



## wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 03:11 PM BST

PDB ID : 3JAH  
EMDB ID: : EMD-3039  
Title : Structure of a mammalian ribosomal termination complex with ABCE1, eRF1(AAQ), and the UAG stop codon  
Authors : Brown, A.; Shao, S.; Murray, J.; Hegde, R.S.; Ramakrishnan, V.  
Deposited on : 2015-06-10  
Resolution : 3.45 Å(reported)  
Based on PDB ID : 1DT9, 4V51, 3J7P, 3J92, 3BK7

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.  
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/EMValidationReportHelp>

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MolProbity : 4.02b-467  
Mogul : 1.7.1 (RC1), CSD as537be (2016)  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk27241

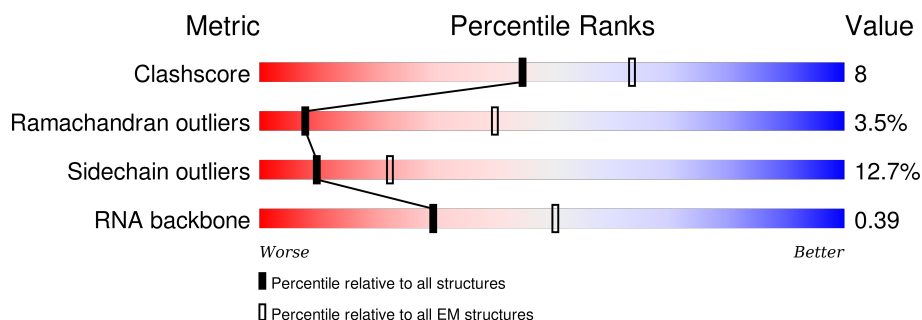
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.45 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.






















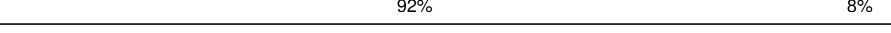





Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	244	76% 18% 5%
2	B	394	76% 21% .
3	C	362	71% 26% .
4	D	292	79% 18% .
5	E	248	65% 25% 5% 5%
6	F	225	76% 20% . .
7	G	241	78% 22% .
8	H	190	81% 17% .














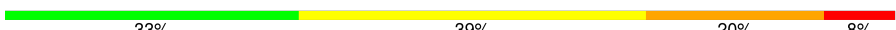


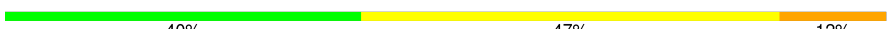
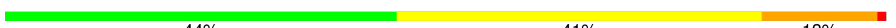







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Mol	Chain	Length	Quality of chain
9	I	213	
10	J	169	
11	L	210	
12	M	138	
13	N	203	
14	O	199	
15	P	153	
16	Q	187	
17	R	180	
18	S	175	
19	T	159	
20	U	99	
21	V	131	
22	W	63	
23	X	119	
24	Y	134	
25	Z	135	
26	a	147	
27	b	75	
28	c	94	
29	d	107	
30	e	128	
31	f	109	
32	g	114	
33	h	122	


























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Mol	Chain	Length	Quality of chain
34	i	102	 91% 9%
35	j	86	 83% 15%
36	k	69	 84% 14%
37	l	50	 84% 16%
38	m	52	 83% 17%
39	n	23	 83% 17%
40	o	104	 86% 13%
41	p	91	 92% 8%
42	r	125	 78% 18%
43	s	198	 90% 10%
44	t	163	 80% 20%
45	1	15	 73% 20% 7%
46	2	76	 59% 32% 8%
47	3	75	 33% 39% 20% 8%
48	5	3662	 46% 40% 13%
49	7	120	 63% 32% 5%
50	8	156	 40% 47% 12%
51	9	1719	 44% 41% 13%
52	AA	208	 70% 28%
53	BB	213	 73% 23%
54	CC	218	 74% 23%
55	DD	227	 81% 18%
56	EE	262	 65% 27% 7%
57	FF	191	 68% 28%
58	GG	237	 75% 21% 5%





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Mol	Chain	Length	Quality of chain
59	HH	189	 71% 24% 5%
60	II	206	 69% 30% .
61	JJ	185	 75% 18% 6% .
62	KK	98	 71% 27% .
63	LL	152	 70% 24% . .
64	MM	124	 75% 24% .
65	NN	150	 76% 22% .
66	OO	136	 67% 23% 7% .
67	PP	127	 75% 21% .
68	QQ	141	 77% 20% .
69	RR	129	 78% 19% .
70	SS	137	 74% 20% . .
71	TT	141	 79% 16% 5% .
72	UU	104	 75% 22% . .
73	VV	83	 73% 24% .
74	WW	129	 65% 29% 5% .
75	XX	141	 72% 23% 5%
76	YY	126	 73% 22% 5%
77	ZZ	75	 77% 23%
78	aa	98	 81% 19%
79	bb	83	 80% 20%
80	cc	61	 80% 20%
81	dd	53	 81% 19%
82	ee	57	 82% 16% .
83	ff	68	 87% . 9%

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Mol	Chain	Length	Quality of chain
84	gg	313	 90%9%
85	hh	12	 42%58%
86	ii	416	 89%10%
87	jj	594	 91%5%•

## 2 Entry composition

There are 91 unique types of molecules in this entry. The entry contains 226454 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
1	A	244	Total	C	N	O	S	0	0
			1868	1171	382	309	6		

- Molecule 2 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	394	Total	C	N	O	S	0	0
			3148	2007	591	537	13		

- Molecule 3 is a protein called uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	362	Total	C	N	O	S	0	0
			2884	1814	578	478	14		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	361	LYS	-	EXPRESSION TAG	UNP G1SVW5
C	362	LYS	-	EXPRESSION TAG	UNP G1SVW5
C	363	SER	-	EXPRESSION TAG	UNP G1SVW5

- Molecule 4 is a protein called uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	292	Total	C	N	O	S	0	0
			2386	1509	437	426	14		

- Molecule 5 is a protein called eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	236	Total	C	N	O	S	0	0
			1898	1215	362	318	3		

- Molecule 6 is a protein called uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 7 is a protein called eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	241	Total	C	N	O	S	0	0
			1934	1233	371	326	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	191	GLY	CYS	CONFLICT	UNP G1STW0

- Molecule 8 is a protein called uL6.

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

- Molecule 9 is a protein called uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	204	Total	C	N	O	S	0	0
			1655	1051	319	272	13		

- Molecule 10 is a protein called uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	169	Total	C	N	O	S	0	0
			1353	855	252	240	6		

- Molecule 11 is a protein called eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	210	Total	C	N	O	S	0	0
			1703	1065	354	280	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
			1638	1056	321	256	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	776	241	216	9		

- Molecule 16 is a protein called uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	187	Total	C	N	O	S	0	0
			1506	941	311	249	5		

- 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	175	Total	C	N	O	S	0	0
			1454	925	284	235	10		

- 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
			808	518	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	63	Total	C	N	O	S	0	0
			528	337	103	85	3		

- Molecule 23 is a protein called uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	119	Total	C	N	O	S	0	0
			976	624	183	168	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		

- Molecule 27 is a protein called eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	75	Total	C	N	O	S	0	0
			609	378	130	98	3		

- Molecule 28 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	c	94	Total	C	N	O	S	0	0
			732	465	130	131	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
			444	281	98	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	23	Total	C	N	O	S	0	0
			222	134	61	25	2		

- 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	125	Total	C	N	O	S	0	0
			1001	621	206	168	6		

- Molecule 43 is a protein called uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	s	198	Total	C	N	O	S	0	0
			1523	969	265	280	9		

- Molecule 44 is a protein called uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	t	163	Total	C	N	O	S	0	0
			1238	773	230	230	5		

- Molecule 45 is a protein called peptide.

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 tRNA(Val).

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 tRNA(Lys).

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	3662	Total	C	N	O	P	0	0
			78486	34947	14363	25515	3661		

- 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	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
51	9	1719	Total	C	N	O	P	0	0
			36680	16371	6586	12005	1718		

- Molecule 52 is a protein called uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	AA	208	Total	C	N	O	S	0	0
			1642	1045	289	300	8		

- Molecule 53 is a protein called eS1.

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

- Molecule 54 is a protein called uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	CC	218	Total	C	N	O	S	0	0
			1692	1102	287	296	7		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CC	194	ARG	HIS	CONFLICT	UNP G1TUT9
CC	228	GLY	SER	CONFLICT	UNP G1TUT9

- Molecule 55 is a protein called uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	DD	227	Total	C	N	O	S	0	0
			1764	1124	317	315	8		

- Molecule 56 is a protein called eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	EE	262	Total	C	N	O	S	0	0
			2073	1323	384	357	9		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
EE	25	GLY	SER	CONFLICT	UNP G1TK17

- Molecule 57 is a protein called uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	FF	191	Total	C	N	O	S	0	0
			1509	943	286	273	7		

- 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	189	Total	C	N	O	S	0	0
			1521	969	280	271	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	98	Total	C	N	O	S	0	0
			827	539	148	134	6		

- Molecule 63 is a protein called uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	LL	152	Total	C	N	O	S	0	0
			1238	788	232	212	6		

- Molecule 64 is a protein called eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	MM	124	Total	C	N	O	S	0	0
			958	600	170	179	9		

- Molecule 65 is a protein called uS15.



Mol	Chain	Residues	Atoms					AltConf	Trace
65	NN	150	Total	C	N	O	S	0	0
			1208	773	229	205	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	127	Total	C	N	O	S	0	0
			1060	673	201	179	7		

- Molecule 68 is a protein called uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	QQ	141	Total	C	N	O	S	0	0
			1124	715	212	194	3		

- Molecule 69 is a protein called eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	RR	129	Total	C	N	O	S	0	0
			1047	658	193	191	5		

- Molecule 70 is a protein called uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SS	137	Total	C	N	O	S	0	0
			1139	714	231	193	1		

- Molecule 71 is a protein called eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	TT	141	Total	C	N	O	S	0	0
			1102	692	212	195	3		

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
72	UU	104	Total	C	N	O	S	0	0
			821	514	155	148	4		

- Molecule 73 is a protein called eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	VV	83	Total	C	N	O	S	0	0
			636	394	118	119	5		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
VV	3	ASN	SER	CONFLICT	UNP G1TM82
VV	4	ASP	ASN	CONFLICT	UNP G1TM82
VV	50	PHE	SER	CONFLICT	UNP G1TM82
VV	75	ALA	SER	CONFLICT	UNP G1TM82

- Molecule 74 is a protein called uS8.

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

- Molecule 75 is a protein called uS12.

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

- Molecule 76 is a protein called eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	YY	126	Total	C	N	O	S	0	0
			1023	646	200	172	5		

- 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	98	Total	C	N	O	S	0	0
			781	486	161	129	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	61	Total	C	N	O	S	0	0
			475	290	92	91	2		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
cc	18	ILE	LEU	CONFLICT	UNP G1TIB4
cc	20	LYS	ARG	CONFLICT	UNP G1TIB4
cc	40	HIS	ARG	CONFLICT	UNP G1TIB4
cc	42	THR	ILE	CONFLICT	UNP G1TIB4

- Molecule 81 is a protein called uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	dd	53	Total	C	N	O	S	0	0
			445	278	90	72	5		

- Molecule 82 is a protein called eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	ee	57	Total	C	N	O	S	0	0
			457	282	101	73	1		

- Molecule 83 is a protein called eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	ff	62	Total	C	N	O	S	0	0
			520	331	98	85	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
ff	?	-	VAL	DELETION	UNP G1SK22

- Molecule 84 is a protein called RACK1.

