



## wwPDB EM Validation Summary Report ⓘ

Sep 28, 2024 – 06:53 pm BST

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

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.dev113  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

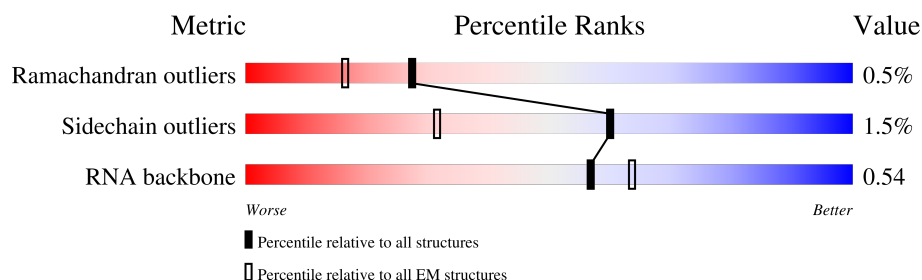
# 1 Overall quality at a glance

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	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	56	
1	00	56	
2	1	50	
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	17% 99%
18	M	136	12% 96%
18	MM	136	8% 96%
19	N	120	5% 98%
19	NN	120	8% 98%
20	O	116	23% 99%
20	OO	116	28% 99%
21	P	114	16% 99%
21	PP	114	11% 99%
22	Q	117	7% 100%
22	QQ	117	6% 100%
23	R	103	31% 98%
23	RR	103	28% 98%
24	S	110	14% 98%
24	SS	110	12% 98%
25	T	93	14% 99%
25	TT	93	20% 99%
26	U	102	25% 100%
26	UU	102	21% 100%
27	V	94	28% 100%
27	VV	94	18% 100%
28	W	75	20% 96%
28	WW	75	15% 96%
29	X	77	• 97%
29	XX	77	5% 97%

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Mol	Chain	Length	Quality of chain
30	Y	63	25% 97% .
30	YY	63	22% 97% .
31	Z	58	12% 97% .
31	ZZ	58	12% 97% .
32	a	1539	. 80% 19% .
32	aa	1539	. 80% 19% .
33	b	226	31% 98% .
33	bb	226	34% 98% .
34	c	206	22% 99% .
34	cc	206	26% 99% .
35	d	205	33% 97% .
35	dd	205	26% 97% .
36	e	157	25% 97% .
36	ee	157	24% 97% .
37	f	100	. 100%
37	ff	100	7% 100%
38	g	161	14% 94% 6% .
38	gg	161	13% 94% 6% .
39	h	129	13% 98% .
39	hh	129	14% 98% .
40	i	127	18% 96% ..
40	ii	127	13% 96% ..
41	j	98	36% 99% .
41	jj	98	34% 99% .
42	k	116	8% 97% ..

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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	<div> <div>45%</div> <div>57%</div> <div>5%</div> <div>37%</div> </div>
55	yy	557	<div> <div>43%</div> <div>57%</div> <div>5%</div> <div>37%</div> </div>
56	w	77	<div> <div>18%</div> <div>48%</div> <div>40%</div> <div>12%</div> </div>
56	ww	77	<div> <div>14%</div> <div>47%</div> <div>39%</div> <div>14%</div> </div>

## 2 Entry composition

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

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

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

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

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

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

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

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

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

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

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



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

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

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

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

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

There are 6 discrepancies between the modelled and reference sequences:

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

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

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

There are 2 discrepancies between the modelled and reference sequences:

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

There are 16 discrepancies between the modelled and reference sequences:

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

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

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

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

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

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

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

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

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

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

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

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

There are 4 discrepancies between the modelled and reference sequences:

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

There are 2 discrepancies between the modelled and reference sequences:

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

*Continued on next page...*

*Continued from previous page...*

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

- Molecule 53 is a protein called Ribosome modulation factor.

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

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

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

There are 4 discrepancies between the modelled and reference sequences:

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

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

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

- Molecule 56 is a RNA chain called tRNA Mixture.

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

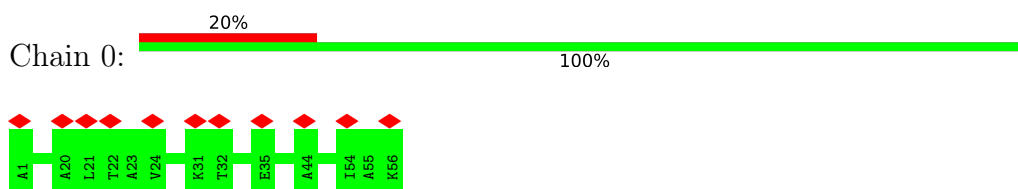
There are 4 discrepancies between the modelled and reference sequences:

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

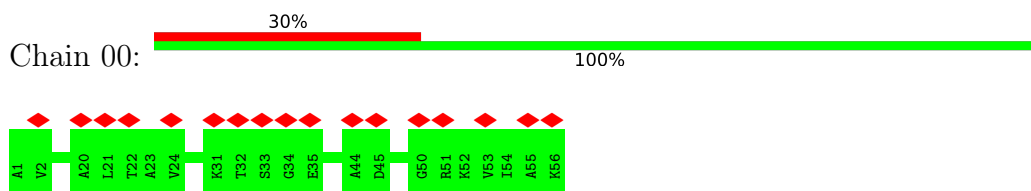
### 3 Residue-property plots [i](#)

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

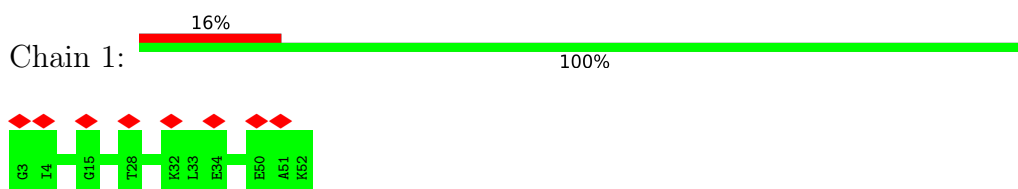
- Molecule 1: 50S ribosomal protein L32



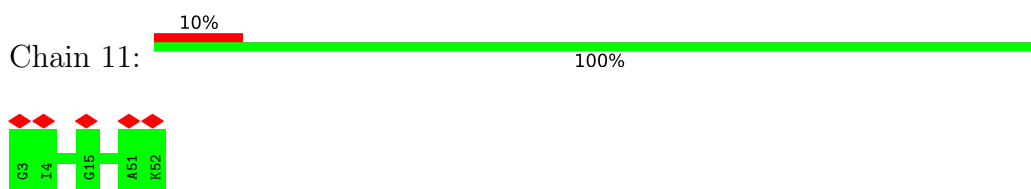
- Molecule 1: 50S ribosomal protein L32



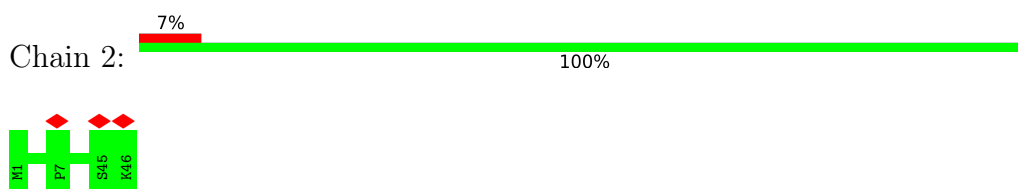
- Molecule 2: 50S ribosomal protein L33



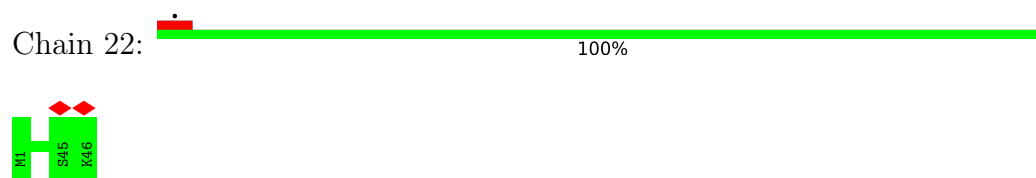
- Molecule 2: 50S ribosomal protein L33



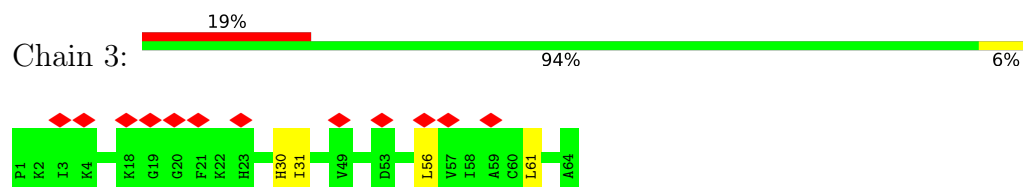
- Molecule 3: 50S ribosomal protein L34



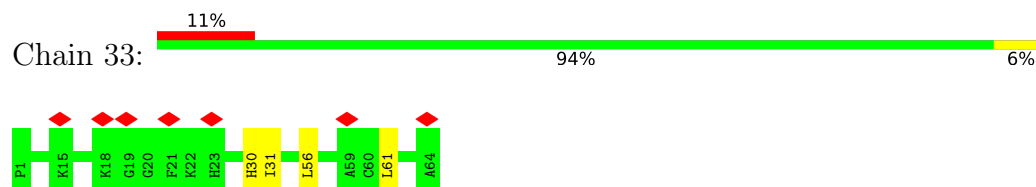
- Molecule 3: 50S ribosomal protein L34



- Molecule 4: 50S ribosomal protein L35



- Molecule 4: 50S ribosomal protein L35

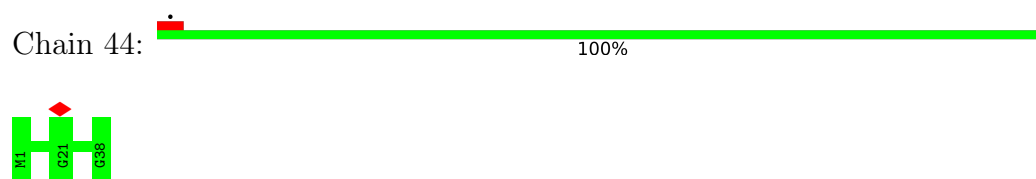


- Molecule 5: 50S ribosomal protein L36

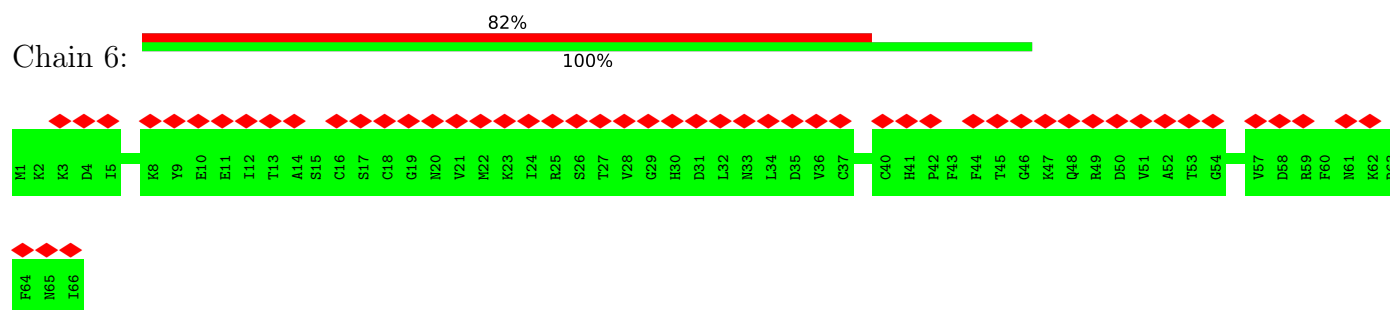


There are no outlier residues recorded for this chain.

