



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 07:56 PM UTC

PDB ID : 6H58 / pdb_00006h58
EMDB ID : EMD-0139
Title : Structure of a hibernating 100S ribosome reveals an inactive conformation of the ribosomal protein S1 - Full 100S Hibernating E. coli Ribosome
Authors : Beckert, B.; Turk, M.; Czech, A.; Berninghausen, O.; Beckmann, R.; Ignatova, Z.; Plitzko, J.; Wilson, D.N.
Deposited on : 2018-07-24
Resolution : 7.90 Å(reported)
Based on initial model : 6H4N

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:

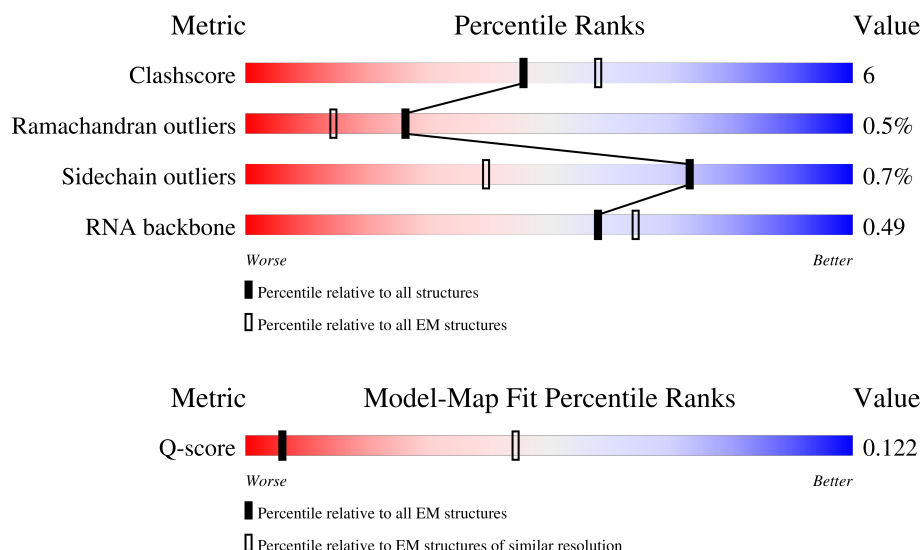
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 7.90 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	366 (7.40 - 8.40)

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

Mol	Chain	Length	Quality of chain
1	0	56	
1	00	56	
2	1	50	

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Mol	Chain	Length	Quality of chain
2	11	50	
3	2	46	
3	22	46	
4	3	64	
4	33	64	
5	4	38	
5	44	38	
6	6	66	
6	66	66	
7	A	2903	
7	AA	2903	
8	B	120	
8	BB	120	
9	C	271	
9	CC	271	
10	D	209	
10	DD	209	
11	E	201	
11	EE	201	
12	F	177	
12	FF	177	
13	G	176	
13	GG	176	
14	H	149	
14	HH	149	

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Mol	Chain	Length	Quality of chain
15	J	142	
15	JJ	142	
16	K	122	
16	KK	122	
17	L	143	
17	LL	143	
18	M	136	
18	MM	136	
19	N	120	
19	NN	120	
20	O	116	
20	OO	116	
21	P	114	
21	PP	114	
22	Q	117	
22	QQ	117	
23	R	103	
23	RR	103	
24	S	110	
24	SS	110	
25	T	93	
25	TT	93	
26	U	102	
26	UU	102	
27	V	94	

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Mol	Chain	Length	Quality of chain
27	VV	94	
28	W	75	
28	WW	75	
29	X	77	
29	XX	77	
30	Y	63	
30	YY	63	
31	Z	58	
31	ZZ	58	
32	a	1539	
32	aa	1539	
33	b	226	
33	bb	226	
34	c	206	
34	cc	206	
35	d	205	
35	dd	205	
36	e	157	
36	ee	157	
37	f	100	
37	ff	100	
38	g	161	
38	gg	161	
39	h	129	
39	hh	129	

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Mol	Chain	Length	Quality of chain
40	i	127	
40	ii	127	
41	j	98	
41	jj	98	
42	k	116	
42	kk	116	
43	l	123	
43	ll	123	
44	m	114	
44	mm	114	
45	n	101	
45	nn	101	
46	o	88	
46	oo	88	
47	p	82	
47	pp	82	
48	q	80	
48	qq	80	
49	r	65	
49	rr	65	
50	s	79	
50	ss	79	
51	t	85	
51	tt	85	
52	u	65	

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Mol	Chain	Length	Quality of chain
52	uu	65	
53	v	55	
53	vv	55	
54	x	95	
54	xx	95	
55	y	557	
55	yy	557	
56	w	77	
56	ww	77	

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 294684 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	56	Total	C	N	O	S	0	0
			444	269	94	80	1		
1	00	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
2	1	50	Total	C	N	O	0	0
			409	263	75	71		
2	11	50	Total	C	N	O	0	0
			409	263	75	71		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		
3	22	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		
4	33	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		
5	44	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 6 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	66	Total	C	N	O	S	0	0
			522	323	99	94	6		
6	66	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 7 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	2900	Total	C	N	O	P	0	0
			62261	27774	11460	20127	2900		
7	AA	2900	Total	C	N	O	P	0	0
			62261	27774	11460	20127	2900		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	747	C	U	conflict	GB 1036415628
A	1847	G	A	conflict	GB 1036415628
A	2069	A	G	conflict	GB 1036415628
AA	747	C	U	conflict	GB 1036415628
AA	1847	G	A	conflict	GB 1036415628
AA	2069	A	G	conflict	GB 1036415628

- Molecule 8 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	120	Total	C	N	O	P	0	0
			2572	1145	471	836	120		
8	BB	120	Total	C	N	O	P	0	0
			2572	1145	471	836	120		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	120	A	U	conflict	GB 1393501787

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Chain	Residue	Modelled	Actual	Comment	Reference
BB	120	A	U	conflict	GB 1393501787

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		
9	CC	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		
12	FF	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

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

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

- Molecule 14 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	H	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		
14	HH	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 15 is a protein called 50S ribosomal protein L13.

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

- Molecule 16 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	122	Total	C	N	O	S	0	0
			938	587	180	165	6		
16	KK	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 17 is a protein called 50S ribosomal protein L15.

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

- Molecule 18 is a protein called 50S ribosomal protein L16.

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

- Molecule 19 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	N	120	Total	C	N	O	S	0	0
			960	593	196	166	5		
19	NN	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 20 is a protein called 50S ribosomal protein L18.

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

- Molecule 21 is a protein called 50S ribosomal protein L19.

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

- Molecule 22 is a protein called 50S ribosomal protein L20.

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

- Molecule 23 is a protein called 50S ribosomal protein L21.

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

- Molecule 24 is a protein called 50S ribosomal protein L22.

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

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

- Molecule 25 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	T	93	Total	C	N	O	S	0	0
			738	466	139	131	2		
25	TT	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 26 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	U	102	Total	C	N	O	S	0	0
			779	492	146	141			
26	UU	102	Total	C	N	O	S	0	0
			779	492	146	141			

- Molecule 27 is a protein called 50S ribosomal protein L25.

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

- Molecule 28 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	W	75	Total	C	N	O	S	0	0
			575	356	116	102	1		
28	WW	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 29 is a protein called 50S ribosomal protein L28.

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

- Molecule 30 is a protein called 50S ribosomal protein L29.

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

- Molecule 31 is a protein called 50S ribosomal protein L30.

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

- Molecule 32 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	a	1539	Total	C	N	O	P	0	0
			33016	14725	6052	10700	1539		
32	aa	1539	Total	C	N	O	P	0	0
			33016	14725	6052	10700	1539		

- Molecule 33 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	b	226	Total	C	N	O	S	0	0
			1764	1115	315	327	7		
33	bb	226	Total	C	N	O	S	0	0
			1764	1115	315	327	7		

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
b	226	GLN	-	expression tag	UNP P0A7V0
b	227	ASP	-	expression tag	UNP P0A7V0
b	228	LEU	-	expression tag	UNP P0A7V0
b	229	ALA	-	expression tag	UNP P0A7V0
b	230	SER	-	expression tag	UNP P0A7V0
b	231	GLN	-	expression tag	UNP P0A7V0
b	232	ALA	-	expression tag	UNP P0A7V0
b	233	GLU	-	expression tag	UNP P0A7V0
bb	226	GLN	-	expression tag	UNP P0A7V0

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Chain	Residue	Modelled	Actual	Comment	Reference
bb	227	ASP	-	expression tag	UNP P0A7V0
bb	228	LEU	-	expression tag	UNP P0A7V0
bb	229	ALA	-	expression tag	UNP P0A7V0
bb	230	SER	-	expression tag	UNP P0A7V0
bb	231	GLN	-	expression tag	UNP P0A7V0
bb	232	ALA	-	expression tag	UNP P0A7V0
bb	233	GLU	-	expression tag	UNP P0A7V0

- Molecule 34 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	c	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		
34	cc	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 35 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	d	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		
35	dd	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 36 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	e	157	Total	C	N	O	S	0	0
			1141	709	218	208	6		
36	ee	157	Total	C	N	O	S	0	0
			1141	709	218	208	6		

- Molecule 37 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	f	100	Total	C	N	O	S	0	0
			817	515	148	148	6		
37	ff	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 38 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	g	161	Total	C	N	O	S	0	0
			1266	791	243	228	4		
38	gg	161	Total	C	N	O	S	0	0
			1266	791	243	228	4		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
g	154	ALA	ARG	conflict	UNP P02359
g	161	ALA	PHE	conflict	UNP P02359
gg	154	ALA	ARG	conflict	UNP P02359
gg	161	ALA	PHE	conflict	UNP P02359

- Molecule 39 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	h	129	Total	C	N	O	S	0	0
			979	616	173	184	6		
39	hh	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 40 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	i	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		
40	ii	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 41 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	j	98	Total	C	N	O	S	0	0
			786	493	150	142	1		
41	jj	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 42 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	k	116	Total	C	N	O	S	0	0
			869	535	173	158	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
42	kk	116	Total	C	N	O	S	0	0
			869	535	173	158	3		

- Molecule 43 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	l	123	Total	C	N	O	S	0	0
			955	590	196	165	4		
43	ll	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 44 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	m	114	Total	C	N	O	S	0	0
			883	546	178	156	3		
44	mm	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 45 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	n	101	Total	C	N	O	S	0	0
			799	498	165	133	3		
45	nn	101	Total	C	N	O	S	0	0
			799	498	165	133	3		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
n	35	ALA	-	insertion	UNP P0AG59
nn	35	ALA	-	insertion	UNP P0AG59

- Molecule 46 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	o	88	Total	C	N	O	S	0	0
			714	439	144	130	1		
46	oo	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 47 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	p	82	Total	C	N	O	S	0	0
			649	406	128	114	1		
47	pp	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 48 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	q	80	Total	C	N	O	S	0	0
			648	411	121	113	3		
48	qq	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 49 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	r	65	Total	C	N	O	0	0
			504	317	96	91		
49	rr	65	Total	C	N	O	0	0
			504	317	96	91		

- Molecule 50 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	s	79	Total	C	N	O	S	0	0
			637	408	120	107	2		
50	ss	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 51 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	t	85	Total	C	N	O	S	0	0
			665	411	137	114	3		
51	tt	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 52 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	u	65	Total	C	N	O	S	0	0
			495	307	100	87	1		

Continued on next page...

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Mol	Chain	Residues	Atoms					AltConf	Trace
52	uu	65	Total	C	N	O	S	0	0
			495	307	100	87	1		

- Molecule 53 is a protein called Ribosome modulation factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	v	55	Total	C	N	O	S	0	0
			453	275	96	77	5		
53	vv	55	Total	C	N	O	S	0	0
			453	275	96	77	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
54	x	95	Total	C	N	O	S	0	0
			754	474	133	145	2		
54	xx	95	Total	C	N	O	S	0	0
			754	474	133	145	2		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
x	57	ASP	ASN	conflict	UNP P0AFX0
x	61	LEU	ILE	conflict	UNP P0AFX0
xx	57	ASP	ASN	conflict	UNP P0AFX0
xx	61	LEU	ILE	conflict	UNP P0AFX0

- Molecule 55 is a protein called 30S ribosomal protein S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	y	351	Total	C	N	O	S	0	0
			2180	1339	397	441	3		
55	yy	351	Total	C	N	O	S	0	0
			2180	1339	397	441	3		

- Molecule 56 is a RNA chain called tRNA Mixture.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	w	77	Total	C	N	O	P	0	0
			1642	732	296	537	77		
56	ww	77	Total	C	N	O	P	0	0
			1642	732	296	537	77		

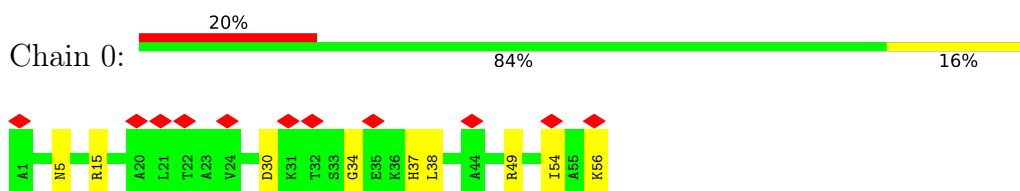
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
w	29	U	G	conflict	GB 1063812051
w	41	A	C	conflict	GB 1063812051
ww	29	U	G	conflict	GB 1063812051
ww	41	A	C	conflict	GB 1063812051

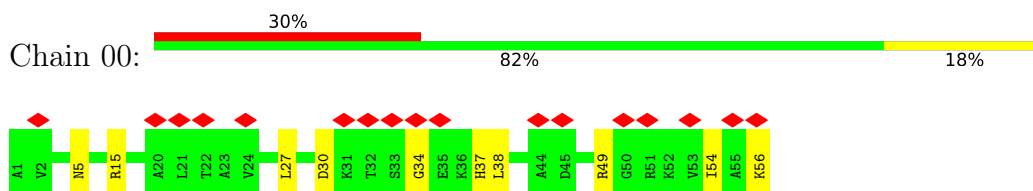
3 Residue-property plots [i](#)

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

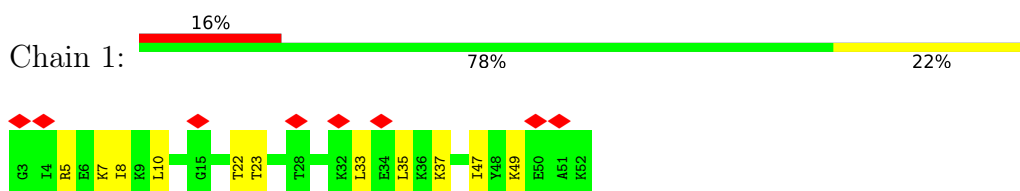
- Molecule 1: 50S ribosomal protein L32



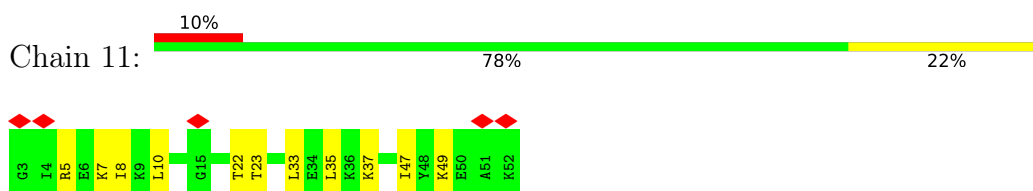
- Molecule 1: 50S ribosomal protein L32



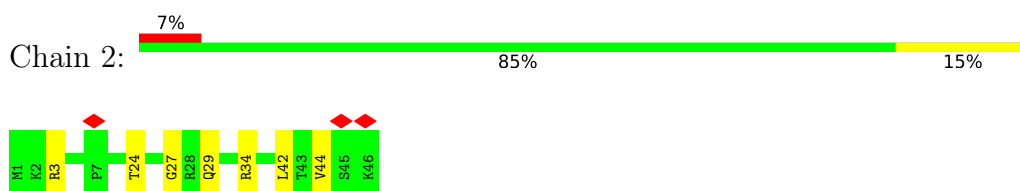
- Molecule 2: 50S ribosomal protein L33



- Molecule 2: 50S ribosomal protein L33



- Molecule 3: 50S ribosomal protein L34



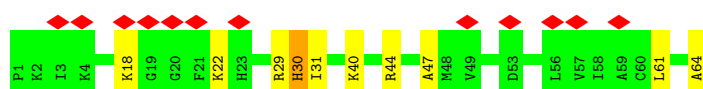
- Molecule 3: 50S ribosomal protein L34

Chain 22:  87% 13%



- Molecule 4: 50S ribosomal protein L35

Chain 3:  19% 84% 14%



- Molecule 4: 50S ribosomal protein L35

Chain 33:  11% 84% 14%



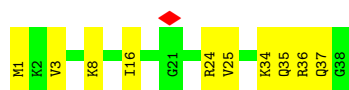
- Molecule 5: 50S ribosomal protein L36

Chain 4:  74% 26%

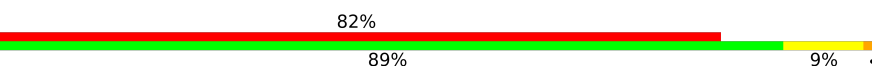


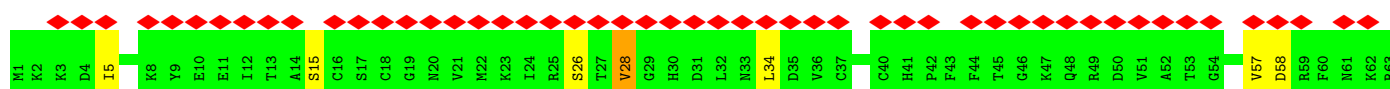
- Molecule 5: 50S ribosomal protein L36

Chain 44:  74% 26%

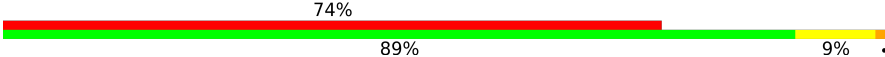


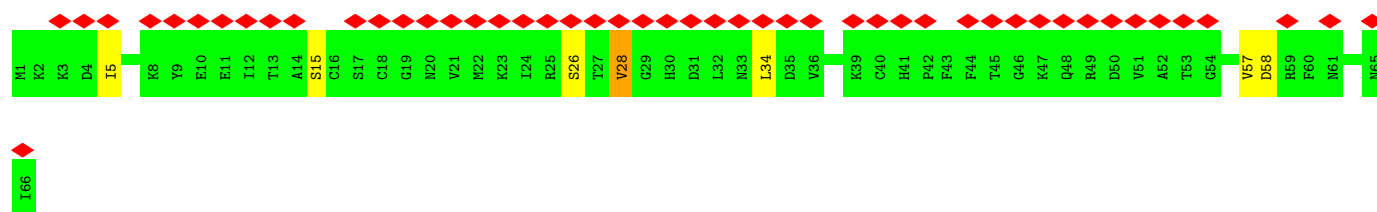
- Molecule 6: 50S ribosomal protein L31

Chain 6:  82% 89% 9%



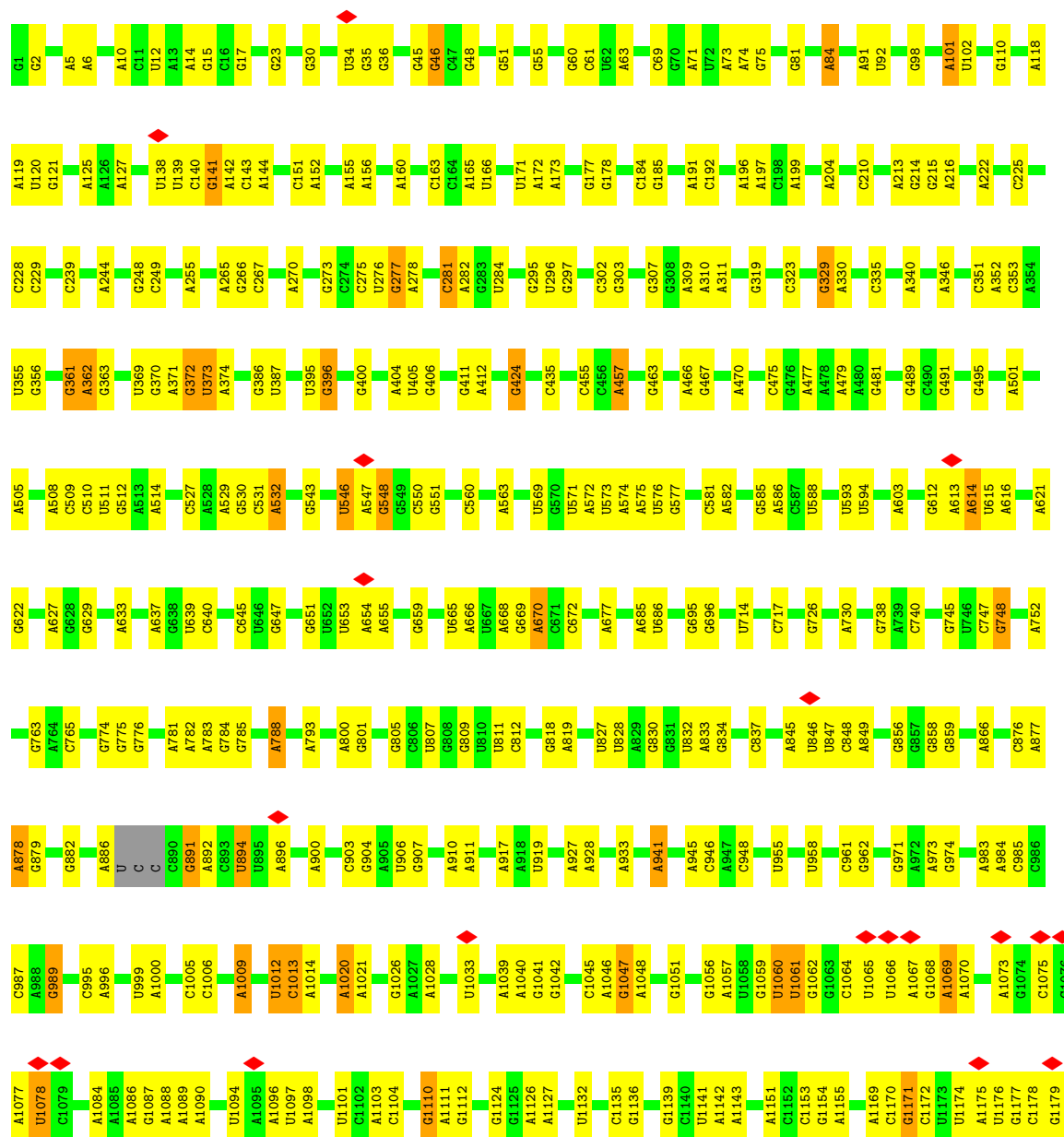
- Molecule 6: 50S ribosomal protein L31

Chain 66: 



• Molecule 7: 23S ribosomal RNA

Chain A: 