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

- Molecule 85 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	hh	12	Total	C	N	O	P	0	0
			257	115	46	84	12		

- Molecule 86 is a protein called eRF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	ii	416	Total	C	N	O	S	0	0
			3280	2087	559	623	11		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
ii	183	ALA	GLY	ENGINEERED MUTATION	UNP P62495
ii	184	ALA	GLY	ENGINEERED MUTATION	UNP P62495

- Molecule 87 is a protein called ABCE1.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	jj	576	Total	C	N	O	S	0	0
			4543	2904	779	829	31		

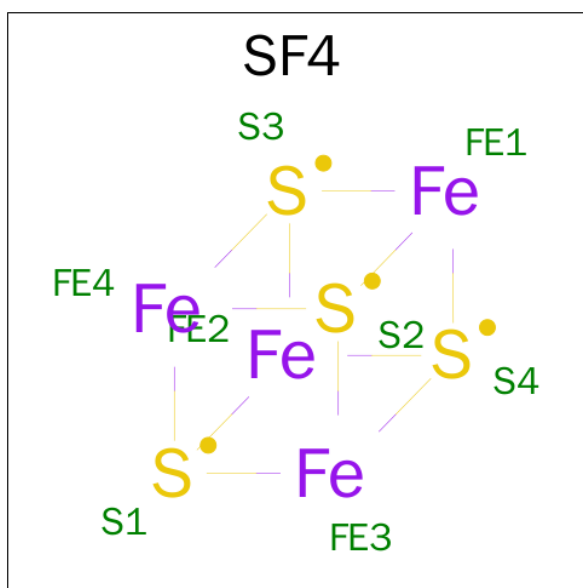
- Molecule 88 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
88	P	1	Total 1	Mg 1	0
88	g	1	Total 1	Mg 1	0
88	LL	1	Total 1	Mg 1	0
88	B	1	Total 1	Mg 1	0
88	I	1	Total 1	Mg 1	0
88	C	1	Total 1	Mg 1	0
88	V	1	Total 1	Mg 1	0
88	7	5	Total 5	Mg 5	0
88	5	146	Total 146	Mg 146	0
88	8	2	Total 2	Mg 2	0
88	9	34	Total 34	Mg 34	0
88	hh	1	Total 1	Mg 1	0

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

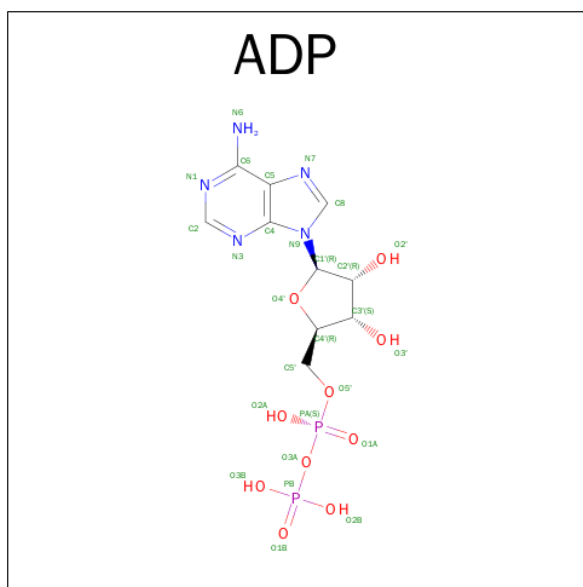
Mol	Chain	Residues	Atoms		AltConf
89	p	1	Total 1	Zn 1	0
89	g	1	Total 1	Zn 1	0
89	j	1	Total 1	Zn 1	0
89	dd	1	Total 1	Zn 1	0
89	ff	1	Total 1	Zn 1	0
89	aa	1	Total 1	Zn 1	0
89	o	1	Total 1	Zn 1	0
89	m	1	Total 1	Zn 1	0

- Molecule 90 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula:  $\text{Fe}_4\text{S}_4$ ).



Mol	Chain	Residues	Atoms			AltConf
90	jj	1	Total	Fe	S	0
			16	8	8	
90	jj	1	Total	Fe	S	0
			16	8	8	

- Molecule 91 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula:  $\text{C}_{10}\text{H}_{15}\text{N}_5\text{O}_{10}\text{P}_2$ ).

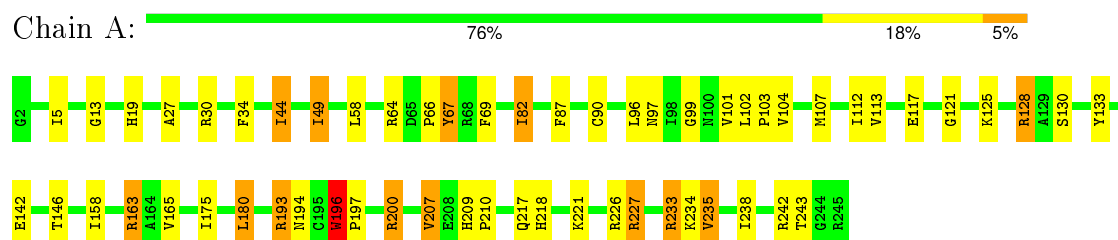


Mol	Chain	Residues	Atoms					AltConf
91	jj	1	Total	C	N	O	P	0
			54	20	10	20	4	
91	jj	1	Total	C	N	O	P	0
			54	20	10	20	4	

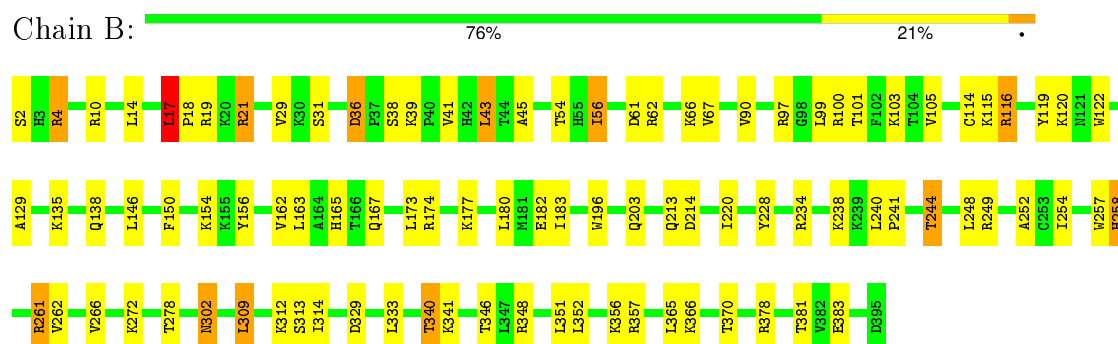
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.

