	48	66
26	b1	44/44 (100%)	43 (98%)	1 (2%)	44	63
26	b2	44/44 (100%)	43 (98%)	1 (2%)	44	63
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%)	50 (98%)	1 (2%)	48	66
28	d2	51/51 (100%)	51 (100%)	0	100	100
31	e1	33/33 (100%)	32 (97%)	1 (3%)	36	57
31	e2	33/33 (100%)	33 (100%)	0	100	100
32	B3	205/205 (100%)	202 (98%)	3 (2%)	57	70
32	B4	205/205 (100%)	203 (99%)	2 (1%)	68	76
33	C3	160/160 (100%)	158 (99%)	2 (1%)	61	72
33	C4	160/160 (100%)	160 (100%)	0	100	100
34	D3	180/180 (100%)	179 (99%)	1 (1%)	78	80
34	D4	180/180 (100%)	178 (99%)	2 (1%)	65	74
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%)	88 (98%)	2 (2%)	45	64
37	G3	126/126 (100%)	124 (98%)	2 (2%)	55	69
37	G4	126/126 (100%)	124 (98%)	2 (2%)	55	69
38	H3	119/119 (100%)	118 (99%)	1 (1%)	73	77
38	H4	119/119 (100%)	118 (99%)	1 (1%)	73	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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%)	88 (99%)	1 (1%)	65	74
41	K3	89/89 (100%)	89 (100%)	0	100	100
41	K4	89/89 (100%)	89 (100%)	0	100	100
42	L3	104/104 (100%)	102 (98%)	2 (2%)	50	66
42	L4	104/104 (100%)	101 (97%)	3 (3%)	37	58
43	M3	94/94 (100%)	94 (100%)	0	100	100
43	M4	94/94 (100%)	94 (100%)	0	100	100
44	N3	49/49 (100%)	49 (100%)	0	100	100
44	N4	49/49 (100%)	49 (100%)	0	100	100
45	O3	79/79 (100%)	79 (100%)	0	100	100
45	O4	79/79 (100%)	79 (100%)	0	100	100
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%)	55 (100%)	0	100	100
48	R4	55/55 (100%)	54 (98%)	1 (2%)	51	67
49	S3	67/67 (100%)	65 (97%)	2 (3%)	36	57
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%)	19 (95%)	1 (5%)	22	45
51	U4	20/20 (100%)	20 (100%)	0	100	100
52	W4	50/50 (100%)	36 (72%)	14 (28%)	0	3
52	X3	50/50 (100%)	32 (64%)	18 (36%)	0	1
54	V3	101/101 (100%)	86 (85%)	15 (15%)	3	15
54	V4	100/101 (99%)	95 (95%)	5 (5%)	22	45
All	All	9775/9776 (100%)	9618 (98%)	157 (2%)	54	69

5 of 157 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
54	V3	62	LEU
52	W4	162	ARG
54	V3	89	THR
38	H4	137	VAL
52	W4	182	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 179 such sidechains are listed below:

Mol	Chain	Res	Type
41	K3	22	HIS
33	C4	108	ASN
43	M3	40	ASN
50	T3	45	GLN
35	E4	72	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
29	A1	2911/2912 (99%)	1375 (47%)	31 (1%)
29	A2	2911/2912 (99%)	1352 (46%)	39 (1%)
30	B1	121/122 (99%)	61 (50%)	1 (0%)
30	B2	121/122 (99%)	61 (50%)	0
53	A3	1505/1506 (99%)	771 (51%)	28 (1%)
53	A4	1505/1506 (99%)	758 (50%)	27 (1%)
All	All	9074/9080 (99%)	4378 (48%)	126 (1%)

5 of 4378 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
29	A1	4	C
29	A1	6	A
29	A1	9	U
29	A1	10	G
29	A1	12	U

5 of 126 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
29	A2	2004	G

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Mol	Chain	Res	Type
53	A4	717	G
53	A3	105	G
53	A4	705	A
53	A4	1144	C

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
37	G3	1
34	D4	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	G3	12:LEU	C	13:GLN	N	1.08
1	D4	187:ARG	C	188:LEU	N	1.06

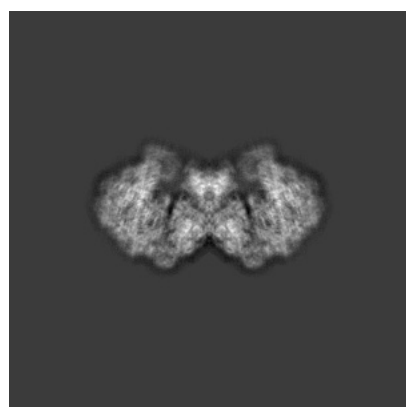
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0105. These allow visual inspection of the internal detail of the map and identification of artifacts.