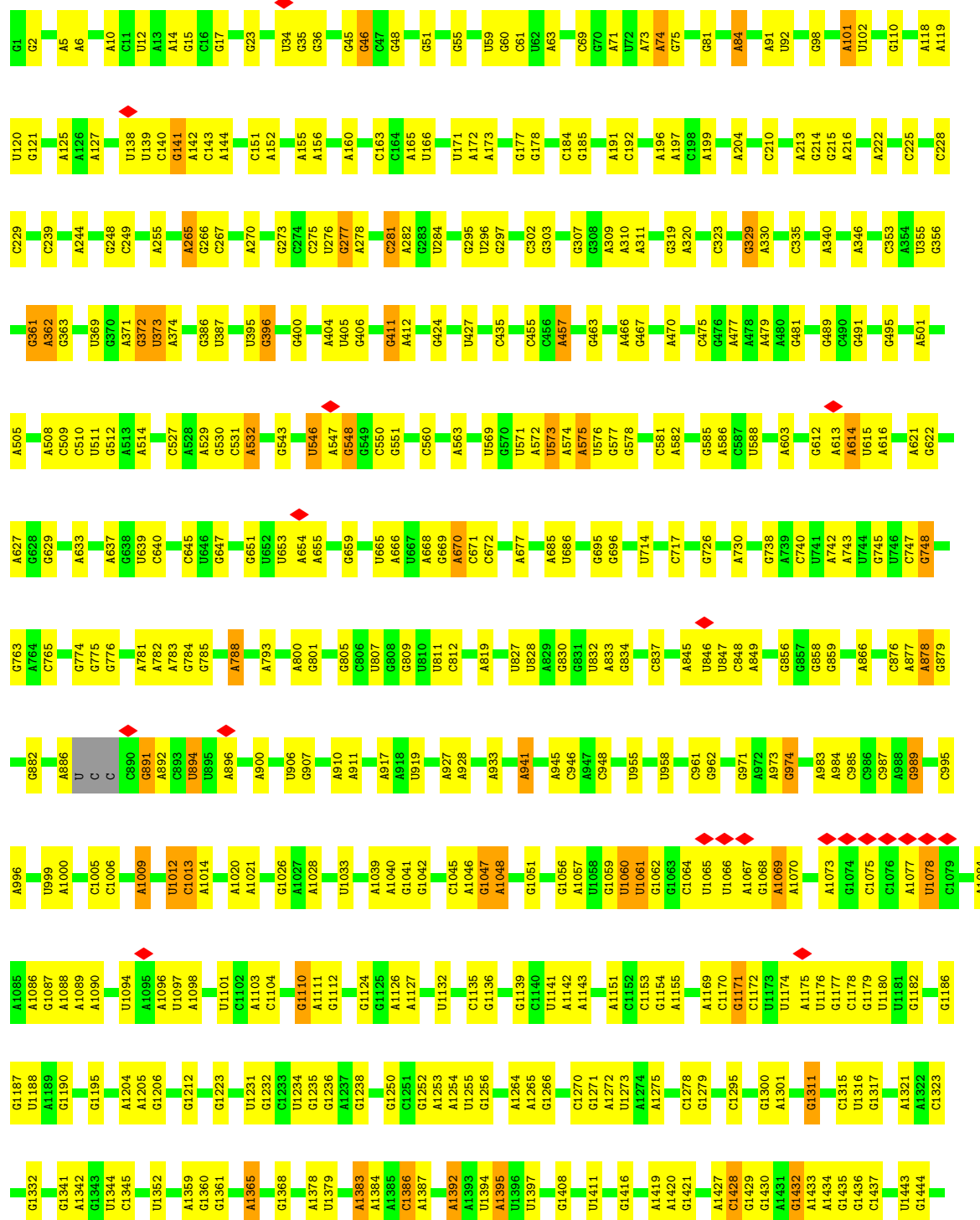


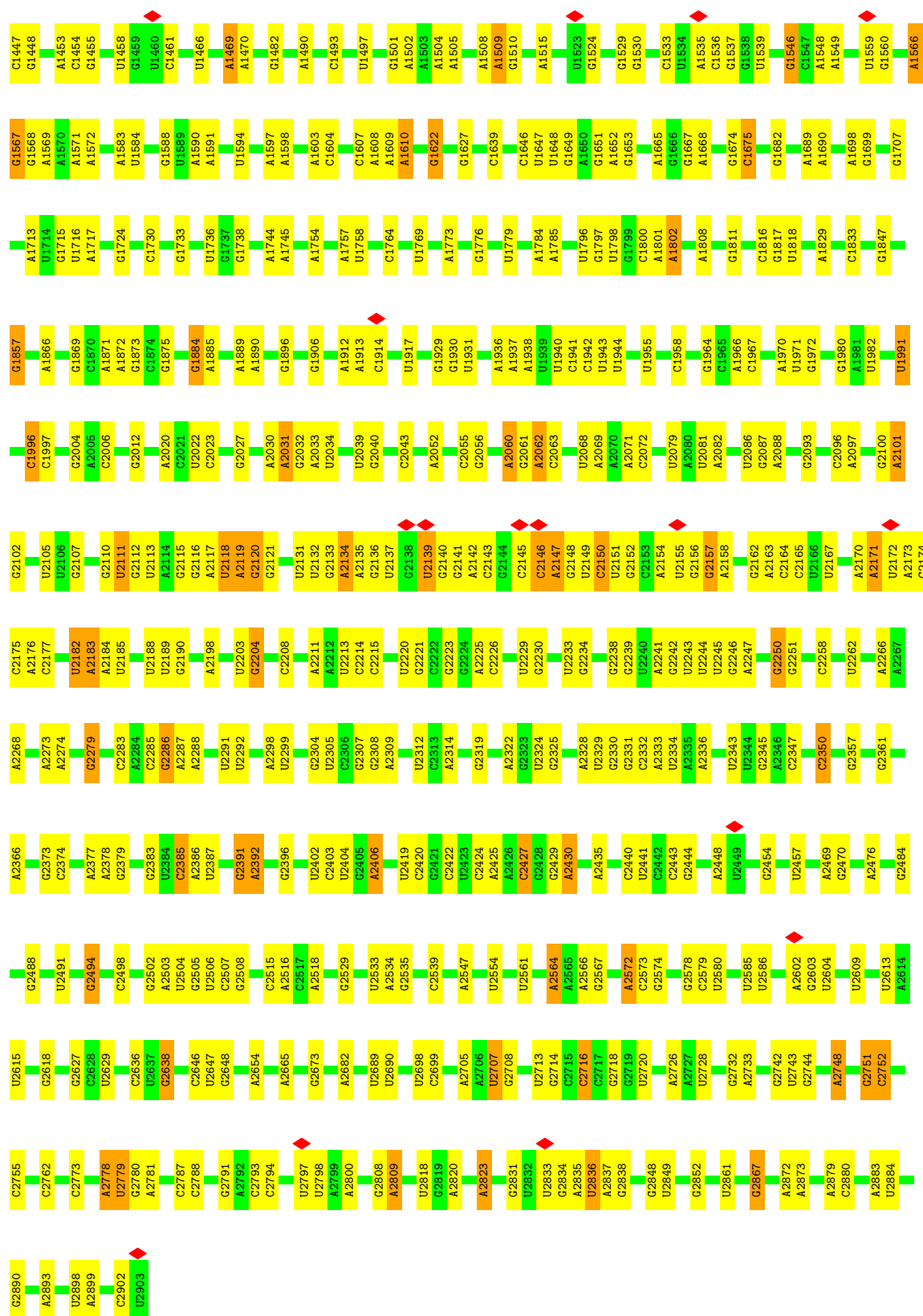
C2762	U2609	G2470	A2366	U2262	A2173	G2100	G1857	G1707	A1566	U1443	C1315	U1180
C2773	U2613	A2476	G2373	A2266	C2174	A2101	A1866	A1713	G1567	G1444	U1316	U1161
A2778	A2614	G2494	C2374	A2267	A2176	G2102	G1869	U1714	G1568	C1447	G1317	G1182
U2779	U2615	G2488	A2377	A2268	C2177	U2106	C1870	G1715	A1570	G1448	A1321	G1186
G2780	G2618	U2491	A2273	C2179	U2180	G2107	A1872	U1716	A1571	A1453	A1322	G1187
C2787	U2629	G2494	G2279	U2181	U2182	G2110	G1874	A1717	A1572	G1455	C1323	U1188
C2788	G2383	C2494	G2280	U2183	U2183	G2111	G1875	G1724	A1583	G1455	G1341	A1189
G2791	U2636	G2498	G2281	A2184	U2184	G2112	G1884	U1729	U1584	U1458	C1345	G1195
A2792	C2637	C2498	G2282	A2184	U2184	G2113	A1885	C1730	G1588	G1459	U1352	A1204
C2793	G2638	C2498	A2284	U2185	U2185	G2115	G1885	G1733	U1589	U1460	A1205	A1206
C2794	C2646	G2502	G2285	U2188	U2188	G2116	A1889	U1736	A1591	U1466	A1369	G1206
U2797	U2503	A2504	G2286	U2189	U2189	G2117	A1890	U1737	A1594	U1469	G1360	G1213
U2798	G2648	U2504	A2288	G2190	U2190	G2118	G1896	G1738	U1594	A1469	G1361	A1212
A2799	A2654	U2506	G2291	A2198	U2198	G2119	G1906	A1744	U1597	A1470	A1365	A1214
C2800	A2665	G2507	U2292	U2203	U2203	G2121	G1906	A1745	A1598	G1482	G1368	G1223
G2808	G2673	U2514	A2298	G2204	U2204	U2131	A1912	A1757	A1603	A1490	A1378	U1231
A2809	A2516	A2516	U2299	C2208	A2033	U2132	A1913	U1758	C1604	A1490	U1379	U1232
U2818	C2517	G2517	G2304	A2211	U2039	U2133	C1914	C1764	A1608	C1493	A1383	C1233
A2819	A2518	G2518	C2305	A2212	G2040	U2136	U1917	U1769	A1610	U1497	A1384	U1234
A2820	G2529	G2529	G2307	U2213	G2040	U2137	G1929	U1773	A1609	G1501	A1385	G1235
A2823	U2533	U2533	G2308	C2214	C2043	G2138	U1931	A1773	G1622	A1502	C1386	A1237
G2831	A2534	A2534	A2309	C2215	A2052	U2139	U1931	A1776	G1627	A1503	A1387	G1238
U2832	G2535	G2535	U2312	U2220	A2052	G2140	A1936	G1776	A1504	A1505	A1392	G1250
U2833	C2539	C2539	G2319	G2221	C2055	G2141	A1937	U1779	A1508	A1509	A1393	C1251
A2835	A2547	A2547	A2322	G2222	G2056	C2142	A1938	A1784	A1509	A1504	A1394	G1252
U2836	U2554	U2554	G2323	A2225	A2061	C2146	U1940	A1785	G1646	A1508	A1395	A1253
A2837	G2428	G2428	G2324	C2226	A2062	C2147	C1941	U1796	U1647	A1509	A1396	A1254
G2838	A2430	A2430	G2325	U2229	C2063	A2147	U1943	U1797	G1651	G1510	U1397	U1255
U2848	U2561	U2561	A2328	G2230	U2068	G2148	U1944	U1798	A1652	A1515	G1408	G1256
U2849	A2564	A2564	U2329	U2233	A2069	U2149	U1955	U1799	A1653	G1524	U1411	A1264
A2850	A2565	A2565	G2330	G2234	A2070	G2150	C1958	C1800	G1666	G1529	A1265	G1266
U2861	A2566	A2566	G2331	G2238	A2071	G2151	G1964	A1801	A1667	G1530	A1416	C1270
G2867	U2728	U2728	C2332	G2239	A2072	G2152	C1965	A1802	A1668	C1533	A1419	G1271
A2868	G2732	A2572	U2334	A2241	U2081	G2153	C1966	A1808	G1674	U1534	A1420	G1272
U2872	A2733	C2573	U2343	G2242	A2082	A2156	C1967	G1811	G1675	A1535	A1427	U1273
A2873	G2742	G2578	U2344	U2243	A2082	G2157	C1967	C1816	G1674	C1536	C1428	C1278
U2879	U2743	U2580	U2345	U2244	A2088	A2158	C1967	G1817	G1675	G1537	G1429	G1279
C2880	G2744	U2580	G2347	U2245	A2088	A2158	C1967	U1818	G1682	U1539	A1431	C1295
U2883	A2748	U2585	C2350	G2246	G2093	G2162	A1970	A1829	A1689	G1546	A1433	G1300
U2884	G2751	U2586	G2357	G2250	G2093	C2164	U1971	A1829	A1690	G1547	A1434	A1301
G2890	C2752	A2602	U2361	G2251	C2096	G2165	A1981	C1833	A1548	A1549	G1435	G1300
U2890	C2755	U2604	G2361	C2258	A2097	U2167	U1982	G1847	G1699	U1559	G1436	G1311



• Molecule 7: 23S ribosomal RNA

Chain AA: 68% 28%



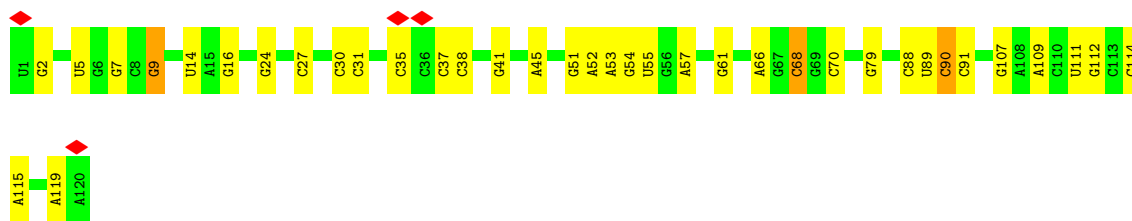


• Molecule 8: 5S ribosomal RNA

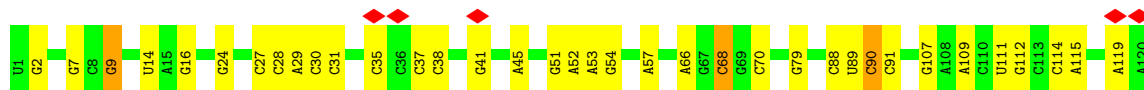
Chain B:

69%

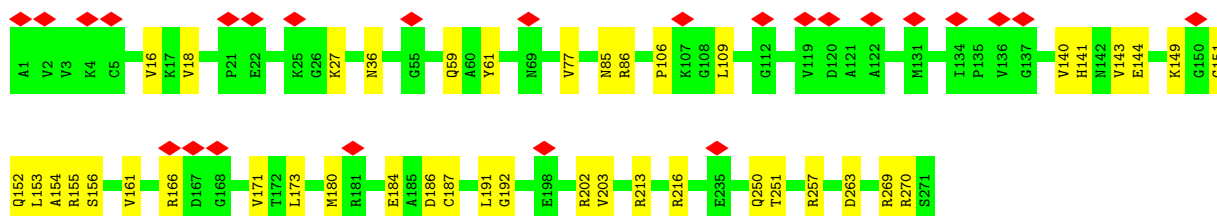
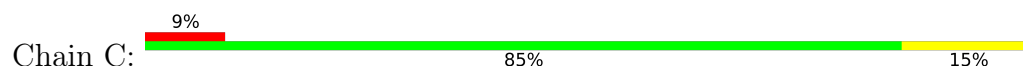
28%



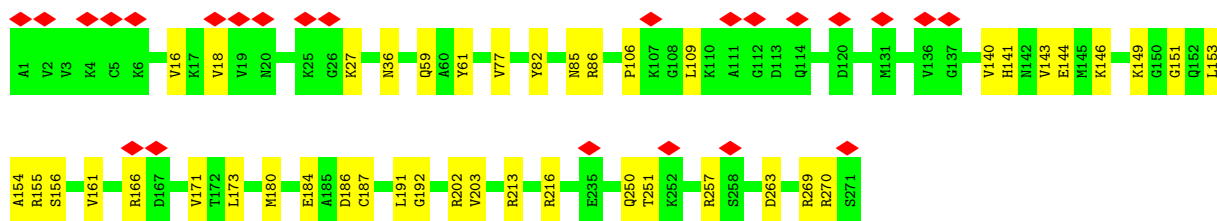
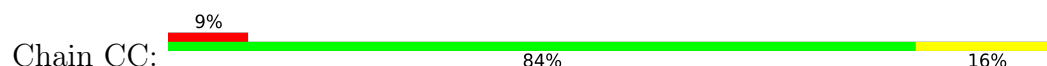
- Molecule 8: 5S ribosomal RNA



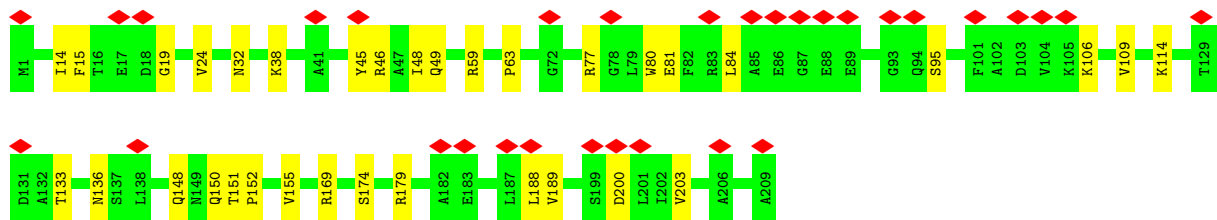
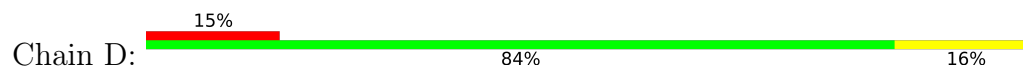
- Molecule 9: 50S ribosomal protein L2



- Molecule 9: 50S ribosomal protein L2

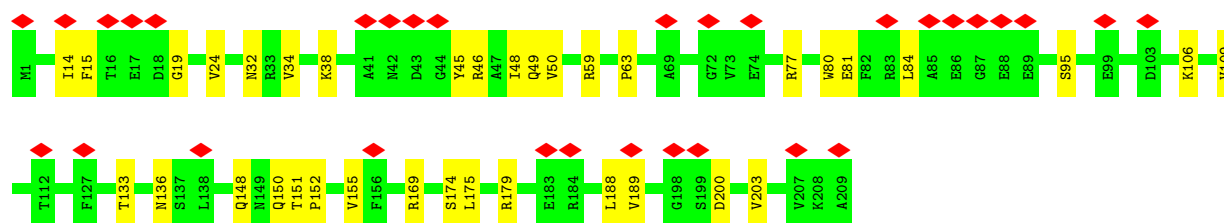


- Molecule 10: 50S ribosomal protein L3



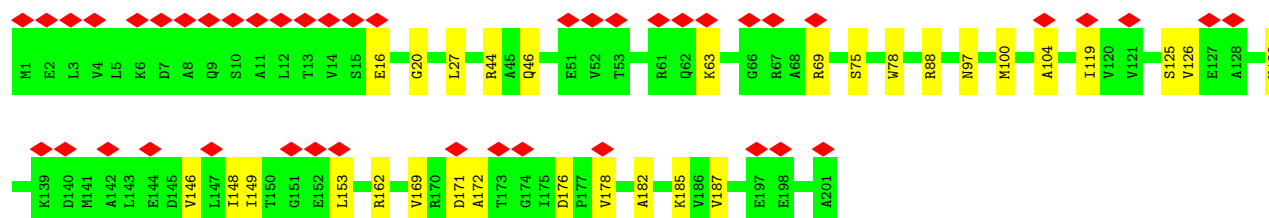
- Molecule 10: 50S ribosomal protein L3

Chain DD: 



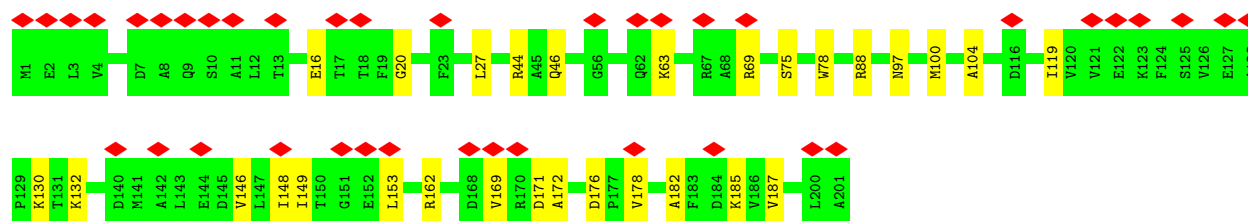
- Molecule 11: 50S ribosomal protein L4

Chain E: 



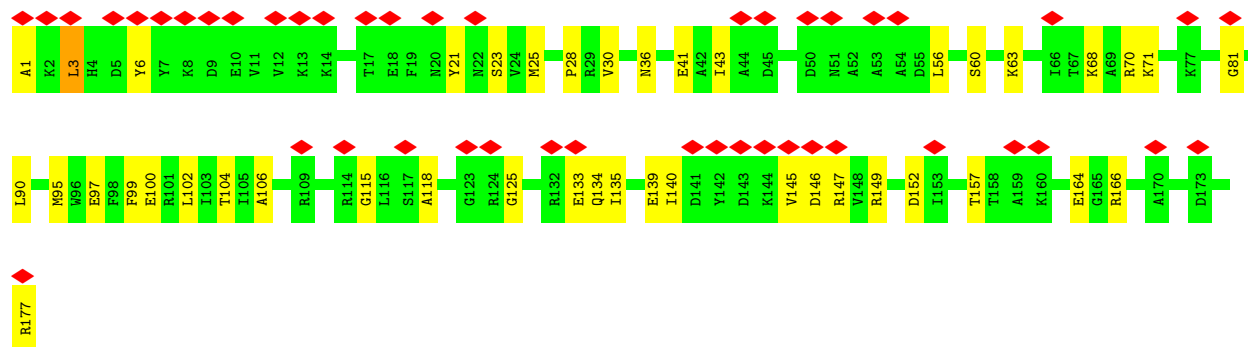
- Molecule 11: 50S ribosomal protein L4

Chain EE: 



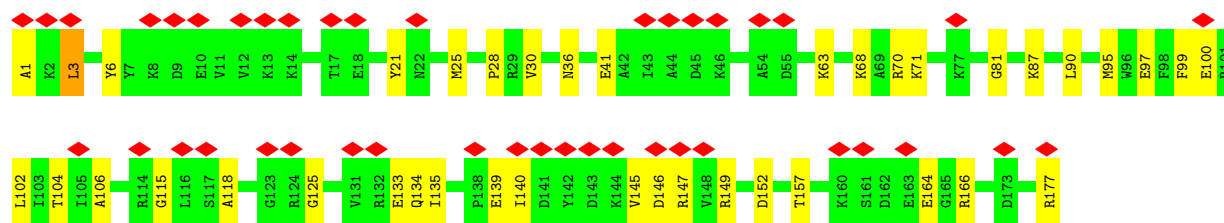
- Molecule 12: 50S ribosomal protein L5

Chain F: 

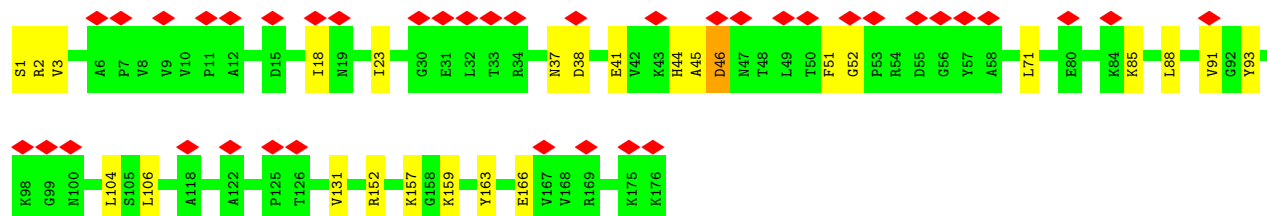
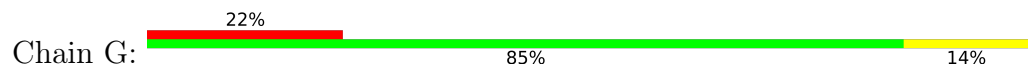


- Molecule 12: 50S ribosomal protein L5

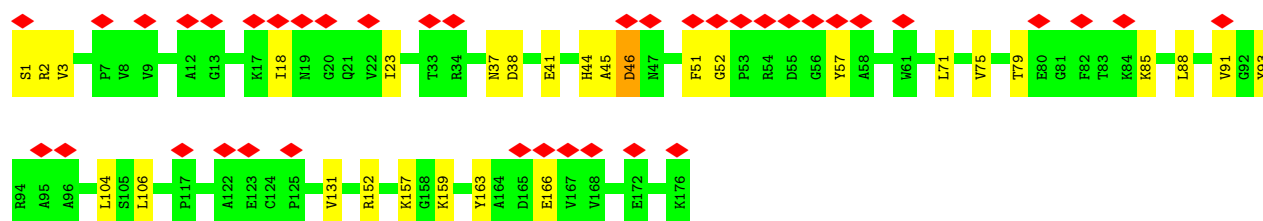
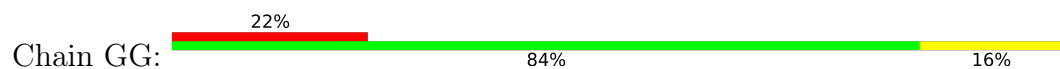
Chain FF: 