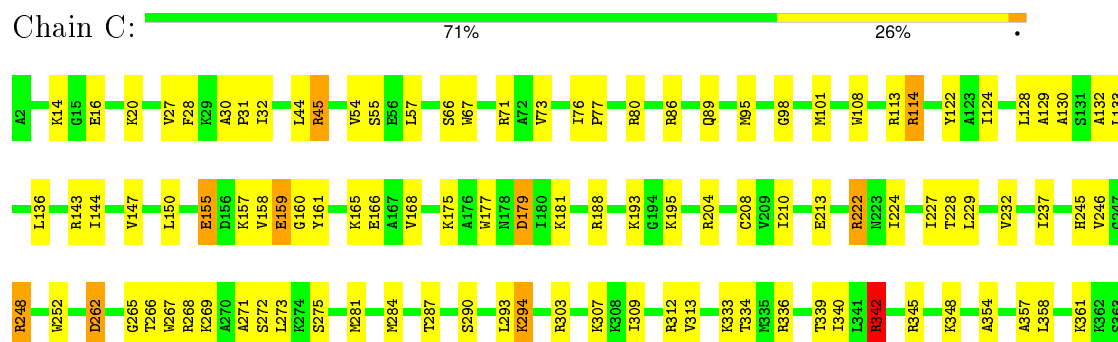
#### • Molecule 1: uL2



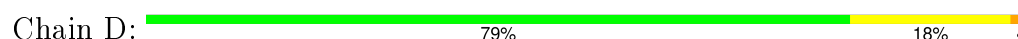
#### • Molecule 2: uL3



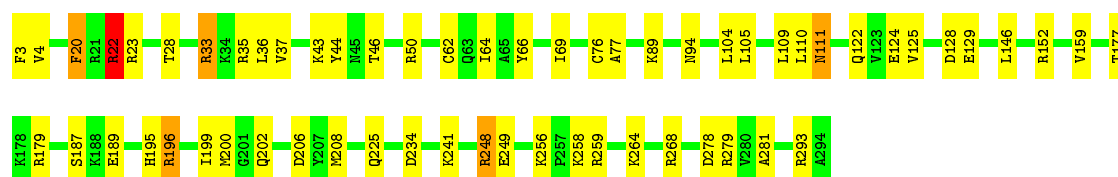
#### • Molecule 3: uL4



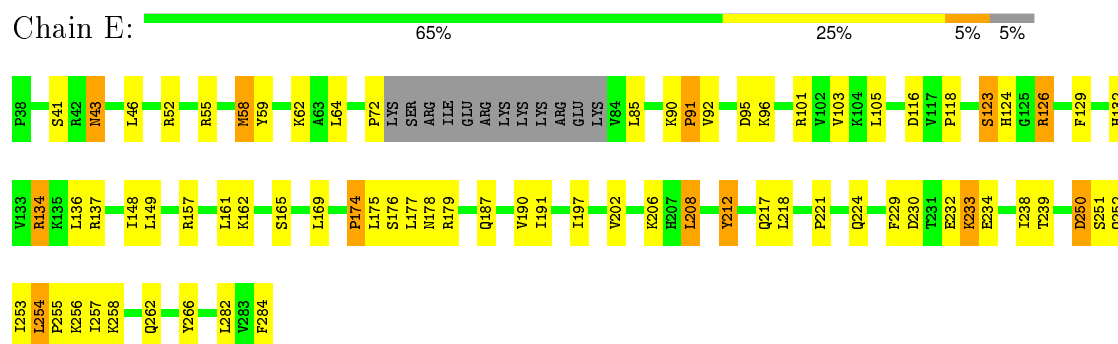
#### • Molecule 4: uL18



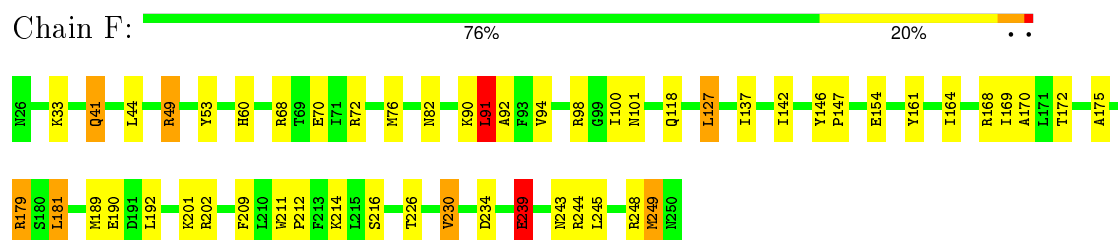




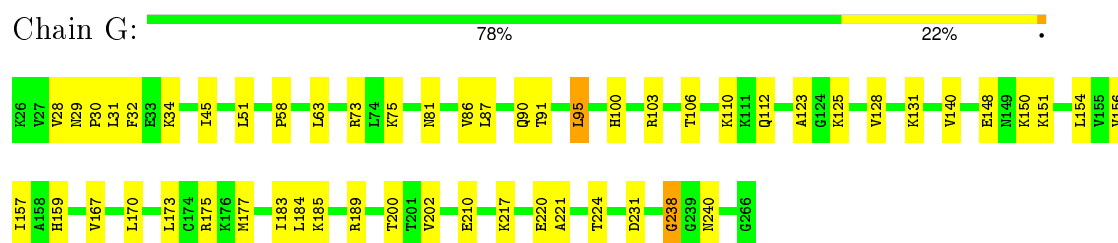
- Molecule 5: eL6



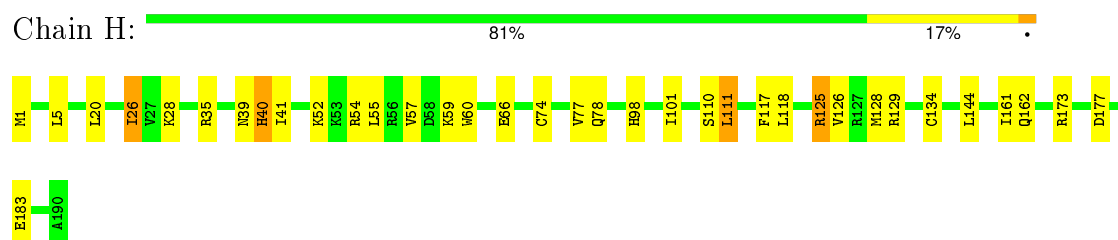
- Molecule 6: uL30



- Molecule 7: eL8

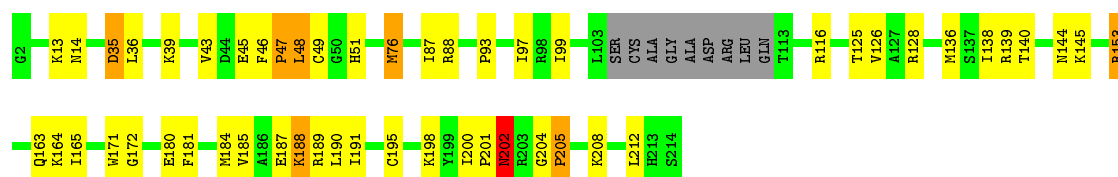


- Molecule 8: uL6



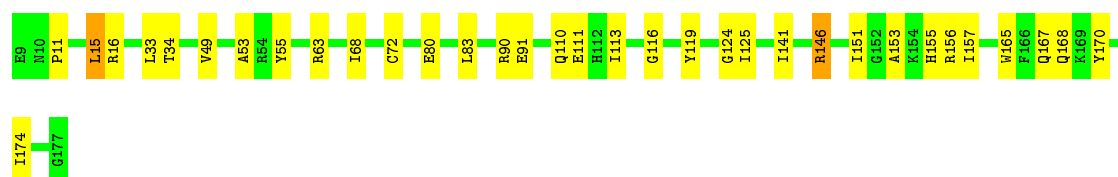
- Molecule 9: uL16





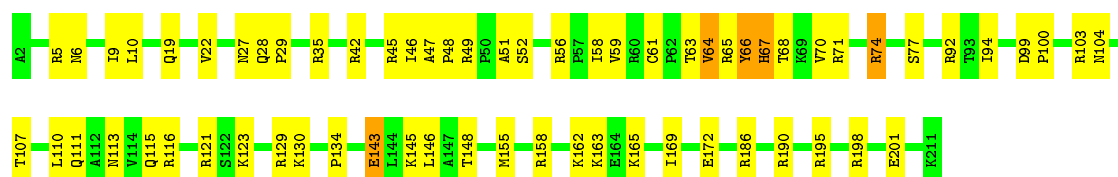
• Molecule 10: uL5

Chain J: 80% 19%



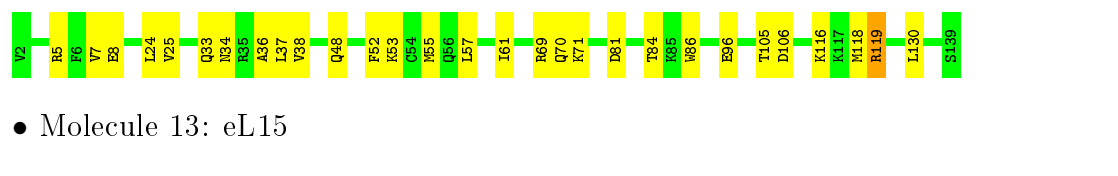
• Molecule 11: eL13

Chain L: 69% 29%



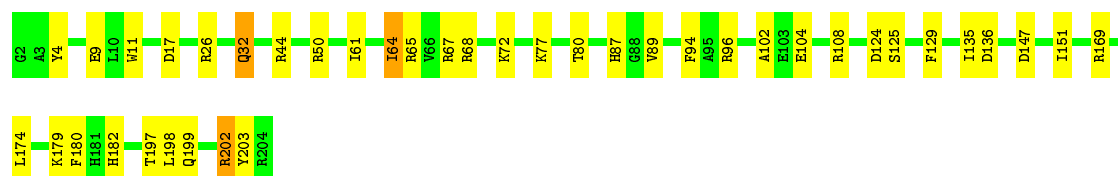
• Molecule 12: eL14

Chain M: 79% 20%



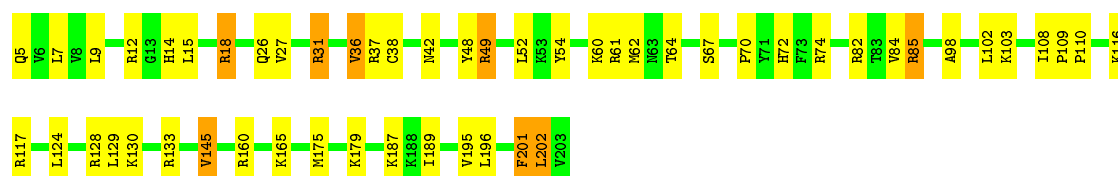
• Molecule 13: eL15

Chain N: 80% 18%




• Molecule 14: uL13

Chain O: 73% 23%




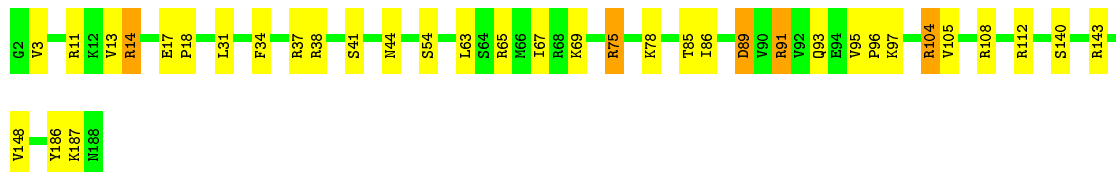
- Molecule 15: uL22

Chain P:  84% 14%



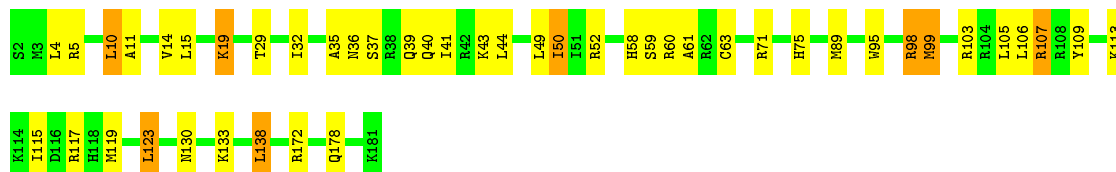
- Molecule 16: uL14

Chain Q:  81% 17%




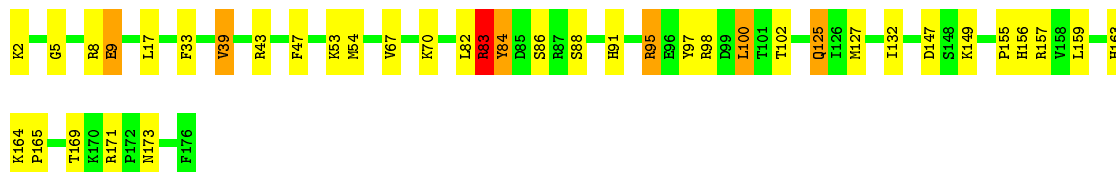
- Molecule 17: eL19

Chain R:  74% 21%




- Molecule 18: eL20

Chain S:  78% 18%




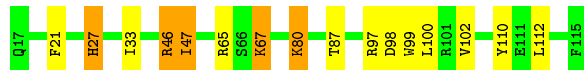
- Molecule 19: eL21

Chain T:  80% 19%




- Molecule 20: eL22

Chain U:  84% 11% 5%




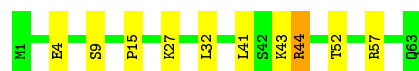
- Molecule 21: uL14

Chain V:  81% 18%




- Molecule 22: eL24