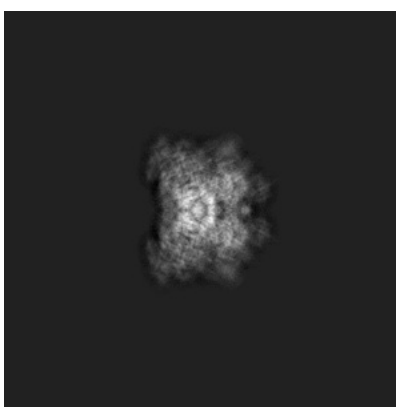
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

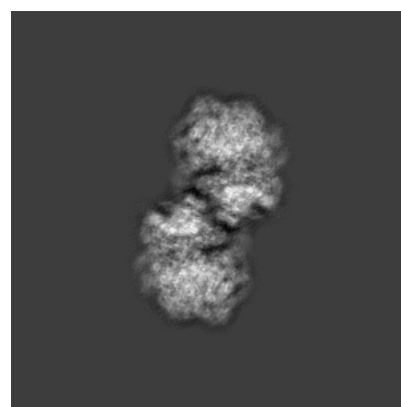
6.1.1 Primary map



X



Y

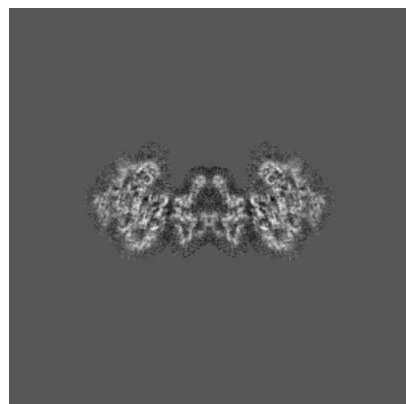


Z

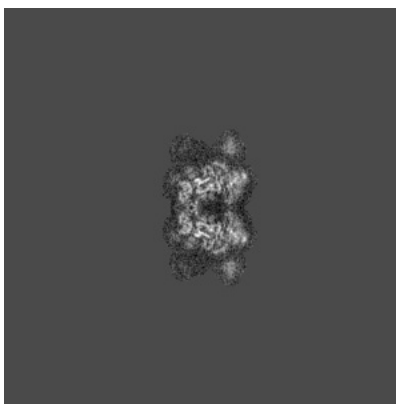
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

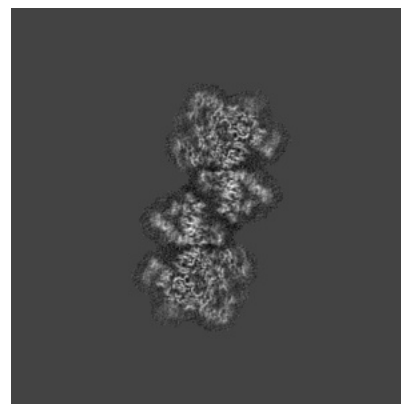
6.2.1 Primary map



X Index: 350



Y Index: 350

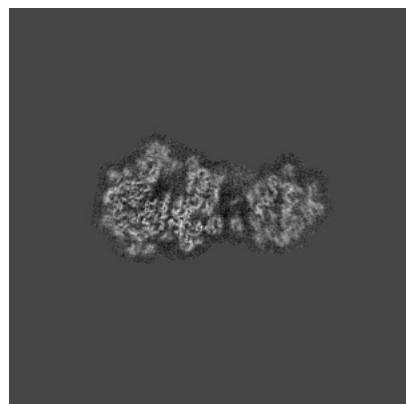


Z Index: 350

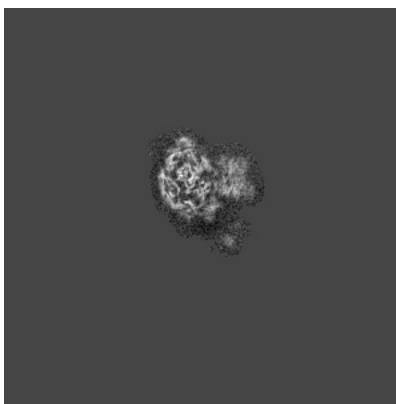
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

