



## Full wwPDB EM Validation Report ⓘ

Nov 19, 2022 – 12:16 pm GMT

PDB ID : 5LZW  
EMDB ID : EMD-4134  
Title : Structure of the mammalian rescue complex with Pelota and Hbs1l assembled on a truncated mRNA.  
Authors : Shao, S.; Murray, J.; Brown, A.; Taunton, J.; Ramakrishnan, V.; Hegde, R.S.  
Deposited on : 2016-10-02  
Resolution : 3.53 Å(reported)

This is a Full wwPDB EM Validation 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:

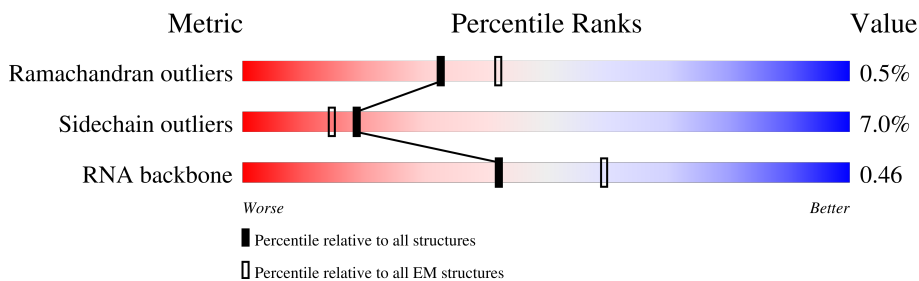
EMDB validation analysis : 0.0.1.dev43  
Mogul : 1.8.4, CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (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 3.53 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.



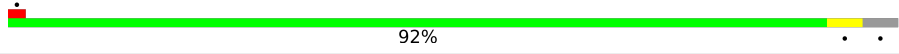
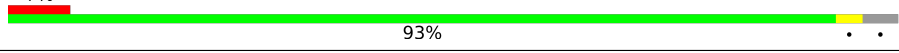
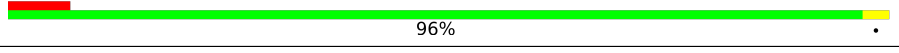
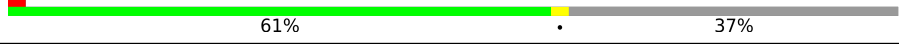
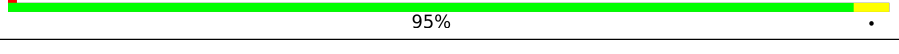
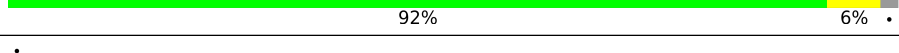

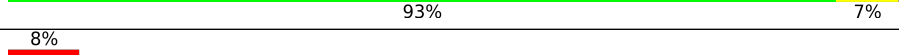
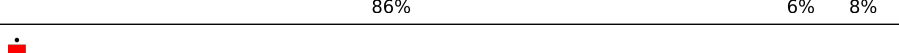
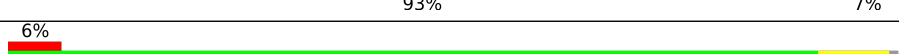
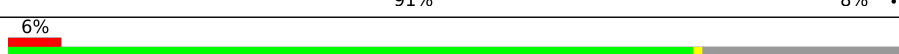

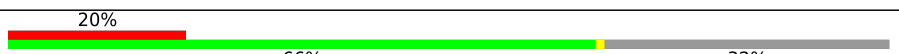
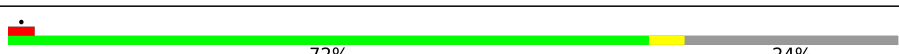
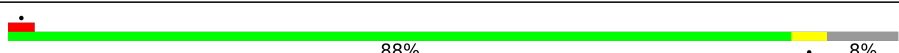
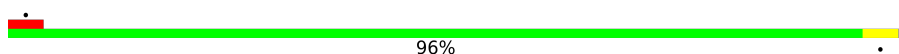
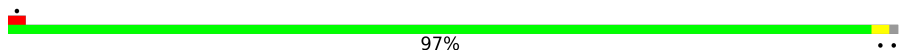


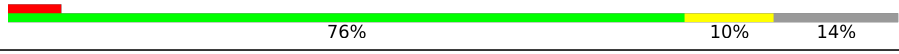

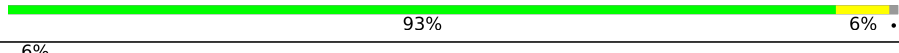
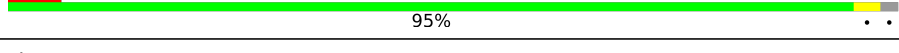
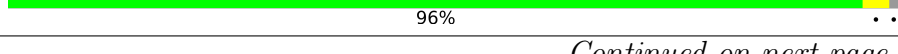

Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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  $\geq 3$ , 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	A	257	
2	B	403	
3	C	425	
4	D	297	
5	E	291	
6	F	247	
7	G	319	
8	H	192	

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Mol	Chain	Length	Quality of chain
9	I	214	 92%
10	J	178	 93%
11	L	211	 96%
12	M	218	 61% 37%
13	N	204	 95%
14	O	203	 92% 6%
15	P	184	 78% 5% 17%
16	Q	188	 93% 7%
17	R	196	 86% 6% 8%
18	S	176	 93% 7%
19	T	160	 91% 8% 6%
20	U	128	 77% 23%
21	V	140	 87% 6% 6%
22	W	157	 66% 32%
23	X	156	 72% 24%
24	Y	145	 88% 8%
25	Z	136	 96%
26	a	148	 97%
27	b	245	 41% 58%
28	c	115	 82% 15%
29	d	125	 76% 10% 14%
30	e	135	 88% 7% 5%
31	f	110	 93% 6%
32	g	116	 95%
33	h	123	 96%

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Mol	Chain	Length	Quality of chain
34	i	105	94%
35	j	97	85% 11%
36	k	70	96%
37	l	51	96%
38	m	102	48% 49%
39	n	25	92% 8%
40	o	106	93% 5%
41	p	92	97%
42	r	137	85% 5% 9%
43	s	318	53% 59% 38%
44	t	165	85% 90% 7%
45	1	15	87% 100%
46	2	76	14% 80% 20%
47	3	75	88% 64% 36%
48	5	3543	74% 25%
49	7	120	88% 12%
50	8	156	72% 24%
51	9	1869	5% 66% 24% 9%
52	AA	295	5% 68% 6% 26%
53	BB	264	5% 74% 6% 19%
54	CC	293	69% 7% 25%
55	DD	243	12% 86% 8% 6%
56	EE	263	5% 94% 6%
57	FF	204	86% 5% 9%
58	GG	249	17% 88% 7% 5%

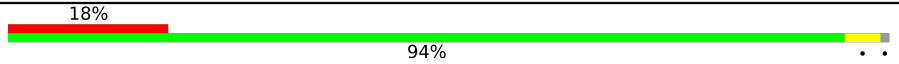
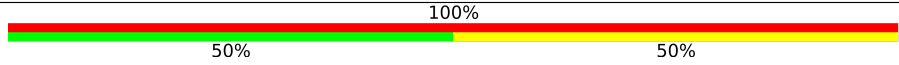


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Mol	Chain	Length	Quality of chain
59	HH	194	
60	II	208	
61	JJ	194	
62	KK	165	
63	LL	158	
64	MM	132	
65	NN	151	
66	OO	168	
67	PP	145	
68	QQ	146	
69	RR	135	
70	SS	152	
71	TT	145	
72	UU	119	
73	VV	83	
74	WW	130	
75	XX	143	
76	YY	130	
77	ZZ	125	
78	aa	115	
79	bb	84	
80	cc	69	
81	dd	56	
82	ee	133	
83	ff	156	

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Mol	Chain	Length	Quality of chain
84	gg	317	
85	hh	8	
86	ii	403	
87	jj	710	

## 2 Entry composition i

There are 90 unique types of molecules in this entry. The entry contains 222130 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 uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 2 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	394	Total	C	N	O	S	0	0
			3172	2020	597	542	13		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1	MET	-	initiating methionine	UNP G1TL06

- Molecule 3 is a protein called uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	362	Total	C	N	O	S	0	0
			2883	1812	577	480	14		

- Molecule 4 is a protein called uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	293	Total	C	N	O	S	0	0
			2391	1512	438	427	14		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	1	MET	LYS	initiating methionine	UNP G1SYJ6

- Molecule 5 is a protein called eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	216	1729	1115	329	282	3	0	0

- Molecule 6 is a protein called uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	225	1875	1205	358	303	9	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	61	ARG	GLY	conflict	UNP G1TUB1
F	93	ARG	GLY	conflict	UNP G1TUB1
F	131	MET	VAL	conflict	UNP G1TUB1
F	153	ILE	VAL	conflict	UNP G1TUB1

- Molecule 7 is a protein called eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	G	233	1879	1199	361	315	4	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	244	GLY	CYS	conflict	UNP G1STW0

- Molecule 8 is a protein called uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	H	190	1516	954	284	272	6	0	0

- Molecule 9 is a protein called uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	I	205	1664	1056	321	274	13	0	0

- Molecule 10 is a protein called uL5.



Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 11 is a protein called eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	210	Total	C	N	O	S	0	0
			1702	1065	354	279	4		

- Molecule 12 is a protein called eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 13 is a protein called eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 14 is a protein called uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	199	Total	C	N	O	S	0	0
			1630	1051	319	255	5		

- Molecule 15 is a protein called uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	153	Total	C	N	O	S	0	0
			1242	777	241	215	9		

- Molecule 16 is a protein called eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	187	Total	C	N	O	S	0	0
			1515	946	315	250	4		

- Molecule 17 is a protein called eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 18 is a protein called eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	176	Total	C	N	O	S	0	0
			1462	930	285	236	11		

- Molecule 19 is a protein called eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 20 is a protein called eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	99	Total	C	N	O	S	0	0
			809	519	141	147	2		

- Molecule 21 is a protein called uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 22 is a protein called eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	106	Total	C	N	O	S	0	0
			860	538	174	144	4		

- Molecule 23 is a protein called uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 24 is a protein called uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Y	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 25 is a protein called eL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Z	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 26 is a protein called uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	a	147	Total	C	N	O	S	0	0
			1162	734	239	185	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	1	MET	GLN	conflict	UNP G1SNY0

- Molecule 27 is a protein called eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	104	Total	C	N	O	S	0	0
			848	527	189	129	3		

- Molecule 28 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	c	98	Total	C	N	O	S	0	0
			761	481	134	140	6		

- Molecule 29 is a protein called eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 30 is a protein called eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 31 is a protein called eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	f	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 32 is a protein called eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	g	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 33 is a protein called uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	h	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 34 is a protein called eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	i	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 35 is a protein called eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	j	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 36 is a protein called eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	k	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 37 is a protein called eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 38 is a protein called eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	m	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 39 is a protein called eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	n	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 40 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	o	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 41 is a protein called eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	p	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 42 is a protein called eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	r	124	Total	C	N	O	S	0	0
			994	616	205	167	6		

- Molecule 43 is a protein called uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	s	196	Total	C	N	O	S	0	0
			1507	959	263	276	9		

- Molecule 44 is a protein called uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	t	153	Total	C	N	O	S	0	0
			1160	722	218	217	3		

- Molecule 45 is a protein called Nascent chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	1	15	Total	C	N	O	S	0	0
			125	82	20	22	1		

- Molecule 46 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	2	76	Total	C	N	O	P	0	0
			1616	723	291	527	75		

- Molecule 47 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	3	75	Total	C	N	O	P	0	0
			1593	712	281	526	74		

- Molecule 48 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	5	3543	Total	C	N	O	P	0	0
			75972	33833	13910	24686	3543		

- Molecule 49 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 50 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	8	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 51 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
51	9	1698	36249	16180	6508	11864	1697	0	0

- Molecule 52 is a protein called uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	AA	217	1710	1086	300	316	8	0	0

- Molecule 53 is a protein called eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	BB	213	1729	1098	309	308	14	0	0

- Molecule 54 is a protein called uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	CC	221	1716	1111	295	301	9	0	0

- Molecule 55 is a protein called uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	DD	228	1768	1126	318	316	8	0	0

- Molecule 56 is a protein called eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	EE	262	2076	1324	386	358	8	0	0

- Molecule 57 is a protein called uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
57	FF	185	1471	921	277	266	7	0	0

- Molecule 58 is a protein called eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	GG	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 59 is a protein called eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	HH	185	Total	C	N	O	S	0	0
			1488	952	271	264	1		

- Molecule 60 is a protein called eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	II	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
II	47	ARG	GLY	conflict	UNP G1TJW1

- Molecule 61 is a protein called uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	JJ	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 62 is a protein called eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	KK	96	Total	C	N	O	S	0	0
			810	530	143	131	6		

- Molecule 63 is a protein called uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	LL	143	Total	C	N	O	S	0	0
			1175	749	222	198	6		

- Molecule 64 is a protein called eS12.



Mol	Chain	Residues	Atoms					AltConf	Trace
64	MM	117	Total	C	N	O	S	0	0
			908	570	161	169	8		

- Molecule 65 is a protein called uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	NN	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 66 is a protein called uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	OO	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 67 is a protein called uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	PP	120	Total	C	N	O	S	0	0
			997	635	187	168	7		

- Molecule 68 is a protein called uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	QQ	142	Total	C	N	O	S	0	0
			1128	717	213	195	3		

- Molecule 69 is a protein called eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	RR	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 70 is a protein called uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SS	144	Total	C	N	O	S	0	0
			1190	746	241	202	1		

- Molecule 71 is a protein called eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
71	TT	141	1097	688	211	195	3	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
TT	119	GLY	TRP	conflict	UNP G1TN62

- Molecule 72 is a protein called uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
72	UU	100	795	498	152	141	4	0	0

- Molecule 73 is a protein called eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
73	VV	83	636	393	117	121	5	0	0

- Molecule 74 is a protein called uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
74	WW	129	1034	659	193	176	6	0	0

- Molecule 75 is a protein called uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
75	XX	141	1098	693	219	183	3	0	0

- Molecule 76 is a protein called eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
76	YY	124	1011	640	198	168	5	0	0

- Molecule 77 is a protein called eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	ZZ	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 78 is a protein called eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	aa	101	Total	C	N	O	S	0	0
			814	507	170	132	5		

- Molecule 79 is a protein called eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	bb	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 80 is a protein called eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	cc	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 81 is a protein called uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	dd	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 82 is a protein called eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	ee	55	Total	C	N	O	S	0	0
			443	274	97	71	1		

- Molecule 83 is a protein called eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	ff	68	Total	C	N	O	S	0	0
			555	351	103	94	7		

- Molecule 84 is a protein called RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
84	gg	313	2436	1535	424	465	12	0	0

- Molecule 85 is a RNA chain called mRNA (truncated).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
85	hh	8	169	76	29	56	8	0	0

- Molecule 86 is a protein called Pelota.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
86	ii	372	2947	1844	528	559	16	0	0

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
ii	221	MET	LEU	conflict	UNP Q9BRX2
ii	386	GLY	-	expression tag	UNP Q9BRX2
ii	387	SER	-	expression tag	UNP Q9BRX2
ii	388	GLU	-	expression tag	UNP Q9BRX2
ii	389	ASN	-	expression tag	UNP Q9BRX2
ii	390	LEU	-	expression tag	UNP Q9BRX2
ii	391	TYR	-	expression tag	UNP Q9BRX2
ii	392	PHE	-	expression tag	UNP Q9BRX2
ii	393	GLN	-	expression tag	UNP Q9BRX2
ii	394	GLY	-	expression tag	UNP Q9BRX2
ii	395	ALA	-	expression tag	UNP Q9BRX2
ii	396	HIS	-	expression tag	UNP Q9BRX2
ii	397	HIS	-	expression tag	UNP Q9BRX2
ii	398	HIS	-	expression tag	UNP Q9BRX2
ii	399	HIS	-	expression tag	UNP Q9BRX2
ii	400	HIS	-	expression tag	UNP Q9BRX2
ii	401	HIS	-	expression tag	UNP Q9BRX2
ii	402	SER	-	expression tag	UNP Q9BRX2
ii	403	THR	-	expression tag	UNP Q9BRX2

- Molecule 87 is a protein called Hbs1l.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
87	jj	425	3292	2100	565	609	18	0	0

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
jj	-25	MET	-	initiating methionine	UNP Q9Y450
jj	-24	ASP	-	expression tag	UNP Q9Y450
jj	-23	TYR	-	expression tag	UNP Q9Y450
jj	-22	LYS	-	expression tag	UNP Q9Y450
jj	-21	ASP	-	expression tag	UNP Q9Y450
jj	-20	HIS	-	expression tag	UNP Q9Y450
jj	-19	ASP	-	expression tag	UNP Q9Y450
jj	-18	GLY	-	expression tag	UNP Q9Y450
jj	-17	ASP	-	expression tag	UNP Q9Y450
jj	-16	TYR	-	expression tag	UNP Q9Y450
jj	-15	LYS	-	expression tag	UNP Q9Y450
jj	-14	ASP	-	expression tag	UNP Q9Y450
jj	-13	HIS	-	expression tag	UNP Q9Y450
jj	-12	ASP	-	expression tag	UNP Q9Y450
jj	-11	ILE	-	expression tag	UNP Q9Y450
jj	-10	ASP	-	expression tag	UNP Q9Y450
jj	-9	TYR	-	expression tag	UNP Q9Y450
jj	-8	LYS	-	expression tag	UNP Q9Y450
jj	-7	ASP	-	expression tag	UNP Q9Y450
jj	-6	ASP	-	expression tag	UNP Q9Y450
jj	-5	ASP	-	expression tag	UNP Q9Y450
jj	-4	ASP	-	expression tag	UNP Q9Y450
jj	-3	LYS	-	expression tag	UNP Q9Y450
jj	-2	ALA	-	expression tag	UNP Q9Y450
jj	-1	GLY	-	expression tag	UNP Q9Y450
jj	0	SER	-	expression tag	UNP Q9Y450

- Molecule 88 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
88	B	1	Total Mg 1 1	0
88	I	1	Total Mg 1 1	0
88	P	2	Total Mg 2 2	0
88	Q	1	Total Mg 1 1	0
88	V	1	Total Mg 1 1	0
88	a	1	Total Mg 1 1	0

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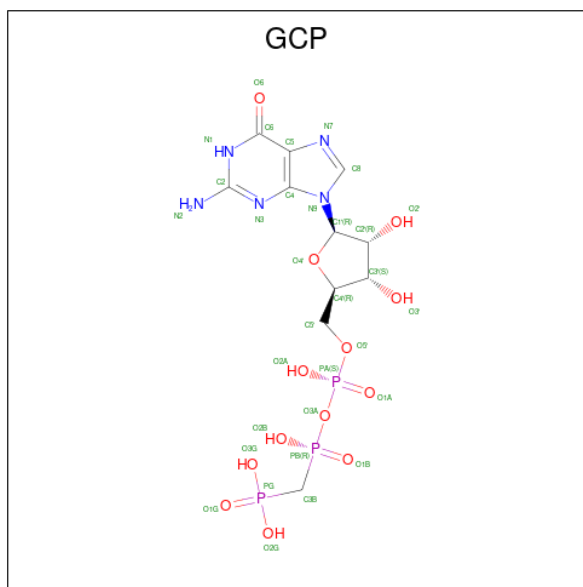
*Continued from previous page...*

Mol	Chain	Residues	Atoms		AltConf
88	e	1	Total 1	Mg 1	0
88	g	1	Total 1	Mg 1	0
88	j	1	Total 1	Mg 1	0
88	5	188	Total 188	Mg 188	0
88	7	5	Total 5	Mg 5	0
88	8	6	Total 6	Mg 6	0
88	9	71	Total 71	Mg 71	0
88	jj	1	Total 1	Mg 1	0

- Molecule 89 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
89	g	1	Total 1	Zn 1	0
89	j	1	Total 1	Zn 1	0
89	m	1	Total 1	Zn 1	0
89	o	1	Total 1	Zn 1	0
89	p	1	Total 1	Zn 1	0
89	aa	1	Total 1	Zn 1	0
89	dd	1	Total 1	Zn 1	0
89	ff	1	Total 1	Zn 1	0

- Molecule 90 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (three-letter code: GCP) (formula: C<sub>11</sub>H<sub>18</sub>N<sub>5</sub>O<sub>13</sub>P<sub>3</sub>).




Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
90	9	1	32	11	5	13	3	0
90	jj	1	32	11	5	13	3	0

### 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.

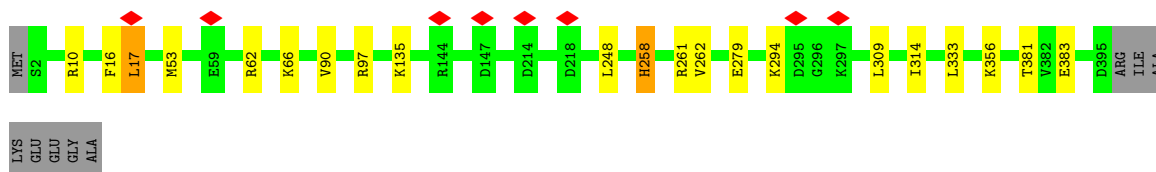
- Molecule 1: uL2

Chain A:  90% 7%




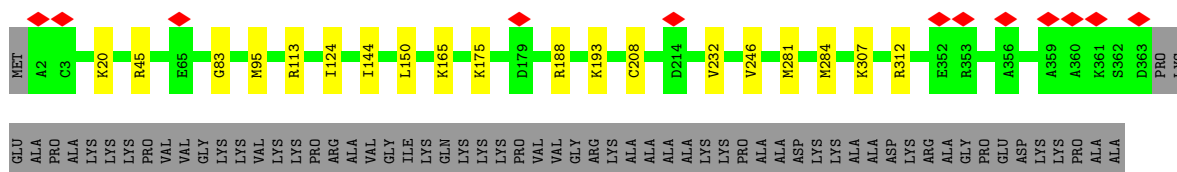
- Molecule 2: uL3

Chain B:  93% 5%



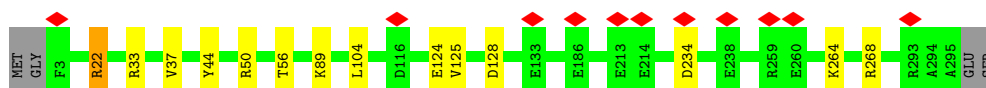
- Molecule 3: uL4

Chain C:  81% 15%



- Molecule 4: uL18

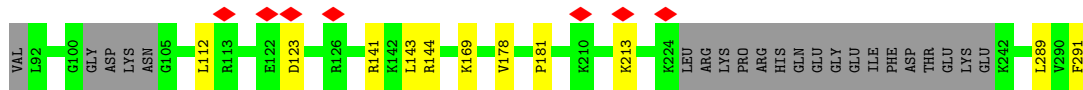
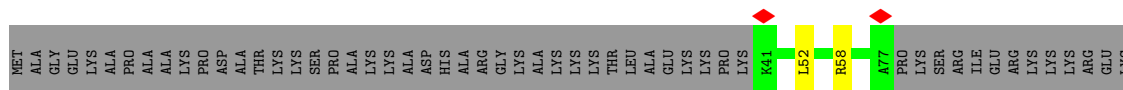
Chain D:  94%



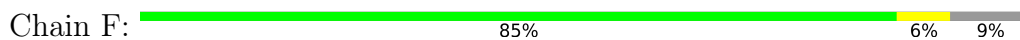
- Molecule 5: eL6

Chain E:  70% 26%

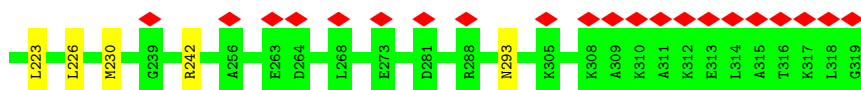
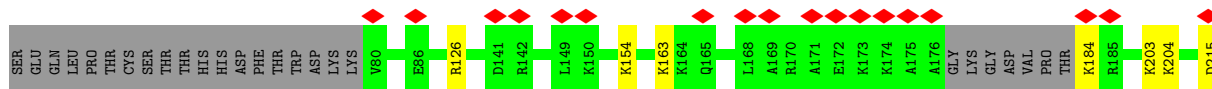
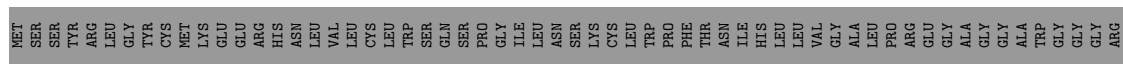




• Molecule 6: uL30



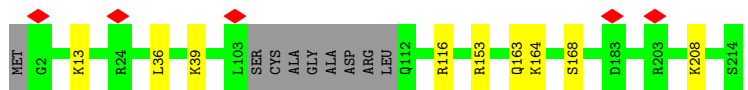
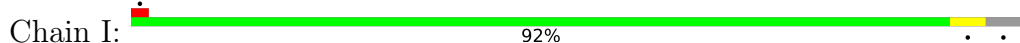
• Molecule 7: eL8



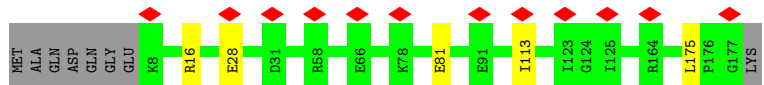
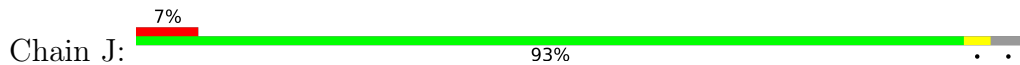
• Molecule 8: uL6