Chain W:  84% 14%




- Molecule 23: uL23

Chain X:  82% 16%



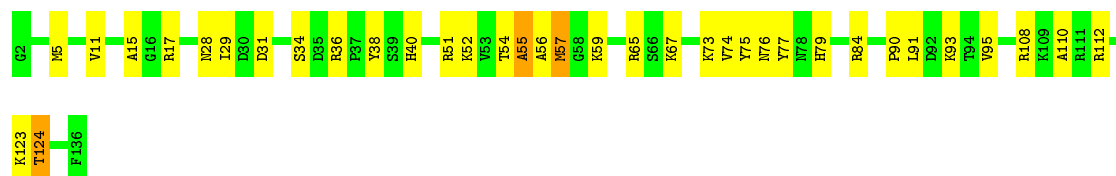
- Molecule 24: uL24

Chain Y:  81% 14%




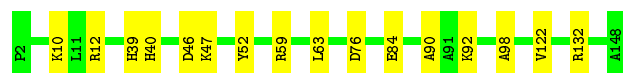
- Molecule 25: eL27

Chain Z:  73% 24%



- Molecule 26: uL15

Chain a:  89% 11%




- Molecule 27: eL29

Chain b:  92% 8%




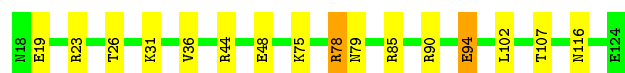
- Molecule 28: eL30

Chain c:  86% 14%




- Molecule 29: eL31

Chain d:  85% 13%




- Molecule 30: eL32

Chain e:  84% 16%




- Molecule 31: eL33

Chain f:  83% 17%




- Molecule 32: eL34

Chain g:  86% 13%




- Molecule 33: uL29

Chain h:  88% 11%




- Molecule 34: eL36

Chain i:  91% 9%

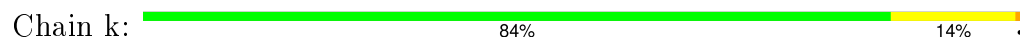


- Molecule 35: eL37

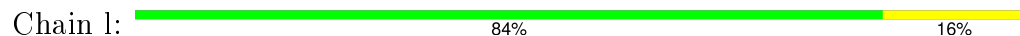
Chain j:  83% 15%



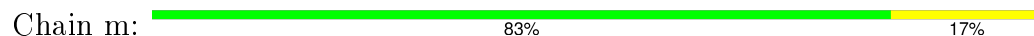
- Molecule 36: eL38



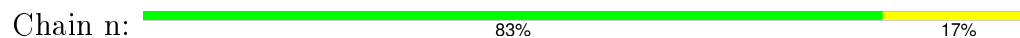
- Molecule 37: eL39



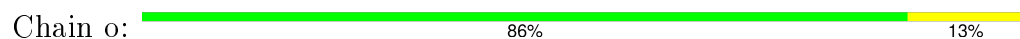
- Molecule 38: eL40



- Molecule 39: eL41



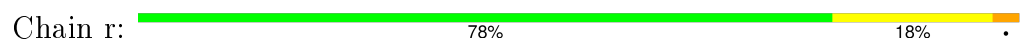
- Molecule 40: eL42



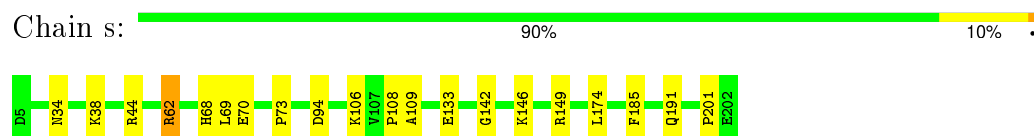
- Molecule 41: eL43



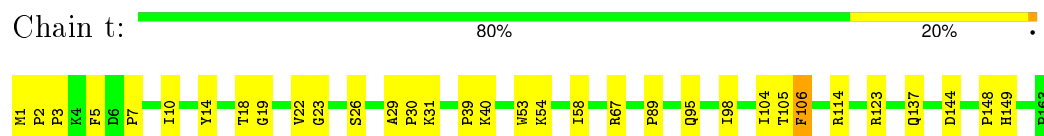
- Molecule 42: eL28



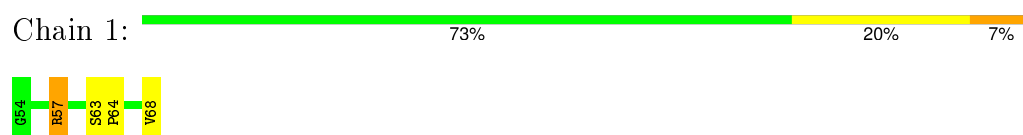
- Molecule 43: uL10



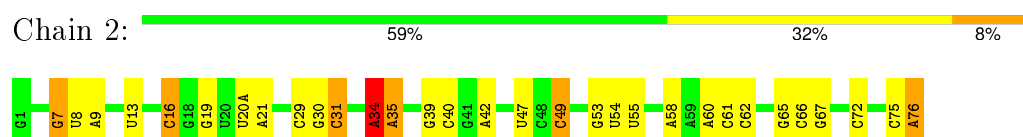
- Molecule 44: uL11



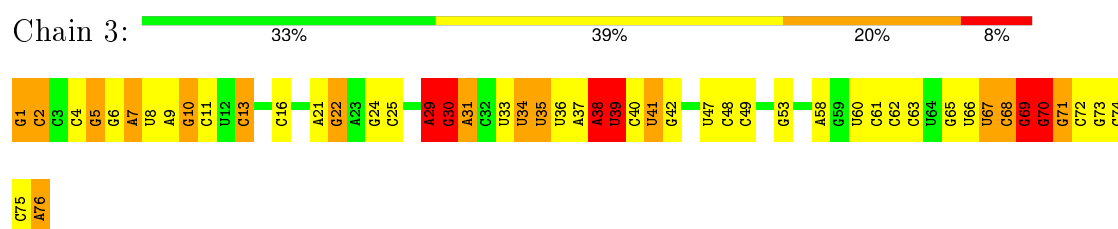
- Molecule 45: peptide



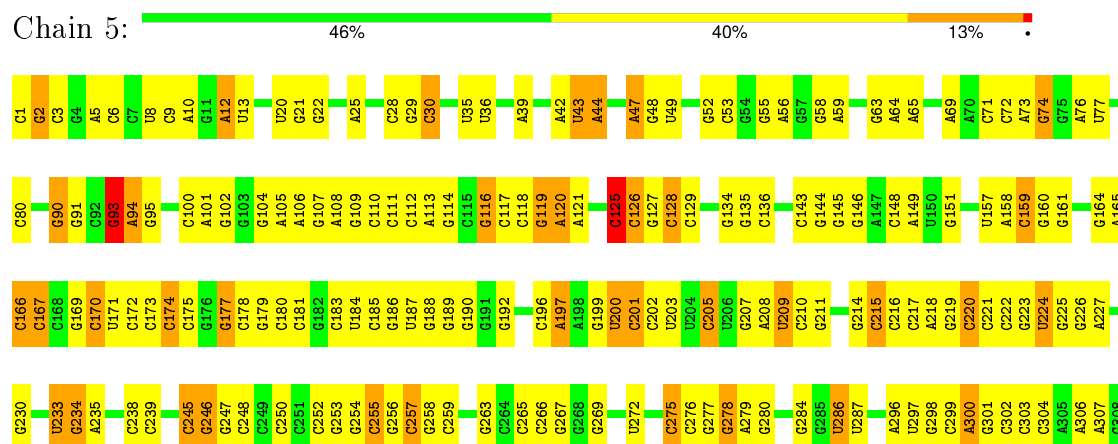
- Molecule 46: tRNA(Val)



- Molecule 47: tRNA(Lys)