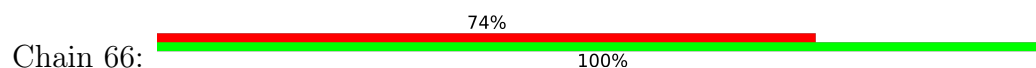
- Molecule 5: 50S ribosomal protein L36

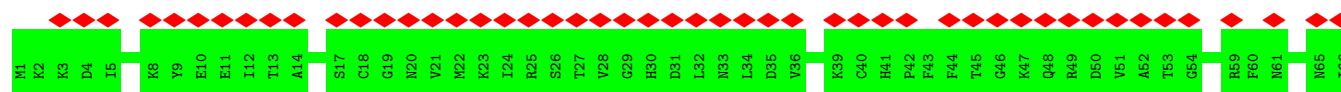


- Molecule 6: 50S ribosomal protein L31



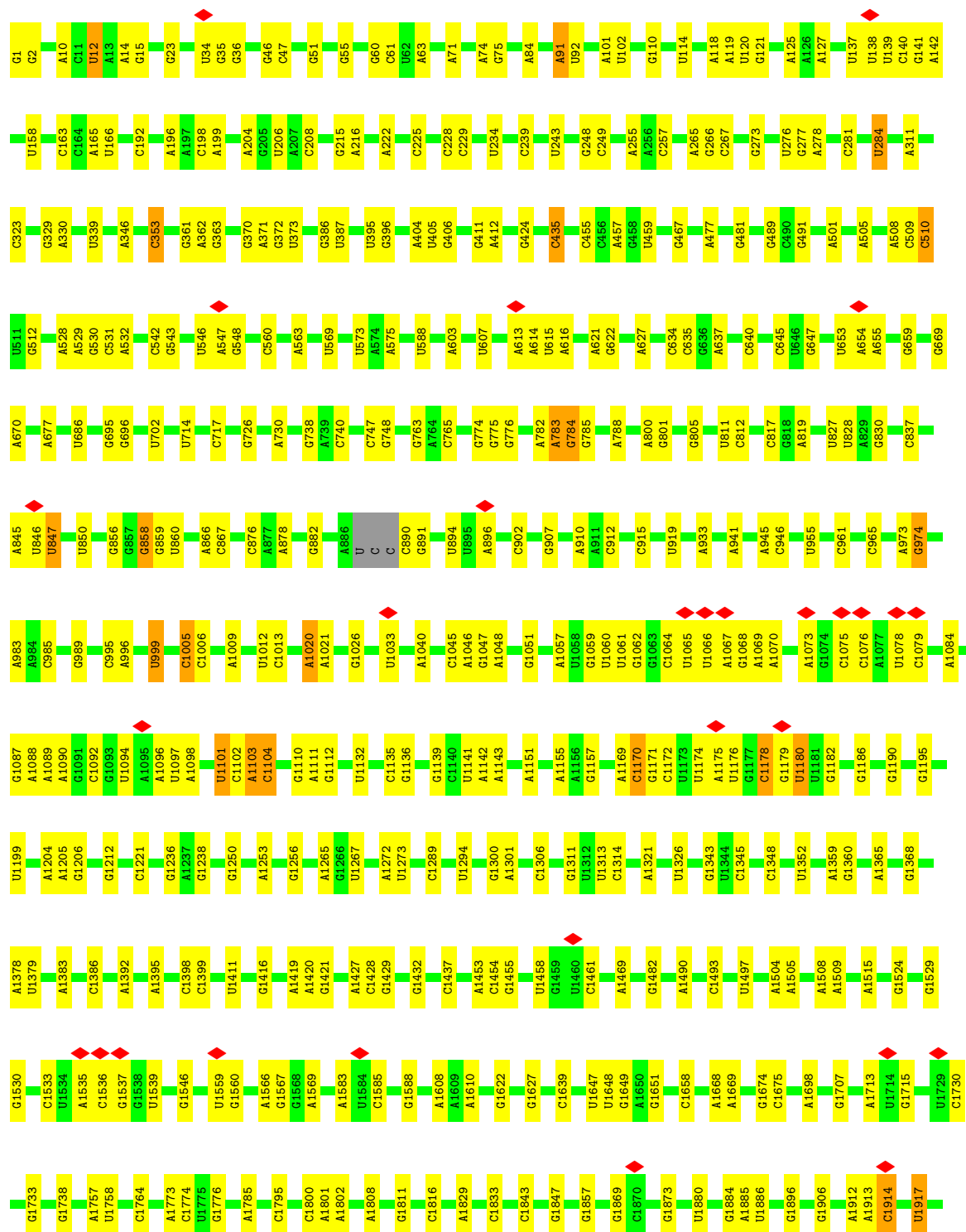
- Molecule 6: 50S ribosomal protein L31

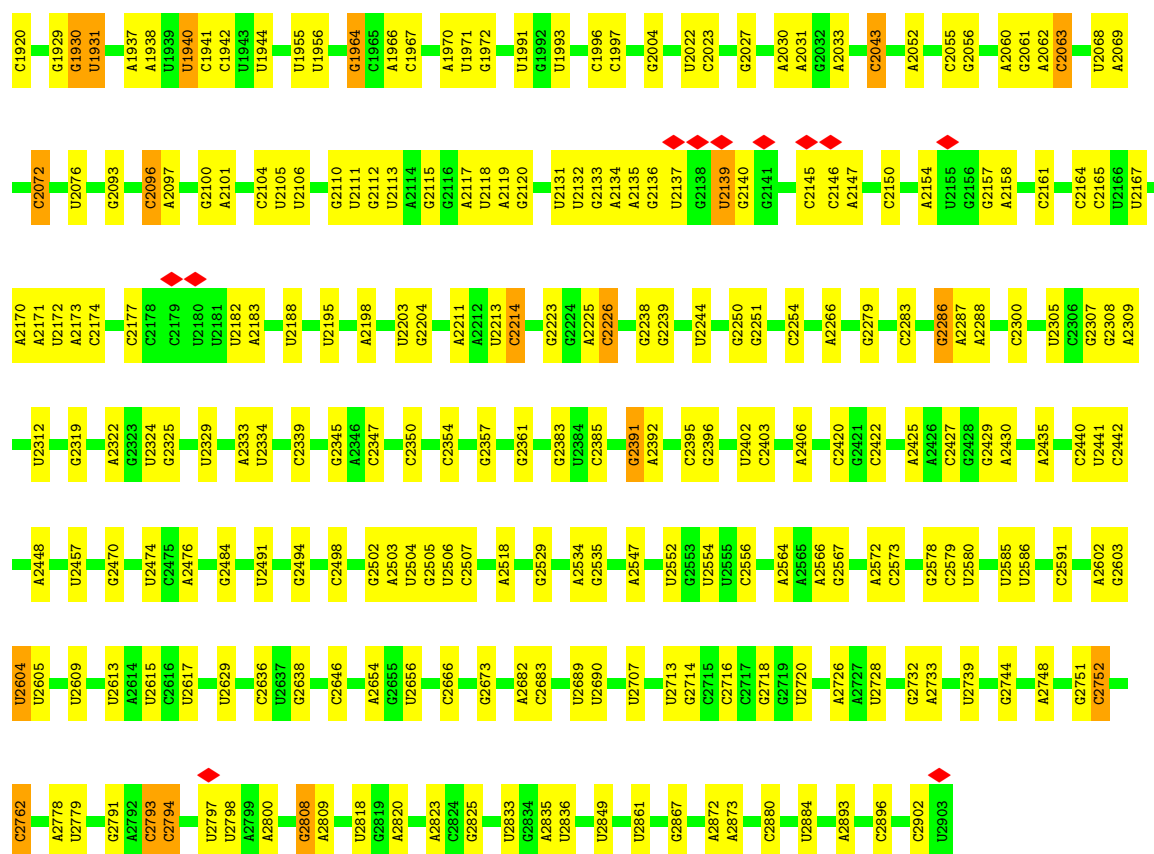




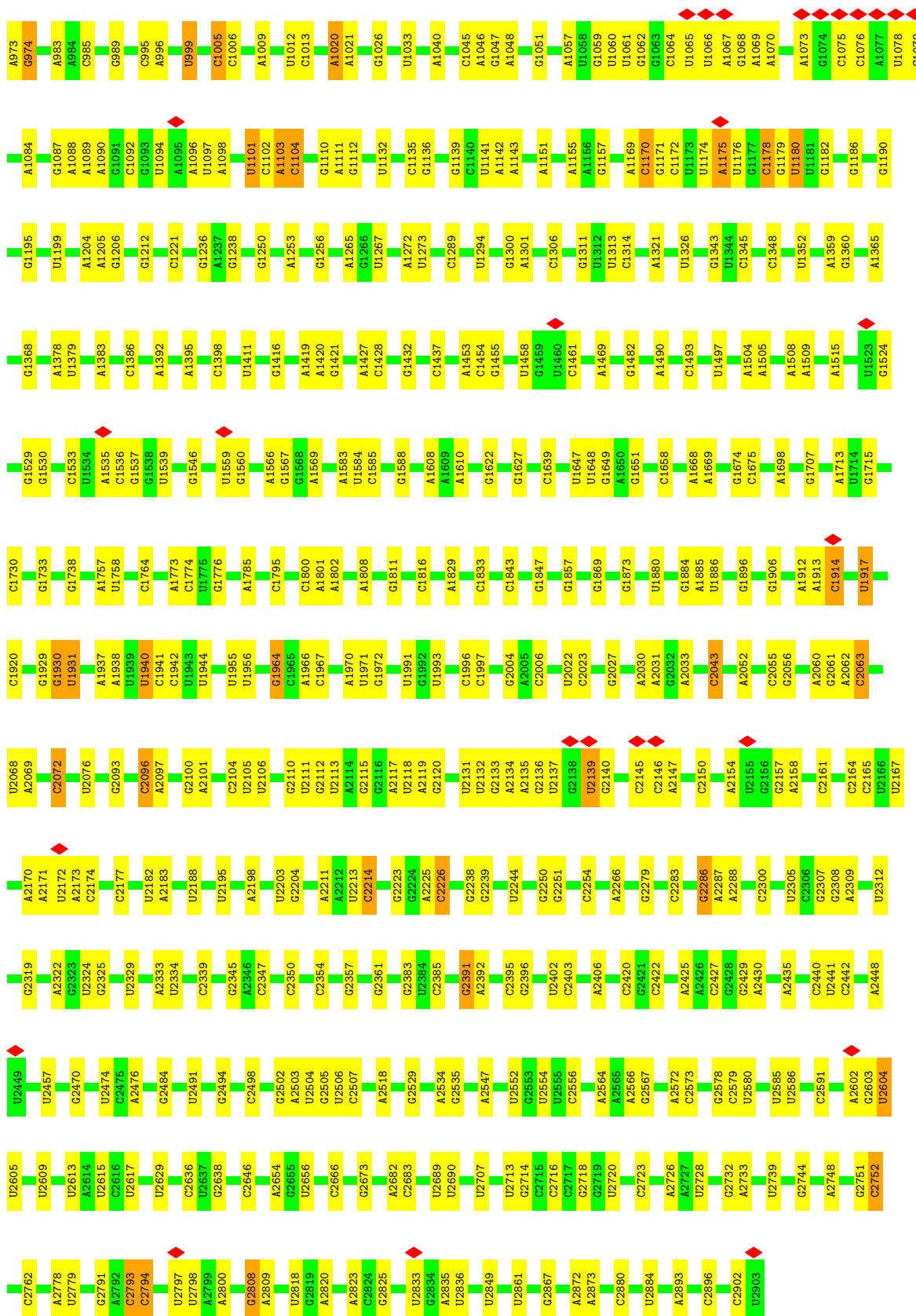
• Molecule 7: 23S ribosomal RNA

Chain A: 77% 22%




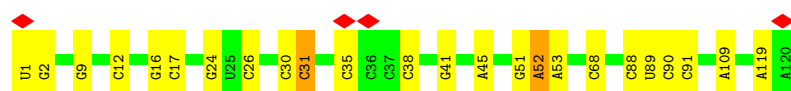







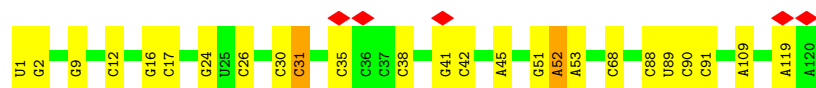
• Molecule 8: 5S ribosomal RNA

Chain B:  80% 18%



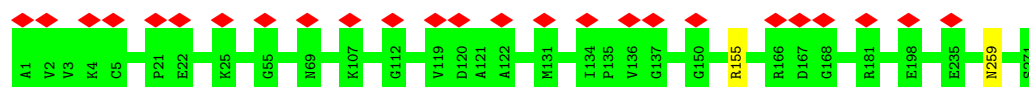
- Molecule 8: 5S ribosomal RNA

Chain BB:  79% 19%



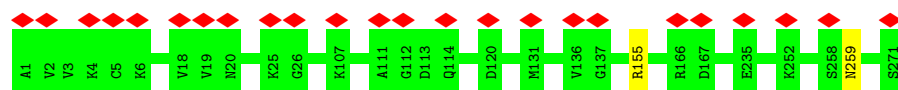
- Molecule 9: 50S ribosomal protein L2

Chain C:  9% 99%



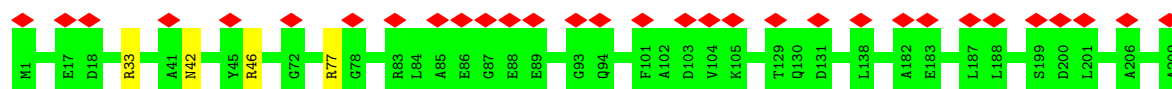
- Molecule 9: 50S ribosomal protein L2

Chain CC:  9% 99%



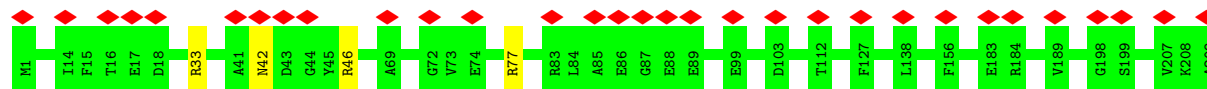
- Molecule 10: 50S ribosomal protein L3

Chain D:  15% 98%



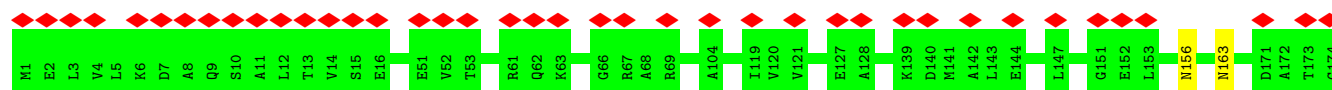
- Molecule 10: 50S ribosomal protein L3

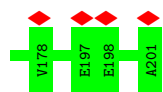
Chain DD:  15% 98%



- Molecule 11: 50S ribosomal protein L4

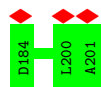
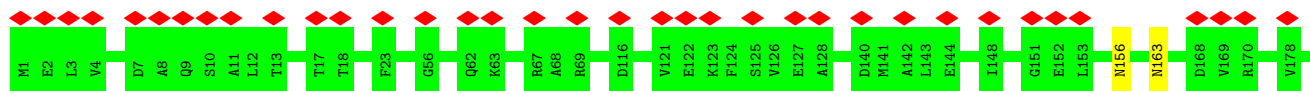
Chain E:  22% 99%