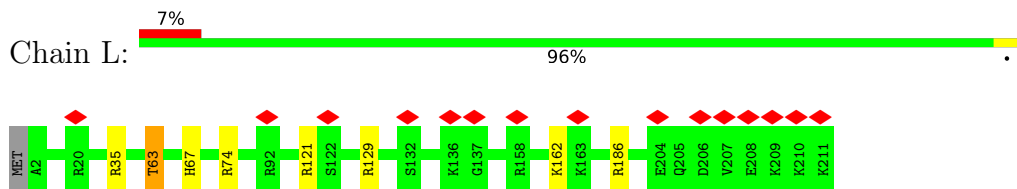
• Molecule 9: uL16



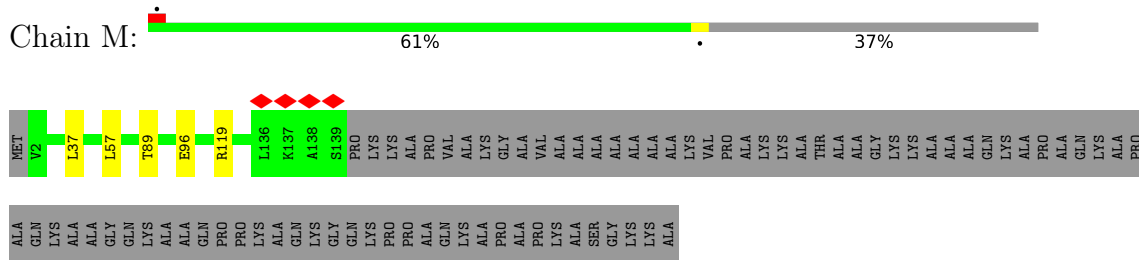
• Molecule 10: uL5



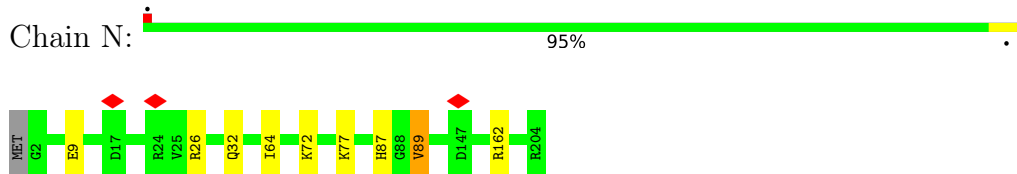
• Molecule 11: eL13



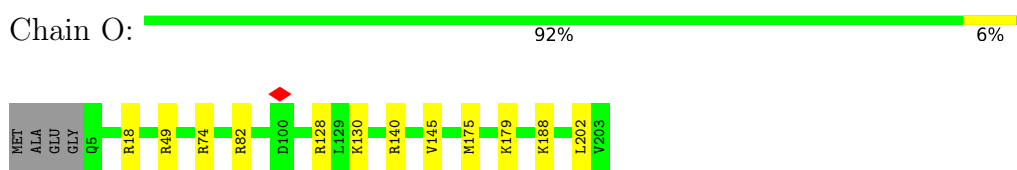
• Molecule 12: eL14



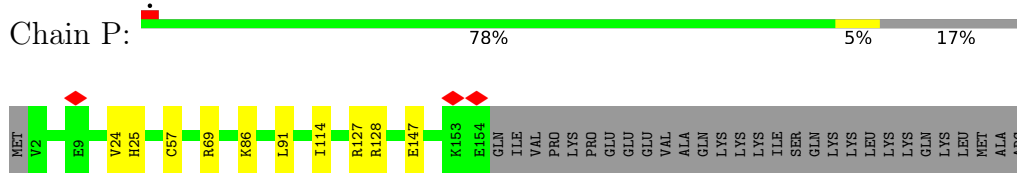
• Molecule 13: eL15



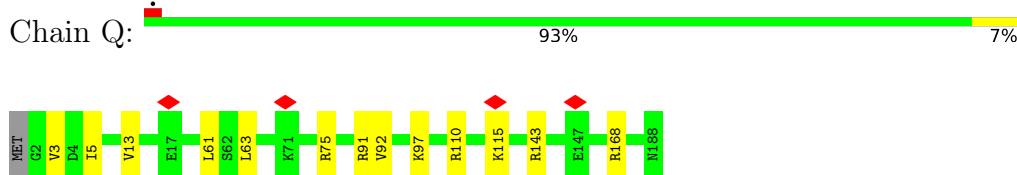
• Molecule 14: uL13



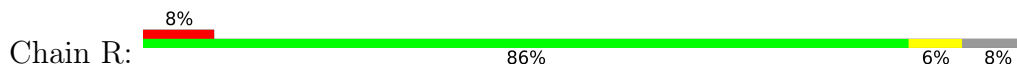
• Molecule 15: uL22

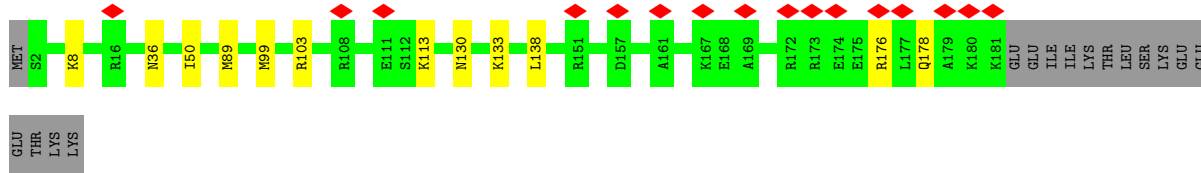


• Molecule 16: eL18

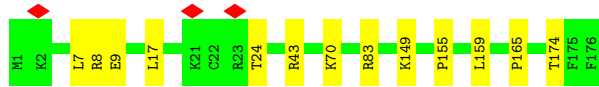
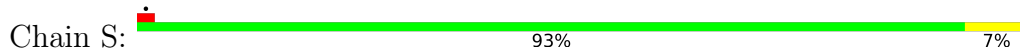


• Molecule 17: eL19

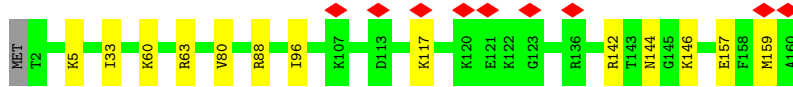
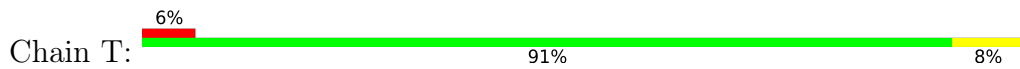




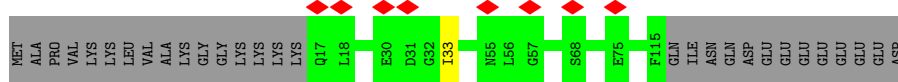
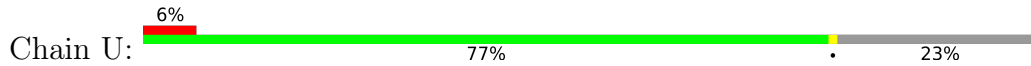
● Molecule 18: eL20



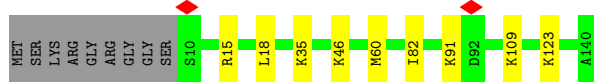
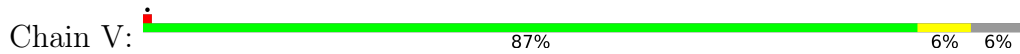
● Molecule 19: eL21



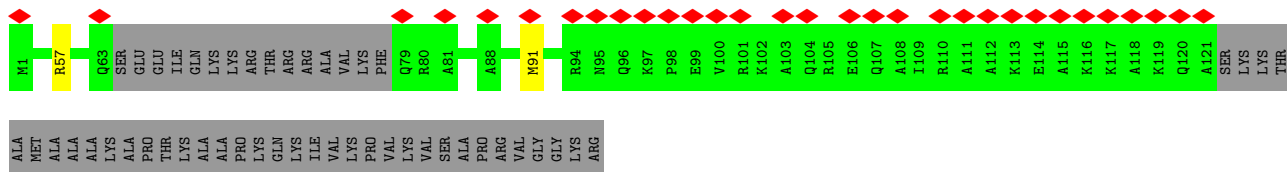
● Molecule 20: eL22



● Molecule 21: uL14

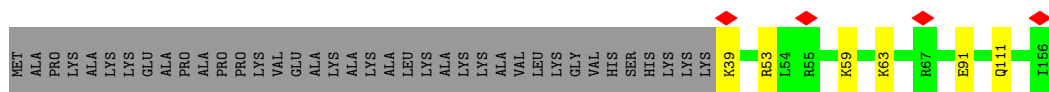


● Molecule 22: eL24

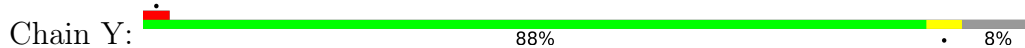


● Molecule 23: uL23

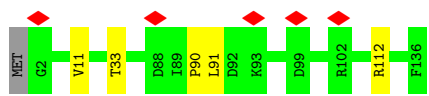




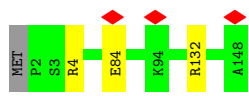
• Molecule 24: uL24



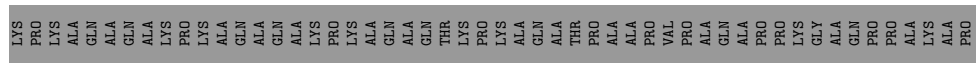
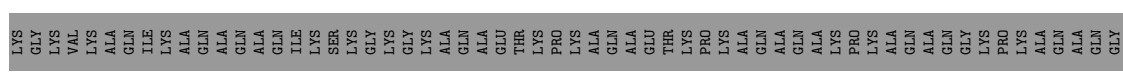
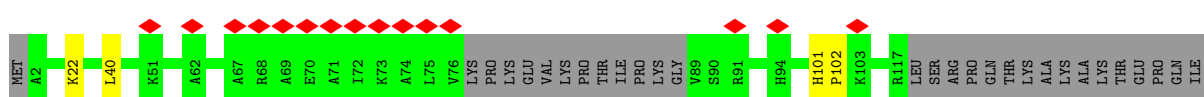
• Molecule 25: eL27



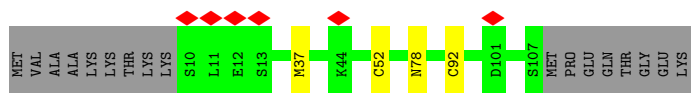
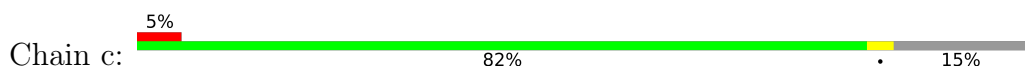
• Molecule 26: uL15



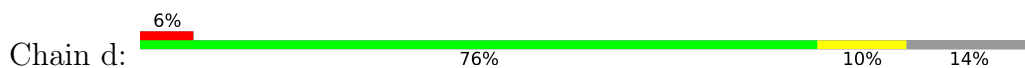
• Molecule 27: eL29



• Molecule 28: eL30

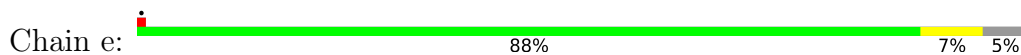


• Molecule 29: eL31

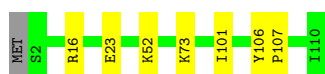




● Molecule 30: eL32



● Molecule 31: eL33



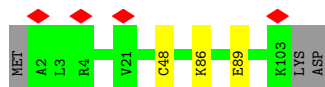
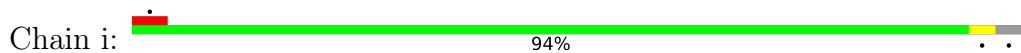
● Molecule 32: eL34



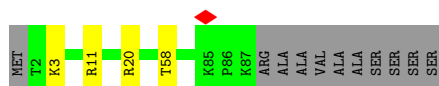
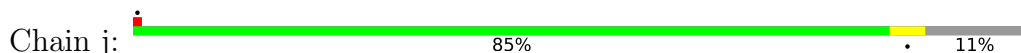
● Molecule 33: uL29



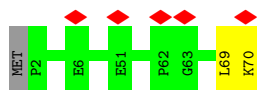
● Molecule 34: eL36



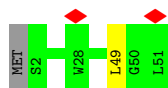
● Molecule 35: eL37



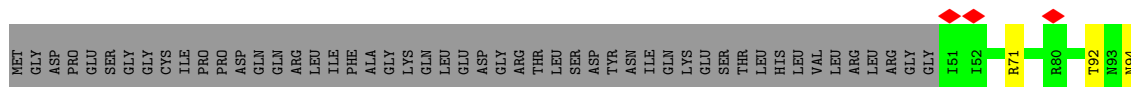
● Molecule 36: eL38



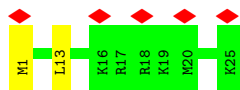
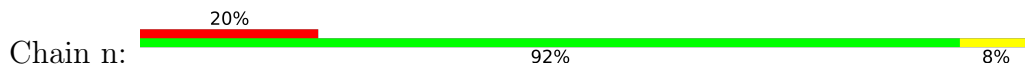
• Molecule 37: eL39



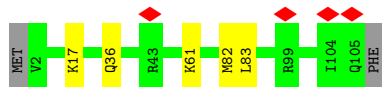
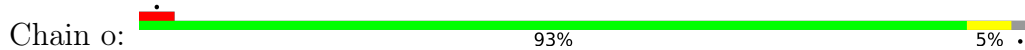
• Molecule 38: eL40



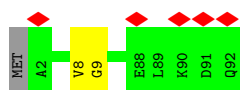
• Molecule 39: eL41



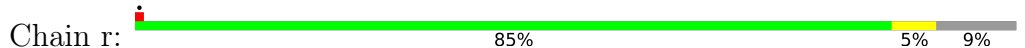
• Molecule 40: eL42

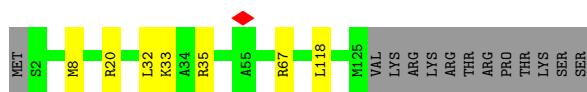


• Molecule 41: eL43

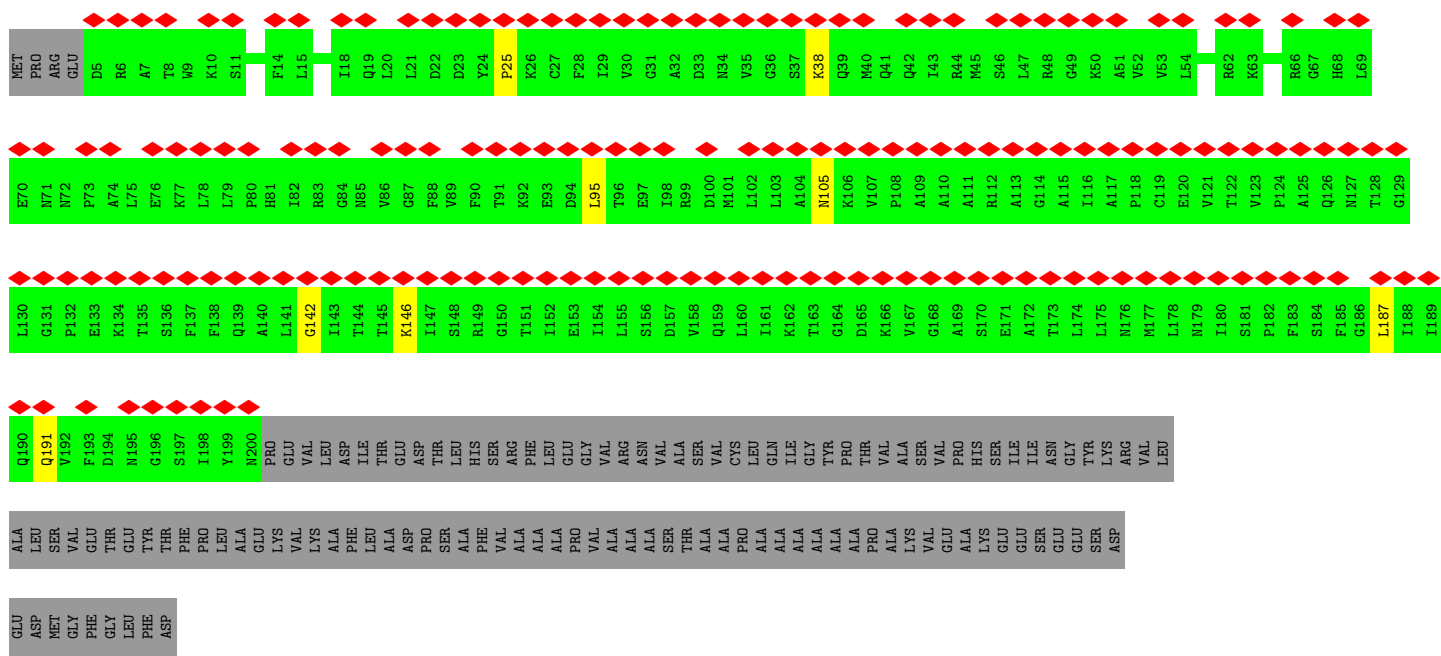


• Molecule 42: eL28

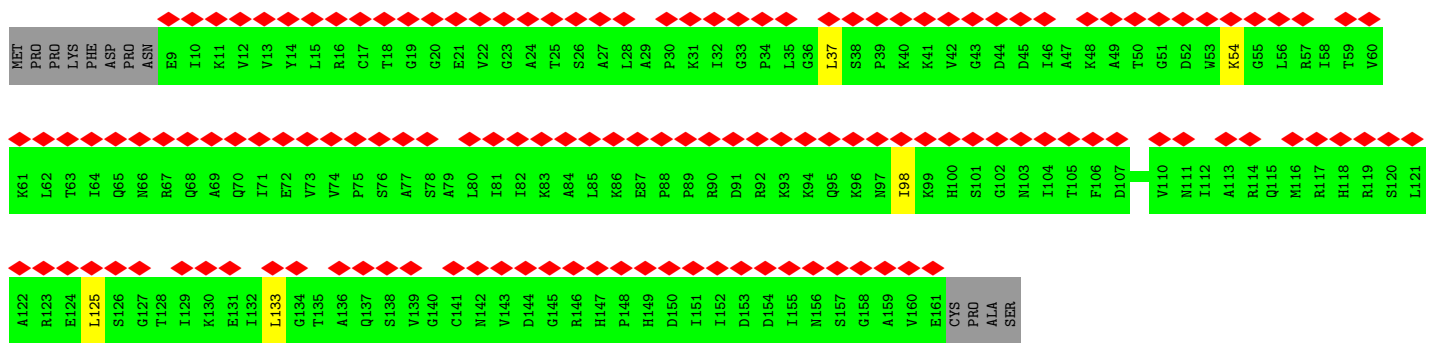
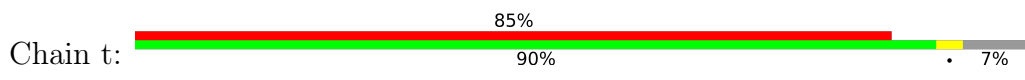




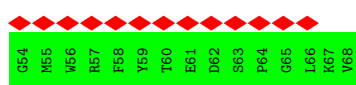
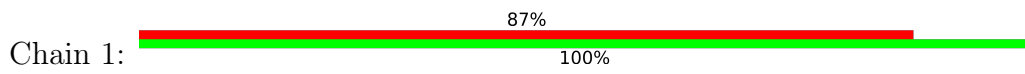
• Molecule 43: uL10



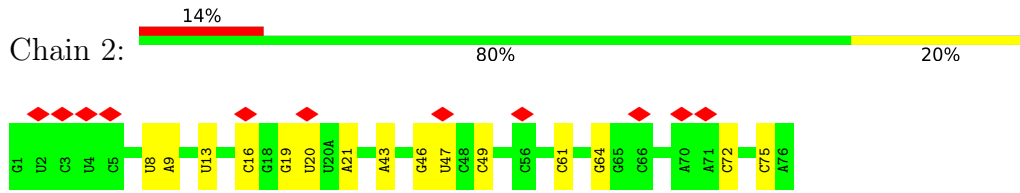
• Molecule 44: uL11



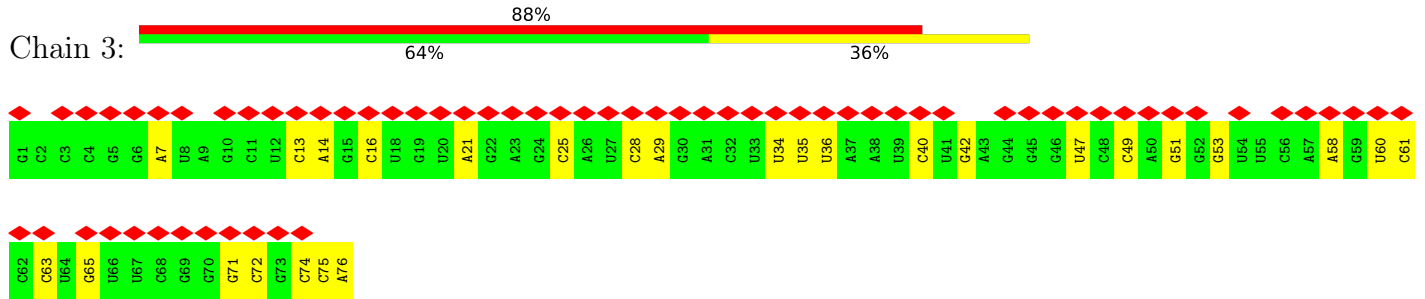
• Molecule 45: Nascent chain



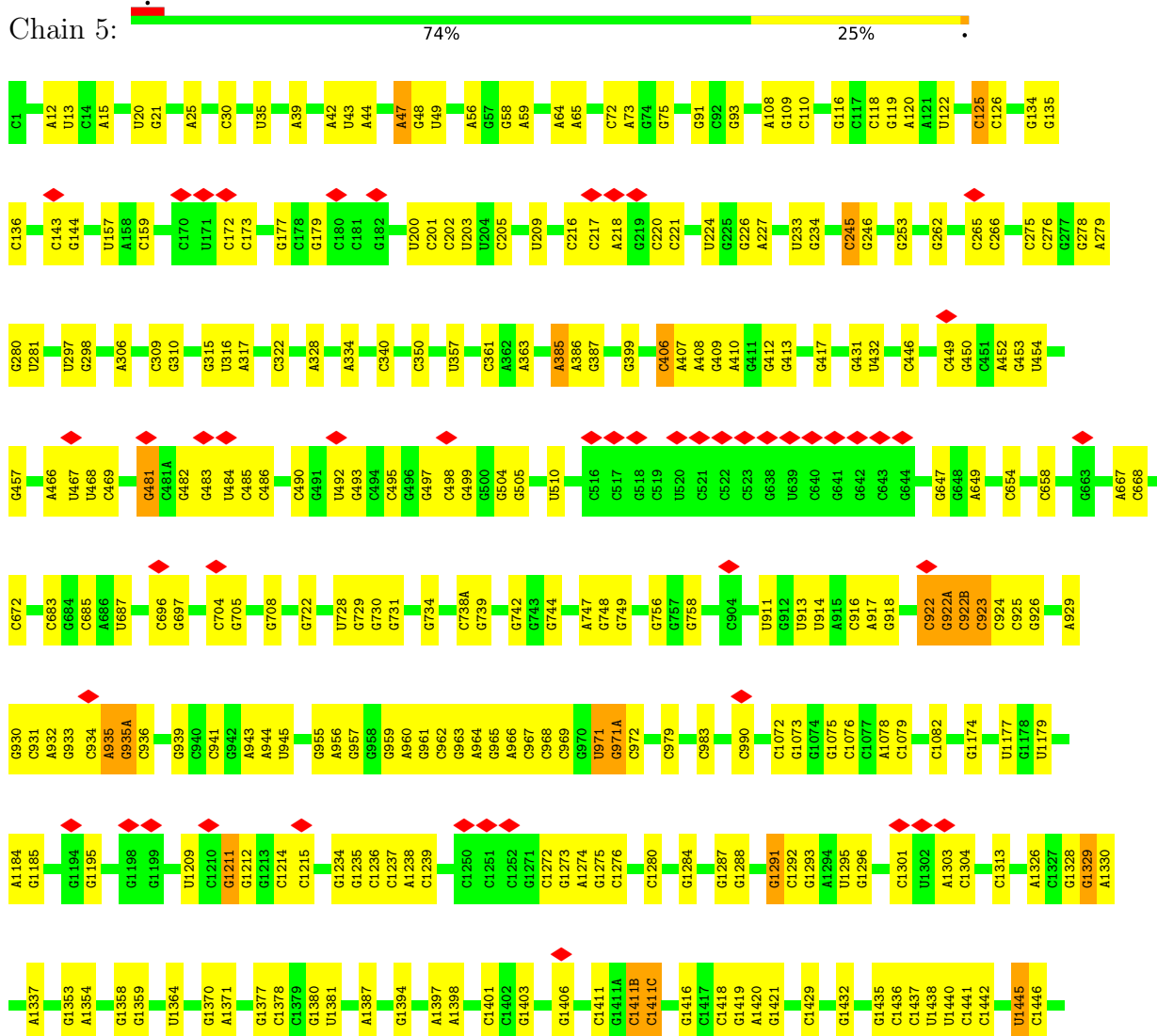
• Molecule 46: P-site tRNA



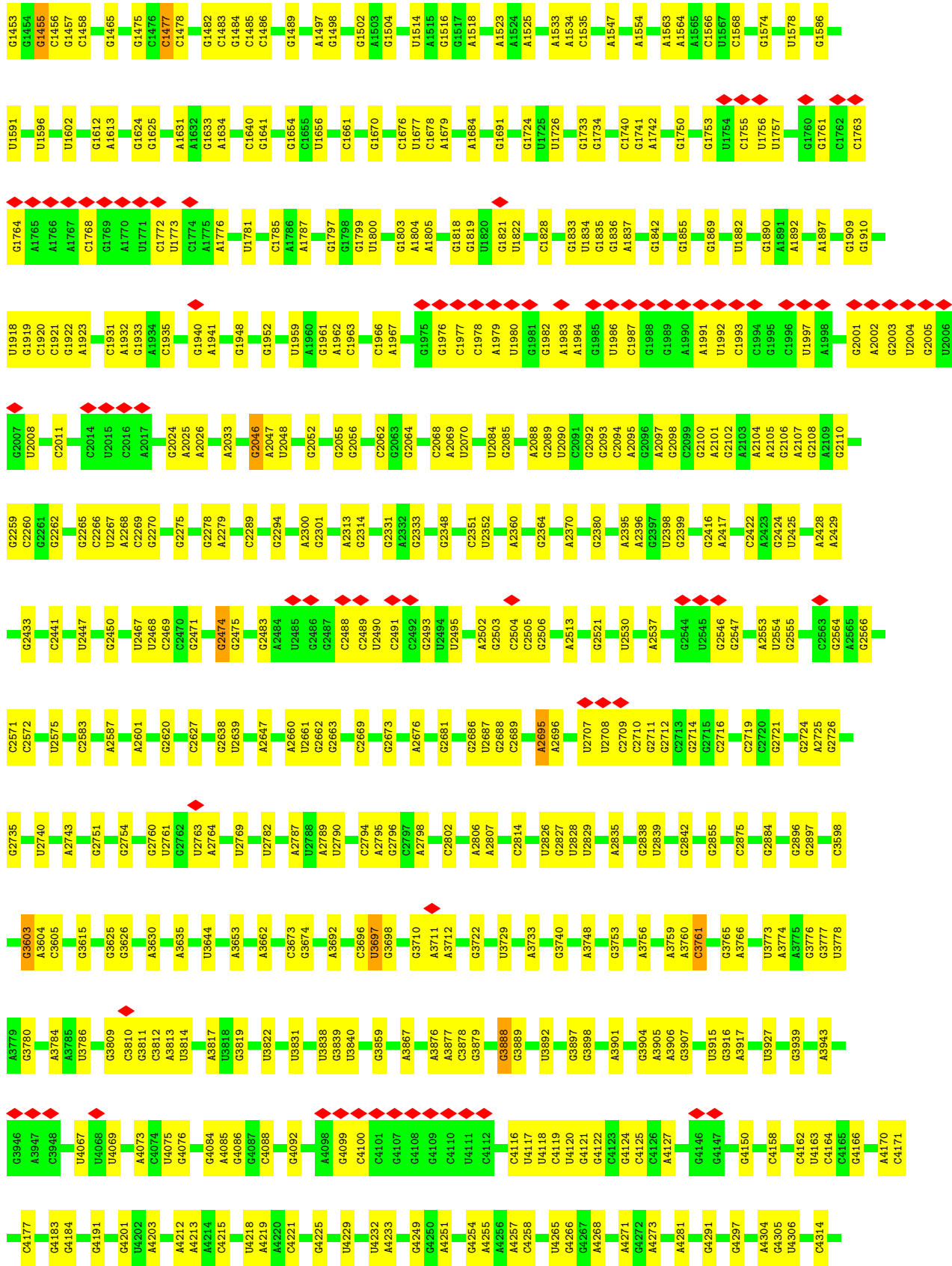
• Molecule 47: E-site tRNA

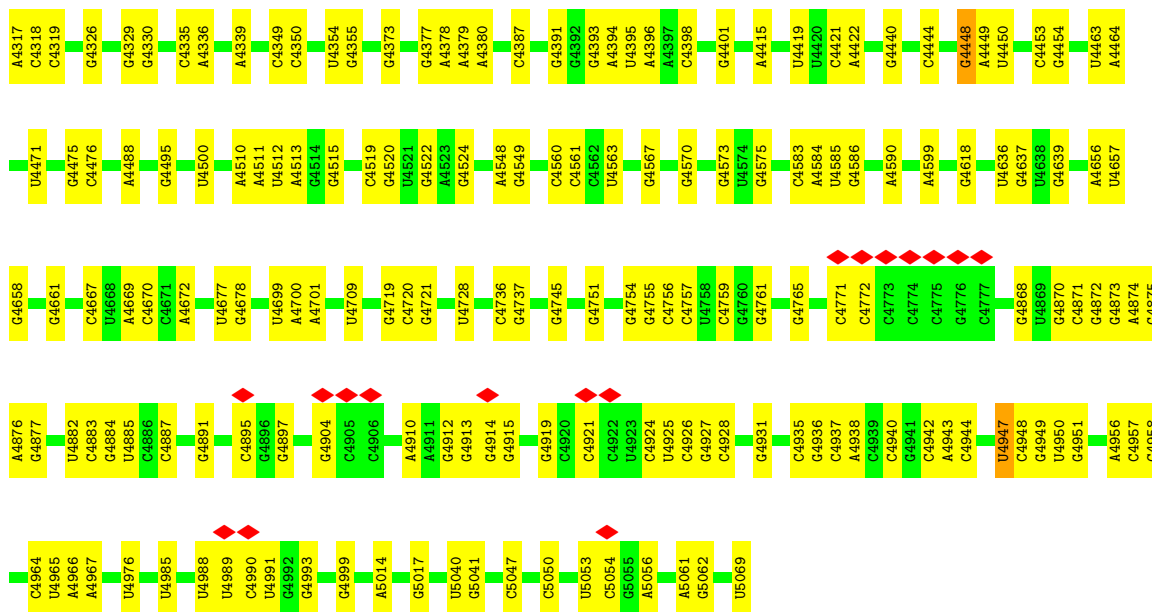


• Molecule 48: 28S ribosomal RNA

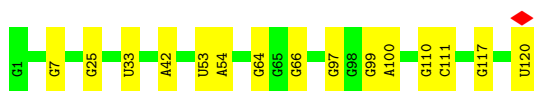
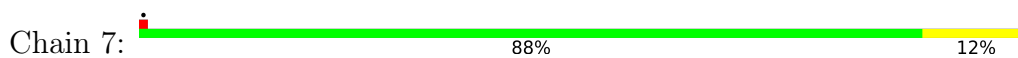