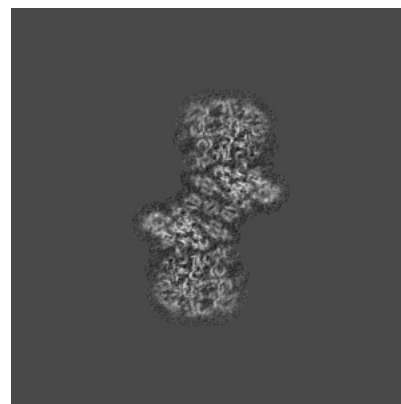
6.3.1 Primary map



X Index: 324



Y Index: 384

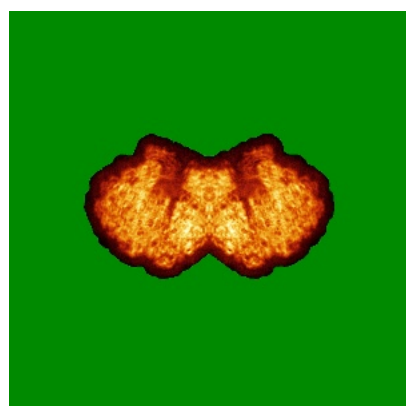


Z Index: 327

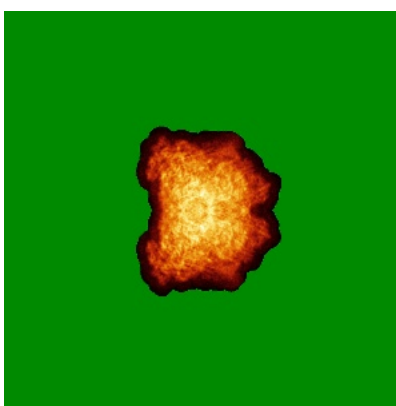
The images above show the largest variance slices of the map in three orthogonal directions.