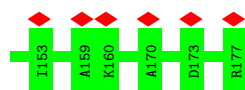
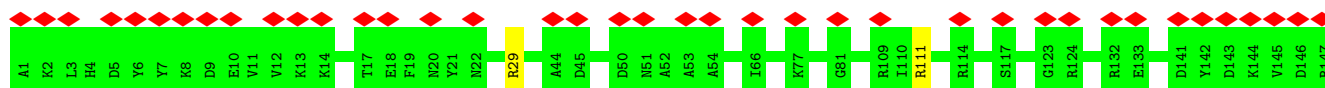
- Molecule 11: 50S ribosomal protein L4

Chain EE: 19% 99%



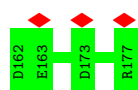
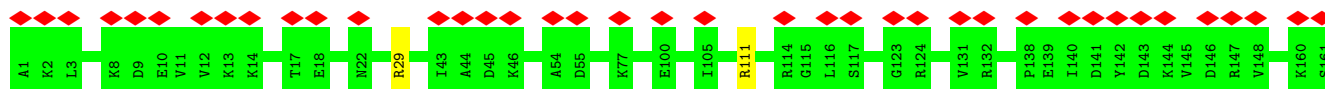
- Molecule 12: 50S ribosomal protein L5

Chain F: 25% 99%



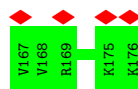
- Molecule 12: 50S ribosomal protein L5

Chain FF: 24% 99%

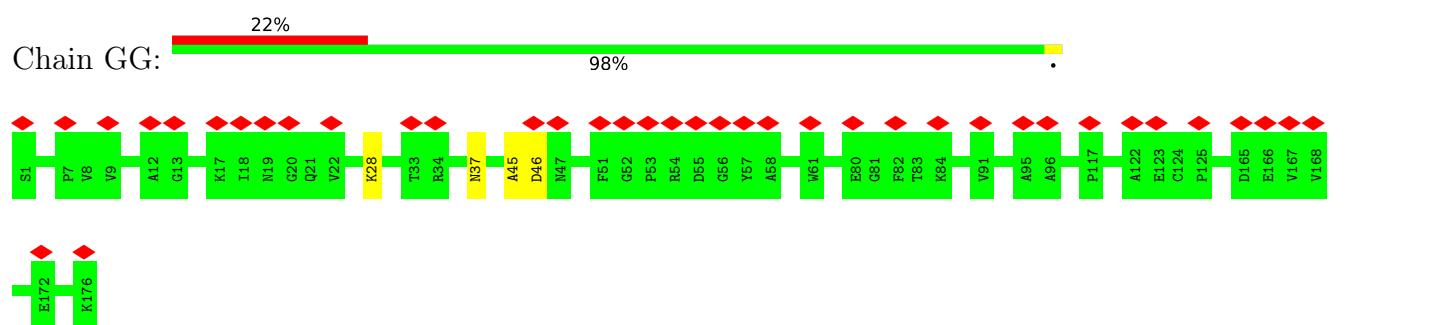


- Molecule 13: 50S ribosomal protein L6

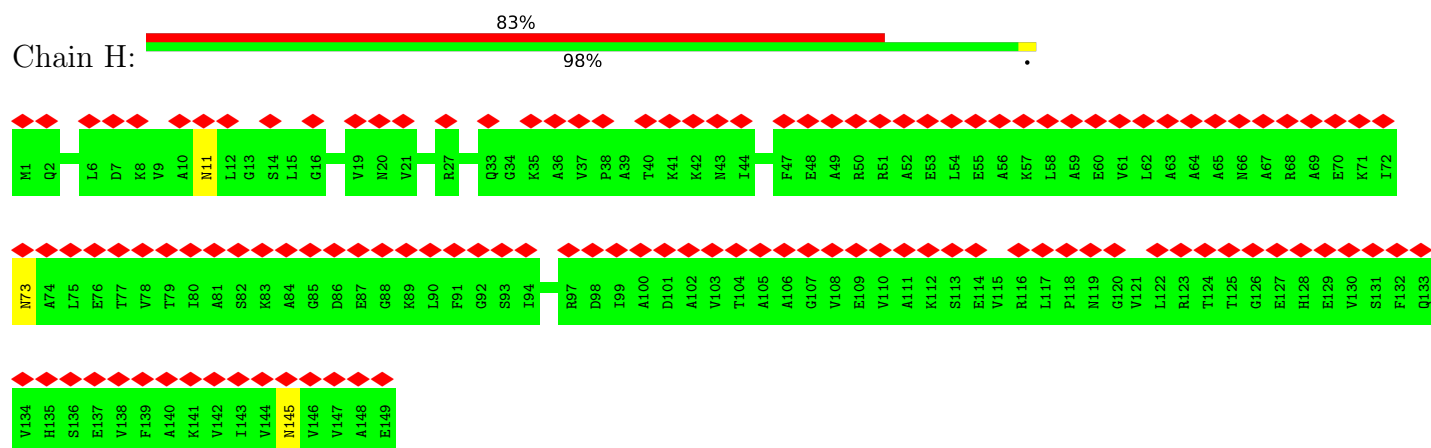
Chain G: 22% 98%



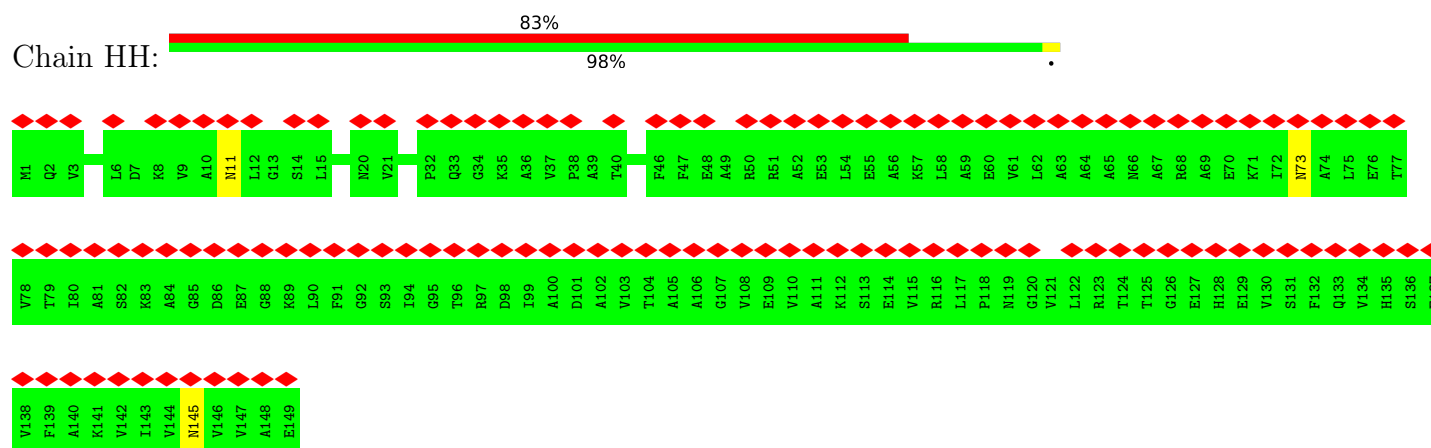
- Molecule 13: 50S ribosomal protein L6



- Molecule 14: 50S ribosomal protein L9



- Molecule 14: 50S ribosomal protein L9

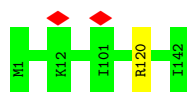


- Molecule 15: 50S ribosomal protein L13

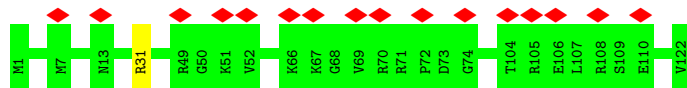


- Molecule 15: 50S ribosomal protein L13

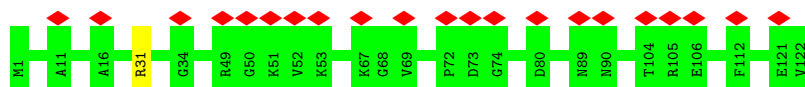




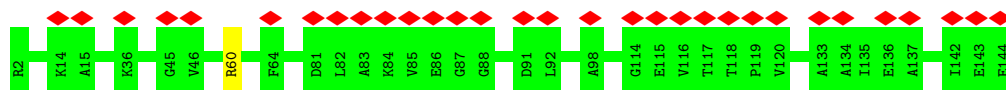
- Molecule 16: 50S ribosomal protein L14



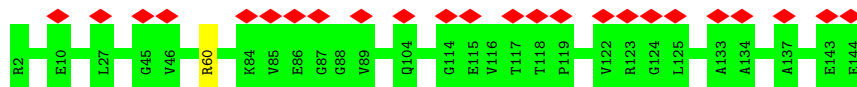
- Molecule 16: 50S ribosomal protein L14



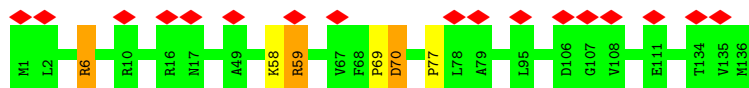
- Molecule 17: 50S ribosomal protein L15



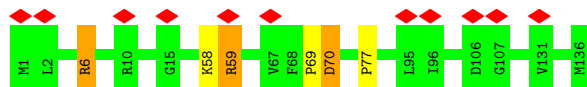
- Molecule 17: 50S ribosomal protein L15



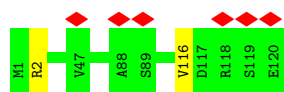
- Molecule 18: 50S ribosomal protein L16



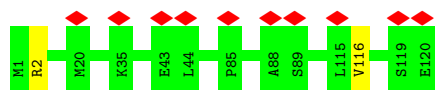
- Molecule 18: 50S ribosomal protein L16



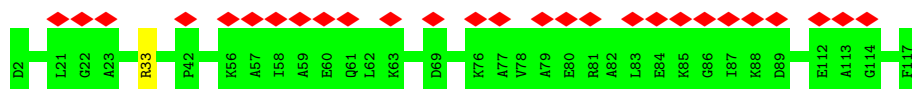
- Molecule 19: 50S ribosomal protein L17



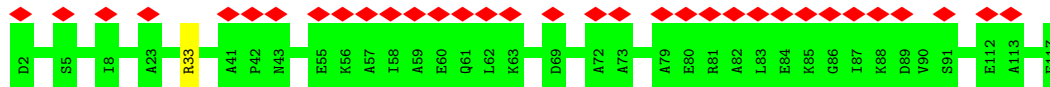
- Molecule 19: 50S ribosomal protein L17



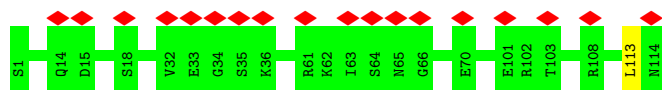
- Molecule 20: 50S ribosomal protein L18



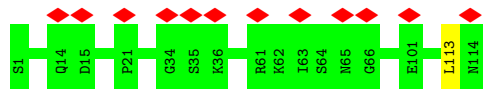
- Molecule 20: 50S ribosomal protein L18



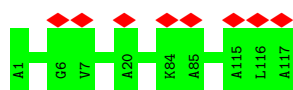
- Molecule 21: 50S ribosomal protein L19



- Molecule 21: 50S ribosomal protein L19

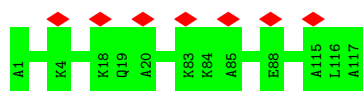


- Molecule 22: 50S ribosomal protein L20



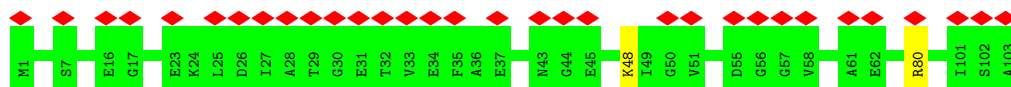
- Molecule 22: 50S ribosomal protein L20

Chain QQ:  6% 100%



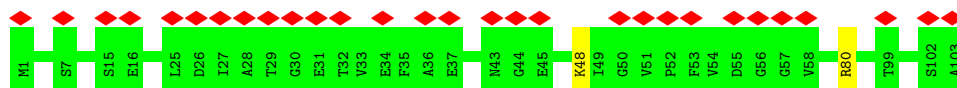
- Molecule 23: 50S ribosomal protein L21

Chain R:  31% 98%



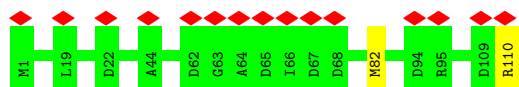
- Molecule 23: 50S ribosomal protein L21

Chain RR:  28% 98%



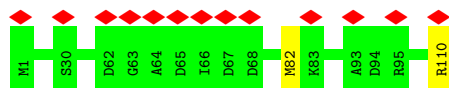
- Molecule 24: 50S ribosomal protein L22

Chain S:  14% 98%



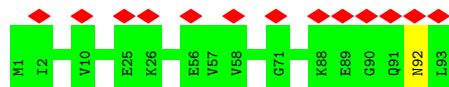
- Molecule 24: 50S ribosomal protein L22