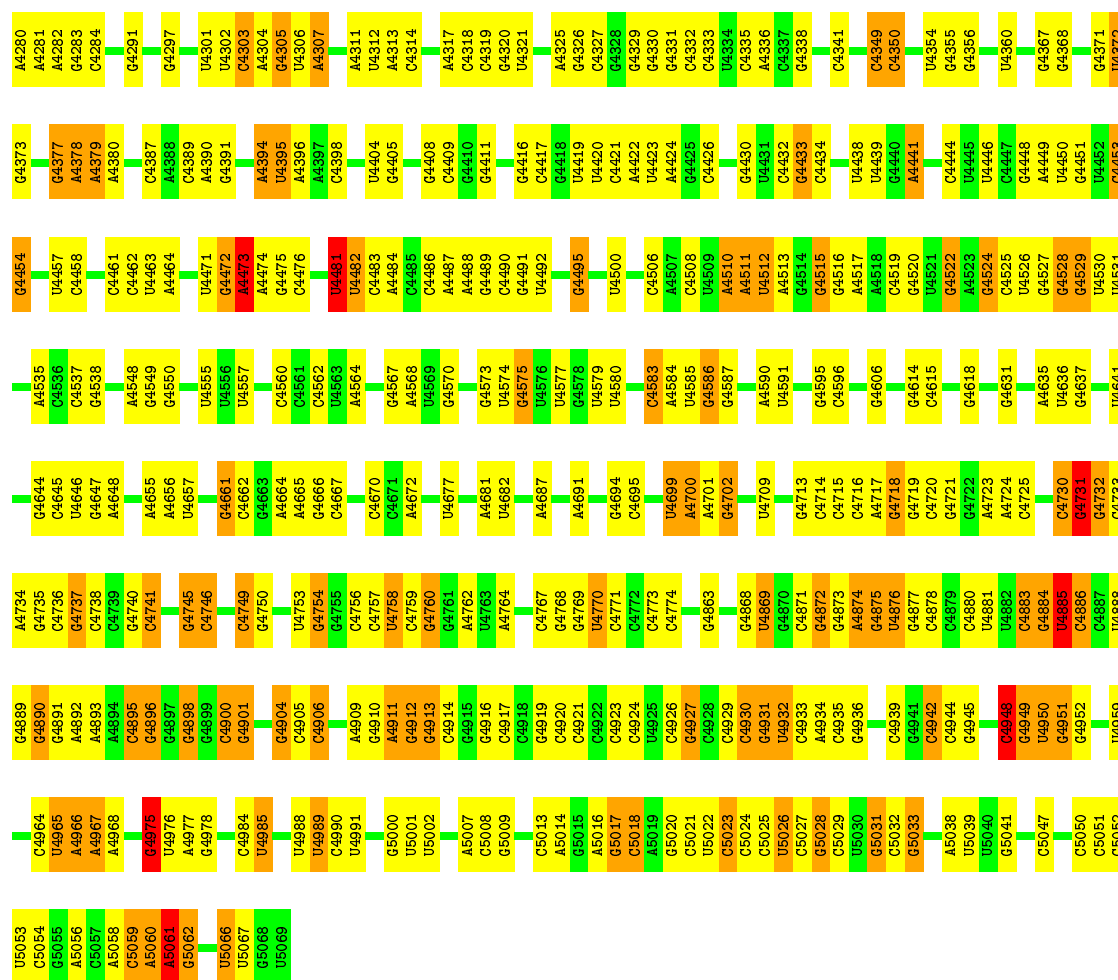
- Molecule 48: 28S ribosomal RNA



C1963	G1878	A1787	G1689	G1592	G1498	C1414	C1346	C1264	U1186	U982	A917	C693	C501	A407	C309
A1964	G1879	A1794	G1690	U1596	C1499	G1415	C1346	G1265	G1187	U982	G918	C694	C502	A408	G310
G1965	U1882	G1798	C1691	U1602	C1500	G1416	C1350	G1266	C1188	C983	C919	G695	C503	A409	G315
G1968	G1885	G1799	C1696	U1612	C1501	C1417	C1350	G1267	G1189	C984	C920	G696	C504	A410	G316
G1969	G1886	U1800	C1697	G1613	A1503	G1418	G1353	G1268	C1190	C985	C921	G697	C505	G411	U316
U1974	U1889	G1803	C1698	U1614	G1504	G1419	A1354	G1269	C1191	C986	C922	G698	C506	G412	A319
G1975	G1890	A1804	C1699	U1615	G1506	G1420	A1354	A1270	C1192	U989	C923	G699	G507	G413	C320
G1976	A1891	A1805	C1718	U1616	C1507	G1421	U1356	C1271	C1193	C990	C924	G700	G508	C422	C322
C1977	A1892	A1806	C1719	U1617	C1507	U1424	C1357	A1274	G1195	C991	G926	G702	U510	G423	C322
C1978	C1893	C1807	G1720	G1619	U1514	G1425	G1359	G1275	C1197	C993	C928	G704	U513	U325	U325
A1979	C1894	C1808	C1722	G1625	G1516	G1429	G1361	G1277	G1199	C995	A929	G706	U514	C326	C326
U1980	A1897	G1811	G1723	G1625	U1517	C1430	U1364	C1278	G1203	G1048	C931	G707	U515	U327	U327
G1981	C1898	C1812	A1724	U1726	A1518	C1431	C1365	A1279	C1204	C1049	A932	G708	A509	G432	A328
G1982	G1899	U1726	U1725	G1629	A1523	G1432	C1366	G1281	G1205	C1050	C934	G709	U518	U432	G330
A1984	C1900	G1815	C1732	A1630	A1524	G1435	C1367	G1282	C1206	G1051	C935	A711	G642	A434	G331
G1985	G1904	G1818	C1733	A1631	A1525	C1436	C1368	G1283	U1209	G1065	C937	G712	C643	C446	A334
U1986	U1910	G1819	G1734	A1633	A1533	C1439	C1370	U1285	C1210	G1066	C938	G715	G645	C447	A335
C1987	G1910	C1820	U1735	A1634	A1534	U1440	A1371	C1286	G1211	G1067	C939	G716	G646	C448	A336
G1988	G1911	G1821	A1736	C1635	A1534	C1441	A1372	G1287	G1212	G1068	C940	G718	G647	C449	U337
G1989	C1912	U1822	U1736	U1636	U1538	C1442	A1373	G1288	G1213	G1069	C941	G719	G648	G451	C340
A1990	C1913	G1823	G1741	A1637	U1539	U1445	G1374	C1289	G1214	G1070	G942	G721	A649	A452	C340
U1992	U1918	A1825	A1742	A1638	C1540	C1446	C1375	G1290	C1215	C1071	A943	G722	C654	G453	A347
C1993	G1919	G1826	A1743	U1639	C1541	U1447	C1376	G1291	C1216	C1072	A944	A723	C655	U454	G348
C1994	C1920	C1827	U1744	C1640	A1547	G1447	G1377	C1292	G1219	G1073	C945	G724	C656	C455	A349
G1995	G1921	G1828	G1745	G1641	A1547	G1448	C1378	G1293	G1220	G1074	C946	G725	C657	C458	C350
C1996	C1921	C1829	A1746	A1642	G1548	C1449	C1379	A1294	G1221	G1075	C947	G726	C657	C458	C351
U1997	G1922	G1830	A1746	A1643	G1549	C1450	G1380	C1295	A1222	C1076	C948	G727	C657	C458	G352
A1998	G1923	G1831	G1750	C1644	G1550	C1451	U1381	G1296	G1232	C1081	C952	G728	G663	G465	A353
U1999	C1924	C1832	A1751	G1654	C1551	C1454	G1382	U1297	G1233	C1082	G953	G729	G664	A466	G356
G2000	G1925	G1833	G1752	C1655	C1557	C1455	C1383	G1298	G1234	U1083	C954	G730	G665	A467	U357
G2001	C1926	U1834	G1753	U1656	C1567	C1456	C1384	U1301	G1235	U1083	C955	G731	G666	U468	C361
A2002	U1927	G1835	U1754	U1656	C1567	C1457	C1385	U1302	C1236	G1086	A956	A733	G667	A470	A362
G2003	C1928	G1836	C1755	U1660	A1563	G1464	C1386	A1303	C1237	C1086	G957	G737	G668	C472	A363
U2004	A1929	A1837	U1756	U1661	A1564	C1464	A1387	C1304	A1238	G1090	G958	G742	G671	C473	C368
C2005	U1930	U1838	U1757	C1661	A1565	G1465	C1387	C1309	C1239	C1091	G959	G743	C673	G476	G369
U2008	C1931	U1839	G1758	U1664	U1566	G1466	C1390	C1308	G1240	C1098	A960	G744	C674	G479	A371
A2009	A1932	G1840	G1759	U1664	U1567	C1467	G1394	C1309	G1241	C1098	C962	G745	C675	C480	U370
C2010	C1933	G1842	G1760	C1665	C1568	C1468	U1397	C1313	G1242	C1099	A964	A746	C676	G479	A371
C2011	C1935	G1846	G1761	C1666	C1568	C1468	A1397	C1322	G1243	C1107	C963	G747	C677	C481	G373
C2016	A1942	C1847	G1764	G1667	U1571	C1474	A1398	A1322	G1244	C1107	A965	A748	C678	G480	G373
A2017	U1947	G1854	C1768	A1668	U1572	G1475	C1399	A1326	G1245	C1109	C967	G749	C679	G481	G374
C2018	U1947	G1855	C1768	U1670	G1574	C1476	G1400	A1326	U1247	C1116	C968	G750	C682	G482	G375
C2019	G1952	C1856	U1771	U1672	U1578	C1478	C1401	G1327	C1248	G1170	C969	G751	G683	U484	A376
U2020	G1952	C1856	U1771	U1673	C1579	C1481	G1404	G1328	C1249	G1171	C970	G752	G684	C485	A376
C2021	G1955	C1772	C1772	U1673	C1580	G1482	C1405	A1329	C1252	C1172	G971	G756	G685	C486	A384
C2022	G1956	A1867	C1776	C1676	U1581	C1483	G1406	A1330	C1253	A1175	C972	G756	C686	G487	A385
C2023	A1956	A1868	U1776	U1677	U1582	G1484	C1407	A1337	A1255	C1176	C973	G756	C687	G488	A386
G2024	U1957	G1869	C1777	C1678	A1583	C1485	G1408	A1338	G1256	U1177	C974	U911	U687	C489	G387
A2025	A1958	G1872	C1777	C1678	A1584	C1486	C1409	U1339	G1259	C1181	C975	U912	U688	G497	G389
A2026	U1959	G1872	A1780	A1682	C1585	G1489	U1410	C1340	G1262	C1182	C976	U913	U689	C498	G399
U2027	C1961	A1874	U1781	U1683	G1586	G1499	C1411	C1344	G1262	C1183	C977	U914	C690	C499	U405
C2028	G1962	A1874	U1782	U1683	G1586	G1497	C1413	A1345	G1263	C1183	C978	U915	C691	G500	C406
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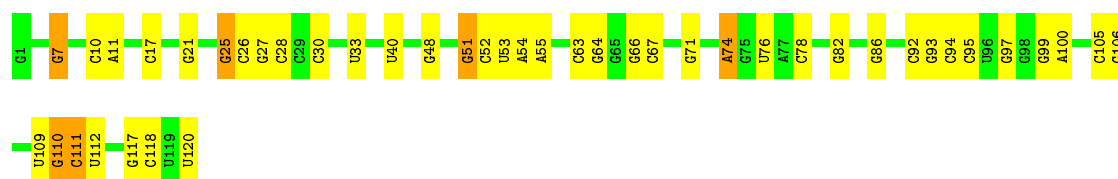


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U4208	C4126	U3940	C3855	G3675	C3587	A2796	G2721	U2554	C2482	C2382	A2282	C2035
U4209	A4127	G3941	C3855	U3680	G3590	A2806	U2722	G2556	U2485	C2383	G2107	
U4210	A4128	A3942	C3859	G3681	G3592	A2807	G2723	G2557	U2384	U2384	G2108	
A4211	C4129	G3765	A3861	A3682	G3593	C2814	G2724	G2558	C2488	U2385	G2109	
A4213	G4131	A3766	A3862	C3685	C3594	A2815	G2725	G2559	C2489	U2386	G2110	
	C4132			G3686	G3595	G2816	G2726	C2560	U2490	A2395	G2111	
G4216	C4133	U4069		G3686	A3596	G2817	C2727	U2561	C2491	A2396	G2112	
G4217	C4134	U4070	A3867	G3689	A3597	G2818	U2728	G2562	C2492	A2397	G2113	
U4218	G4135	U4071	G3868	U3689	A3598	C2819	G2729	G2563	C2493	G2397	G2114	
A4219	G4136	A4072	C3869	G3690	G3599	G2820	U2730	G2564	C2494	G2398	G2115	
A4220	A4137	A4073	C3870	G3691	A3599	G2821	G2731	G2565	U2495	G2399	G2116	
G4221	C4138	C4074	A3875	A3692	G3600	G2822	G2732	G2566	U2496	U2398	G2117	
G4222	G4139	U4075	A3876	G3693	G3601	A2823	C2733	G2567	G2497	G2399	G2118	
C4223	G4140	G4076	G3776	C3696	C3602	U2824	U2734	G2568	U2498	G2400	G2119	
A4224	G4141	A4077	U3778	U3697	G3603	G2825		G2569	C2499	A2300	G2120	
G4225	C4142	A3779	G3698	G3698	C3604	U2826	U2735	G2570	C2500	G2301	G2121	
G4226	G4143	G3780	G3800	G3699	G3605	U2827	U2736	G2571	A2417	C2302	G2122	
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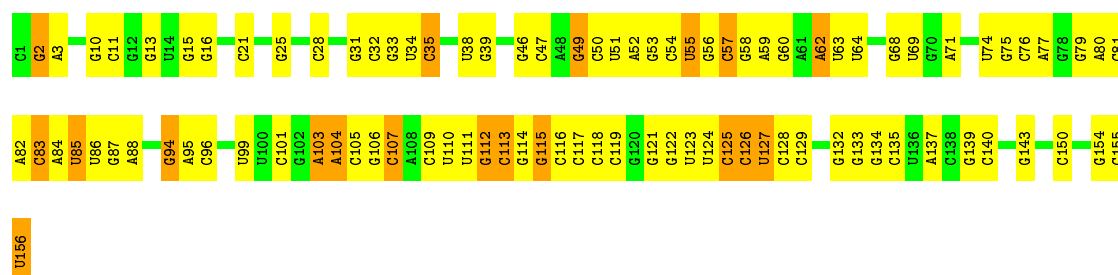
• Molecule 49: 5S ribosomal RNA

