wwPDB EM Validation Summary Report (i)

Nov 20, 2022 – 07:24 am GMT

PDB ID	:	6H58
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

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

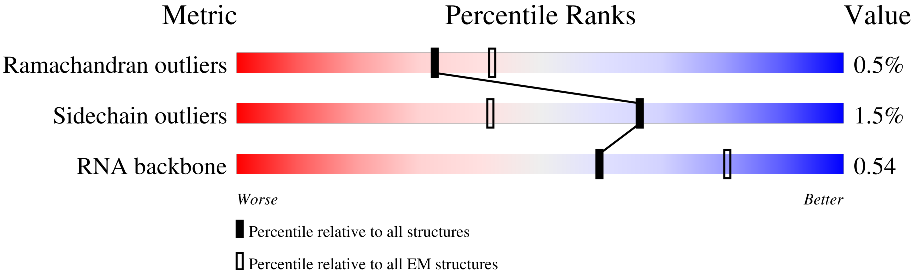
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance ⓘ

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

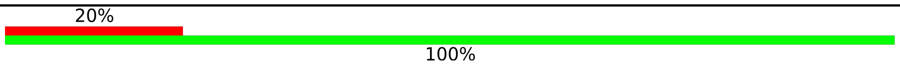
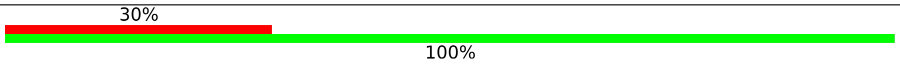
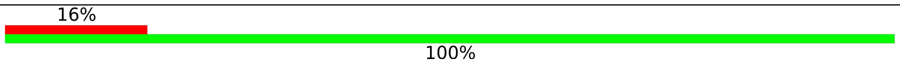
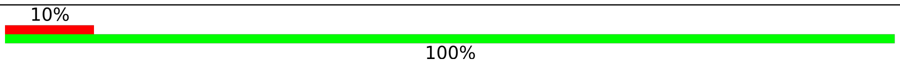
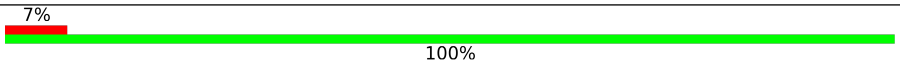
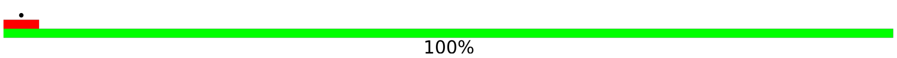
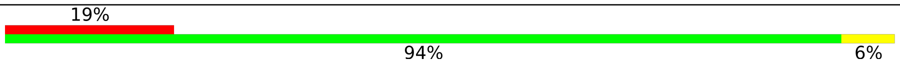
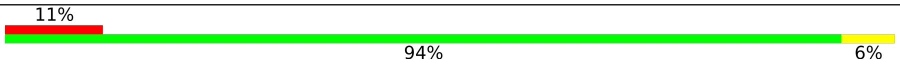
The reported resolution of this entry is 7.90 Å.

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)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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 <=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	
2	11	50	
3	2	46	
3	22	46	
4	3	64	
4	33	64	

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Mol	Chain	Length	Quality of chain
5	4	38	100%
5	44	38	• 100%
6	6	66	82% 100%
6	66	66	74% 100%
7	A	2903	• 77% 22% •
7	AA	2903	• 77% 22% •
8	B	120	• 80% 18% •
8	BB	120	• 79% 19% •
9	C	271	9% 99% •
9	CC	271	9% 99% •
10	D	209	15% 98% •
10	DD	209	15% 98% •
11	E	201	22% 99% •
11	EE	201	19% 99% •
12	F	177	25% 99% •
12	FF	177	24% 99% •
13	G	176	22% 98% •
13	GG	176	22% 98% •
14	H	149	83% 98% •
14	HH	149	83% 98% •
15	J	142	6% 99% •
15	JJ	142	• 99% •
16	K	122	13% 99% •
16	KK	122	17% 99% •
17	L	143	22% 99% •

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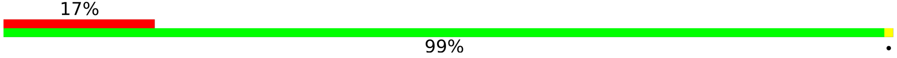
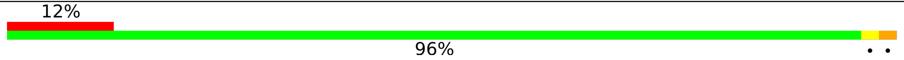
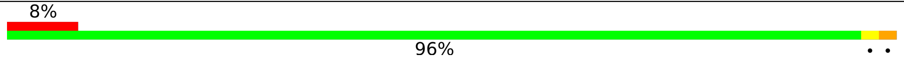
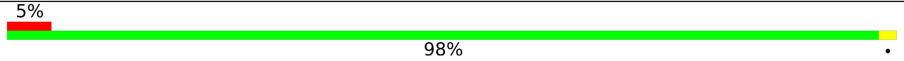
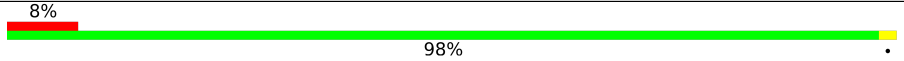
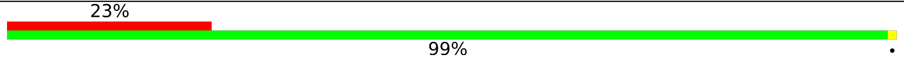
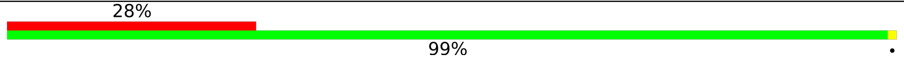
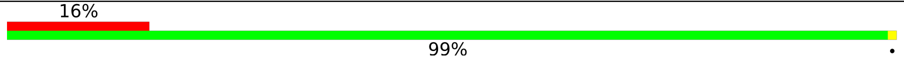
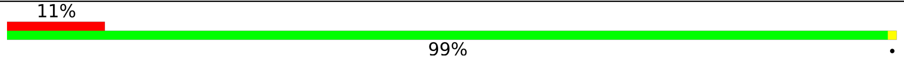
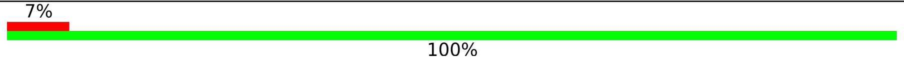
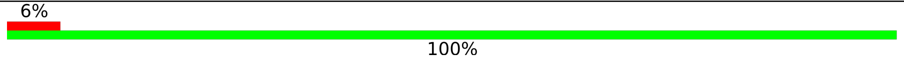
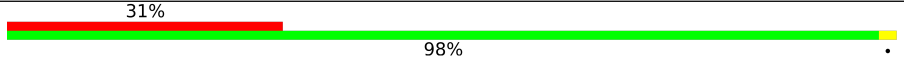
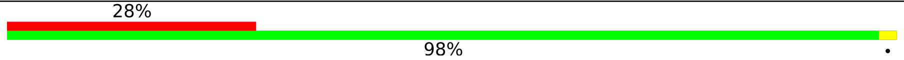
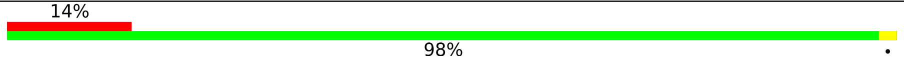
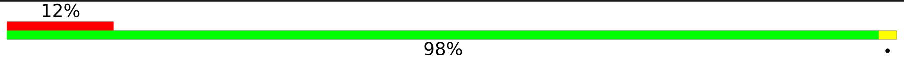
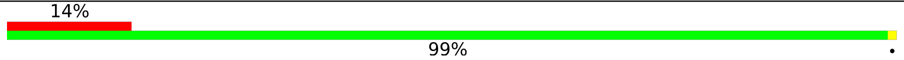
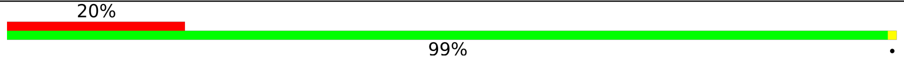
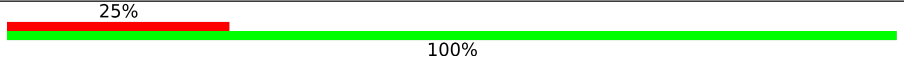
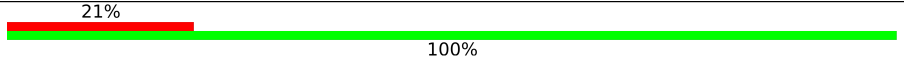
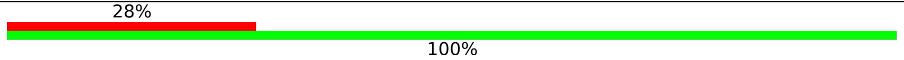
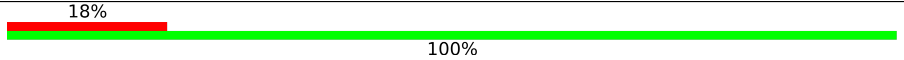
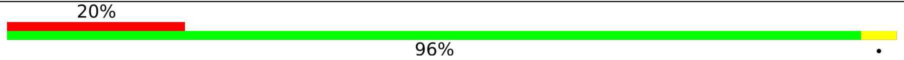
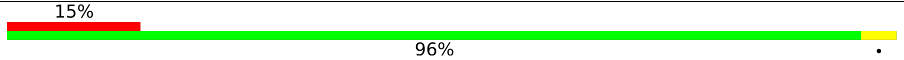
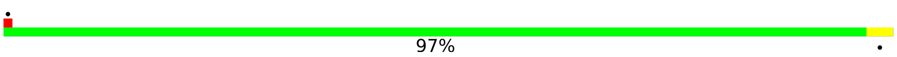
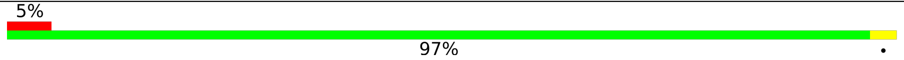
Mol	Chain	Length	Quality of chain
17	LL	143	
18	M	136	
18	MM	136	
19	N	120	
19	NN	120	
20	O	116	
20	OO	116	
21	P	114	
21	PP	114	
22	Q	117	
22	QQ	117	
23	R	103	
23	RR	103	
24	S	110	
24	SS	110	
25	T	93	
25	TT	93	
26	U	102	
26	UU	102	
27	V	94	
27	VV	94	
28	W	75	
28	WW	75	
29	X	77	
29	XX	77	

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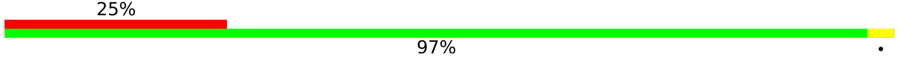
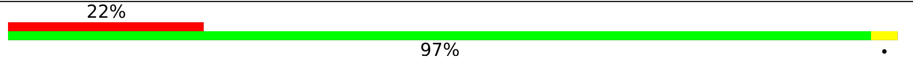
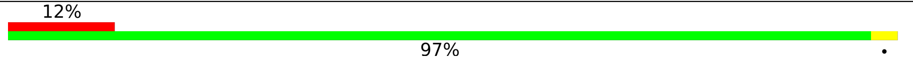
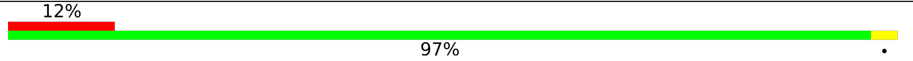
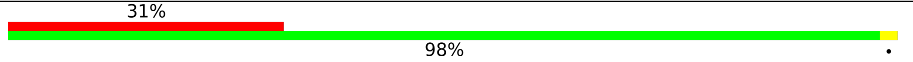
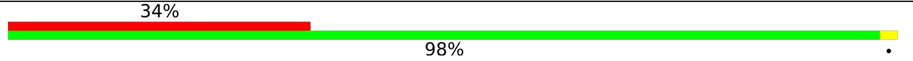
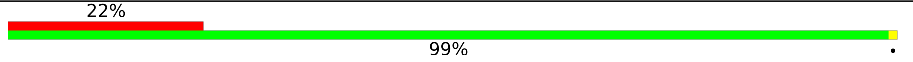
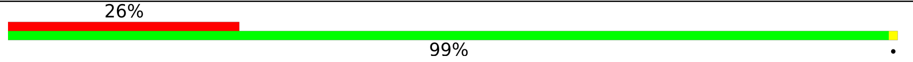
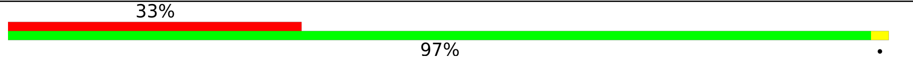
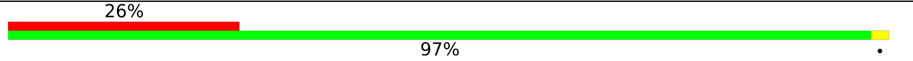
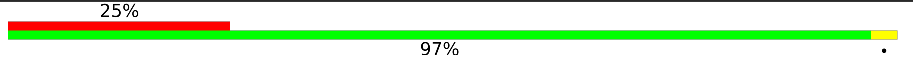
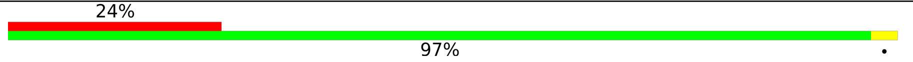
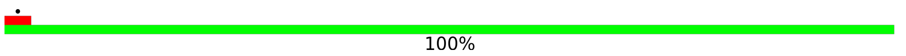
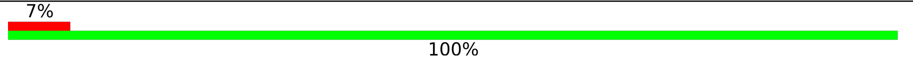
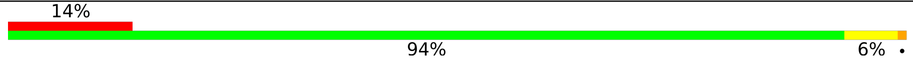
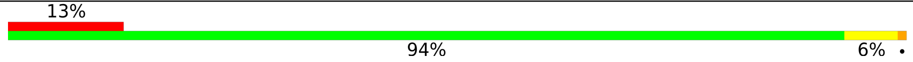
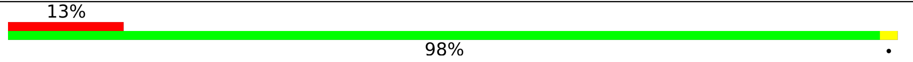
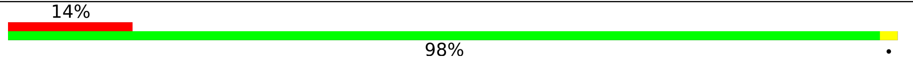
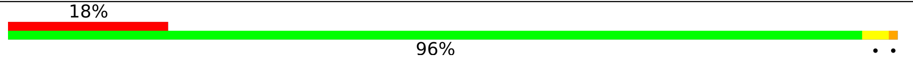
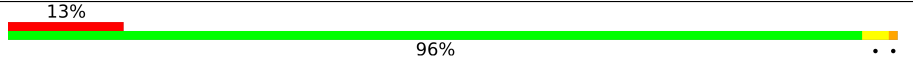
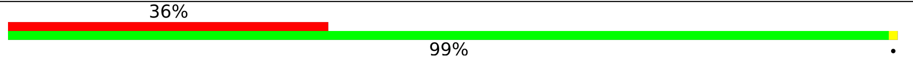
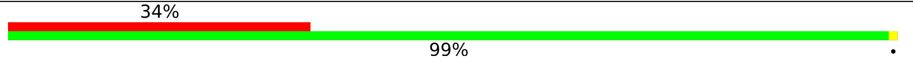
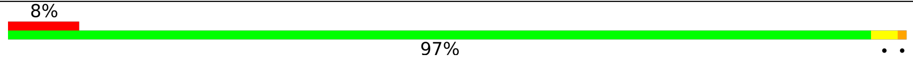
Mol	Chain	Length	Quality of chain
30	Y	63	
30	YY	63	
31	Z	58	
31	ZZ	58	
32	a	1539	
32	aa	1539	
33	b	226	
33	bb	226	
34	c	206	
34	cc	206	
35	d	205	
35	dd	205	
36	e	157	
36	ee	157	
37	f	100	
37	ff	100	
38	g	161	
38	gg	161	
39	h	129	
39	hh	129	
40	i	127	
40	ii	127	
41	j	98	
41	jj	98	
42	k	116	

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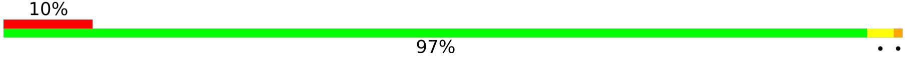
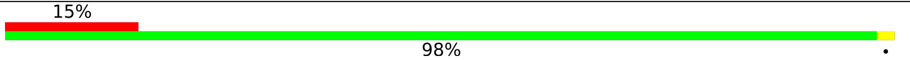
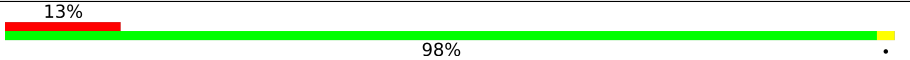
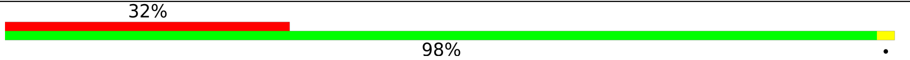
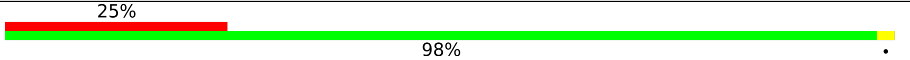
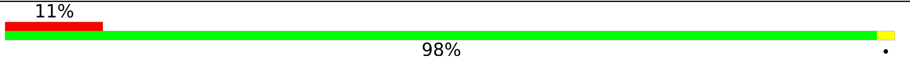
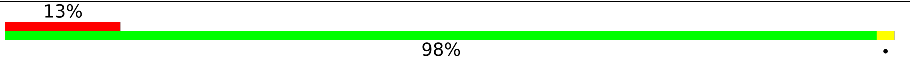
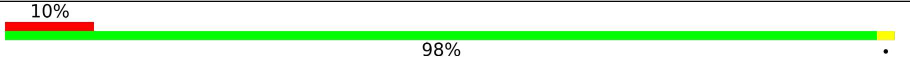
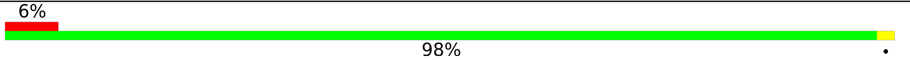
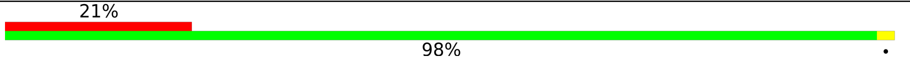
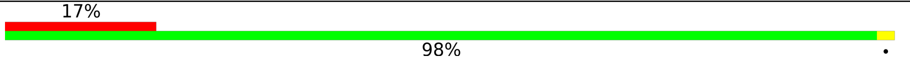
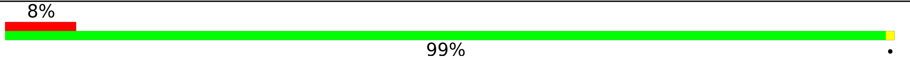
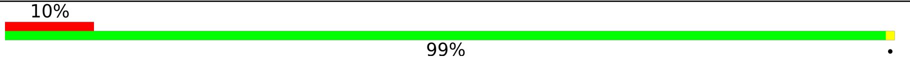
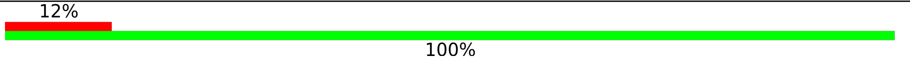
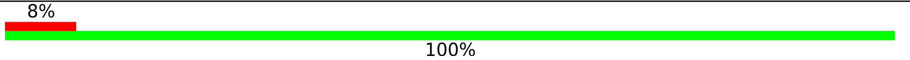
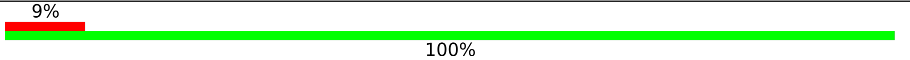
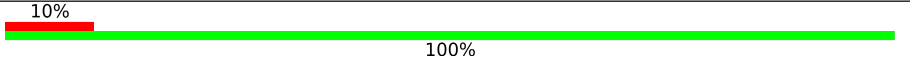
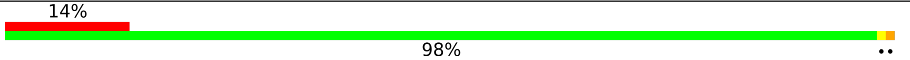
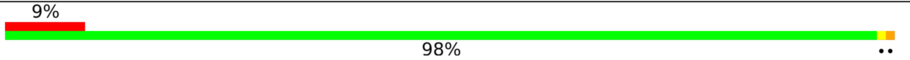
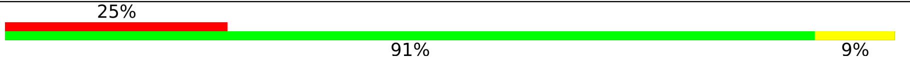
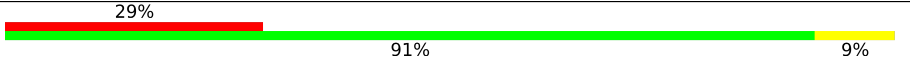
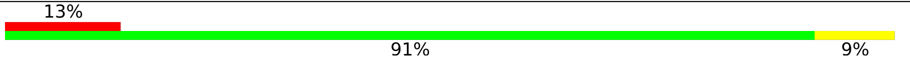
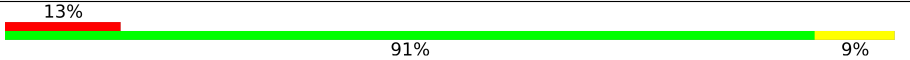
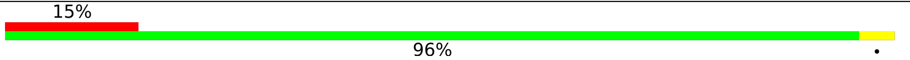
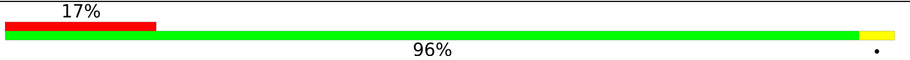
Mol	Chain	Length	Quality of chain
42	kk	116	
43	l	123	
43	ll	123	
44	m	114	
44	mm	114	
45	n	101	
45	nn	101	
46	o	88	
46	oo	88	
47	p	82	
47	pp	82	
48	q	80	
48	qq	80	
49	r	65	
49	rr	65	
50	s	79	
50	ss	79	
51	t	85	
51	tt	85	
52	u	65	
52	uu	65	
53	v	55	
53	vv	55	
54	x	95	
54	xx	95	

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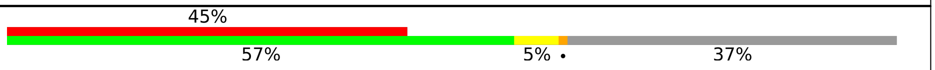
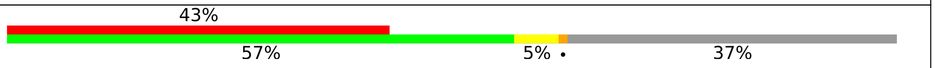
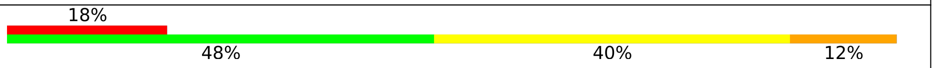
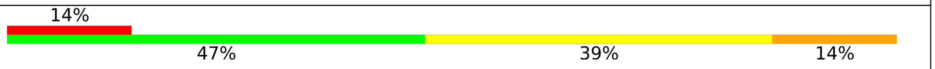
Mol	Chain	Length	Quality of chain
55	y	557	
55	yy	557	
56	w	77	
56	ww	77	

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
			Total	C	N	O	S		
1	0	56	444	269	94	80	1	0	0
			Total	C	N	O	S		
1	00	56	444	269	94	80	1	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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 2572 1145 471 836 120	0	0
8	BB	120	Total C N O P 2572 1145 471 836 120	0	0

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 2082	C 1288	N 423	O 364	S 7	0	0
9	CC	271	Total 2082	C 1288	N 423	O 364	S 7	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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	0	0
			892	552	178	162		
20	OO	116	Total	C	N	O	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	0	0
			947	604	192	151		
22	QQ	117	Total	C	N	O	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
			Total	C	N	O	S		
24	SS	110	857	532	166	156	3	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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 1624	C 1028	N 305	O 288	S 3	0	0
34	cc	206	Total 1624	C 1028	N 305	O 288	S 3	0	0

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

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

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

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

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

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

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

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

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 979	C 616	N 173	O 184	S 6	0	0
39	hh	129	Total 979	C 616	N 173	O 184	S 6	0	0

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

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

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

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

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

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

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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 649	C 406	N 128	O 114	S 1	0	0
47	pp	82	Total 649	C 406	N 128	O 114	S 1	0	0

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

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

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

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

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

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

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

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

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

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

Continued on next page...