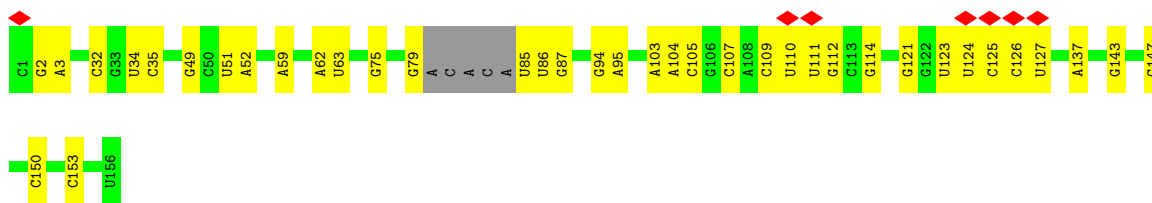




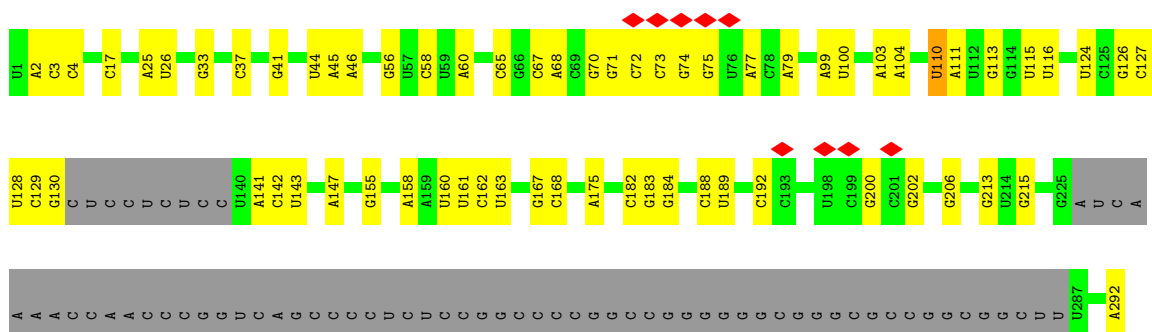
• Molecule 49: 5S ribosomal RNA



• Molecule 50: 5.8S ribosomal RNA

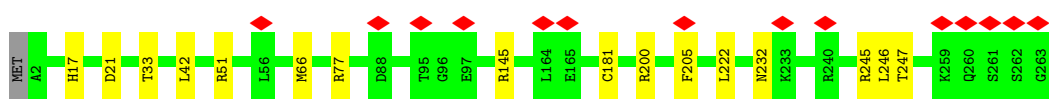


• Molecule 51: 18S ribosomal RNA

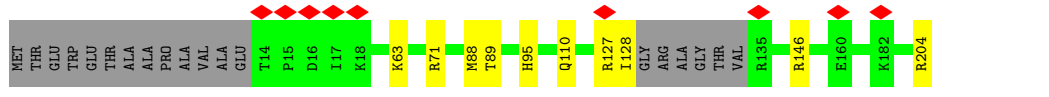
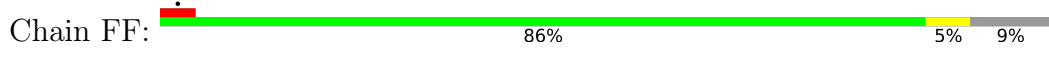




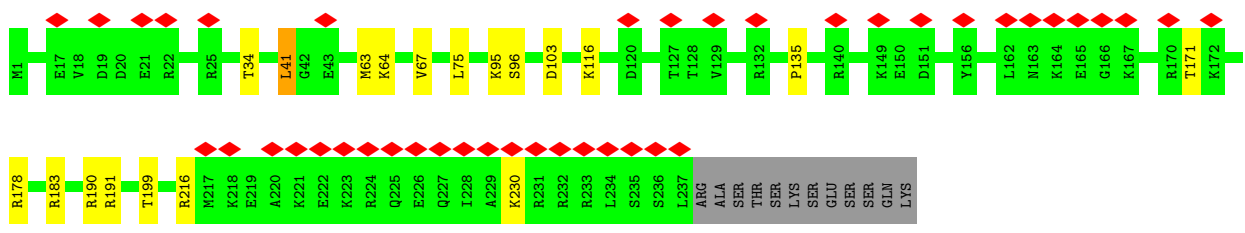
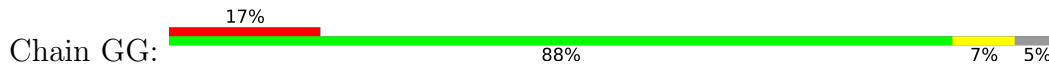




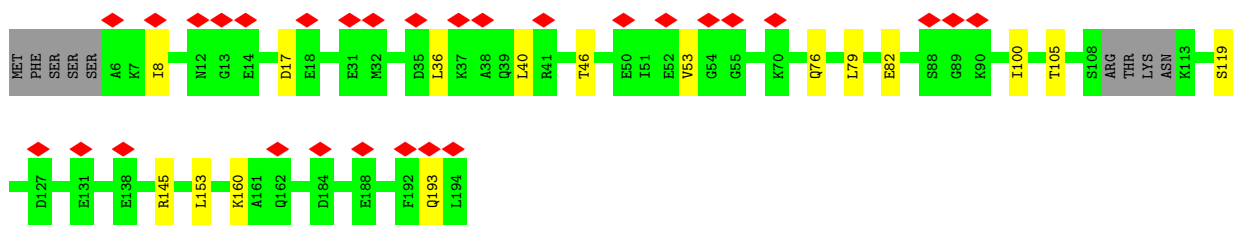
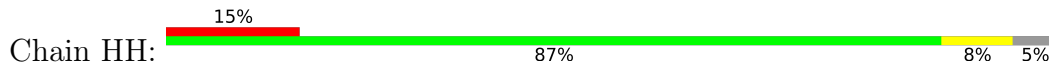
• Molecule 57: uS7



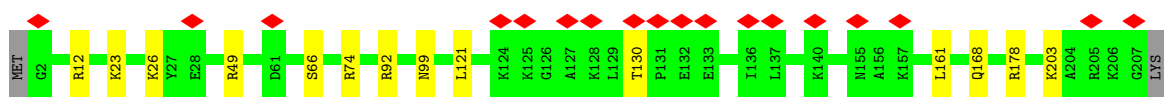
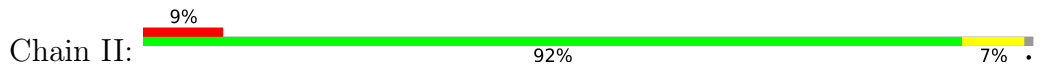
• Molecule 58: eS6



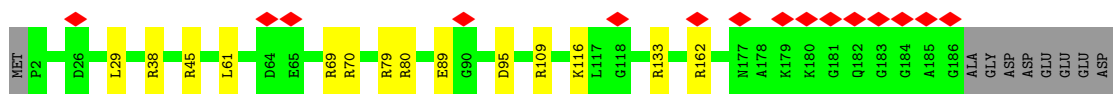
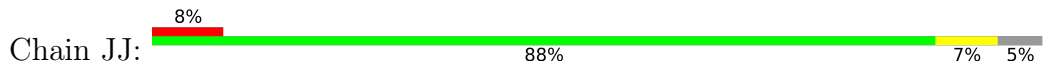
• Molecule 59: eS7



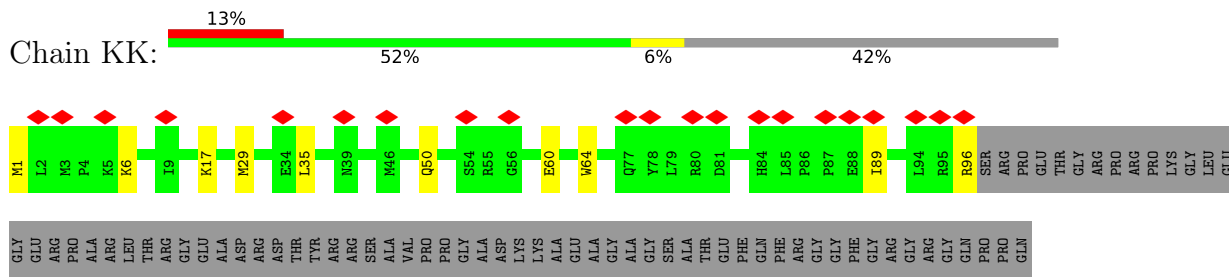
• Molecule 60: eS8



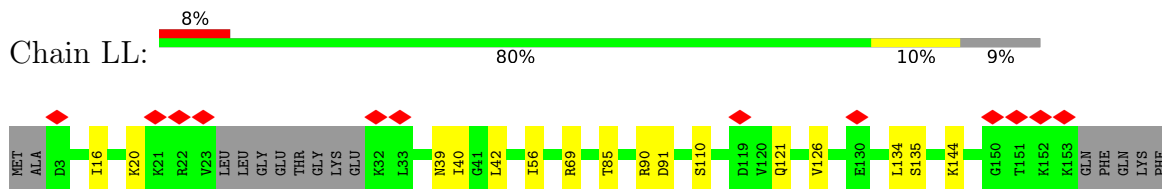
• Molecule 61: uS4



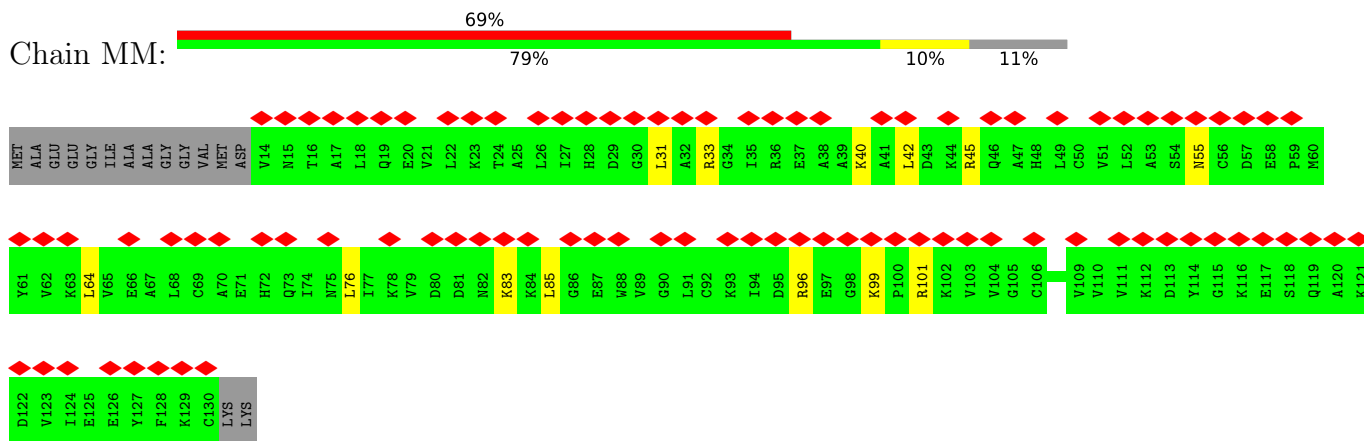
• Molecule 62: eS10



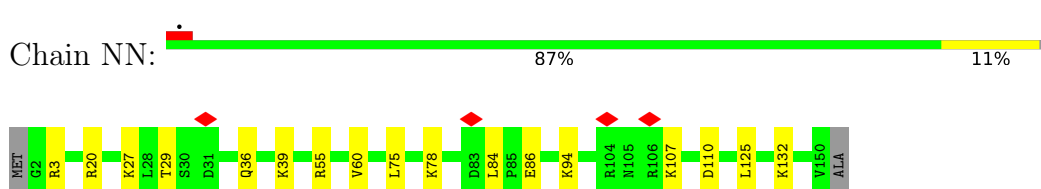
• Molecule 63: uS17



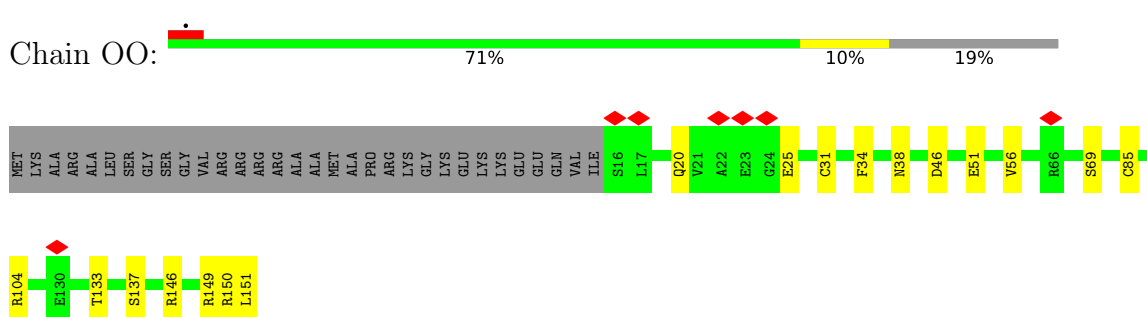
• Molecule 64: eS12



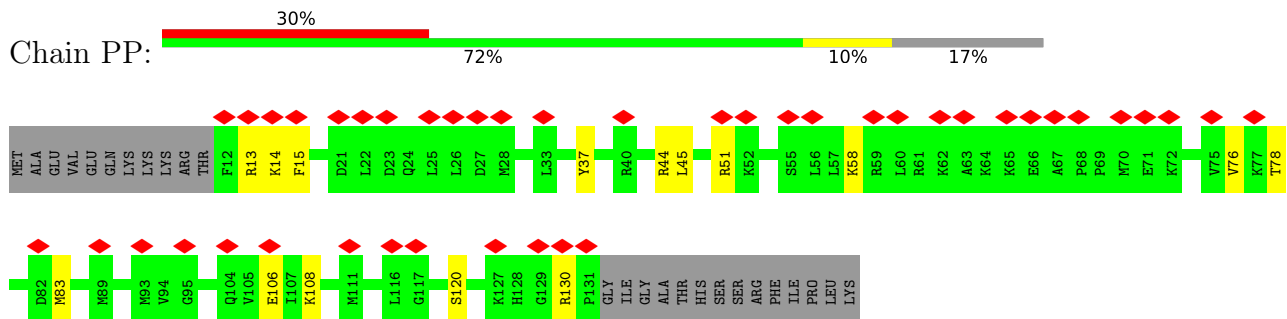
• Molecule 65: uS15



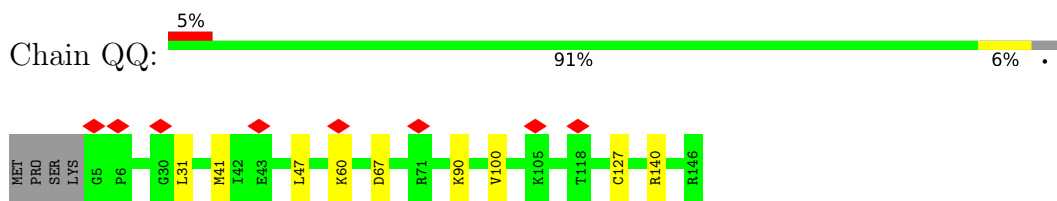
• Molecule 66: uS11



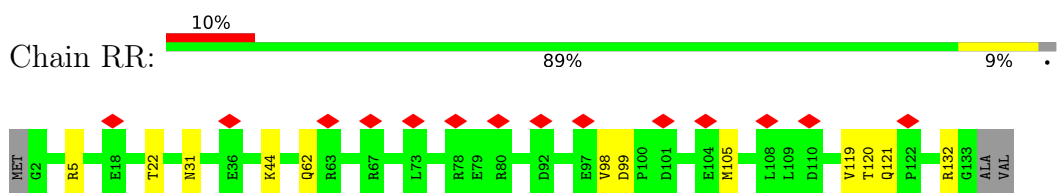
• Molecule 67: uS19



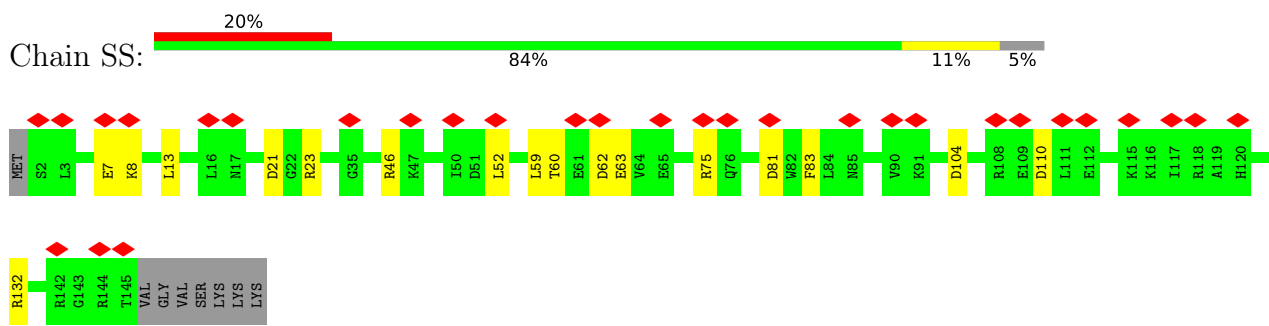
• Molecule 68: uS9



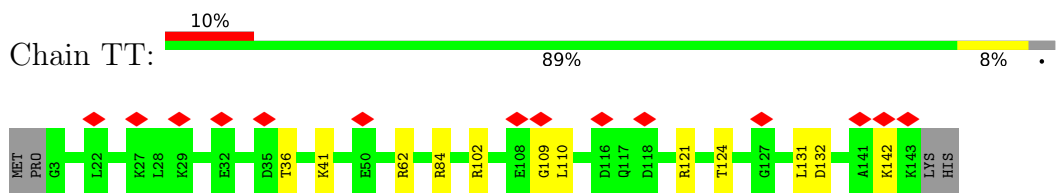
• Molecule 69: eS17



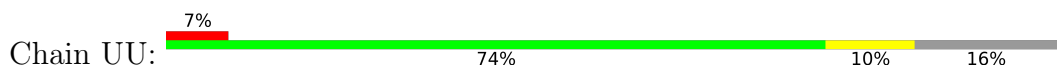
• Molecule 70: uS13



• Molecule 71: eS19

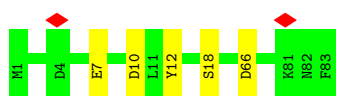


• Molecule 72: uS10

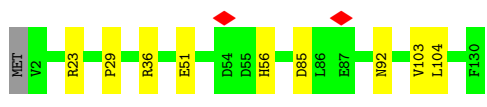




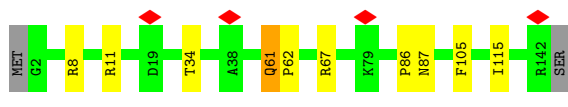
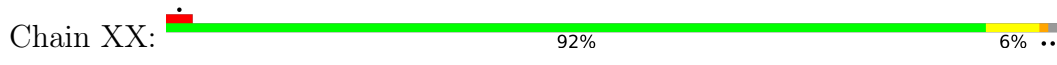
• Molecule 73: eS21



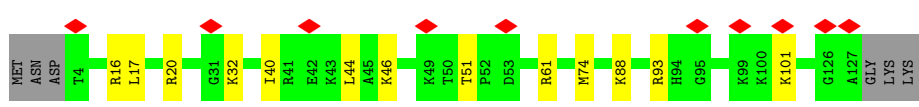
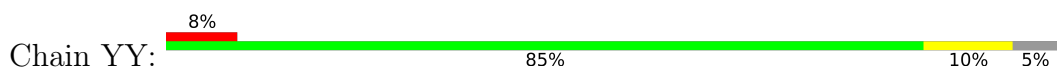
• Molecule 74: uS8



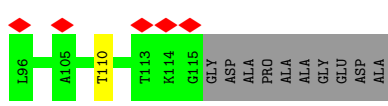
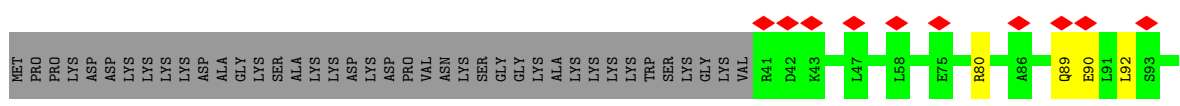
• Molecule 75: uS12



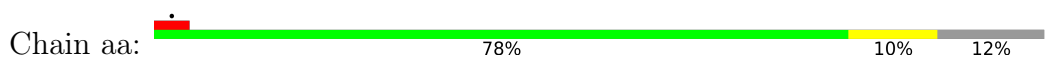
• Molecule 76: eS24



• Molecule 77: eS25



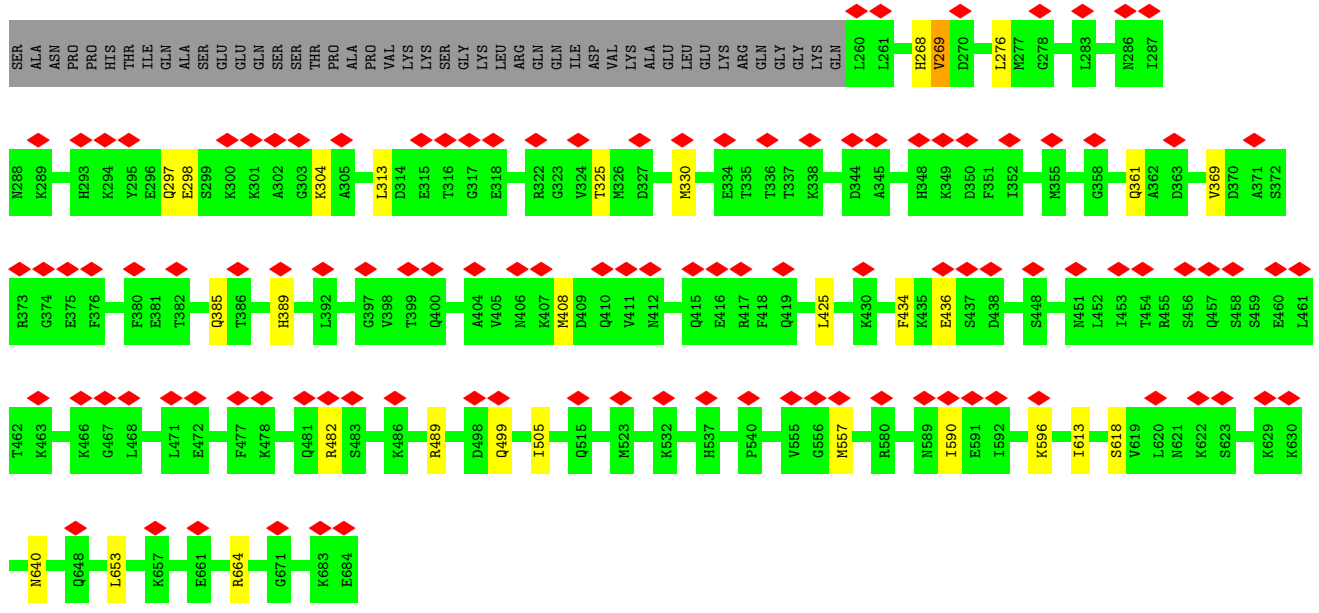
• Molecule 78: eS26











## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	42011	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 ( $e^-/\text{\AA}^2$ )	30	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	104478	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.703	Depositor
Minimum map value	-0.451	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.022	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	562.8, 562.8, 562.8	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3399999, 1.3399999, 1.3399999	Depositor