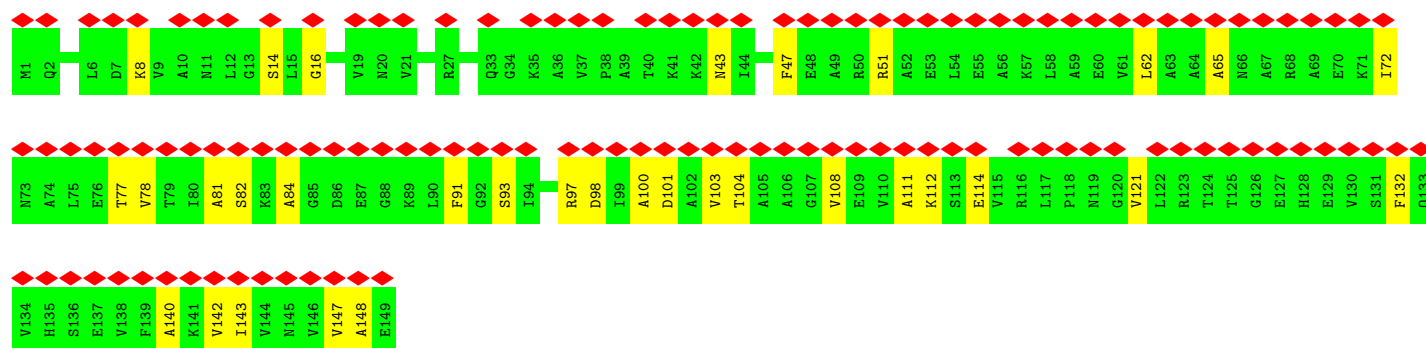
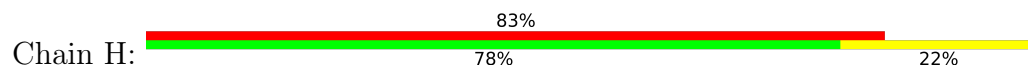
• Molecule 13: 50S ribosomal protein L6



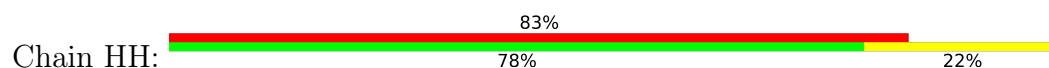
• Molecule 13: 50S ribosomal protein L6

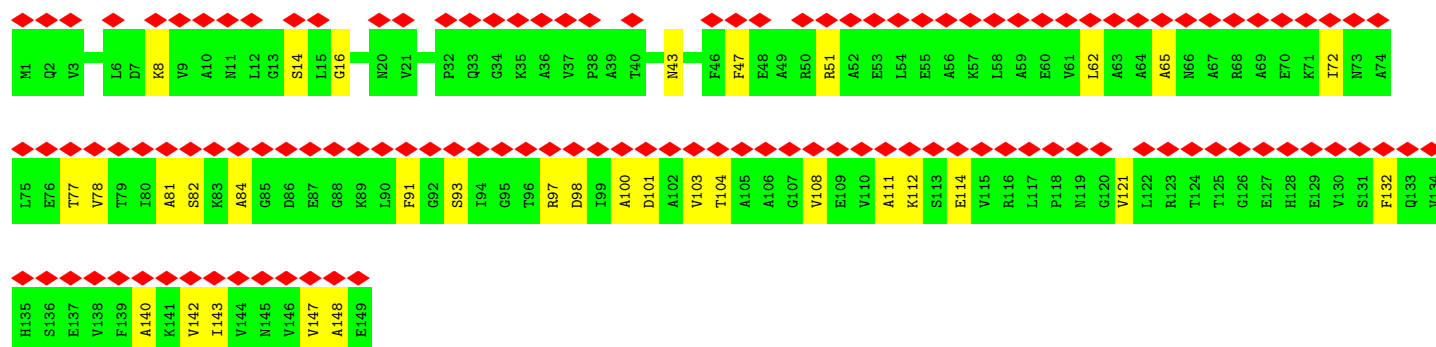


• Molecule 14: 50S ribosomal protein L9

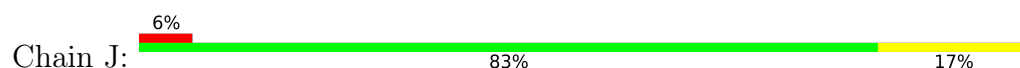


• Molecule 14: 50S ribosomal protein L9

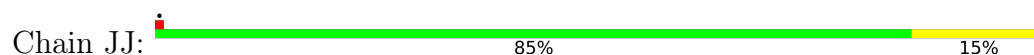




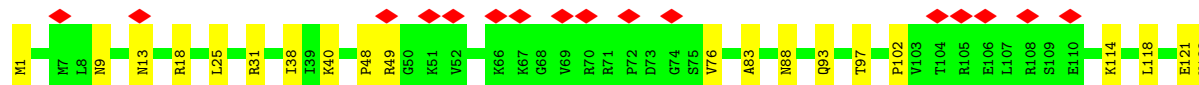
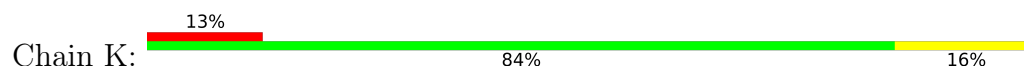
• Molecule 15: 50S ribosomal protein L13



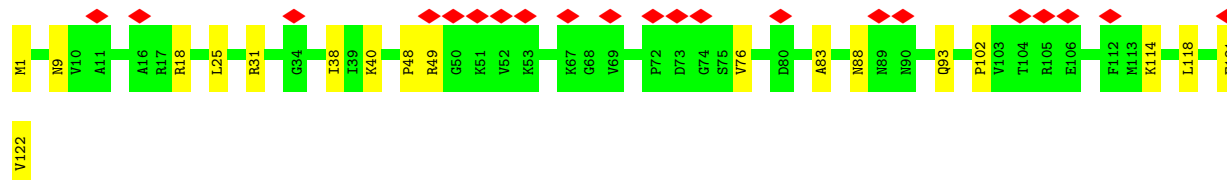
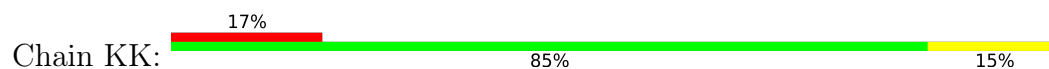
• Molecule 15: 50S ribosomal protein L13



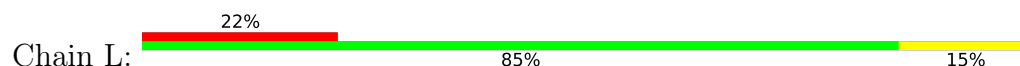
• Molecule 16: 50S ribosomal protein L14

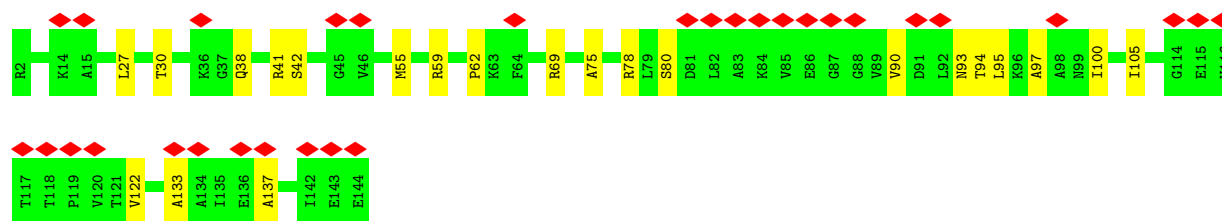


• Molecule 16: 50S ribosomal protein L14

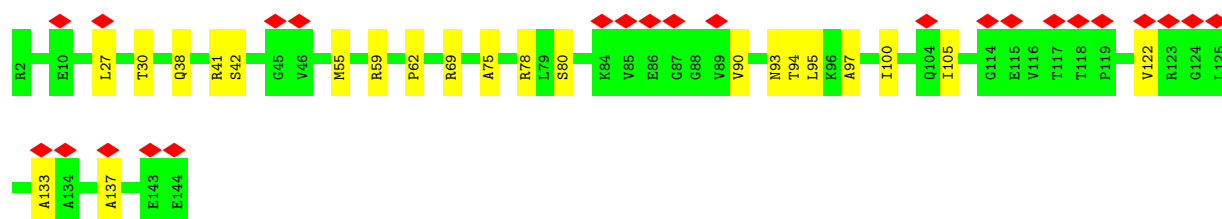
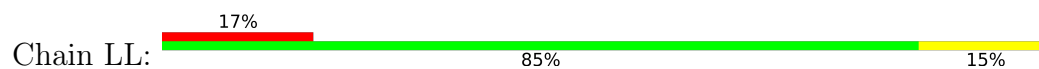


• Molecule 17: 50S ribosomal protein L15

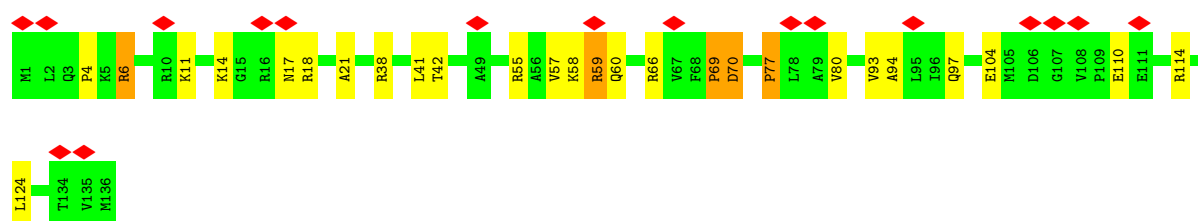
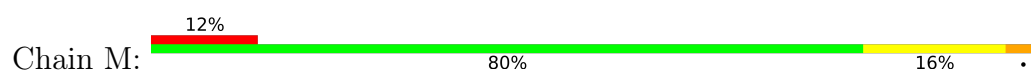




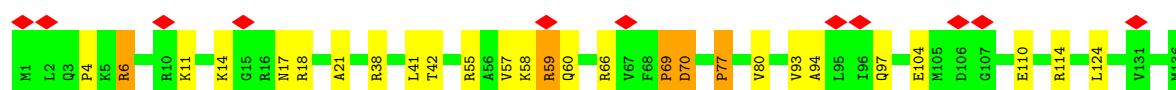
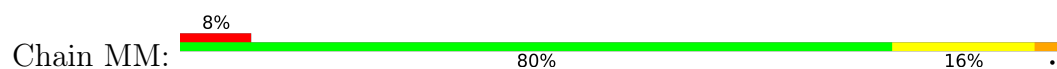
- Molecule 17: 50S ribosomal protein L15



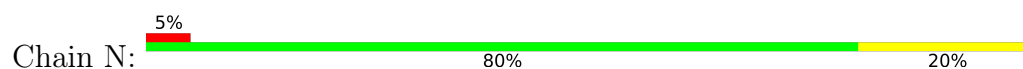
- Molecule 18: 50S ribosomal protein L16



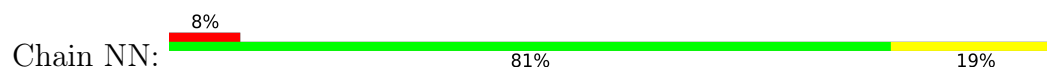
- Molecule 18: 50S ribosomal protein L16



- Molecule 19: 50S ribosomal protein L17

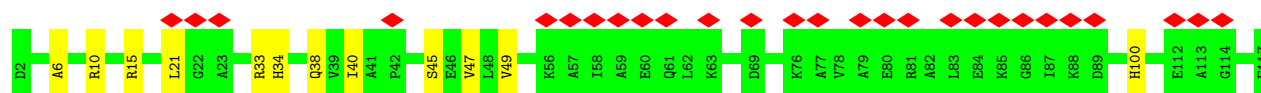
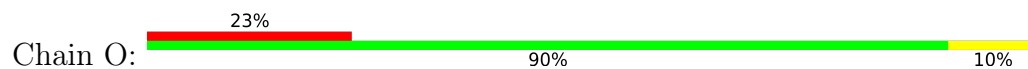


- Molecule 19: 50S ribosomal protein L17

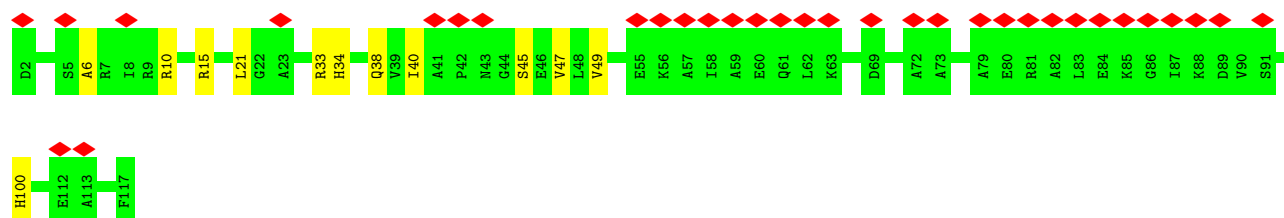
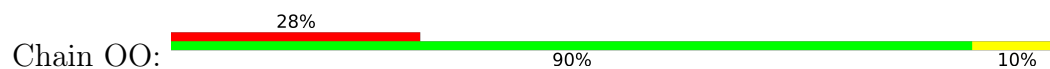




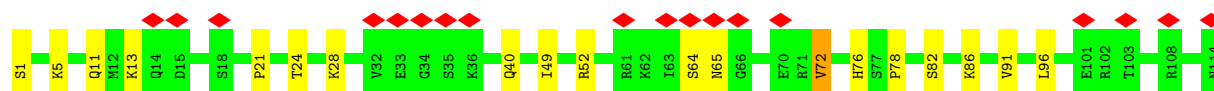
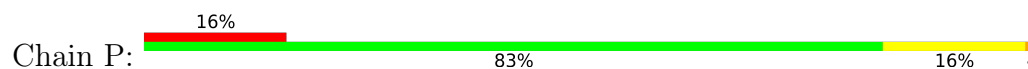
- Molecule 20: 50S ribosomal protein L18



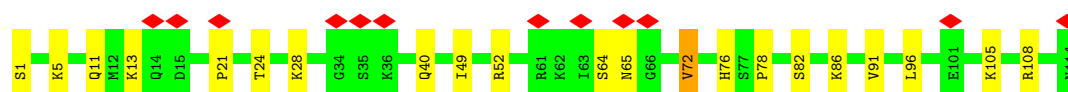
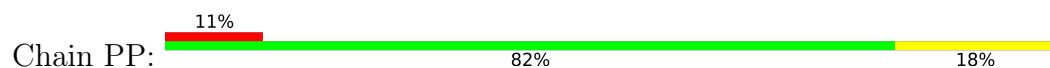
- Molecule 20: 50S ribosomal protein L18



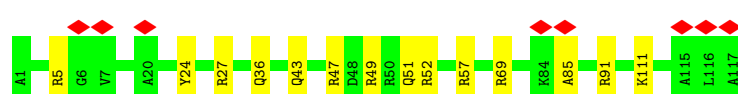
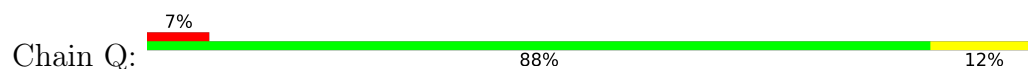
- Molecule 21: 50S ribosomal protein L19



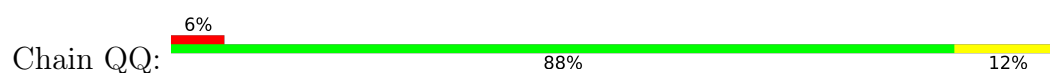
- Molecule 21: 50S ribosomal protein L19



- Molecule 22: 50S ribosomal protein L20

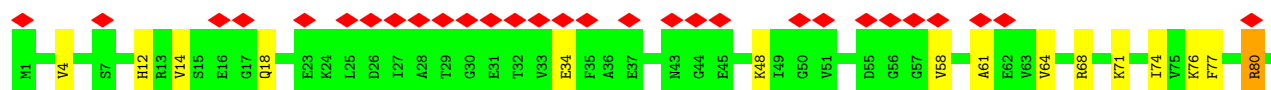
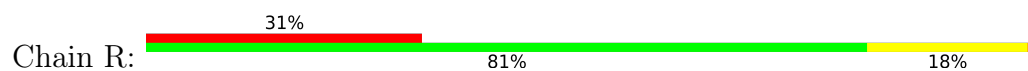


- Molecule 22: 50S ribosomal protein L20

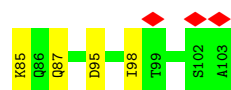
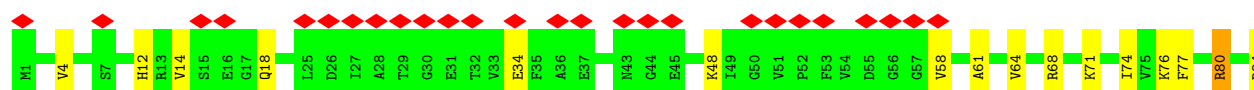
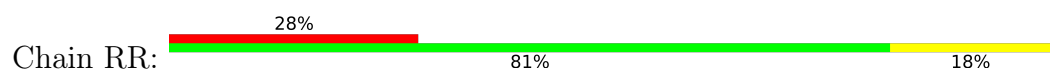




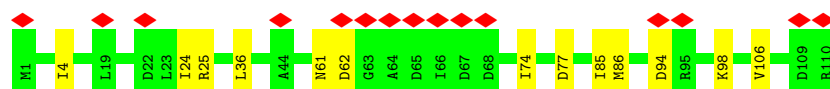
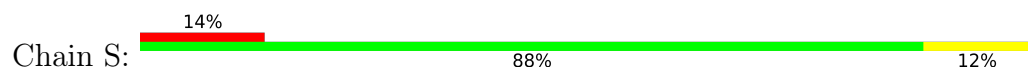
- Molecule 23: 50S ribosomal protein L21



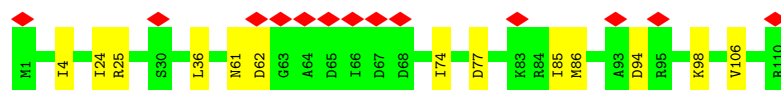
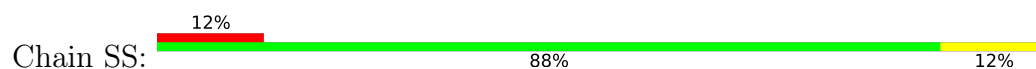
- Molecule 23: 50S ribosomal protein L21



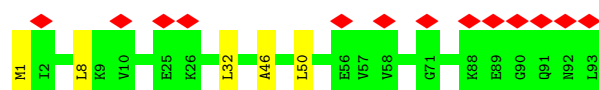
- Molecule 24: 50S ribosomal protein L22



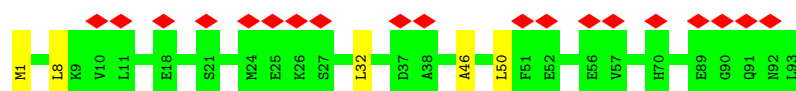
- Molecule 24: 50S ribosomal protein L22



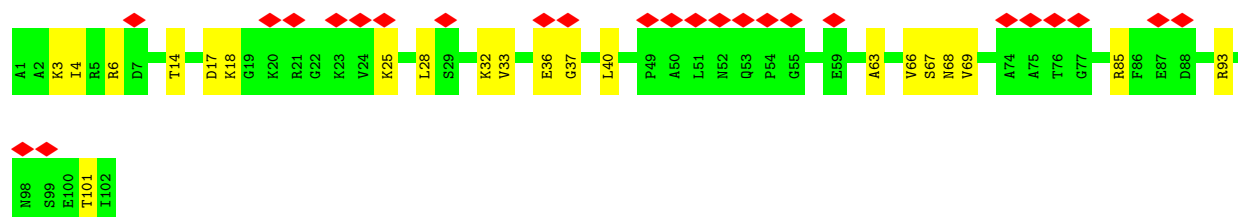
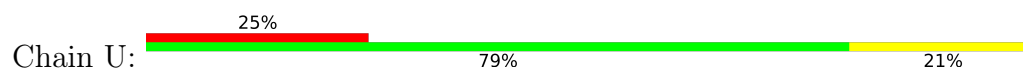
- Molecule 25: 50S ribosomal protein L23



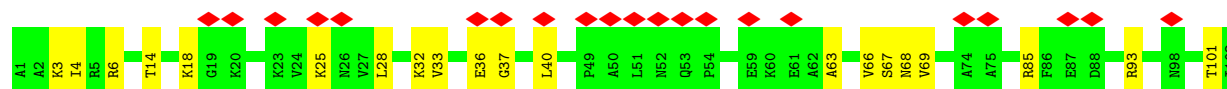
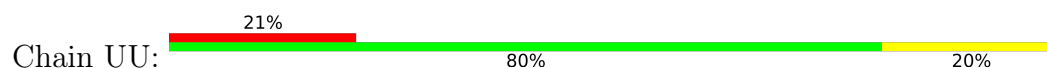
- Molecule 25: 50S ribosomal protein L23



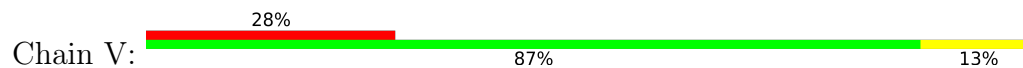
- Molecule 26: 50S ribosomal protein L24



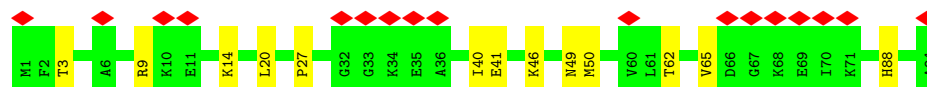
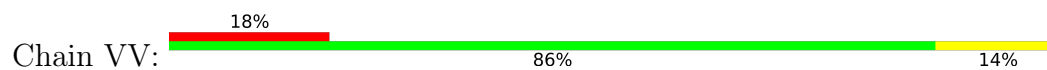
- Molecule 26: 50S ribosomal protein L24



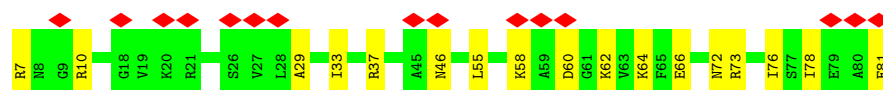
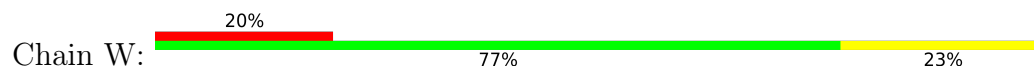
- Molecule 27: 50S ribosomal protein L25



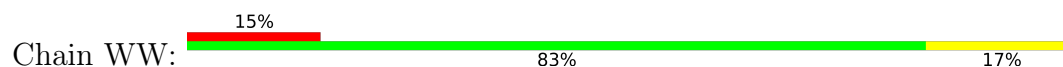
- Molecule 27: 50S ribosomal protein L25

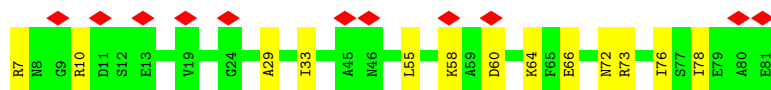


- Molecule 28: 50S ribosomal protein L27

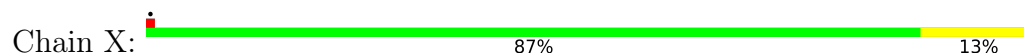


- Molecule 28: 50S ribosomal protein L27

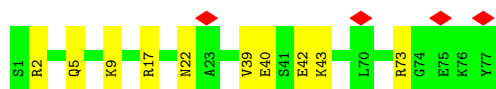




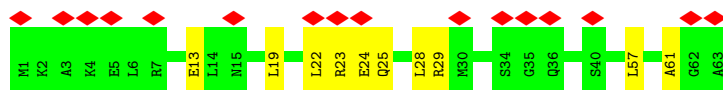
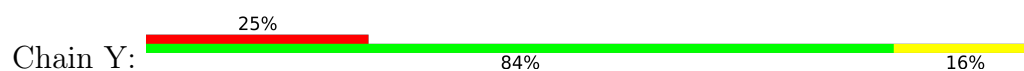
- Molecule 29: 50S ribosomal protein L28



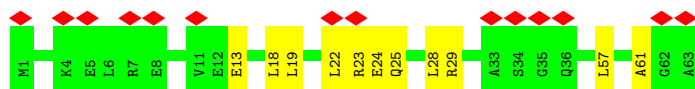
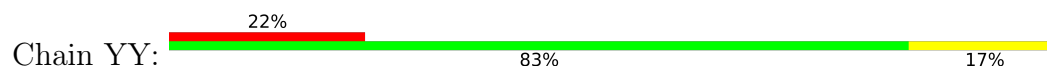
- Molecule 29: 50S ribosomal protein L28



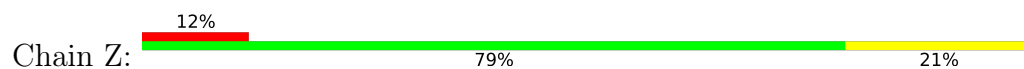
- Molecule 30: 50S ribosomal protein L29