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

- Molecule 53 is a protein called Ribosome modulation factor.

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

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

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

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
			Total	C	N	O	S		
55	y	351	2180	1339	397	441	3	0	0
55	yy	351	2180	1339	397	441	3	0	0

- Molecule 56 is a RNA chain called tRNA Mixture.

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

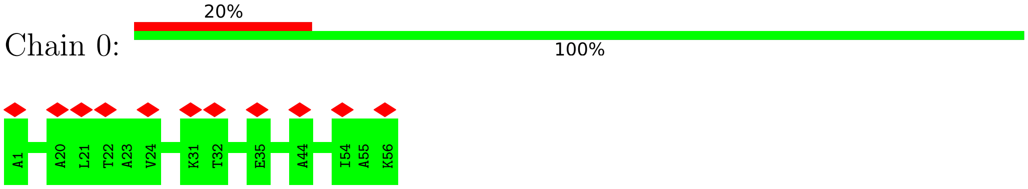
There are 4 discrepancies between the modelled and reference sequences:

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

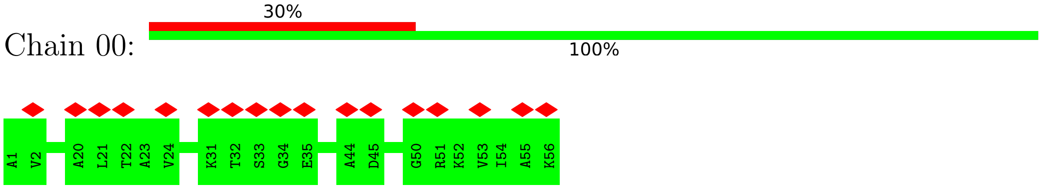
3 Residue-property plots ⓘ

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.

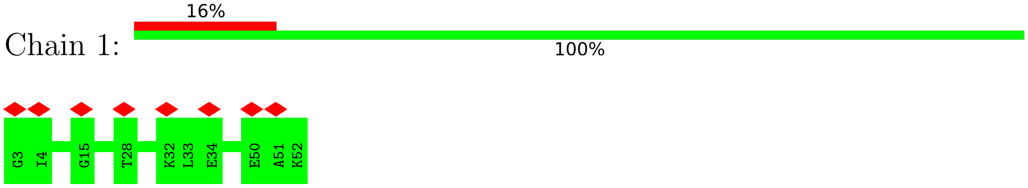
- Molecule 1: 50S ribosomal protein L32



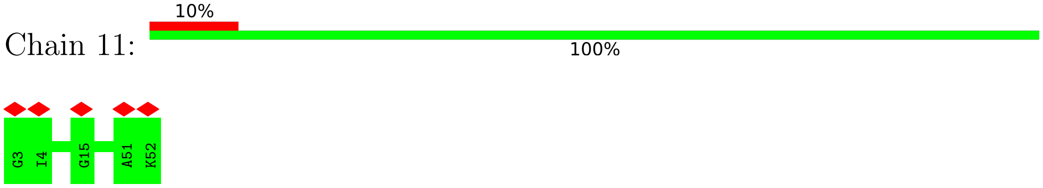
- Molecule 1: 50S ribosomal protein L32



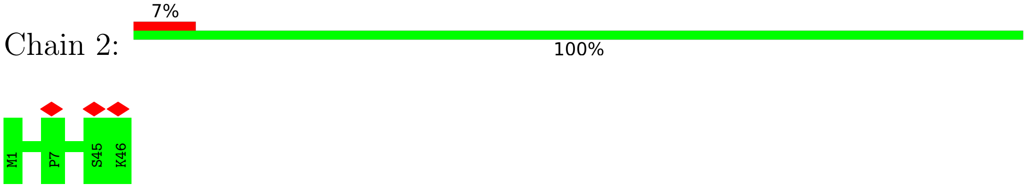
- Molecule 2: 50S ribosomal protein L33



- Molecule 2: 50S ribosomal protein L33

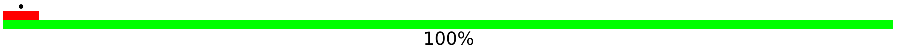


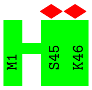
- Molecule 3: 50S ribosomal protein L34



- Molecule 3: 50S ribosomal protein L34

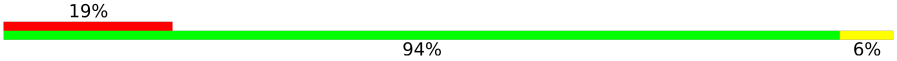
Chain 22:

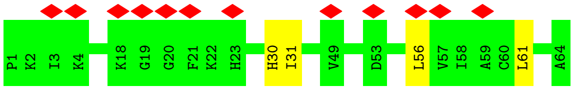




- Molecule 4: 50S ribosomal protein L35

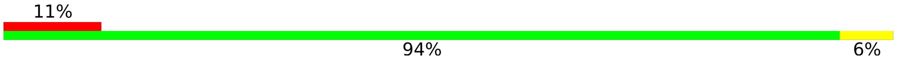
Chain 3:

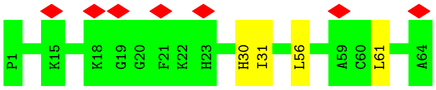




- Molecule 4: 50S ribosomal protein L35

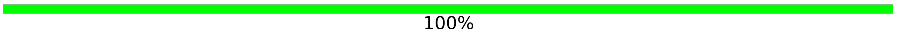
Chain 33:





- Molecule 5: 50S ribosomal protein L36

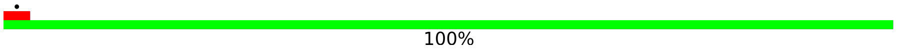
Chain 4:

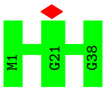


There are no outlier residues recorded for this chain.

- Molecule 5: 50S ribosomal protein L36

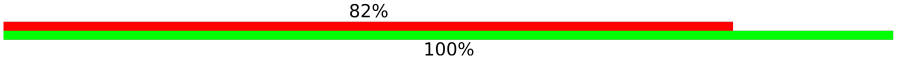
Chain 44:

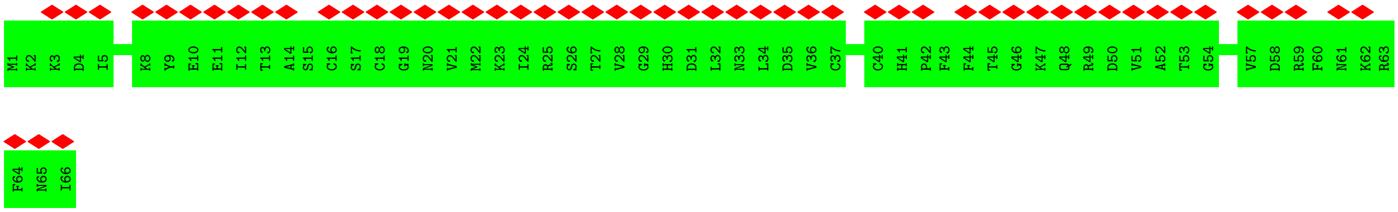




- Molecule 6: 50S ribosomal protein L31

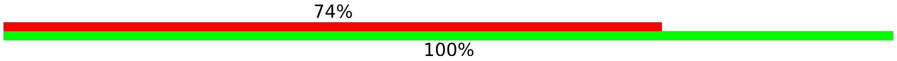
Chain 6:

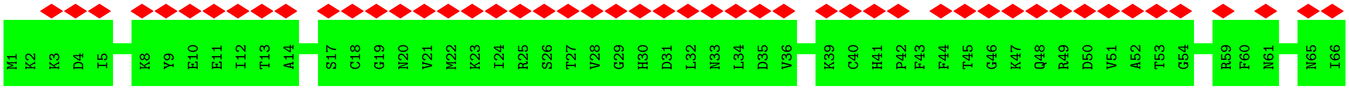




- Molecule 6: 50S ribosomal protein L31

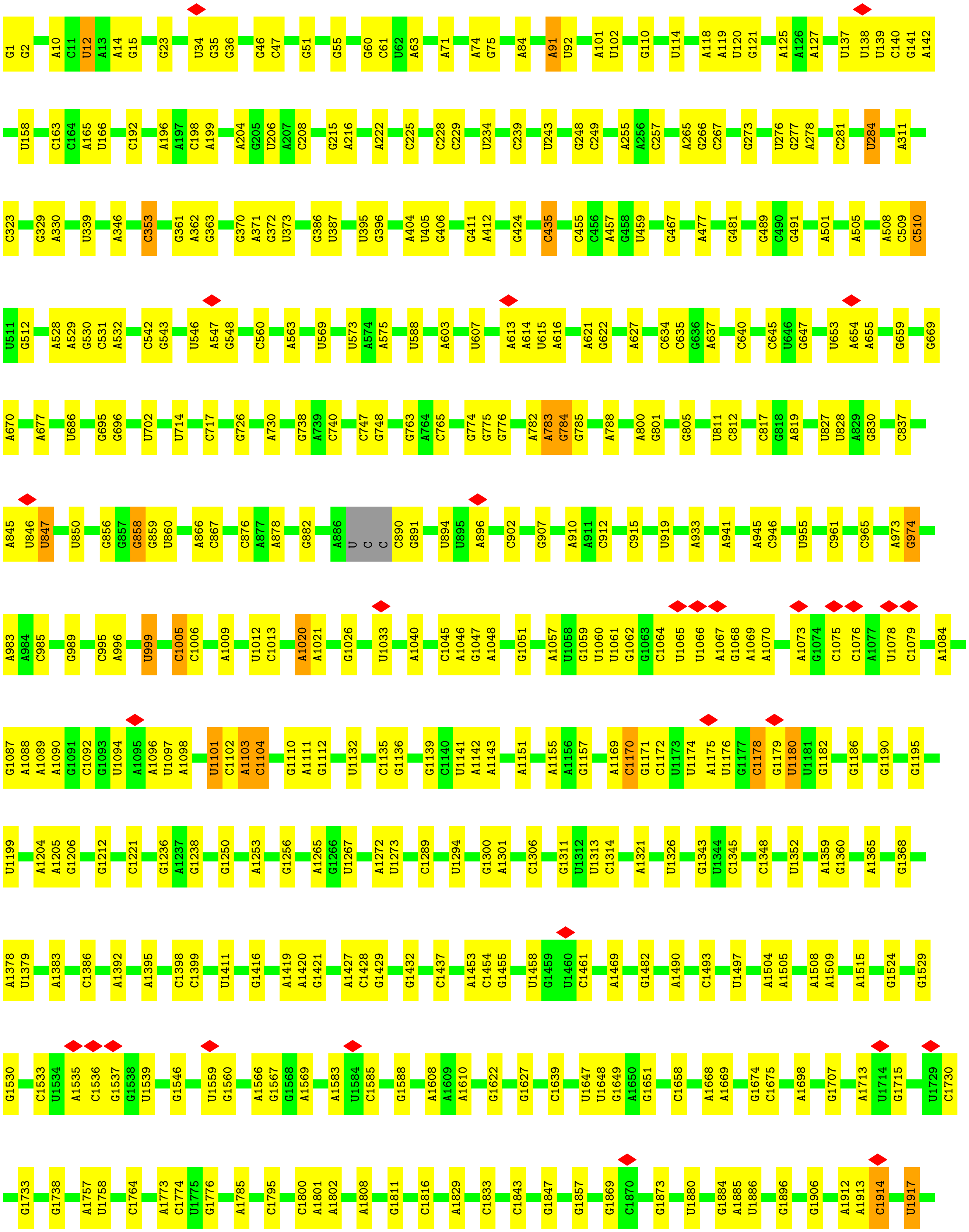
Chain 66:

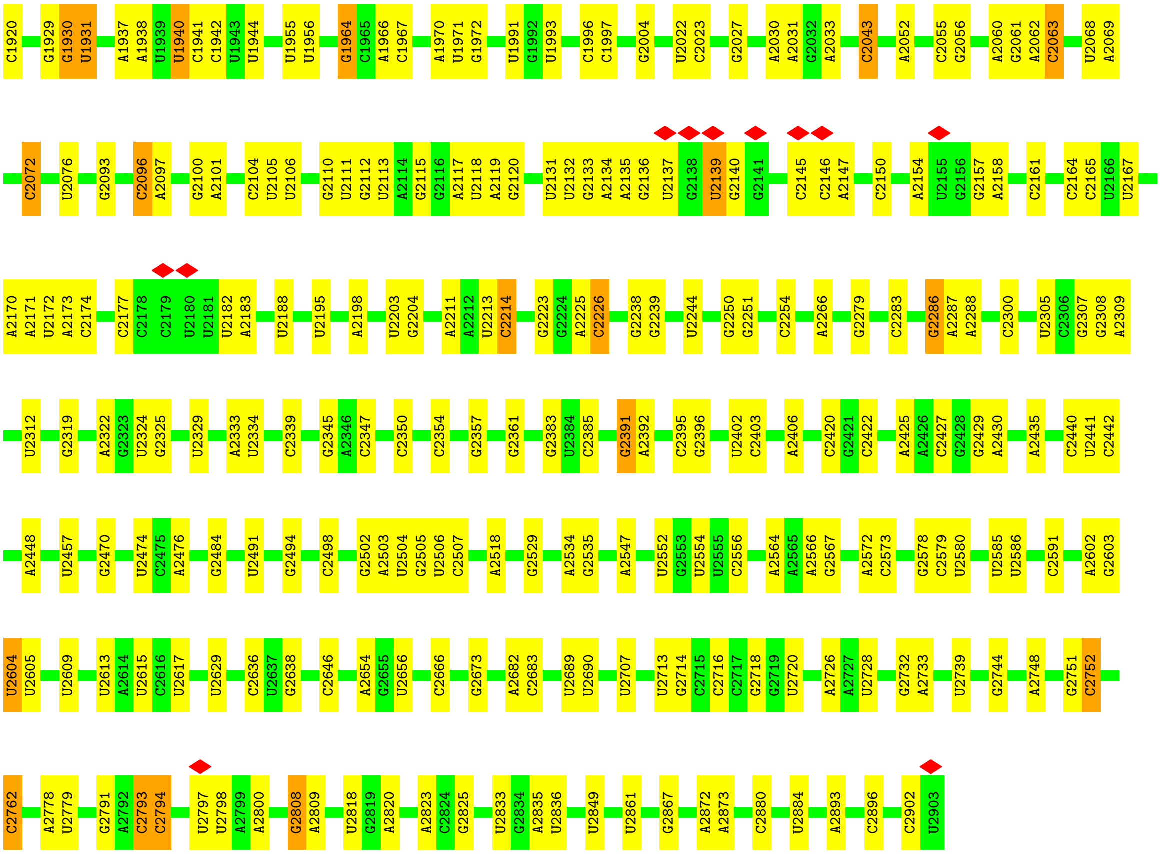




• Molecule 7: 23S ribosomal RNA

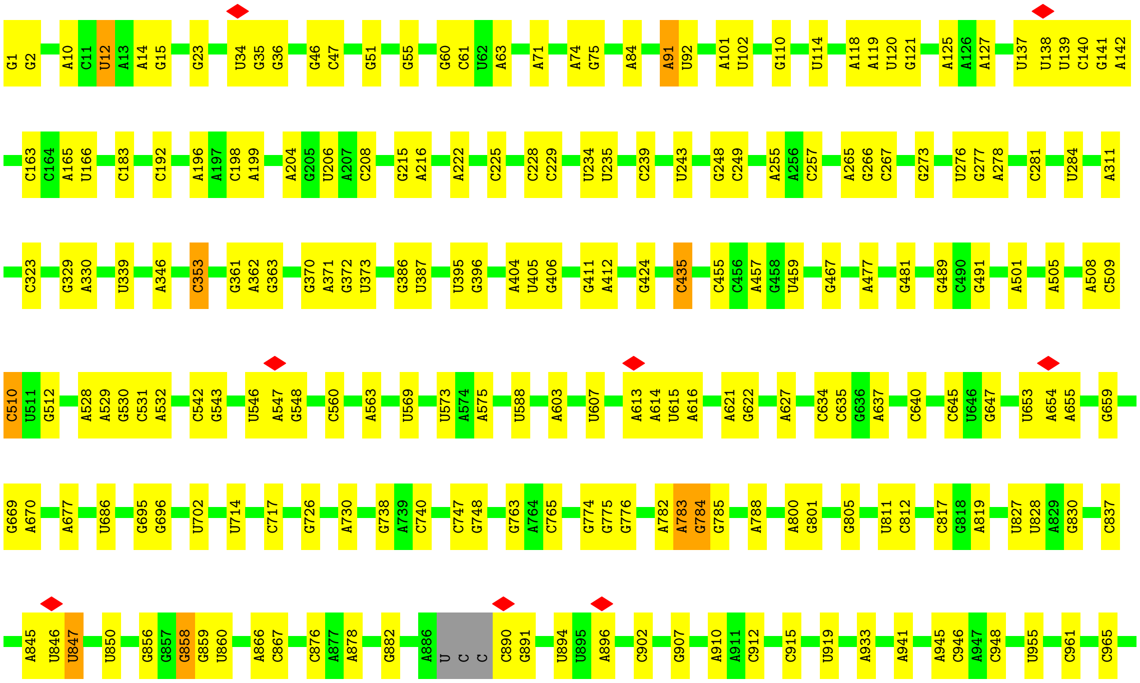
Chain A:

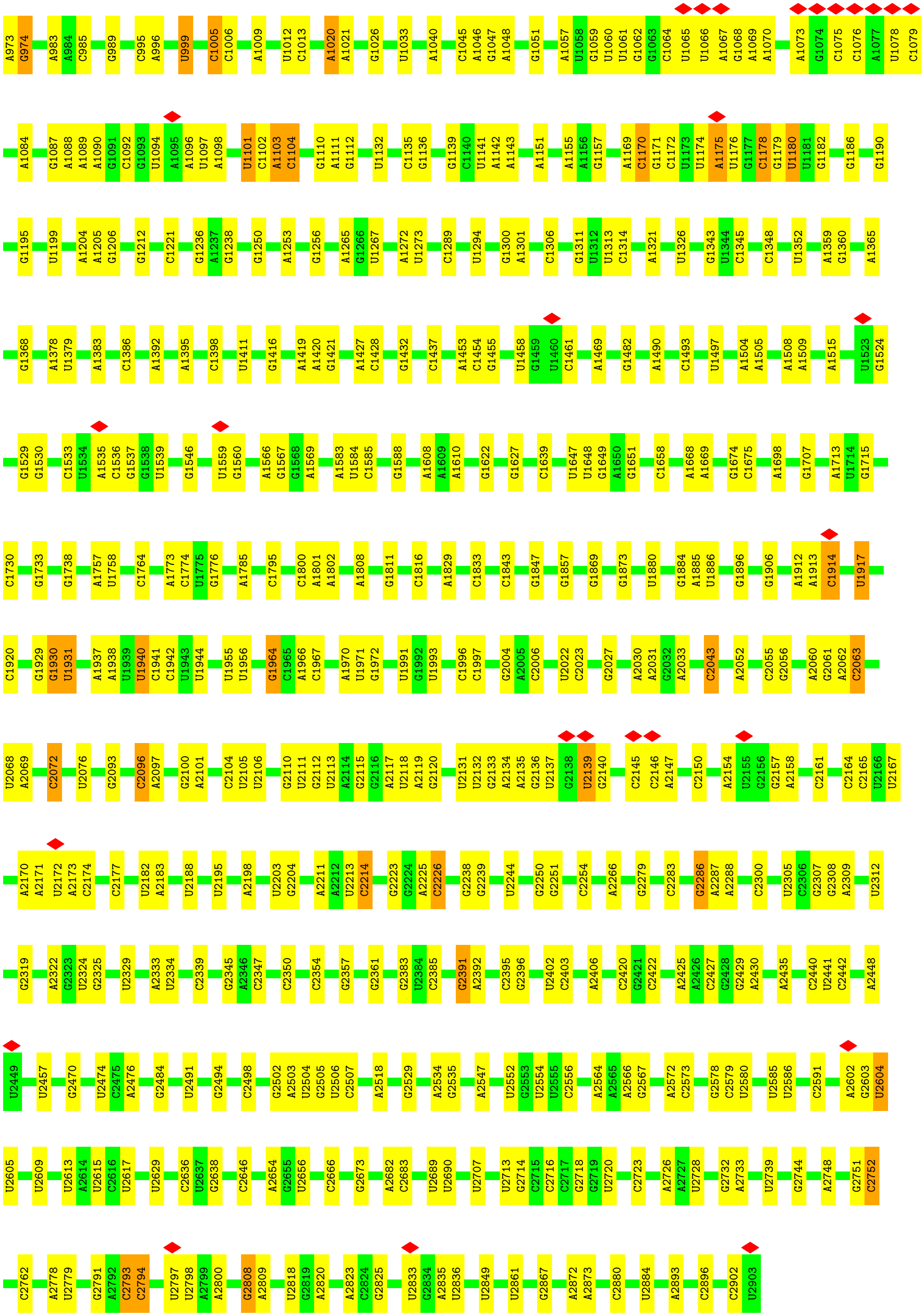




- Molecule 7: 23S ribosomal RNA

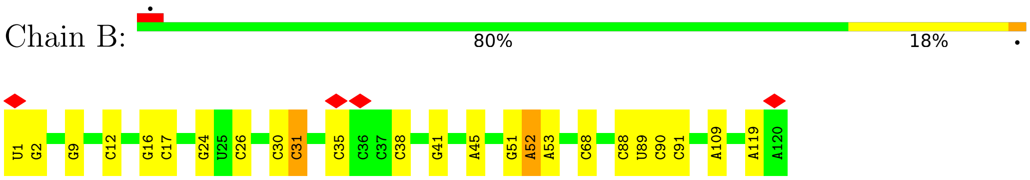
Chain AA:





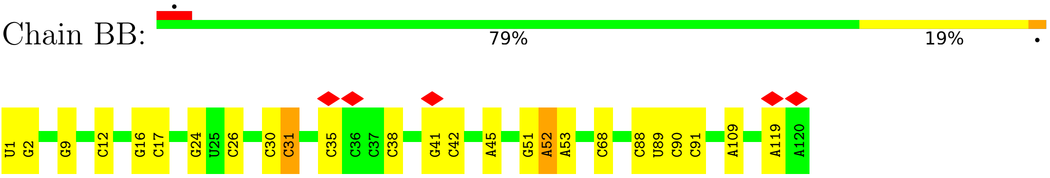
- Molecule 8: 5S ribosomal RNA

Chain B:



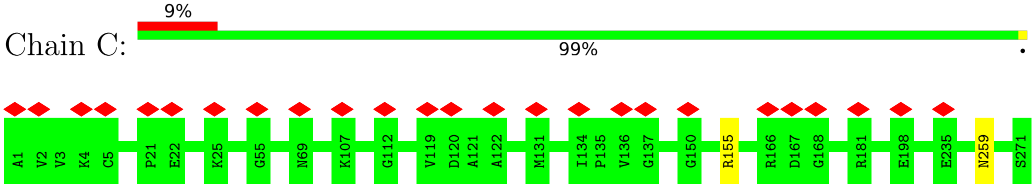
- Molecule 8: 5S ribosomal RNA

Chain BB:



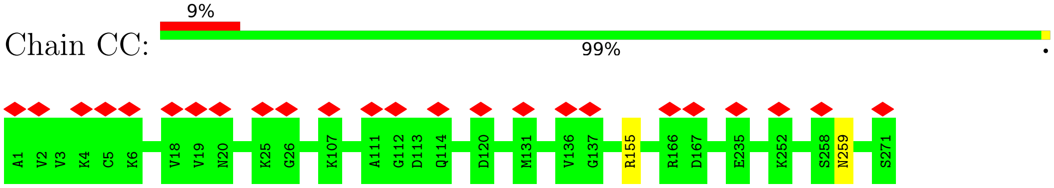
- Molecule 9: 50S ribosomal protein L2

Chain C:



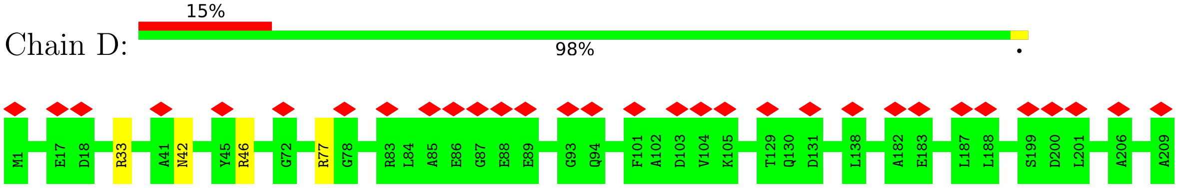
- Molecule 9: 50S ribosomal protein L2

Chain CC:



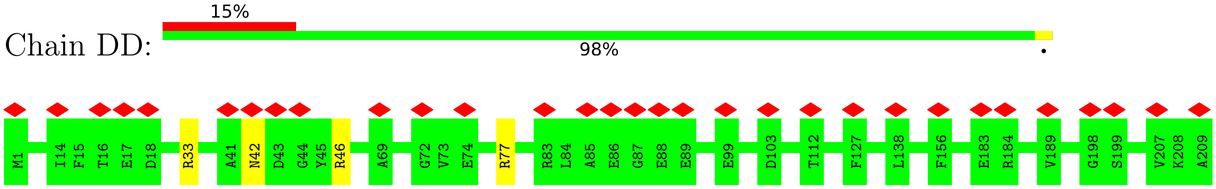
- Molecule 10: 50S ribosomal protein L3

Chain D:



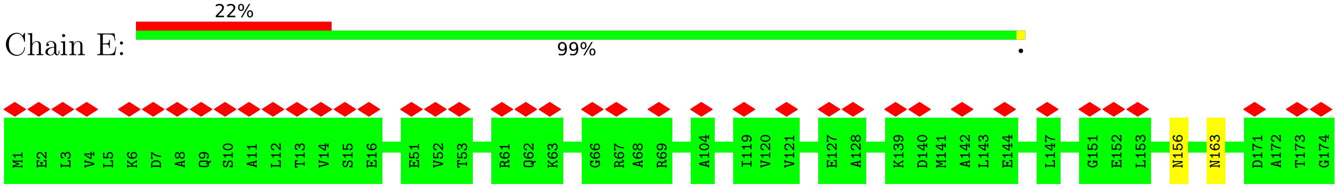
- Molecule 10: 50S ribosomal protein L3

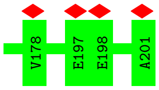
Chain DD:



- Molecule 11: 50S ribosomal protein L4

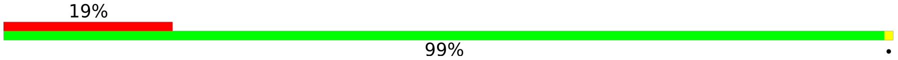
Chain E:

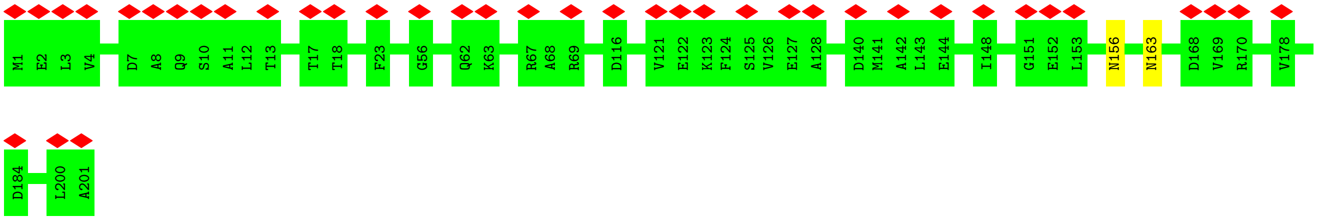




- Molecule 11: 50S ribosomal protein L4

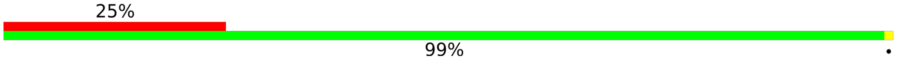
Chain EE:

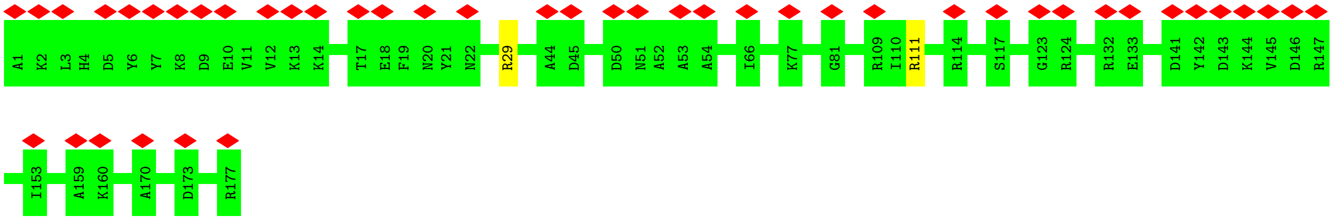




- Molecule 12: 50S ribosomal protein L5

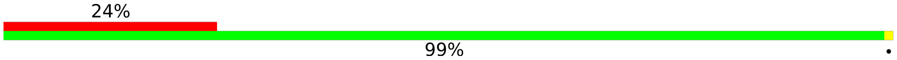
Chain F:

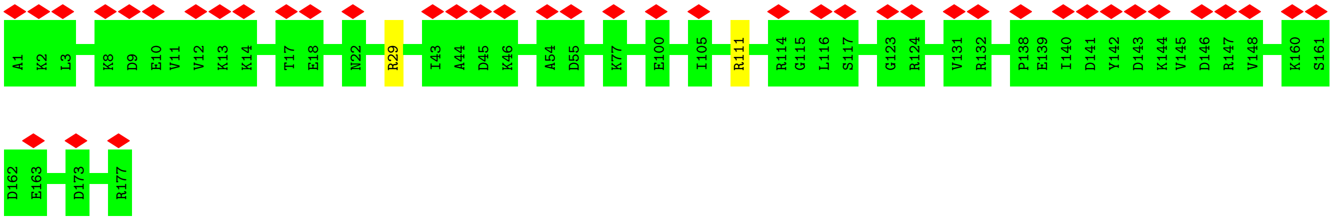




- Molecule 12: 50S ribosomal protein L5

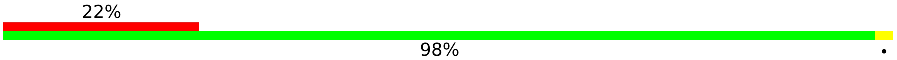
Chain FF:

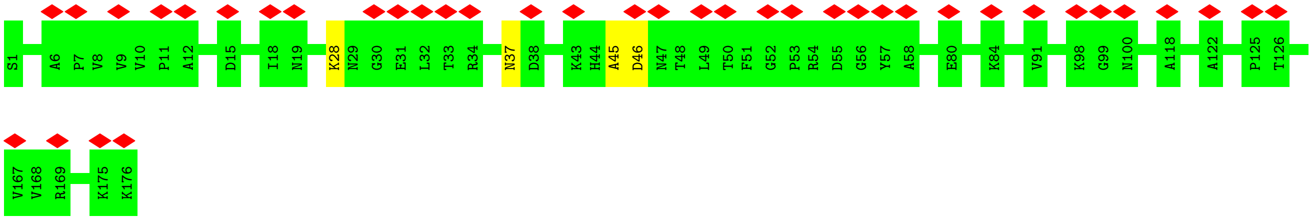




- Molecule 13: 50S ribosomal protein L6

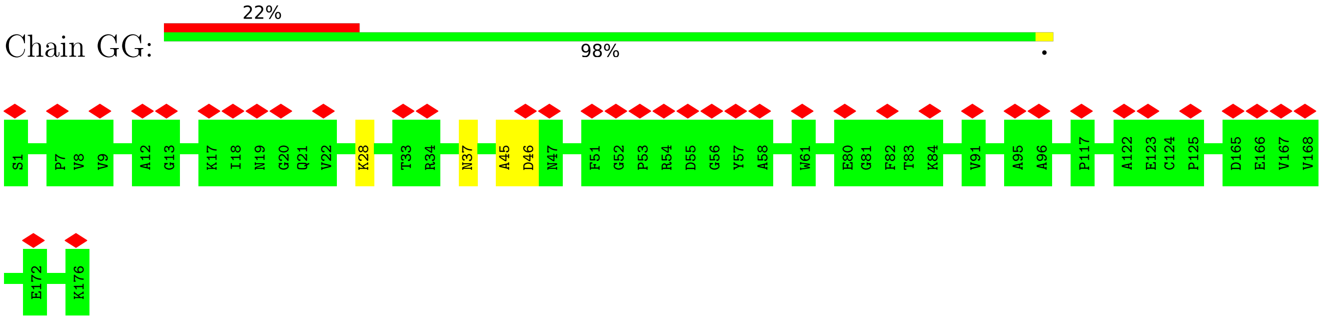
Chain G:





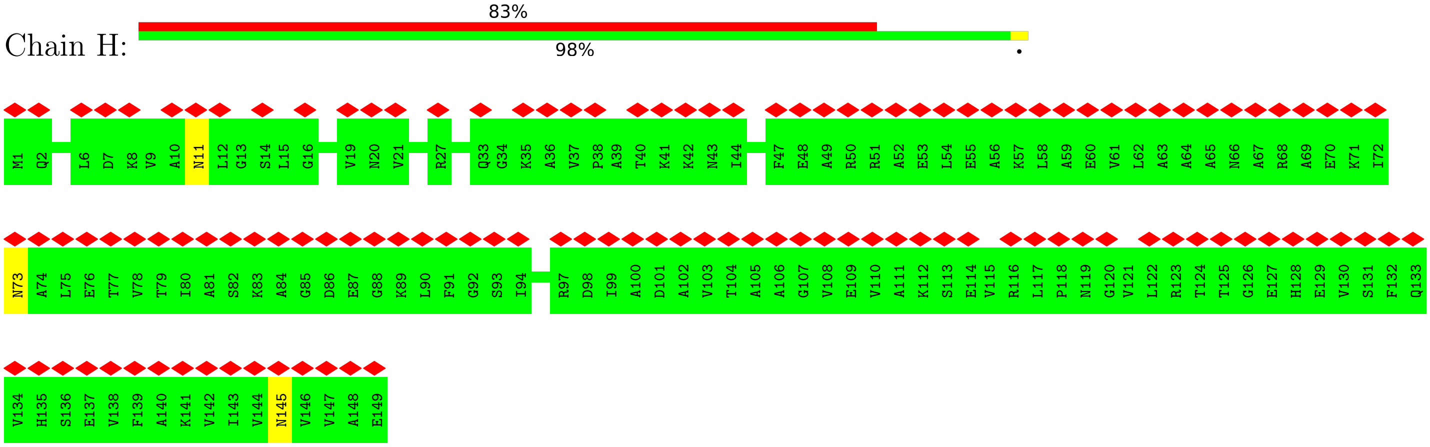
- Molecule 13: 50S ribosomal protein L6

Chain GG:



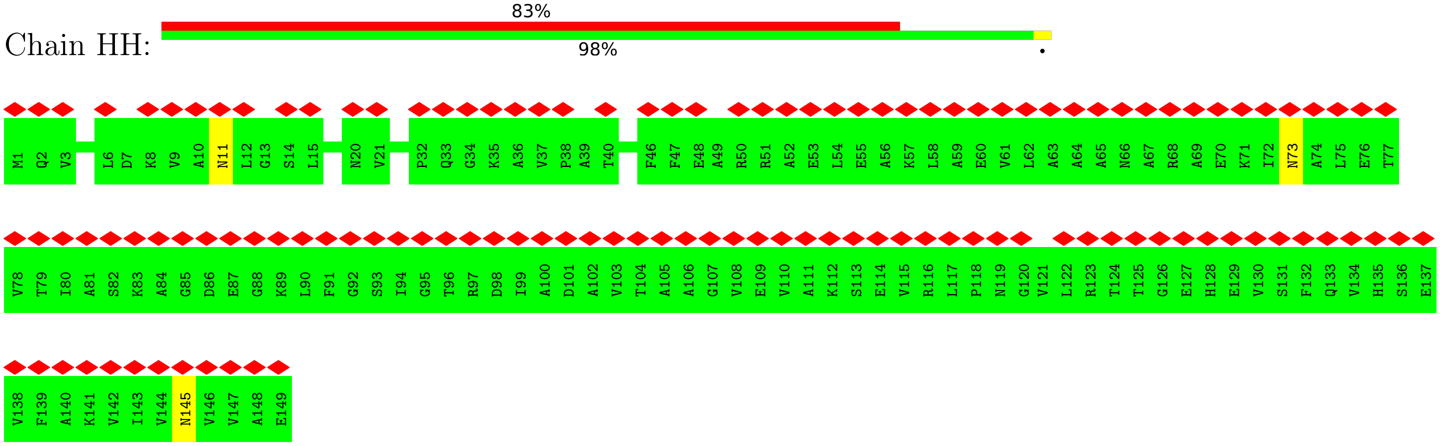
- Molecule 14: 50S ribosomal protein L9

Chain H:



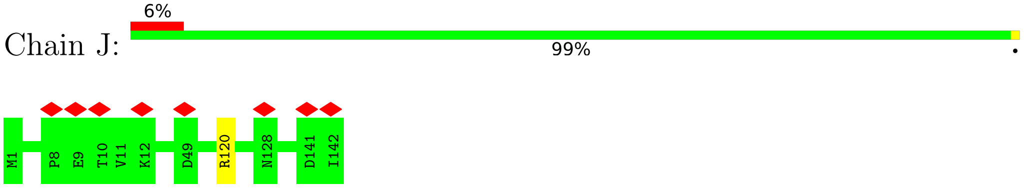
- Molecule 14: 50S ribosomal protein L9

Chain HH:



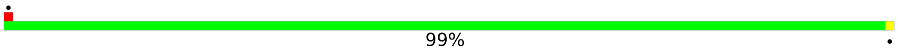
- Molecule 15: 50S ribosomal protein L13

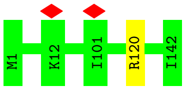
Chain J:



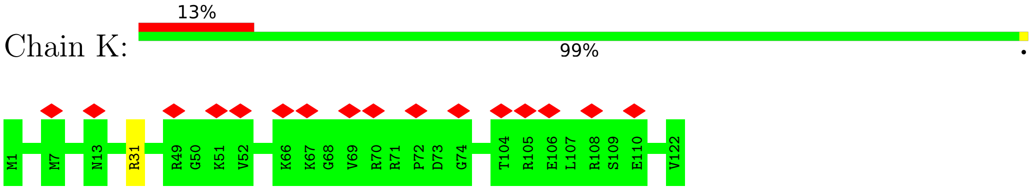
- Molecule 15: 50S ribosomal protein L13

Chain JJ:

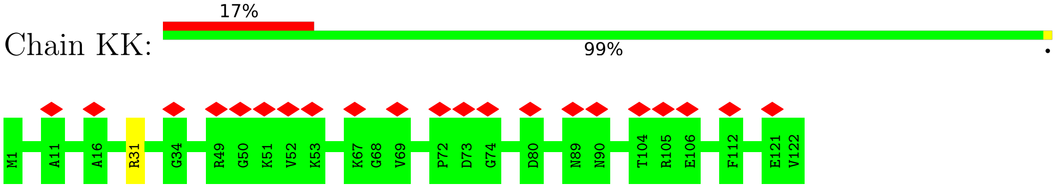




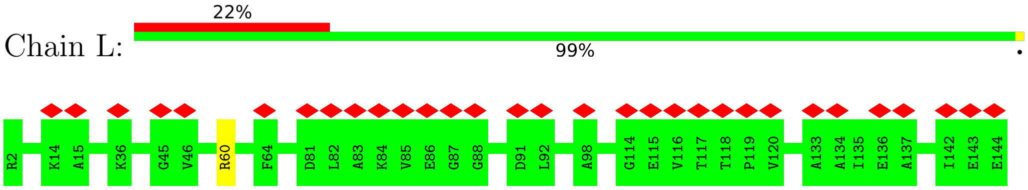
- Molecule 16: 50S ribosomal protein L14



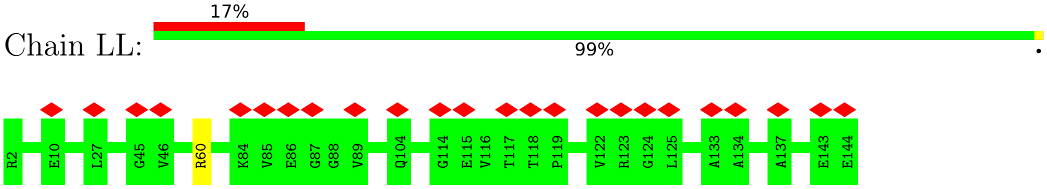
- Molecule 16: 50S ribosomal protein L14



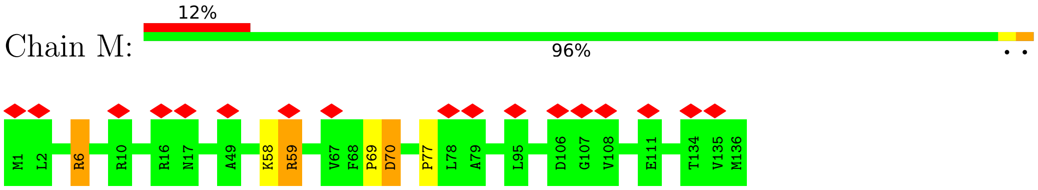
- Molecule 17: 50S ribosomal protein L15



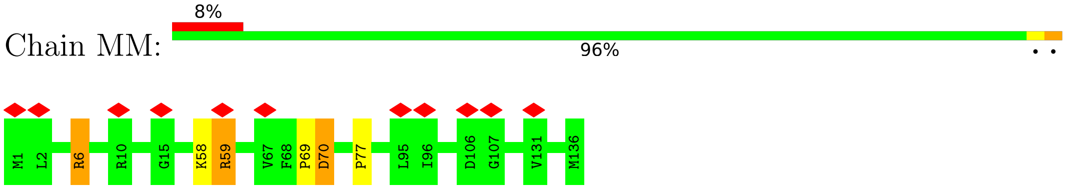
- Molecule 17: 50S ribosomal protein L15



- Molecule 18: 50S ribosomal protein L16

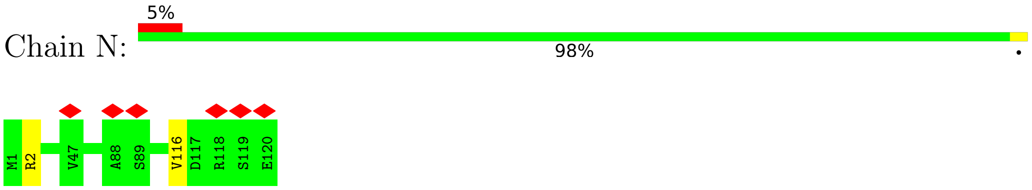


- Molecule 18: 50S ribosomal protein L16



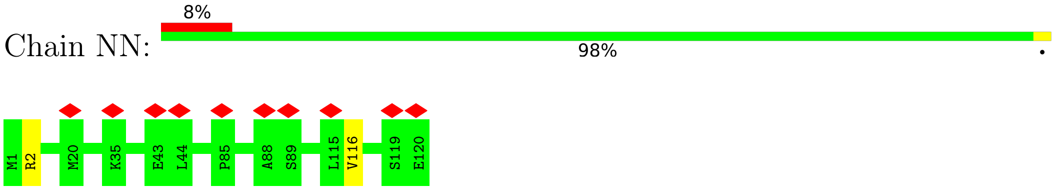
- Molecule 19: 50S ribosomal protein L17