## 5 Model quality i

### 5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, GCP, MG

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	A	0.36	0/1936	0.71	0/2596
2	B	0.34	0/3240	0.64	0/4339
3	C	0.35	0/2937	0.67	0/3946
4	D	0.34	0/2437	0.61	1/3264 (0.0%)
5	E	0.34	0/1762	0.62	0/2362
6	F	0.36	0/1911	0.67	0/2549
7	G	0.34	0/1910	0.61	0/2569
8	H	0.33	0/1535	0.62	0/2063
9	I	0.35	0/1702	0.63	0/2272
10	J	0.33	0/1385	0.60	0/1852
11	L	0.35	0/1733	0.66	0/2316
12	M	0.37	0/1158	0.68	0/1547
13	N	0.36	0/1746	0.69	0/2338
14	O	0.36	0/1662	0.67	0/2222
15	P	0.36	0/1268	0.65	0/1700
16	Q	0.36	0/1539	0.73	0/2054
17	R	0.35	0/1524	0.67	0/2013
18	S	0.35	0/1501	0.65	0/2012
19	T	0.37	0/1326	0.63	0/1770
20	U	0.36	0/823	0.56	0/1104
21	V	0.37	0/993	0.67	0/1332
22	W	0.35	0/873	0.57	0/1158
23	X	0.33	0/984	0.60	0/1323
24	Y	0.35	0/1132	0.64	0/1504
25	Z	0.35	0/1130	0.61	0/1507
26	a	0.34	0/1191	0.63	0/1590
27	b	0.33	0/861	0.58	0/1138
28	c	0.33	0/771	0.54	0/1034
29	d	0.35	0/903	0.67	0/1216
30	e	0.38	0/1071	0.68	0/1429
31	f	0.36	0/895	0.70	0/1198
32	g	0.34	0/916	0.70	0/1220

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	h	0.32	0/1021	0.59	0/1348
34	i	0.34	0/841	0.59	0/1112
35	j	0.35	0/720	0.70	0/952
36	k	0.32	0/575	0.54	0/761
37	l	0.34	0/459	0.62	0/608
38	m	0.35	0/435	0.63	0/575
39	n	0.35	0/240	0.68	0/305
40	o	0.33	0/864	0.61	0/1140
41	p	0.33	0/718	0.60	0/953
42	r	0.36	0/1010	0.66	0/1354
43	s	0.36	0/1530	0.50	0/2064
44	t	0.36	0/1174	0.53	0/1582
45	1	0.44	0/129	0.61	0/173
46	2	0.21	0/1805	0.66	0/2809
47	3	0.21	0/1777	0.66	0/2763
48	5	0.74	31/84961 (0.0%)	0.78	72/132460 (0.1%)
49	7	0.26	0/2858	0.65	0/4455
50	8	0.26	0/3581	0.68	0/5577
51	9	0.27	0/40523	0.71	14/63130 (0.0%)
52	AA	0.36	0/1747	0.61	0/2374
53	BB	0.34	0/1756	0.59	0/2350
54	CC	0.36	0/1753	0.66	0/2369
55	DD	0.36	0/1796	0.63	0/2417
56	EE	0.36	0/2118	0.64	0/2849
57	FF	0.34	0/1492	0.60	0/2005
58	GG	0.36	0/1946	0.68	1/2590 (0.0%)
59	HH	0.36	0/1510	0.58	0/2022
60	II	0.36	0/1715	0.67	0/2287
61	JJ	0.35	0/1550	0.68	0/2069
62	KK	0.39	0/834	0.61	0/1125
63	LL	0.35	0/1195	0.68	0/1597
64	MM	0.37	0/918	0.59	0/1233
65	NN	0.36	0/1226	0.64	0/1649
66	OO	0.36	0/1029	0.73	0/1380
67	PP	0.38	0/1017	0.65	0/1358
68	QQ	0.35	0/1146	0.63	0/1534
69	RR	0.36	0/1082	0.61	0/1452
70	SS	0.37	0/1208	0.67	0/1618
71	TT	0.38	0/1115	0.65	0/1493
72	UU	0.35	0/805	0.65	0/1081
73	VV	0.38	0/643	0.66	0/860
74	WW	0.36	0/1051	0.71	0/1406
75	XX	0.33	0/1116	0.65	0/1490

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
76	YY	0.37	0/1028	0.64	0/1366
77	ZZ	0.36	0/604	0.60	0/810
78	aa	0.38	0/828	0.71	0/1109
79	bb	0.35	0/665	0.63	0/891
80	cc	0.38	0/490	0.73	1/656 (0.2%)
81	dd	0.39	0/470	0.65	0/623
82	ee	0.36	0/447	0.66	0/587
83	ff	0.38	0/567	0.55	0/753
84	gg	0.33	0/2493	0.55	0/3394
85	hh	0.29	0/188	0.82	0/290
86	ii	0.33	0/2996	0.56	0/4050
87	jj	0.34	0/3352	0.55	0/4523
All	All	0.52	31/237872 (0.0%)	0.71	89/348318 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	2
6	F	0	1
48	5	0	3
75	XX	0	1
86	ii	0	2
All	All	0	9

All (31) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
48	5	935	A	C6-N6	192.84	2.88	1.33
48	5	935	A	C5-C6	-20.65	1.22	1.41
48	5	922(A)	G	O3'-P	17.07	1.81	1.61
48	5	481	G	C2-N3	-13.50	1.22	1.32
48	5	971	U	C2-O2	-13.31	1.10	1.22
48	5	922	C	O3'-P	13.02	1.76	1.61
48	5	1411(C)	C	O5'-C5'	11.09	1.62	1.44
48	5	1411	C	P-O5'	10.73	1.70	1.59
48	5	935	A	C5-C4	-10.67	1.31	1.38
48	5	935	A	C6-N1	-10.62	1.28	1.35
48	5	935	A	N1-C2	-9.43	1.25	1.34
48	5	935	A	C2-N3	9.23	1.41	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
48	5	935	A	N3-C4	9.04	1.40	1.34
48	5	1411	C	P-OP1	-8.94	1.33	1.49
48	5	481	G	N1-C2	-8.66	1.30	1.37
48	5	971	U	N1-C2	-8.63	1.30	1.38
48	5	481	G	C5-C6	8.39	1.50	1.42
48	5	922(B)	C	O3'-P	7.49	1.70	1.61
48	5	1411	C	C5'-C4'	6.95	1.59	1.51
48	5	1411(C)	C	P-O5'	6.66	1.66	1.59
48	5	481	G	N9-C8	-6.64	1.33	1.37
48	5	922(A)	G	C3'-O3'	6.48	1.51	1.42
48	5	922	C	C3'-O3'	6.22	1.50	1.42
48	5	1411(C)	C	C5'-C4'	6.09	1.58	1.51
48	5	935(A)	G	P-O5'	5.99	1.65	1.59
48	5	922(B)	C	O5'-C5'	5.75	1.53	1.44
48	5	971	U	C2-N3	-5.72	1.33	1.37
48	5	1411(B)	C	O3'-P	5.59	1.67	1.61
48	5	1411	C	C4'-C3'	5.52	1.59	1.53
48	5	1406	G	P-O5'	5.47	1.65	1.59
48	5	922(B)	C	C5'-C4'	5.21	1.57	1.51

All (89) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	5	481	G	C8-N9-C1'	-61.05	47.63	127.00
48	5	935	A	C6-N1-C2	-39.97	94.62	118.60
48	5	935	A	C5-C6-N6	-39.04	92.47	123.70
48	5	481	G	N1-C2-N2	-38.45	81.59	116.20
48	5	481	G	N3-C2-N2	-37.53	93.63	119.90
48	5	935	A	C4-C5-C6	-36.79	98.61	117.00
48	5	481	G	C4-N9-C1'	-36.47	79.09	126.50
48	5	481	G	C2-N3-C4	-29.02	97.39	111.90
48	5	481	G	C6-N1-C2	-25.25	109.95	125.10
48	5	971	U	N3-C2-O2	-22.99	106.11	122.20
48	5	971	U	N1-C2-O2	-21.48	107.77	122.80
48	5	935	A	N1-C6-N6	-21.18	105.89	118.60
48	5	935	A	N3-C4-C5	-18.98	113.52	126.80
48	5	935	A	N1-C2-N3	-16.36	121.12	129.30
48	5	922	C	C2'-C3'-O3'	13.28	138.72	109.50
48	5	971	U	C2-N3-C4	-11.55	120.07	127.00
48	5	971	U	C6-N1-C2	-10.89	114.47	121.00
48	5	1411(C)	C	P-O5'-C5'	10.66	137.95	120.90
48	5	481	G	C5-C6-N1	-10.50	106.25	111.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	5	935	A	O5'-P-OP2	-10.33	96.40	105.70
48	5	935	A	C5-C6-N1	-10.03	112.69	117.70
51	9	1821	U	N1-C1'-C2'	-9.95	101.05	112.00
48	5	922	C	C4'-C3'-C2'	-9.39	93.21	102.60
48	5	922(B)	C	O4'-C1'-N1	9.27	115.62	108.20
48	5	922	C	C5'-C4'-O4'	9.13	120.06	109.10
48	5	481	G	N3-C4-C5	-8.85	124.17	128.60
48	5	922	C	N1-C1'-C2'	-8.53	102.62	112.00
51	9	1835	A	C2'-C3'-O3'	8.38	127.93	109.50
48	5	935	A	C1'-O4'-C4'	-8.17	103.37	109.90
48	5	481	G	N9-C1'-C2'	8.16	124.60	114.00
48	5	3888	G	C2'-C3'-O3'	8.09	127.30	109.50
51	9	1394	G	C2'-C3'-O3'	8.08	127.28	109.50
51	9	1820	G	N9-C1'-C2'	-7.83	103.38	112.00
48	5	922	C	O4'-C4'-C3'	-7.64	96.36	104.00
4	D	22	ARG	NE-CZ-NH1	7.45	124.02	120.30
48	5	481	G	N7-C8-N9	-7.17	109.52	113.10
48	5	922(A)	G	P-O3'-C3'	7.11	128.23	119.70
48	5	481	G	N9-C4-C5	-7.04	102.58	105.40
48	5	3761	C	N1-C1'-C2'	-6.83	104.48	112.00
48	5	3697	U	C2'-C3'-O3'	6.68	124.39	113.70
48	5	1477	C	C2'-C3'-O3'	6.64	124.33	113.70
48	5	922(A)	G	N9-C1'-C2'	6.62	122.61	114.00
48	5	922(B)	C	P-O5'-C5'	6.58	131.44	120.90
48	5	1411	C	C4'-C3'-O3'	6.58	126.17	113.00
48	5	935	A	C4-N9-C1'	-6.50	114.60	126.30
48	5	1329	G	C2'-C3'-O3'	6.44	124.00	113.70
48	5	406	C	C2'-C3'-O3'	6.39	123.92	113.70
48	5	1455	G	C2'-C3'-O3'	6.37	123.89	113.70
48	5	1411	C	C5'-C4'-O4'	6.36	116.73	109.10
48	5	2046	G	C2'-C3'-O3'	6.33	123.83	113.70
48	5	935	A	C8-N9-C1'	6.26	138.97	127.70
48	5	935	A	O4'-C1'-N9	6.24	113.19	108.20
48	5	1211	G	C2'-C3'-O3'	6.20	123.62	113.70
48	5	481	G	C8-N9-C4	6.19	108.88	106.40
48	5	1411	C	C5'-C4'-C3'	6.13	125.81	116.00
48	5	922(B)	C	C4'-C3'-O3'	6.09	125.19	113.00
48	5	47	A	C4'-C3'-O3'	5.99	124.98	113.00
48	5	385	A	C4'-C3'-O3'	5.99	124.97	113.00
48	5	2695	A	C2'-C3'-O3'	5.97	123.25	113.70
48	5	923	C	P-O5'-C5'	5.94	130.41	120.90
48	5	935(A)	G	C2'-C3'-O3'	5.93	123.19	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	9	1646	C	C2'-C3'-O3'	5.89	123.12	113.70
48	5	1411	C	O4'-C1'-N1	5.86	112.88	108.20
48	5	4947	U	C2'-C3'-O3'	5.82	123.02	113.70
48	5	1411(C)	C	C5'-C4'-O4'	5.74	115.98	109.10
48	5	1291	G	C2'-C3'-O3'	5.66	122.75	113.70
48	5	1411	C	O4'-C4'-C3'	-5.63	98.37	104.00
48	5	245	C	C2'-C3'-O3'	5.61	122.68	113.70
48	5	922	C	O4'-C1'-N1	5.60	112.68	108.20
48	5	125	C	C2'-C3'-O3'	5.60	122.65	113.70
51	9	1820	G	C1'-C2'-O2'	-5.59	93.81	110.60
80	cc	66	ARG	NE-CZ-NH2	5.57	123.09	120.30
48	5	922(B)	C	C5'-C4'-C3'	5.54	124.86	116.00
48	5	922(B)	C	N1-C1'-C2'	5.51	121.17	114.00
51	9	1820	G	C4'-C3'-O3'	5.39	123.79	113.00
51	9	110	U	C2'-C3'-O3'	5.37	122.29	113.70
48	5	1445	U	C2'-C3'-O3'	5.27	122.13	113.70
48	5	4448	G	C4'-C3'-O3'	5.23	123.47	113.00
48	5	922(B)	C	C1'-C2'-O2'	-5.22	94.94	110.60
48	5	3603	G	C2'-C3'-O3'	5.19	122.00	113.70
51	9	1130	G	C4'-C3'-O3'	5.16	123.32	113.00
51	9	434	G	C2'-C3'-O3'	5.14	121.93	113.70
48	5	2474	G	C2'-C3'-O3'	5.10	121.86	113.70
51	9	1137	U	C2'-C3'-O3'	5.10	121.86	113.70
51	9	532	C	C2'-C3'-O3'	5.09	121.84	113.70
48	5	971(A)	G	C4'-C3'-O3'	5.09	123.17	113.00
51	9	1060	A	N9-C1'-C2'	5.06	120.57	114.00
58	GG	41	LEU	CA-CB-CG	5.05	126.91	115.30
51	9	1863	A	O4'-C1'-N9	5.02	112.22	108.20

There are no chirality outliers.

All (9) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
48	5	481	G	Sidechain
48	5	935	A	Sidechain
48	5	971	U	Sidechain
2	B	16	PHE	Peptide
2	B	258	HIS	Peptide
6	F	235	ARG	Peptide
75	XX	61	GLN	Peptide
86	ii	45	ARG	Sidechain
86	ii	62	ARG	Sidechain

## 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	A	246/257 (96%)	222 (90%)	23 (9%)	1 (0%)	34	71
2	B	392/403 (97%)	363 (93%)	26 (7%)	3 (1%)	19	60
3	C	360/425 (85%)	339 (94%)	20 (6%)	1 (0%)	41	75
4	D	291/297 (98%)	276 (95%)	13 (4%)	2 (1%)	22	62
5	E	208/291 (72%)	190 (91%)	17 (8%)	1 (0%)	29	68
6	F	223/247 (90%)	209 (94%)	12 (5%)	2 (1%)	17	58
7	G	229/319 (72%)	222 (97%)	7 (3%)	0	100	100
8	H	188/192 (98%)	178 (95%)	10 (5%)	0	100	100
9	I	201/214 (94%)	182 (90%)	19 (10%)	0	100	100
10	J	168/178 (94%)	162 (96%)	6 (4%)	0	100	100
11	L	208/211 (99%)	200 (96%)	7 (3%)	1 (0%)	29	68
12	M	136/218 (62%)	126 (93%)	10 (7%)	0	100	100
13	N	201/204 (98%)	187 (93%)	13 (6%)	1 (0%)	29	68
14	O	197/203 (97%)	188 (95%)	9 (5%)	0	100	100
15	P	151/184 (82%)	143 (95%)	7 (5%)	1 (1%)	22	62
16	Q	185/188 (98%)	169 (91%)	15 (8%)	1 (0%)	29	68
17	R	178/196 (91%)	172 (97%)	6 (3%)	0	100	100
18	S	174/176 (99%)	164 (94%)	8 (5%)	2 (1%)	14	54
19	T	157/160 (98%)	145 (92%)	12 (8%)	0	100	100
20	U	97/128 (76%)	85 (88%)	12 (12%)	0	100	100
21	V	129/140 (92%)	114 (88%)	15 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	W	102/157 (65%)	96 (94%)	6 (6%)	0	100	100
23	X	116/156 (74%)	110 (95%)	6 (5%)	0	100	100
24	Y	132/145 (91%)	122 (92%)	10 (8%)	0	100	100
25	Z	133/136 (98%)	127 (96%)	4 (3%)	2 (2%)	10	47
26	a	145/148 (98%)	130 (90%)	15 (10%)	0	100	100
27	b	100/245 (41%)	92 (92%)	7 (7%)	1 (1%)	15	55
28	c	96/115 (84%)	90 (94%)	5 (5%)	1 (1%)	15	55
29	d	105/125 (84%)	89 (85%)	15 (14%)	1 (1%)	15	55
30	e	126/135 (93%)	120 (95%)	6 (5%)	0	100	100
31	f	107/110 (97%)	99 (92%)	6 (6%)	2 (2%)	8	42
32	g	112/116 (97%)	105 (94%)	7 (6%)	0	100	100
33	h	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
34	i	100/105 (95%)	93 (93%)	7 (7%)	0	100	100
35	j	84/97 (87%)	78 (93%)	6 (7%)	0	100	100
36	k	67/70 (96%)	64 (96%)	3 (4%)	0	100	100
37	l	48/51 (94%)	44 (92%)	4 (8%)	0	100	100
38	m	50/102 (49%)	49 (98%)	0	1 (2%)	7	42
39	n	23/25 (92%)	23 (100%)	0	0	100	100
40	o	102/106 (96%)	96 (94%)	6 (6%)	0	100	100
41	p	89/92 (97%)	82 (92%)	6 (7%)	1 (1%)	14	54
42	r	122/137 (89%)	111 (91%)	10 (8%)	1 (1%)	19	60
43	s	194/318 (61%)	175 (90%)	17 (9%)	2 (1%)	15	55
44	t	151/165 (92%)	135 (89%)	14 (9%)	2 (1%)	12	50
45	1	13/15 (87%)	10 (77%)	3 (23%)	0	100	100
52	AA	215/295 (73%)	200 (93%)	13 (6%)	2 (1%)	17	58
53	BB	211/264 (80%)	197 (93%)	14 (7%)	0	100	100
54	CC	219/293 (75%)	206 (94%)	13 (6%)	0	100	100
55	DD	226/243 (93%)	209 (92%)	14 (6%)	3 (1%)	12	50
56	EE	260/263 (99%)	242 (93%)	18 (7%)	0	100	100
57	FF	181/204 (89%)	170 (94%)	11 (6%)	0	100	100
58	GG	235/249 (94%)	227 (97%)	7 (3%)	1 (0%)	34	71

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
59	HH	181/194 (93%)	170 (94%)	11 (6%)	0	100	100
60	II	204/208 (98%)	192 (94%)	12 (6%)	0	100	100
61	JJ	183/194 (94%)	173 (94%)	10 (6%)	0	100	100
62	KK	94/165 (57%)	85 (90%)	8 (8%)	1 (1%)	14	54
63	LL	139/158 (88%)	129 (93%)	10 (7%)	0	100	100
64	MM	115/132 (87%)	103 (90%)	12 (10%)	0	100	100
65	NN	147/151 (97%)	141 (96%)	6 (4%)	0	100	100
66	OO	134/168 (80%)	122 (91%)	10 (8%)	2 (2%)	10	47
67	PP	118/145 (81%)	106 (90%)	12 (10%)	0	100	100
68	QQ	140/146 (96%)	131 (94%)	9 (6%)	0	100	100
69	RR	130/135 (96%)	122 (94%)	7 (5%)	1 (1%)	19	60
70	SS	142/152 (93%)	135 (95%)	7 (5%)	0	100	100
71	TT	139/145 (96%)	130 (94%)	8 (6%)	1 (1%)	22	62
72	UU	98/119 (82%)	91 (93%)	7 (7%)	0	100	100
73	VV	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
74	WW	127/130 (98%)	118 (93%)	7 (6%)	2 (2%)	9	46
75	XX	139/143 (97%)	129 (93%)	7 (5%)	3 (2%)	6	39
76	YY	122/130 (94%)	112 (92%)	10 (8%)	0	100	100
77	ZZ	73/125 (58%)	71 (97%)	2 (3%)	0	100	100
78	aa	99/115 (86%)	92 (93%)	6 (6%)	1 (1%)	15	55
79	bb	81/84 (96%)	74 (91%)	6 (7%)	1 (1%)	13	52
80	cc	60/69 (87%)	57 (95%)	3 (5%)	0	100	100
81	dd	53/56 (95%)	47 (89%)	5 (9%)	1 (2%)	8	42
82	ee	53/133 (40%)	51 (96%)	2 (4%)	0	100	100
83	ff	66/156 (42%)	60 (91%)	6 (9%)	0	100	100
84	gg	311/317 (98%)	285 (92%)	23 (7%)	3 (1%)	15	55
86	ii	370/403 (92%)	338 (91%)	31 (8%)	1 (0%)	41	75
87	jj	423/710 (60%)	387 (92%)	32 (8%)	4 (1%)	17	58
All	All	12325/14502 (85%)	11474 (93%)	794 (6%)	57 (0%)	32	68

All (57) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
75	XX	62	PRO
1	A	14	SER
3	C	83	GLY
11	L	63	THR
15	P	114	ILE
18	S	155	PRO
31	f	107	PRO
43	s	142	GLY
44	t	125	LEU
75	XX	86	PRO
13	N	89	VAL
27	b	102	PRO
28	c	92	CYS
29	d	58	GLY
31	f	106	TYR
38	m	94	ASN
62	KK	64	TRP
66	OO	20	GLN
66	OO	149	ARG
79	bb	6	ASP
86	ii	12	ASN
87	jj	618	SER
2	B	17	LEU
4	D	44	TYR
25	Z	90	PRO
25	Z	91	LEU
52	AA	102	ARG
52	AA	159	ILE
55	DD	93	THR
81	dd	7	TYR
87	jj	268	HIS
87	jj	596	LYS
18	S	165	PRO
42	r	33	LYS
44	t	54	LYS
55	DD	44	THR
55	DD	48	ILE
58	GG	135	PRO
71	TT	109	GLY
78	aa	47	ALA
87	jj	269	VAL
2	B	258	HIS
6	F	196	VAL

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Mol	Chain	Res	Type
74	WW	56	HIS
75	XX	61	GLN
16	Q	92	VAL
43	s	25	PRO
4	D	125	VAL
69	RR	119	VAL
84	gg	61	GLY
84	gg	224	GLY
5	E	181	PRO
6	F	99	GLY
41	p	9	GLY
84	gg	13	GLY
2	B	90	VAL
74	WW	29	PRO

### 5.3.2 Protein sidechains [i](#)

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	A	190/199 (96%)	174 (92%)	16 (8%)	11 41
2	B	342/348 (98%)	324 (95%)	18 (5%)	22 57
3	C	302/347 (87%)	284 (94%)	18 (6%)	19 53
4	D	247/250 (99%)	235 (95%)	12 (5%)	25 59
5	E	190/251 (76%)	178 (94%)	12 (6%)	18 52
6	F	196/215 (91%)	183 (93%)	13 (7%)	16 50
7	G	200/272 (74%)	188 (94%)	12 (6%)	19 53
8	H	169/171 (99%)	157 (93%)	12 (7%)	14 47
9	I	175/181 (97%)	166 (95%)	9 (5%)	24 58
10	J	143/149 (96%)	138 (96%)	5 (4%)	36 68
11	L	175/176 (99%)	167 (95%)	8 (5%)	27 61
12	M	117/161 (73%)	112 (96%)	5 (4%)	29 63
13	N	171/172 (99%)	162 (95%)	9 (5%)	22 57

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	O	171/173 (99%)	159 (93%)	12 (7%)	15	47
15	P	134/163 (82%)	125 (93%)	9 (7%)	16	49
16	Q	164/165 (99%)	152 (93%)	12 (7%)	14	46
17	R	159/175 (91%)	147 (92%)	12 (8%)	13	45
18	S	157/157 (100%)	146 (93%)	11 (7%)	15	47
19	T	139/140 (99%)	126 (91%)	13 (9%)	8	37
20	U	89/114 (78%)	88 (99%)	1 (1%)	73	88
21	V	101/107 (94%)	92 (91%)	9 (9%)	9	39
22	W	86/126 (68%)	84 (98%)	2 (2%)	50	77
23	X	106/134 (79%)	100 (94%)	6 (6%)	20	55
24	Y	124/135 (92%)	118 (95%)	6 (5%)	25	60
25	Z	117/118 (99%)	114 (97%)	3 (3%)	46	75
26	a	119/120 (99%)	116 (98%)	3 (2%)	47	76
27	b	84/184 (46%)	81 (96%)	3 (4%)	35	67
28	c	84/98 (86%)	81 (96%)	3 (4%)	35	67
29	d	98/110 (89%)	87 (89%)	11 (11%)	6	30
30	e	114/121 (94%)	105 (92%)	9 (8%)	12	43
31	f	88/89 (99%)	83 (94%)	5 (6%)	20	55
32	g	98/99 (99%)	94 (96%)	4 (4%)	30	64
33	h	109/110 (99%)	105 (96%)	4 (4%)	34	66
34	i	86/89 (97%)	83 (96%)	3 (4%)	36	68
35	j	73/80 (91%)	69 (94%)	4 (6%)	21	56
36	k	64/65 (98%)	62 (97%)	2 (3%)	40	71
37	l	47/48 (98%)	46 (98%)	1 (2%)	53	79
38	m	48/90 (53%)	46 (96%)	2 (4%)	30	63
39	n	24/24 (100%)	22 (92%)	2 (8%)	11	41
40	o	92/94 (98%)	87 (95%)	5 (5%)	22	56
41	p	74/75 (99%)	73 (99%)	1 (1%)	67	85
42	r	108/121 (89%)	102 (94%)	6 (6%)	21	55
43	s	164/258 (64%)	158 (96%)	6 (4%)	34	66
44	t	126/137 (92%)	123 (98%)	3 (2%)	49	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	1	13/13 (100%)	13 (100%)	0	100	100
52	AA	180/245 (74%)	165 (92%)	15 (8%)	11	41
53	BB	194/231 (84%)	177 (91%)	17 (9%)	10	39
54	CC	187/225 (83%)	167 (89%)	20 (11%)	6	32
55	DD	190/202 (94%)	173 (91%)	17 (9%)	9	39
56	EE	224/225 (100%)	208 (93%)	16 (7%)	14	47
57	FF	158/170 (93%)	148 (94%)	10 (6%)	18	52
58	GG	207/218 (95%)	189 (91%)	18 (9%)	10	40
59	HH	165/174 (95%)	149 (90%)	16 (10%)	8	35
60	II	178/180 (99%)	164 (92%)	14 (8%)	12	43
61	JJ	161/168 (96%)	147 (91%)	14 (9%)	10	40
62	KK	87/136 (64%)	78 (90%)	9 (10%)	7	33
63	LL	130/142 (92%)	114 (88%)	16 (12%)	4	25
64	MM	99/108 (92%)	86 (87%)	13 (13%)	4	23
65	NN	130/131 (99%)	113 (87%)	17 (13%)	4	23
66	OO	106/130 (82%)	91 (86%)	15 (14%)	3	21
67	PP	109/130 (84%)	94 (86%)	15 (14%)	3	21
68	QQ	117/121 (97%)	108 (92%)	9 (8%)	13	44
69	RR	119/121 (98%)	108 (91%)	11 (9%)	9	38
70	SS	125/132 (95%)	108 (86%)	17 (14%)	3	22
71	TT	111/115 (96%)	100 (90%)	11 (10%)	8	35
72	UU	92/107 (86%)	80 (87%)	12 (13%)	4	23
73	VV	67/67 (100%)	62 (92%)	5 (8%)	13	45
74	WW	112/113 (99%)	105 (94%)	7 (6%)	18	52
75	XX	113/115 (98%)	106 (94%)	7 (6%)	18	52
76	YY	107/112 (96%)	94 (88%)	13 (12%)	5	26
77	ZZ	66/103 (64%)	61 (92%)	5 (8%)	13	44
78	aa	88/98 (90%)	78 (89%)	10 (11%)	5	29
79	bb	75/76 (99%)	69 (92%)	6 (8%)	12	42
80	cc	55/62 (89%)	50 (91%)	5 (9%)	9	38
81	dd	48/49 (98%)	46 (96%)	2 (4%)	30	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
82	ee	46/106 (43%)	41 (89%)	5 (11%)	6	31
83	ff	61/140 (44%)	55 (90%)	6 (10%)	8	35
84	gg	272/275 (99%)	261 (96%)	11 (4%)	31	65
86	ii	326/353 (92%)	309 (95%)	17 (5%)	23	58
87	jj	358/608 (59%)	332 (93%)	26 (7%)	14	46
All	All	10740/12312 (87%)	9991 (93%)	749 (7%)	19	47