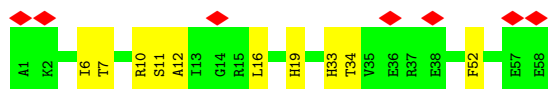
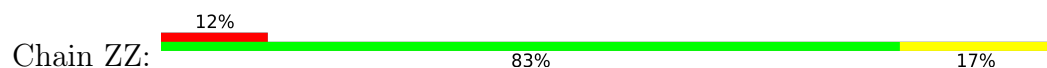
- Molecule 30: 50S ribosomal protein L29



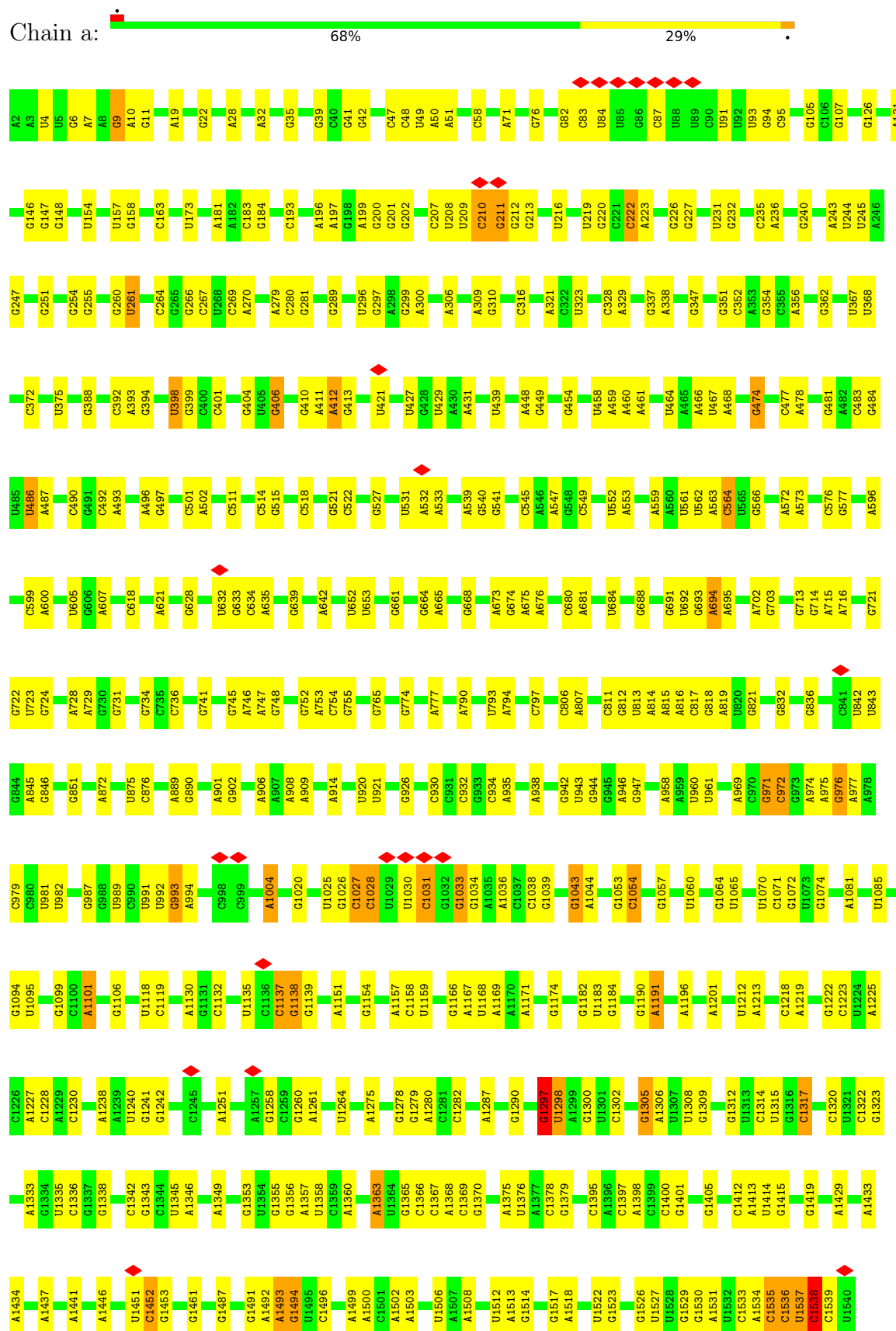
- Molecule 31: 50S ribosomal protein L30



- Molecule 31: 50S ribosomal protein L30

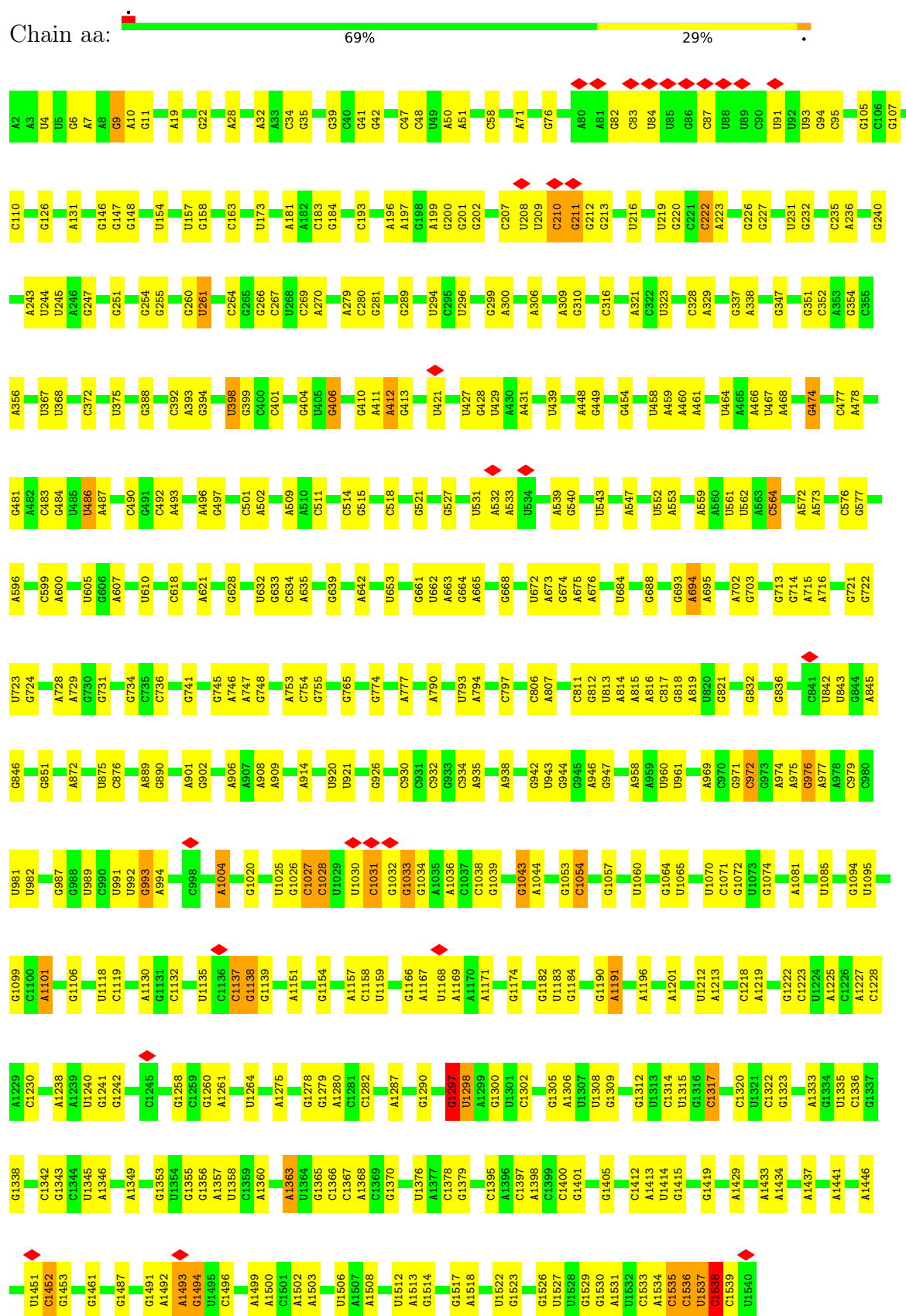


- Molecule 32: 16S ribosomal RNA

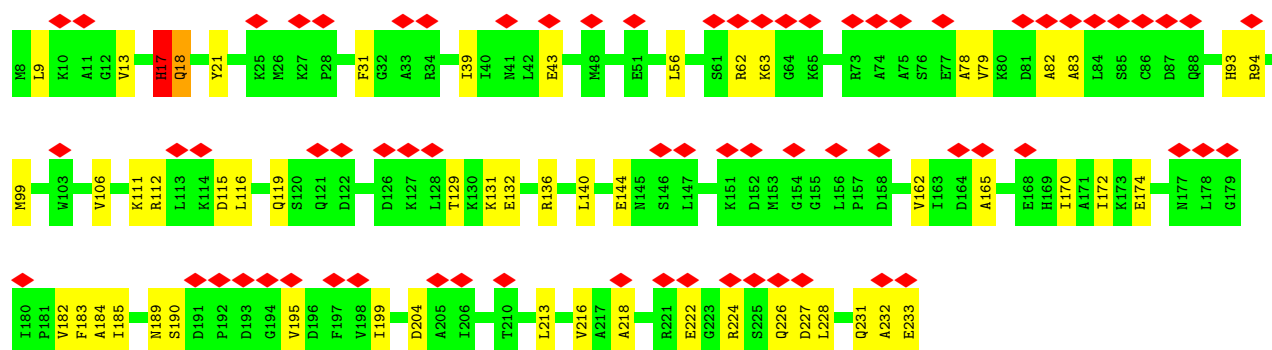
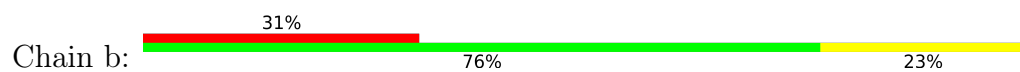


• Molecule 32: 16S ribosomal RNA

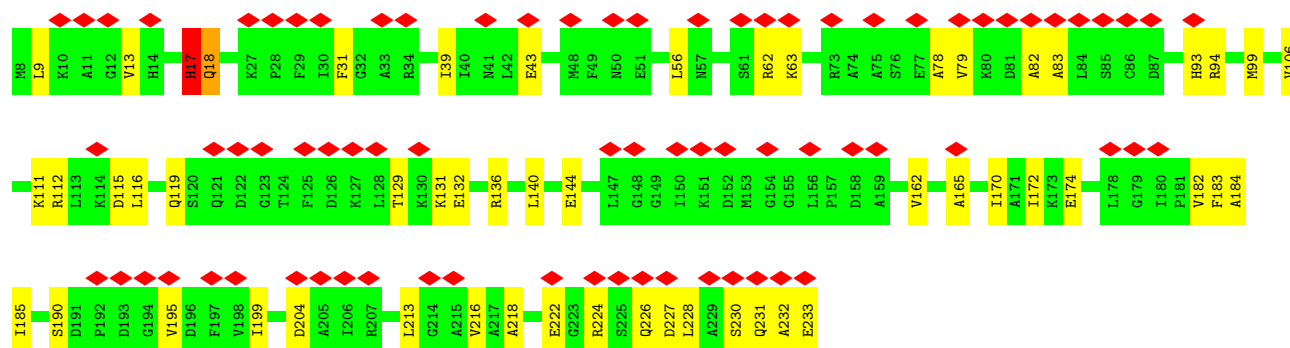
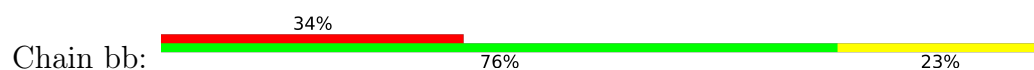
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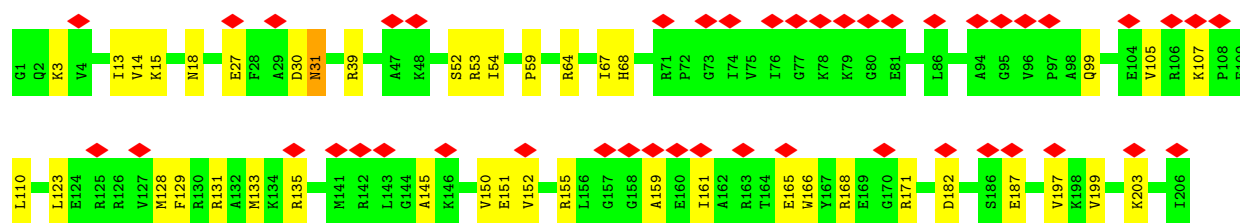
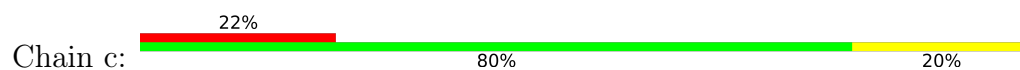
- Molecule 33: 30S ribosomal protein S2



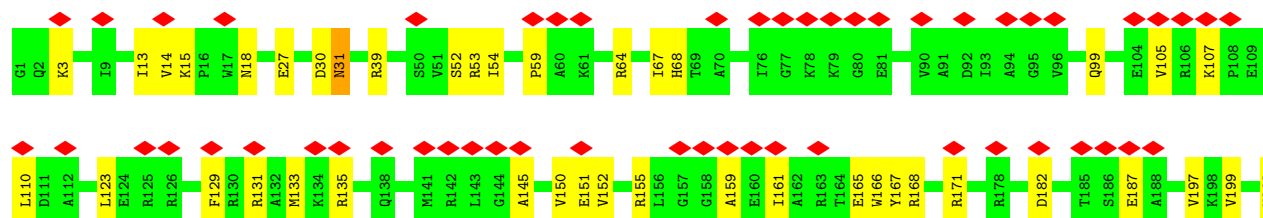
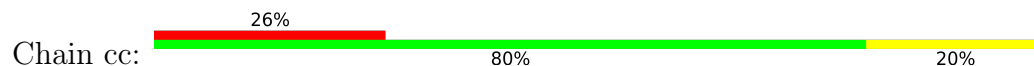
• Molecule 33: 30S ribosomal protein S2



• Molecule 34: 30S ribosomal protein S3

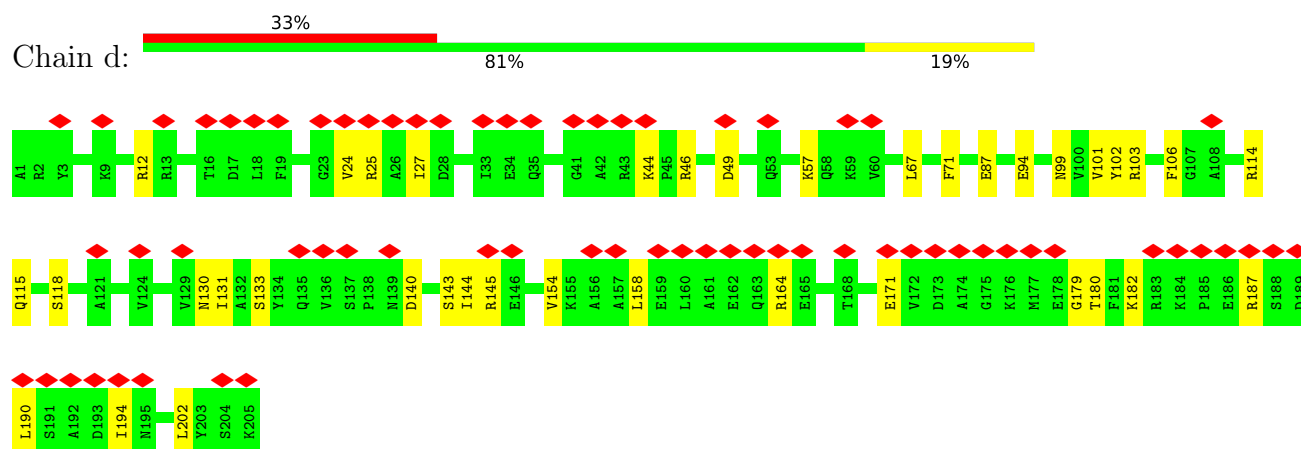


• Molecule 34: 30S ribosomal protein S3

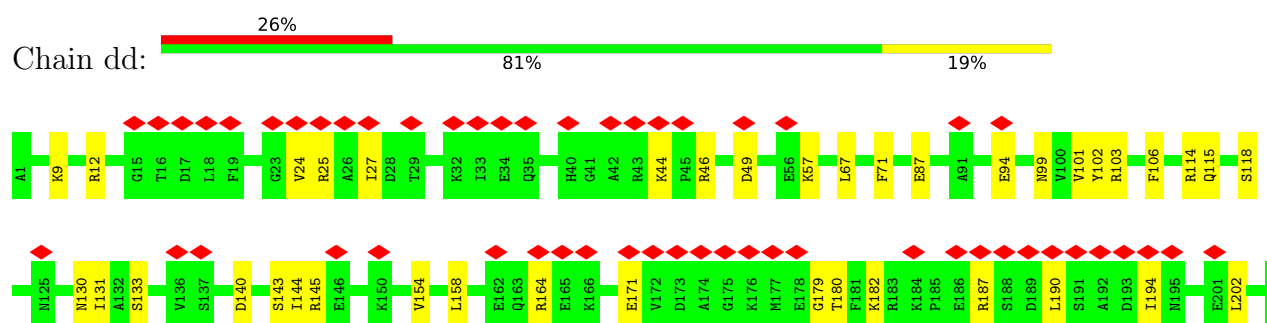




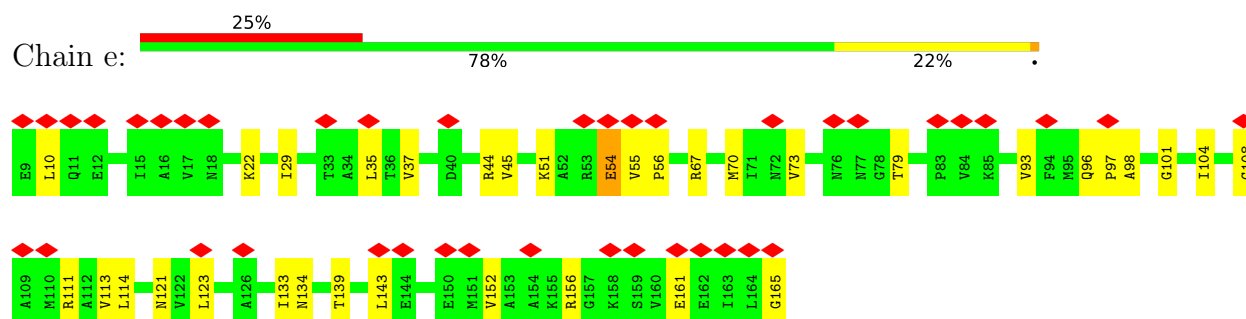
- Molecule 35: 30S ribosomal protein S4



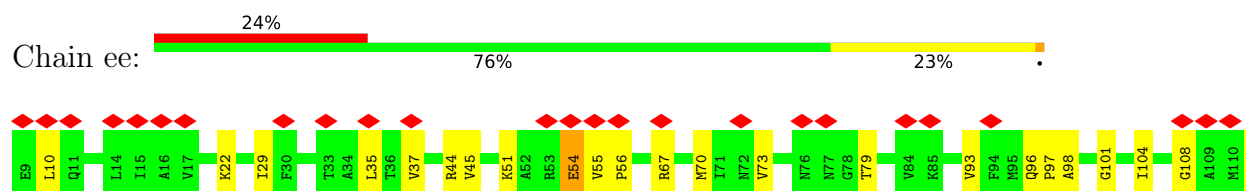
- Molecule 35: 30S ribosomal protein S4

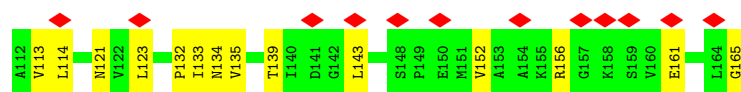


- Molecule 36: 30S ribosomal protein S5

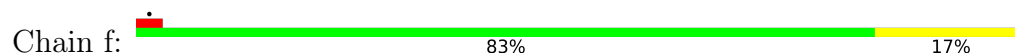


- Molecule 36: 30S ribosomal protein S5

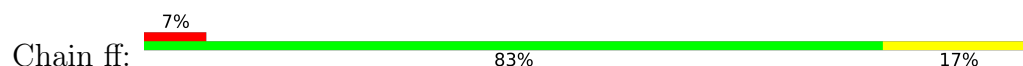




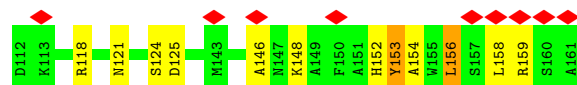
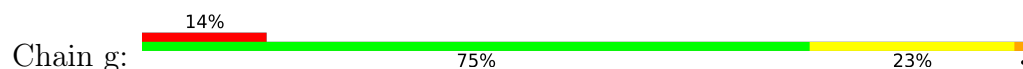
- Molecule 37: 30S ribosomal protein S6



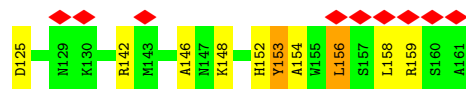
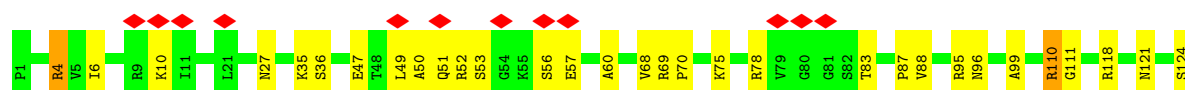
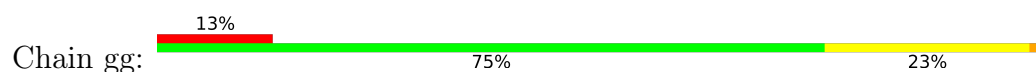
- Molecule 37: 30S ribosomal protein S6



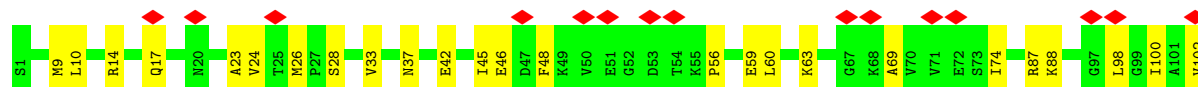
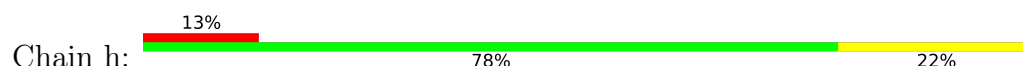
- Molecule 38: 30S ribosomal protein S7

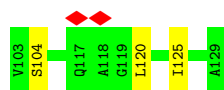


- Molecule 38: 30S ribosomal protein S7

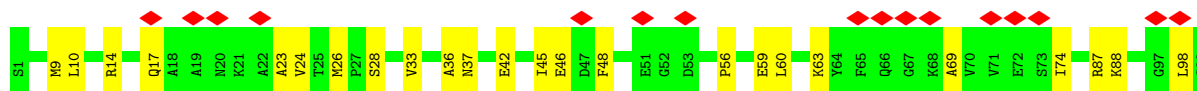
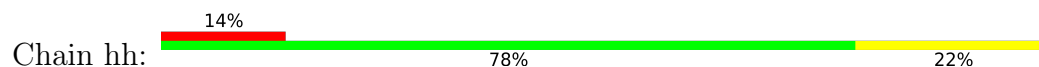


- Molecule 39: 30S ribosomal protein S8

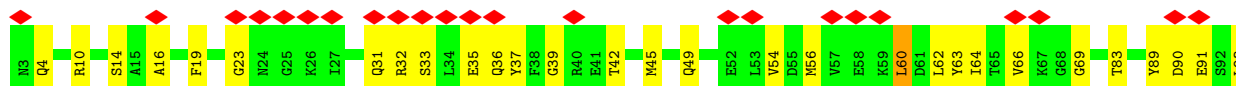




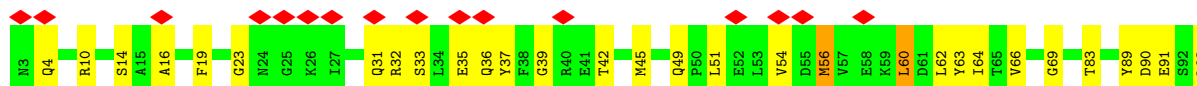
- Molecule 39: 30S ribosomal protein S8



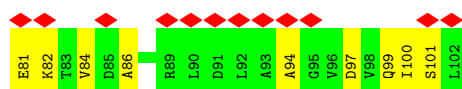
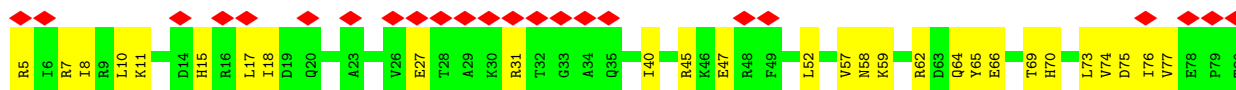
- Molecule 40: 30S ribosomal protein S9