Chain 7: 63% 32% 5%



• Molecule 50: 5.8S ribosomal RNA

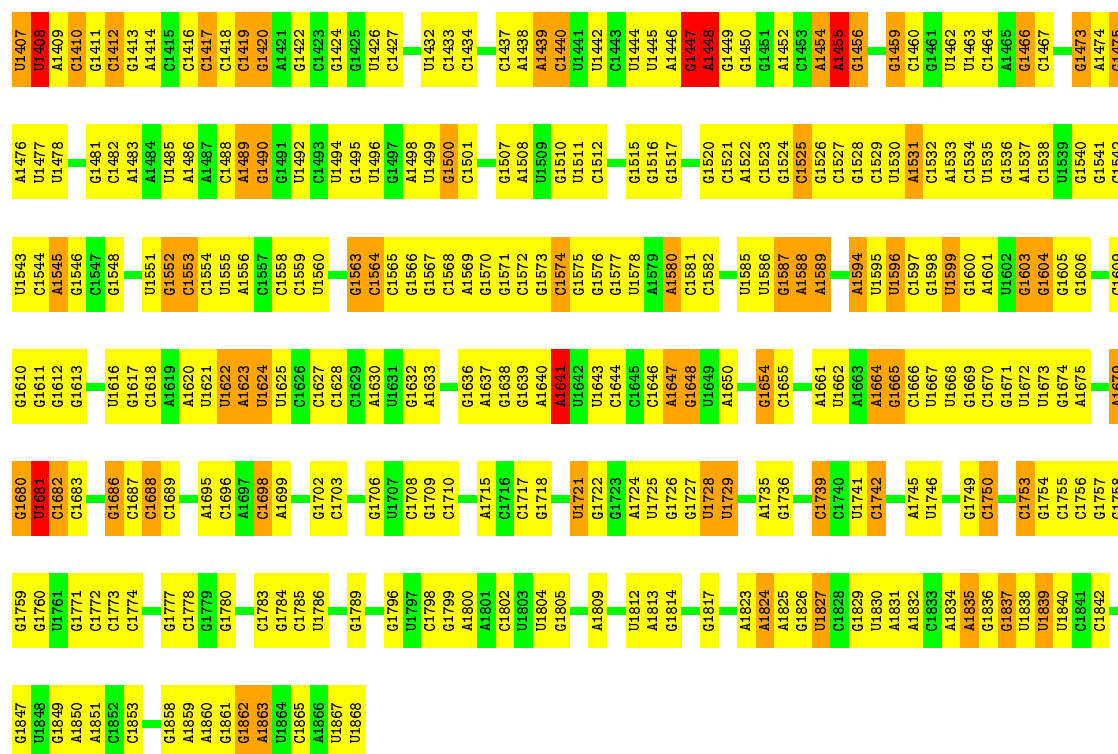
Chain 8: 40% 47% 12%



• Molecule 51: 18S ribosomal RNA

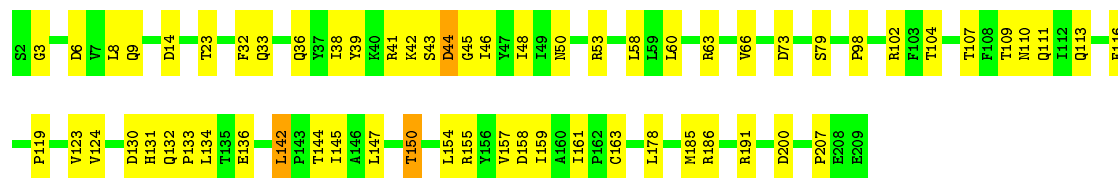
Chain 9: 

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G70	G71	C72	C73	G74	G75	U76	A77	C78	A79	G80	C86	U87	G88	C89	A92	U93	G94	G95	C96	A99	U100	C101	A102	G103	C107	G108	U109	U110	A111	U112	G113	G114	U115	U116	U119	G123	A209	U124	C125	G126	C139	U140	G141	C142	U143	U144	G145	A147	A150	C151	G155																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
G156	U157	A158	A159	U160	U161	C162	U163	A164	G165	A166	G167	C168	U172	A173	G180	U183	C182	G183	C96	A92	U93	G94	G95	C96	A99	U100	C101	A102	G103	C107	G108	U109	U110	A111	U112	G113	G114	U115	U116	U119	G123	A209	U124	C125	G126	C139	U140	G141	C142	U143	U144	G145	A147	A150	C151	G155																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																													
U294	A301	A302	C303	C304	U305	C306	G307	A308	G309	C310	C311	G312	A313	U314	G180	U183	C182	G183	C96	A92	U93	G94	G95	C96	A99	U100	C101	A102	G103	C107	G108	U109	U110	A111	U112	G113	G114	U115	U116	U119	G123	A209	U124	C125	G126	C139	U140	G141	C142	U143	U144	G145	A147	A150	C151	G155																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																													
U378	C379	G380	G383	U384	C385	G386	C391	A392	G393	C394	G395	C396	A397	U398	G401	U402	C403	G404	A405	U406	C407	A408	C409	G412	U416	C417	A418	U427	U428	C429	G432	A433	G434	A435	G436	G437	G438	C441	G446	A447	A448	A449	C450	U457	A458	C459	A460	C463	A464	G465	G466	G467	A468	A469																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
C472	A473	C474	A475	U476	C477	G478	C479	A480	C481	G482	C483	U487	A488	C489	A490	U491	C492	A493	A500	C501	G502	C503	G506	U507	A508	C509	G510	U511	A512	A516	A522	A523	U524	A525	A528	A529	U530	A531	C532	A533	G534	G535	C536	U537	A538	C539	A540	G541	C542	A543	G544	A545	G546	G547	C548	C549	C550	U551																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
G552	U553	A554	A555	U556	G557	C558	G559	A560	U561	G562	C563	A564	U565	A566	U567	C568	A569	G570	A583	A587	G588	C589	A590	U591	C592	A593	G594	U595	U596	G597	G598	A599	G600	C603	A604	A605	G606	U607	C608	U609	G613	C614	G620	C621	C622	C624	U627	A628	G629	U630	U631	C632																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
G635	C636	U637	C638	G639	A640	U641	G642	A643	U644	A654	U655	A656	U657	C658	A659	U660	C663	A664	G665	U666	C667	A668	U669	A670	C671	G672	U673	C674	U678	G684	A685	U686	C687	U688	U689	G696	C697	G698	C730	U731	G732	C733	C734	C735	G736	U737	C738	G746	U747	C748	U749	C750																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
G751	U752	C753	G754	U755	G756	C757	G758	U759	C760	A761	G762	C763	A764	U765	A766	U767	C768	A769	G770	U771	C772	A773	U774	G775	C776	U777	A778	C779	G780	U781	C782	A783	U784	G785	C786	U787	A788	C789	G790	U791	C792	A793	U794	G795	C796	U797	A798	C799	U800	A810	A811	A812	G821	U822	C823	A824	U827	G828	C829	A830	U831	G832	C833	A834	U835	G836	A837	G838	C839	U840	G841	C842	U843	G844	C845	U846	A847	C853	C856	G859	U860	A861	U869	A870	U871																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
A872	G873	U874	A875	C876	G877	U878	C879	A880	U881	G882	U883	A884	U885	G886	U887	C888	A889	U890	G891	U892	U893	G901	A902	C903	A908	G909	U910	C911	A912	U913	G914	A915	U916	C917	U918	A919	G920	U921	A922	C930	G933	U934	C935	G936	U937	A938	U942	A943	A944	U945	U946	G947	U948	A949	U950	C951	U956	A957	U958	C959	U960	G966	A967	U968	C969	U970	U971																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
G959	A963	U964	G965	U966	G967	U968	C969	A970	U971	G972	A973	U974	G975	C976	U977	A978	C979	U980	G981	U982	U983	G984	A985	U986	C987	U988	A989	U990	G991	U992	C993	A994	U995	G996	U997	A998	U999	C1000	A1001	U1002	G1003	U1004	A1005	U1006	C1007	A1008	U1009	G1010	U1011	C1012	A1013	U1014	G1015	C1016	U1017	A1018	U1019	C1020	A1021	U1022	C1023	G1024	U1025	A1026	U1027	C1028	U1029	G1030	U1031	C1032	A1033	U1034	G1035	C1036	U1037	A1038	U1039	G1040	C1041	U1042	A1043	U1044	C1045	A1046	U1047	C1048	U1049	G1050	A1051	U1052	C1053	U1054	A1055	U1056	C1057	A1058	U1059	G1060	U1061	C1062	A1063	U1064	G1065	C1066	U1067	A1068	U1069	C1070	A1071	U1072	C1073	A1074	U1075	G1076	C1077	A1078	U1079	C1080	U1081	G1082	A1083	U1084	C1085	U1086	A1087	U1088	C1089	U1090	G1091	A1092	U1093	C1094	A1095	U1096	C1097	A1098	U1099	G1100	C1101	A1102	U1103	G1104	C1105	A1106	U1107	C1108	U1109	G1110	C1111	A1112	U1113	G1114	C1115	A1116	U1117	C1118	A1119	U1120	G1121	C1122	A1123	U1124	G1125	C1126	U1127	A1128	C1129	G1130	U1131	C1132	A1133	U1134	G1135	C1136	U1137	A1138	U1139	G1140	C1141	U1142	A1143	U1144	C1145	U1146	A1147	C1148	U1149	G1150	C1151	A1152	U1153	G1154	C1155	U1156	A1157	U1158	C1159	U1160	G1161	C1162	A1163	U1164	G1165	C1166	A1167	U1168	C1169	U1170	G1171	C1172	A1173	U1174	G1175	C1176	A1177	U1178	C1179	A1180	U1181	G1182	C1183	U1184	A1185	U1186	C1187	A1188	U1189	G1190	C1191	A1192	U1193	G1194	C1195	A1196	U1197	C1198	A1199	U1200	G1201	C1202	A1203	U1204	G1205	C1206	U1207	A1208	U1209	G1210	C1211	A1212	U1213	G1214	C1215	A1216	U1217	C1218	A1219	U1220	G1221	C1222	A1223	U1224	G1225	C1226	U1227	A1228	C1229	G1230	U1231	C1232	A1233	U1234	G1235	C1236	U1237	A1238	U1239	G1240	C1241	A1242	U1243	G1244	C1245	A1246	U1247	G1248	C1249	A1250	U1251	C1252	A1253	U1254	G1255	C1256	U1257	A1258	U1259	G1260	C1261	A1262	U1263	G1264	C1265	U1266	A1267	C1268	U1269	G1270	C1271	A1272	U1273	G1274	C1275	A1276	U1277	G1278	C1279	A1280	U1281	G1282	C1283	U1284	A1285	U1286	C1287	A1288	U1289	G1290	C1291	A1292	U1293	G1294	C1295	A1296	U1297	G1298	C1299	U1300	A1301	G1302	C1303	U1304	A1305	U1306	C1307	A1308	U1309	G1310	C1311	U1312	A1313	U1314	G1315	C1316	U1317	A1318	U1319	G1320	C1321	A1322	U1323	G1324	C1325	A1326	U1327	G1328	C1329	U1330	A1331	U1332	G1333	C1334	U1335	A1336	U1337	G1338	C1339	U1340	A1341	U1342	G1343	C1344	U1345	A1346	U1347	G1348	C1349	U1350	A1351	U1352	G1353	C1354	U1355	A1356	U1357	G1358	C1359	U1360	A1361	U1362	G1363	C1364	U1365	A1366	U1367	G1368	C1369	U1370	A1371	U1372	C1373	A1374	U1375	G1376	C1377	A1378	U1379	G1380	C1381	U1382	A1383	U1384	G1385	C1386	U1387	A1388	U1389	G1390	C1391	U1392	A1393	U1394	G1395	C1396	U1397	A1398	U1399	G1400	C1401	U1402	A1403	U1404	G1405	C1406	U1407	A1408	U1409	G1410	C1411	U1412	A1413	U1414	G1415	C1416	U1417	A1418	U1419	G1420	C1421	A1422	U1423	G1424	C1425	A1426	U1427	G1428	C1429	U1430	A1431	U1432	G1433	C1434	U1435	A1436	U1437	G1438	C1439	U1440	A1441	U1442	G1443	C1444	U1445	A1446	U1447	G1448	C1449	U1450	A1451	U1452	G1453	C1454	U1455	A1456	U1457	G1458	C1459	U1460	A1461	U1462	G1463	C1464	U1465	A1466	U1467	G1468	C1469	U1470	A1471	U1472	G1473	C1474	U1475	A1476	U1477	G1478	C1479	A1480	U1481	G1482	C1483	U1484	A1485	U1486	G1487	C1488	U1489	A1490	U1491	G1492	C1493	U1494	A1495	U1496	G1497	C1498	U1499	A1500	U1501	G1502	C1503	U1504	A1505	U1506	G1507	C1508	U1509	A1510	U1511	G1512	C1513	U1514	A1515	U1516	G1517	C1518	U1519	A1520	U1521	G1522	C1523	U1524	A1525	U1526	G1527	C1528	U1529	A1530	U1531	G1532	C1533	U1534	A1535	U1536	G1537	C1538	U1539	A1540	U1541	G1542	C1543	U1544	A1545	U1546	G1547	C1548	U1549	A1550	U1551	G1552	C1553	U1554	A1555	U1556	G1557	C1558	U1559	A1560	U1561	G1562	C1563	U1564	A1565	U1566	G1567	C1568	U1569	A1570	U1571	G1572	C1573	U1574	A1575	U1576	G1577	C1578	U1579	A1580	U1581	G1582	C1583	U1584	A1585	U1586	G1587	C1588	U1589	A1590	U1591	G1592	C1593	U1594	A1595	U1596	G1597	C1598	U1599	A1600	U1601	G1602	C1603	U1604	A1605	U1606	G1607	C1608	U1609	A1610	U1611	G1612	C1613	U1614	A1615	U1616	G1617	C1618	U1619	A1620	U1621	G1622	C1623	U1624	A1625	U1626	G1627	C1628	U1629	A1630	U1631	G1632	C1633	U1634	A1635	U1636	G1637	C1638	U1639	A1640	U1641	G1642	C1643	U1644	A1645	U1646	G1647	C1648	U1649	A1650	U1651	G1652	C1653	U1654	A1655	U1656	G1657	C1658	U1659	A1660	U1661	G1662	C1663	U1664	A1665	U1666	G1667	C1668	U1669	A1670	U1671	G1672	C1673	U1674	A1675	U1676	G1677	C1678	U1679	A1680	U1681	G1682	C1683	U1684	A1685	U1686	G1687	C1688	U1689	A1690	U1691	G1692	C1693	U1694	A1695	U1696	G1697	C1698	U1699	A1700	U1701	G1702	C1703	U1704	A1705	U1706	G1707	C1708	U1709	A1710	U1711	G1712	C1713	U1714	A1715	U1716	G1717	C1718	U1719	A1720	U1721	G1722	C1723	U1724	A1725	U1726	G1727	C1728	U1729	A1730	U1731	G1732	C1733	U1734	A1735</