All (749) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	ILE
1	A	64	ARG
1	A	102	LEU
1	A	109	GLU
1	A	115	CYS
1	A	125	LYS
1	A	128	ARG
1	A	142	GLU
1	A	163	ARG
1	A	175	ILE
1	A	200	ARG
1	A	209	HIS
1	A	221	LYS
1	A	226	ARG
1	A	233	ARG
1	A	242	ARG
2	B	10	ARG
2	B	17	LEU
2	B	53	MET
2	B	62	ARG
2	B	66	LYS
2	B	97	ARG
2	B	135	LYS
2	B	248	LEU
2	B	261	ARG
2	B	262	VAL
2	B	279	GLU
2	B	294	LYS
2	B	309	LEU
2	B	314	ILE

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
2	B	333	LEU
2	B	356	LYS
2	B	381	THR
2	B	383	GLU
3	C	20	LYS
3	C	45	ARG
3	C	95	MET
3	C	113	ARG
3	C	124	ILE
3	C	144	ILE
3	C	150	LEU
3	C	165	LYS
3	C	175	LYS
3	C	188	ARG
3	C	193	LYS
3	C	208	CYS
3	C	232	VAL
3	C	246	VAL
3	C	281	MET
3	C	284	MET
3	C	307	LYS
3	C	312	ARG
4	D	22	ARG
4	D	33	ARG
4	D	37	VAL
4	D	50	ARG
4	D	56	THR
4	D	89	LYS
4	D	104	LEU
4	D	124	GLU
4	D	128	ASP
4	D	234	ASP
4	D	264	LYS
4	D	268	ARG
5	E	52	LEU
5	E	58	ARG
5	E	112	LEU
5	E	123	ASP
5	E	141	ARG
5	E	143	LEU
5	E	144	ARG
5	E	169	LYS

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
5	E	178	VAL
5	E	213	LYS
5	E	289	LEU
5	E	291	PHE
6	F	30	LYS
6	F	38	GLN
6	F	46	ARG
6	F	65	ARG
6	F	88	LEU
6	F	134	ILE
6	F	151	GLU
6	F	187	GLU
6	F	198	LYS
6	F	211	LYS
6	F	231	ASP
6	F	245	ARG
6	F	246	MET
7	G	126	ARG
7	G	154	LYS
7	G	163	LYS
7	G	184	LYS
7	G	203	LYS
7	G	204	LYS
7	G	215	ASP
7	G	223	LEU
7	G	226	LEU
7	G	230	MET
7	G	242	ARG
7	G	293	ASN
8	H	1	MET
8	H	20	LEU
8	H	23	ARG
8	H	52	LYS
8	H	54	ARG
8	H	59	LYS
8	H	66	GLU
8	H	105	ILE
8	H	108	ASN
8	H	128	MET
8	H	173	ARG
8	H	177	ASP
9	I	13	LYS

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
9	I	36	LEU
9	I	39	LYS
9	I	116	ARG
9	I	153	ARG
9	I	163	GLN
9	I	164	LYS
9	I	168	SER
9	I	208	LYS
10	J	16	ARG
10	J	28	GLU
10	J	81	GLU
10	J	113	ILE
10	J	175	LEU
11	L	35	ARG
11	L	63	THR
11	L	67	HIS
11	L	74	ARG
11	L	121	ARG
11	L	129	ARG
11	L	162	LYS
11	L	186	ARG
12	M	37	LEU
12	M	57	LEU
12	M	89	THR
12	M	96	GLU
12	M	119	ARG
13	N	9	GLU
13	N	26	ARG
13	N	32	GLN
13	N	64	ILE
13	N	72	LYS
13	N	77	LYS
13	N	87	HIS
13	N	89	VAL
13	N	162	ARG
14	O	18	ARG
14	O	49	ARG
14	O	74	ARG
14	O	82	ARG
14	O	128	ARG
14	O	130	LYS
14	O	140	ARG

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
14	O	145	VAL
14	O	175	MET
14	O	179	LYS
14	O	188	LYS
14	O	202	LEU
15	P	24	VAL
15	P	25	HIS
15	P	57	CYS
15	P	69	ARG
15	P	86	LYS
15	P	91	LEU
15	P	127	ARG
15	P	128	ARG
15	P	147	GLU
16	Q	3	VAL
16	Q	5	ILE
16	Q	13	VAL
16	Q	61	LEU
16	Q	63	LEU
16	Q	75	ARG
16	Q	91	ARG
16	Q	97	LYS
16	Q	110	ARG
16	Q	115	LYS
16	Q	143	ARG
16	Q	168	ARG
17	R	8	LYS
17	R	36	ASN
17	R	50	ILE
17	R	89	MET
17	R	99	MET
17	R	103	ARG
17	R	113	LYS
17	R	130	ASN
17	R	133	LYS
17	R	138	LEU
17	R	176	ARG
17	R	178	GLN
18	S	7	LEU
18	S	8	ARG
18	S	9	GLU
18	S	17	LEU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
18	S	24	THR
18	S	43	ARG
18	S	70	LYS
18	S	83	ARG
18	S	149	LYS
18	S	159	LEU
18	S	174	THR
19	T	5	LYS
19	T	33	ILE
19	T	60	LYS
19	T	63	ARG
19	T	80	VAL
19	T	88	ARG
19	T	96	ILE
19	T	117	LYS
19	T	142	ARG
19	T	144	ASN
19	T	146	LYS
19	T	157	GLU
19	T	159	MET
20	U	33	ILE
21	V	15	ARG
21	V	18	LEU
21	V	35	LYS
21	V	46	LYS
21	V	60	MET
21	V	82	ILE
21	V	91	LYS
21	V	109	LYS
21	V	123	LYS
22	W	57	ARG
22	W	91	MET
23	X	39	LYS
23	X	53	ARG
23	X	59	LYS
23	X	63	LYS
23	X	91	GLU
23	X	111	GLN
24	Y	2	LYS
24	Y	8	THR
24	Y	50	ARG
24	Y	72	GLN

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
24	Y	74	TYR
24	Y	104	VAL
25	Z	11	VAL
25	Z	33	THR
25	Z	112	ARG
26	a	4	ARG
26	a	84	GLU
26	a	132	ARG
27	b	22	LYS
27	b	40	LEU
27	b	101	HIS
28	c	37	MET
28	c	52	CYS
28	c	78	ASN
29	d	23	ARG
29	d	26	THR
29	d	31	LYS
29	d	44	ARG
29	d	48	GLU
29	d	78	ARG
29	d	79	ASN
29	d	83	ARG
29	d	85	ARG
29	d	98	SER
29	d	102	LEU
30	e	21	ILE
30	e	22	ARG
30	e	48	ARG
30	e	64	LYS
30	e	78	LEU
30	e	86	GLU
30	e	89	LEU
30	e	106	LYS
30	e	128	ARG
31	f	16	ARG
31	f	23	GLU
31	f	52	LYS
31	f	73	LYS
31	f	101	ILE
32	g	54	ARG
32	g	60	ARG
32	g	66	ARG

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
32	g	114	GLN
33	h	16	GLU
33	h	67	GLU
33	h	77	LYS
33	h	89	ARG
34	i	48	CYS
34	i	86	LYS
34	i	89	GLU
35	j	3	LYS
35	j	11	ARG
35	j	20	ARG
35	j	58	THR
36	k	69	LEU
36	k	70	LYS
37	l	49	LEU
38	m	71	ARG
38	m	92	THR
39	n	1	MET
39	n	13	LEU
40	o	17	LYS
40	o	36	GLN
40	o	61	LYS
40	o	82	MET
40	o	83	LEU
41	p	8	VAL
42	r	8	MET
42	r	20	ARG
42	r	32	LEU
42	r	35	ARG
42	r	67	ARG
42	r	118	LEU
43	s	38	LYS
43	s	95	LEU
43	s	105	ASN
43	s	146	LYS
43	s	187	LEU
43	s	191	GLN
44	t	37	LEU
44	t	98	ILE
44	t	133	LEU
52	AA	12	GLU
52	AA	23	THR

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
52	AA	25	LEU
52	AA	50	ASN
52	AA	56	GLU
52	AA	58	LEU
52	AA	59	LEU
52	AA	60	LEU
52	AA	111	GLN
52	AA	136	GLU
52	AA	142	LEU
52	AA	155	ARG
52	AA	169	HIS
52	AA	178	LEU
52	AA	200	ASP
53	BB	29	ASP
53	BB	38	MET
53	BB	71	LEU
53	BB	82	ARG
53	BB	96	CYS
53	BB	105	LEU
53	BB	125	VAL
53	BB	126	ASP
53	BB	157	GLN
53	BB	163	GLN
53	BB	175	GLU
53	BB	180	ASP
53	BB	181	LEU
53	BB	184	VAL
53	BB	207	LEU
53	BB	209	ASP
53	BB	213	ARG
54	CC	78	LEU
54	CC	79	GLU
54	CC	105	GLU
54	CC	114	LYS
54	CC	117	ARG
54	CC	120	GLN
54	CC	121	ARG
54	CC	132	ASP
54	CC	144	SER
54	CC	167	ARG
54	CC	185	THR
54	CC	188	CYS

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
54	CC	192	LEU
54	CC	196	ILE
54	CC	236	PHE
54	CC	244	ILE
54	CC	248	TYR
54	CC	252	THR
54	CC	255	LEU
54	CC	271	ASP
55	DD	28	GLU
55	DD	31	GLU
55	DD	45	ARG
55	DD	72	VAL
55	DD	76	ARG
55	DD	127	MET
55	DD	134	CYS
55	DD	142	LEU
55	DD	145	GLN
55	DD	146	ARG
55	DD	168	VAL
55	DD	179	GLN
55	DD	182	LEU
55	DD	190	LEU
55	DD	218	LEU
55	DD	220	THR
55	DD	227	LYS
56	EE	17	HIS
56	EE	21	ASP
56	EE	33	THR
56	EE	42	LEU
56	EE	51	ARG
56	EE	66	MET
56	EE	77	ARG
56	EE	145	ARG
56	EE	181	CYS
56	EE	200	ARG
56	EE	205	PHE
56	EE	222	LEU
56	EE	232	ASN
56	EE	245	ARG
56	EE	246	LEU
56	EE	247	THR
57	FF	63	LYS

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
57	FF	71	ARG
57	FF	88	MET
57	FF	89	THR
57	FF	95	HIS
57	FF	110	GLN
57	FF	127	ARG
57	FF	128	ILE
57	FF	146	ARG
57	FF	204	ARG
58	GG	34	THR
58	GG	41	LEU
58	GG	63	MET
58	GG	64	LYS
58	GG	67	VAL
58	GG	75	LEU
58	GG	95	LYS
58	GG	96	SER
58	GG	103	ASP
58	GG	116	LYS
58	GG	171	THR
58	GG	178	ARG
58	GG	183	ARG
58	GG	190	ARG
58	GG	191	ARG
58	GG	199	THR
58	GG	216	ARG
58	GG	230	LYS
59	HH	8	ILE
59	HH	17	ASP
59	HH	36	LEU
59	HH	40	LEU
59	HH	46	THR
59	HH	53	VAL
59	HH	76	GLN
59	HH	79	LEU
59	HH	82	GLU
59	HH	100	ILE
59	HH	105	THR
59	HH	119	SER
59	HH	145	ARG
59	HH	153	LEU
59	HH	160	LYS

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
59	HH	193	GLN
60	II	12	ARG
60	II	23	LYS
60	II	26	LYS
60	II	49	ARG
60	II	66	SER
60	II	74	ARG
60	II	92	ARG
60	II	99	ASN
60	II	121	LEU
60	II	130	THR
60	II	161	LEU
60	II	168	GLN
60	II	178	ARG
60	II	203	LYS
61	JJ	29	LEU
61	JJ	38	ARG
61	JJ	45	ARG
61	JJ	61	LEU
61	JJ	69	ARG
61	JJ	70	ARG
61	JJ	79	ARG
61	JJ	80	ARG
61	JJ	89	GLU
61	JJ	95	ASP
61	JJ	109	ARG
61	JJ	116	LYS
61	JJ	133	ARG
61	JJ	162	ARG
62	KK	1	MET
62	KK	6	LYS
62	KK	17	LYS
62	KK	29	MET
62	KK	35	LEU
62	KK	50	GLN
62	KK	60	GLU
62	KK	89	ILE
62	KK	96	ARG
63	LL	16	ILE
63	LL	20	LYS
63	LL	39	ASN
63	LL	40	ILE

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
63	LL	42	LEU
63	LL	56	ILE
63	LL	69	ARG
63	LL	85	THR
63	LL	90	ARG
63	LL	91	ASP
63	LL	110	SER
63	LL	121	GLN
63	LL	126	VAL
63	LL	134	LEU
63	LL	135	SER
63	LL	144	LYS
64	MM	31	LEU
64	MM	33	ARG
64	MM	40	LYS
64	MM	42	LEU
64	MM	45	ARG
64	MM	55	ASN
64	MM	64	LEU
64	MM	76	LEU
64	MM	83	LYS
64	MM	85	LEU
64	MM	96	ARG
64	MM	99	LYS
64	MM	101	ARG
65	NN	3	ARG
65	NN	20	ARG
65	NN	27	LYS
65	NN	29	THR
65	NN	36	GLN
65	NN	39	LYS
65	NN	55	ARG
65	NN	60	VAL
65	NN	75	LEU
65	NN	78	LYS
65	NN	84	LEU
65	NN	86	GLU
65	NN	94	LYS
65	NN	107	LYS
65	NN	110	ASP
65	NN	125	LEU
65	NN	132	LYS

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
66	OO	25	GLU
66	OO	31	CYS
66	OO	34	PHE
66	OO	38	ASN
66	OO	46	ASP
66	OO	51	GLU
66	OO	56	VAL
66	OO	69	SER
66	OO	85	CYS
66	OO	104	ARG
66	OO	133	THR
66	OO	137	SER
66	OO	146	ARG
66	OO	150	ARG
66	OO	151	LEU
67	PP	13	ARG
67	PP	14	LYS
67	PP	15	PHE
67	PP	37	TYR
67	PP	44	ARG
67	PP	45	LEU
67	PP	51	ARG
67	PP	58	LYS
67	PP	76	VAL
67	PP	78	THR
67	PP	83	MET
67	PP	106	GLU
67	PP	108	LYS
67	PP	120	SER
67	PP	130	ARG
68	QQ	31	LEU
68	QQ	41	MET
68	QQ	47	LEU
68	QQ	60	LYS
68	QQ	67	ASP
68	QQ	90	LYS
68	QQ	100	VAL
68	QQ	127	CYS
68	QQ	140	ARG
69	RR	5	ARG
69	RR	22	THR
69	RR	31	ASN

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
69	RR	44	LYS
69	RR	62	GLN
69	RR	98	VAL
69	RR	99	ASP
69	RR	105	MET
69	RR	120	THR
69	RR	121	GLN
69	RR	132	ARG
70	SS	7	GLU
70	SS	8	LYS
70	SS	13	LEU
70	SS	21	ASP
70	SS	23	ARG
70	SS	46	ARG
70	SS	52	LEU
70	SS	59	LEU
70	SS	60	THR
70	SS	62	ASP
70	SS	63	GLU
70	SS	75	ARG
70	SS	81	ASP
70	SS	83	PHE
70	SS	104	ASP
70	SS	110	ASP
70	SS	132	ARG
71	TT	36	THR
71	TT	41	LYS
71	TT	62	ARG
71	TT	84	ARG
71	TT	102	ARG
71	TT	110	LEU
71	TT	121	ARG
71	TT	124	THR
71	TT	131	LEU
71	TT	132	ASP
71	TT	142	LYS
72	UU	18	HIS
72	UU	19	ARG
72	UU	25	THR
72	UU	36	CYS
72	UU	44	LYS
72	UU	56	MET

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
72	UU	60	THR
72	UU	79	ARG
72	UU	88	LEU
72	UU	90	ASP
72	UU	106	ILE
72	UU	111	GLU
73	VV	7	GLU
73	VV	10	ASP
73	VV	12	TYR
73	VV	18	SER
73	VV	66	ASP
74	WW	23	ARG
74	WW	36	ARG
74	WW	51	GLU
74	WW	85	ASP
74	WW	92	ASN
74	WW	103	VAL
74	WW	104	LEU
75	XX	8	ARG
75	XX	11	ARG
75	XX	34	THR
75	XX	67	ARG
75	XX	87	ASN
75	XX	105	PHE
75	XX	115	ILE
76	YY	16	ARG
76	YY	17	LEU
76	YY	20	ARG
76	YY	32	LYS
76	YY	40	ILE
76	YY	44	LEU
76	YY	46	LYS
76	YY	51	THR
76	YY	61	ARG
76	YY	74	MET
76	YY	88	LYS
76	YY	93	ARG
76	YY	101	LYS
77	ZZ	80	ARG
77	ZZ	89	GLN
77	ZZ	90	GLU
77	ZZ	92	LEU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
77	ZZ	110	THR
78	aa	2	THR
78	aa	18	VAL
78	aa	19	GLN
78	aa	21	ILE
78	aa	23	CYS
78	aa	41	ILE
78	aa	42	ARG
78	aa	55	GLU
78	aa	74	CYS
78	aa	100	ARG
79	bb	17	ARG
79	bb	37	CYS
79	bb	42	LYS
79	bb	65	GLN
79	bb	80	ARG
79	bb	81	ARG
80	cc	31	ARG
80	cc	40	ARG
80	cc	44	ARG
80	cc	51	ARG
80	cc	68	LEU
81	dd	4	GLN
81	dd	22	ARG
82	ee	98	LYS
82	ee	99	LYS
82	ee	107	ARG
82	ee	109	MET
82	ee	113	ARG
83	ff	83	LYS
83	ff	94	LYS
83	ff	99	LYS
83	ff	110	GLU
83	ff	138	ARG
83	ff	140	TYR
84	gg	17	TRP
84	gg	20	GLN
84	gg	36	ARG
84	gg	38	LYS
84	gg	113	PHE
84	gg	119	GLN
84	gg	198	VAL

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
84	gg	207	CYS
84	gg	273	GLU
84	gg	289	LEU
84	gg	306	LEU
86	ii	40	ARG
86	ii	68	CYS
86	ii	81	LEU
86	ii	107	ASN
86	ii	148	HIS
86	ii	149	ILE
86	ii	156	MET
86	ii	170	LYS
86	ii	183	GLU
86	ii	198	HIS
86	ii	243	VAL
86	ii	258	CYS
86	ii	297	LYS
86	ii	311	LEU
86	ii	313	ILE
86	ii	319	ARG
86	ii	349	LEU
87	jj	269	VAL
87	jj	276	LEU
87	jj	297	GLN
87	jj	298	GLU
87	jj	304	LYS
87	jj	313	LEU
87	jj	325	THR
87	jj	330	MET
87	jj	361	GLN
87	jj	369	VAL
87	jj	385	GLN
87	jj	389	HIS
87	jj	408	MET
87	jj	425	LEU
87	jj	434	PHE
87	jj	436	GLU
87	jj	482	ARG
87	jj	489	ARG
87	jj	499	GLN
87	jj	505	ILE
87	jj	557	MET

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Mol	Chain	Res	Type
87	jj	590	ILE
87	jj	613	ILE
87	jj	640	ASN
87	jj	653	LEU
87	jj	664	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (35) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	162	ASN
3	C	223	ASN
5	E	45	HIS
7	G	134	ASN
7	G	135	GLN
7	G	194	ASN
11	L	28	GLN
11	L	87	HIS
14	O	50	ASN
16	Q	188	ASN
17	R	130	ASN
22	W	48	GLN
23	X	105	ASN
24	Y	14	ASN
42	r	70	GLN
42	r	103	HIS
43	s	34	ASN
55	DD	4	GLN
55	DD	179	GLN
56	EE	67	GLN
56	EE	260	GLN
59	HH	193	GLN
61	JJ	111	GLN
61	JJ	154	GLN
63	LL	100	ASN
66	OO	38	ASN
68	QQ	142	GLN
70	SS	10	GLN
71	TT	42	HIS
74	WW	92	ASN
86	ii	109	GLN
86	ii	166	ASN
87	jj	361	GLN

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Mol	Chain	Res	Type
87	jj	385	GLN
87	jj	389	HIS

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
46	2	74/76 (97%)	15 (20%)	0
47	3	72/75 (96%)	27 (37%)	2 (2%)
48	5	3506/3543 (98%)	868 (24%)	165 (4%)
49	7	119/120 (99%)	15 (12%)	0
50	8	150/156 (96%)	37 (24%)	7 (4%)
51	9	1680/1869 (89%)	434 (25%)	87 (5%)
85	hh	7/8 (87%)	4 (57%)	0
All	All	5608/5847 (95%)	1400 (24%)	261 (4%)