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

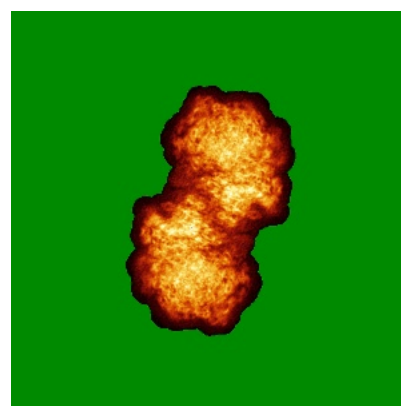
6.4.1 Primary map



X



Y

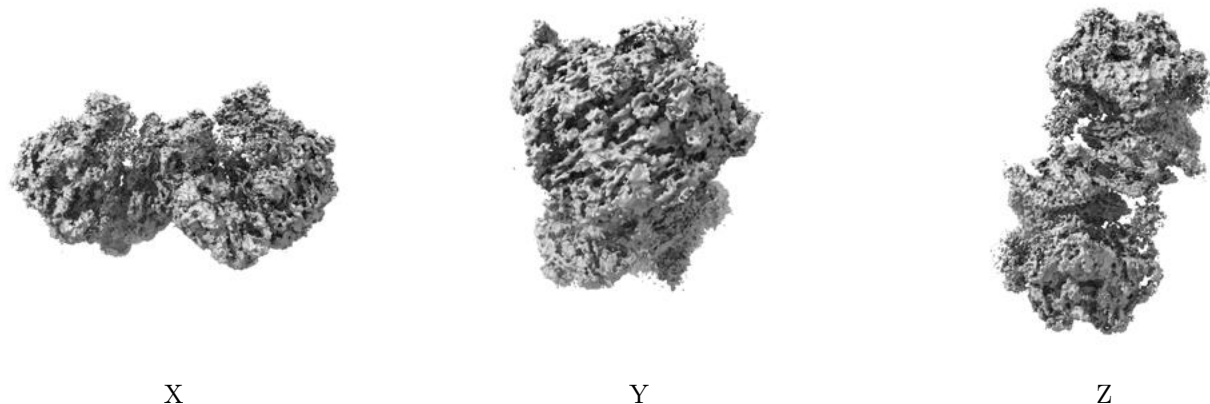


Z

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

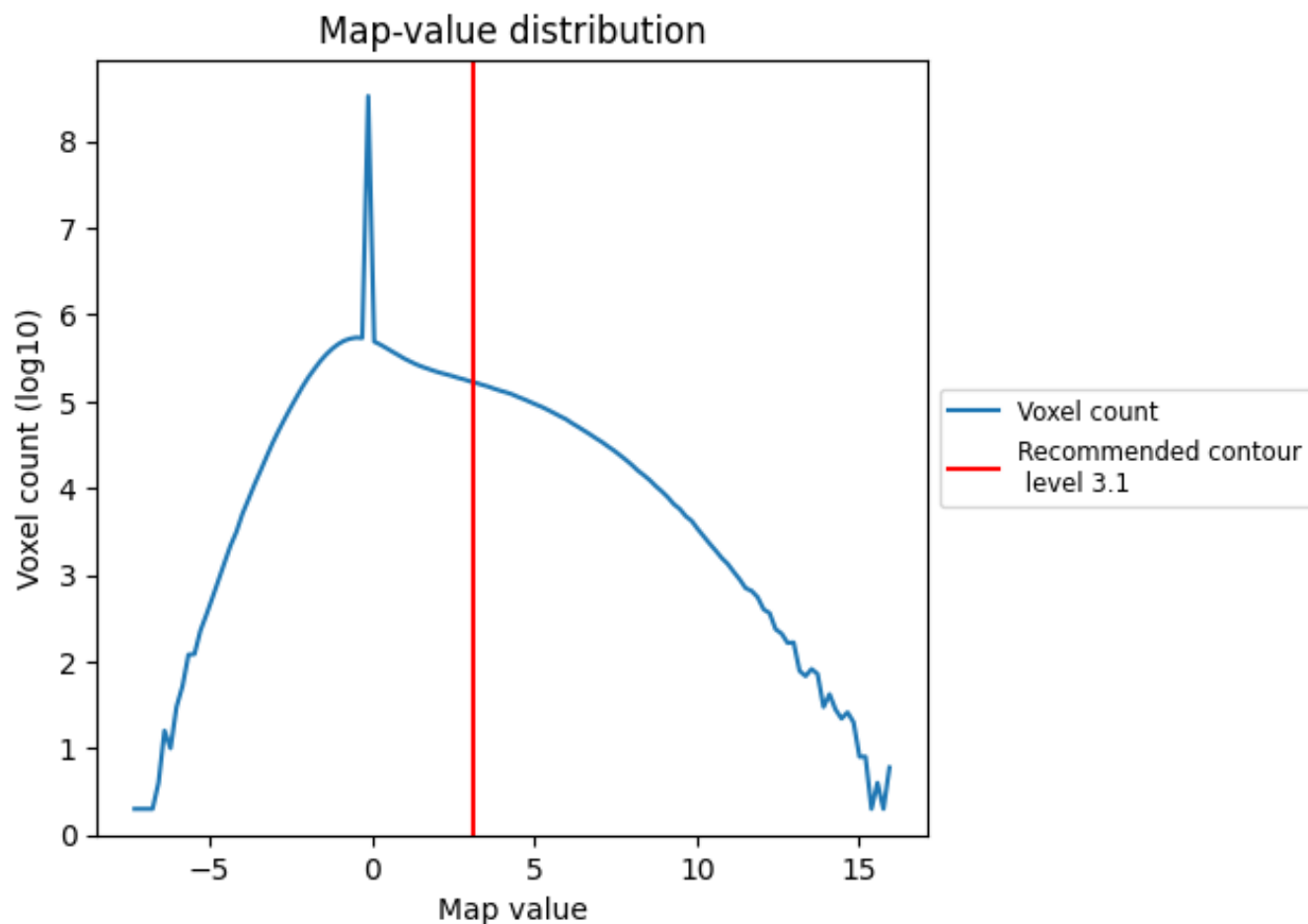
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

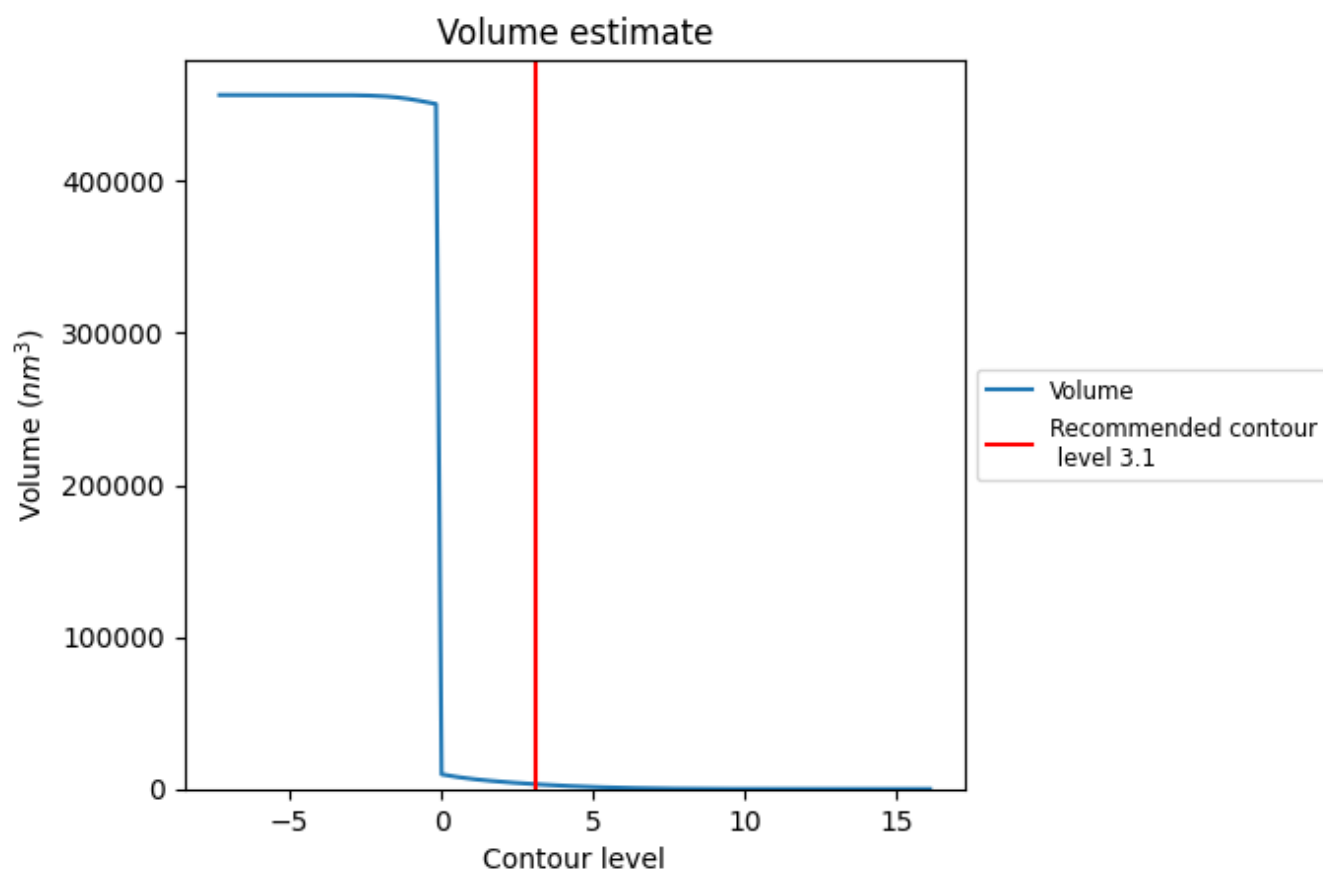
This section contains the results of statistical analysis of the map.