Chain SS:  12% 98%



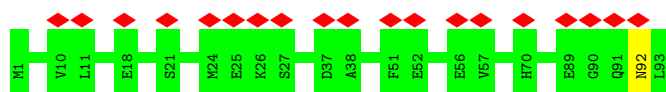
- Molecule 25: 50S ribosomal protein L23

Chain T:  14% 99%

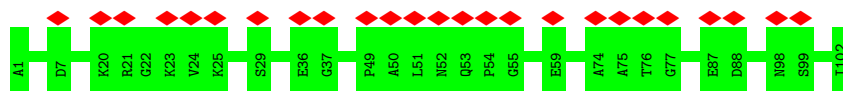


- Molecule 25: 50S ribosomal protein L23

Chain TT:  20% 99%



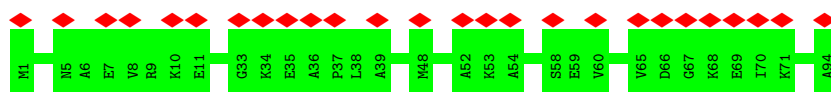
- Molecule 26: 50S ribosomal protein L24



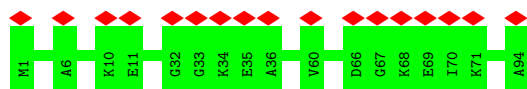
- Molecule 26: 50S ribosomal protein L24



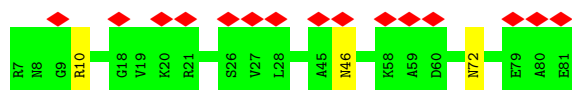
- Molecule 27: 50S ribosomal protein L25



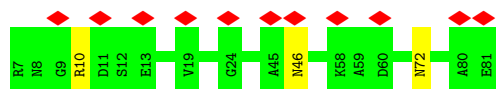
- Molecule 27: 50S ribosomal protein L25



- Molecule 28: 50S ribosomal protein L27



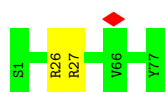
- Molecule 28: 50S ribosomal protein L27



- Molecule 29: 50S ribosomal protein L28



Chain X:  97%



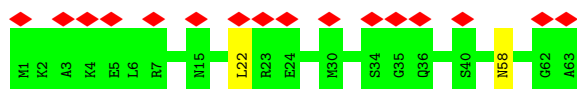
- Molecule 29: 50S ribosomal protein L28

Chain XX:  97%



- Molecule 30: 50S ribosomal protein L29

Chain Y:  97%



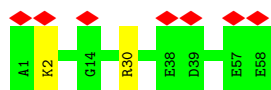
- Molecule 30: 50S ribosomal protein L29

Chain YY:  97%



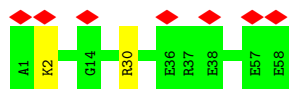
- Molecule 31: 50S ribosomal protein L30

Chain Z:  97%




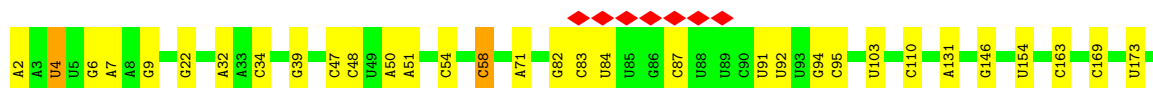
- Molecule 31: 50S ribosomal protein L30

Chain ZZ:  97%

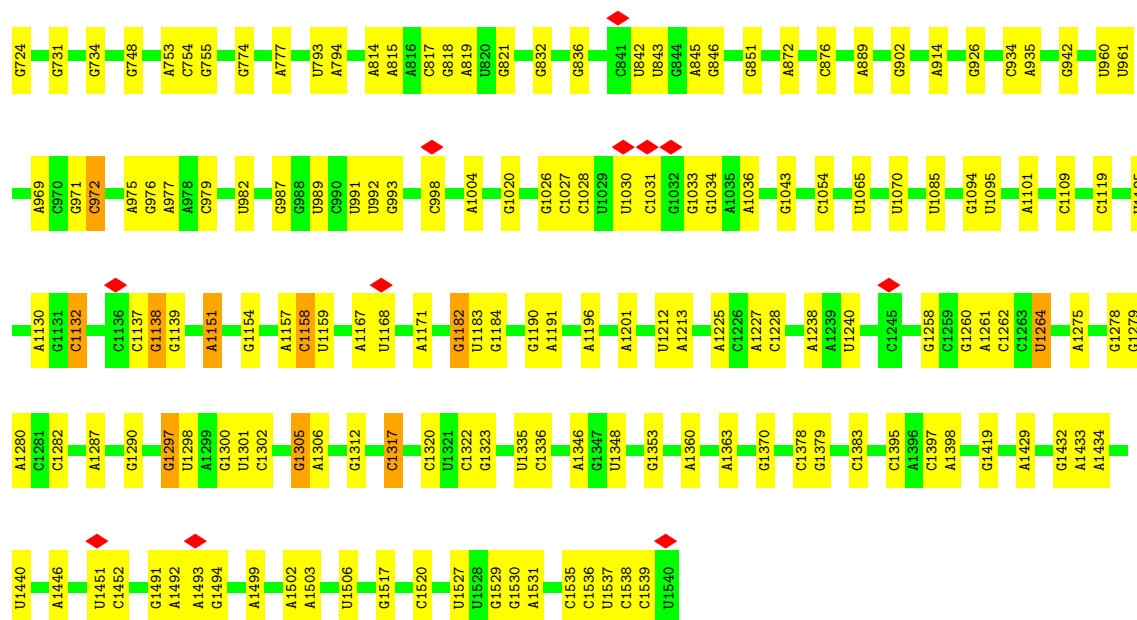


- Molecule 32: 16S ribosomal RNA

Chain a:  80% 19%







• Molecule 33: 30S ribosomal protein S2

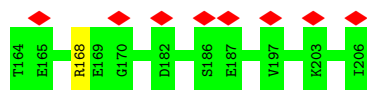


• Molecule 33: 30S ribosomal protein S2



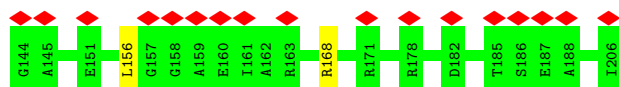
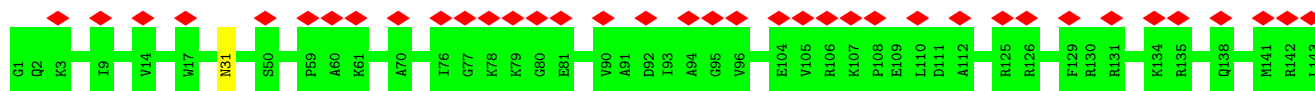
• Molecule 34: 30S ribosomal protein S3





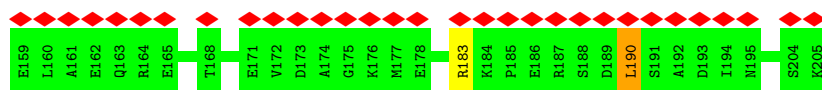
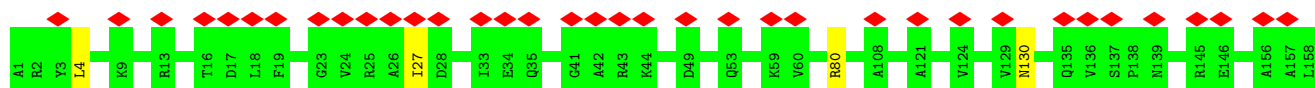
- Molecule 34: 30S ribosomal protein S3

Chain cc: 26% 99%



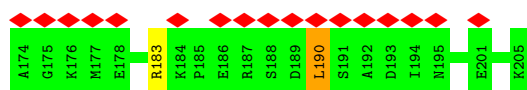
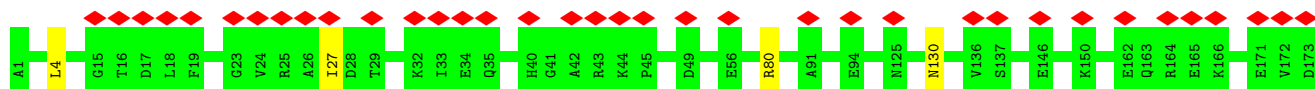
- Molecule 35: 30S ribosomal protein S4

Chain d: 33% 97%



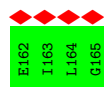
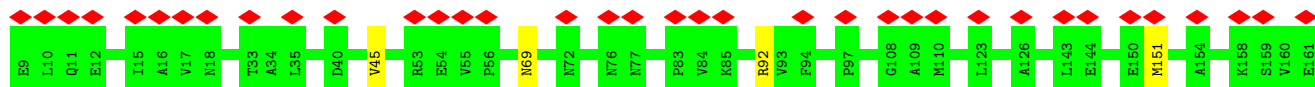
- Molecule 35: 30S ribosomal protein S4