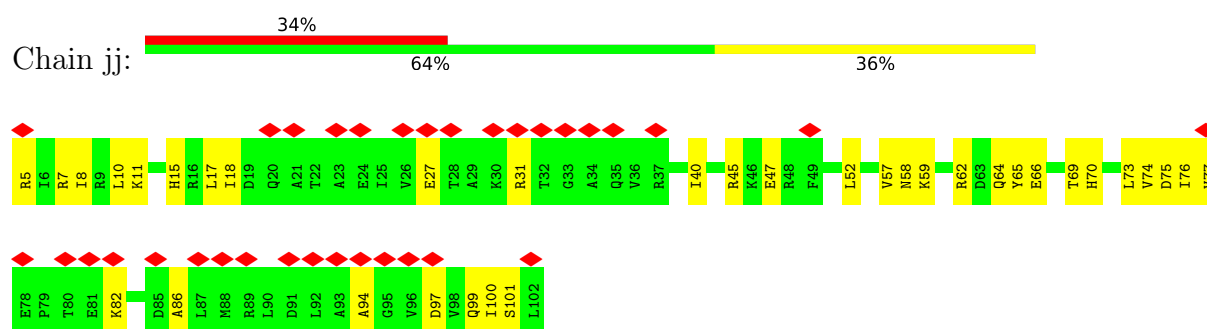
- Molecule 40: 30S ribosomal protein S9



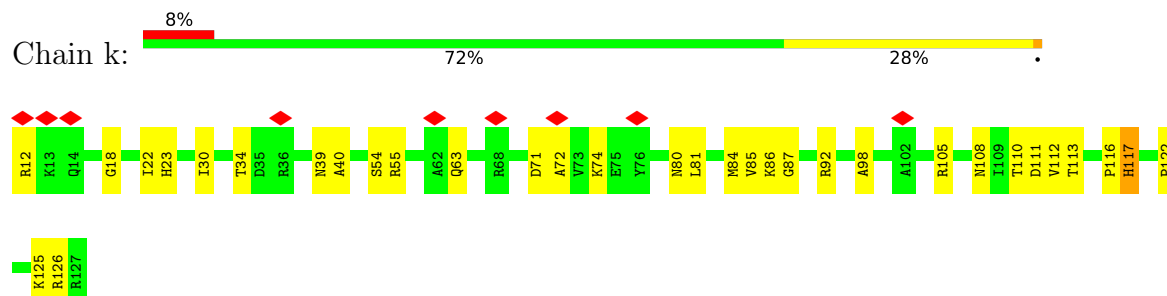
- Molecule 41: 30S ribosomal protein S10



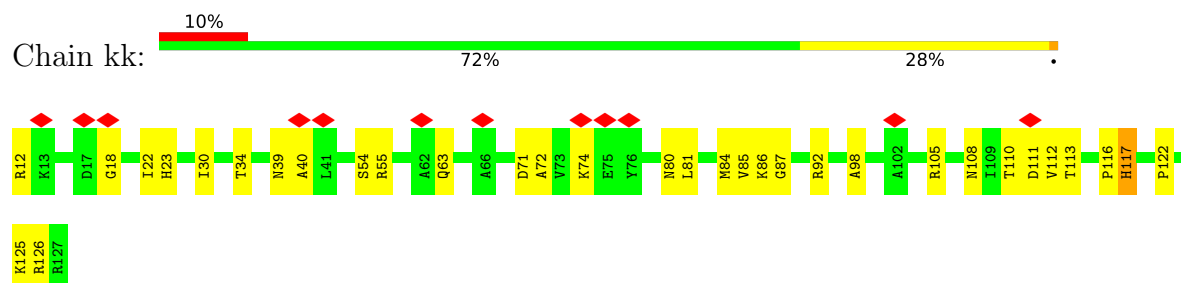
- Molecule 41: 30S ribosomal protein S10



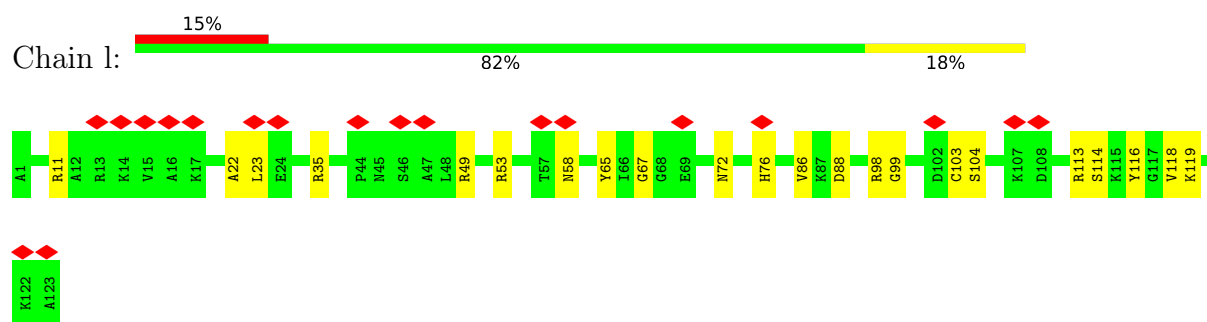
- Molecule 42: 30S ribosomal protein S11



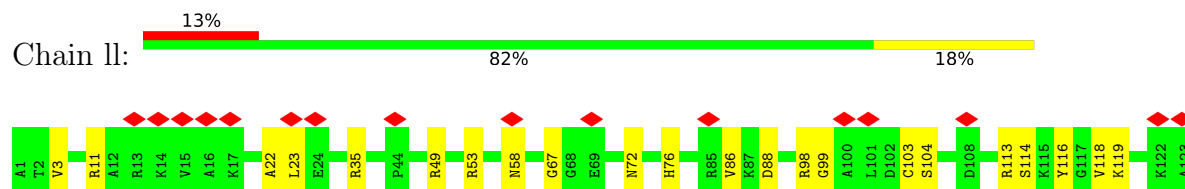
- Molecule 42: 30S ribosomal protein S11



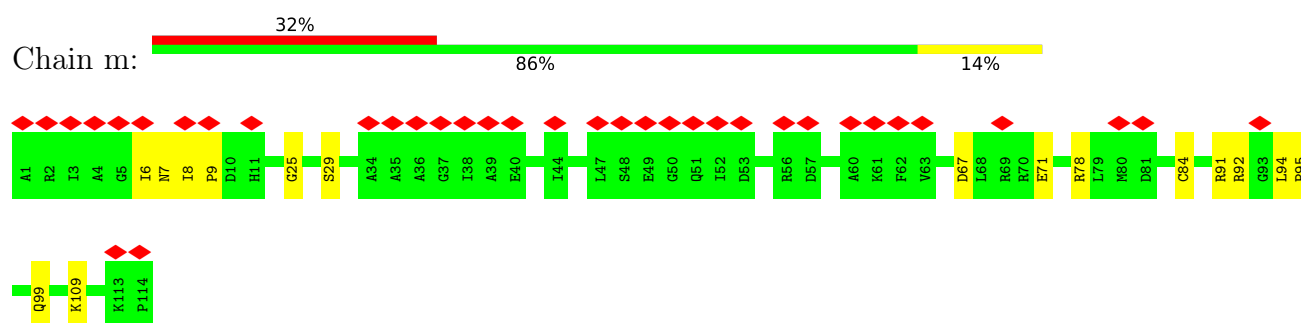
- Molecule 43: 30S ribosomal protein S12



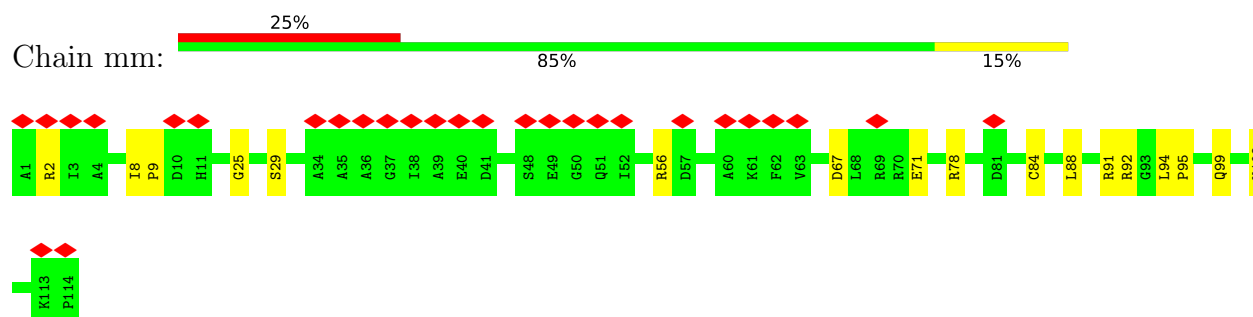
- Molecule 43: 30S ribosomal protein S12



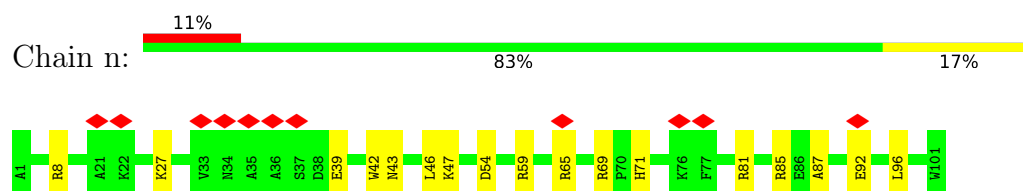
- Molecule 44: 30S ribosomal protein S13



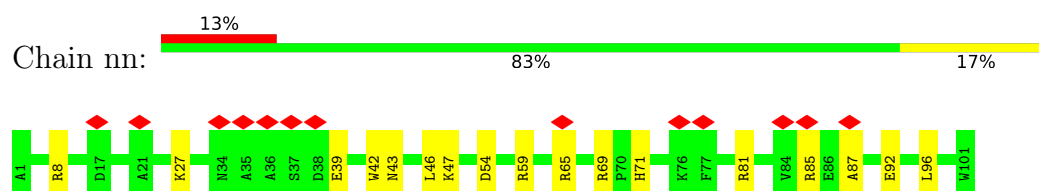
- Molecule 44: 30S ribosomal protein S13



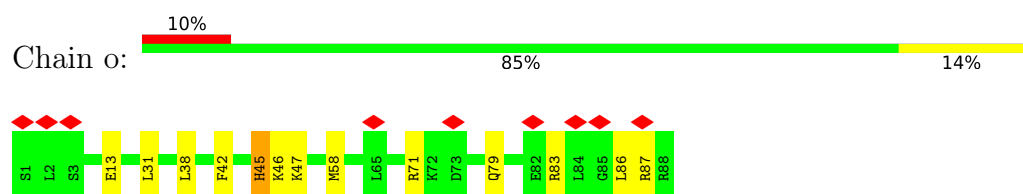
- Molecule 45: 30S ribosomal protein S14



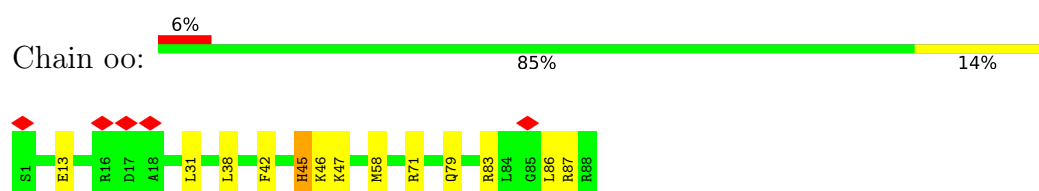
- Molecule 45: 30S ribosomal protein S14



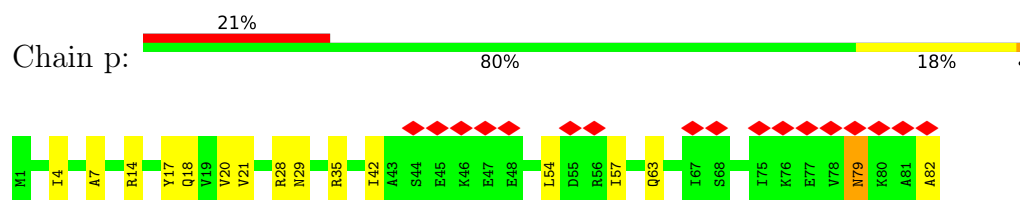
- Molecule 46: 30S ribosomal protein S15



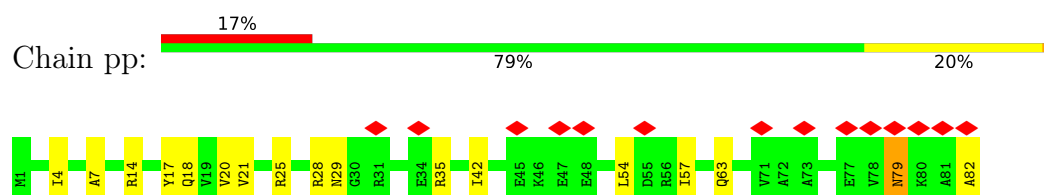
- Molecule 46: 30S ribosomal protein S15



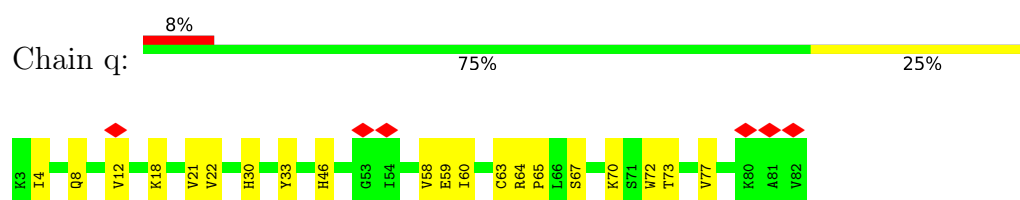
- Molecule 47: 30S ribosomal protein S16



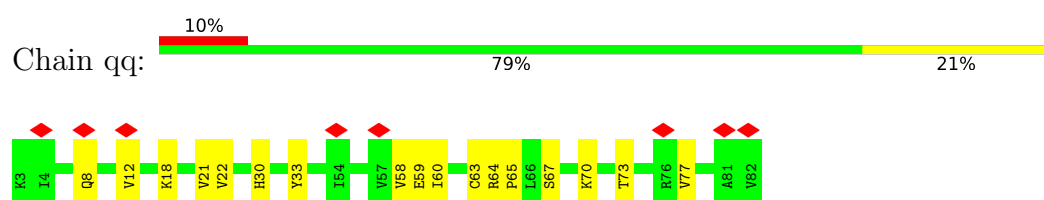
- Molecule 47: 30S ribosomal protein S16



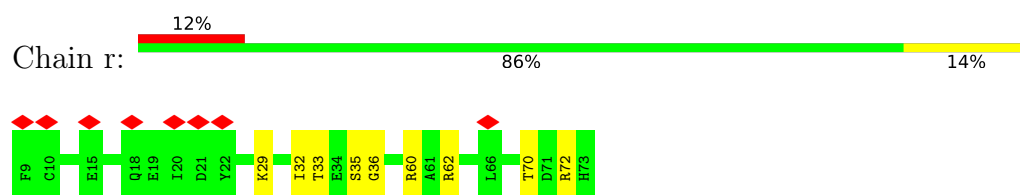
- Molecule 48: 30S ribosomal protein S17



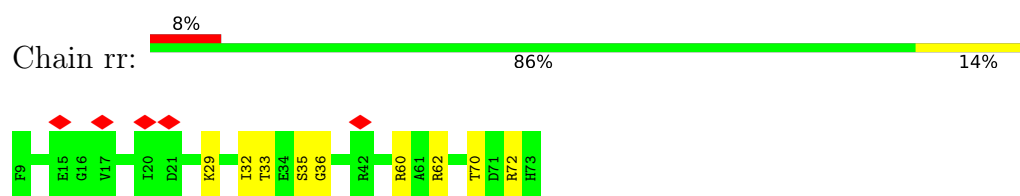
- Molecule 48: 30S ribosomal protein S17



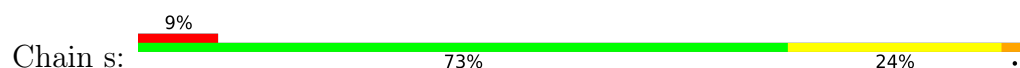
- Molecule 49: 30S ribosomal protein S18

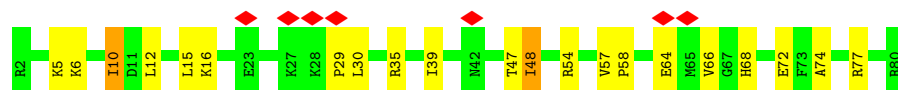


- Molecule 49: 30S ribosomal protein S18

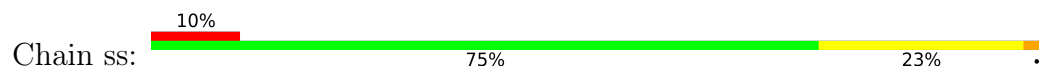


- Molecule 50: 30S ribosomal protein S19

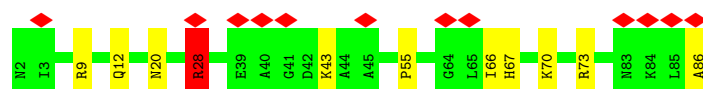
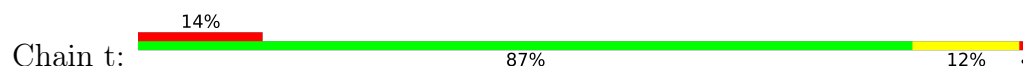




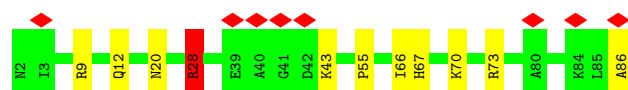
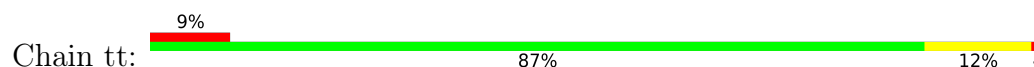
- Molecule 50: 30S ribosomal protein S19



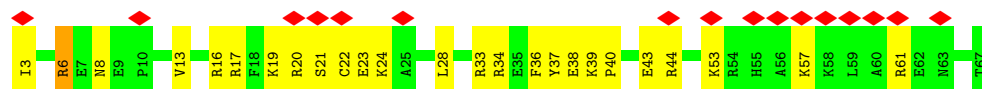
- Molecule 51: 30S ribosomal protein S20



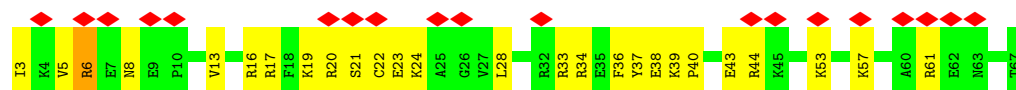
- Molecule 51: 30S ribosomal protein S20



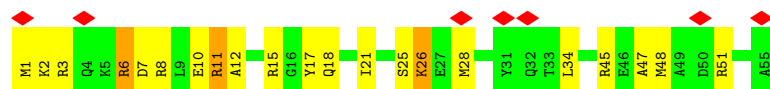
- Molecule 52: 30S ribosomal protein S21



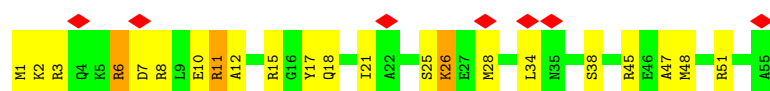
- Molecule 52: 30S ribosomal protein S21



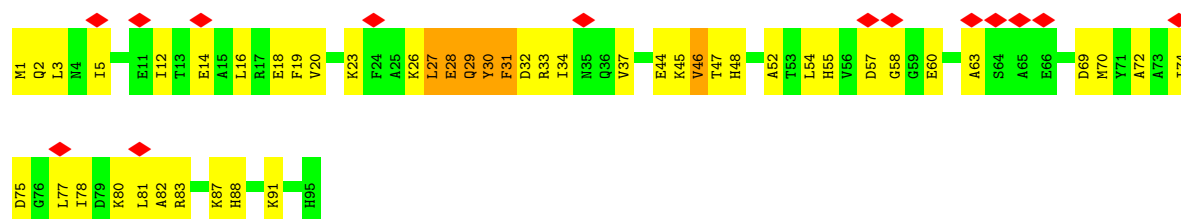
- Molecule 53: Ribosome modulation factor



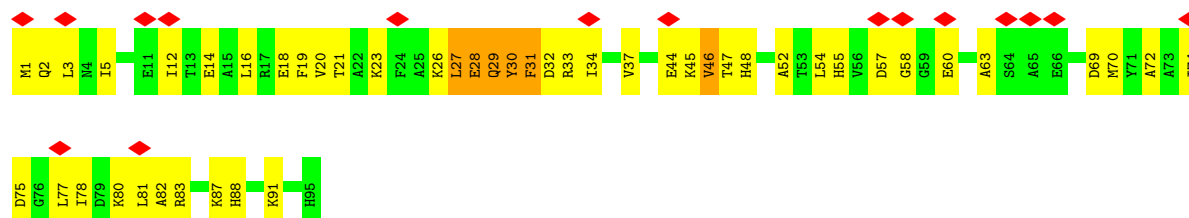
- Molecule 53: Ribosome modulation factor



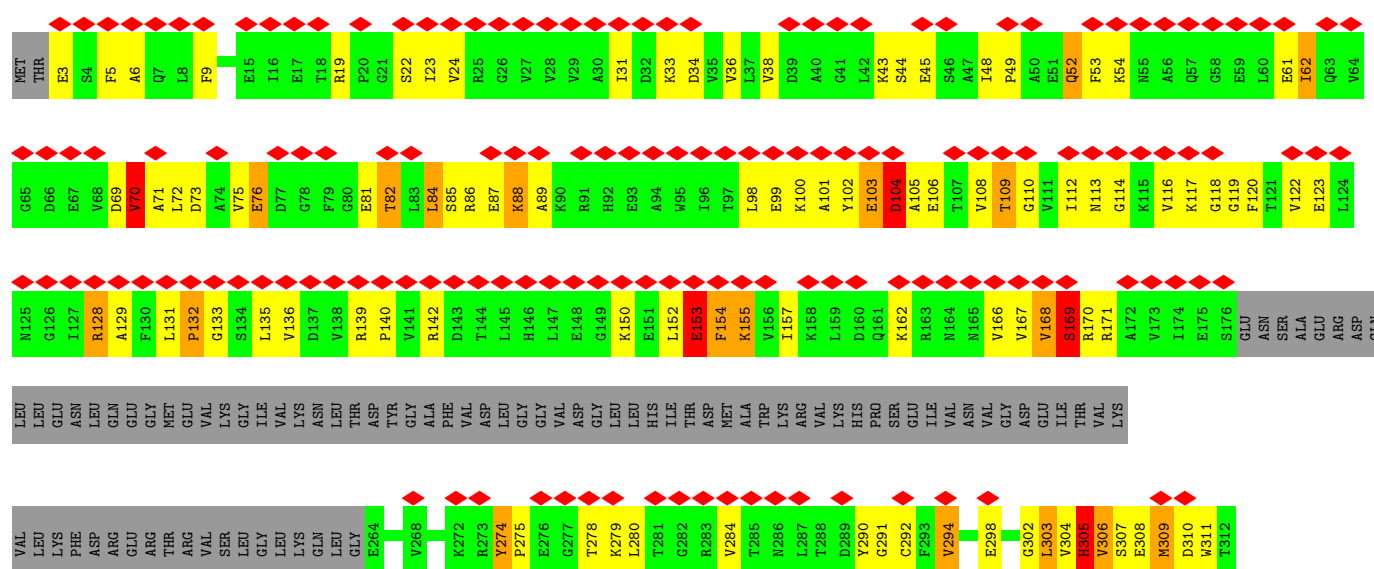
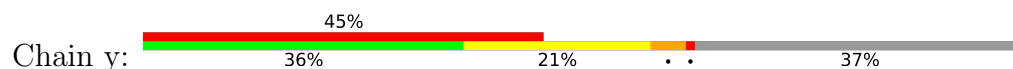
- Molecule 54: Ribosome hibernation promoting factor