All (1400) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
46	2	8	U
46	2	9	A
46	2	13	U
46	2	16	C
46	2	19	G
46	2	20	U
46	2	21	A
46	2	43	A
46	2	46	G
46	2	47	U
46	2	49	C
46	2	61	C
46	2	64	G
46	2	72	C
46	2	75	C
47	3	7	A
47	3	13	C
47	3	14	A
47	3	16	C
47	3	21	A
47	3	25	C
47	3	28	C
47	3	29	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
47	3	34	U
47	3	35	U
47	3	36	U
47	3	40	C
47	3	42	G
47	3	47	U
47	3	49	C
47	3	51	G
47	3	53	G
47	3	58	A
47	3	60	U
47	3	61	C
47	3	63	C
47	3	65	G
47	3	71	G
47	3	72	C
47	3	74	C
47	3	75	C
47	3	76	A
48	5	12	A
48	5	13	U
48	5	15	A
48	5	21	G
48	5	25	A
48	5	30	C
48	5	35	U
48	5	39	A
48	5	42	A
48	5	43	U
48	5	44	A
48	5	48	G
48	5	49	U
48	5	56	A
48	5	58	G
48	5	59	A
48	5	64	A
48	5	65	A
48	5	72	C
48	5	73	A
48	5	75	G
48	5	91	G
48	5	93	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
48	5	108	A
48	5	109	G
48	5	110	C
48	5	116	G
48	5	118	C
48	5	119	G
48	5	120	A
48	5	122	U
48	5	126	C
48	5	134	G
48	5	135	G
48	5	136	C
48	5	143	C
48	5	144	G
48	5	157	U
48	5	159	C
48	5	172	C
48	5	173	C
48	5	177	G
48	5	179	G
48	5	200	U
48	5	201	C
48	5	202	C
48	5	203	U
48	5	205	C
48	5	209	U
48	5	216	C
48	5	217	C
48	5	218	A
48	5	220	C
48	5	221	C
48	5	224	U
48	5	226	G
48	5	227	A
48	5	233	U
48	5	234	G
48	5	245	C
48	5	246	G
48	5	253	G
48	5	262	G
48	5	265	C
48	5	266	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
48	5	276	C
48	5	279	A
48	5	280	G
48	5	281	U
48	5	297	U
48	5	298	G
48	5	306	A
48	5	309	C
48	5	310	G
48	5	315	G
48	5	316	U
48	5	317	A
48	5	322	C
48	5	328	A
48	5	334	A
48	5	340	C
48	5	350	C
48	5	357	U
48	5	361	C
48	5	363	A
48	5	386	A
48	5	387	G
48	5	399	G
48	5	407	A
48	5	409	G
48	5	410	A
48	5	412	G
48	5	413	G
48	5	431	G
48	5	432	U
48	5	446	C
48	5	449	C
48	5	450	G
48	5	452	A
48	5	453	G
48	5	454	U
48	5	457	G
48	5	466	A
48	5	467	U
48	5	468	U
48	5	469	C
48	5	482	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
48	5	483	G
48	5	484	U
48	5	485	C
48	5	486	C
48	5	490	C
48	5	492	U
48	5	493	G
48	5	495	C
48	5	497	G
48	5	498	C
48	5	499	G
48	5	505	G
48	5	510	U
48	5	647	G
48	5	649	A
48	5	654	C
48	5	658	C
48	5	667	A
48	5	668	C
48	5	672	C
48	5	683	C
48	5	685	C
48	5	687	U
48	5	696	C
48	5	697	G
48	5	704	C
48	5	705	G
48	5	708	G
48	5	722	G
48	5	729	G
48	5	730	G
48	5	731	G
48	5	734	G
48	5	739	G
48	5	742	G
48	5	744	G
48	5	747	A
48	5	748	G
48	5	749	G
48	5	756	G
48	5	758	G
48	5	911	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
48	5	913	U
48	5	914	U
48	5	917	A
48	5	918	G
48	5	922(A)	G
48	5	922(B)	C
48	5	923	C
48	5	924	C
48	5	925	C
48	5	926	G
48	5	929	A
48	5	931	C
48	5	932	A
48	5	933	G
48	5	934	C
48	5	936	C
48	5	939	G
48	5	941	C
48	5	943	A
48	5	944	A
48	5	945	U
48	5	955	G
48	5	956	A
48	5	957	G
48	5	959	G
48	5	960	A
48	5	961	G
48	5	962	C
48	5	963	G
48	5	964	A
48	5	965	G
48	5	966	A
48	5	967	C
48	5	968	C
48	5	969	C
48	5	972	C
48	5	979	C
48	5	983	C
48	5	990	C
48	5	1072	C
48	5	1073	G
48	5	1075	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
48	5	1076	C
48	5	1078	A
48	5	1079	C
48	5	1082	C
48	5	1174	G
48	5	1177	U
48	5	1179	U
48	5	1184	A
48	5	1185	G
48	5	1195	G
48	5	1211	G
48	5	1212	G
48	5	1214	C
48	5	1215	C
48	5	1234	G
48	5	1235	G
48	5	1236	C
48	5	1237	C
48	5	1238	A
48	5	1239	C
48	5	1272	C
48	5	1273	G
48	5	1274	A
48	5	1275	G
48	5	1276	C
48	5	1280	C
48	5	1284	G
48	5	1287	G
48	5	1288	G
48	5	1291	G
48	5	1292	C
48	5	1293	G
48	5	1295	U
48	5	1296	G
48	5	1301	C
48	5	1303	A
48	5	1304	C
48	5	1313	C
48	5	1326	A
48	5	1328	G
48	5	1330	A
48	5	1337	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
48	5	1353	G
48	5	1354	A
48	5	1359	G
48	5	1364	U
48	5	1370	G
48	5	1371	A
48	5	1377	G
48	5	1378	C
48	5	1380	G
48	5	1381	U
48	5	1387	A
48	5	1394	G
48	5	1397	A
48	5	1398	A
48	5	1401	C
48	5	1403	G
48	5	1411(B)	C
48	5	1411(C)	C
48	5	1416	G
48	5	1418	C
48	5	1419	G
48	5	1420	A
48	5	1421	G
48	5	1429	C
48	5	1435	G
48	5	1436	C
48	5	1437	C
48	5	1438	U
48	5	1441	C
48	5	1442	C
48	5	1445	U
48	5	1446	C
48	5	1453	G
48	5	1455	G
48	5	1456	C
48	5	1457	G
48	5	1458	C
48	5	1465	G
48	5	1475	G
48	5	1478	C
48	5	1482	G
48	5	1483	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
48	5	1484	G
48	5	1485	C
48	5	1486	C
48	5	1489	G
48	5	1497	A
48	5	1498	G
48	5	1502	G
48	5	1504	G
48	5	1514	U
48	5	1516	G
48	5	1518	A
48	5	1523	A
48	5	1525	A
48	5	1534	A
48	5	1535	C
48	5	1547	A
48	5	1554	A
48	5	1563	A
48	5	1564	A
48	5	1566	C
48	5	1568	C
48	5	1574	G
48	5	1578	U
48	5	1586	G
48	5	1591	U
48	5	1596	U
48	5	1602	U
48	5	1612	G
48	5	1613	A
48	5	1624	G
48	5	1625	G
48	5	1631	A
48	5	1633	G
48	5	1634	A
48	5	1640	C
48	5	1641	G
48	5	1654	G
48	5	1656	U
48	5	1661	C
48	5	1670	G
48	5	1676	C
48	5	1677	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
48	5	1679	A
48	5	1684	A
48	5	1691	G
48	5	1724	G
48	5	1726	U
48	5	1733	G
48	5	1734	G
48	5	1740	C
48	5	1741	G
48	5	1742	A
48	5	1750	G
48	5	1753	G
48	5	1755	C
48	5	1756	U
48	5	1757	U
48	5	1761	G
48	5	1763	C
48	5	1764	G
48	5	1768	C
48	5	1772	C
48	5	1773	U
48	5	1776	A
48	5	1781	U
48	5	1785	C
48	5	1787	A
48	5	1797	G
48	5	1799	G
48	5	1800	U
48	5	1803	G
48	5	1804	A
48	5	1805	A
48	5	1819	G
48	5	1821	G
48	5	1822	U
48	5	1828	C
48	5	1833	G
48	5	1834	U
48	5	1835	G
48	5	1836	G
48	5	1837	A
48	5	1842	G
48	5	1855	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
48	5	1869	G
48	5	1882	U
48	5	1890	G
48	5	1897	A
48	5	1909	G
48	5	1910	G
48	5	1918	U
48	5	1920	C
48	5	1921	C
48	5	1922	G
48	5	1923	A
48	5	1931	C
48	5	1932	A
48	5	1933	G
48	5	1940	G
48	5	1941	A
48	5	1948	G
48	5	1952	G
48	5	1959	U
48	5	1961	G
48	5	1962	A
48	5	1963	C
48	5	1966	C
48	5	1967	A
48	5	1976	G
48	5	1977	C
48	5	1978	C
48	5	1980	U
48	5	1982	G
48	5	1983	A
48	5	1984	A
48	5	1986	U
48	5	1987	C
48	5	1991	A
48	5	1992	U
48	5	1993	C
48	5	1997	U
48	5	2001	G
48	5	2002	A
48	5	2003	G
48	5	2004	U
48	5	2005	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
48	5	2008	U
48	5	2011	C
48	5	2024	G
48	5	2025	A
48	5	2026	A
48	5	2033	A
48	5	2046	G
48	5	2047	A
48	5	2048	U
48	5	2052	G
48	5	2055	G
48	5	2056	G
48	5	2062	C
48	5	2064	G
48	5	2069	A
48	5	2070	U
48	5	2084	U
48	5	2085	G
48	5	2089	G
48	5	2090	U
48	5	2092	G
48	5	2093	G
48	5	2094	C
48	5	2095	A
48	5	2097	A
48	5	2098	G
48	5	2100	G
48	5	2101	A
48	5	2102	G
48	5	2104	A
48	5	2105	A
48	5	2106	G
48	5	2107	A
48	5	2108	G
48	5	2110	G
48	5	2259	G
48	5	2260	C
48	5	2262	G
48	5	2266	C
48	5	2267	U
48	5	2268	A
48	5	2269	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
48	5	2270	G
48	5	2275	G
48	5	2279	A
48	5	2289	C
48	5	2294	G
48	5	2300	A
48	5	2301	G
48	5	2313	A
48	5	2314	G
48	5	2331	G
48	5	2333	G
48	5	2348	G
48	5	2351	C
48	5	2352	U
48	5	2360	A
48	5	2364	G
48	5	2370	A
48	5	2380	G
48	5	2395	A
48	5	2396	A
48	5	2399	G
48	5	2416	G
48	5	2417	A
48	5	2422	C
48	5	2424	G
48	5	2425	U
48	5	2428	A
48	5	2429	A
48	5	2433	G
48	5	2441	C
48	5	2447	U
48	5	2450	G
48	5	2467	U
48	5	2468	U
48	5	2469	C
48	5	2471	G
48	5	2475	G
48	5	2483	G
48	5	2488	C
48	5	2489	C
48	5	2490	U
48	5	2491	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
48	5	2493	G
48	5	2495	U
48	5	2503	G
48	5	2504	C
48	5	2505	C
48	5	2506	G
48	5	2513	A
48	5	2521	G
48	5	2530	U
48	5	2537	A
48	5	2546	G
48	5	2547	G
48	5	2553	A
48	5	2554	U
48	5	2555	G
48	5	2564	G
48	5	2566	G
48	5	2571	C
48	5	2572	C
48	5	2575	U
48	5	2583	C
48	5	2587	A
48	5	2601	A
48	5	2620	G
48	5	2627	C
48	5	2638	G
48	5	2639	U
48	5	2647	A
48	5	2660	A
48	5	2662	G
48	5	2663	G
48	5	2669	C
48	5	2673	G
48	5	2676	A
48	5	2681	G
48	5	2686	G
48	5	2687	U
48	5	2688	G
48	5	2689	C
48	5	2695	A
48	5	2696	A
48	5	2707	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
48	5	2708	U
48	5	2709	C
48	5	2710	C
48	5	2711	G
48	5	2712	G
48	5	2714	G
48	5	2716	C
48	5	2719	C
48	5	2721	G
48	5	2725	A
48	5	2726	G
48	5	2735	G
48	5	2740	U
48	5	2743	A
48	5	2751	G
48	5	2754	G
48	5	2760	G
48	5	2761	U
48	5	2763	U
48	5	2764	A
48	5	2769	U
48	5	2787	A
48	5	2789	A
48	5	2790	U
48	5	2795	A
48	5	2796	G
48	5	2798	A
48	5	2802	C
48	5	2806	A
48	5	2807	A
48	5	2814	C
48	5	2826	U
48	5	2827	G
48	5	2828	U
48	5	2829	U
48	5	2835	A
48	5	2838	G
48	5	2839	U
48	5	2842	G
48	5	2855	G
48	5	2875	C
48	5	2884	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
48	5	2896	G
48	5	2897	G
48	5	3598	C
48	5	3604	A
48	5	3605	C
48	5	3615	G
48	5	3625	G
48	5	3626	G
48	5	3630	A
48	5	3635	A
48	5	3644	U
48	5	3653	A
48	5	3662	A
48	5	3674	G
48	5	3692	A
48	5	3696	C
48	5	3698	G
48	5	3711	A
48	5	3712	A
48	5	3722	G
48	5	3729	U
48	5	3733	A
48	5	3740	G
48	5	3748	A
48	5	3753	G
48	5	3756	A
48	5	3759	A
48	5	3760	A
48	5	3761	C
48	5	3765	G
48	5	3766	A
48	5	3773	U
48	5	3774	A
48	5	3776	G
48	5	3777	G
48	5	3778	U
48	5	3780	G
48	5	3784	A
48	5	3786	U
48	5	3810	C
48	5	3811	G
48	5	3812	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
48	5	3813	A
48	5	3814	U
48	5	3817	A
48	5	3819	G
48	5	3822	U
48	5	3831	U
48	5	3838	U
48	5	3839	G
48	5	3840	U
48	5	3859	G
48	5	3867	A
48	5	3876	A
48	5	3877	A
48	5	3878	C
48	5	3879	G
48	5	3888	G
48	5	3889	G
48	5	3892	U
48	5	3897	G
48	5	3898	G
48	5	3901	A
48	5	3905	A
48	5	3906	A
48	5	3907	G
48	5	3915	U
48	5	3916	G
48	5	3917	A
48	5	3927	U
48	5	3939	G
48	5	3943	A
48	5	4067	U
48	5	4069	U
48	5	4073	A
48	5	4076	G
48	5	4084	G
48	5	4085	A
48	5	4086	G
48	5	4088	C
48	5	4092	G
48	5	4099	G
48	5	4100	C
48	5	4116	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
48	5	4117	U
48	5	4118	U
48	5	4119	C
48	5	4120	U
48	5	4121	G
48	5	4122	G
48	5	4125	C
48	5	4127	A
48	5	4150	G
48	5	4158	C
48	5	4162	C
48	5	4163	U
48	5	4164	C
48	5	4166	G
48	5	4171	C
48	5	4177	C
48	5	4183	G
48	5	4184	G
48	5	4191	G
48	5	4201	G
48	5	4203	A
48	5	4212	A
48	5	4213	A
48	5	4215	C
48	5	4218	U
48	5	4219	A
48	5	4225	G
48	5	4229	U
48	5	4232	U
48	5	4233	A
48	5	4249	G
48	5	4251	A
48	5	4255	A
48	5	4257	A
48	5	4258	C
48	5	4265	U
48	5	4268	A
48	5	4271	A
48	5	4273	A
48	5	4281	A
48	5	4291	G
48	5	4297	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
48	5	4304	A
48	5	4305	G
48	5	4306	U
48	5	4314	C
48	5	4317	A
48	5	4318	C
48	5	4319	C
48	5	4326	G
48	5	4329	G
48	5	4330	G
48	5	4335	C
48	5	4336	A
48	5	4339	A
48	5	4349	C
48	5	4350	C
48	5	4354	U
48	5	4355	G
48	5	4373	G
48	5	4377	G
48	5	4378	A
48	5	4379	A
48	5	4380	A
48	5	4387	C
48	5	4391	G
48	5	4393	G
48	5	4394	A
48	5	4395	U
48	5	4396	A
48	5	4398	C
48	5	4401	G
48	5	4415	A
48	5	4419	U
48	5	4421	C
48	5	4422	A
48	5	4440	G
48	5	4444	C
48	5	4448	G
48	5	4449	A
48	5	4450	U
48	5	4453	C
48	5	4454	G
48	5	4464	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
48	5	4471	U
48	5	4475	G
48	5	4476	C
48	5	4488	A
48	5	4495	G
48	5	4500	U
48	5	4510	A
48	5	4511	A
48	5	4512	U
48	5	4513	A
48	5	4515	G
48	5	4519	C
48	5	4520	G
48	5	4522	G
48	5	4524	G
48	5	4548	A
48	5	4549	G
48	5	4560	C
48	5	4561	C
48	5	4563	U
48	5	4567	G
48	5	4570	G
48	5	4573	G
48	5	4575	G
48	5	4584	A
48	5	4585	U
48	5	4586	G
48	5	4590	A
48	5	4599	A
48	5	4618	G
48	5	4636	U
48	5	4637	G
48	5	4639	G
48	5	4656	A
48	5	4657	U
48	5	4658	G
48	5	4661	G
48	5	4667	C
48	5	4669	A
48	5	4670	C
48	5	4672	A
48	5	4677	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
48	5	4678	G
48	5	4700	A
48	5	4701	A
48	5	4709	U
48	5	4719	G
48	5	4720	C
48	5	4721	G
48	5	4728	U
48	5	4736	C
48	5	4737	G
48	5	4745	G
48	5	4751	G
48	5	4754	G
48	5	4755	G
48	5	4756	C
48	5	4757	C
48	5	4759	C
48	5	4761	G
48	5	4765	G
48	5	4771	C
48	5	4772	C
48	5	4868	G
48	5	4870	G
48	5	4871	C
48	5	4872	G
48	5	4873	G
48	5	4874	A
48	5	4875	G
48	5	4876	A
48	5	4877	G
48	5	4882	U
48	5	4883	C
48	5	4885	U
48	5	4887	C
48	5	4891	G
48	5	4895	C
48	5	4897	G
48	5	4904	G
48	5	4910	A
48	5	4912	G
48	5	4913	G
48	5	4914	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
48	5	4915	G
48	5	4919	G
48	5	4921	C
48	5	4924	C
48	5	4925	U
48	5	4926	C
48	5	4927	G
48	5	4928	C
48	5	4931	G
48	5	4935	C
48	5	4937	C
48	5	4938	A
48	5	4940	C
48	5	4942	C
48	5	4943	A
48	5	4944	C
48	5	4948	C
48	5	4949	G
48	5	4950	U
48	5	4951	G
48	5	4956	A
48	5	4957	C
48	5	4958	C
48	5	4964	C
48	5	4965	U
48	5	4966	A
48	5	4967	A
48	5	4976	U
48	5	4985	U
48	5	4988	U
48	5	4989	U
48	5	4990	C
48	5	4991	U
48	5	4993	G
48	5	4999	G
48	5	5014	A
48	5	5017	G
48	5	5040	U
48	5	5041	G
48	5	5047	C
48	5	5050	C
48	5	5053	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
48	5	5054	C
48	5	5056	A
48	5	5061	A
48	5	5062	G
48	5	5069	U
49	7	7	G
49	7	25	G
49	7	33	U
49	7	42	A
49	7	53	U
49	7	54	A
49	7	64	G
49	7	66	G
49	7	97	G
49	7	99	G
49	7	100	A
49	7	110	G
49	7	111	C
49	7	117	G
49	7	120	U
50	8	2	G
50	8	3	A
50	8	32	C
50	8	34	U
50	8	35	C
50	8	49	G
50	8	51	U
50	8	52	A
50	8	59	A
50	8	62	A
50	8	63	U
50	8	75	G
50	8	79	G
50	8	86	U
50	8	87	G
50	8	94	G
50	8	95	A
50	8	103	A
50	8	104	A
50	8	105	C
50	8	107	C
50	8	109	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
50	8	110	U
50	8	111	U
50	8	112	G
50	8	114	G
50	8	121	G
50	8	123	U
50	8	124	U
50	8	125	C
50	8	126	C
50	8	127	U
50	8	137	A
50	8	143	G
50	8	147	G
50	8	150	C
50	8	153	C
51	9	2	A
51	9	3	C
51	9	4	C
51	9	17	C
51	9	25	A
51	9	26	U
51	9	33	G
51	9	37	C
51	9	41	G
51	9	44	U
51	9	45	A
51	9	46	A
51	9	56	G
51	9	58	C
51	9	60	A
51	9	65	C
51	9	67	C
51	9	68	A
51	9	70	G
51	9	71	G
51	9	73	C
51	9	74	G
51	9	75	G
51	9	77	A
51	9	79	A
51	9	99	A
51	9	100	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
51	9	103	A
51	9	104	A
51	9	110	U
51	9	111	A
51	9	113	G
51	9	115	U
51	9	116	U
51	9	124	U
51	9	126	G
51	9	127	C
51	9	128	U
51	9	129	C
51	9	130	G
51	9	141	A
51	9	143	U
51	9	147	A
51	9	155	G
51	9	158	A
51	9	161	U
51	9	162	C
51	9	163	U
51	9	167	G
51	9	168	C
51	9	175	A
51	9	182	C
51	9	183	G
51	9	184	G
51	9	188	C
51	9	189	U
51	9	192	C
51	9	200	G
51	9	202	G
51	9	206	G
51	9	213	G
51	9	215	G
51	9	292	A
51	9	294	U
51	9	302	A
51	9	304	C
51	9	307	G
51	9	308	G
51	9	309	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
51	9	312	G
51	9	313	A
51	9	314	U
51	9	317	C
51	9	318	A
51	9	319	C
51	9	322	C
51	9	331	C
51	9	332	G
51	9	335	G
51	9	343	A
51	9	347	G
51	9	351	G
51	9	360	A
51	9	362	C
51	9	364	A
51	9	368	U
51	9	370	G
51	9	379	C
51	9	381	C
51	9	382	C
51	9	385	G
51	9	386	C
51	9	400	C
51	9	407	G
51	9	409	C
51	9	410	G
51	9	417	C
51	9	418	A
51	9	435	A
51	9	438	G
51	9	448	A
51	9	449	A
51	9	450	C
51	9	459	C
51	9	460	A
51	9	462	C
51	9	464	A
51	9	465	A
51	9	466	G
51	9	468	A
51	9	472	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
51	9	473	A
51	9	474	G
51	9	476	A
51	9	482	G
51	9	487	U
51	9	492	C
51	9	496	C
51	9	501	C
51	9	503	C
51	9	523	A
51	9	525	A
51	9	528	A
51	9	531	A
51	9	532	C
51	9	533	A
51	9	544	G
51	9	545	A
51	9	546	G
51	9	548	C
51	9	549	C
51	9	550	C
51	9	551	U
51	9	554	A
51	9	555	A
51	9	556	U
51	9	557	U
51	9	559	G
51	9	560	A
51	9	563	G
51	9	564	A
51	9	568	C
51	9	576	A
51	9	583	A
51	9	587	A
51	9	588	G
51	9	589	G
51	9	590	A
51	9	591	U
51	9	592	C
51	9	595	U
51	9	597	G
51	9	604	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
51	9	606	G
51	9	607	U
51	9	608	C
51	9	613	G
51	9	614	C
51	9	615	C
51	9	616	A
51	9	617	G
51	9	625	G
51	9	626	G
51	9	627	U
51	9	628	A
51	9	629	A
51	9	630	U
51	9	632	C
51	9	637	U
51	9	643	A
51	9	644	G
51	9	655	A
51	9	659	G
51	9	660	C
51	9	663	C
51	9	668	A
51	9	669	A
51	9	670	A
51	9	671	A
51	9	672	A
51	9	683	G
51	9	684	G
51	9	688	U
51	9	689	U
51	9	732	U
51	9	752	G
51	9	753	C
51	9	754	G
51	9	811	A
51	9	812	A
51	9	821	G
51	9	822	U
51	9	830	A
51	9	834	C
51	9	847	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
51	9	849	A
51	9	861	A
51	9	868	G
51	9	869	A
51	9	870	A
51	9	871	U
51	9	872	A
51	9	873	G
51	9	874	G
51	9	875	A
51	9	877	C
51	9	878	G
51	9	885	U
51	9	887	U
51	9	890	U
51	9	892	U
51	9	911	C
51	9	913	A
51	9	914	U
51	9	920	A
51	9	922	A
51	9	930	C
51	9	933	G
51	9	934	G
51	9	943	U
51	9	971	G
51	9	985	G
51	9	990	A
51	9	992	A
51	9	999	G
51	9	1016	U
51	9	1017	U
51	9	1023	A
51	9	1041	G
51	9	1055	A
51	9	1060	A
51	9	1061	U
51	9	1062	A
51	9	1067	C
51	9	1078	C
51	9	1083	A
51	9	1085	C

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
51	9	1089	G
51	9	1099	G
51	9	1100	A
51	9	1113	A
51	9	1114	U
51	9	1115	U
51	9	1116	C
51	9	1117	C
51	9	1118	C
51	9	1121	G
51	9	1131	G
51	9	1138	C
51	9	1139	C
51	9	1144	A
51	9	1148	A
51	9	1149	A
51	9	1153	C
51	9	1154	U
51	9	1161	U
51	9	1165	G
51	9	1166	G
51	9	1195	A
51	9	1196	A
51	9	1207	G
51	9	1208	A
51	9	1211	G
51	9	1213	C
51	9	1215	C
51	9	1221	G
51	9	1223	A
51	9	1224	G
51	9	1227	G
51	9	1230	C
51	9	1240	A
51	9	1242	U
51	9	1251	A
51	9	1253	A
51	9	1254	C
51	9	1256	G
51	9	1257	G
51	9	1258	A
51	9	1259	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
51	9	1265	A
51	9	1266	C
51	9	1268	C
51	9	1271	C
51	9	1274	G
51	9	1275	G
51	9	1281	G
51	9	1284	A
51	9	1285	G
51	9	1286	G
51	9	1287	A
51	9	1289	U
51	9	1291	A
51	9	1293	A
51	9	1298	G
51	9	1299	A
51	9	1300	U
51	9	1301	A
51	9	1302	G
51	9	1303	C
51	9	1307	U
51	9	1308	U
51	9	1313	A
51	9	1314	U
51	9	1316	C
51	9	1322	G
51	9	1330	G
51	9	1331	C
51	9	1337	C
51	9	1342	U
51	9	1348	G
51	9	1354	G
51	9	1369	A
51	9	1371	U
51	9	1372	U
51	9	1378	A
51	9	1395	C
51	9	1396	A
51	9	1397	U
51	9	1401	A
51	9	1402	A
51	9	1404	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
51	9	1410	C
51	9	1412	C
51	9	1424	G
51	9	1428	G
51	9	1429	G
51	9	1439	A
51	9	1449	G
51	9	1454	A
51	9	1459	G
51	9	1462	U
51	9	1463	U
51	9	1466	G
51	9	1473	G
51	9	1476	A
51	9	1477	U
51	9	1478	U
51	9	1489	A
51	9	1490	G
51	9	1493	C
51	9	1494	U
51	9	1498	A
51	9	1507	G
51	9	1509	U
51	9	1510	G
51	9	1521	C
51	9	1522	A
51	9	1531	A
51	9	1533	A
51	9	1536	G
51	9	1539	U
51	9	1544	C
51	9	1545	A
51	9	1548	G
51	9	1552	G
51	9	1553	C
51	9	1555	U
51	9	1556	A
51	9	1557	C
51	9	1560	U
51	9	1570	G
51	9	1574	C
51	9	1575	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
51	9	1580	A
51	9	1581	C
51	9	1585	U
51	9	1587	G
51	9	1588	A
51	9	1589	A
51	9	1600	G
51	9	1601	A
51	9	1602	U
51	9	1604	G
51	9	1621	U
51	9	1622	U
51	9	1623	A
51	9	1624	U
51	9	1625	U
51	9	1637	A
51	9	1638	G
51	9	1641	A
51	9	1647	A
51	9	1648	G
51	9	1654	G
51	9	1664	A
51	9	1665	G
51	9	1671	G
51	9	1680	G
51	9	1682	C
51	9	1683	C
51	9	1686	G
51	9	1689	C
51	9	1695	A
51	9	1698	C
51	9	1715	A
51	9	1721	U
51	9	1722	G
51	9	1726	G
51	9	1728	U
51	9	1729	U
51	9	1730	U
51	9	1732	G
51	9	1737	G
51	9	1744	G
51	9	1745	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
51	9	1753	C
51	9	1758	G
51	9	1760	G
51	9	1772	C
51	9	1783	C
51	9	1785	C
51	9	1800	A
51	9	1801	A
51	9	1805	G
51	9	1823	A
51	9	1824	A
51	9	1825	A
51	9	1826	G
51	9	1829	G
51	9	1831	A
51	9	1835	A
51	9	1836	G
51	9	1838	U
51	9	1849	G
51	9	1850	A
51	9	1851	A
51	9	1861	G
51	9	1862	G
51	9	1863	A
51	9	1865	C
51	9	1866	A
51	9	1867	U
51	9	1868	U
51	9	1869	A
85	hh	42	C
85	hh	43	A
85	hh	45	A
85	hh	46	G

All (261) RNA pucker outliers are listed below:

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
47	3	7	A
47	3	74	C
48	5	12	A
48	5	20	U
48	5	47	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
48	5	48	G
48	5	64	A
48	5	119	G
48	5	125	C
48	5	134	G
48	5	143	C
48	5	159	C
48	5	217	C
48	5	226	G
48	5	245	C
48	5	265	C
48	5	275	C
48	5	278	G
48	5	315	G
48	5	385	A
48	5	387	G
48	5	406	C
48	5	408	A
48	5	409	G
48	5	417	G
48	5	449	C
48	5	484	U
48	5	485	C
48	5	492	U
48	5	497	G
48	5	498	C
48	5	504	G
48	5	696	C
48	5	728	U
48	5	729	G
48	5	738(A)	C
48	5	747	A
48	5	748	G
48	5	916	C
48	5	922	C
48	5	922(B)	C
48	5	930	G
48	5	933	G
48	5	935(A)	G
48	5	936	C
48	5	955	G
48	5	956	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
48	5	959	G
48	5	963	G
48	5	965	G
48	5	966	A
48	5	968	C
48	5	969	C
48	5	971(A)	G
48	5	1072	C
48	5	1209	U
48	5	1211	G
48	5	1214	C
48	5	1236	C
48	5	1238	A
48	5	1287	G
48	5	1291	G
48	5	1295	U
48	5	1329	G
48	5	1358	G
48	5	1359	G
48	5	1370	G
48	5	1378	C
48	5	1380	G
48	5	1420	A
48	5	1432	G
48	5	1440	U
48	5	1445	U
48	5	1455	G
48	5	1477	C
48	5	1484	G
48	5	1485	C
48	5	1533	A
48	5	1563	A
48	5	1633	G
48	5	1678	C
48	5	1733	G
48	5	1740	C
48	5	1804	A
48	5	1818	G
48	5	1833	G
48	5	1834	U
48	5	1835	G
48	5	1892	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
48	5	1919	G
48	5	1921	C
48	5	1935	C
48	5	1979	A
48	5	1983	A
48	5	1986	U
48	5	2001	G
48	5	2046	G
48	5	2068	C
48	5	2088	A
48	5	2089	G
48	5	2100	G
48	5	2265	G
48	5	2266	C
48	5	2278	G
48	5	2313	A
48	5	2396	A
48	5	2398	U
48	5	2428	A
48	5	2467	U
48	5	2468	U
48	5	2474	G
48	5	2475	G
48	5	2490	U
48	5	2502	A
48	5	2546	G
48	5	2553	A
48	5	2661	U
48	5	2695	A
48	5	2724	G
48	5	2754	G
48	5	2782	U
48	5	2789	A
48	5	2794	C
48	5	2806	A
48	5	3603	G
48	5	3625	G
48	5	3673	C
48	5	3697	U
48	5	3710	G
48	5	3759	A
48	5	3760	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
48	5	3809	G
48	5	3876	A
48	5	3888	G
48	5	3904	G
48	5	4075	U
48	5	4076	G
48	5	4084	G
48	5	4119	C
48	5	4121	G
48	5	4124	G
48	5	4162	C
48	5	4170	A
48	5	4221	C
48	5	4232	U
48	5	4254	G
48	5	4266	G
48	5	4378	A
48	5	4395	U
48	5	4448	G
48	5	4449	A
48	5	4463	U
48	5	4488	A
48	5	4510	A
48	5	4583	C
48	5	4699	U
48	5	4719	G
48	5	4871	C
48	5	4872	G
48	5	4873	G
48	5	4876	A
48	5	4884	G
48	5	4925	U
48	5	4936	G
48	5	4942	C
48	5	4947	U
48	5	4965	U
50	8	2	G
50	8	51	U
50	8	85	U
50	8	86	U
50	8	94	G
50	8	110	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
50	8	124	U
51	9	2	A
51	9	3	C
51	9	72	C
51	9	110	U
51	9	126	G
51	9	127	C
51	9	128	U
51	9	142	C
51	9	160	U
51	9	182	C
51	9	293	C
51	9	312	G
51	9	369	C
51	9	434	G
51	9	465	A
51	9	500	A
51	9	516	A
51	9	532	C
51	9	550	C
51	9	553	U
51	9	555	A
51	9	559	G
51	9	563	G
51	9	591	U
51	9	594	A
51	9	606	G
51	9	607	U
51	9	613	G
51	9	614	C
51	9	615	C
51	9	625	G
51	9	626	G
51	9	627	U
51	9	628	A
51	9	629	A
51	9	642	U
51	9	670	A
51	9	688	U
51	9	752	G
51	9	821	G
51	9	869	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
51	9	870	A
51	9	872	A
51	9	874	G
51	9	932	G
51	9	990	A
51	9	1016	U
51	9	1087	A
51	9	1114	U
51	9	1115	U
51	9	1137	U
51	9	1165	G
51	9	1253	A
51	9	1264	C
51	9	1274	G
51	9	1284	A
51	9	1285	G
51	9	1286	G
51	9	1313	A
51	9	1330	G
51	9	1394	G
51	9	1395	C
51	9	1396	A
51	9	1438	A
51	9	1476	A
51	9	1489	A
51	9	1493	C
51	9	1519	U
51	9	1520	G
51	9	1578	U
51	9	1581	C
51	9	1587	G
51	9	1621	U
51	9	1622	U
51	9	1636	G
51	9	1637	A
51	9	1646	C
51	9	1663	A
51	9	1664	A
51	9	1679	A
51	9	1721	U
51	9	1744	G
51	9	1824	A

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Mol	Chain	Res	Type
51	9	1825	A
51	9	1835	A
51	9	1867	U
51	9	1868	U

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

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 291 ligands modelled in this entry, 289 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
90	GCP	jj	700	88	27,34,34	1.58	6 (22%)	34,54,54	1.88	8 (23%)
90	GCP	9	1972	-	27,34,34	1.41	5 (18%)	34,54,54	2.04	8 (23%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
90	GCP	jj	700	88	-	4/15/38/38	0/3/3/3
90	GCP	9	1972	-	-	5/15/38/38	0/3/3/3

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
90	jj	700	GCP	C5-C6	4.56	1.49	1.41
90	9	1972	GCP	C5-C6	3.96	1.48	1.41
90	jj	700	GCP	PG-O3G	2.88	1.61	1.54
90	jj	700	GCP	PG-O2G	2.88	1.61	1.54
90	9	1972	GCP	PG-O2G	2.80	1.61	1.54
90	9	1972	GCP	PG-O3G	2.71	1.61	1.54
90	jj	700	GCP	C5-C4	2.62	1.47	1.40
90	jj	700	GCP	PB-O3A	2.47	1.61	1.58
90	9	1972	GCP	C5-C4	2.23	1.46	1.40
90	jj	700	GCP	PB-O2B	2.17	1.61	1.56
90	9	1972	GCP	PB-O2B	2.04	1.61	1.56

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
90	jj	700	GCP	C2-N3-C4	5.06	121.14	115.36
90	9	1972	GCP	C2-N3-C4	4.89	120.94	115.36
90	9	1972	GCP	PB-O3A-PA	-4.85	117.17	132.56
90	9	1972	GCP	C4-C5-C6	-4.19	116.79	120.80
90	9	1972	GCP	C2-N1-C6	4.01	122.31	115.93
90	9	1972	GCP	C5-C6-N1	-3.83	118.19	123.43
90	jj	700	GCP	C2-N1-C6	3.82	122.00	115.93
90	jj	700	GCP	C5-C6-N1	-3.81	118.22	123.43
90	jj	700	GCP	C4-C5-C6	-3.71	117.25	120.80
90	9	1972	GCP	N3-C2-N1	-3.45	122.62	127.22
90	jj	700	GCP	N3-C2-N1	-3.31	122.80	127.22
90	jj	700	GCP	C4-C5-N7	-2.87	106.41	109.40
90	jj	700	GCP	C3'-C2'-C1'	2.82	105.23	100.98
90	jj	700	GCP	PB-O3A-PA	-2.74	123.88	132.56
90	9	1972	GCP	C3'-C2'-C1'	2.67	105.00	100.98
90	9	1972	GCP	C4-C5-N7	-2.60	106.69	109.40

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
90	9	1972	GCP	C5'-O5'-PA-O1A
90	9	1972	GCP	C5'-O5'-PA-O2A
90	jj	700	GCP	PG-C3B-PB-O1B
90	jj	700	GCP	PG-C3B-PB-O2B
90	jj	700	GCP	PG-C3B-PB-O3A
90	9	1972	GCP	C3'-C4'-C5'-O5'

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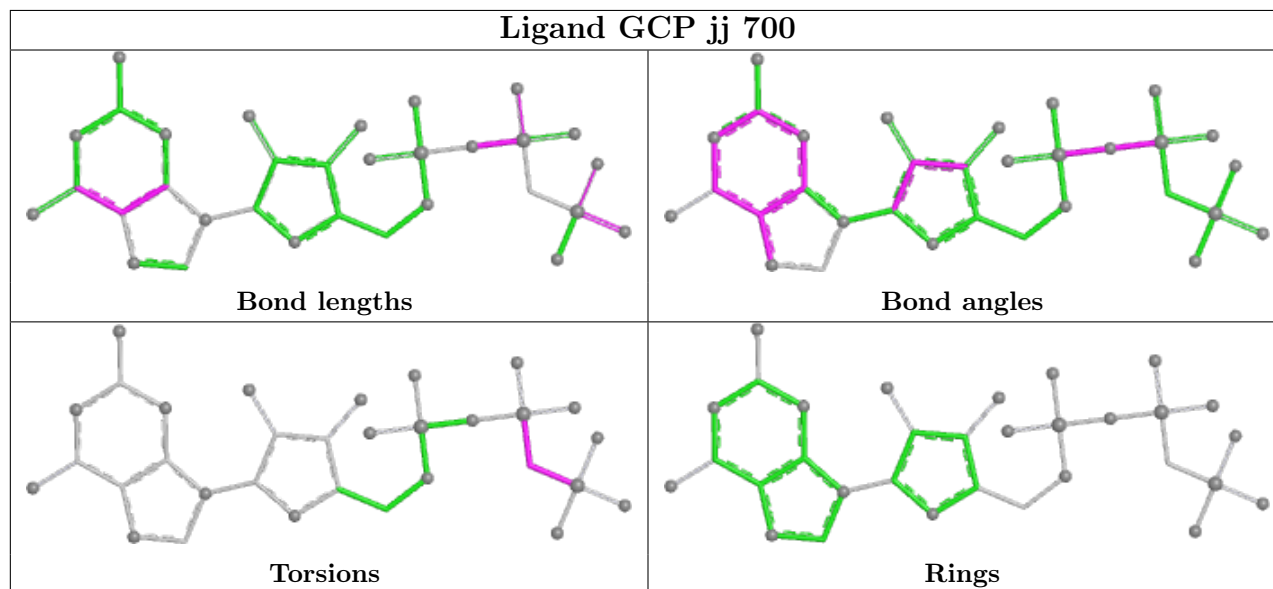
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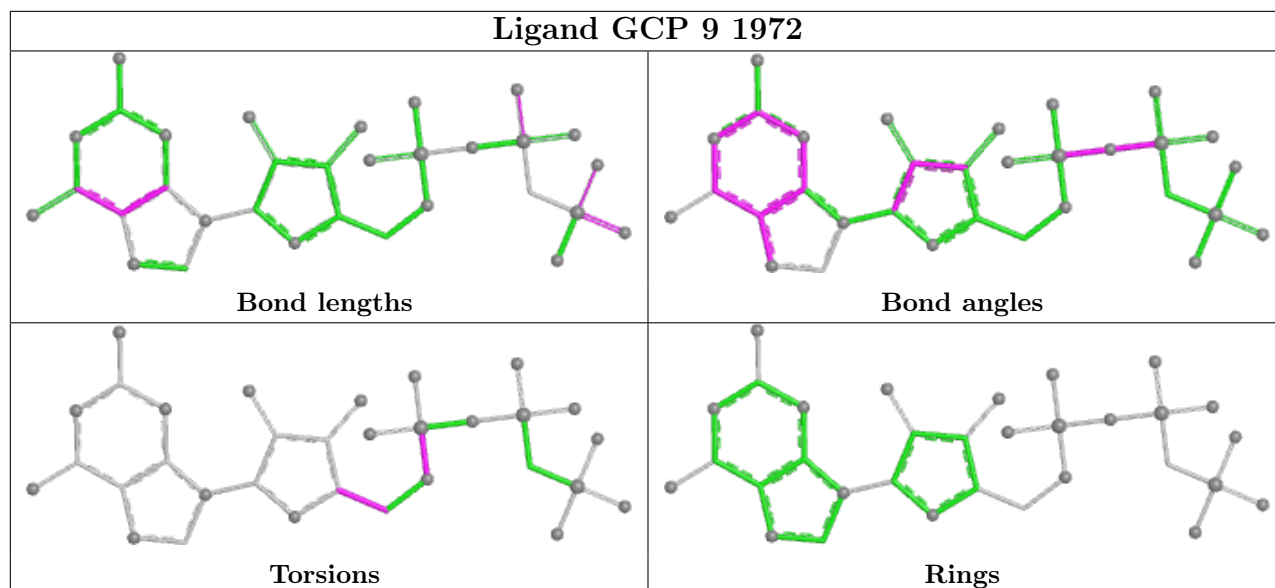
Mol	Chain	Res	Type	Atoms
90	9	1972	GCP	O4'-C4'-C5'-O5'
90	jj	700	GCP	PB-C3B-PG-O1G
90	9	1972	GCP	C5'-O5'-PA-O3A

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





## 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
48	5	44
51	9	8
47	3	2
46	2	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	2113:G	O3'	2258:C	P	40.78
1	5	1252:C	O3'	1271:G	P	35.85
1	5	1219:G	O3'	1233:G	P	22.84
1	5	1405:C	O3'	1406:G	P	22.78
1	5	3948:C	O3'	4065:G	P	19.74
1	5	1406:G	O3'	1406(A):G	P	19.63
1	5	4138:C	O3'	4146:G	P	18.06
1	5	990:C	O3'	1064:G	P	18.05
1	5	523:C	O3'	638:G	P	17.99
1	5	4101:C	O3'	4107:G	P	17.46
1	5	1406(C):G	O3'	1411:C	P	17.15

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	4777:C	O3'	4859:C	P	16.56
1	5	760:G	O3'	904:C	P	14.90
1	5	5022:U	O3'	5028:G	P	14.80
1	5	1696:C	O3'	1720:C	P	14.57
1	5	1364:U	O3'	1368:A	P	14.45
1	5	1411:C	O3'	1411(A):G	P	14.41
1	5	182:G	O3'	189:G	P	14.04
1	5	921:C	O3'	922:C	P	13.49
1	5	2901:G	O3'	3597:G	P	13.37
1	5	970:G	O3'	971:U	P	10.82
1	5	512:U	O3'	515:C	P	9.81
1	5	4729:A	O3'	4735:G	P	9.78
1	5	971:U	O3'	971(A):G	P	9.74
1	5	934:C	O3'	935:A	P	9.42
1	5	737:C	O3'	738:C	P	9.01
1	5	1180:C	O3'	1183:C	P	9.01
1	5	481:G	O3'	481(A):C	P	8.81
1	5	500:G	O3'	504:G	P	6.68
1	5	480:C	O3'	481:G	P	5.80
1	5	1100:U	O3'	1168:G	P	5.73
1	3	19:G	O3'	20:U	P	5.67
1	5	1239:C	O3'	1244:G	P	5.22
1	9	322:C	O3'	323:C	P	5.10
1	5	4740:G	O3'	4743:G	P	4.93
1	3	16:C	O3'	18:U	P	4.79
1	9	309:G	O3'	310:C	P	4.68
1	9	798:G	O3'	799:U	P	4.57
1	5	935:A	O3'	935(A):G	P	4.49
1	9	304:C	O3'	305:U	P	4.39
1	2	16:C	O3'	18:G	P	4.25
1	5	738:C	O3'	738(A):C	P	4.14
1	5	170:C	O3'	171:U	P	3.93
1	5	4899:G	O3'	4902:C	P	3.39
1	9	902:G	O3'	903:A	P	3.39
1	9	903:A	O3'	904:A	P	3.34
1	9	1295:A	O3'	1296:U	P	3.34
1	5	1438:U	O3'	1440:U	P	3.33
1	5	5020:G	O3'	5021:C	P	3.21
1	5	267:G	O3'	268:G	P	3.16
1	5	751:G	O3'	752:G	P	3.13
1	9	593:C	O3'	594:A	P	3.06
1	5	2031:C	O3'	2032:U	P	2.65

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	922(A):G	O3'	922(B):C	P	1.81
1	5	922:C	O3'	922(A):G	P	1.76

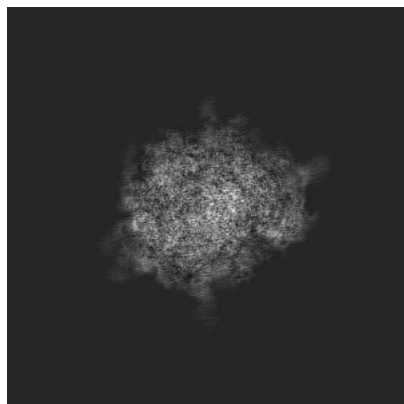
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4134. These allow visual inspection of the internal detail of the map and identification of artifacts.

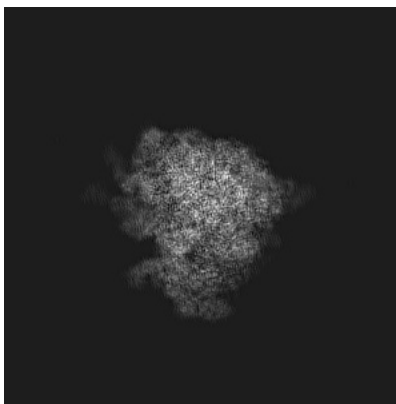
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

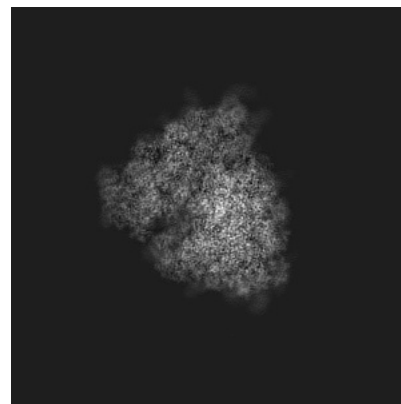
#### 6.1.1 Primary map



X

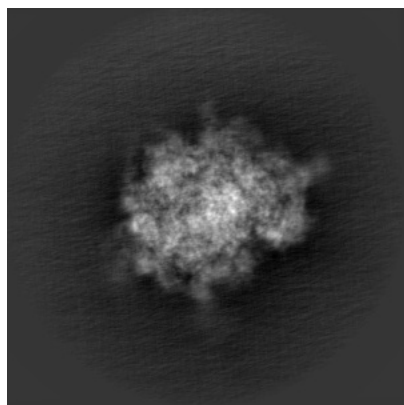


Y

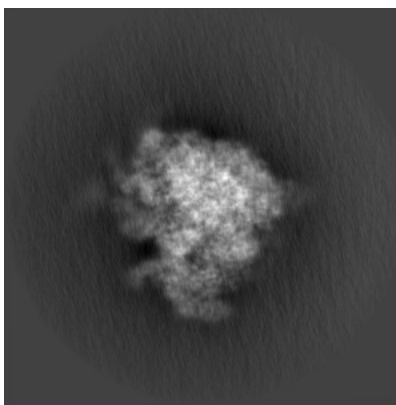


Z

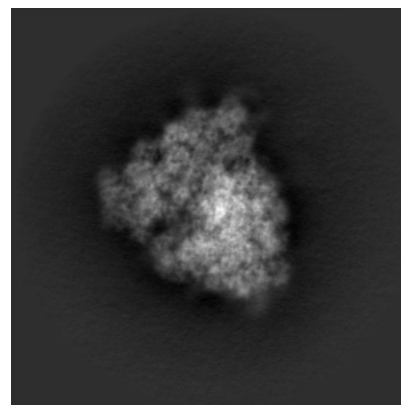
#### 6.1.2 Raw map



X



Y

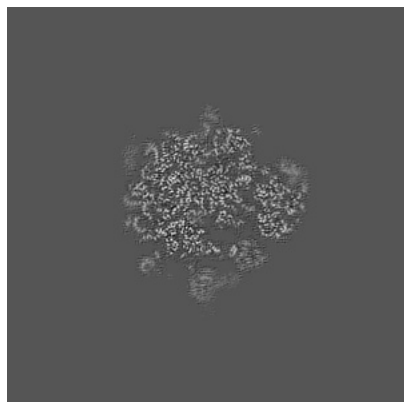


Z

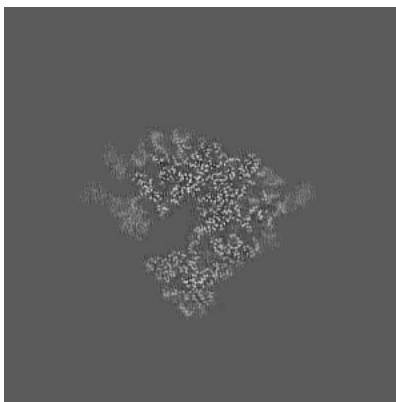
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

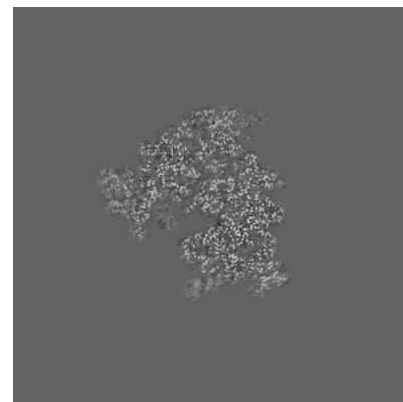
### 6.2.1 Primary map



X Index: 210

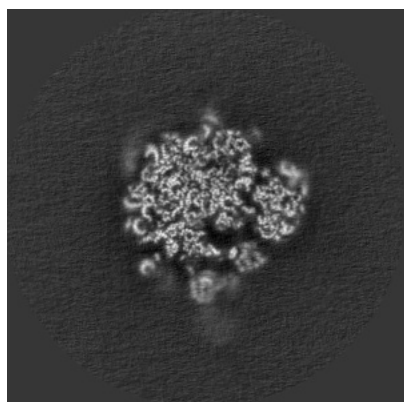


Y Index: 210

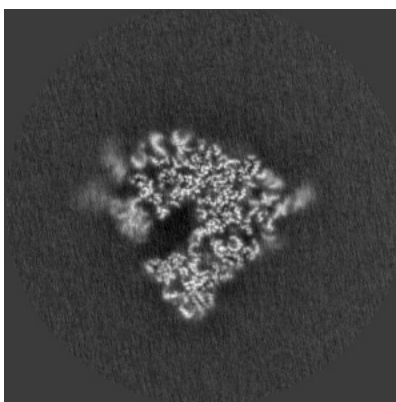


Z Index: 210

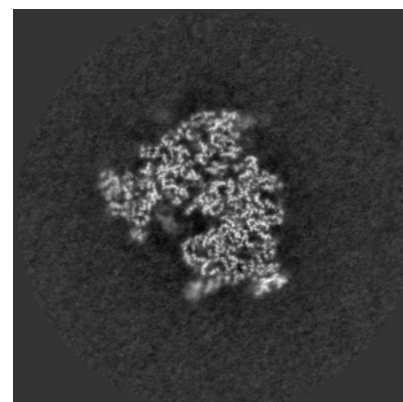
### 6.2.2 Raw map



X Index: 210



Y Index: 210

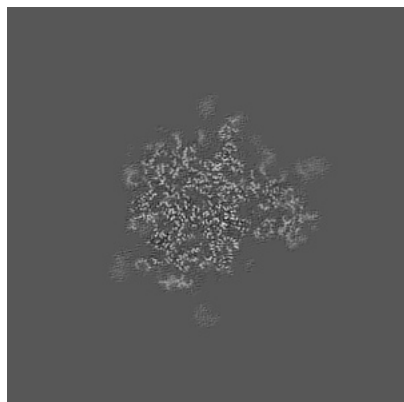


Z Index: 210

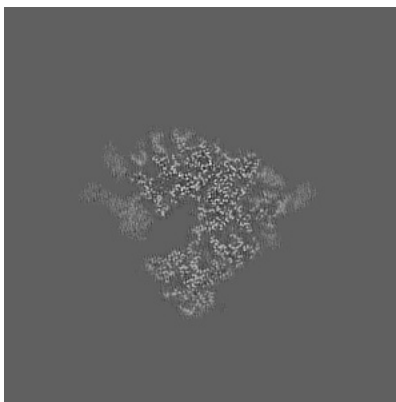
The images above show central slices of the map in three orthogonal directions.