Chain dd: 26% 97%

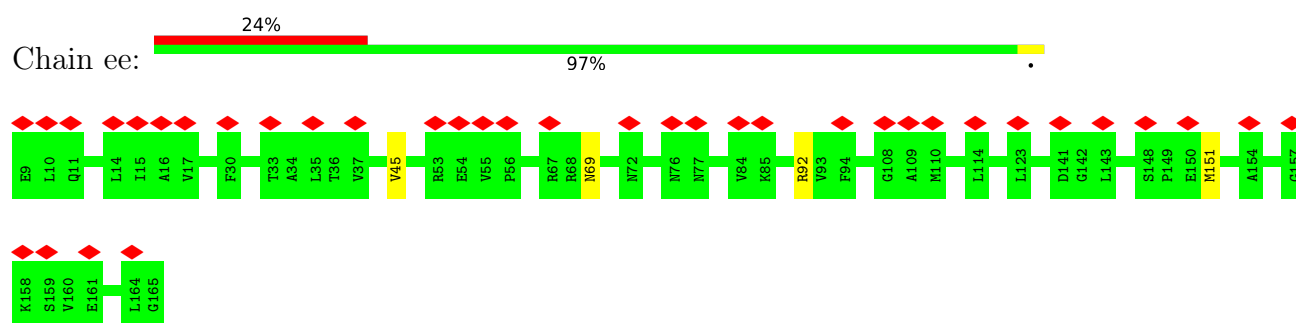


- Molecule 36: 30S ribosomal protein S5

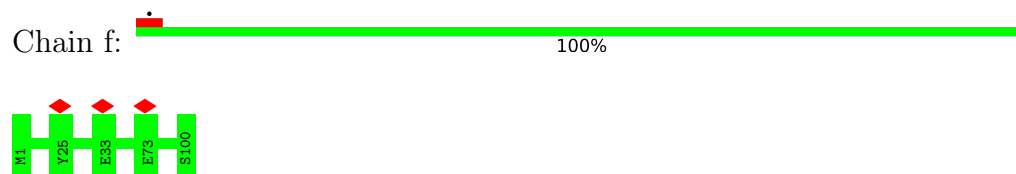
Chain e: 25% 97%



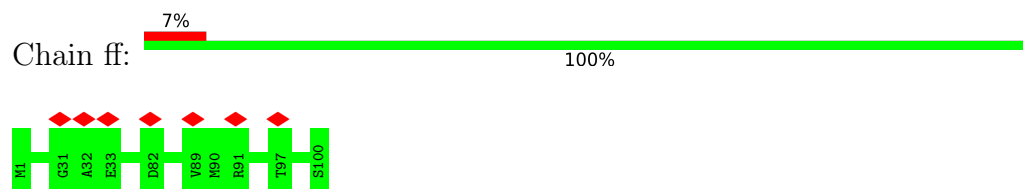
- Molecule 36: 30S ribosomal protein S5



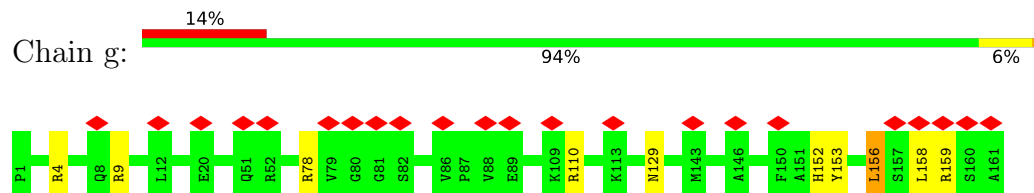
- Molecule 37: 30S ribosomal protein S6



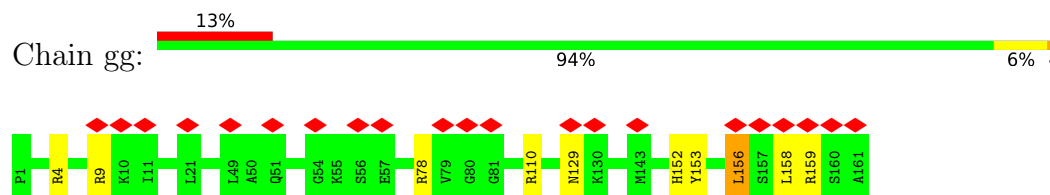
- Molecule 37: 30S ribosomal protein S6



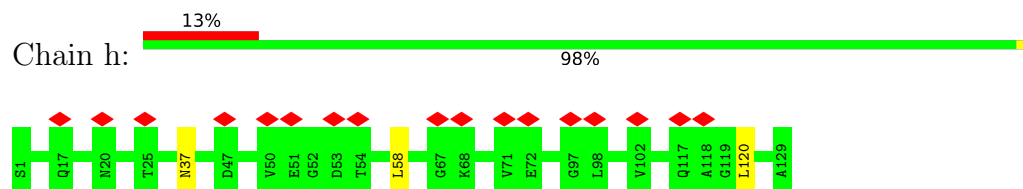
- Molecule 38: 30S ribosomal protein S7



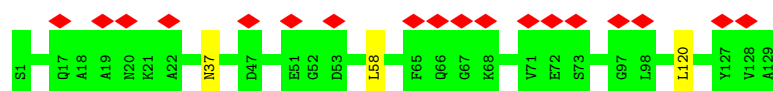
- Molecule 38: 30S ribosomal protein S7



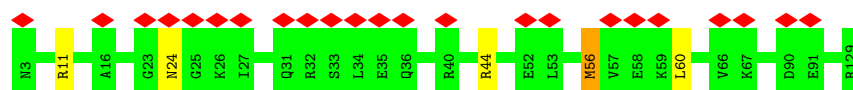
- Molecule 39: 30S ribosomal protein S8



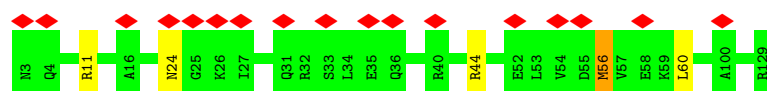
- Molecule 39: 30S ribosomal protein S8



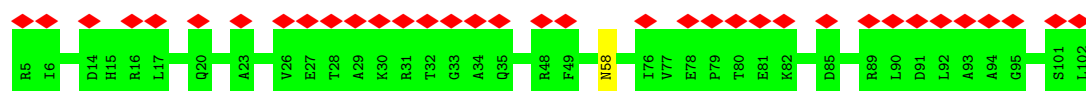
- Molecule 40: 30S ribosomal protein S9



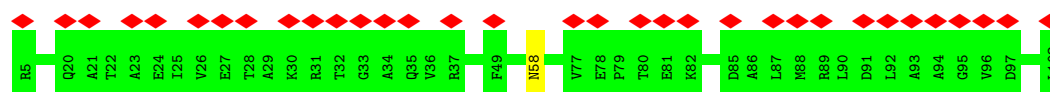
- Molecule 40: 30S ribosomal protein S9



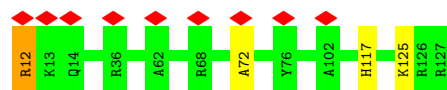
- Molecule 41: 30S ribosomal protein S10



- Molecule 41: 30S ribosomal protein S10

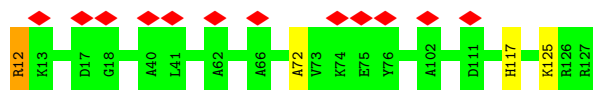


- Molecule 42: 30S ribosomal protein S11

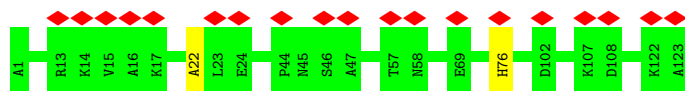


- Molecule 42: 30S ribosomal protein S11

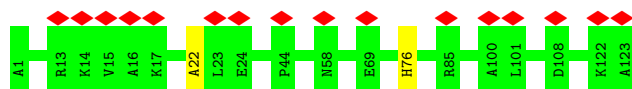




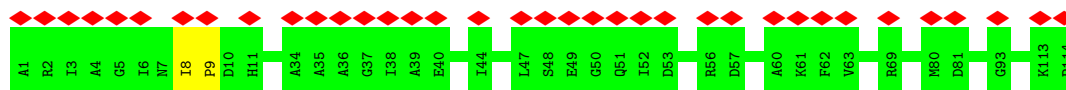
- Molecule 43: 30S ribosomal protein S12



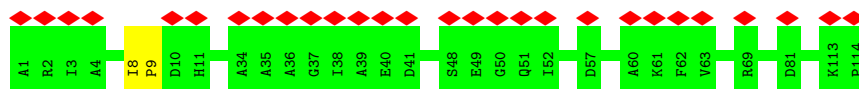
- Molecule 43: 30S ribosomal protein S12



- Molecule 44: 30S ribosomal protein S13



- Molecule 44: 30S ribosomal protein S13



- Molecule 45: 30S ribosomal protein S14



- Molecule 45: 30S ribosomal protein S14



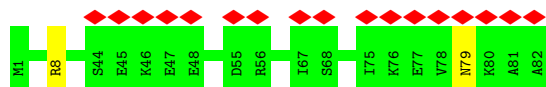
- Molecule 46: 30S ribosomal protein S15



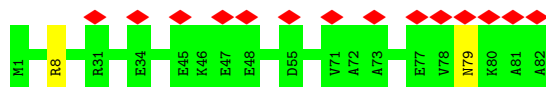
- Molecule 46: 30S ribosomal protein S15



- Molecule 47: 30S ribosomal protein S16



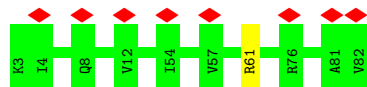
- Molecule 47: 30S ribosomal protein S16



- Molecule 48: 30S ribosomal protein S17



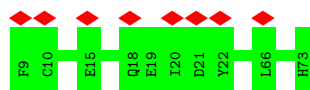
- Molecule 48: 30S ribosomal protein S17



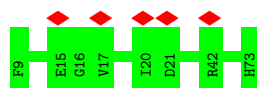
- Molecule 49: 30S ribosomal protein S18



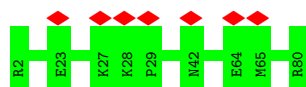




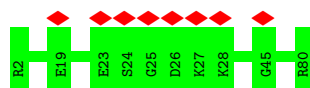
- Molecule 49: 30S ribosomal protein S18



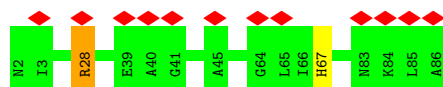
- Molecule 50: 30S ribosomal protein S19



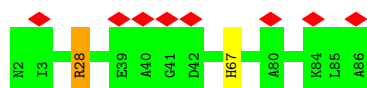
- Molecule 50: 30S ribosomal protein S19



- Molecule 51: 30S ribosomal protein S20



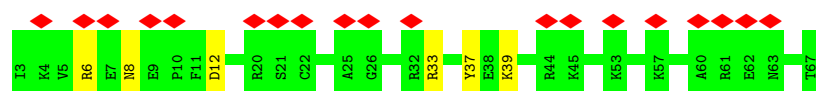
- Molecule 51: 30S ribosomal protein S20



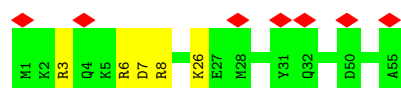
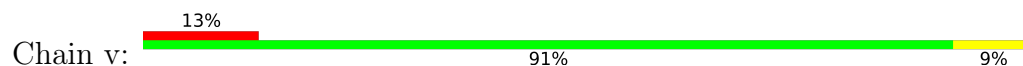
- Molecule 52: 30S ribosomal protein S21



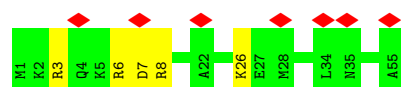
- Molecule 52: 30S ribosomal protein S21



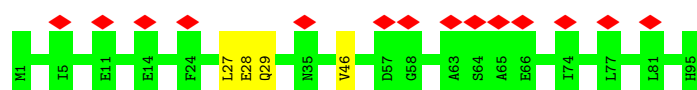
- Molecule 53: Ribosome modulation factor



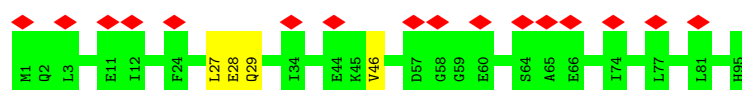
- Molecule 53: Ribosome modulation factor



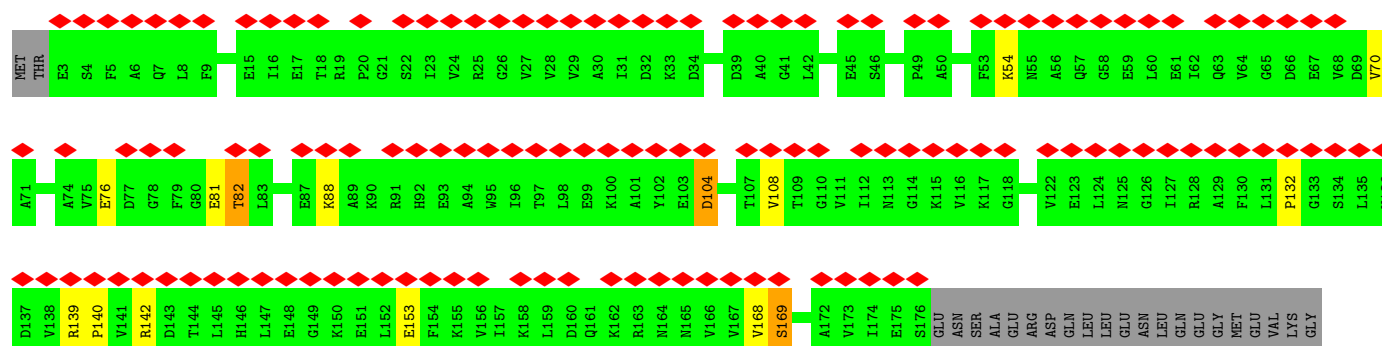
- Molecule 54: Ribosome hibernation promoting factor



- Molecule 54: Ribosome hibernation promoting factor



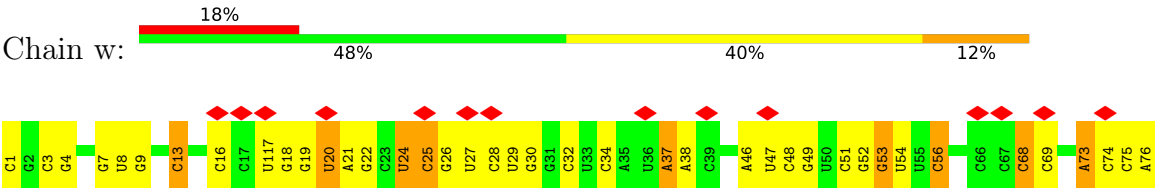
- Molecule 55: 30S ribosomal protein S1



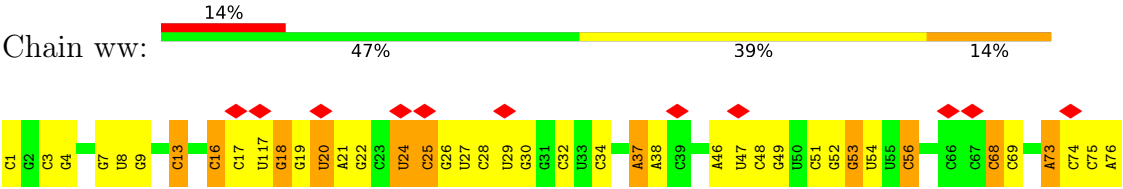


ALA	ASP	GLU	LYS	ASP	ALA	TLE	THR	VAL	ASN	LYS	GLN	GLU	ASP	ALA	ASN	PHE	SER	ASN	ALA	MET	ALA	GLU	ALA	LYS	ALA	ALA	LYS	GLY	GLU
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

● Molecule 56: tRNA Mixture



● Molecule 56: tRNA Mixture



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	18000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	1.15	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.312	Depositor
Minimum map value	-0.097	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.019	Depositor
Recommended contour level	0.075	Depositor
Map size ( $\text{\AA}$ )	615.60004, 615.60004, 615.60004	wwPDB
Map dimensions	228, 228, 228	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	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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*Continued from previous page...*

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(°)	Ideal(°)
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 [i](#)

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

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

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

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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%)	8	38
4	33	62/64 (97%)	57 (92%)	4 (6%)	1 (2%)	8	38
5	4	36/38 (95%)	34 (94%)	2 (6%)	0	100	100
5	44	36/38 (95%)	34 (94%)	2 (6%)	0	100	100
6	6	64/66 (97%)	56 (88%)	8 (12%)	0	100	100
6	66	64/66 (97%)	55 (86%)	9 (14%)	0	100	100
9	C	269/271 (99%)	244 (91%)	25 (9%)	0	100	100
9	CC	269/271 (99%)	244 (91%)	25 (9%)	0	100	100
10	D	207/209 (99%)	192 (93%)	15 (7%)	0	100	100
10	DD	207/209 (99%)	192 (93%)	15 (7%)	0	100	100
11	E	199/201 (99%)	188 (94%)	11 (6%)	0	100	100
11	EE	199/201 (99%)	188 (94%)	11 (6%)	0	100	100
12	F	175/177 (99%)	163 (93%)	12 (7%)	0	100	100
12	FF	175/177 (99%)	163 (93%)	12 (7%)	0	100	100
13	G	174/176 (99%)	160 (92%)	13 (8%)	1 (1%)	22	60
13	GG	174/176 (99%)	160 (92%)	13 (8%)	1 (1%)	22	60
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%)	3	23
18	MM	134/136 (98%)	126 (94%)	4 (3%)	4 (3%)	3	23
19	N	118/120 (98%)	108 (92%)	10 (8%)	0	100	100