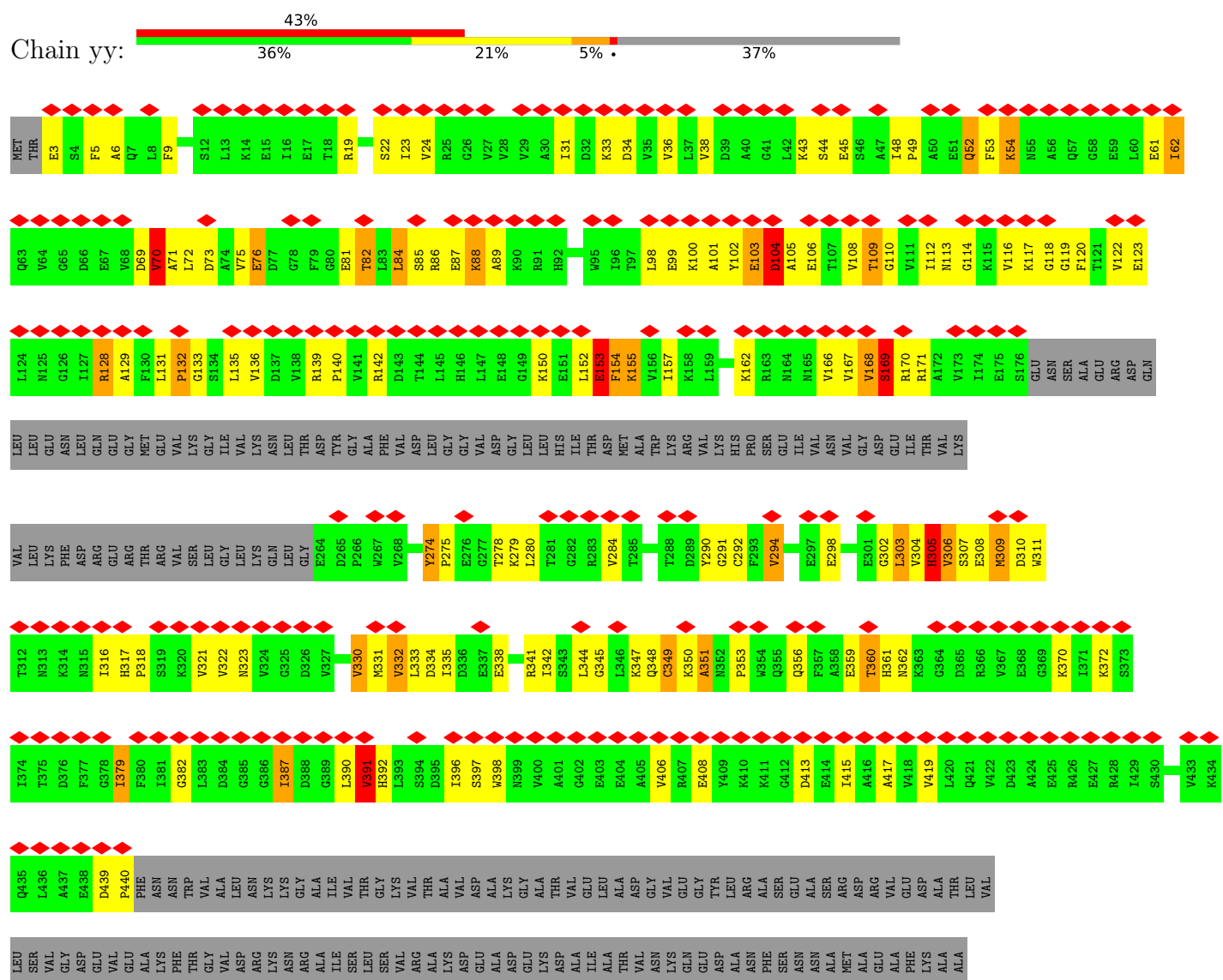
- Molecule 54: Ribosome hibernation promoting factor



- Molecule 55: 30S ribosomal protein S1

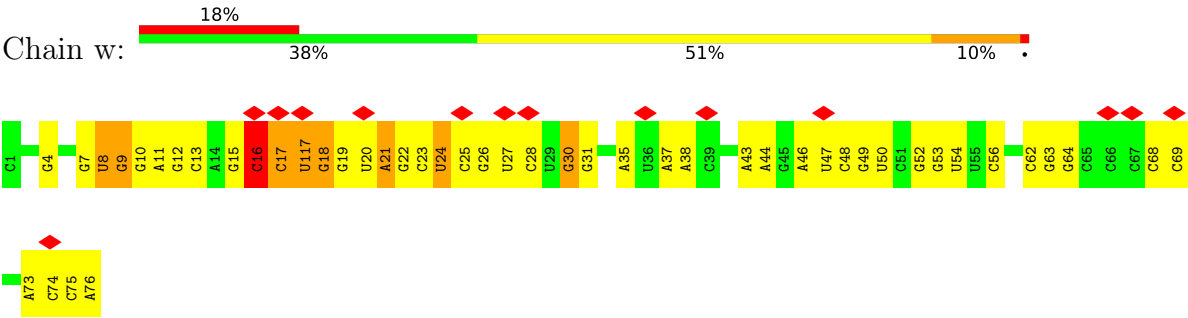


- Molecule 55: 30S ribosomal protein S1

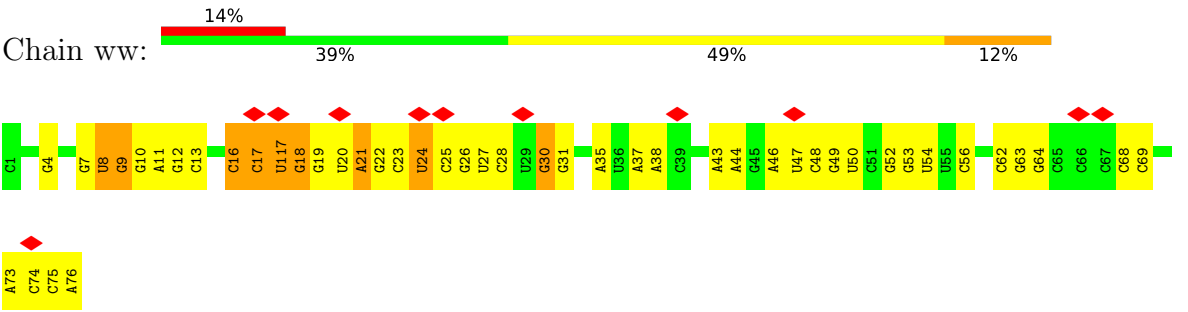


LYS
GLY
GLU

● Molecule 56: tRNA Mixture



● Molecule 56: tRNA Mixture



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	18000	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 ($e^-/\text{\AA}^2$)	1.15	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	0.312	Depositor
Minimum map value	-0.097	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.019	Depositor
Recommended contour level	0.075	Depositor
Map size (Å)	615.60004, 615.60004, 615.60004	wwPDB
Map dimensions	228, 228, 228	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.7, 2.7, 2.7	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	0	0.35	0/450	0.61	0/599
1	00	0.34	0/450	0.60	0/599
2	1	0.31	0/416	0.54	0/554
2	11	0.31	0/416	0.54	0/554
3	2	0.40	0/380	0.62	0/498
3	22	0.40	0/380	0.62	0/498
4	3	0.40	0/513	0.71	0/676
4	33	0.40	0/513	0.71	0/676
5	4	0.39	0/303	0.60	0/397
5	44	0.39	0/303	0.60	0/397
6	6	0.27	0/531	0.60	0/709
6	66	0.27	0/531	0.60	0/709
7	A	0.38	0/69733	0.41	1/108786 (0.0%)
7	AA	0.38	0/69733	0.41	0/108786
8	B	0.33	0/2876	0.39	0/4483
8	BB	0.33	0/2876	0.39	0/4483
9	C	0.42	0/2121	0.63	0/2852
9	CC	0.42	0/2121	0.63	0/2852
10	D	0.38	0/1586	0.60	0/2134
10	DD	0.38	0/1586	0.59	0/2134
11	E	0.32	0/1571	0.54	0/2113
11	EE	0.32	0/1571	0.54	0/2113
12	F	0.32	0/1434	0.61	0/1926
12	FF	0.32	0/1434	0.61	0/1926
13	G	0.27	0/1343	0.55	0/1816
13	GG	0.27	0/1343	0.55	0/1816
14	H	0.24	0/1122	0.56	0/1515
14	HH	0.24	0/1122	0.56	0/1515
15	J	0.37	0/1152	0.55	0/1551
15	JJ	0.37	0/1152	0.55	0/1551
16	K	0.36	0/947	0.66	0/1268
16	KK	0.36	0/947	0.66	0/1268
17	L	0.38	0/1054	0.73	2/1403 (0.1%)
17	LL	0.38	0/1054	0.73	2/1403 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
18	M	0.36	0/1093	0.66	3/1460 (0.2%)
18	MM	0.36	0/1093	0.66	3/1460 (0.2%)
19	N	0.38	0/973	0.75	0/1301
19	NN	0.38	0/973	0.75	0/1301
20	O	0.31	0/902	0.58	0/1209
20	OO	0.30	0/902	0.58	0/1209
21	P	0.36	0/929	0.59	0/1242
21	PP	0.36	0/929	0.59	0/1242
22	Q	0.39	0/960	0.57	0/1278
22	QQ	0.39	0/960	0.57	0/1278
23	R	0.36	0/829	0.60	0/1107
23	RR	0.36	0/829	0.60	0/1107
24	S	0.39	0/864	0.61	0/1156
24	SS	0.39	0/864	0.61	0/1156
25	T	0.31	0/744	0.60	0/994
25	TT	0.31	0/744	0.61	0/994
26	U	0.29	0/787	0.60	0/1051
26	UU	0.29	0/787	0.60	0/1051
27	V	0.34	0/766	0.60	0/1025
27	VV	0.34	0/766	0.60	0/1025
28	W	0.39	0/582	0.56	0/769
28	WW	0.38	0/582	0.56	0/769
29	X	0.39	0/635	0.56	0/848
29	XX	0.39	0/635	0.56	0/848
30	Y	0.33	0/510	0.59	0/677
30	YY	0.33	0/510	0.58	0/677
31	Z	0.34	0/453	0.54	0/605
31	ZZ	0.34	0/453	0.54	0/605
32	a	0.36	0/36967	0.41	7/57666 (0.0%)
32	aa	0.36	0/36967	0.41	6/57666 (0.0%)
33	b	0.35	0/1795	0.77	4/2418 (0.2%)
33	bb	0.35	0/1795	0.77	4/2418 (0.2%)
34	c	0.35	0/1651	0.60	0/2225
34	cc	0.34	0/1651	0.60	0/2225
35	d	0.33	0/1665	0.71	0/2227
35	dd	0.34	0/1665	0.71	0/2227
36	e	0.36	0/1154	0.74	2/1554 (0.1%)
36	ee	0.36	0/1154	0.74	2/1554 (0.1%)
37	f	0.34	0/835	0.78	2/1128 (0.2%)
37	ff	0.34	0/835	0.78	2/1128 (0.2%)
38	g	0.32	0/1284	0.68	0/1724
38	gg	0.32	0/1284	0.68	0/1724
39	h	0.33	0/989	0.58	0/1326

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
39	hh	0.33	0/989	0.59	0/1326
40	i	0.34	0/1034	0.70	0/1375
40	ii	0.34	0/1034	0.70	0/1375
41	j	0.35	0/796	0.71	3/1077 (0.3%)
41	jj	0.35	0/796	0.71	3/1077 (0.3%)
42	k	0.35	0/885	0.69	0/1195
42	kk	0.35	0/885	0.69	0/1195
43	l	0.37	0/969	0.68	2/1300 (0.2%)
43	ll	0.37	0/969	0.68	2/1300 (0.2%)
44	m	0.30	0/892	0.70	0/1193
44	mm	0.30	0/892	0.70	0/1193
45	n	0.34	0/811	0.61	0/1081
45	nn	0.34	0/811	0.61	0/1081
46	o	0.32	0/722	0.62	0/964
46	oo	0.32	0/722	0.62	0/964
47	p	0.36	0/659	0.60	0/884
47	pp	0.36	0/659	0.60	0/884
48	q	0.32	0/657	0.64	0/881
48	qq	0.32	0/657	0.64	0/881
49	r	0.33	0/511	0.56	0/689
49	rr	0.33	0/511	0.56	0/689
50	s	0.39	1/652 (0.2%)	0.64	0/877
50	ss	0.38	1/652 (0.2%)	0.64	0/877
51	t	0.29	0/671	0.65	2/888 (0.2%)
51	tt	0.29	0/671	0.65	2/888 (0.2%)
52	u	0.42	0/500	0.95	0/668
52	uu	0.43	0/500	0.95	0/668
53	v	0.35	0/460	0.83	1/611 (0.2%)
53	vv	0.35	0/460	0.83	1/611 (0.2%)
54	x	0.38	0/764	0.83	2/1028 (0.2%)
54	xx	0.38	0/764	0.83	2/1028 (0.2%)
55	y	0.69	4/2196 (0.2%)	1.50	43/3006 (1.4%)
55	yy	0.69	4/2196 (0.2%)	1.50	43/3006 (1.4%)
56	w	0.26	0/1833	0.58	3/2851 (0.1%)
56	ww	0.32	2/1834 (0.1%)	0.56	1/2855 (0.0%)
All	All	0.37	12/319823 (0.0%)	0.51	150/477680 (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
4	3	0	1
4	33	0	1
13	G	0	1
13	GG	0	1
18	M	0	1
18	MM	0	1
19	N	0	1
19	NN	0	1
20	O	0	1
20	OO	0	1
33	b	0	1
33	bb	0	1
35	d	0	2
35	dd	0	2
38	g	0	4
38	gg	0	4
40	i	0	1
40	ii	0	1
42	k	0	4
42	kk	0	4
43	l	0	2
43	ll	0	2
44	m	0	1
44	mm	0	1
46	o	0	1
46	oo	0	1
51	t	0	1
51	tt	0	1
52	u	0	3
52	uu	0	3
53	v	0	2
53	vv	0	2
55	y	0	6
55	yy	0	6
All	All	0	66

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	y	169	SER	N-CA	11.72	1.61	1.46
55	yy	169	SER	N-CA	11.71	1.61	1.46
55	y	88	LYS	N-CA	6.97	1.55	1.46
55	yy	88	LYS	N-CA	6.94	1.55	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	y	168	VAL	C-N	6.40	1.42	1.33

The worst 5 of 150 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	yy	88	LYS	CA-C-N	16.97	143.62	120.38
55	yy	88	LYS	C-N-CA	16.97	143.62	120.38
55	y	88	LYS	CA-C-N	16.93	143.57	120.38
55	y	88	LYS	C-N-CA	16.93	143.57	120.38
55	y	332	VAL	N-CA-C	13.74	124.64	110.62

There are no chirality outliers.

5 of 66 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	3	30	HIS	Peptide
13	G	45	ALA	Peptide
18	M	58	LYS	Peptide
19	N	116	VAL	Peptide
20	O	33	ARG	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	444	0	461	7	0
1	00	444	0	461	8	0
2	1	409	0	440	7	0
2	11	409	0	440	7	0
3	2	377	0	418	4	0
3	22	377	0	418	3	0
4	3	504	0	574	7	0
4	33	504	0	574	7	0
5	4	302	0	343	7	0
5	44	302	0	343	7	0
6	6	522	0	522	6	0
6	66	522	0	522	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A	62261	0	31314	321	0
7	AA	62261	0	31314	332	0
8	B	2572	0	1302	16	0
8	BB	2572	0	1302	15	0
9	C	2082	0	2157	27	0
9	CC	2082	0	2157	28	0
10	D	1565	0	1616	24	0
10	DD	1565	0	1616	25	0
11	E	1552	0	1619	22	0
11	EE	1552	0	1619	23	0
12	F	1410	0	1447	31	0
12	FF	1410	0	1447	29	0
13	G	1323	0	1374	15	0
13	GG	1323	0	1374	18	0
14	H	1111	0	1148	22	0
14	HH	1111	0	1148	22	0
15	J	1129	0	1162	16	0
15	JJ	1129	0	1162	15	0
16	K	938	0	1012	14	0
16	KK	938	0	1012	13	0
17	L	1045	0	1117	15	0
17	LL	1045	0	1117	14	0
18	M	1074	0	1157	15	0
18	MM	1074	0	1157	15	0
19	N	960	0	1000	14	0
19	NN	960	0	1000	13	0
20	O	892	0	923	9	0
20	OO	892	0	923	9	0
21	P	917	0	965	13	0
21	PP	917	0	965	14	0
22	Q	947	0	1022	14	0
22	QQ	947	0	1022	13	0
23	R	816	0	839	15	0
23	RR	816	0	839	15	0
24	S	857	0	922	10	0
24	SS	857	0	922	10	0
25	T	738	0	807	3	0
25	TT	738	0	807	3	0
26	U	779	0	834	13	0
26	UU	779	0	834	13	0
27	V	753	0	780	7	0
27	VV	753	0	780	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	W	575	0	592	10	0
28	WW	575	0	592	8	0
29	X	625	0	655	7	0
29	XX	625	0	655	7	0
30	Y	509	0	543	6	0
30	YY	509	0	543	7	0
31	Z	449	0	491	6	0
31	ZZ	449	0	491	5	0
32	a	33016	0	16616	238	0
32	aa	33016	0	16616	233	0
33	b	1764	0	1779	84	0
33	bb	1764	0	1779	83	0
34	c	1624	0	1697	28	0
34	cc	1624	0	1698	29	0
35	d	1643	0	1707	33	0
35	dd	1643	0	1707	34	0
36	e	1141	0	1170	48	0
36	ee	1141	0	1170	50	0
37	f	817	0	808	11	0
37	ff	817	0	808	11	0
38	g	1266	0	1320	50	0
38	gg	1266	0	1320	50	0
39	h	979	0	1034	21	0
39	hh	979	0	1034	22	0
40	i	1022	0	1070	29	0
40	ii	1022	0	1070	30	0
41	j	786	0	828	26	0
41	jj	786	0	828	24	0
42	k	869	0	878	25	0
42	kk	869	0	878	25	0
43	l	955	0	1019	13	0
43	ll	955	0	1019	13	0
44	m	883	0	944	10	0
44	mm	883	0	944	10	0
45	n	799	0	841	15	0
45	nn	799	0	841	15	0
46	o	714	0	737	9	0
46	oo	714	0	737	9	0
47	p	649	0	666	11	0
47	pp	649	0	666	12	0
48	q	648	0	691	12	0
48	qq	648	0	691	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
49	r	504	0	502	8	0
49	rr	504	0	502	8	0
50	s	637	0	665	15	0
50	ss	637	0	665	13	0
51	t	665	0	714	9	0
51	tt	665	0	714	9	0
52	u	495	0	486	22	0
52	uu	495	0	486	24	0
53	v	453	0	453	48	0
53	vv	453	0	453	51	0
54	x	754	0	756	96	0
54	xx	754	0	756	106	0
55	y	2180	0	1667	243	0
55	yy	2180	0	1667	248	0
56	w	1642	0	836	22	0
56	ww	1642	0	835	14	0
All	All	294684	0	198880	2976	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 6.

The worst 5 of 2976 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)
55:yy:311:TRP:CZ2	55:yy:351:ALA:CB	1.75	1.68
55:y:100:LYS:CB	55:y:106:GLU:CB	1.75	1.65
55:y:311:TRP:CZ2	55:y:351:ALA:HB2	1.11	1.62
55:y:311:TRP:CZ2	55:y:351:ALA:CB	1.75	1.61
55:yy:100:LYS:CB	55:yy:106:GLU:CB	1.75	1.60

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	0	54/56 (96%)	52 (96%)	2 (4%)	0	100	100
1	00	54/56 (96%)	52 (96%)	2 (4%)	0	100	100
2	1	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
2	11	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
3	2	44/46 (96%)	41 (93%)	3 (7%)	0	100	100
3	22	44/46 (96%)	41 (93%)	3 (7%)	0	100	100
4	3	62/64 (97%)	57 (92%)	4 (6%)	1 (2%)	7	38
4	33	62/64 (97%)	57 (92%)	4 (6%)	1 (2%)	7	38
5	4	36/38 (95%)	34 (94%)	2 (6%)	0	100	100
5	44	36/38 (95%)	34 (94%)	2 (6%)	0	100	100
6	6	64/66 (97%)	56 (88%)	8 (12%)	0	100	100
6	66	64/66 (97%)	55 (86%)	9 (14%)	0	100	100
9	C	269/271 (99%)	244 (91%)	25 (9%)	0	100	100
9	CC	269/271 (99%)	244 (91%)	25 (9%)	0	100	100
10	D	207/209 (99%)	192 (93%)	15 (7%)	0	100	100
10	DD	207/209 (99%)	192 (93%)	15 (7%)	0	100	100
11	E	199/201 (99%)	188 (94%)	11 (6%)	0	100	100
11	EE	199/201 (99%)	188 (94%)	11 (6%)	0	100	100
12	F	175/177 (99%)	163 (93%)	12 (7%)	0	100	100
12	FF	175/177 (99%)	163 (93%)	12 (7%)	0	100	100
13	G	174/176 (99%)	160 (92%)	13 (8%)	1 (1%)	21	59
13	GG	174/176 (99%)	160 (92%)	13 (8%)	1 (1%)	21	59
14	H	147/149 (99%)	127 (86%)	20 (14%)	0	100	100
14	HH	147/149 (99%)	127 (86%)	20 (14%)	0	100	100
15	J	140/142 (99%)	134 (96%)	6 (4%)	0	100	100
15	JJ	140/142 (99%)	135 (96%)	5 (4%)	0	100	100
16	K	120/122 (98%)	103 (86%)	17 (14%)	0	100	100
16	KK	120/122 (98%)	103 (86%)	17 (14%)	0	100	100
17	L	141/143 (99%)	127 (90%)	14 (10%)	0	100	100
17	LL	141/143 (99%)	126 (89%)	15 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	M	134/136 (98%)	126 (94%)	4 (3%)	4 (3%)	3	23
18	MM	134/136 (98%)	126 (94%)	4 (3%)	4 (3%)	3	23
19	N	118/120 (98%)	108 (92%)	10 (8%)	0	100	100
19	NN	118/120 (98%)	108 (92%)	10 (8%)	0	100	100
20	O	114/116 (98%)	103 (90%)	11 (10%)	0	100	100
20	OO	114/116 (98%)	103 (90%)	11 (10%)	0	100	100
21	P	112/114 (98%)	105 (94%)	7 (6%)	0	100	100
21	PP	112/114 (98%)	105 (94%)	7 (6%)	0	100	100
22	Q	115/117 (98%)	114 (99%)	1 (1%)	0	100	100
22	QQ	115/117 (98%)	114 (99%)	1 (1%)	0	100	100
23	R	101/103 (98%)	89 (88%)	12 (12%)	0	100	100
23	RR	101/103 (98%)	89 (88%)	12 (12%)	0	100	100
24	S	108/110 (98%)	100 (93%)	8 (7%)	0	100	100
24	SS	108/110 (98%)	100 (93%)	8 (7%)	0	100	100
25	T	91/93 (98%)	82 (90%)	9 (10%)	0	100	100
25	TT	91/93 (98%)	82 (90%)	9 (10%)	0	100	100
26	U	100/102 (98%)	86 (86%)	14 (14%)	0	100	100
26	UU	100/102 (98%)	86 (86%)	14 (14%)	0	100	100
27	V	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
27	VV	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
28	W	73/75 (97%)	68 (93%)	5 (7%)	0	100	100
28	WW	73/75 (97%)	68 (93%)	5 (7%)	0	100	100
29	X	75/77 (97%)	72 (96%)	3 (4%)	0	100	100
29	XX	75/77 (97%)	72 (96%)	3 (4%)	0	100	100
30	Y	61/63 (97%)	57 (93%)	4 (7%)	0	100	100
30	YY	61/63 (97%)	57 (93%)	4 (7%)	0	100	100
31	Z	56/58 (97%)	54 (96%)	2 (4%)	0	100	100
31	ZZ	56/58 (97%)	54 (96%)	2 (4%)	0	100	100
33	b	224/226 (99%)	190 (85%)	33 (15%)	1 (0%)	30	67
33	bb	224/226 (99%)	190 (85%)	33 (15%)	1 (0%)	30	67
34	c	204/206 (99%)	191 (94%)	13 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	cc	204/206 (99%)	191 (94%)	13 (6%)	0	100	100
35	d	203/205 (99%)	181 (89%)	22 (11%)	0	100	100
35	dd	203/205 (99%)	181 (89%)	22 (11%)	0	100	100
36	e	155/157 (99%)	142 (92%)	13 (8%)	0	100	100
36	ee	155/157 (99%)	142 (92%)	13 (8%)	0	100	100
37	f	98/100 (98%)	86 (88%)	12 (12%)	0	100	100
37	ff	98/100 (98%)	86 (88%)	12 (12%)	0	100	100
38	g	159/161 (99%)	137 (86%)	21 (13%)	1 (1%)	21	59
38	gg	159/161 (99%)	136 (86%)	22 (14%)	1 (1%)	21	59
39	h	127/129 (98%)	119 (94%)	8 (6%)	0	100	100
39	hh	127/129 (98%)	119 (94%)	8 (6%)	0	100	100
40	i	125/127 (98%)	102 (82%)	23 (18%)	0	100	100
40	ii	125/127 (98%)	102 (82%)	23 (18%)	0	100	100
41	j	96/98 (98%)	82 (85%)	13 (14%)	1 (1%)	12	49
41	jj	96/98 (98%)	82 (85%)	13 (14%)	1 (1%)	12	49
42	k	114/116 (98%)	97 (85%)	17 (15%)	0	100	100
42	kk	114/116 (98%)	97 (85%)	17 (15%)	0	100	100
43	l	121/123 (98%)	103 (85%)	18 (15%)	0	100	100
43	ll	121/123 (98%)	103 (85%)	18 (15%)	0	100	100
44	m	112/114 (98%)	96 (86%)	15 (13%)	1 (1%)	14	51
44	mm	112/114 (98%)	96 (86%)	15 (13%)	1 (1%)	14	51
45	n	99/101 (98%)	85 (86%)	14 (14%)	0	100	100
45	nn	99/101 (98%)	85 (86%)	14 (14%)	0	100	100
46	o	86/88 (98%)	77 (90%)	8 (9%)	1 (1%)	10	44
46	oo	86/88 (98%)	77 (90%)	8 (9%)	1 (1%)	10	44
47	p	80/82 (98%)	73 (91%)	7 (9%)	0	100	100
47	pp	80/82 (98%)	73 (91%)	7 (9%)	0	100	100
48	q	78/80 (98%)	66 (85%)	12 (15%)	0	100	100
48	qq	78/80 (98%)	66 (85%)	12 (15%)	0	100	100
49	r	63/65 (97%)	61 (97%)	2 (3%)	0	100	100
49	rr	63/65 (97%)	61 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
50	s	77/79 (98%)	71 (92%)	6 (8%)	0	100	100
50	ss	77/79 (98%)	71 (92%)	6 (8%)	0	100	100
51	t	83/85 (98%)	80 (96%)	3 (4%)	0	100	100
51	tt	83/85 (98%)	80 (96%)	3 (4%)	0	100	100
52	u	63/65 (97%)	46 (73%)	16 (25%)	1 (2%)	7	38
52	uu	63/65 (97%)	46 (73%)	16 (25%)	1 (2%)	7	38
53	v	53/55 (96%)	43 (81%)	9 (17%)	1 (2%)	6	32
53	vv	53/55 (96%)	43 (81%)	9 (17%)	1 (2%)	6	32
54	x	93/95 (98%)	86 (92%)	6 (6%)	1 (1%)	11	46
54	xx	93/95 (98%)	86 (92%)	6 (6%)	1 (1%)	11	46
55	y	347/557 (62%)	253 (73%)	75 (22%)	19 (6%)	1	15
55	yy	347/557 (62%)	253 (73%)	75 (22%)	19 (6%)	1	15
All	All	12180/12804 (95%)	10888 (89%)	1226 (10%)	66 (0%)	26	63