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

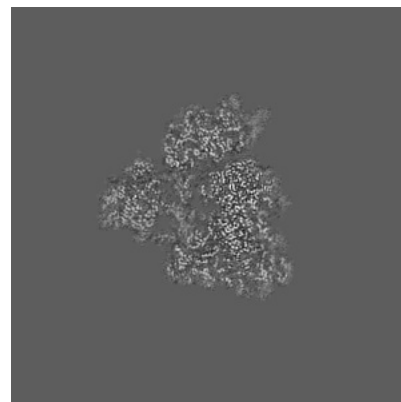
### 6.3.1 Primary map



X Index: 228

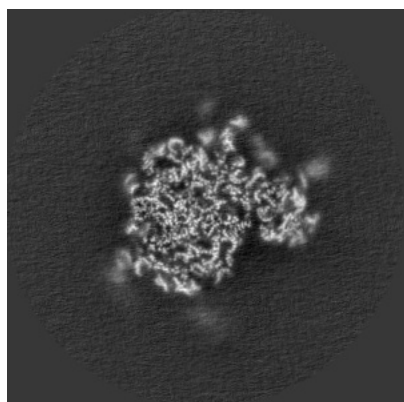


Y Index: 211

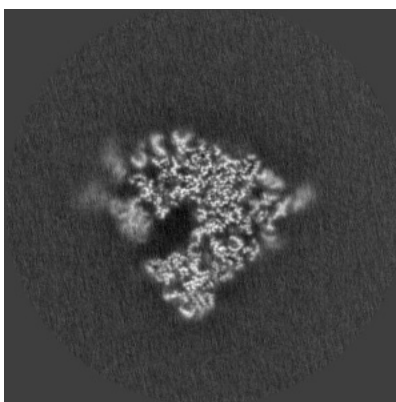


Z Index: 195

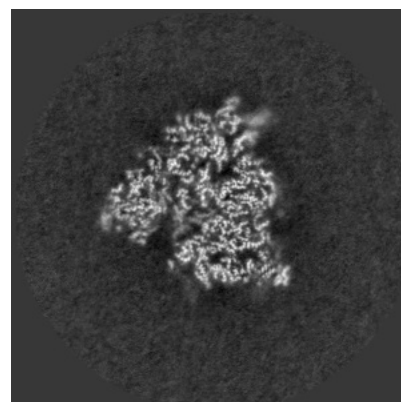
### 6.3.2 Raw map



X Index: 233



Y Index: 211



Z Index: 201

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

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

### 6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.4.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

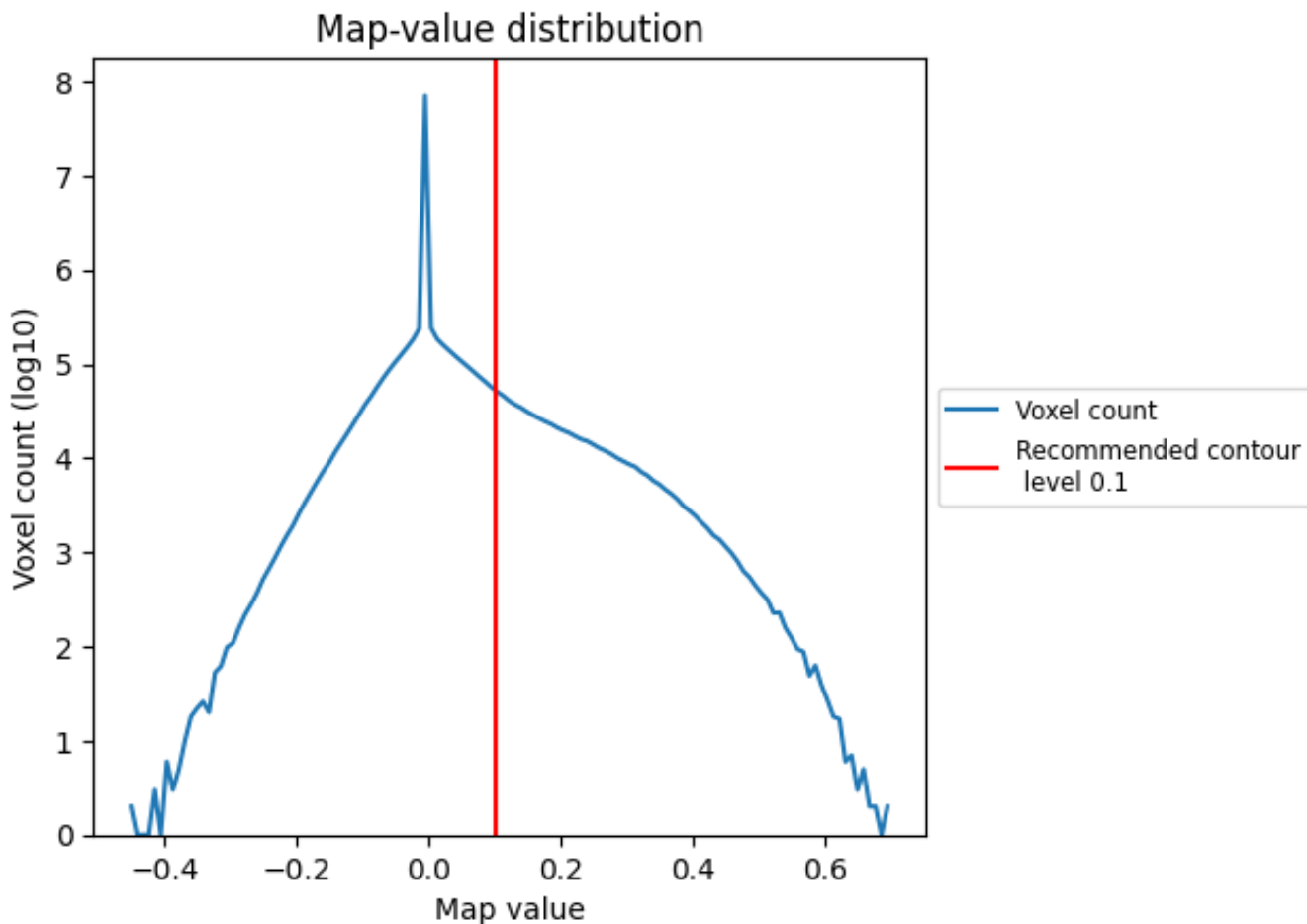
## 6.5 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

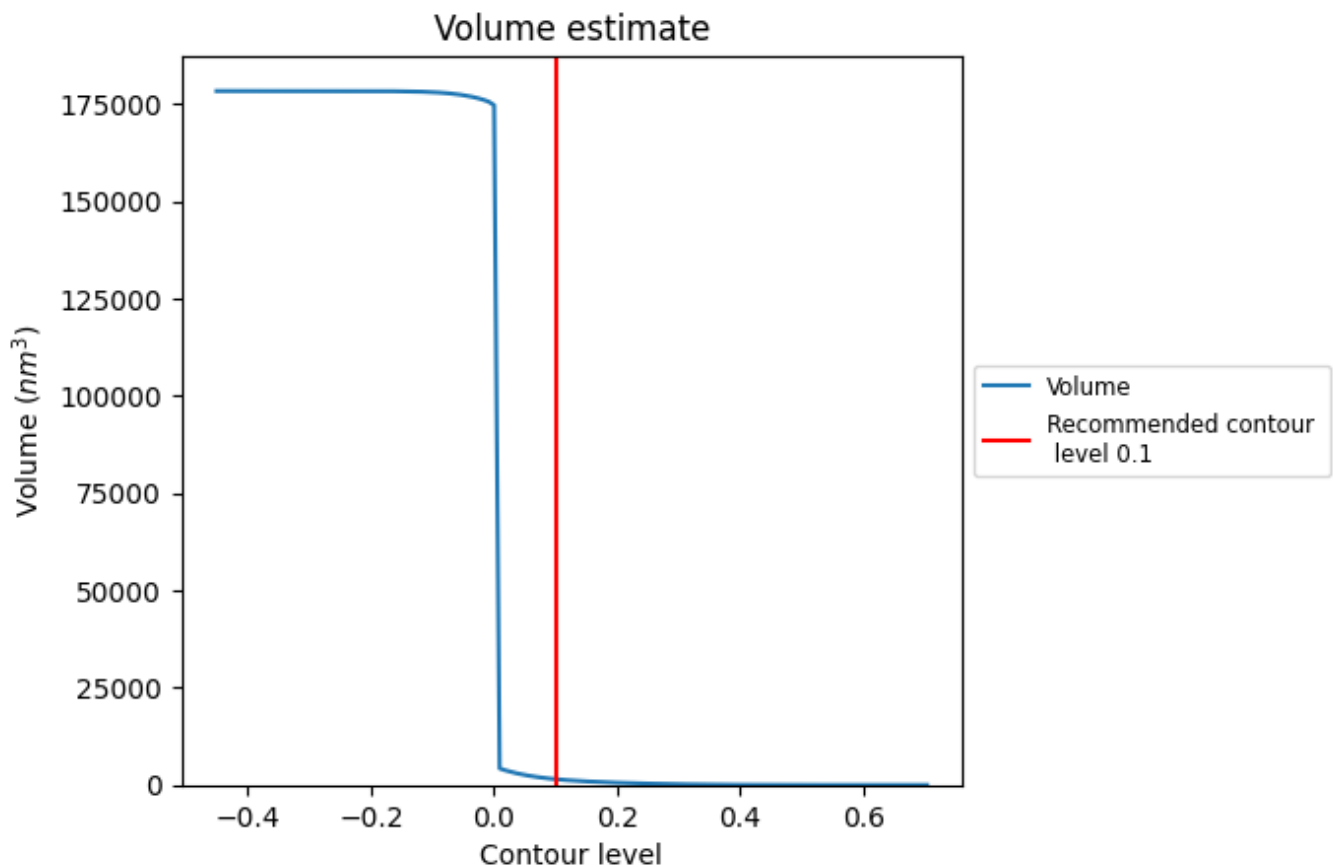
This section contains the results of statistical analysis of the map.

### 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](#)

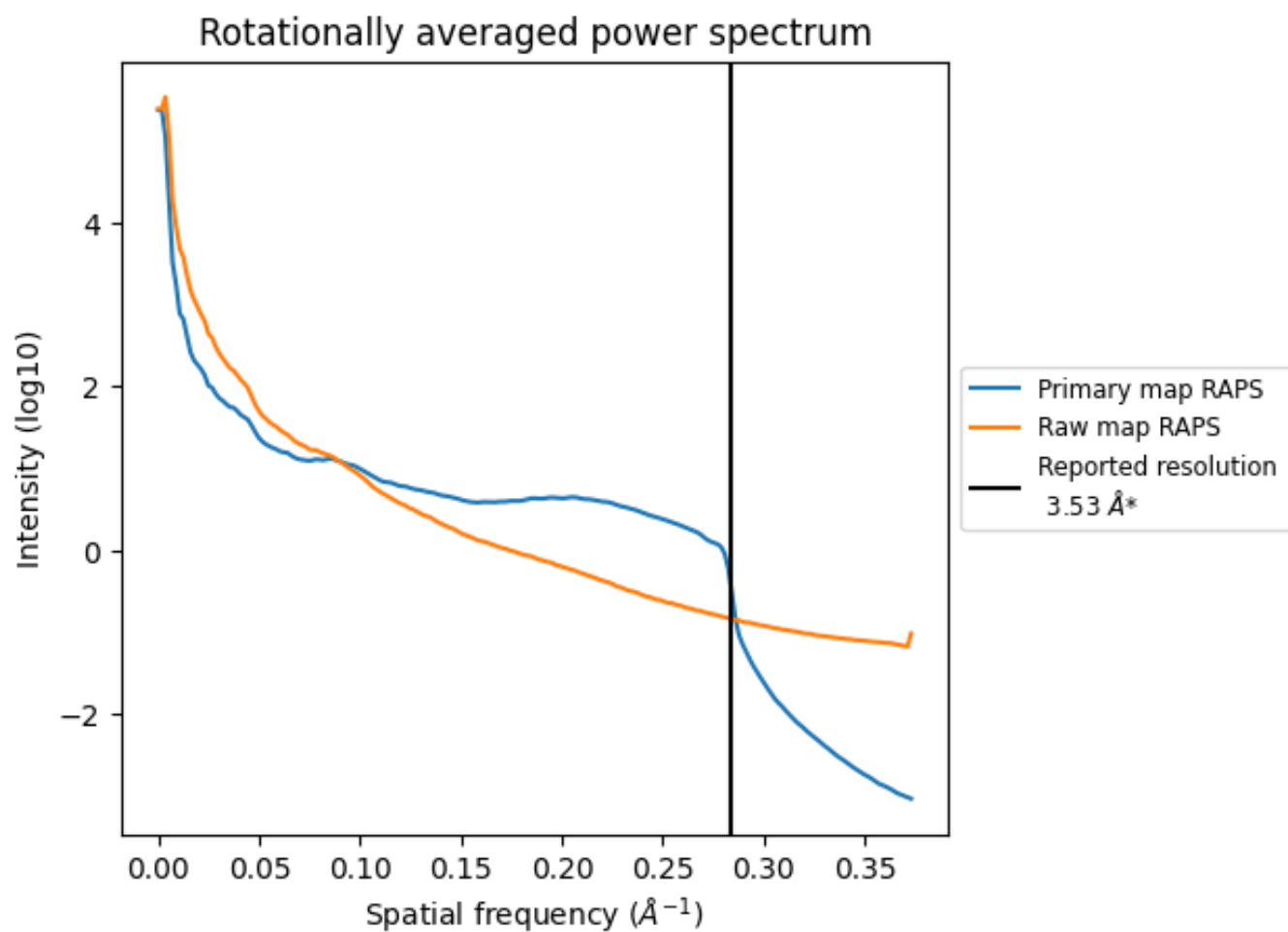


The volume at the recommended contour level is 1479 nm<sup>3</sup>; this corresponds to an approximate mass of 1336 kDa.

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 i

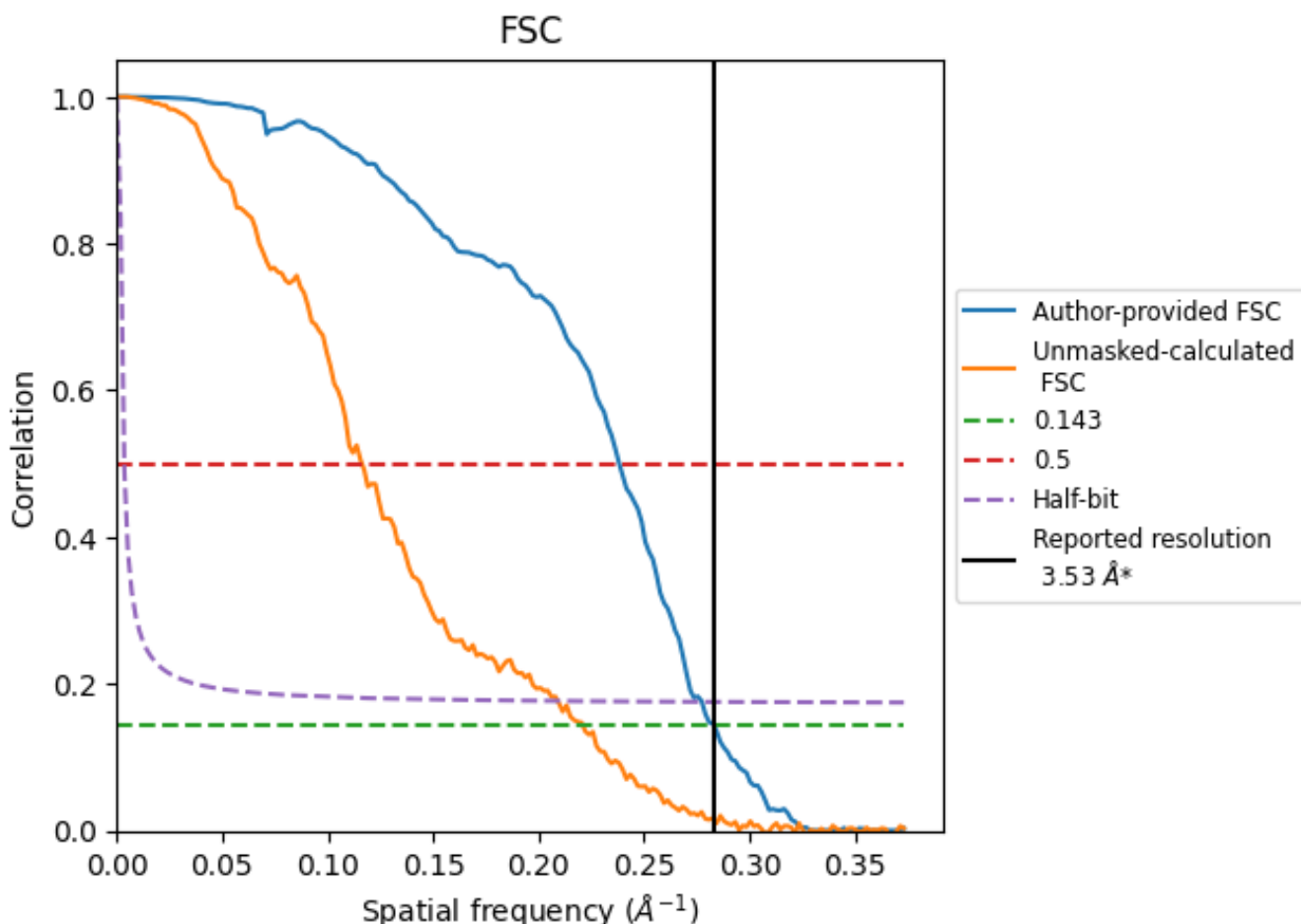


\*Reported resolution corresponds to spatial frequency of  $0.283 \text{ \AA}^{-1}$

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

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.283 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

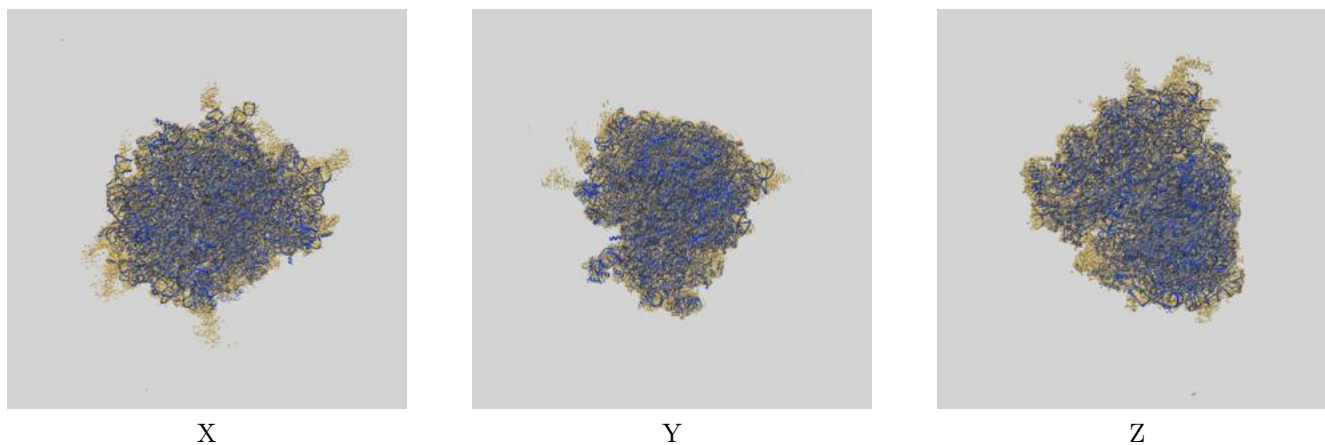
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.53	-	-
Author-provided FSC curve	3.53	4.20	3.61
Unmasked-calculated*	4.53	8.61	4.79

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.53 differs from the reported value 3.53 by more than 10 %

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

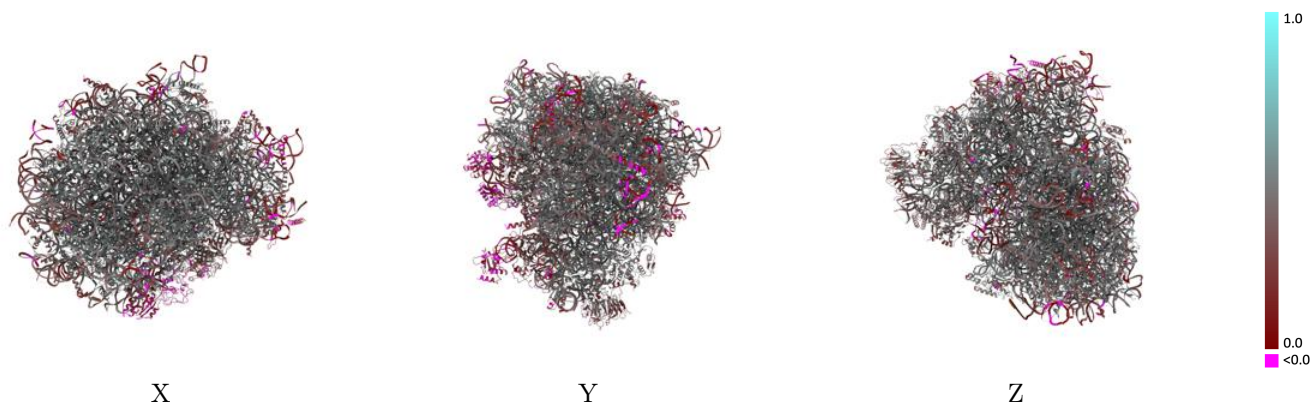
This section contains information regarding the fit between EMDB map EMD-4134 and PDB model 5LZW. Per-residue inclusion information can be found in section 3 on page 24.

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



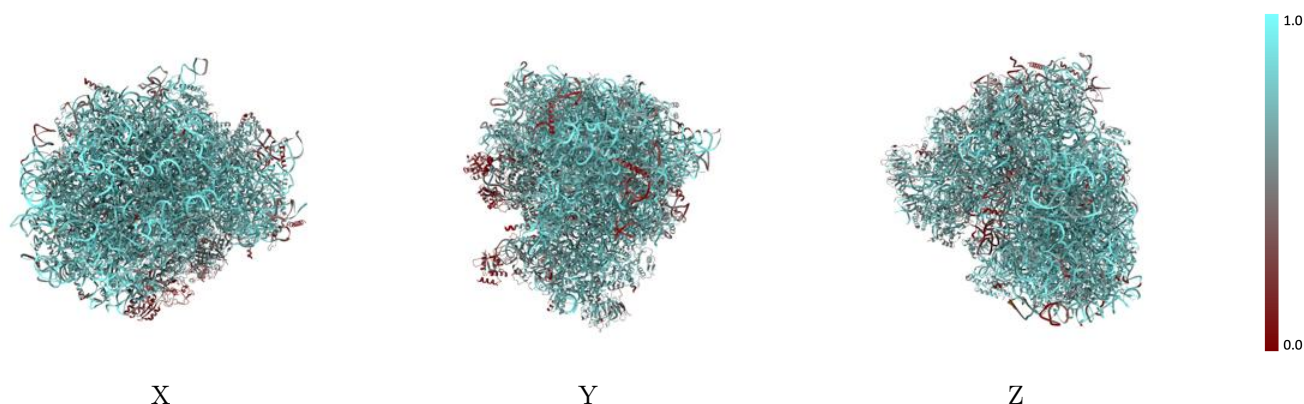
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



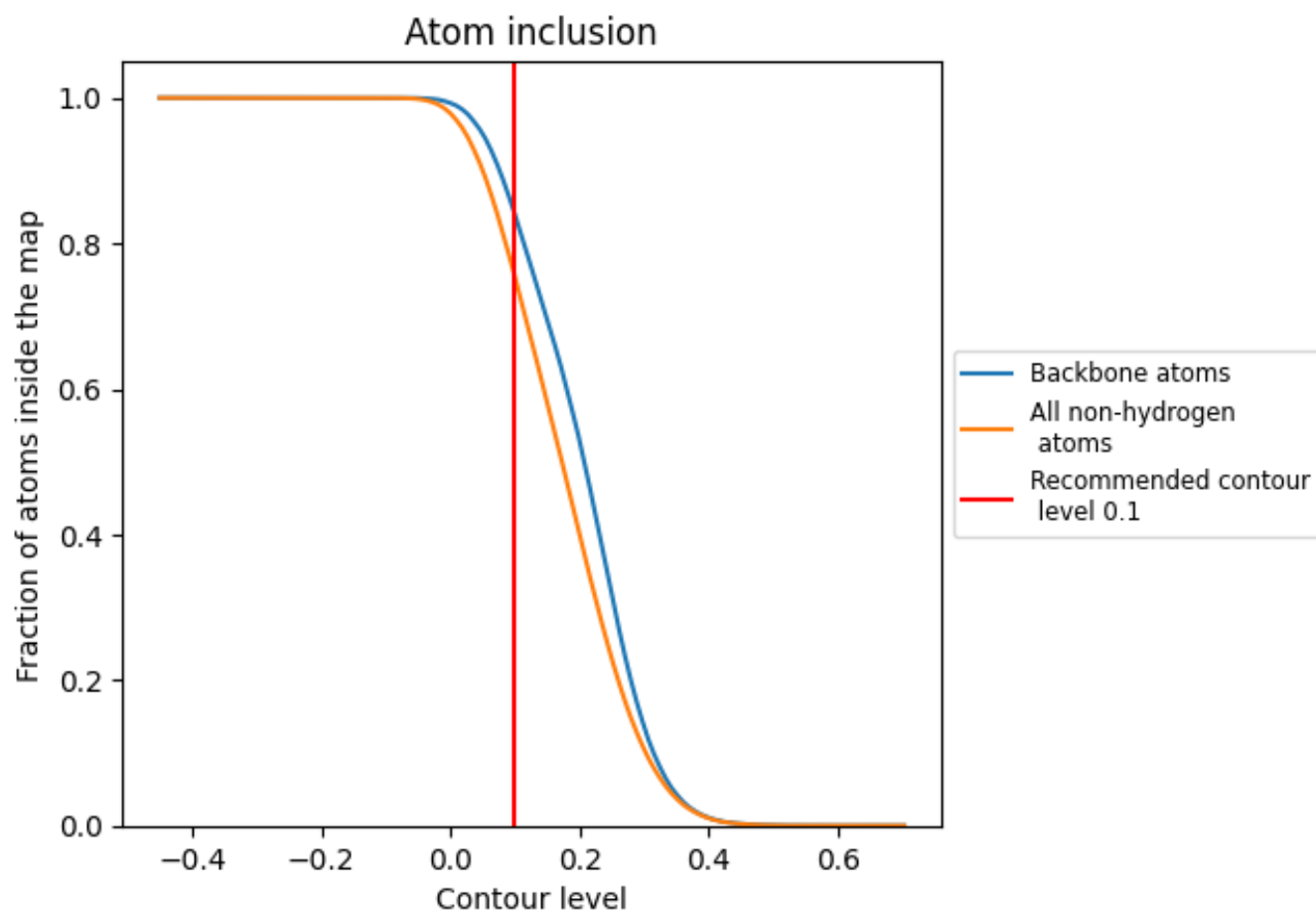
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.1).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 75% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary





















































































The table lists the average atom inclusion at the recommended contour level (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7534	 0.4220
1	 0.2066	 0.3400
2	 0.5582	 0.3580
3	 0.2078	 0.1650
5	 0.8374	 0.4320
7	 0.9075	 0.4740
8	 0.8457	 0.4320
9	 0.8142	 0.4080
A	 0.7569	 0.4930
AA	 0.7202	 0.4500
B	 0.7536	 0.4910
BB	 0.7028	 0.4540
C	 0.7529	 0.4830
CC	 0.7215	 0.4740
D	 0.7555	 0.4540
DD	 0.6243	 0.3920
E	 0.7612	 0.4670
EE	 0.6988	 0.4370
F	 0.7674	 0.4890
FF	 0.6704	 0.4260
G	 0.6373	 0.3990
GG	 0.6108	 0.3420
H	 0.7131	 0.4660
HH	 0.6112	 0.3890
I	 0.7505	 0.4900
II	 0.6878	 0.4320
J	 0.6927	 0.4320
JJ	 0.6894	 0.4280
KK	 0.5873	 0.3100
L	 0.7001	 0.4430
LL	 0.6965	 0.4600
M	 0.7716	 0.4730
MM	 0.2371	 0.0820
N	 0.7735	 0.4950
NN	 0.7247	 0.4650



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Chain	Atom inclusion	Q-score
O	 0.7679	 0.4870
OO	 0.7042	 0.4540
P	 0.7624	 0.4920
PP	 0.5306	 0.2700
Q	 0.7567	 0.4850
QQ	 0.6960	 0.4240
R	 0.6933	 0.4440
RR	 0.6368	 0.4140
S	 0.7720	 0.4950
SS	 0.6087	 0.3300
T	 0.7237	 0.4660
TT	 0.6954	 0.3830
U	 0.6726	 0.4010
UU	 0.6550	 0.4060
V	 0.7411	 0.4980
VV	 0.7106	 0.4550
W	 0.5764	 0.3400
WW	 0.7495	 0.4910
X	 0.7085	 0.4530
XX	 0.7021	 0.4730
Y	 0.7403	 0.4600
YY	 0.7136	 0.4130
Z	 0.7596	 0.4540
ZZ	 0.5780	 0.3210
a	 0.7715	 0.4960
aa	 0.7302	 0.4730
b	 0.6663	 0.3820
bb	 0.6761	 0.4240
c	 0.7231	 0.4430
cc	 0.6426	 0.4160
d	 0.7316	 0.4750
dd	 0.7557	 0.4520
e	 0.7593	 0.4890
ee	 0.6432	 0.4030
f	 0.7874	 0.5090
ff	 0.2680	 0.1100
g	 0.7268	 0.4690
gg	 0.5889	 0.3540
h	 0.6936	 0.4400
hh	 0.0710	 0.0650
i	 0.7010	 0.4260
ii	 0.4894	 0.3670

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Chain	Atom inclusion	Q-score
j	 0.7804	 0.4900
jj	 0.5236	 0.3550
k	 0.6391	 0.3900
l	 0.7190	 0.4620
m	 0.7356	 0.4750
n	 0.5596	 0.4330
o	 0.7131	 0.4720
p	 0.7228	 0.4760
r	 0.7764	 0.4940
s	 0.1636	 0.0900
t	 0.1063	 0.0190