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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%)	30	68
33	bb	224/226 (99%)	190 (85%)	33 (15%)	1 (0%)	30	68
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%)	22	60
38	gg	159/161 (99%)	136 (86%)	22 (14%)	1 (1%)	22	60
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%)	13	49
41	jj	96/98 (98%)	82 (85%)	13 (14%)	1 (1%)	13	49
42	k	114/116 (98%)	97 (85%)	17 (15%)	0	100	100
42	kk	114/116 (98%)	97 (85%)	17 (15%)	0	100	100
43	l	121/123 (98%)	103 (85%)	18 (15%)	0	100	100
43	ll	121/123 (98%)	103 (85%)	18 (15%)	0	100	100
44	m	112/114 (98%)	96 (86%)	15 (13%)	1 (1%)	14	52
44	mm	112/114 (98%)	96 (86%)	15 (13%)	1 (1%)	14	52
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%)	11	44
46	oo	86/88 (98%)	77 (90%)	8 (9%)	1 (1%)	11	44
47	p	80/82 (98%)	73 (91%)	7 (9%)	0	100	100
47	pp	80/82 (98%)	73 (91%)	7 (9%)	0	100	100
48	q	78/80 (98%)	66 (85%)	12 (15%)	0	100	100
48	qq	78/80 (98%)	66 (85%)	12 (15%)	0	100	100
49	r	63/65 (97%)	61 (97%)	2 (3%)	0	100	100
49	rr	63/65 (97%)	61 (97%)	2 (3%)	0	100	100
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%)	8	38
52	uu	63/65 (97%)	46 (73%)	16 (25%)	1 (2%)	8	38
53	v	53/55 (96%)	43 (81%)	9 (17%)	1 (2%)	6	32
53	vv	53/55 (96%)	43 (81%)	9 (17%)	1 (2%)	6	32
54	x	93/95 (98%)	86 (92%)	6 (6%)	1 (1%)	12	47
54	xx	93/95 (98%)	86 (92%)	6 (6%)	1 (1%)	12	47
55	y	347/557 (62%)	253 (73%)	75 (22%)	19 (6%)	1	15
55	yy	347/557 (62%)	253 (73%)	75 (22%)	19 (6%)	1	15
All	All	12180/12804 (95%)	10888 (89%)	1226 (10%)	66 (0%)	27	64

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%)	75	83
9	CC	216/216 (100%)	214 (99%)	2 (1%)	75	83
10	D	164/164 (100%)	160 (98%)	4 (2%)	44	62
10	DD	164/164 (100%)	160 (98%)	4 (2%)	44	62
11	E	165/165 (100%)	163 (99%)	2 (1%)	67	78
11	EE	165/165 (100%)	163 (99%)	2 (1%)	67	78
12	F	148/148 (100%)	146 (99%)	2 (1%)	62	75
12	FF	148/148 (100%)	146 (99%)	2 (1%)	62	75
13	G	137/137 (100%)	135 (98%)	2 (2%)	60	75
13	GG	137/137 (100%)	135 (98%)	2 (2%)	60	75
14	H	114/114 (100%)	111 (97%)	3 (3%)	41	59
14	HH	114/114 (100%)	111 (97%)	3 (3%)	41	59
15	J	116/116 (100%)	115 (99%)	1 (1%)	75	83
15	JJ	116/116 (100%)	115 (99%)	1 (1%)	75	83
16	K	103/103 (100%)	102 (99%)	1 (1%)	73	82
16	KK	103/103 (100%)	102 (99%)	1 (1%)	73	82
17	L	102/102 (100%)	101 (99%)	1 (1%)	73	82
17	LL	102/102 (100%)	101 (99%)	1 (1%)	73	82
18	M	109/109 (100%)	107 (98%)	2 (2%)	54	71
18	MM	109/109 (100%)	107 (98%)	2 (2%)	54	71
19	N	100/100 (100%)	99 (99%)	1 (1%)	73	82
19	NN	100/100 (100%)	99 (99%)	1 (1%)	73	82
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%)	44	62
23	RR	84/84 (100%)	82 (98%)	2 (2%)	44	62
24	S	93/93 (100%)	91 (98%)	2 (2%)	47	65
24	SS	93/93 (100%)	91 (98%)	2 (2%)	47	65
25	T	80/80 (100%)	79 (99%)	1 (1%)	65	77
25	TT	80/80 (100%)	79 (99%)	1 (1%)	65	77
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%)	19	40
28	WW	57/57 (100%)	54 (95%)	3 (5%)	19	40
29	X	67/67 (100%)	65 (97%)	2 (3%)	36	55
29	XX	67/67 (100%)	65 (97%)	2 (3%)	36	55
30	Y	55/55 (100%)	54 (98%)	1 (2%)	54	71
30	YY	55/55 (100%)	54 (98%)	1 (2%)	54	71
31	Z	48/48 (100%)	46 (96%)	2 (4%)	25	46
31	ZZ	48/48 (100%)	46 (96%)	2 (4%)	25	46
33	b	186/186 (100%)	184 (99%)	2 (1%)	70	80
33	bb	186/186 (100%)	184 (99%)	2 (1%)	70	80
34	c	170/170 (100%)	168 (99%)	2 (1%)	67	78
34	cc	170/170 (100%)	168 (99%)	2 (1%)	67	78
35	d	172/172 (100%)	169 (98%)	3 (2%)	56	72
35	dd	172/172 (100%)	169 (98%)	3 (2%)	56	72
36	e	114/119 (96%)	110 (96%)	4 (4%)	31	51
36	ee	114/119 (96%)	110 (96%)	4 (4%)	31	51
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%)	28	49

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	gg	132/132 (100%)	127 (96%)	5 (4%)	28	49
39	h	104/104 (100%)	102 (98%)	2 (2%)	52	69
39	hh	104/104 (100%)	102 (98%)	2 (2%)	52	69
40	i	105/105 (100%)	100 (95%)	5 (5%)	21	43
40	ii	105/105 (100%)	100 (95%)	5 (5%)	21	43
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%)	70	80
42	kk	89/89 (100%)	88 (99%)	1 (1%)	70	80
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%)	42	61
45	nn	79/83 (95%)	77 (98%)	2 (2%)	42	61
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%)	35	54
47	pp	65/65 (100%)	63 (97%)	2 (3%)	35	54
48	q	74/74 (100%)	73 (99%)	1 (1%)	62	75
48	qq	74/74 (100%)	73 (99%)	1 (1%)	62	75
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%)	60	75
51	tt	65/65 (100%)	64 (98%)	1 (2%)	60	75
52	u	44/55 (80%)	43 (98%)	1 (2%)	45	64
52	uu	44/55 (80%)	43 (98%)	1 (2%)	45	64
53	v	44/44 (100%)	42 (96%)	2 (4%)	23	45
53	vv	44/44 (100%)	42 (96%)	2 (4%)	23	45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
54	x	80/81 (99%)	77 (96%)	3 (4%)	28	49
54	xx	80/81 (99%)	77 (96%)	3 (4%)	28	49
55	y	137/461 (30%)	134 (98%)	3 (2%)	47	65
55	yy	137/461 (30%)	134 (98%)	3 (2%)	47	65
All	All	9778/10484 (93%)	9632 (98%)	146 (2%)	60	75

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 [i](#)

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
56	w	1

All chain breaks are listed below:

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

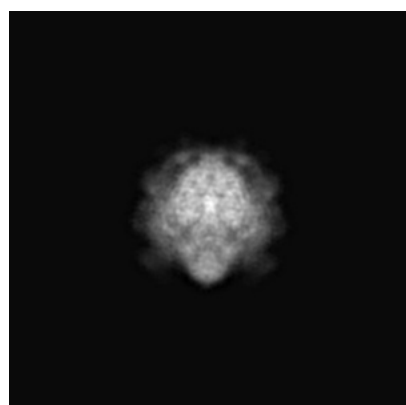
## 6 Map visualisation [i](#)

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

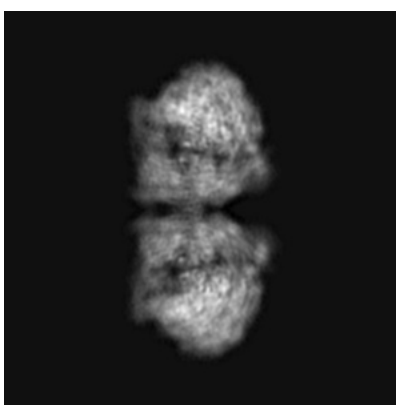
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

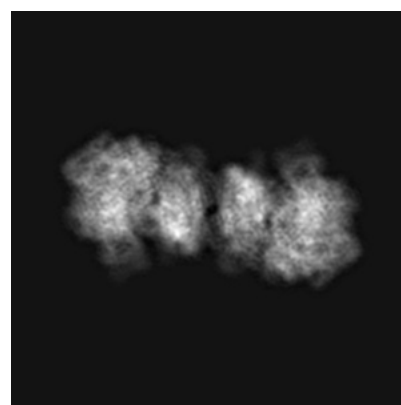
#### 6.1.1 Primary map



X



Y



Z

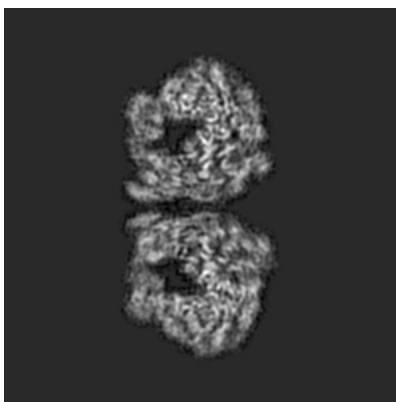
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

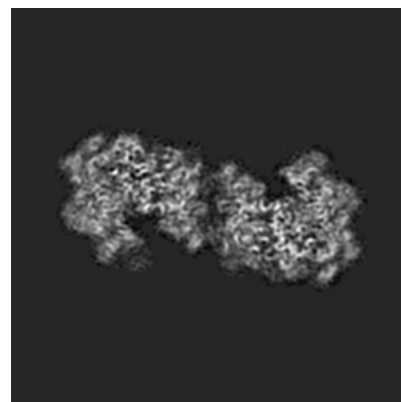
#### 6.2.1 Primary map



X Index: 114



Y Index: 114

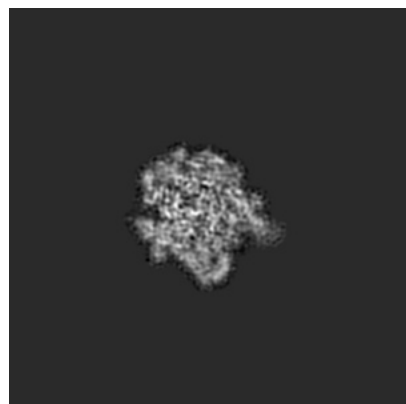


Z Index: 114

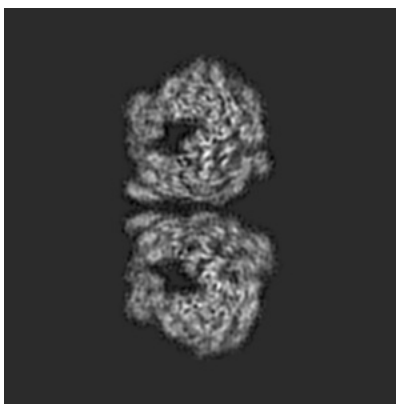
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

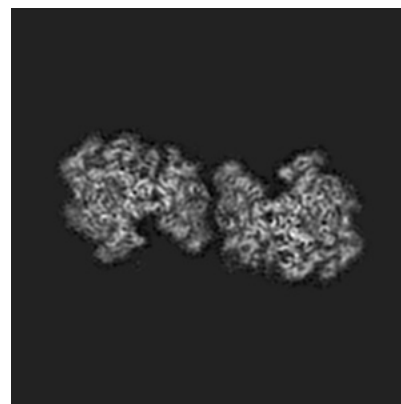
### 6.3.1 Primary map



X Index: 169



Y Index: 113

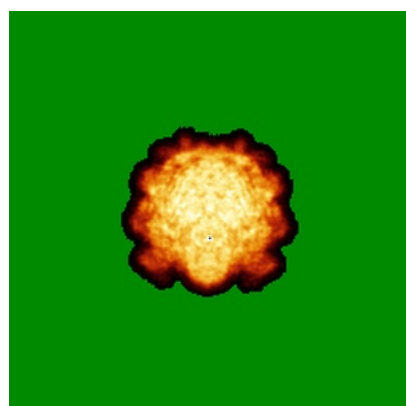


Z Index: 117

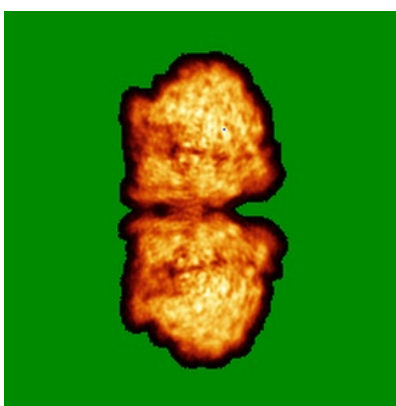
The images above show the largest variance slices of the map in three orthogonal directions.