Chain N:



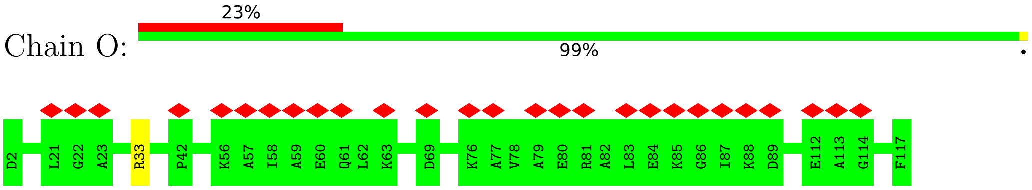
- Molecule 19: 50S ribosomal protein L17

Chain NN:



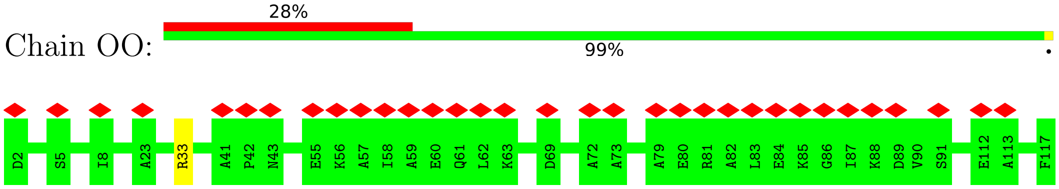
- Molecule 20: 50S ribosomal protein L18

Chain O:



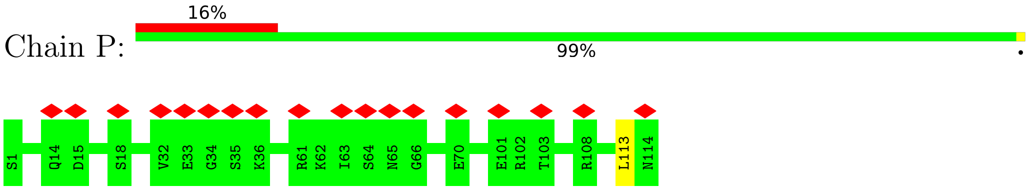
- Molecule 20: 50S ribosomal protein L18

Chain OO:



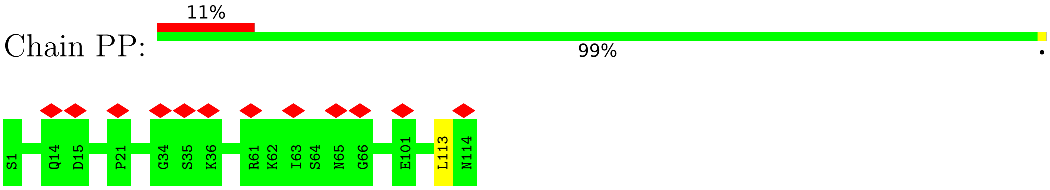
- Molecule 21: 50S ribosomal protein L19

Chain P:



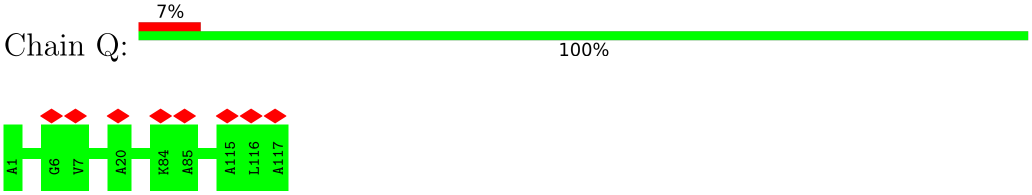
- Molecule 21: 50S ribosomal protein L19

Chain PP:



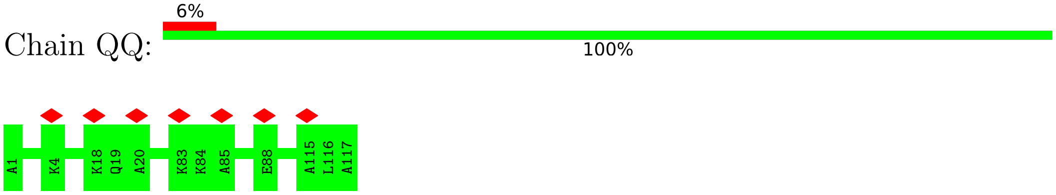
- Molecule 22: 50S ribosomal protein L20

Chain Q:



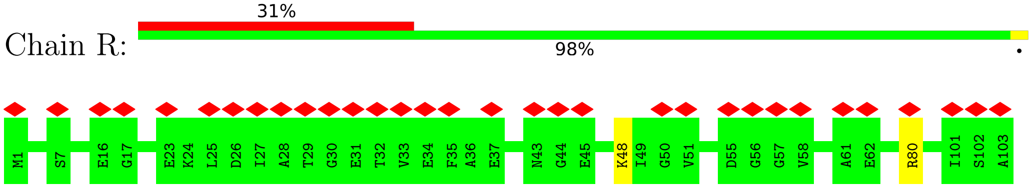
- Molecule 22: 50S ribosomal protein L20

Chain QQ:



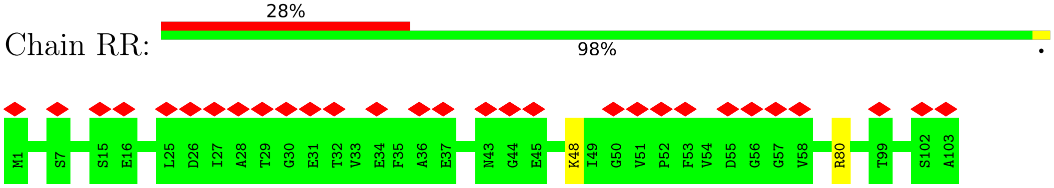
- Molecule 23: 50S ribosomal protein L21

Chain R:



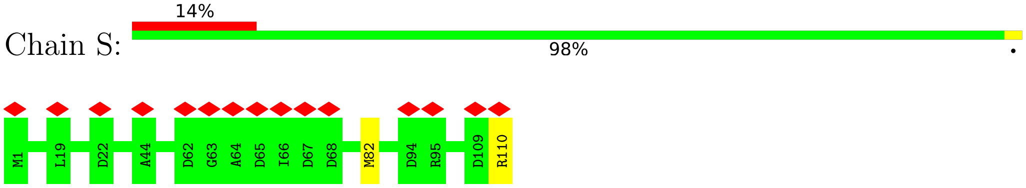
- Molecule 23: 50S ribosomal protein L21

Chain RR:



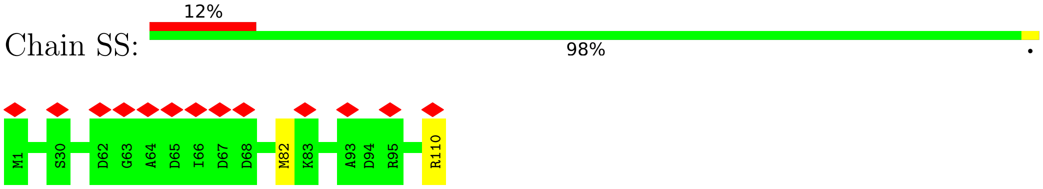
- Molecule 24: 50S ribosomal protein L22

Chain S:



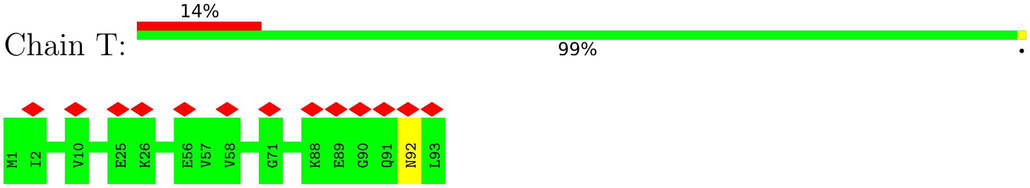
- Molecule 24: 50S ribosomal protein L22

Chain SS:



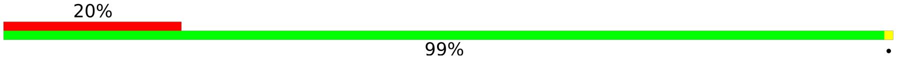
- Molecule 25: 50S ribosomal protein L23

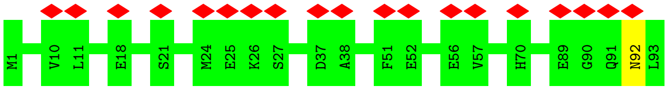
Chain T:



- Molecule 25: 50S ribosomal protein L23

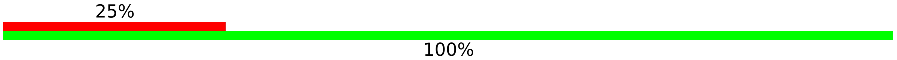
Chain TT:

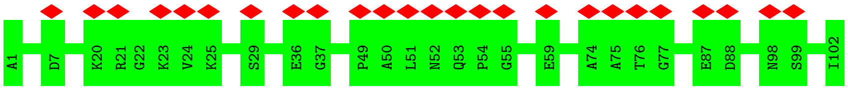




- Molecule 26: 50S ribosomal protein L24

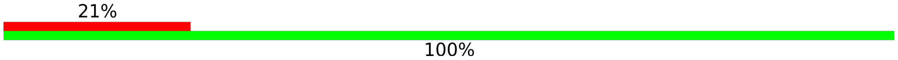
Chain U:

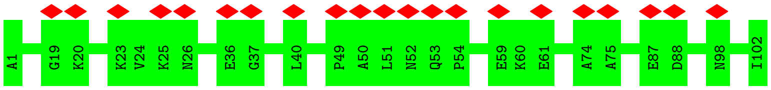




- Molecule 26: 50S ribosomal protein L24

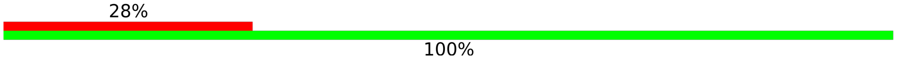
Chain UU:

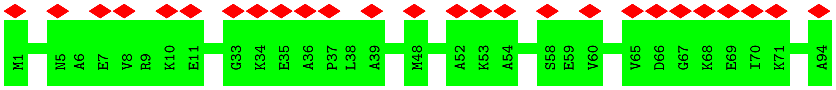




- Molecule 27: 50S ribosomal protein L25

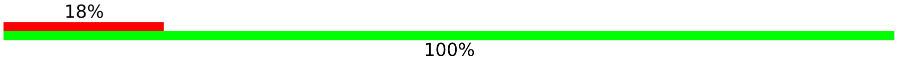
Chain V:

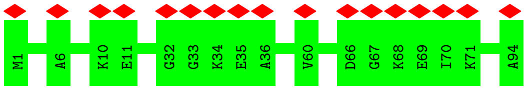




- Molecule 27: 50S ribosomal protein L25

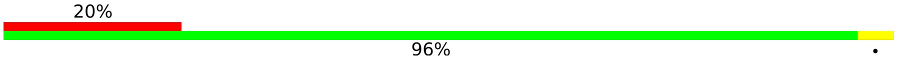
Chain VV:

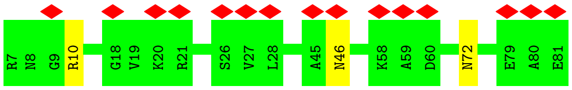




- Molecule 28: 50S ribosomal protein L27

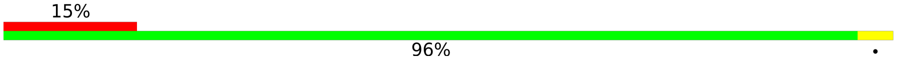
Chain W:

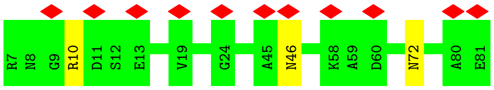




- Molecule 28: 50S ribosomal protein L27

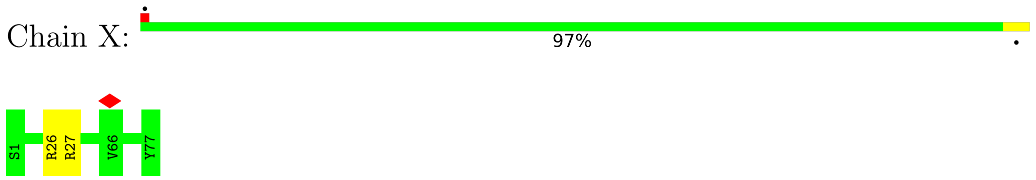
Chain WW:





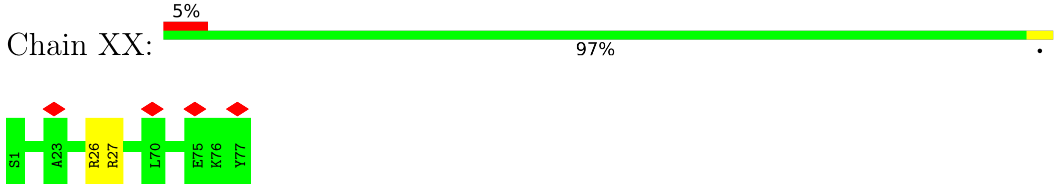
- Molecule 29: 50S ribosomal protein L28

Chain X:



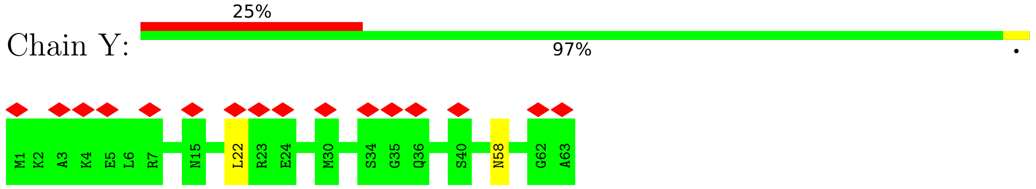
- Molecule 29: 50S ribosomal protein L28

Chain XX:



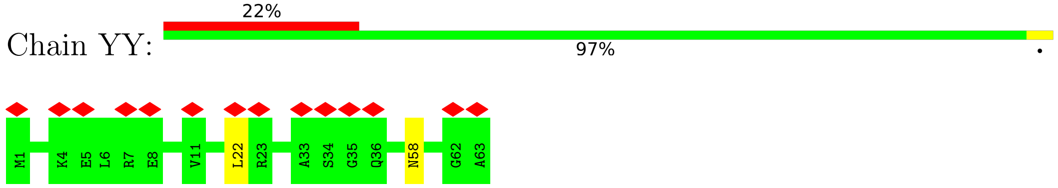
- Molecule 30: 50S ribosomal protein L29

Chain Y:



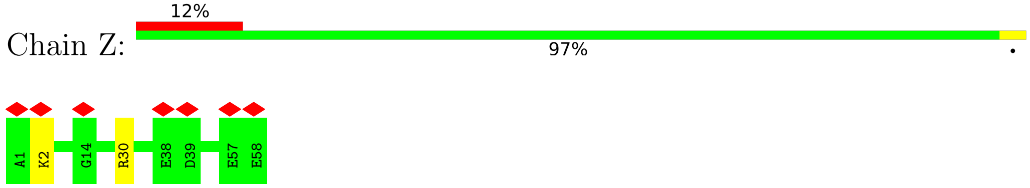
- Molecule 30: 50S ribosomal protein L29

Chain YY:



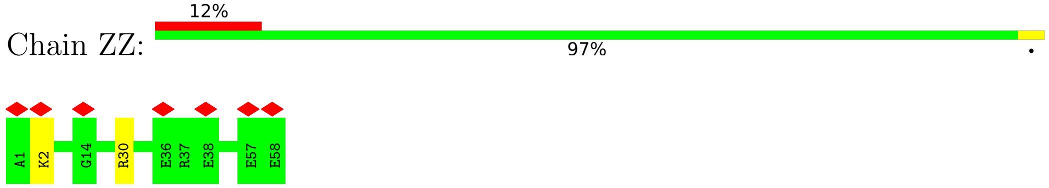
- Molecule 31: 50S ribosomal protein L30

Chain Z:



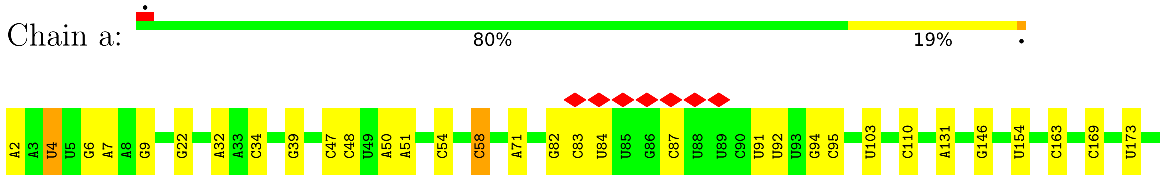
- Molecule 31: 50S ribosomal protein L30

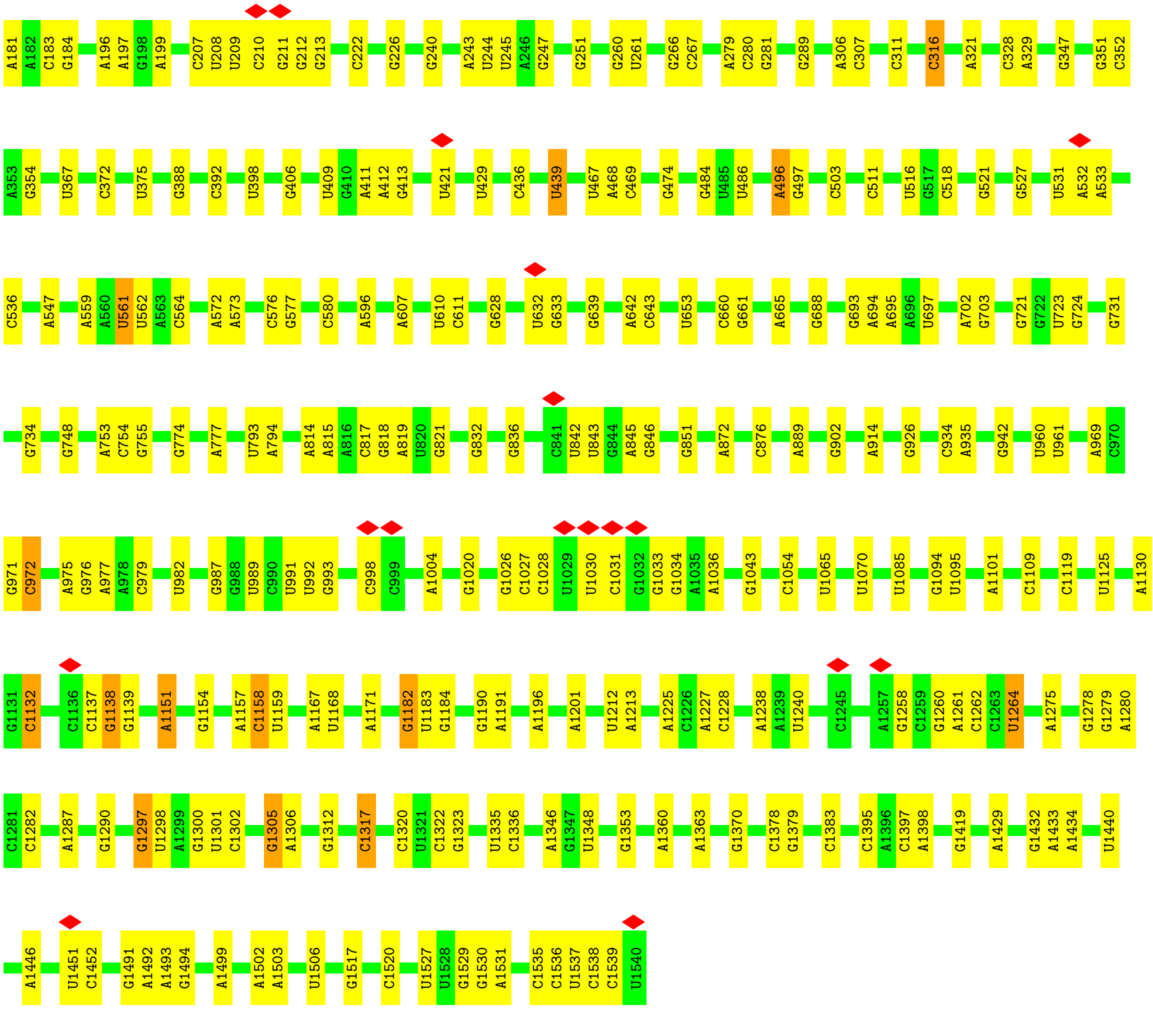
Chain ZZ:



- Molecule 32: 16S ribosomal RNA

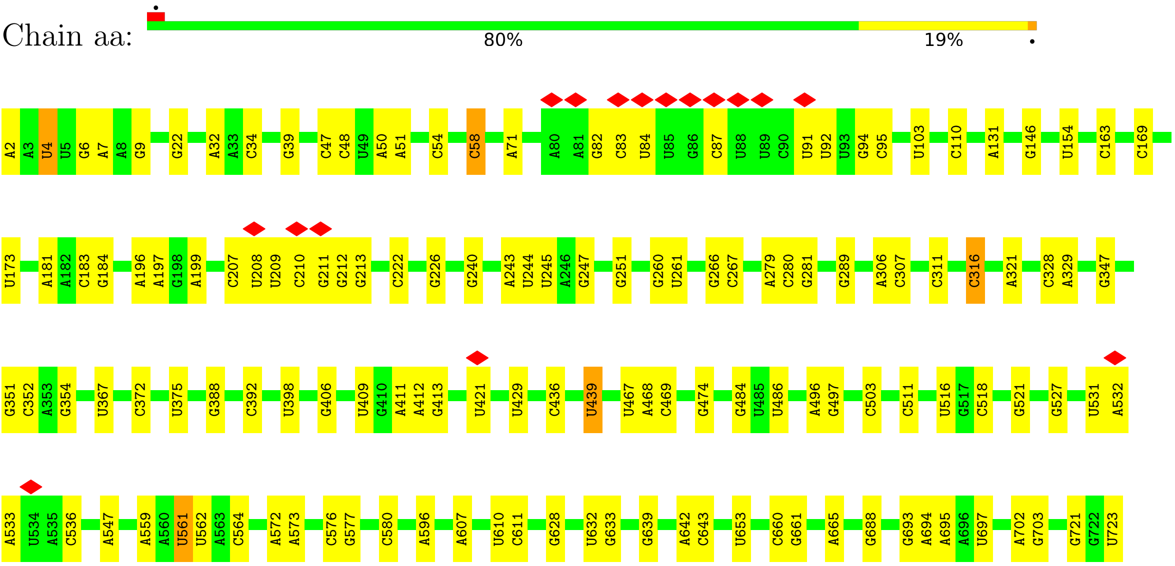
Chain a:

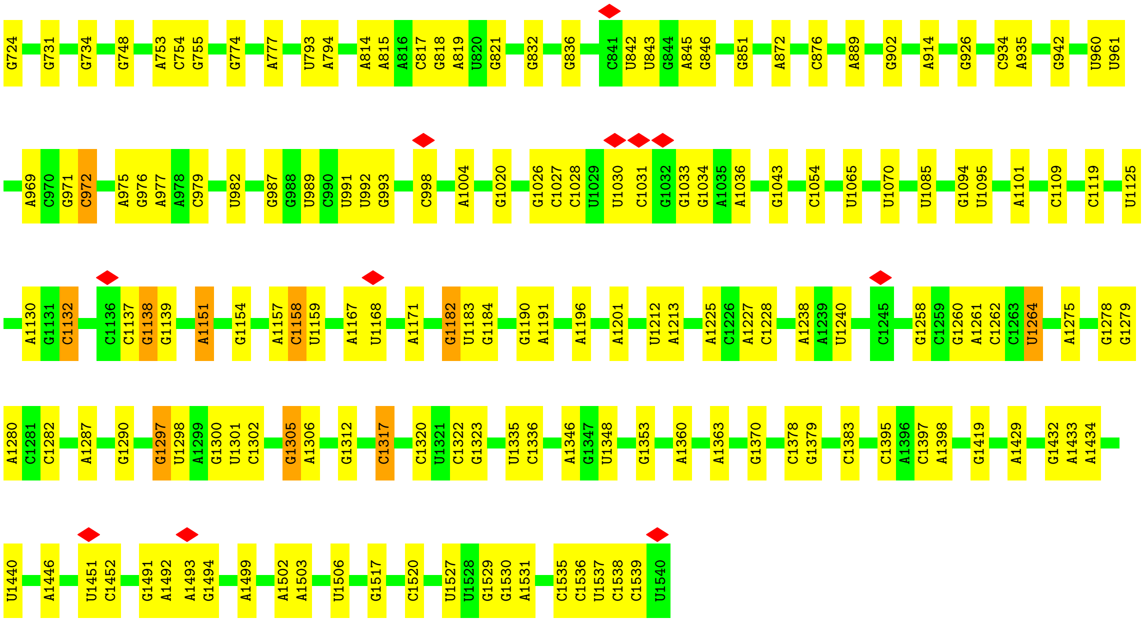




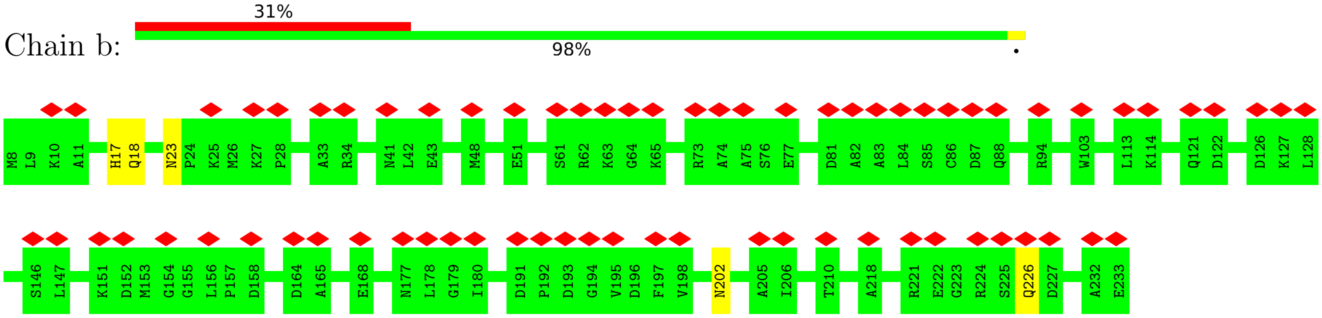
- Molecule 32: 16S ribosomal RNA

Chain aa:

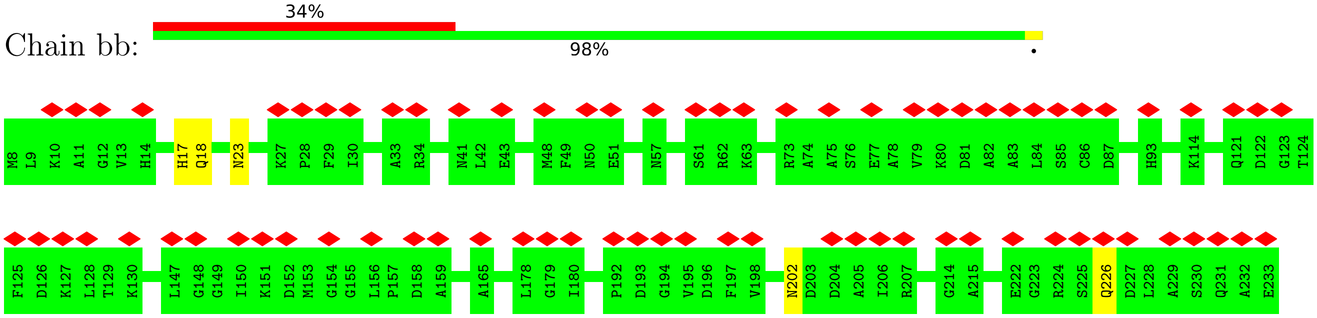




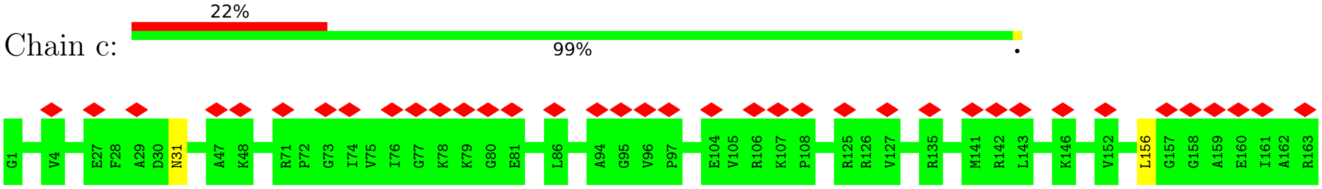
- Molecule 33: 30S ribosomal protein S2

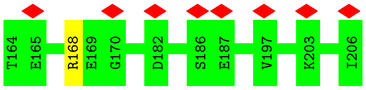


- Molecule 33: 30S ribosomal protein S2



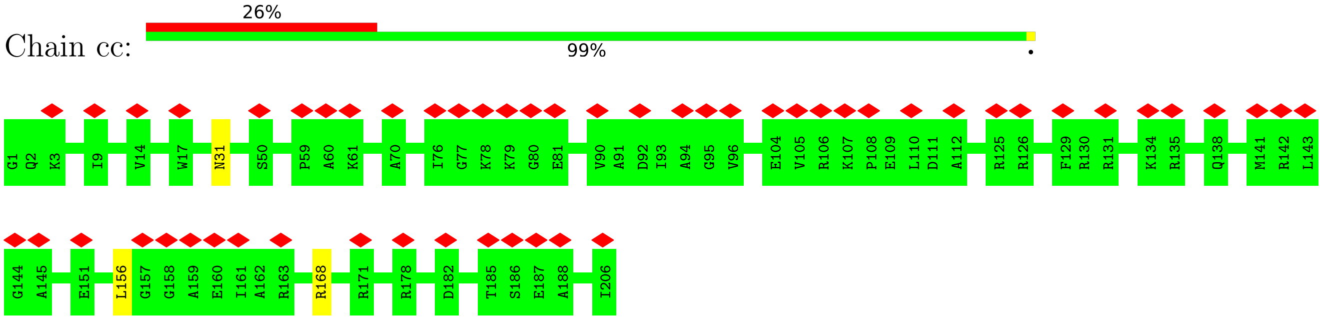
- Molecule 34: 30S ribosomal protein S3





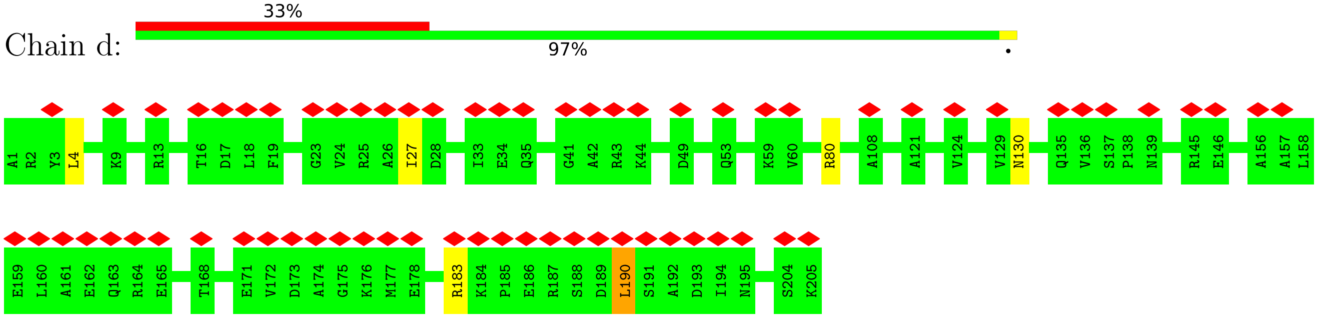
- Molecule 34: 30S ribosomal protein S3

Chain cc:



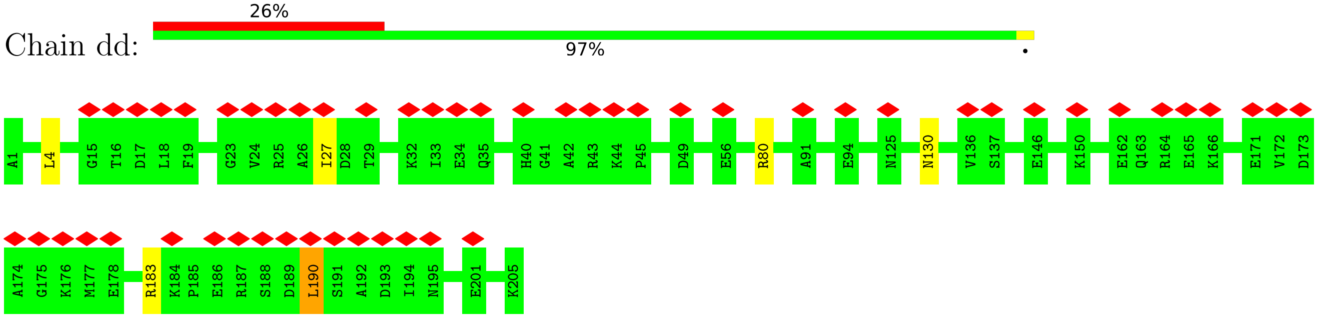
- Molecule 35: 30S ribosomal protein S4

Chain d:



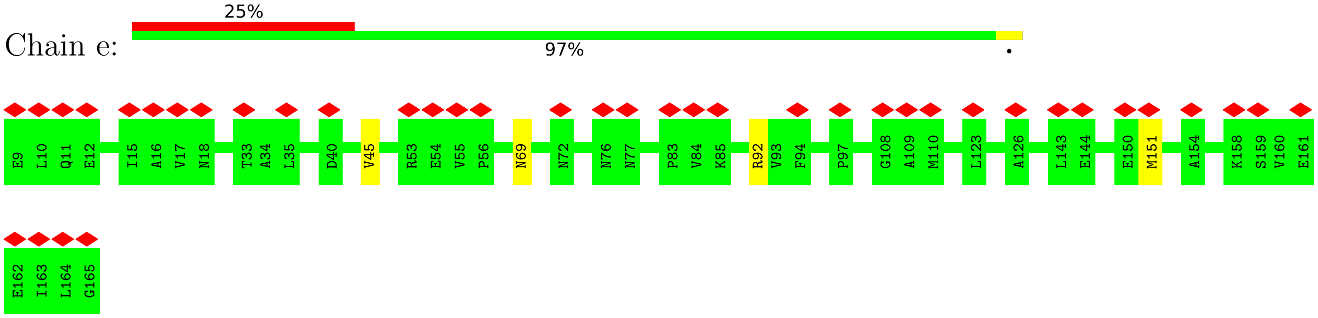
- Molecule 35: 30S ribosomal protein S4

Chain dd:

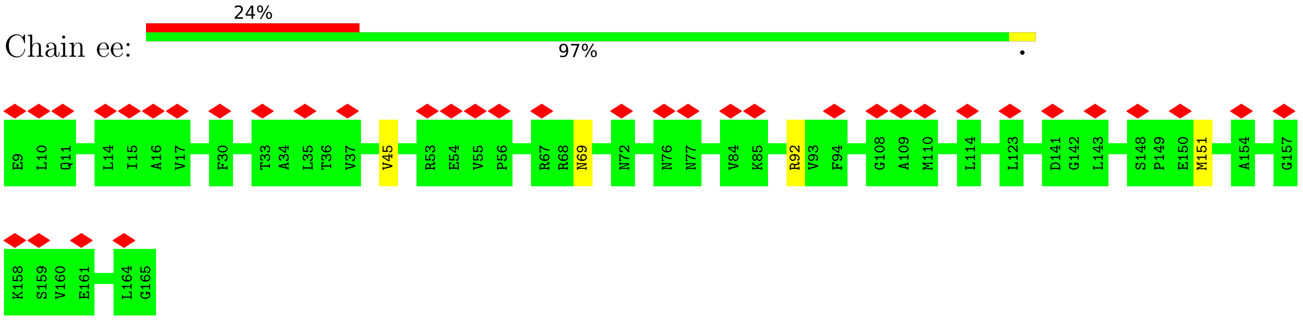


- Molecule 36: 30S ribosomal protein S5

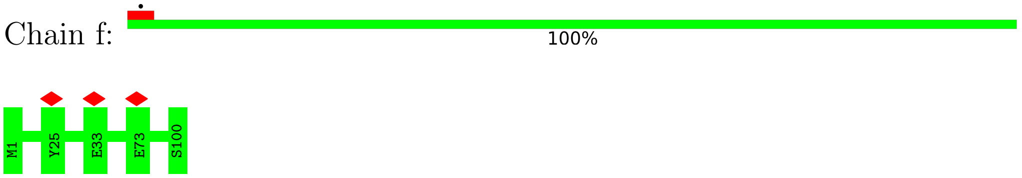
Chain e:



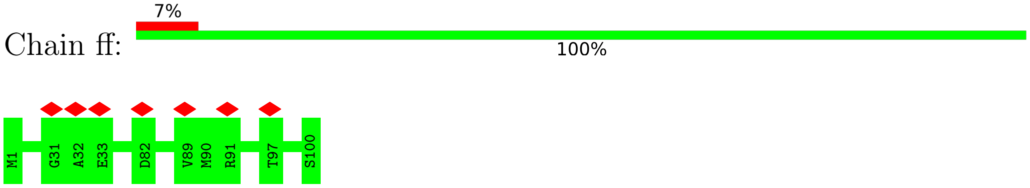
- Molecule 36: 30S ribosomal protein S5



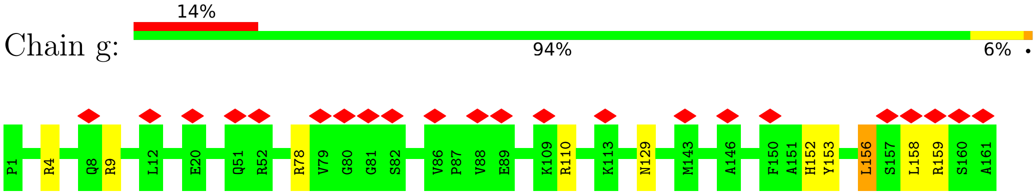
- Molecule 37: 30S ribosomal protein S6



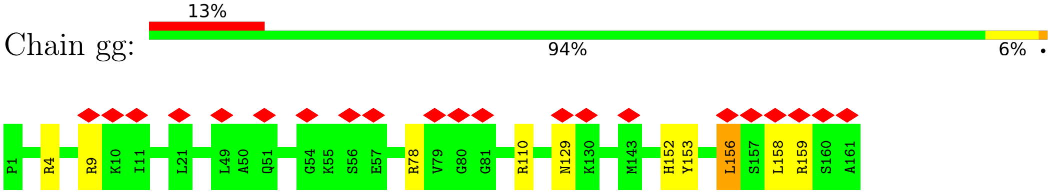
- Molecule 37: 30S ribosomal protein S6



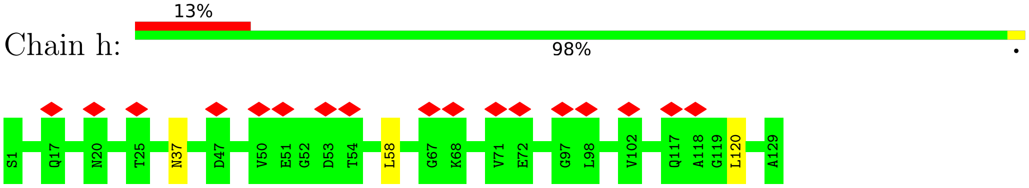
- Molecule 38: 30S ribosomal protein S7



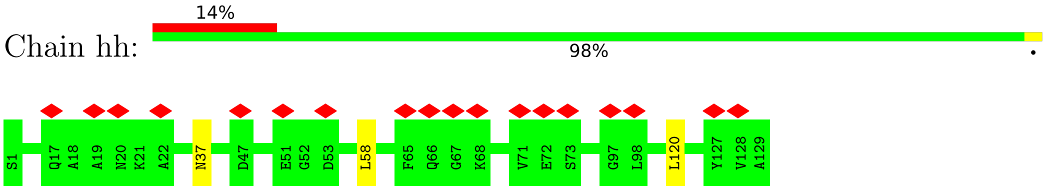
- Molecule 38: 30S ribosomal protein S7



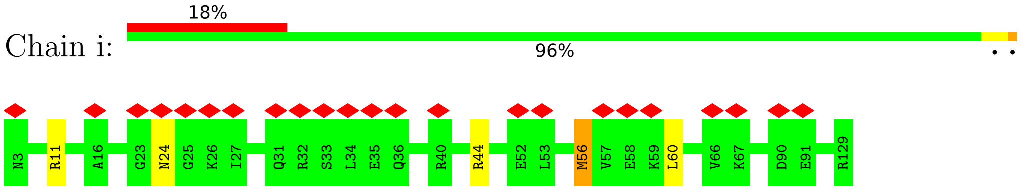
- Molecule 39: 30S ribosomal protein S8



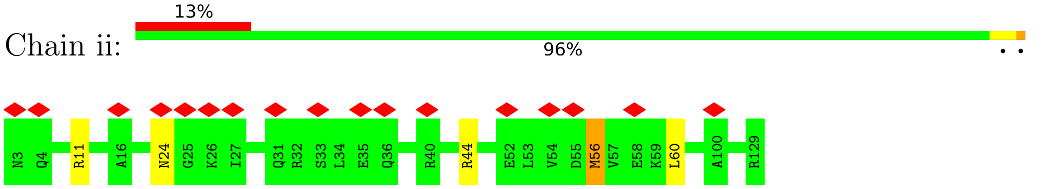
- Molecule 39: 30S ribosomal protein S8



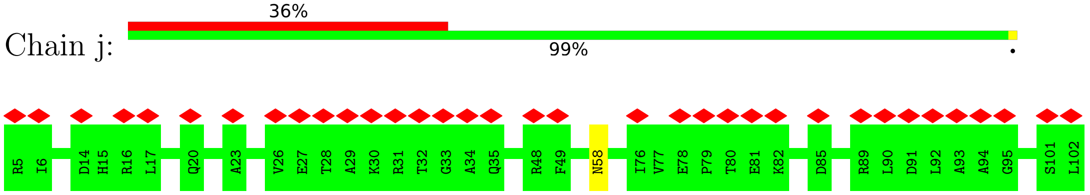
• Molecule 40: 30S ribosomal protein S9



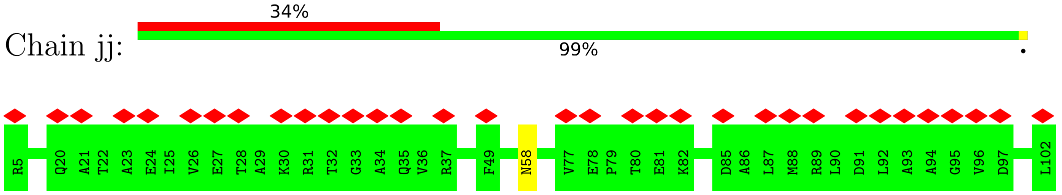
• Molecule 40: 30S ribosomal protein S9



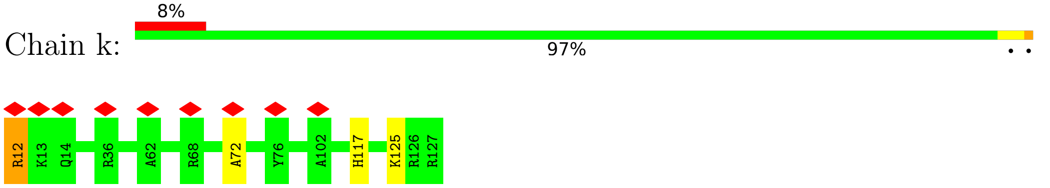
• Molecule 41: 30S ribosomal protein S10



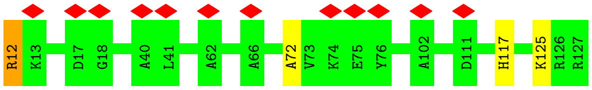
• Molecule 41: 30S ribosomal protein S10



• Molecule 42: 30S ribosomal protein S11

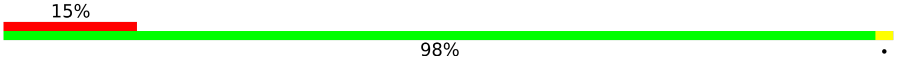


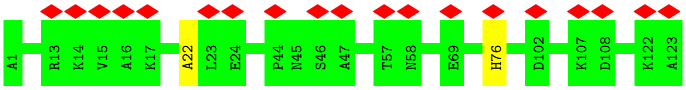
• Molecule 42: 30S ribosomal protein S11



- Molecule 43: 30S ribosomal protein S12

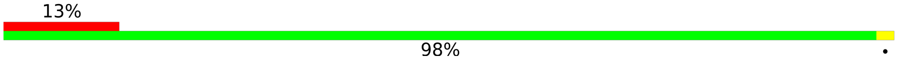
Chain l:

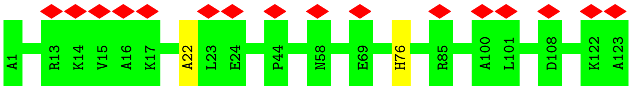




- Molecule 43: 30S ribosomal protein S12

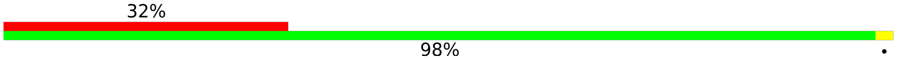
Chain ll:

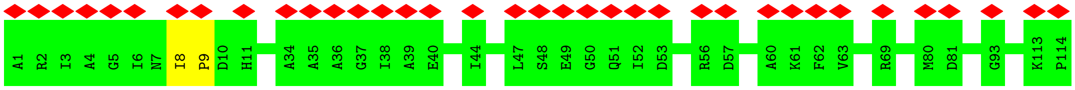




- Molecule 44: 30S ribosomal protein S13

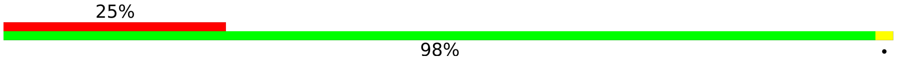
Chain m:

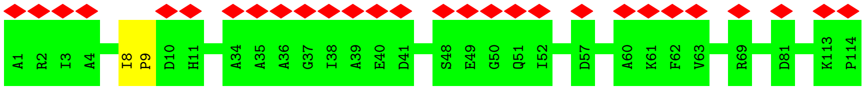




- Molecule 44: 30S ribosomal protein S13

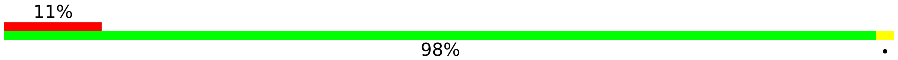
Chain mm:

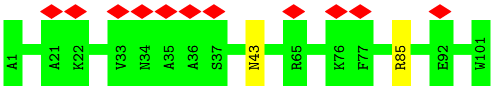




- Molecule 45: 30S ribosomal protein S14

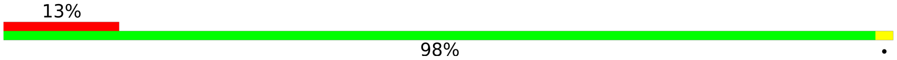
Chain n:

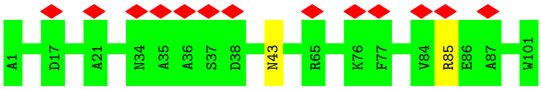




- Molecule 45: 30S ribosomal protein S14

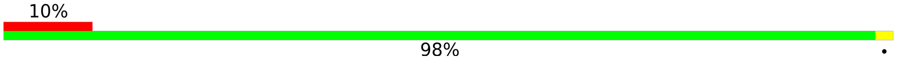
Chain nn:

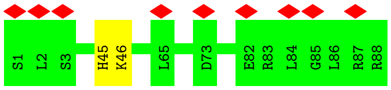




- Molecule 46: 30S ribosomal protein S15

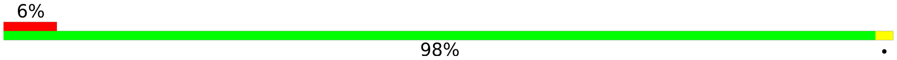
Chain o:

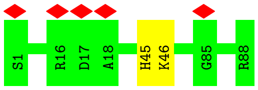




- Molecule 46: 30S ribosomal protein S15

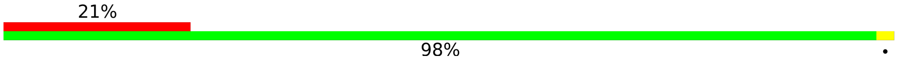
Chain oo:

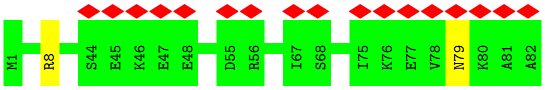




- Molecule 47: 30S ribosomal protein S16

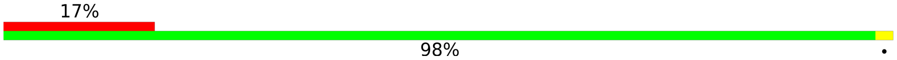
Chain p:

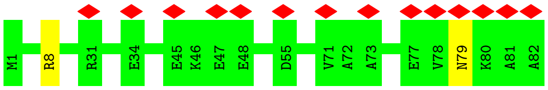




- Molecule 47: 30S ribosomal protein S16

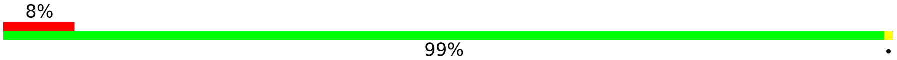
Chain pp:

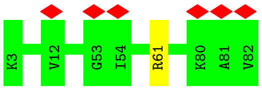




- Molecule 48: 30S ribosomal protein S17

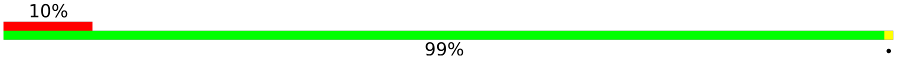
Chain q:

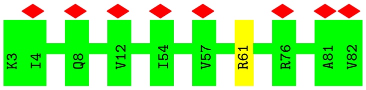




- Molecule 48: 30S ribosomal protein S17

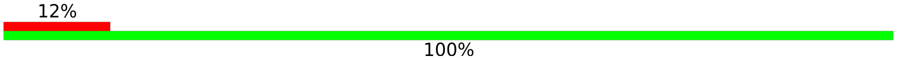
Chain qq:

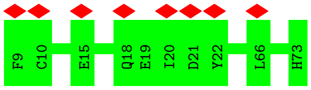




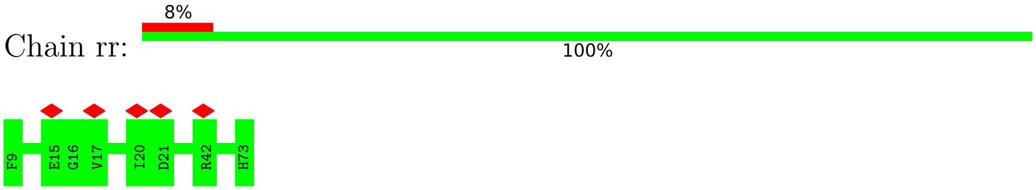
- Molecule 49: 30S ribosomal protein S18

Chain r:

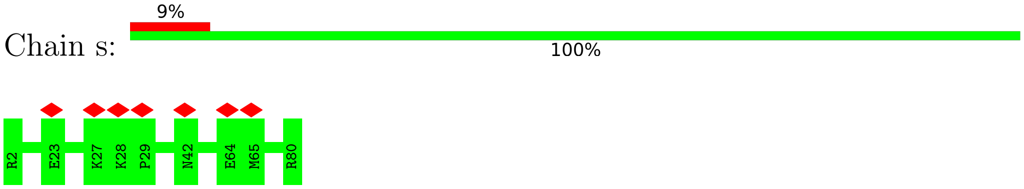




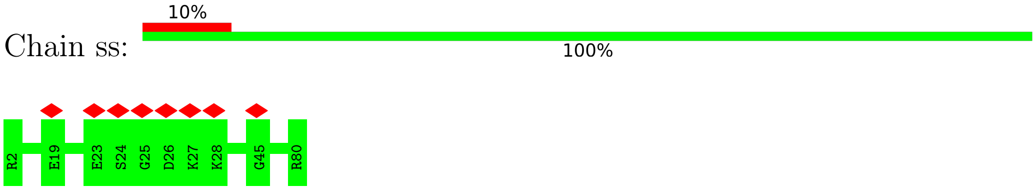
- Molecule 49: 30S ribosomal protein S18



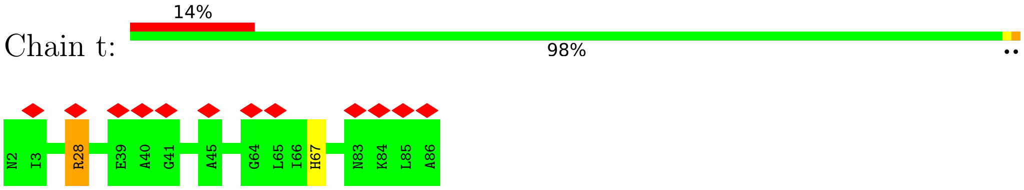
- Molecule 50: 30S ribosomal protein S19



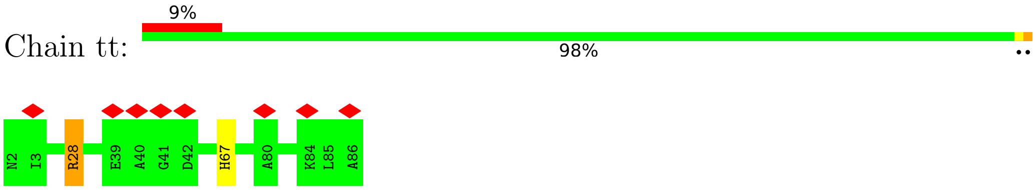
- Molecule 50: 30S ribosomal protein S19



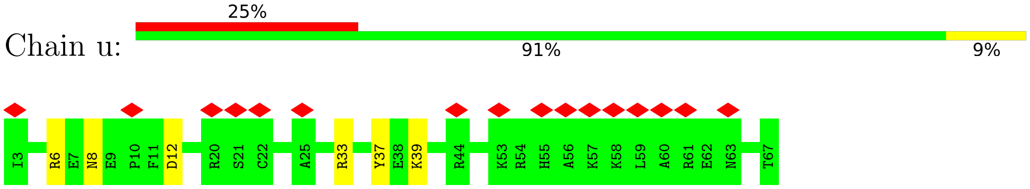
- Molecule 51: 30S ribosomal protein S20



- Molecule 51: 30S ribosomal protein S20

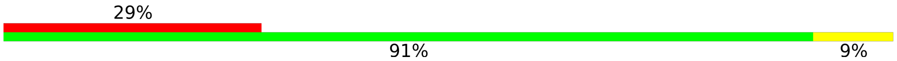


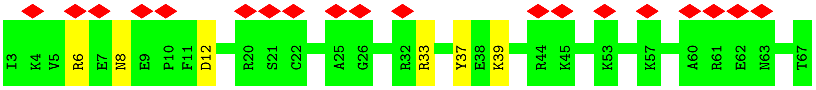
- Molecule 52: 30S ribosomal protein S21



- Molecule 52: 30S ribosomal protein S21

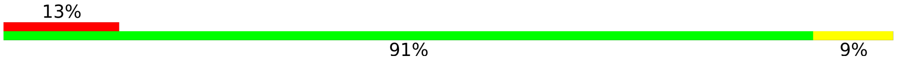
Chain uu:

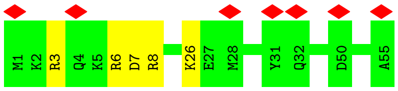




- Molecule 53: Ribosome modulation factor

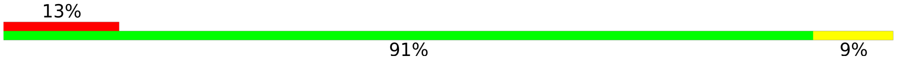
Chain v:

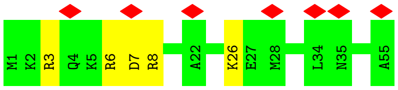




- Molecule 53: Ribosome modulation factor

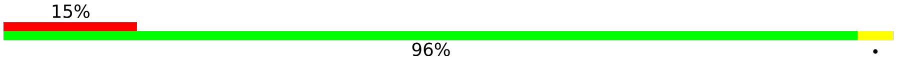
Chain vv:

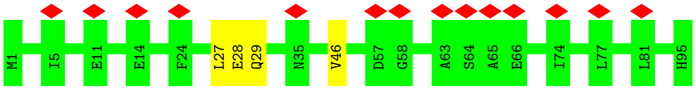




- Molecule 54: Ribosome hibernation promoting factor

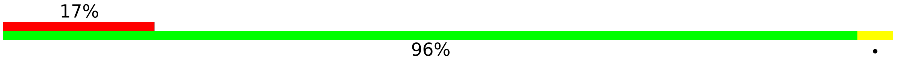
Chain x:

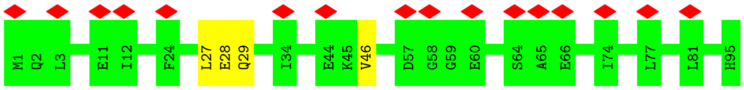




- Molecule 54: Ribosome hibernation promoting factor

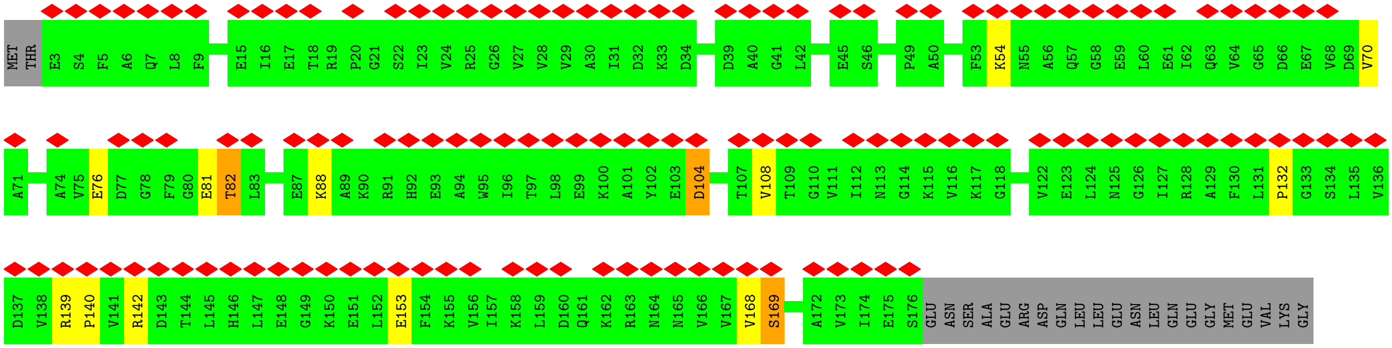
Chain xx:

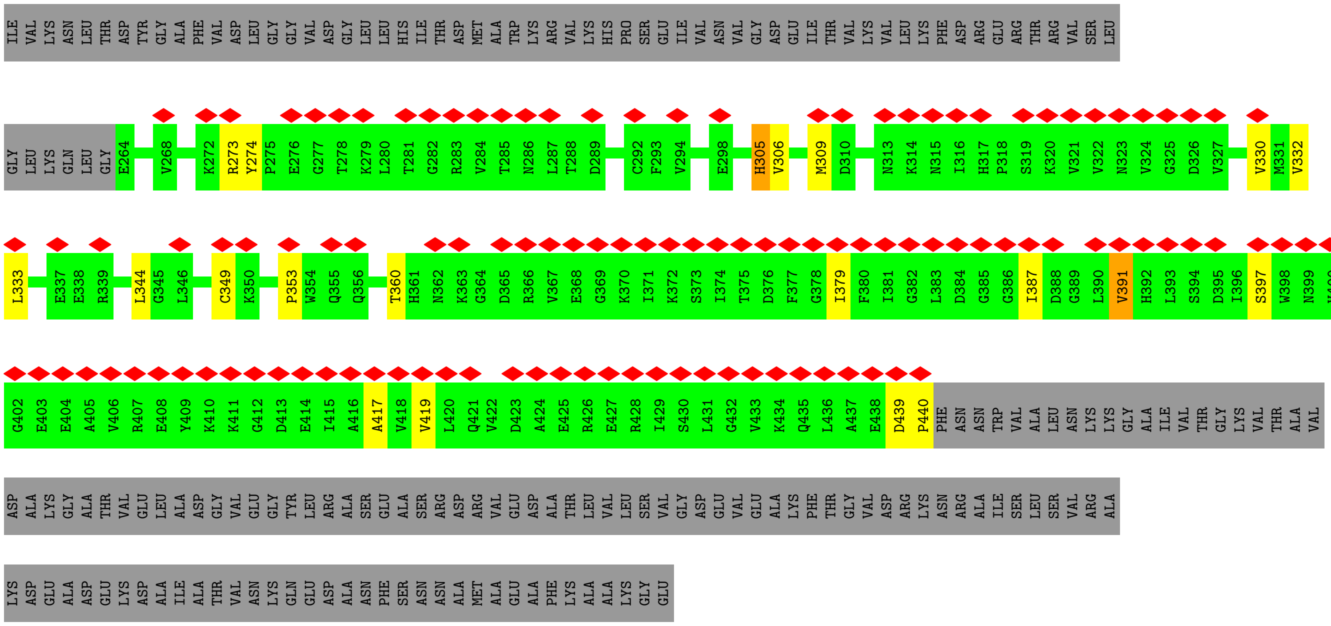




- Molecule 55: 30S ribosomal protein S1

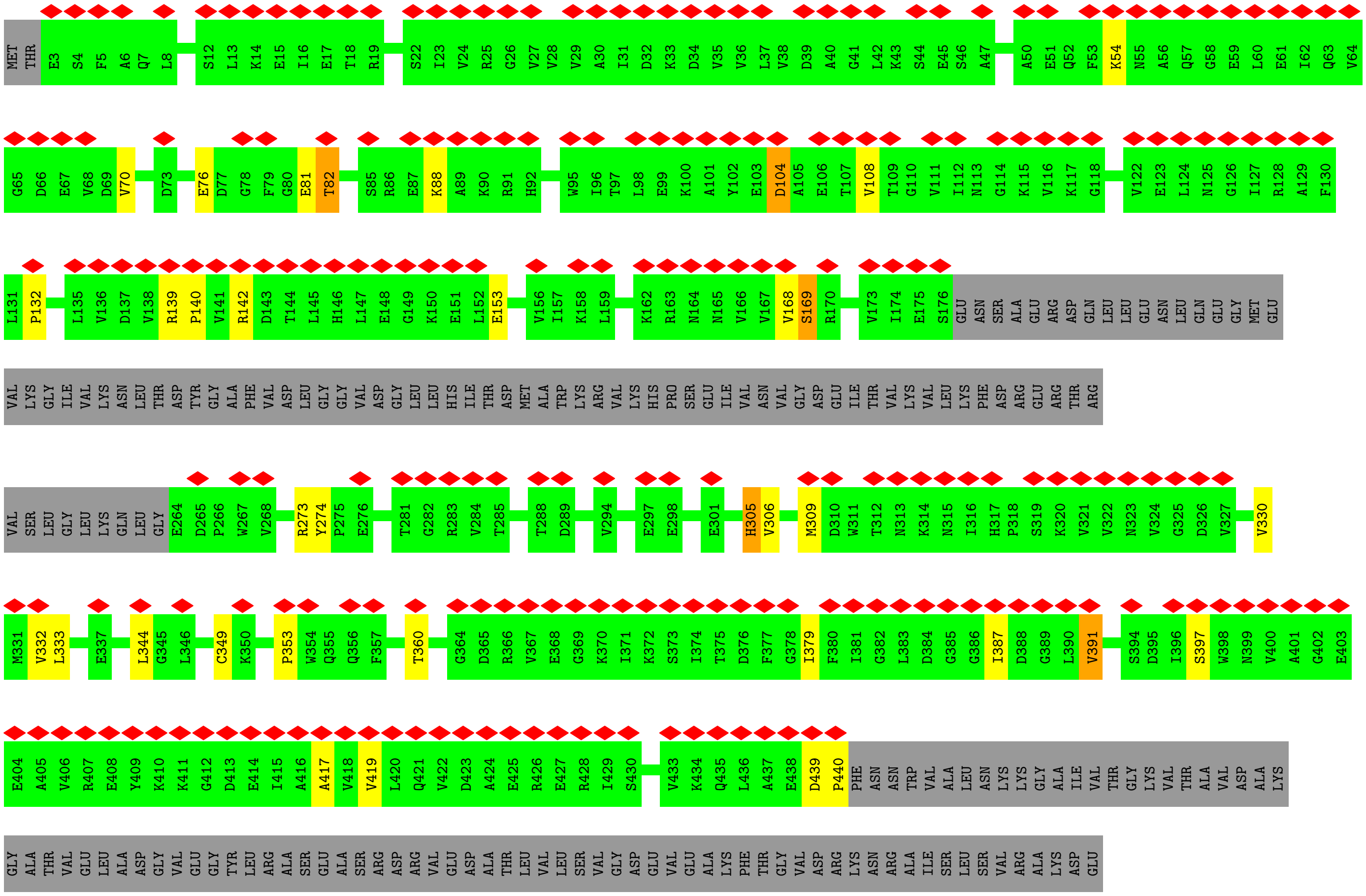
Chain y:



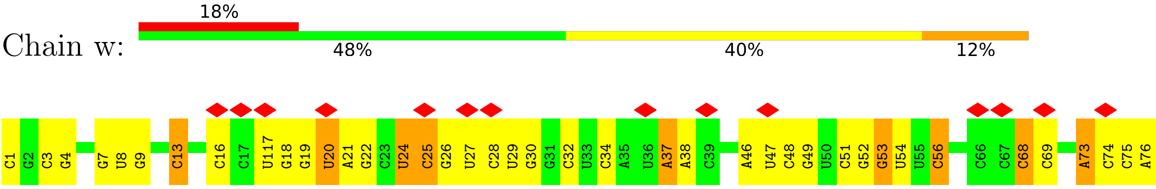


- Molecule 55: 30S ribosomal protein S1

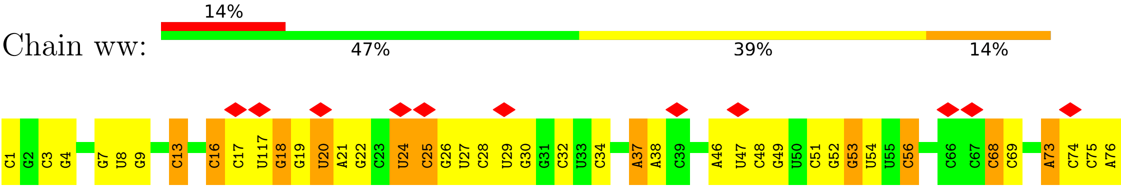
Chain yy:



- 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 ($e^-/\text{Å}^2$)	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	0.38	0/450	0.59	0/599
1	00	0.38	0/450	0.59	0/599
2	1	0.38	0/416	0.58	0/554
2	11	0.38	0/416	0.58	0/554
3	2	0.41	0/380	0.57	0/498
3	22	0.41	0/380	0.57	0/498
4	3	0.41	0/513	0.68	2/676 (0.3%)
4	33	0.41	0/513	0.68	2/676 (0.3%)
5	4	0.44	0/303	0.59	0/397
5	44	0.44	0/303	0.59	0/397
6	6	0.33	0/531	0.58	0/709
6	66	0.33	0/531	0.58	0/709
7	A	0.81	2/69733 (0.0%)	1.07	264/108786 (0.2%)
7	AA	0.81	2/69733 (0.0%)	1.07	269/108786 (0.2%)
8	B	0.73	1/2876 (0.0%)	1.09	10/4483 (0.2%)
8	BB	0.73	1/2876 (0.0%)	1.09	11/4483 (0.2%)
9	C	0.46	0/2121	0.61	0/2852
9	CC	0.46	0/2121	0.61	0/2852
10	D	0.43	0/1586	0.58	0/2134
10	DD	0.42	0/1586	0.58	0/2134
11	E	0.38	0/1571	0.54	0/2113
11	EE	0.38	0/1571	0.54	0/2113
12	F	0.37	0/1434	0.60	0/1926
12	FF	0.37	0/1434	0.60	0/1926
13	G	0.35	0/1343	0.56	0/1816
13	GG	0.35	0/1343	0.56	0/1816
14	H	0.32	0/1122	0.58	0/1515
14	HH	0.32	0/1122	0.58	0/1515
15	J	0.43	0/1152	0.57	0/1551
15	JJ	0.43	0/1152	0.57	0/1551
16	K	0.41	0/947	0.62	0/1268
16	KK	0.41	0/947	0.62	0/1268
17	L	0.42	0/1054	0.65	0/1403
17	LL	0.42	0/1054	0.65	0/1403