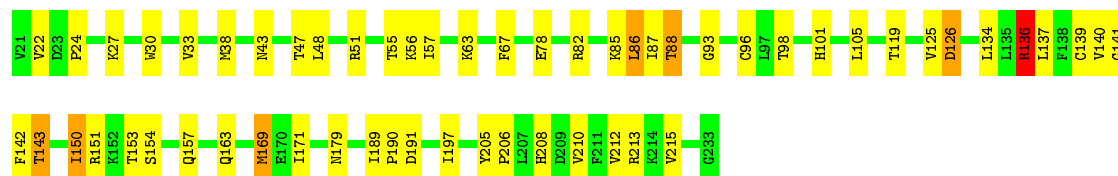
### • Molecule 52: uS2

Chain AA: 70% 28% .



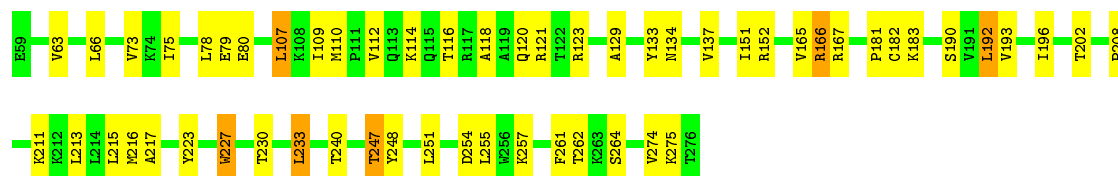
### • Molecule 53: eS1

Chain BB: 73% 23% .




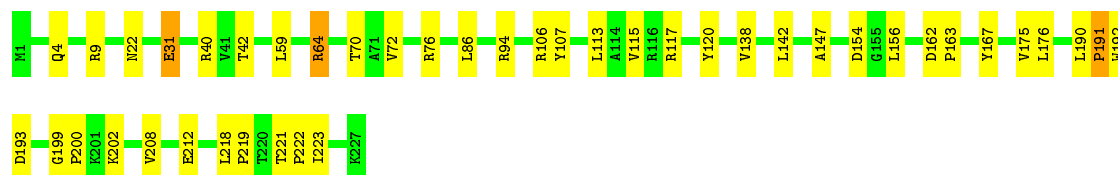
### • Molecule 54: uS5

Chain CC: 74% 23% .



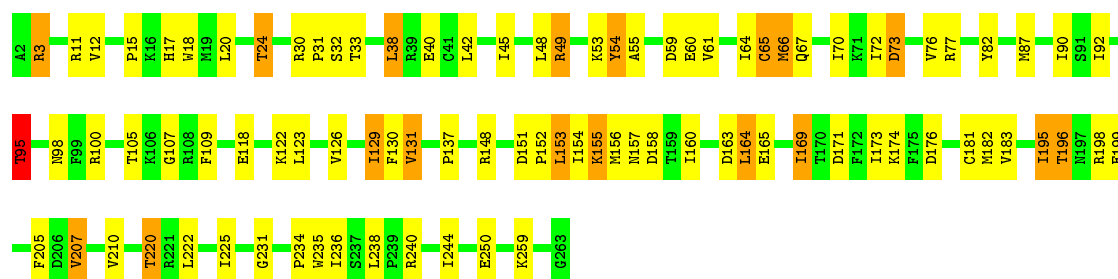
- Molecule 55: uS3

Chain DD: 



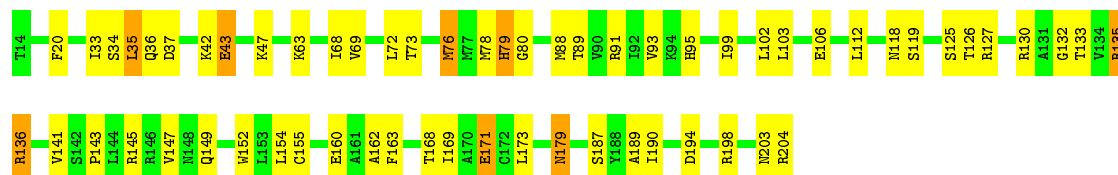
- Molecule 56: eS4

Chain EE: 




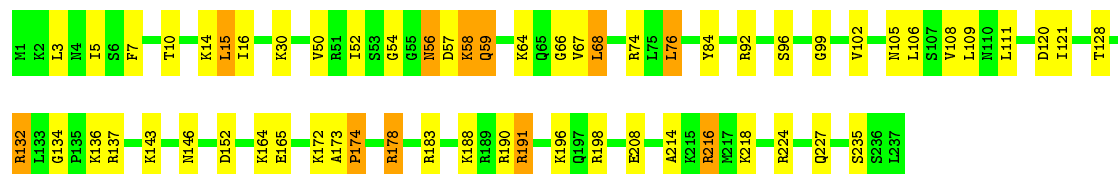
- Molecule 57: uS7

Chain FF: 



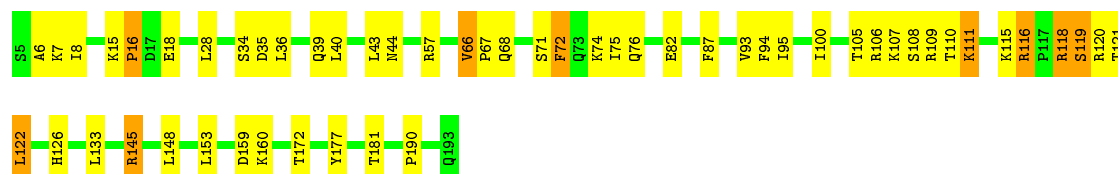
- Molecule 58: eS6

Chain GG: 



- Molecule 59: eS7

Chain HH: 

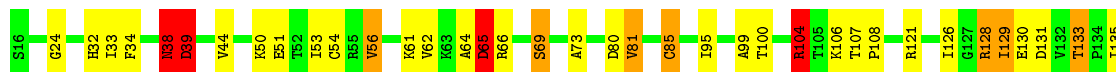


G2	R3	R4	R5	Q13	T24	I25	L26	K27	L28	L40	L45	V52	I53	I54	S57	V60	R64	F65	V66	K70	R73	I74	L75	K76	S77	K78	L84	R85	E86	D87	L88	K94	L102	K107	D110	R114	S120	R121	L125	Y126
----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------



• Molecule 66: uS11

Chain OO: 67% 23% 7% •



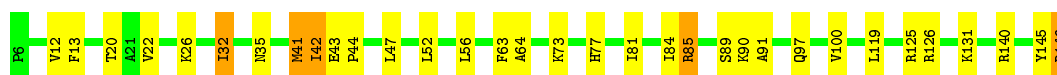
• Molecule 67: uS19

Chain PP: 75% 21% •



• Molecule 68: uS9

Chain QQ: 77% 20% •



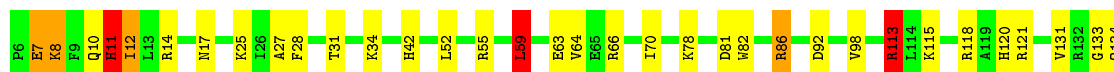
• Molecule 69: eS17

Chain RR: 78% 19% •



• Molecule 70: uS13

Chain SS: 74% 20% • •




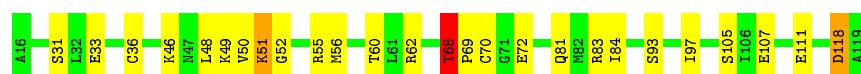
• Molecule 71: eS19

Chain TT: 79% 16% 5% •




• Molecule 72: uS10

Chain UU:  75% 22% ..



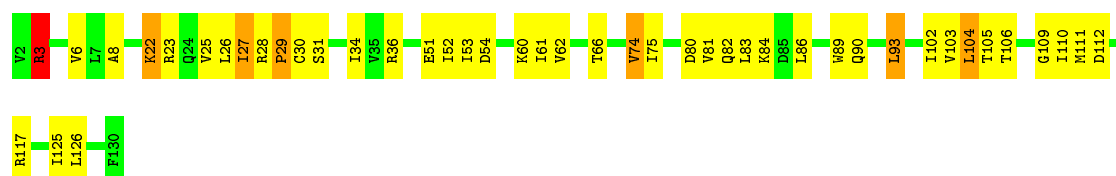
- Molecule 73: eS21

Chain VV:  73% 24% .



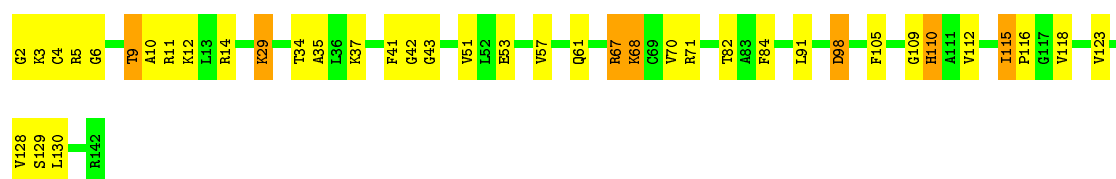
- Molecule 74: uS8

Chain WW:  65% 29% 5% .