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

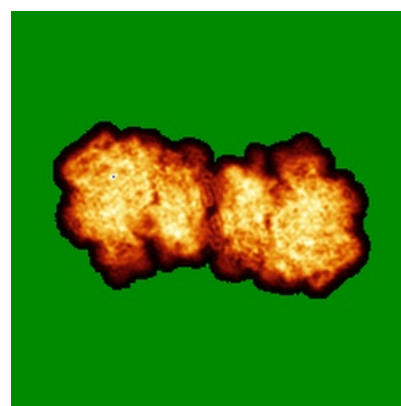
### 6.4.1 Primary map



X



Y

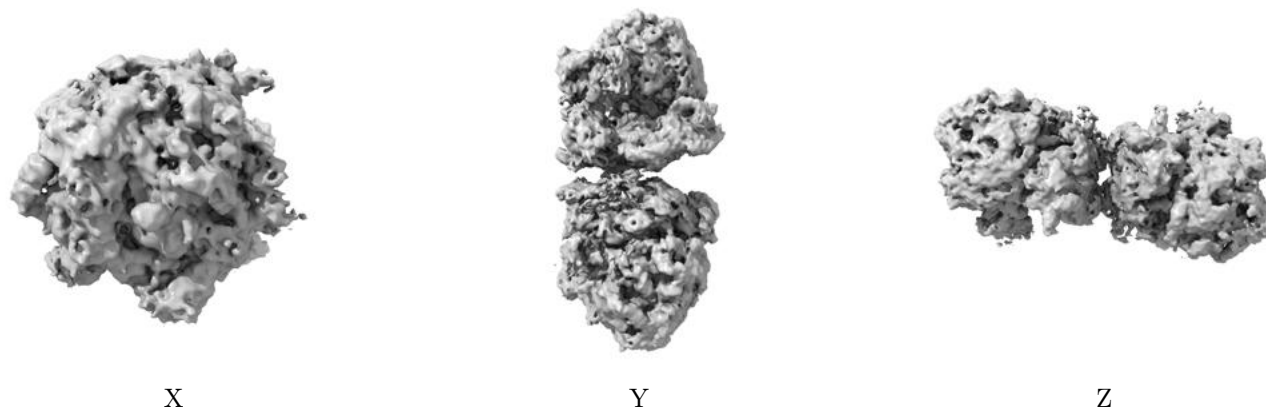


Z

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

## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



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

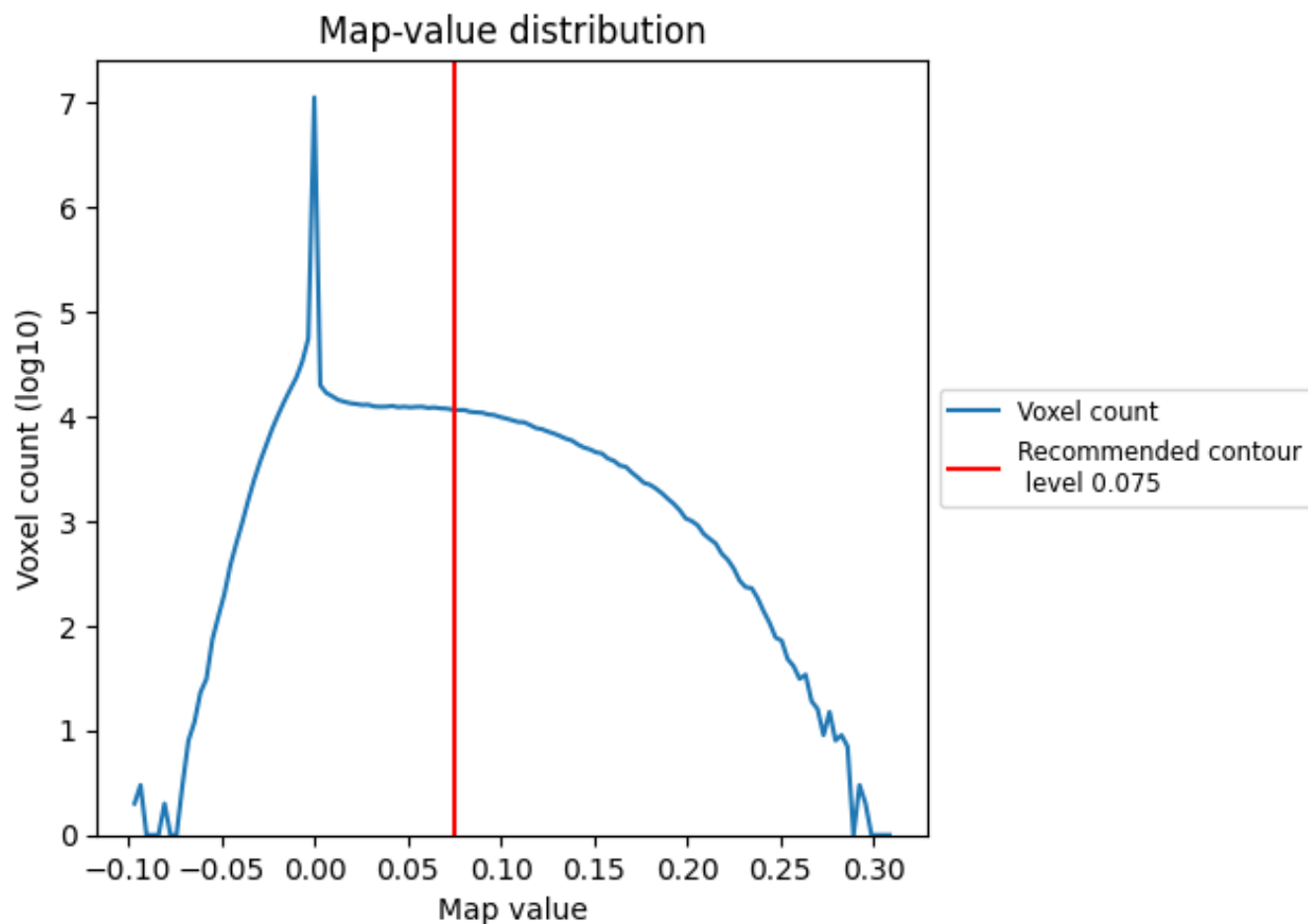
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

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

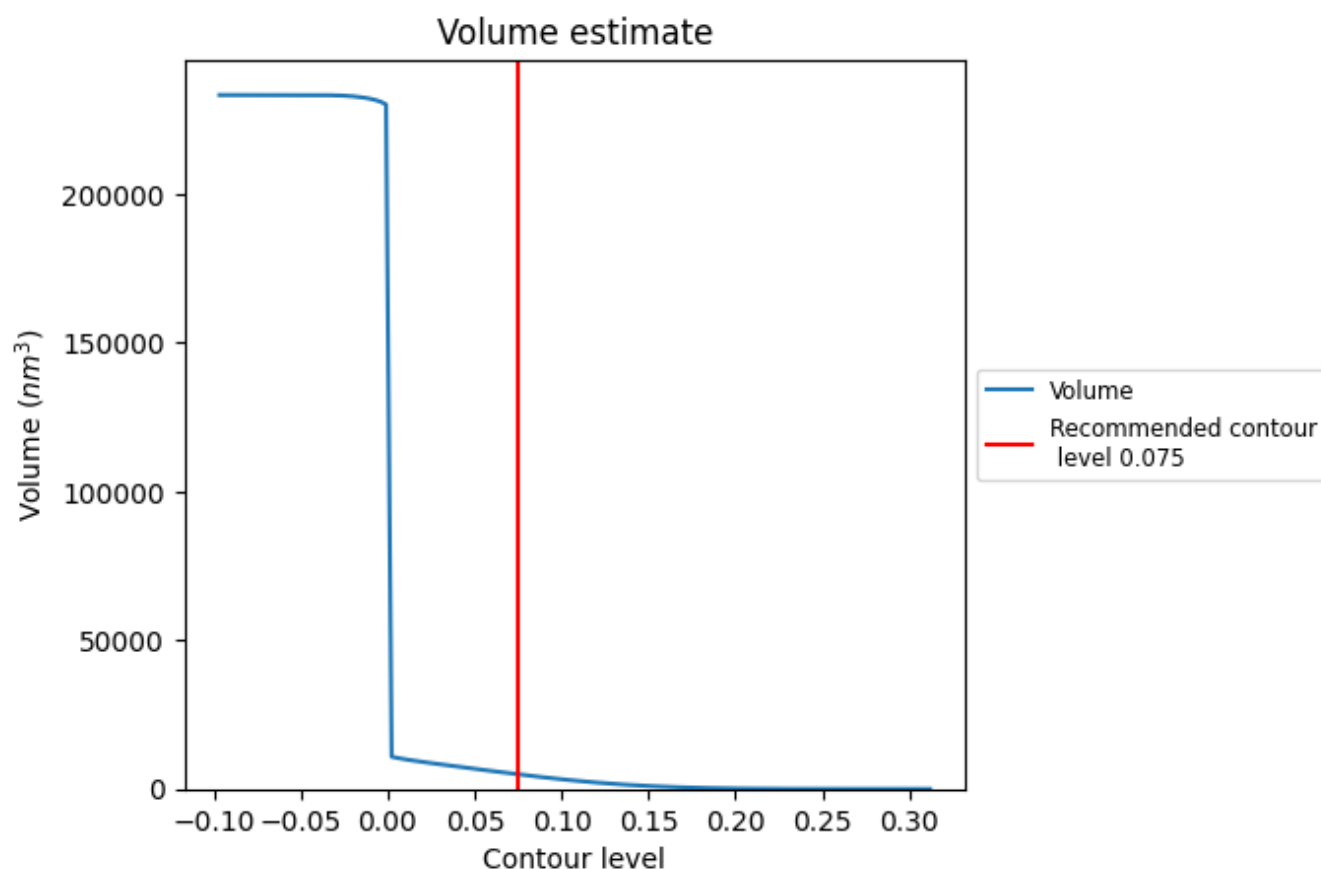
### 7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.



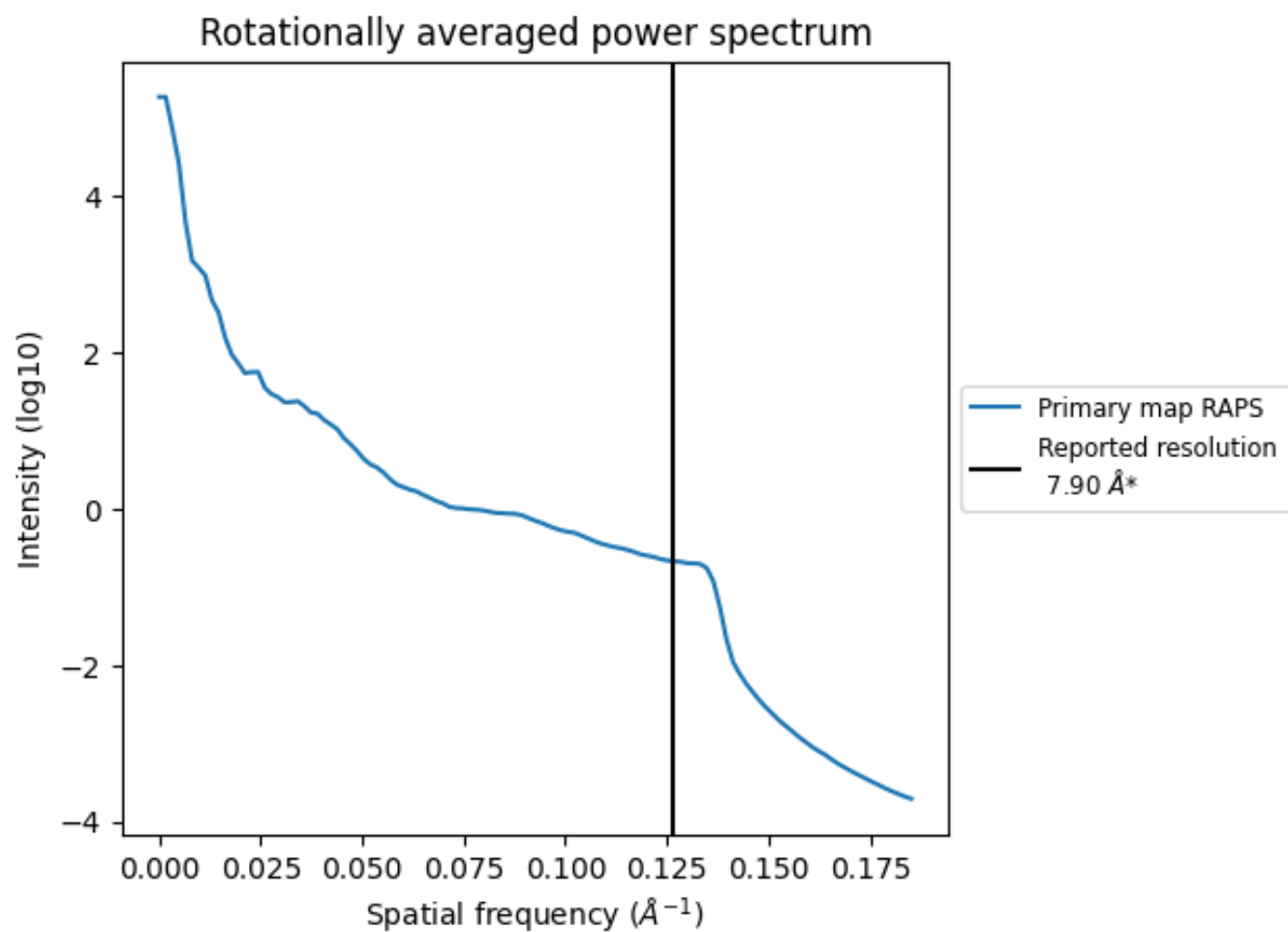
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4934 nm<sup>3</sup>; 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 ⓘ