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
18	M	0.41	0/1093	0.62	2/1460 (0.1%)
18	MM	0.41	0/1093	0.62	2/1460 (0.1%)
19	N	0.39	0/973	0.63	0/1301
19	NN	0.39	0/973	0.63	0/1301
20	O	0.37	0/902	0.54	0/1209
20	OO	0.37	0/902	0.54	0/1209
21	P	0.42	0/929	0.62	1/1242 (0.1%)
21	PP	0.42	0/929	0.62	1/1242 (0.1%)
22	Q	0.46	0/960	0.53	0/1278
22	QQ	0.46	0/960	0.53	0/1278
23	R	0.43	0/829	0.62	0/1107
23	RR	0.43	0/829	0.62	0/1107
24	S	0.42	0/864	0.59	0/1156
24	SS	0.42	0/864	0.59	0/1156
25	T	0.37	0/744	0.60	0/994
25	TT	0.37	0/744	0.60	0/994
26	U	0.37	0/787	0.62	0/1051
26	UU	0.37	0/787	0.62	0/1051
27	V	0.40	0/766	0.59	0/1025
27	VV	0.40	0/766	0.59	0/1025
28	W	0.42	0/582	0.52	0/769
28	WW	0.42	0/582	0.52	0/769
29	X	0.42	0/635	0.56	0/848
29	XX	0.42	0/635	0.56	0/848
30	Y	0.34	0/510	0.63	1/677 (0.1%)
30	YY	0.34	0/510	0.63	1/677 (0.1%)
31	Z	0.36	0/453	0.58	0/605
31	ZZ	0.35	0/453	0.58	0/605
32	a	0.77	1/36967 (0.0%)	1.04	96/57666 (0.2%)
32	aa	0.77	1/36967 (0.0%)	1.05	92/57666 (0.2%)
33	b	0.37	0/1795	0.66	1/2418 (0.0%)
33	bb	0.37	0/1795	0.66	1/2418 (0.0%)
34	c	0.41	0/1651	0.59	1/2225 (0.0%)
34	cc	0.41	0/1651	0.59	1/2225 (0.0%)
35	d	0.38	0/1665	0.64	2/2227 (0.1%)
35	dd	0.38	0/1665	0.64	2/2227 (0.1%)
36	e	0.41	0/1154	0.66	0/1554
36	ee	0.41	0/1154	0.66	0/1554
37	f	0.39	0/835	0.64	0/1128
37	ff	0.39	0/835	0.64	0/1128
38	g	0.36	0/1284	0.66	1/1724 (0.1%)
38	gg	0.36	0/1284	0.66	1/1724 (0.1%)
39	h	0.38	0/989	0.61	1/1326 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
39	hh	0.38	0/989	0.61	1/1326 (0.1%)
40	i	0.40	0/1034	0.65	0/1375
40	ii	0.40	0/1034	0.65	0/1375
41	j	0.38	0/796	0.63	0/1077
41	jj	0.38	0/796	0.63	0/1077
42	k	0.39	0/885	0.67	0/1195
42	kk	0.39	0/885	0.67	0/1195
43	l	0.41	0/969	0.63	0/1300
43	ll	0.42	0/969	0.63	0/1300
44	m	0.34	0/892	0.63	0/1193
44	mm	0.34	0/892	0.63	0/1193
45	n	0.38	0/811	0.55	0/1081
45	nn	0.37	0/811	0.55	0/1081
46	o	0.35	0/722	0.61	0/964
46	oo	0.35	0/722	0.61	0/964
47	p	0.42	0/659	0.60	0/884
47	pp	0.42	0/659	0.60	0/884
48	q	0.37	0/657	0.63	0/881
48	qq	0.37	0/657	0.63	0/881
49	r	0.41	0/511	0.55	0/689
49	rr	0.40	0/511	0.55	0/689
50	s	0.40	0/652	0.63	0/877
50	ss	0.40	0/652	0.63	0/877
51	t	0.33	0/671	0.58	1/888 (0.1%)
51	tt	0.33	0/671	0.58	1/888 (0.1%)
52	u	0.45	0/500	0.85	1/668 (0.1%)
52	uu	0.45	0/500	0.85	1/668 (0.1%)
53	v	0.36	0/460	0.65	0/611
53	vv	0.36	0/460	0.65	0/611
54	x	0.32	0/764	0.67	0/1028
54	xx	0.32	0/764	0.67	0/1028
55	y	0.50	1/2196 (0.0%)	0.98	13/3006 (0.4%)
55	yy	0.50	1/2196 (0.0%)	0.98	13/3006 (0.4%)
56	w	0.54	1/1833 (0.1%)	1.28	26/2851 (0.9%)
56	ww	0.59	3/1834 (0.2%)	1.29	28/2855 (1.0%)
All	All	0.69	14/319823 (0.0%)	0.97	850/477680 (0.2%)

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 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	BB	1	U	OP3-P	-10.77	1.48	1.61
7	A	1	G	OP3-P	-10.71	1.48	1.61
8	B	1	U	OP3-P	-10.70	1.48	1.61
7	AA	1	G	OP3-P	-10.69	1.48	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	w	1	C	OP3-P	-10.52	1.48	1.61

The worst 5 of 850 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
32	a	516	U	N3-C2-O2	-10.91	114.56	122.20
32	aa	516	U	N3-C2-O2	-10.86	114.60	122.20
32	aa	961	U	N3-C2-O2	-10.65	114.75	122.20
32	a	961	U	N3-C2-O2	-10.56	114.81	122.20
7	A	2580	U	N3-C2-O2	-10.55	114.82	122.20

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 ⓘ

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	54/56 (96%)	52 (96%)	2 (4%)	0	100	100
1	00	54/56 (96%)	52 (96%)	2 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	9	44
4	33	62/64 (97%)	57 (92%)	4 (6%)	1 (2%)	9	44
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%)	25	66
13	GG	174/176 (99%)	160 (92%)	13 (8%)	1 (1%)	25	66
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
18	M	134/136 (98%)	126 (94%)	4 (3%)	4 (3%)	4	28
18	MM	134/136 (98%)	126 (94%)	4 (3%)	4 (3%)	4	28
19	N	118/120 (98%)	108 (92%)	10 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	34	72
33	bb	224/226 (99%)	190 (85%)	33 (15%)	1 (0%)	34	72
34	c	204/206 (99%)	191 (94%)	13 (6%)	0	100	100
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	25	66
38	gg	159/161 (99%)	136 (86%)	22 (14%)	1 (1%)	25	66
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%)	15	55
41	jj	96/98 (98%)	82 (85%)	13 (14%)	1 (1%)	15	55
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%)	17	57
44	mm	112/114 (98%)	96 (86%)	15 (13%)	1 (1%)	17	57
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%)	13	50
46	oo	86/88 (98%)	77 (90%)	8 (9%)	1 (1%)	13	50
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
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	tt	83/85 (98%)	80 (96%)	3 (4%)	0	100	100
52	u	63/65 (97%)	46 (73%)	16 (25%)	1 (2%)	9	44
52	uu	63/65 (97%)	46 (73%)	16 (25%)	1 (2%)	9	44
53	v	53/55 (96%)	43 (81%)	9 (17%)	1 (2%)	8	38
53	vv	53/55 (96%)	43 (81%)	9 (17%)	1 (2%)	8	38
54	x	93/95 (98%)	86 (92%)	6 (6%)	1 (1%)	14	52
54	xx	93/95 (98%)	86 (92%)	6 (6%)	1 (1%)	14	52
55	y	347/557 (62%)	253 (73%)	75 (22%)	19 (6%)	2	19
55	yy	347/557 (62%)	253 (73%)	75 (22%)	19 (6%)	2	19
All	All	12180/12804 (95%)	10888 (89%)	1226 (10%)	66 (0%)	32	69

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
3	2	38/38 (100%)	38 (100%)	0	100	100
3	22	38/38 (100%)	38 (100%)	0	100	100
4	3	51/51 (100%)	51 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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%)	59 (100%)	0	100	100
6	66	59/59 (100%)	59 (100%)	0	100	100
9	C	216/216 (100%)	214 (99%)	2 (1%)	78	87
9	CC	216/216 (100%)	214 (99%)	2 (1%)	78	87
10	D	164/164 (100%)	160 (98%)	4 (2%)	49	69
10	DD	164/164 (100%)	160 (98%)	4 (2%)	49	69
11	E	165/165 (100%)	163 (99%)	2 (1%)	71	83
11	EE	165/165 (100%)	163 (99%)	2 (1%)	71	83
12	F	148/148 (100%)	146 (99%)	2 (1%)	67	80
12	FF	148/148 (100%)	146 (99%)	2 (1%)	67	80
13	G	137/137 (100%)	135 (98%)	2 (2%)	65	80
13	GG	137/137 (100%)	135 (98%)	2 (2%)	65	80
14	H	114/114 (100%)	111 (97%)	3 (3%)	46	66
14	HH	114/114 (100%)	111 (97%)	3 (3%)	46	66
15	J	116/116 (100%)	115 (99%)	1 (1%)	78	87
15	JJ	116/116 (100%)	115 (99%)	1 (1%)	78	87
16	K	103/103 (100%)	102 (99%)	1 (1%)	76	86
16	KK	103/103 (100%)	102 (99%)	1 (1%)	76	86
17	L	102/102 (100%)	101 (99%)	1 (1%)	76	86
17	LL	102/102 (100%)	101 (99%)	1 (1%)	76	86
18	M	109/109 (100%)	107 (98%)	2 (2%)	59	77
18	MM	109/109 (100%)	107 (98%)	2 (2%)	59	77
19	N	100/100 (100%)	99 (99%)	1 (1%)	76	86
19	NN	100/100 (100%)	99 (99%)	1 (1%)	76	86
20	O	86/86 (100%)	86 (100%)	0	100	100
20	OO	86/86 (100%)	86 (100%)	0	100	100
21	P	99/99 (100%)	99 (100%)	0	100	100
21	PP	99/99 (100%)	99 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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%)	82 (98%)	2 (2%)	49	69
23	RR	84/84 (100%)	82 (98%)	2 (2%)	49	69
24	S	93/93 (100%)	91 (98%)	2 (2%)	52	71
24	SS	93/93 (100%)	91 (98%)	2 (2%)	52	71
25	T	80/80 (100%)	79 (99%)	1 (1%)	69	81
25	TT	80/80 (100%)	79 (99%)	1 (1%)	69	81
26	U	83/83 (100%)	83 (100%)	0	100	100
26	UU	83/83 (100%)	83 (100%)	0	100	100
27	V	78/78 (100%)	78 (100%)	0	100	100
27	VV	78/78 (100%)	78 (100%)	0	100	100
28	W	57/57 (100%)	54 (95%)	3 (5%)	22	47
28	WW	57/57 (100%)	54 (95%)	3 (5%)	22	47
29	X	67/67 (100%)	65 (97%)	2 (3%)	41	63
29	XX	67/67 (100%)	65 (97%)	2 (3%)	41	63
30	Y	55/55 (100%)	54 (98%)	1 (2%)	59	77
30	YY	55/55 (100%)	54 (98%)	1 (2%)	59	77
31	Z	48/48 (100%)	46 (96%)	2 (4%)	30	54
31	ZZ	48/48 (100%)	46 (96%)	2 (4%)	30	54
33	b	186/186 (100%)	184 (99%)	2 (1%)	73	84
33	bb	186/186 (100%)	184 (99%)	2 (1%)	73	84
34	c	170/170 (100%)	168 (99%)	2 (1%)	71	83
34	cc	170/170 (100%)	168 (99%)	2 (1%)	71	83
35	d	172/172 (100%)	169 (98%)	3 (2%)	60	78
35	dd	172/172 (100%)	169 (98%)	3 (2%)	60	78
36	e	114/119 (96%)	110 (96%)	4 (4%)	36	59
36	ee	114/119 (96%)	110 (96%)	4 (4%)	36	59
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%)	127 (96%)	5 (4%)	33	57

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	gg	132/132 (100%)	127 (96%)	5 (4%)	33	57
39	h	104/104 (100%)	102 (98%)	2 (2%)	57	75
39	hh	104/104 (100%)	102 (98%)	2 (2%)	57	75
40	i	105/105 (100%)	100 (95%)	5 (5%)	25	51
40	ii	105/105 (100%)	100 (95%)	5 (5%)	25	51
41	j	86/86 (100%)	86 (100%)	0	100	100
41	jj	86/86 (100%)	86 (100%)	0	100	100
42	k	89/89 (100%)	88 (99%)	1 (1%)	73	84
42	kk	89/89 (100%)	88 (99%)	1 (1%)	73	84
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%)	77 (98%)	2 (2%)	47	68
45	nn	79/83 (95%)	77 (98%)	2 (2%)	47	68
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%)	63 (97%)	2 (3%)	40	62
47	pp	65/65 (100%)	63 (97%)	2 (3%)	40	62
48	q	74/74 (100%)	73 (99%)	1 (1%)	67	80
48	qq	74/74 (100%)	73 (99%)	1 (1%)	67	80
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%)	70 (100%)	0	100	100
50	ss	70/70 (100%)	70 (100%)	0	100	100
51	t	65/65 (100%)	64 (98%)	1 (2%)	65	80
51	tt	65/65 (100%)	64 (98%)	1 (2%)	65	80
52	u	44/55 (80%)	43 (98%)	1 (2%)	50	70
52	uu	44/55 (80%)	43 (98%)	1 (2%)	50	70
53	v	44/44 (100%)	42 (96%)	2 (4%)	27	52
53	vv	44/44 (100%)	42 (96%)	2 (4%)	27	52

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
54	x	80/81 (99%)	77 (96%)	3 (4%)	33	57
54	xx	80/81 (99%)	77 (96%)	3 (4%)	33	57
55	y	137/461 (30%)	134 (98%)	3 (2%)	52	71
55	yy	137/461 (30%)	134 (98%)	3 (2%)	52	71
All	All	9778/10484 (93%)	9632 (98%)	146 (2%)	66	80

5 of 146 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
36	ee	69	ASN
55	yy	54	LYS
38	gg	78	ARG
42	kk	12	ARG
38	g	156	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 142 such sidechains are listed below:

Mol	Chain	Res	Type
37	ff	3	HIS
39	hh	37	ASN
47	pp	79	ASN
39	h	37	ASN
38	g	129	ASN

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	75/77 (97%)	34 (45%)	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%)
8	BB	119/120 (99%)	18 (15%)	1 (0%)
All	All	9261/9278 (99%)	1767 (19%)	28 (0%)

5 of 1767 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 ⓘ

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

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

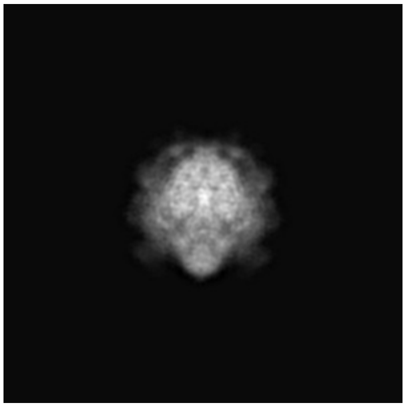
6 Map visualisation

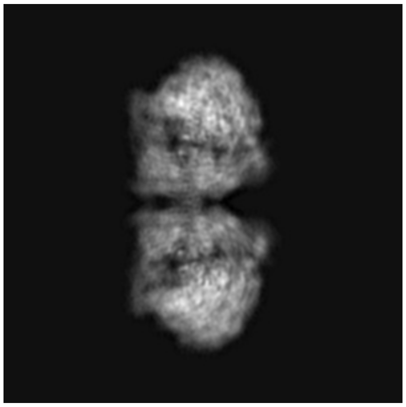
This section contains visualisations of the EMDB entry EMD-0139. These allow visual inspection of the internal detail of the map and identification of artifacts.

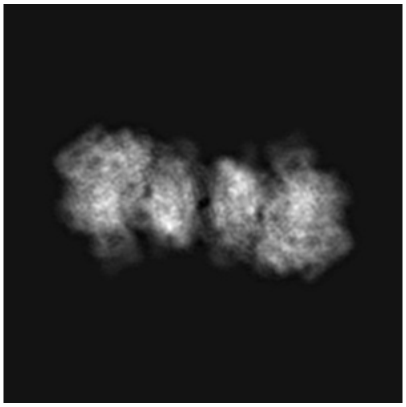
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

6.1.1 Primary map


X


Y

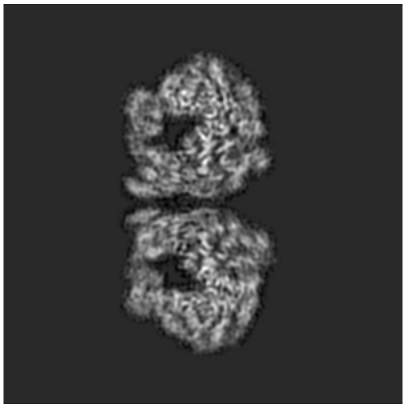

Z

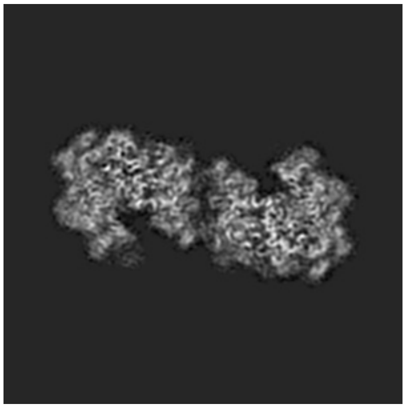
The images above show the map projected in three orthogonal directions.

6.2 Central slices

6.2.1 Primary map


X Index: 114

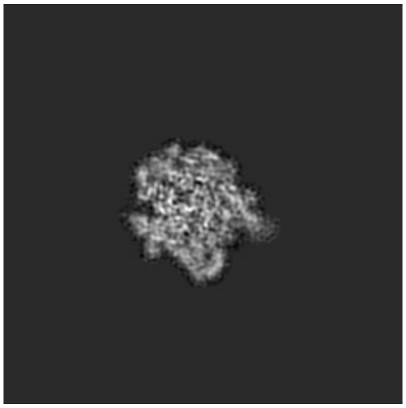

Y Index: 114


Z Index: 114

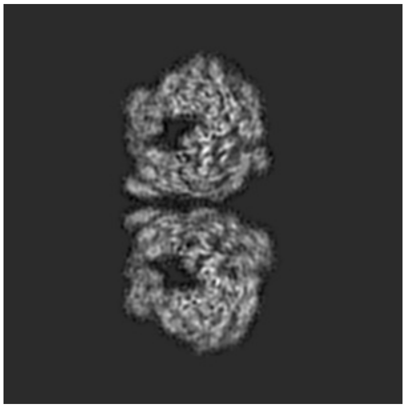
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices

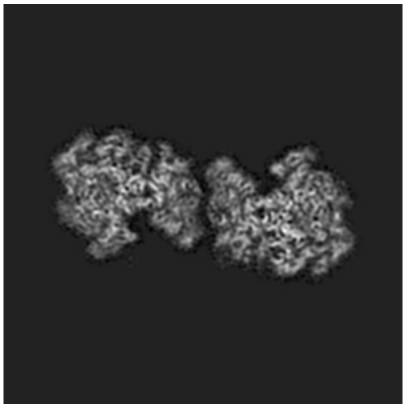
6.3.1 Primary map



X Index: 169



Y Index: 113



Z Index: 117

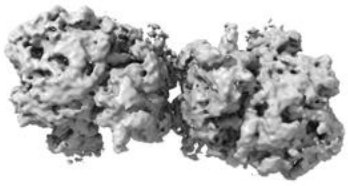
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views

6.4.1 Primary map

X

Y



Z

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.