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.

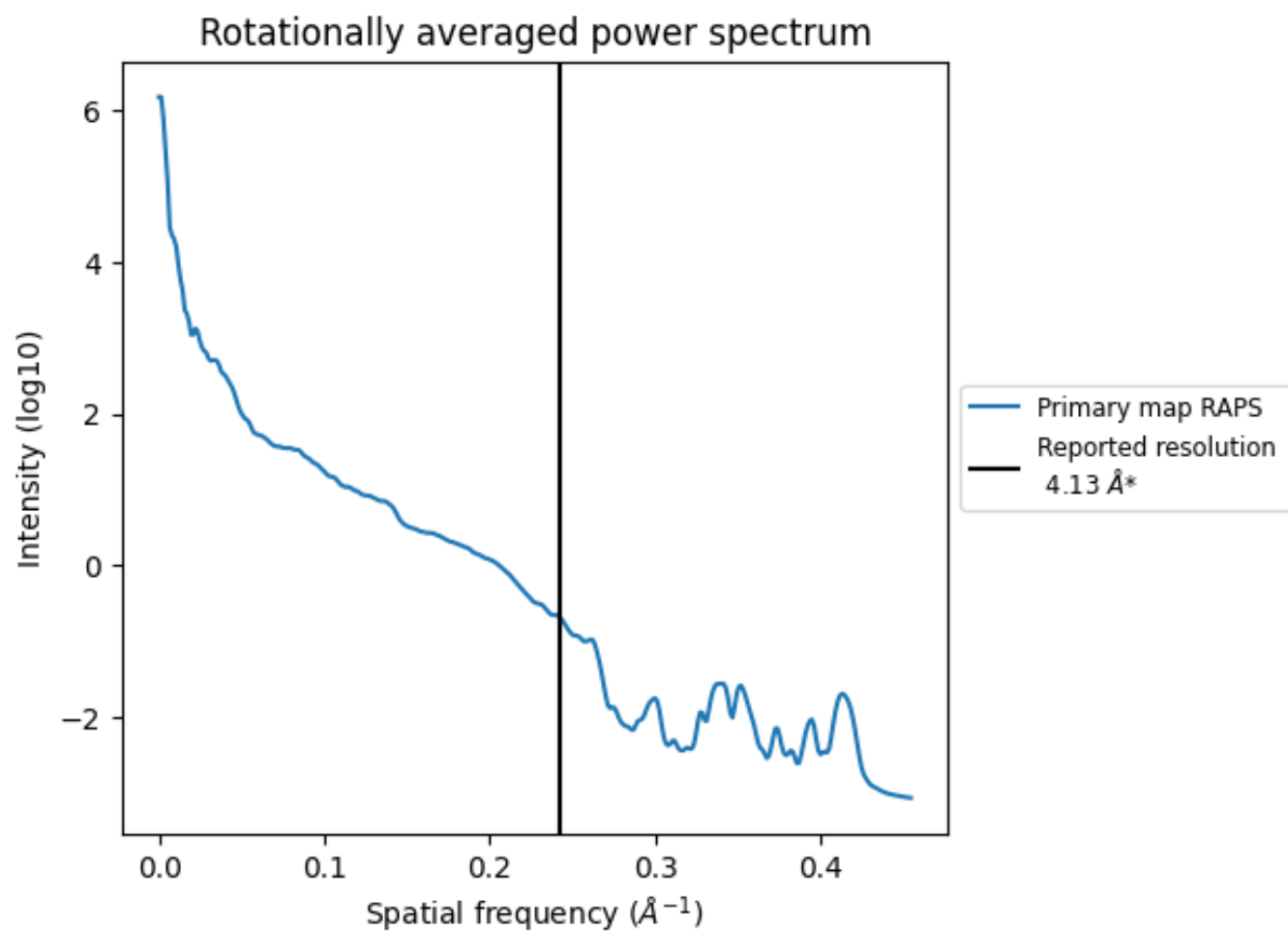
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3146 nm^3 ; this corresponds to an approximate mass of 2842 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 0.242 Å⁻¹