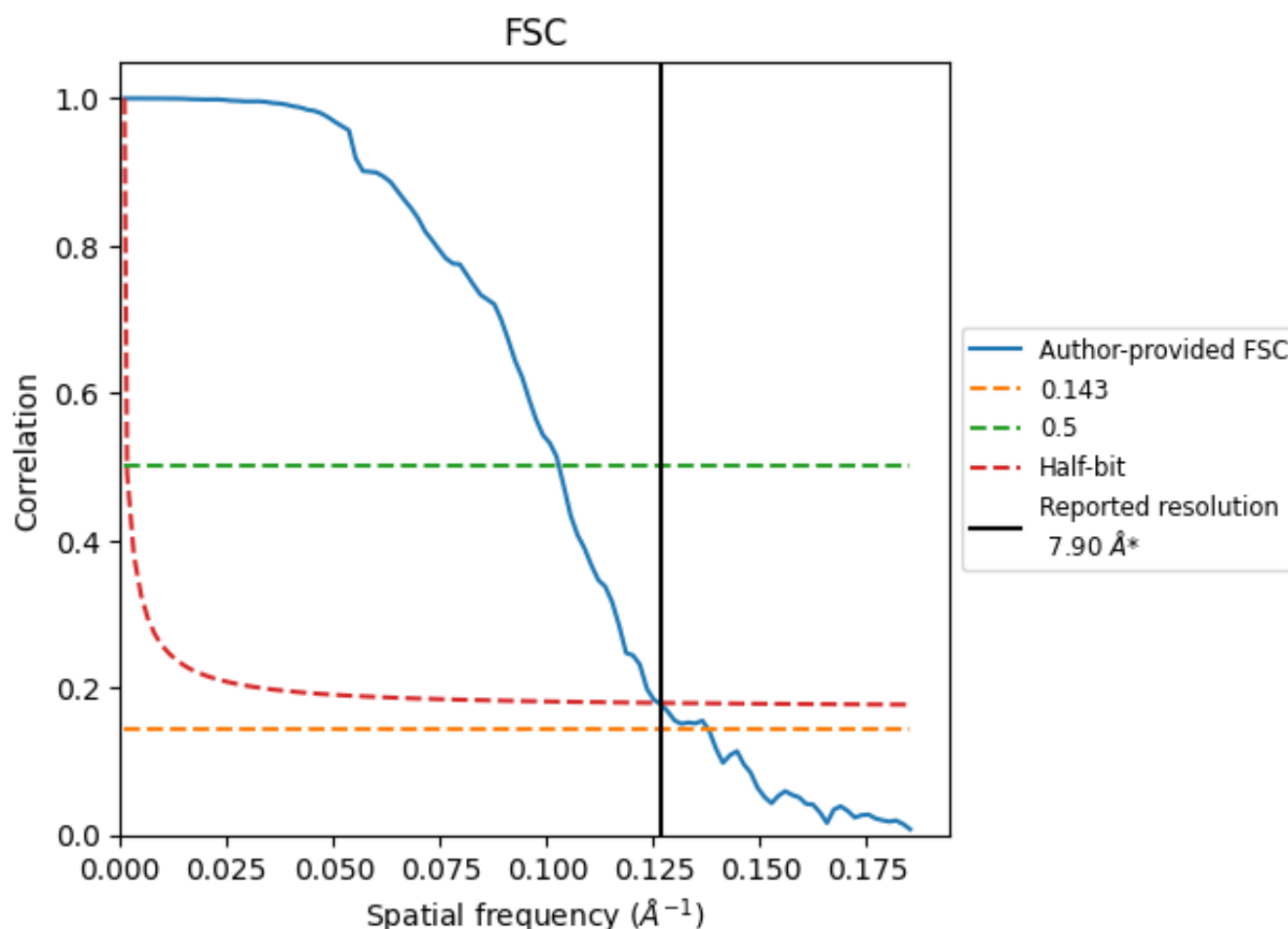


\*Reported resolution corresponds to spatial frequency of 0.127 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.127 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

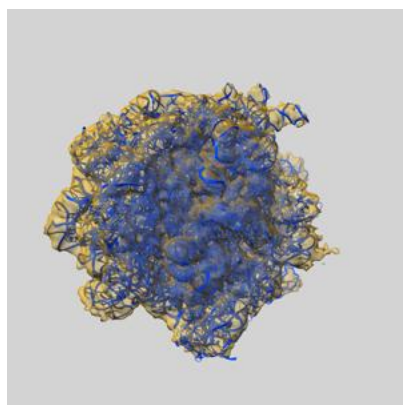
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.90	-	-
Author-provided FSC curve	7.26	9.72	7.92
Unmasked-calculated*	-	-	-

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

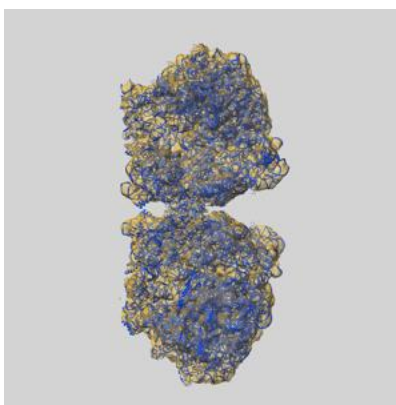
## 9 Map-model fit [i](#)

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

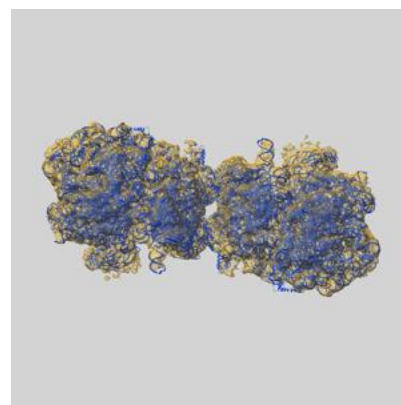
### 9.1 Map-model overlay [i](#)



X



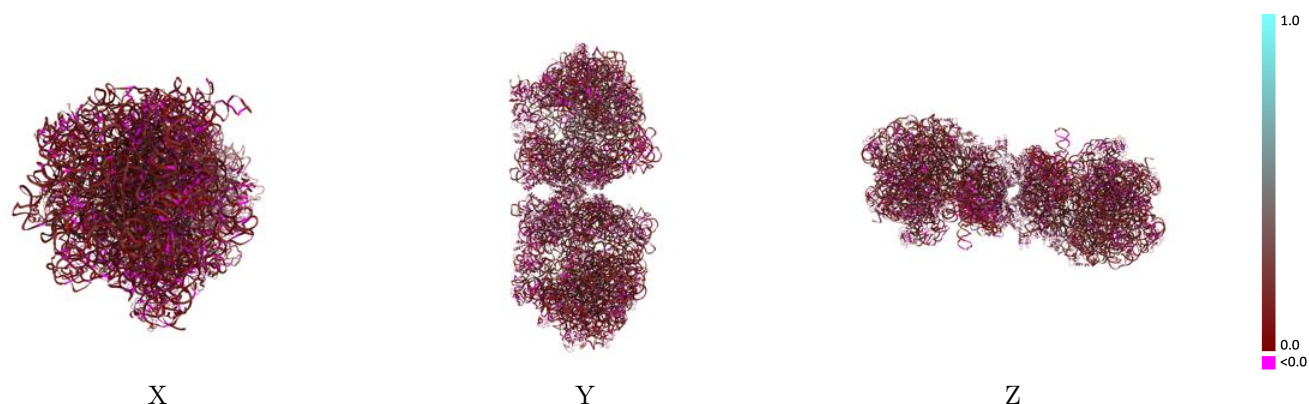
Y



Z

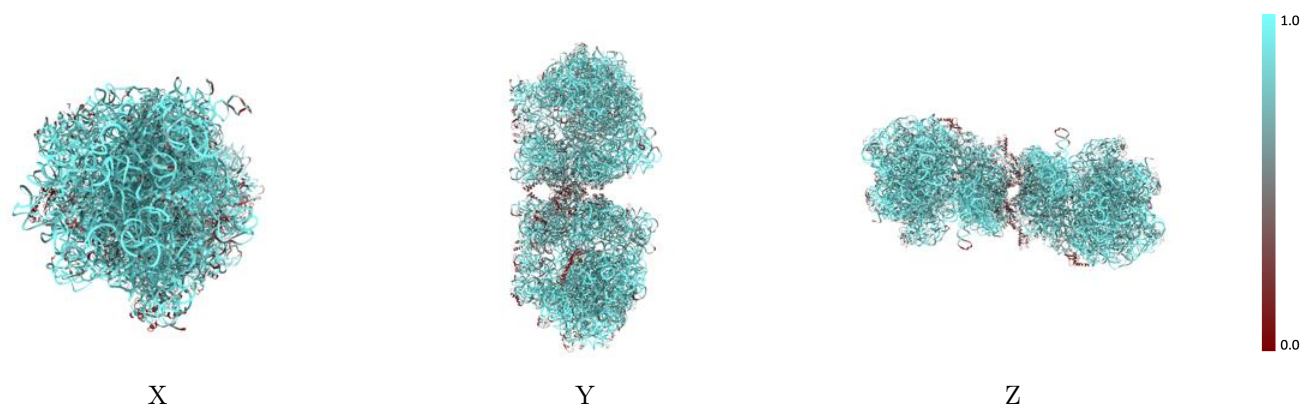
The images above show the 3D surface view of the map at the recommended contour level 0.075 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



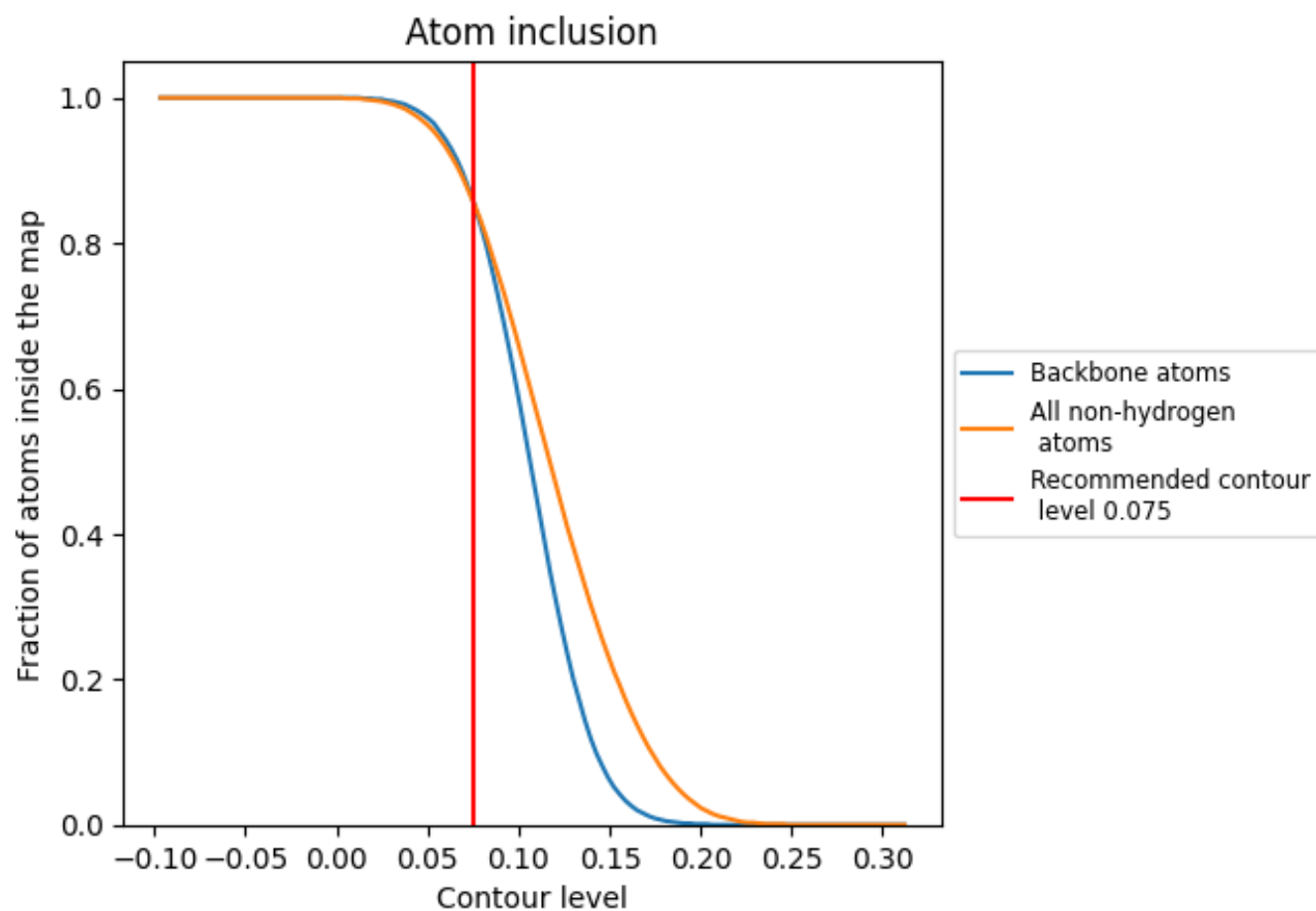
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



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







































































## 9.4 Atom inclusion [i](#)



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

## 9.5 Map-model fit summary ⓘ

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





















































































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



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

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