5 of 66 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
33	b	18	GLN
52	u	37	TYR
55	y	139	ARG
55	y	153	GLU
55	y	169	SER

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	47/47 (100%)	47 (100%)	0	100	100
1	00	47/47 (100%)	47 (100%)	0	100	100
2	1	45/45 (100%)	45 (100%)	0	100	100
2	11	45/45 (100%)	45 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	2	38/38 (100%)	37 (97%)	1 (3%)	40	62
3	22	38/38 (100%)	37 (97%)	1 (3%)	40	62
4	3	51/51 (100%)	51 (100%)	0	100	100
4	33	51/51 (100%)	51 (100%)	0	100	100
5	4	34/34 (100%)	34 (100%)	0	100	100
5	44	34/34 (100%)	34 (100%)	0	100	100
6	6	59/59 (100%)	58 (98%)	1 (2%)	53	69
6	66	59/59 (100%)	58 (98%)	1 (2%)	53	69
9	C	216/216 (100%)	216 (100%)	0	100	100
9	CC	216/216 (100%)	216 (100%)	0	100	100
10	D	164/164 (100%)	164 (100%)	0	100	100
10	DD	164/164 (100%)	164 (100%)	0	100	100
11	E	165/165 (100%)	165 (100%)	0	100	100
11	EE	165/165 (100%)	165 (100%)	0	100	100
12	F	148/148 (100%)	146 (99%)	2 (1%)	59	72
12	FF	148/148 (100%)	146 (99%)	2 (1%)	59	72
13	G	137/137 (100%)	136 (99%)	1 (1%)	76	81
13	GG	137/137 (100%)	136 (99%)	1 (1%)	76	81
14	H	114/114 (100%)	114 (100%)	0	100	100
14	HH	114/114 (100%)	114 (100%)	0	100	100
15	J	116/116 (100%)	116 (100%)	0	100	100
15	JJ	116/116 (100%)	116 (100%)	0	100	100
16	K	103/103 (100%)	103 (100%)	0	100	100
16	KK	103/103 (100%)	103 (100%)	0	100	100
17	L	102/102 (100%)	101 (99%)	1 (1%)	68	78
17	LL	102/102 (100%)	101 (99%)	1 (1%)	68	78
18	M	109/109 (100%)	108 (99%)	1 (1%)	70	79
18	MM	109/109 (100%)	108 (99%)	1 (1%)	70	79
19	N	100/100 (100%)	100 (100%)	0	100	100
19	NN	100/100 (100%)	100 (100%)	0	100	100
20	O	86/86 (100%)	86 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	OO	86/86 (100%)	86 (100%)	0	100	100
21	P	99/99 (100%)	98 (99%)	1 (1%)	68	78
21	PP	99/99 (100%)	98 (99%)	1 (1%)	68	78
22	Q	89/89 (100%)	89 (100%)	0	100	100
22	QQ	89/89 (100%)	89 (100%)	0	100	100
23	R	84/84 (100%)	83 (99%)	1 (1%)	63	75
23	RR	84/84 (100%)	83 (99%)	1 (1%)	63	75
24	S	93/93 (100%)	93 (100%)	0	100	100
24	SS	93/93 (100%)	93 (100%)	0	100	100
25	T	80/80 (100%)	79 (99%)	1 (1%)	61	74
25	TT	80/80 (100%)	79 (99%)	1 (1%)	61	74
26	U	83/83 (100%)	82 (99%)	1 (1%)	63	75
26	UU	83/83 (100%)	82 (99%)	1 (1%)	63	75
27	V	78/78 (100%)	77 (99%)	1 (1%)	61	74
27	VV	78/78 (100%)	77 (99%)	1 (1%)	61	74
28	W	57/57 (100%)	55 (96%)	2 (4%)	32	53
28	WW	57/57 (100%)	56 (98%)	1 (2%)	51	68
29	X	67/67 (100%)	67 (100%)	0	100	100
29	XX	67/67 (100%)	67 (100%)	0	100	100
30	Y	55/55 (100%)	55 (100%)	0	100	100
30	YY	55/55 (100%)	55 (100%)	0	100	100
31	Z	48/48 (100%)	48 (100%)	0	100	100
31	ZZ	48/48 (100%)	48 (100%)	0	100	100
33	b	186/186 (100%)	186 (100%)	0	100	100
33	bb	186/186 (100%)	186 (100%)	0	100	100
34	c	170/170 (100%)	167 (98%)	3 (2%)	51	68
34	cc	170/170 (100%)	167 (98%)	3 (2%)	51	68
35	d	172/172 (100%)	172 (100%)	0	100	100
35	dd	172/172 (100%)	172 (100%)	0	100	100
36	e	114/119 (96%)	113 (99%)	1 (1%)	70	79
36	ee	114/119 (96%)	113 (99%)	1 (1%)	70	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	f	87/87 (100%)	87 (100%)	0	100	100
37	ff	87/87 (100%)	87 (100%)	0	100	100
38	g	132/132 (100%)	131 (99%)	1 (1%)	73	80
38	gg	132/132 (100%)	131 (99%)	1 (1%)	73	80
39	h	104/104 (100%)	103 (99%)	1 (1%)	68	78
39	hh	104/104 (100%)	103 (99%)	1 (1%)	68	78
40	i	105/105 (100%)	104 (99%)	1 (1%)	68	78
40	ii	105/105 (100%)	104 (99%)	1 (1%)	68	78
41	j	86/86 (100%)	85 (99%)	1 (1%)	63	75
41	jj	86/86 (100%)	85 (99%)	1 (1%)	63	75
42	k	89/89 (100%)	89 (100%)	0	100	100
42	kk	89/89 (100%)	89 (100%)	0	100	100
43	l	103/103 (100%)	103 (100%)	0	100	100
43	ll	103/103 (100%)	103 (100%)	0	100	100
44	m	92/92 (100%)	92 (100%)	0	100	100
44	mm	92/92 (100%)	92 (100%)	0	100	100
45	n	79/83 (95%)	79 (100%)	0	100	100
45	nn	79/83 (95%)	79 (100%)	0	100	100
46	o	76/76 (100%)	76 (100%)	0	100	100
46	oo	76/76 (100%)	76 (100%)	0	100	100
47	p	65/65 (100%)	64 (98%)	1 (2%)	57	72
47	pp	65/65 (100%)	64 (98%)	1 (2%)	57	72
48	q	74/74 (100%)	73 (99%)	1 (1%)	59	72
48	qq	74/74 (100%)	73 (99%)	1 (1%)	59	72
49	r	48/56 (86%)	48 (100%)	0	100	100
49	rr	48/56 (86%)	48 (100%)	0	100	100
50	s	70/70 (100%)	68 (97%)	2 (3%)	37	58
50	ss	70/70 (100%)	68 (97%)	2 (3%)	37	58
51	t	65/65 (100%)	64 (98%)	1 (2%)	57	72
51	tt	65/65 (100%)	64 (98%)	1 (2%)	57	72
52	u	44/55 (80%)	44 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	uu	44/55 (80%)	44 (100%)	0	100	100
53	v	44/44 (100%)	44 (100%)	0	100	100
53	vv	44/44 (100%)	44 (100%)	0	100	100
54	x	80/81 (99%)	77 (96%)	3 (4%)	29	50
54	xx	80/81 (99%)	77 (96%)	3 (4%)	29	50
55	y	137/461 (30%)	131 (96%)	6 (4%)	25	47
55	yy	137/461 (30%)	131 (96%)	6 (4%)	25	47
All	All	9778/10484 (93%)	9707 (99%)	71 (1%)	73	81

5 of 71 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
47	pp	79	ASN
50	ss	10	ILE
55	yy	31	ILE
50	s	10	ILE
48	q	18	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 193 such sidechains are listed below:

Mol	Chain	Res	Type
13	GG	115	GLN
31	ZZ	8	GLN
15	JJ	40	HIS
22	QQ	36	GLN
34	cc	99	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
32	a	1538/1539 (99%)	263 (17%)	0
32	aa	1538/1539 (99%)	263 (17%)	0
56	w	76/77 (98%)	35 (46%)	0
56	ww	76/77 (98%)	35 (46%)	0
7	A	2898/2903 (99%)	568 (19%)	13 (0%)
7	AA	2898/2903 (99%)	568 (19%)	13 (0%)
8	B	119/120 (99%)	18 (15%)	1 (0%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
8	BB	119/120 (99%)	18 (15%)	1 (0%)
All	All	9262/9278 (99%)	1768 (19%)	28 (0%)

5 of 1768 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	A	2	G
7	A	10	A
7	A	12	U
7	A	14	A
7	A	15	G

5 of 28 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
7	AA	91	A
8	BB	52	A
7	AA	1020	A
7	AA	2324	U
7	AA	858	G

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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
56	w	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	w	16:C	O3'	17:C	P	2.35

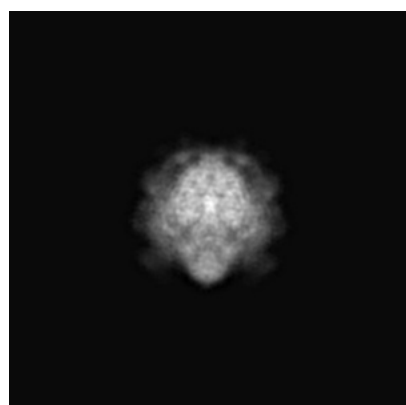
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0139. These allow visual inspection of the internal detail of the map and identification of artifacts.

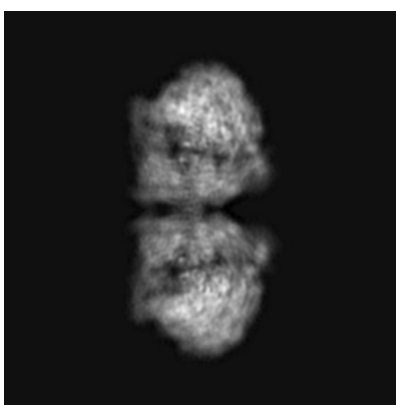
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

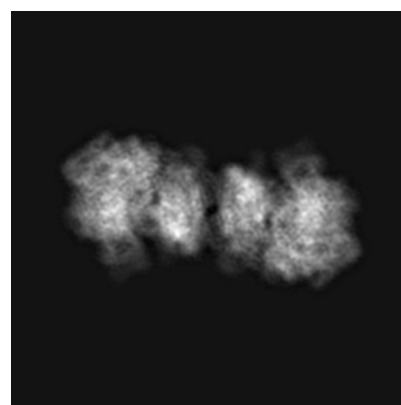
6.1.1 Primary map



X



Y



Z

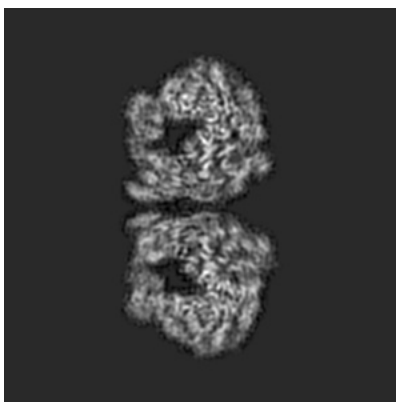
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

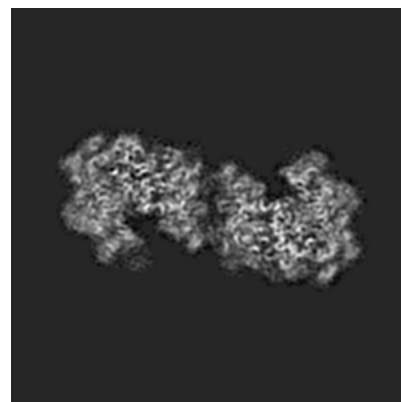
6.2.1 Primary map



X Index: 114



Y Index: 114

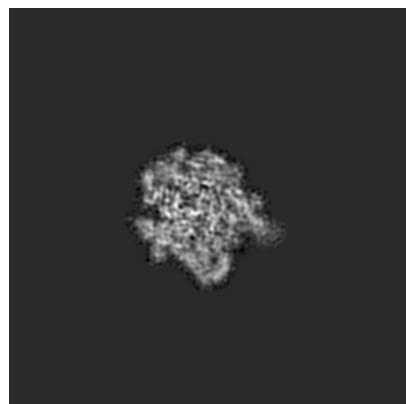


Z Index: 114

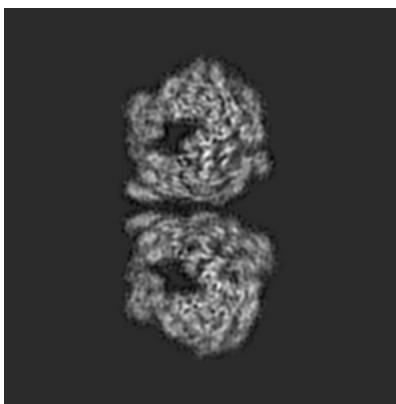
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

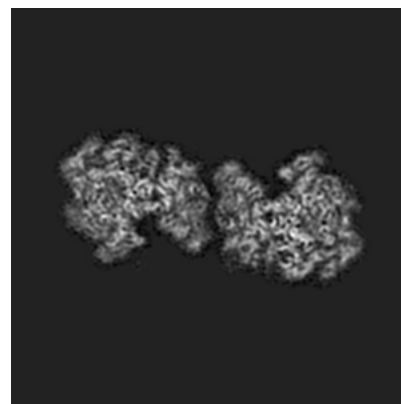
6.3.1 Primary map



X Index: 169



Y Index: 113

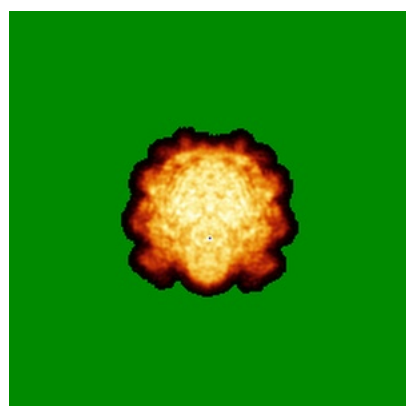


Z Index: 117

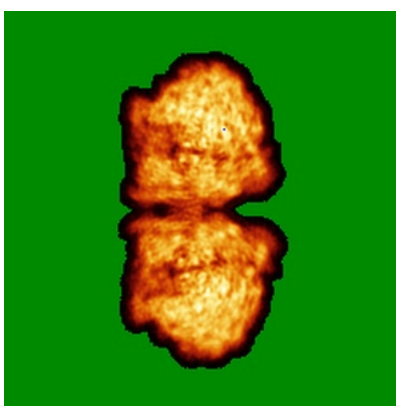
The images above show the largest variance slices of the map in three orthogonal directions.

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

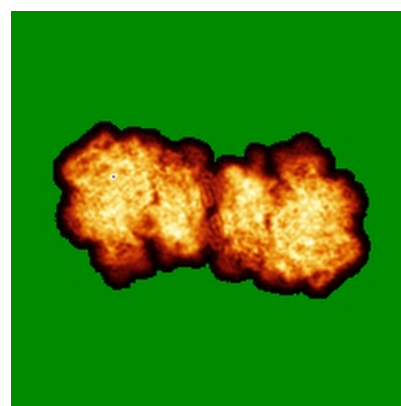
6.4.1 Primary map



X



Y

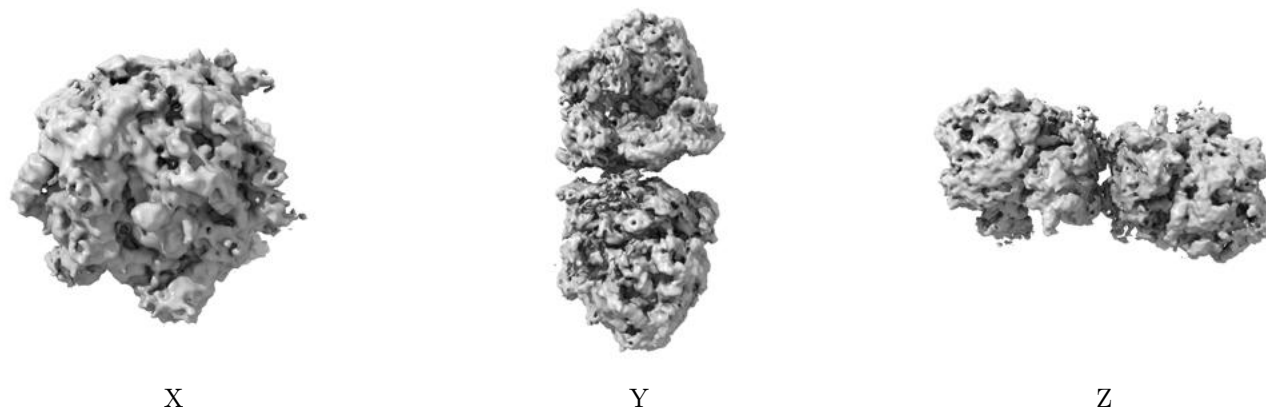


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.075. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

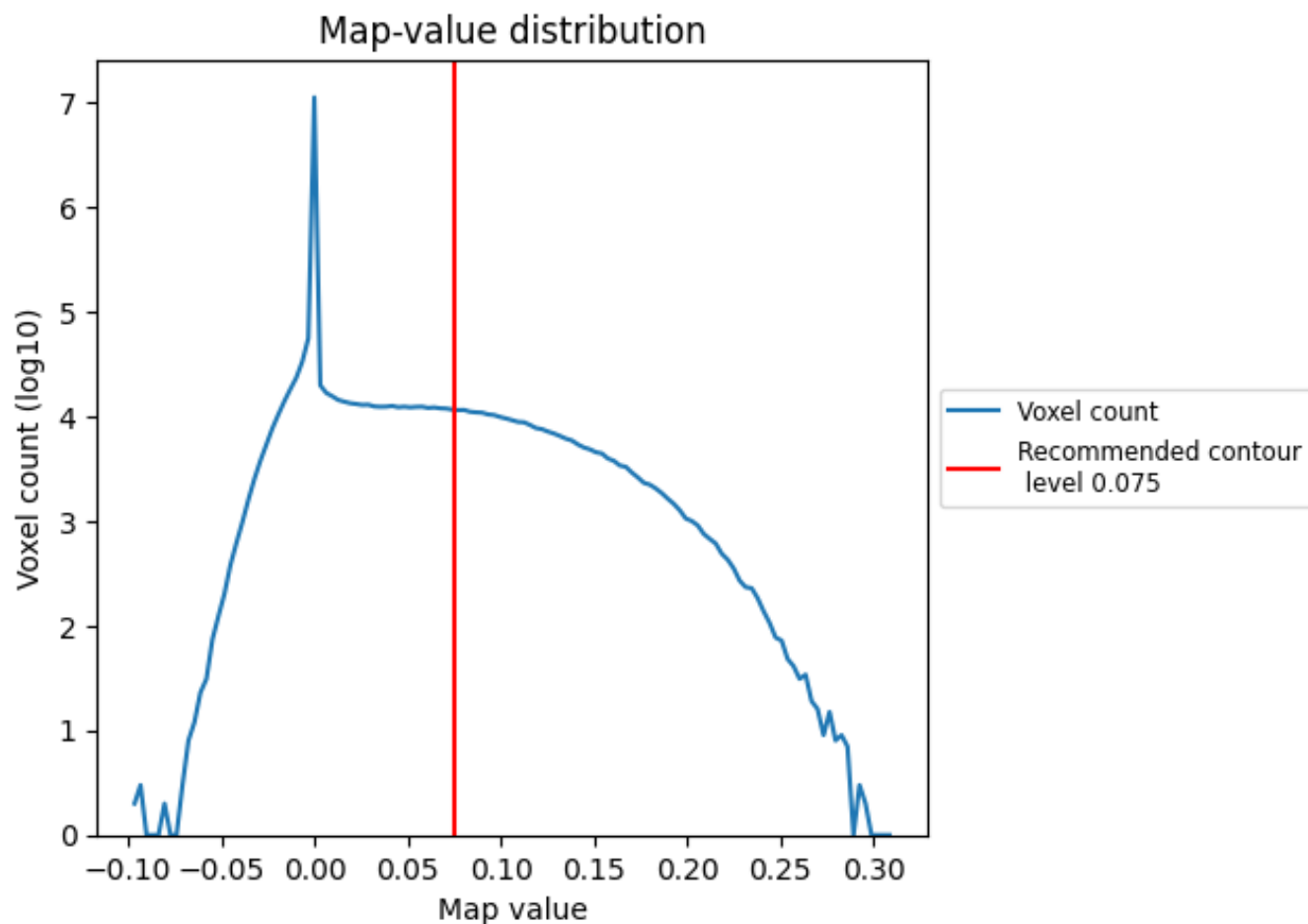
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

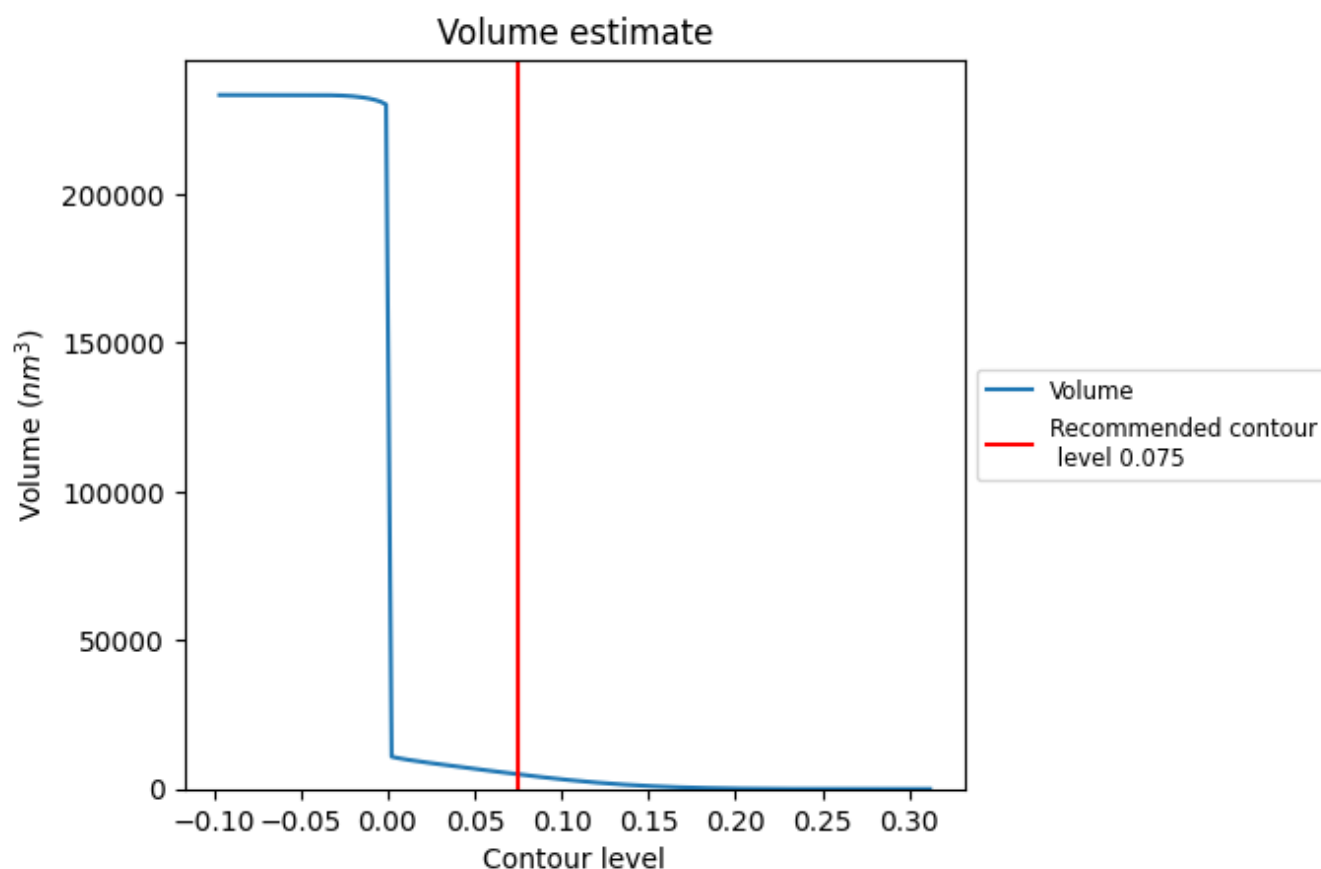
This section contains the results of statistical analysis of the map.