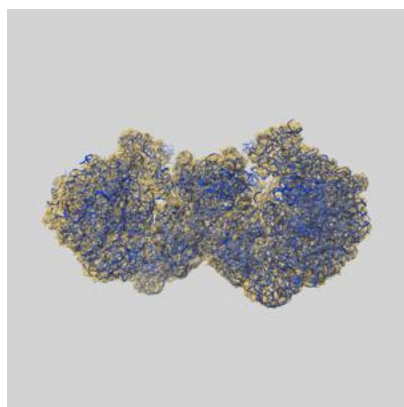
8 Fourier-Shell correlation ⓘ

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

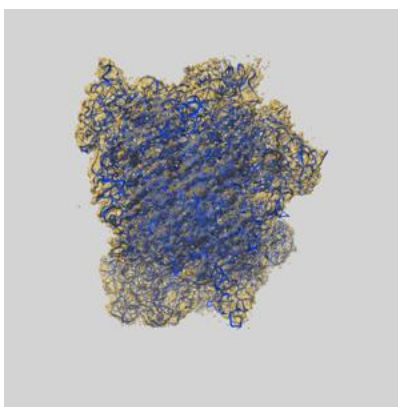
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0105 and PDB model 6GZZ. Per-residue inclusion information can be found in [section 3](#) on [page 19](#).

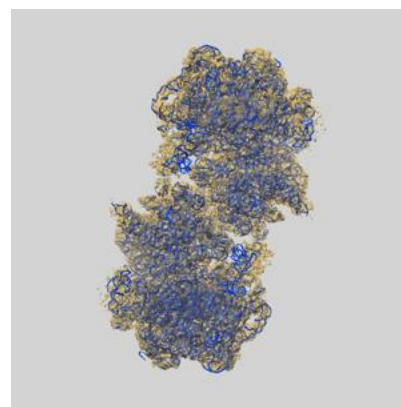
9.1 Map-model overlay [i](#)