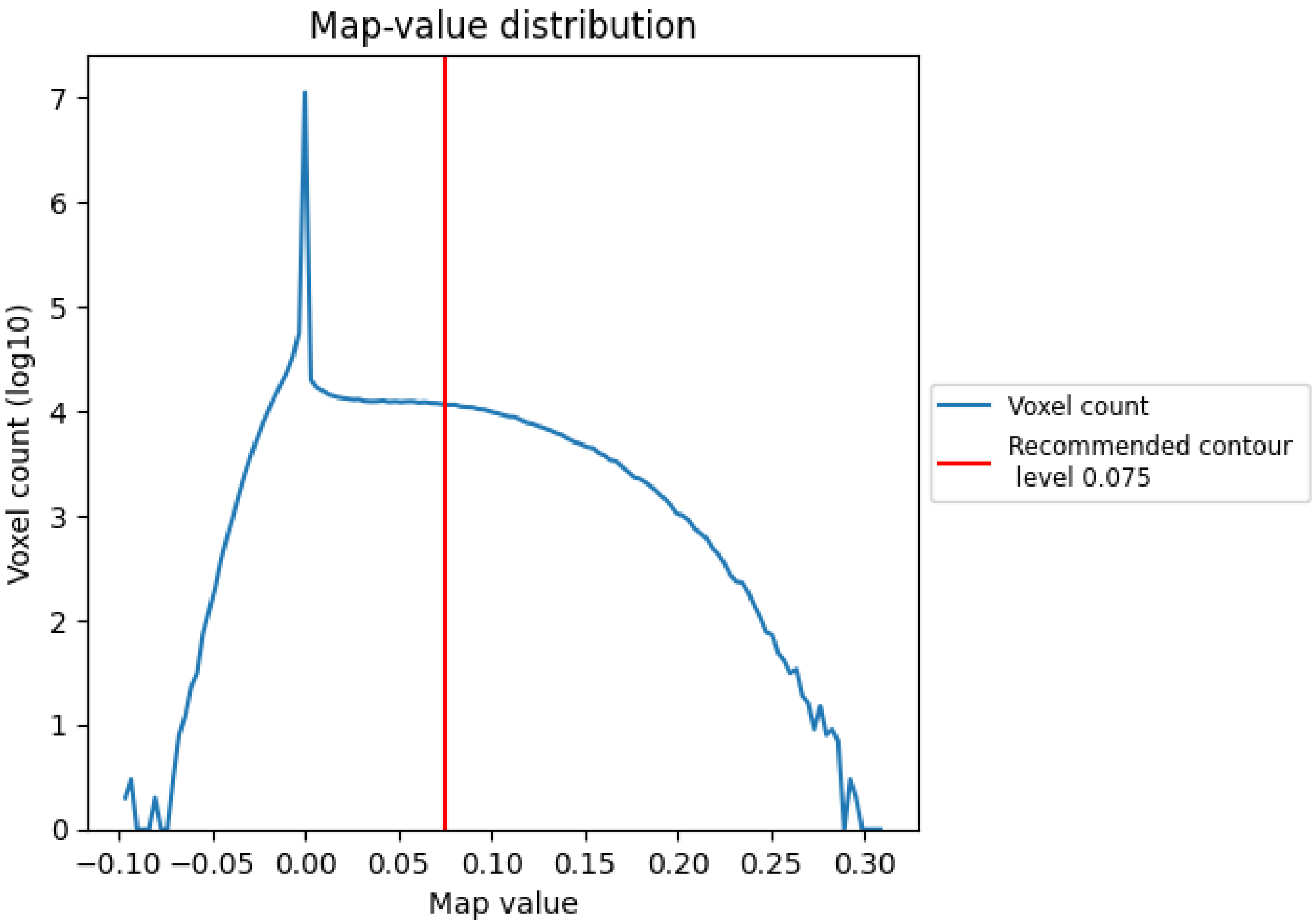
6.5 Mask visualisation ⓘ

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

7 Map analysis ⓘ

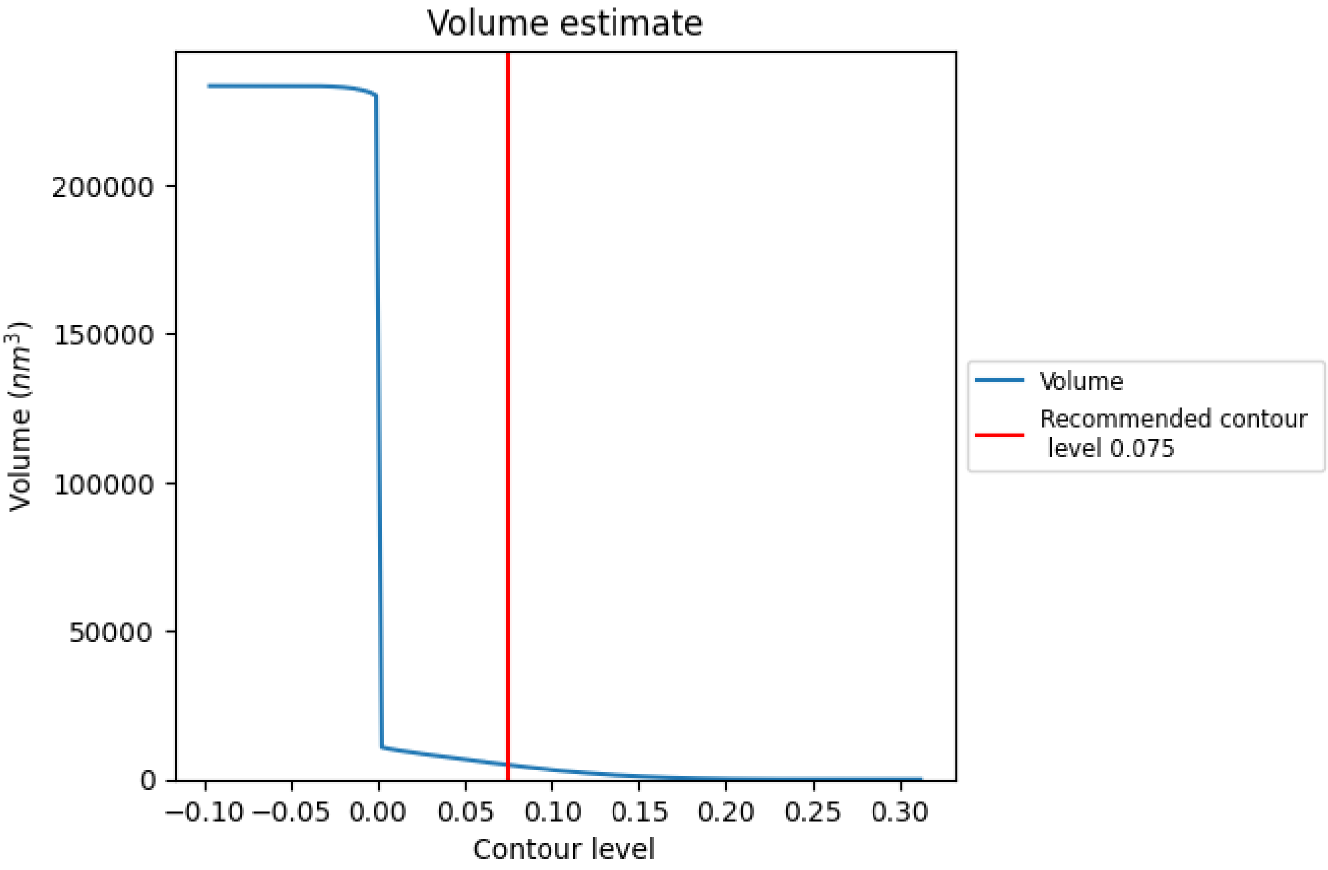
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ



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.

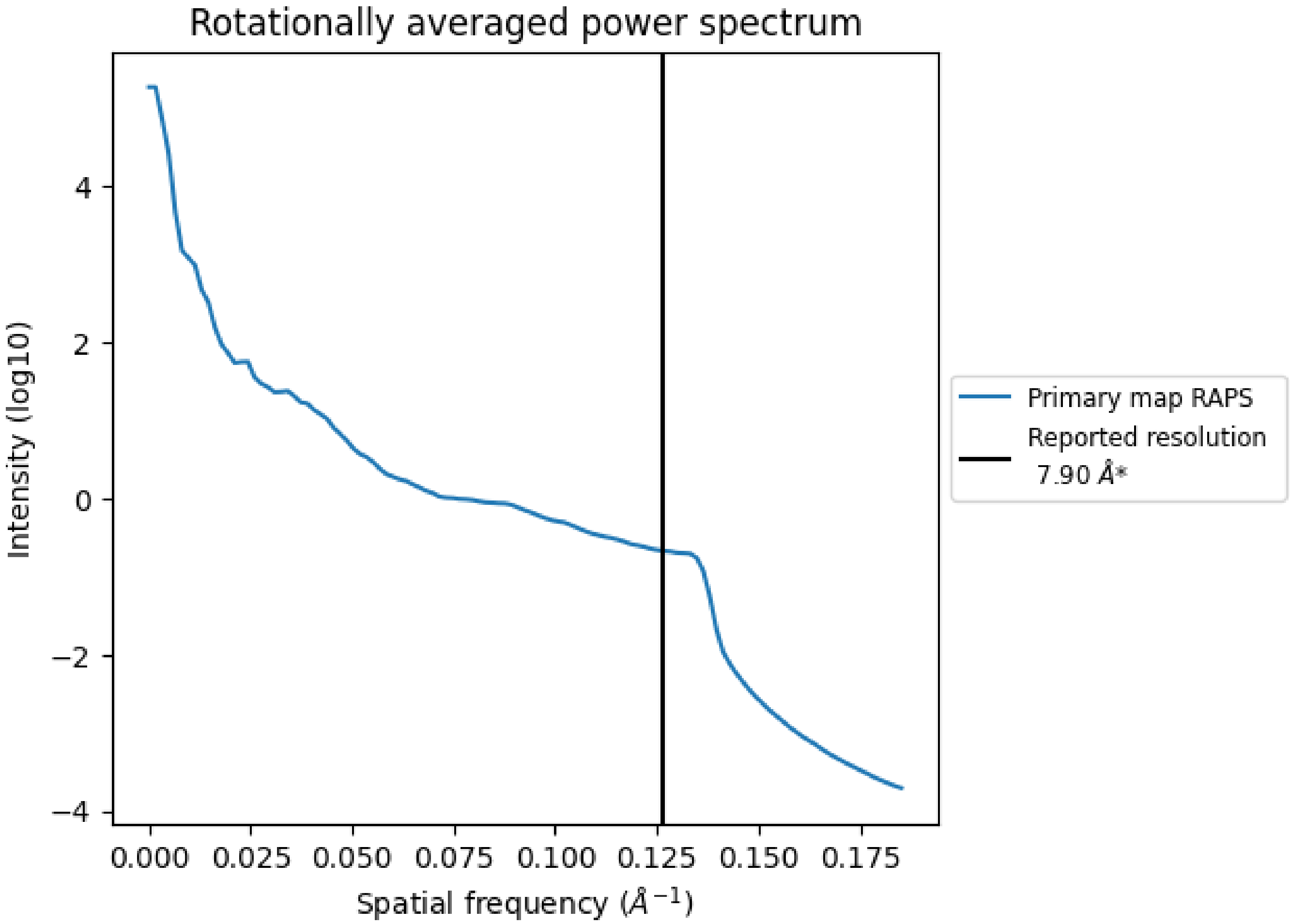
7.2 Volume estimate ⓘ



The volume at the recommended contour level is 4934 nm^3; 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 ⓘ

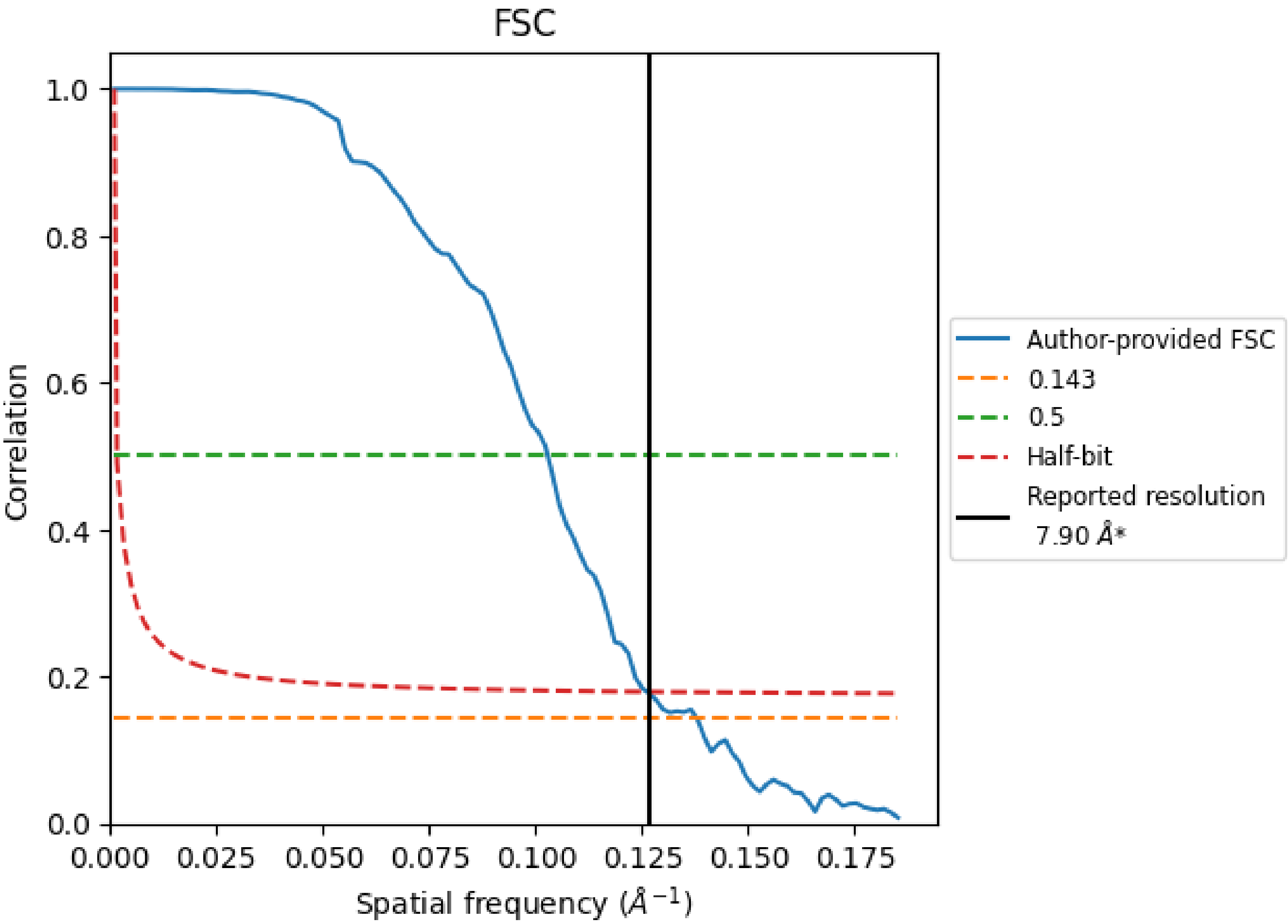


*Reported resolution corresponds to spatial frequency of 0.127 Å^{-1}

8 Fourier-Shell correlation ⓘ

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 ⓘ



*Reported resolution corresponds to spatial frequency of 0.127 $Å^{-1}$

8.2 Resolution estimates (i)

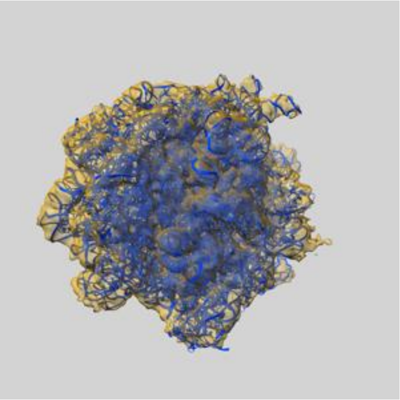
Resolution estimate (Å)	**Estimation criterion (FSC cut-off)**		
	0.143	0.5	Half-bit
Reported by author	7.90	-	-
Author-provided FSC curve	7.26	9.72	7.92
Unmasked-calculated*	-	-	-

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

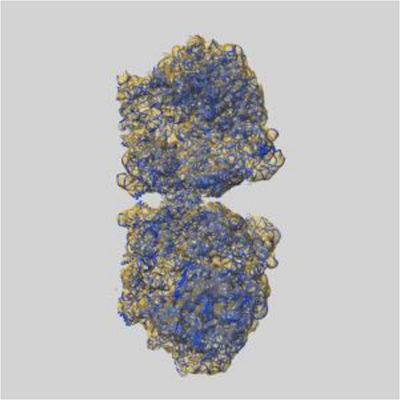
9 Map-model fit

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.

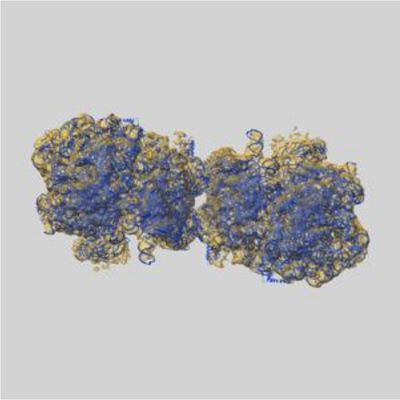
9.1 Map-model overlay



X



Y



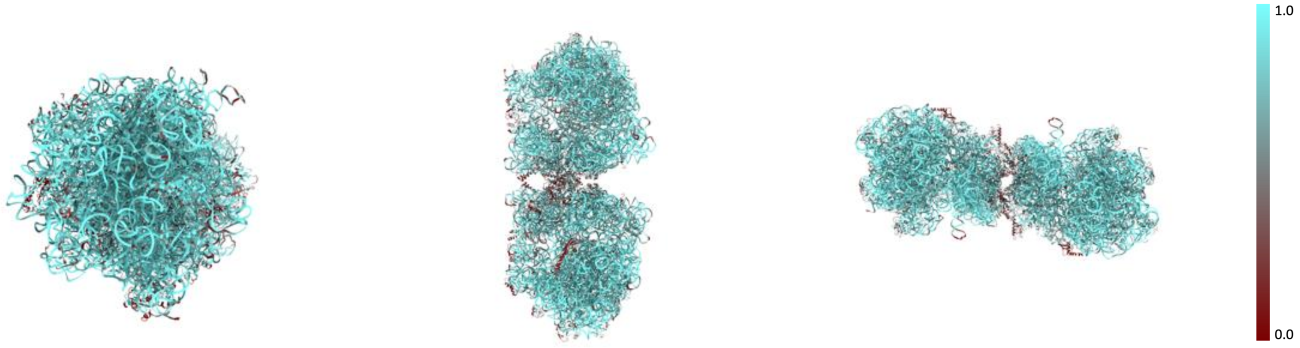
Z

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 ⓘ

This section was not generated.

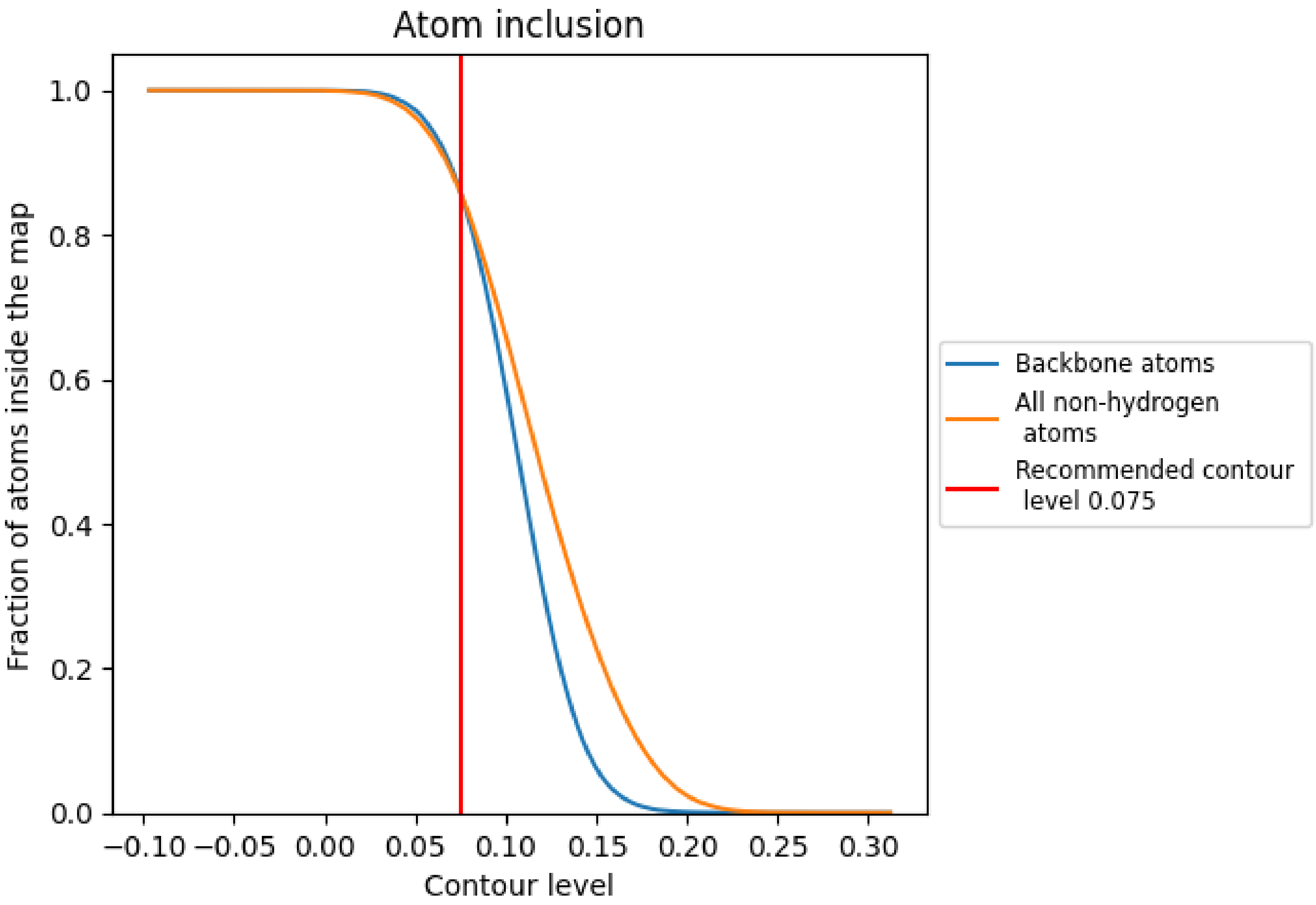
9.3 Atom inclusion mapped to coordinate model ⓘ



X Y Z

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 ⓘ



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
All	▬ 0.8579
0	▬ 0.7430
00	▬ 0.6916
1	▬ 0.7805
11	▬ 0.7905
2	▬ 0.8197
22	▬ 0.8338
3	▬ 0.7352
33	▬ 0.7576
4	▬ 0.8870
44	▬ 0.9212
6	▬ 0.1663
66	▬ 0.2250
A	▬ 0.9487
AA	▬ 0.9510
B	▬ 0.8892
BB	▬ 0.9032
C	▬ 0.7644
CC	▬ 0.7604
D	▬ 0.7562
DD	▬ 0.7575
E	▬ 0.7112
EE	▬ 0.7164
F	▬ 0.6438
FF	▬ 0.6628
G	▬ 0.6577
GG	▬ 0.6816
H	▬ 0.1697
HH	▬ 0.1588
J	▬ 0.8555
JJ	▬ 0.8727
K	▬ 0.7262
KK	▬ 0.6878
L	▬ 0.7087
LL	▬ 0.7421

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Chain	Atom inclusion
M	▬ 0.7562
MM	▬ 0.7476
N	▬ 0.8460
NN	▬ 0.8427
O	▬ 0.6871
OO	▬ 0.6709
P	▬ 0.7365
PP	▬ 0.7691
Q	▬ 0.8359
QQ	▬ 0.8359
R	▬ 0.6424
RR	▬ 0.6600
S	▬ 0.7955
SS	▬ 0.7751
T	▬ 0.7452
TT	▬ 0.7382
U	▬ 0.7184
UU	▬ 0.7197
V	▬ 0.6491
VV	▬ 0.7033
W	▬ 0.7209
WW	▬ 0.7657
X	▬ 0.7720
XX	▬ 0.7770
Y	▬ 0.6660
YY	▬ 0.7183
Z	▬ 0.7963
ZZ	▬ 0.8124
a	▬ 0.9348
aa	▬ 0.9405
b	▬ 0.5585
bb	▬ 0.5545
c	▬ 0.6293
cc	▬ 0.6248
d	▬ 0.5994
dd	▬ 0.6220
e	▬ 0.6300
ee	▬ 0.6479
f	▬ 0.7990
ff	▬ 0.7613
g	▬ 0.7731
gg	▬ 0.7567

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Chain	Atom inclusion
h	🟦 0.7146
hh	🟦 0.7271
i	🟦 0.7579
ii	🟦 0.7589
j	🟦 0.5769
jj	🟦 0.5940
k	🟦 0.7822
kk	🟦 0.7598
l	🟦 0.7546
ll	🟦 0.7372
m	🟦 0.6345
mm	🟦 0.6733
n	🟦 0.7891
nn	🟦 0.7747
o	🟦 0.7942
oo	🟦 0.8261
p	🟦 0.7081
pp	🟦 0.7464
q	🟦 0.7801
qq	🟦 0.7674
r	🟦 0.7856
rr	🟦 0.8247
s	🟦 0.7939
ss	🟦 0.8293
t	🟦 0.7892
tt	🟦 0.8200
u	🟦 0.6345
uu	🟦 0.6408
v	🟦 0.7657
vv	🟦 0.7425
w	🟦 0.6401
ww	🟦 0.6504
x	🟦 0.6470
xx	🟦 0.6738
y	🟫 0.2623
yy	🟫 0.2969