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.

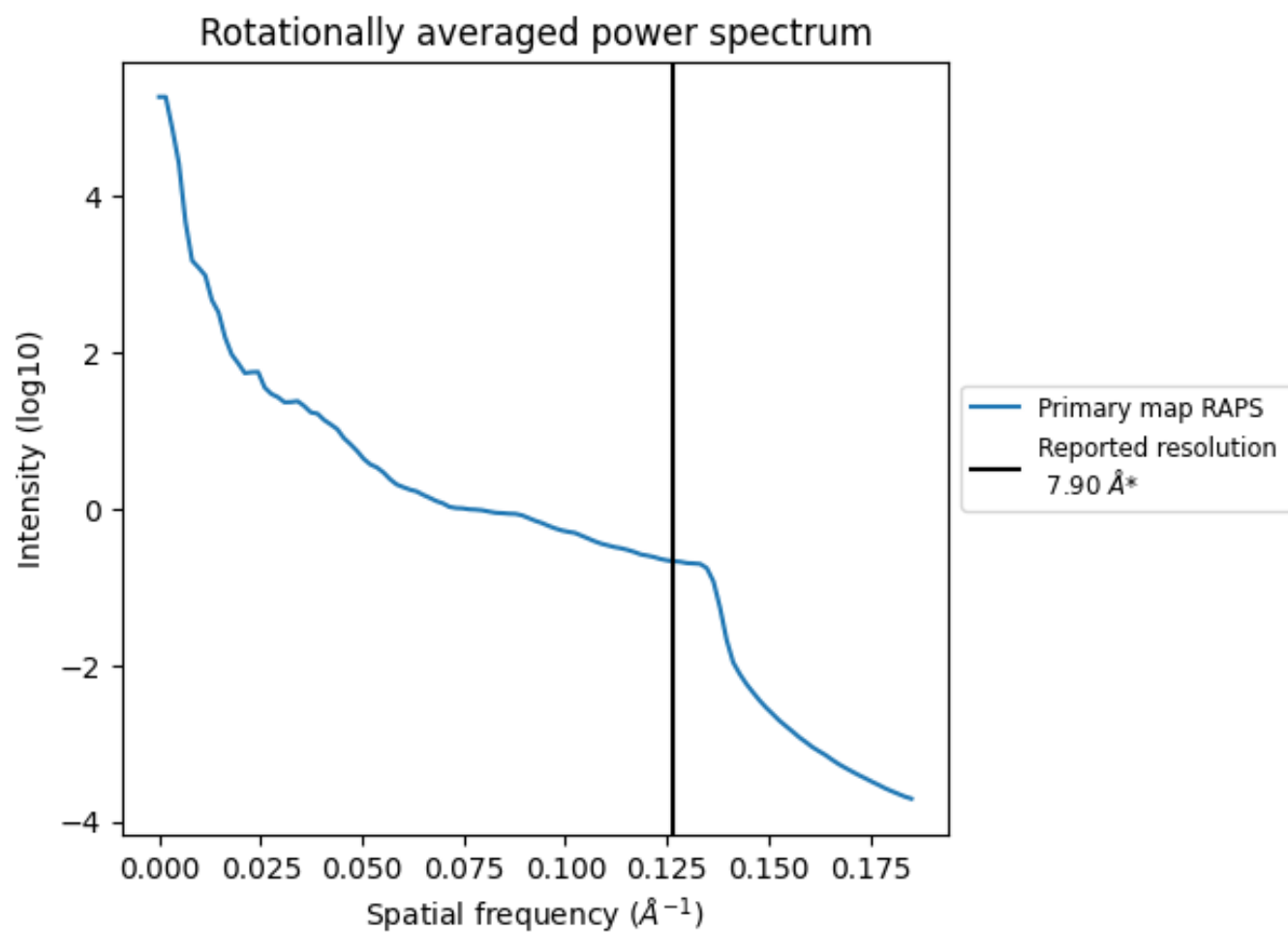
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4934 nm³; this corresponds to an approximate mass of 4457 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 ⓘ

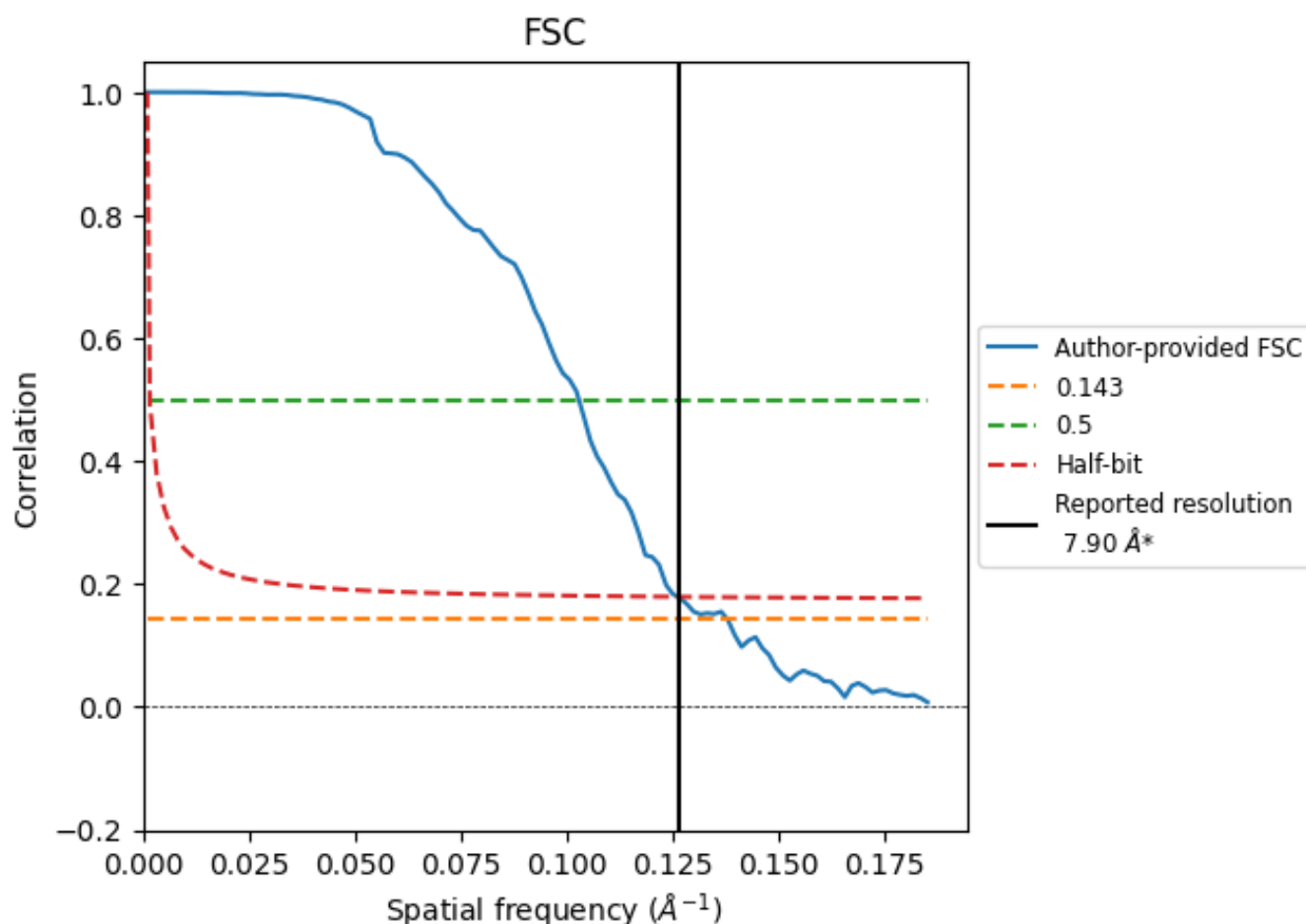


*Reported resolution corresponds to spatial frequency of 0.127 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.127 Å⁻¹

8.2 Resolution estimates [i](#)

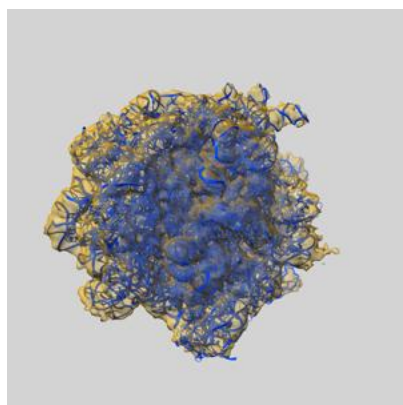
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.90	-	-
Author-provided FSC curve	7.26	9.72	7.92
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

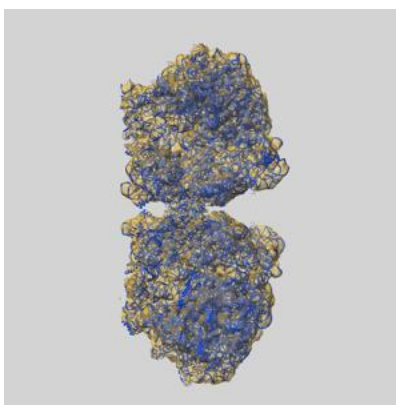
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0139 and PDB model 6H58. Per-residue inclusion information can be found in section [3](#) on page [21](#).

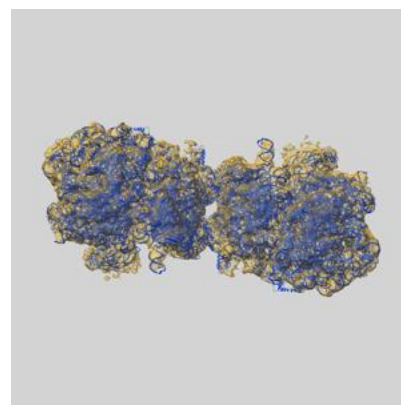
9.1 Map-model overlay [i](#)



X



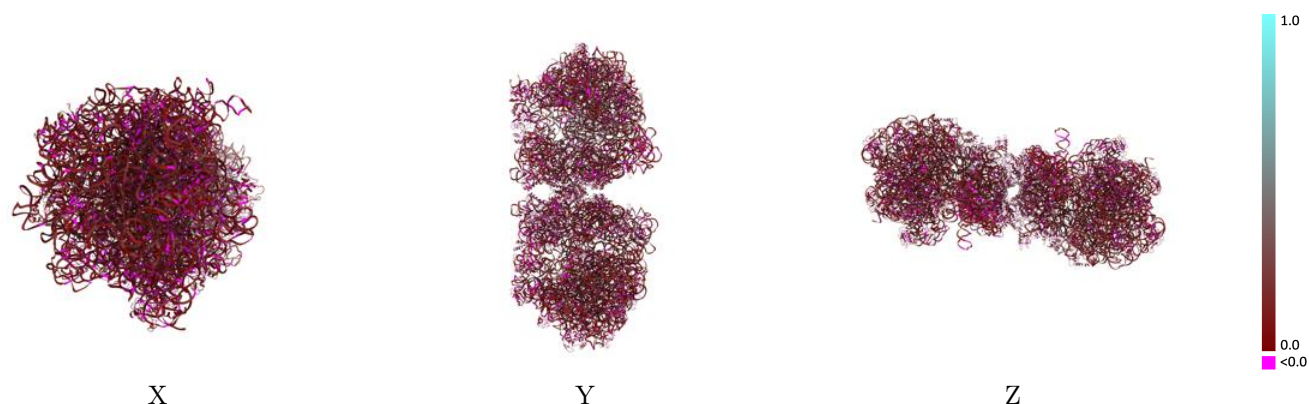
Y



Z

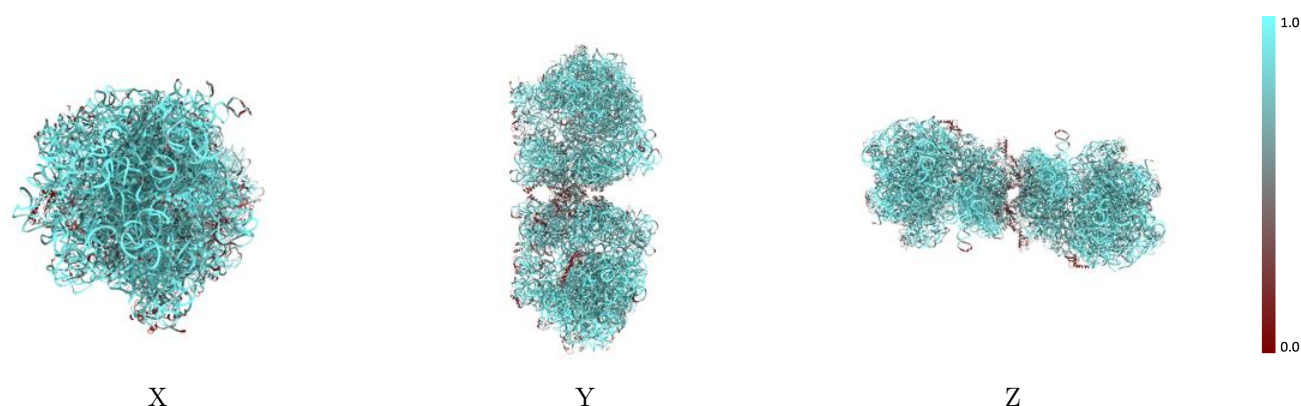
The images above show the 3D surface view of the map at the recommended contour level 0.075 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



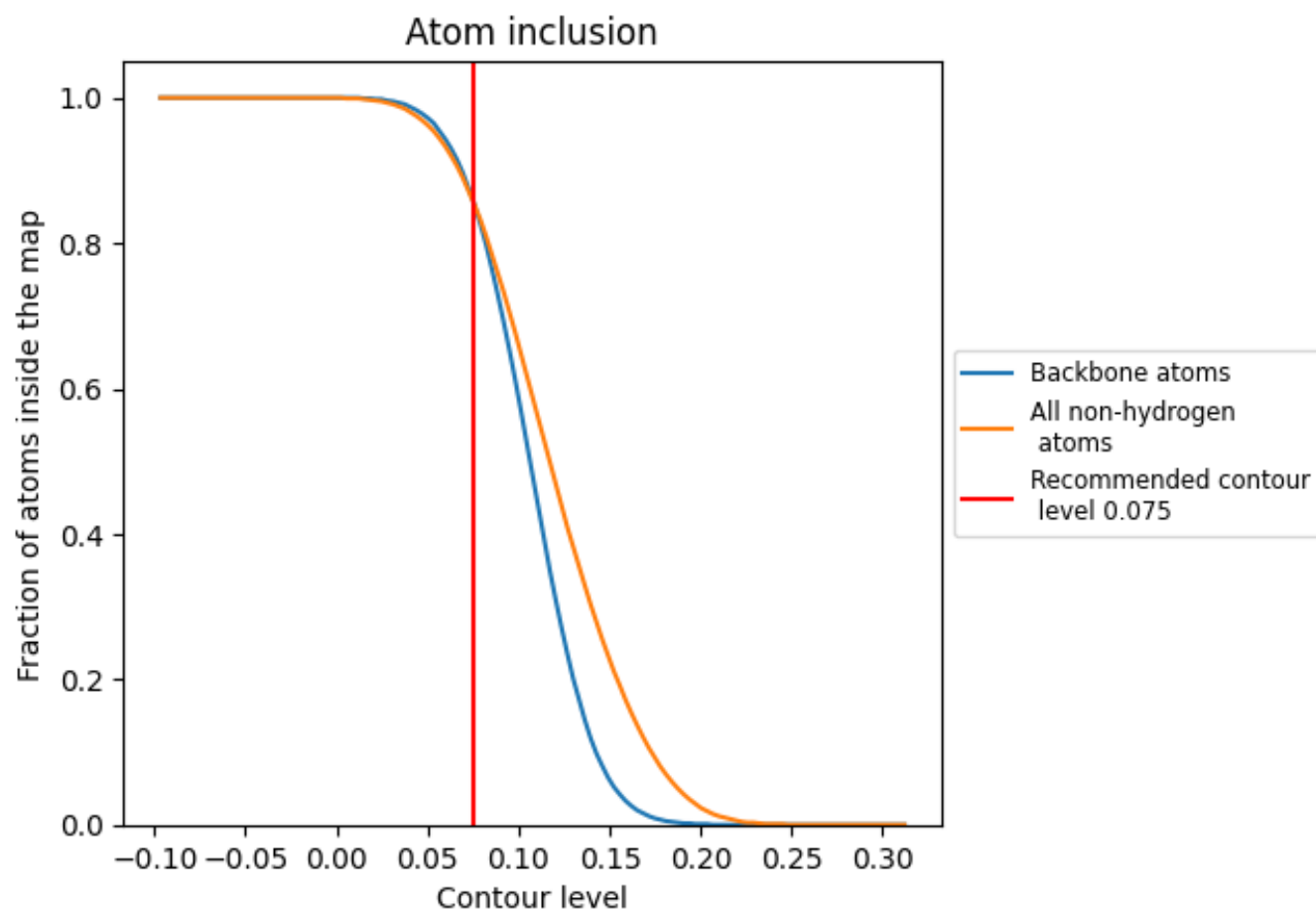
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.075).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 86% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.075) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8580	 0.1220
0	 0.7430	 0.0670
00	 0.6920	 0.0410
1	 0.7800	 0.0580
11	 0.7900	 0.0960
2	 0.8200	 0.0900
22	 0.8340	 0.0980
3	 0.7350	 0.0610
33	 0.7580	 0.0700
4	 0.8870	 0.0600
44	 0.9210	 0.0890
6	 0.1660	 0.0460
66	 0.2250	 0.0650
A	 0.9490	 0.1410
AA	 0.9510	 0.1440
B	 0.8890	 0.1150
BB	 0.9030	 0.1220
C	 0.7640	 0.1050
CC	 0.7600	 0.1090
D	 0.7560	 0.0680
DD	 0.7570	 0.0730
E	 0.7110	 0.0820
EE	 0.7160	 0.0900
F	 0.6440	 0.0860
FF	 0.6630	 0.0730
G	 0.6580	 0.0910
GG	 0.6820	 0.0930
H	 0.1700	 0.1020
HH	 0.1590	 0.1230
J	 0.8560	 0.1210
JJ	 0.8730	 0.1040
K	 0.7260	 0.0940
KK	 0.6880	 0.0950
L	 0.7090	 0.0680
LL	 0.7420	 0.0770



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Chain	Atom inclusion	Q-score
M	 0.7560	 0.0950
MM	 0.7480	 0.0840
N	 0.8460	 0.0800
NN	 0.8430	 0.0840
O	 0.6870	 0.0520
OO	 0.6710	 0.0530
P	 0.7370	 0.0920
PP	 0.7690	 0.0860
Q	 0.8360	 0.0780
QQ	 0.8360	 0.0720
R	 0.6420	 0.0800
RR	 0.6600	 0.0850
S	 0.7950	 0.0790
SS	 0.7750	 0.0840
T	 0.7450	 0.0910
TT	 0.7380	 0.0640
U	 0.7180	 0.0920
UU	 0.7200	 0.0840
V	 0.6490	 0.1020
VV	 0.7030	 0.1110
W	 0.7210	 0.0580
WW	 0.7660	 0.0520
X	 0.7720	 0.1010
XX	 0.7770	 0.1080
Y	 0.6660	 0.0640
YY	 0.7180	 0.0860
Z	 0.7960	 0.1190
ZZ	 0.8120	 0.1080
a	 0.9350	 0.1260
aa	 0.9410	 0.1330
b	 0.5580	 0.1080
bb	 0.5540	 0.1150
c	 0.6290	 0.0980
cc	 0.6250	 0.1030
d	 0.5990	 0.0630
dd	 0.6220	 0.0870
e	 0.6300	 0.0930
ee	 0.6480	 0.0960
f	 0.7990	 0.1280
ff	 0.7610	 0.1170
g	 0.7730	 0.0840
gg	 0.7570	 0.1010

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Chain	Atom inclusion	Q-score
h	 0.7150	 0.0870
hh	 0.7270	 0.0880
i	 0.7580	 0.0670
ii	 0.7590	 0.0660
j	 0.5770	 0.0360
jj	 0.5940	 0.0560
k	 0.7820	 0.1070
kk	 0.7600	 0.1110
l	 0.7550	 0.0920
ll	 0.7370	 0.1010
m	 0.6340	 0.0840
mm	 0.6730	 0.0980
n	 0.7890	 0.0880
nn	 0.7750	 0.0900
o	 0.7940	 0.1030
oo	 0.8260	 0.1320
p	 0.7080	 0.0540
pp	 0.7460	 0.0730
q	 0.7800	 0.0800
qq	 0.7670	 0.0800
r	 0.7860	 0.1050
rr	 0.8250	 0.1200
s	 0.7940	 0.0720
ss	 0.8290	 0.0740
t	 0.7890	 0.1010
tt	 0.8200	 0.1050
u	 0.6340	 0.1340
uu	 0.6410	 0.1150
v	 0.7660	 0.0990
vv	 0.7430	 0.0850
w	 0.6400	 0.1320
ww	 0.6500	 0.1290
x	 0.6470	 0.1030
xx	 0.6740	 0.1190
y	 0.2620	 0.0920
yy	 0.2970	 0.0860