X



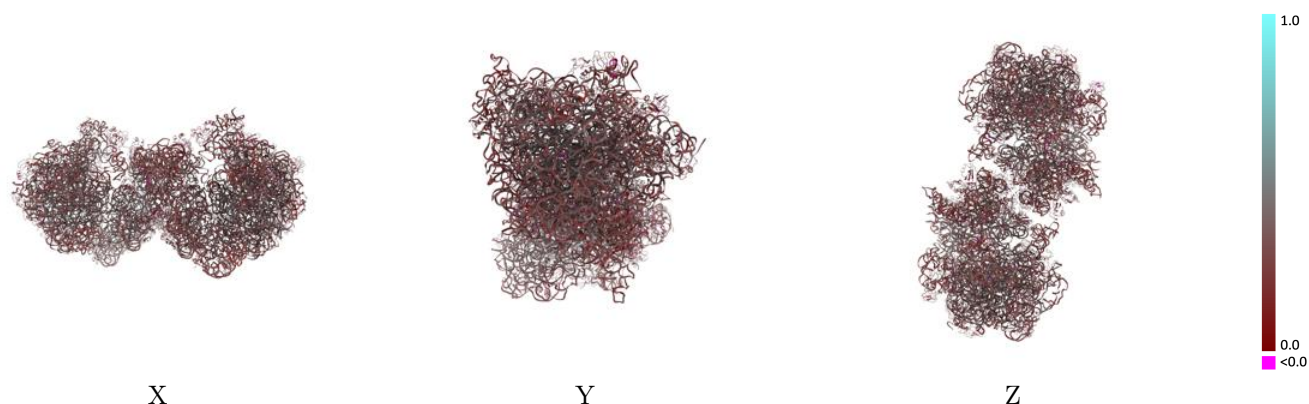
Y



Z

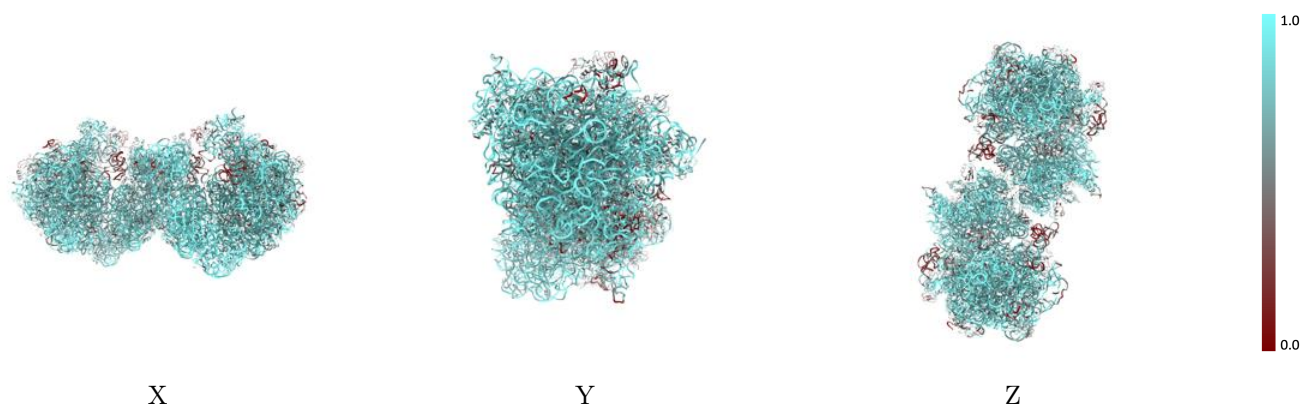
The images above show the 3D surface view of the map at the recommended contour level 3.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



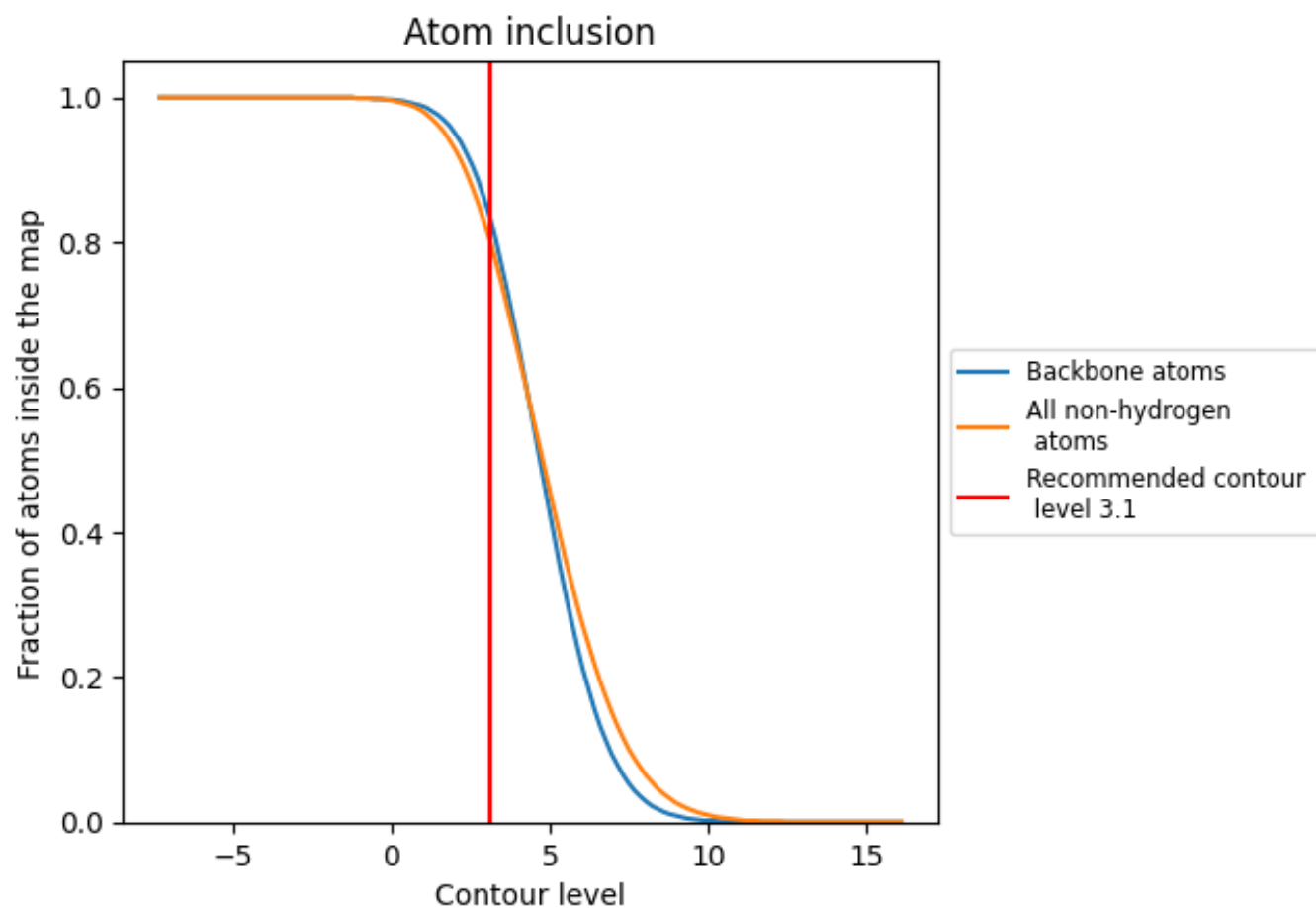
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 81% 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 (3.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8060	 0.3170
A1	 0.8440	 0.3320
A2	 0.8450	 0.3330
A3	 0.9340	 0.3190
A4	 0.9320	 0.3200
B1	 0.8960	 0.2920
B2	 0.9010	 0.2950
B3	 0.7010	 0.2960
B4	 0.6960	 0.2900
C1	 0.6580	 0.3220
C2	 0.6530	 0.3320
C3	 0.6390	 0.2870
C4	 0.6340	 0.2840
D1	 0.6560	 0.3400
D2	 0.6510	 0.3470
D3	 0.8080	 0.2650
D4	 0.8040	 0.2600
E1	 0.5360	 0.3020
E2	 0.5430	 0.3040
E3	 0.8210	 0.3280
E4	 0.8220	 0.3330
F1	 0.5440	 0.2530
F2	 0.5330	 0.2540
F3	 0.7150	 0.2650
F4	 0.7320	 0.2600
G1	 0.5270	 0.2670
G2	 0.5370	 0.2700
G3	 0.7060	 0.2940
G4	 0.7130	 0.3000
H1	 0.4830	 0.2930
H2	 0.4850	 0.2940
H3	 0.8600	 0.3210
H4	 0.8560	 0.3260
I1	 0.6890	 0.3250
I2	 0.7020	 0.3330



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Chain	Atom inclusion	Q-score
I3	 0.7110	 0.2810
I4	 0.7320	 0.2790
J1	 0.4920	 0.3600
J2	 0.5030	 0.3650
J3	 0.5270	 0.2370
J4	 0.5490	 0.2530
K1	 0.4820	 0.3110
K2	 0.4730	 0.3130
K3	 0.6760	 0.2940
K4	 0.6850	 0.3010
L1	 0.6560	 0.3190
L2	 0.6360	 0.3150
L3	 0.8060	 0.3260
L4	 0.8000	 0.3310
M1	 0.6340	 0.3170
M2	 0.6410	 0.3180
M3	 0.6570	 0.2640
M4	 0.6440	 0.2450
N1	 0.7630	 0.2860
N2	 0.7590	 0.2970
N3	 0.7300	 0.2420
N4	 0.7280	 0.2440
O1	 0.6480	 0.3300
O2	 0.6470	 0.3260
O3	 0.7940	 0.2790
O4	 0.7950	 0.2930
P1	 0.7060	 0.2950
P2	 0.6970	 0.2980
P3	 0.8190	 0.3120
P4	 0.8310	 0.3210
Q1	 0.5620	 0.3240
Q2	 0.5770	 0.3230
Q3	 0.6940	 0.3090
Q4	 0.6860	 0.3160
R1	 0.6740	 0.3260
R2	 0.6560	 0.3210
R3	 0.5750	 0.3050
R4	 0.5490	 0.2890
S1	 0.6260	 0.2830
S2	 0.6230	 0.2910
S3	 0.8020	 0.2330
S4	 0.7770	 0.2300

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Chain	Atom inclusion	Q-score
T1	 0.6870	 0.2750
T2	 0.7020	 0.2860
T3	 0.6790	 0.2830
T4	 0.6860	 0.2860
U1	 0.5180	 0.2520
U2	 0.5300	 0.2610
U3	 0.7070	 0.2710
U4	 0.6970	 0.2680
V1	 0.7730	 0.2890
V2	 0.7710	 0.2880
V3	 0.6950	 0.2990
V4	 0.7140	 0.3000
W1	 0.5200	 0.3120
W2	 0.5050	 0.3020
W4	 0.6210	 0.2710
X1	 0.6110	 0.2770
X2	 0.6010	 0.2820
X3	 0.6320	 0.2780
Y1	 0.6840	 0.3300
Y2	 0.6600	 0.3210
Z1	 0.1540	 0.1940
Z2	 0.2160	 0.1880
a1	 0.7630	 0.3140
a2	 0.7360	 0.3190
b1	 0.7470	 0.2680
b2	 0.7790	 0.2410
c1	 0.6860	 0.2960
c2	 0.7110	 0.2980
d1	 0.5690	 0.3180
d2	 0.5500	 0.3160
e1	 0.6150	 0.2360
e2	 0.5940	 0.2760