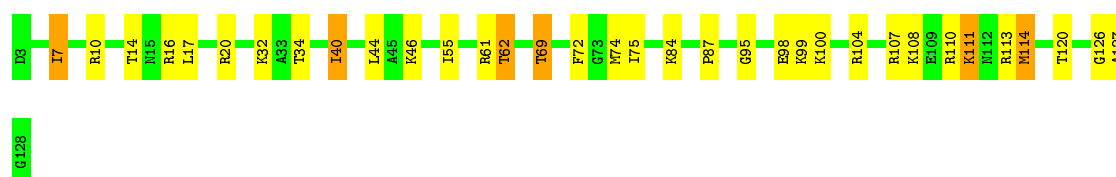
- Molecule 75: uS12

Chain XX:  72% 23% 5%




- Molecule 76: eS24

Chain YY:  73% 22% 5%




- Molecule 77: eS25

Chain ZZ:  77% 23%



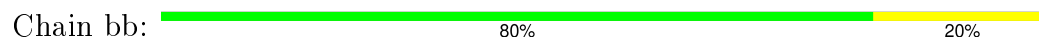
- Molecule 78: eS26

Chain aa:  81% 19%

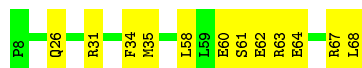




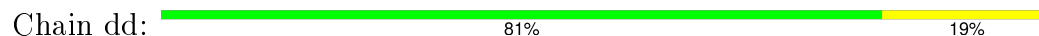
- Molecule 79: eS27



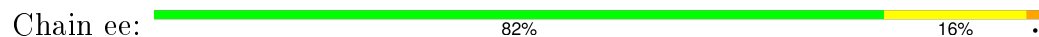
- Molecule 80: eS28



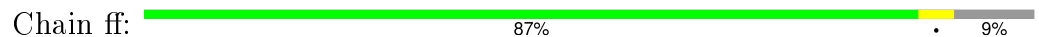
- Molecule 81: uS14



- Molecule 82: eS30



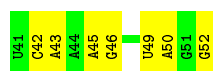
- Molecule 83: eS31



- Molecule 84: RACK1



- Molecule 85: mRNA

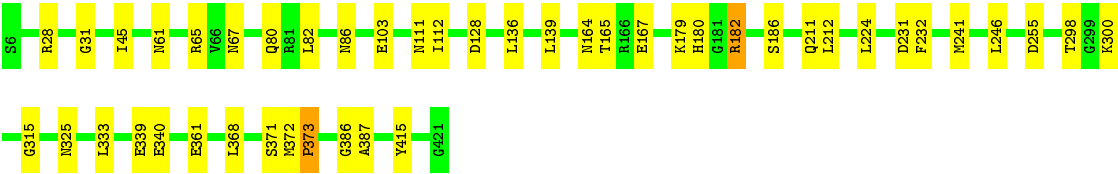


- Molecule 86: eRF1

Chain ii: 

89%

10%

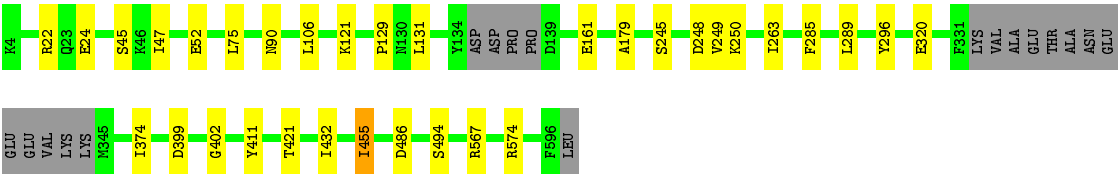


● Molecule 87: ABCE1

Chain jj: 

91%

5%



## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	20515	Depositor
Resolution determination method	FSC 0.143	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	30	Depositor
Minimum defocus (nm)	1700	Depositor
Maximum defocus (nm)	3600	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG, SF4, ADP

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  > 2$	RMSZ	# $ Z  > 2$
1	A	0.46	0/1906	0.79	0/2556
10	J	0.38	0/1376	0.73	0/1841
11	L	0.41	0/1734	0.79	0/2317
12	M	0.37	0/1158	0.74	0/1547
13	N	0.43	0/1746	0.83	0/2338
14	O	0.40	0/1671	0.77	0/2234
15	P	0.42	0/1268	0.75	0/1701
16	Q	0.41	0/1530	0.81	1/2041 (0.0%)
17	R	0.41	0/1524	0.79	0/2013
18	S	0.40	0/1493	0.85	3/2002 (0.1%)
19	T	0.41	0/1326	0.72	0/1770
2	B	0.40	0/3216	0.78	1/4311 (0.0%)
20	U	0.41	0/822	0.68	0/1103
21	V	0.40	0/993	0.73	0/1332
22	W	0.48	0/541	0.83	1/720 (0.1%)
23	X	0.42	0/993	0.74	0/1334
24	Y	0.37	0/1132	0.80	2/1504 (0.1%)
25	Z	0.39	0/1130	0.72	0/1507
26	a	0.40	0/1191	0.79	0/1590
27	b	0.44	0/619	0.73	0/818
28	c	0.36	0/742	0.69	0/996
29	d	0.38	0/903	0.81	1/1216 (0.1%)
3	C	0.43	0/2938	0.80	5/3946 (0.1%)
30	e	0.47	0/1071	0.85	0/1429
31	f	0.52	0/895	0.87	0/1198
32	g	0.42	0/916	0.81	1/1220 (0.1%)
33	h	0.36	0/1021	0.77	1/1348 (0.1%)
34	i	0.40	0/841	0.82	2/1112 (0.2%)
35	j	0.45	0/720	0.93	1/952 (0.1%)
36	k	0.37	0/575	0.68	0/761
37	l	0.50	0/454	0.84	0/599
38	m	0.37	0/435	0.76	0/575

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
39	n	0.41	0/223	0.91	0/284
4	D	0.37	0/2432	0.70	2/3257 (0.1%)
40	o	0.39	0/864	0.75	0/1140
41	p	0.42	0/718	0.71	0/953
42	r	0.48	0/1017	0.80	1/1364 (0.1%)
43	s	0.38	0/1547	0.58	0/2088
44	t	0.41	0/1257	0.69	0/1697
45	1	0.45	0/129	0.72	0/173
46	2	0.26	0/1805	0.72	1/2809 (0.0%)
47	3	0.36	0/1777	0.97	10/2763 (0.4%)
48	5	0.37	4/87790 (0.0%)	0.79	75/136937 (0.1%)
49	7	0.30	0/2858	0.69	0/4455
5	E	0.46	0/1936	0.82	2/2600 (0.1%)
50	8	0.36	0/3701	0.74	0/5766
51	9	0.32	1/41013 (0.0%)	0.79	45/63919 (0.1%)
52	AA	0.36	0/1679	0.70	0/2283
53	BB	0.38	0/1756	0.77	4/2350 (0.2%)
54	CC	0.41	0/1730	0.76	1/2344 (0.0%)
55	DD	0.37	0/1792	0.72	0/2412
56	EE	0.39	0/2115	0.78	0/2843
57	FF	0.49	0/1531	0.78	1/2059 (0.0%)
58	GG	0.37	0/1946	0.78	0/2590
59	HH	0.44	0/1544	0.72	1/2068 (0.0%)
6	F	0.40	0/1905	0.75	1/2539 (0.0%)
60	II	0.41	0/1715	0.78	0/2287
61	JJ	0.41	0/1550	0.88	4/2069 (0.2%)
62	KK	0.47	0/851	0.73	0/1147
63	LL	0.40	0/1259	0.78	0/1684
64	MM	0.42	0/968	0.64	0/1296
65	NN	0.39	0/1232	0.77	0/1656
66	OO	0.42	0/1029	0.88	1/1380 (0.1%)
67	PP	0.39	0/1079	0.76	0/1437
68	QQ	0.37	0/1142	0.70	0/1528
69	RR	0.42	0/1060	0.71	0/1421
7	G	0.38	0/1967	0.73	1/2647 (0.0%)
70	SS	0.38	0/1157	0.84	1/1548 (0.1%)
71	TT	0.43	0/1120	0.78	2/1499 (0.1%)
72	UU	0.36	0/831	0.71	0/1115
73	VV	0.39	0/645	0.75	0/865
74	WW	0.38	0/1051	0.79	0/1406
75	XX	0.38	0/1116	0.80	0/1490
76	YY	0.39	0/1040	0.74	0/1382
77	ZZ	0.37	0/604	0.75	0/810

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
78	aa	0.39	0/794	0.83	0/1065
79	bb	0.37	0/665	0.67	0/891
8	H	0.37	0/1535	0.71	0/2063
80	cc	0.36	0/478	0.78	0/640
81	dd	0.40	0/455	0.80	0/603
82	ee	0.46	0/462	0.75	0/607
83	ff	0.39	0/531	0.62	0/703
84	gg	0.37	0/2493	0.65	0/3394
85	hh	0.29	0/287	0.76	0/445
86	ii	0.39	0/3333	0.63	2/4483 (0.0%)
87	jj	0.47	1/4625 (0.0%)	0.58	0/6238
9	I	0.41	0/1693	0.69	0/2260
All	All	0.38	6/242712 (0.0%)	0.78	174/355683 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
11	L	0	3
17	R	0	1
18	S	0	2
19	T	0	1
2	B	0	4
20	U	0	1
24	Y	0	1
3	C	0	2
31	f	0	1
4	D	0	1
42	r	0	2
48	5	0	1
5	E	0	1
51	9	0	1
52	AA	0	1
56	EE	0	2
57	FF	0	2
59	HH	0	1
60	II	0	1
61	JJ	0	2
66	OO	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
68	QQ	0	1
7	G	0	1
70	SS	0	1
71	TT	0	1
72	UU	0	2
73	VV	0	1
74	WW	0	2
75	XX	0	1
78	aa	0	1
86	ii	0	3
9	I	0	2
All	All	0	49

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
48	5	1965	G	O3'-P	-23.01	1.33	1.61
87	jj	121	LYS	CE-NZ	19.94	1.99	1.49
51	9	908	A	O3'-P	8.98	1.72	1.61
48	5	1847	C	O3'-P	-6.16	1.53	1.61
48	5	957	G	O3'-P	5.62	1.67	1.61

The worst 5 of 174 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	9	909	G	O5'-P-OP2	-16.21	91.11	105.70
47	3	70	G	N9-C1'-C2'	-13.18	96.87	114.00
48	5	3753	G	N9-C1'-C2'	-11.91	98.52	114.00
51	9	1235	G	N9-C1'-C2'	-11.46	99.11	114.00
48	5	3718	A	N9-C1'-C2'	-10.30	100.61	114.00

There are no chirality outliers.

5 of 49 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	196	TRP	Peptide
2	B	17	LEU	Peptide
2	B	257	TRP	Peptide
2	B	258	HIS	Peptide
2	B	351	LEU	Peptide

## 5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1868	0	1959	31	0
2	B	3148	0	3267	55	0
3	C	2884	0	3062	45	0
4	D	2386	0	2419	31	0
5	E	1898	0	2035	66	0
6	F	1870	0	1994	27	0
7	G	1934	0	2087	32	0
8	H	1516	0	1597	10	0
9	I	1655	0	1704	45	0
10	J	1353	0	1386	16	0
11	L	1703	0	1820	22	0
12	M	1137	0	1211	16	0
13	N	1701	0	1749	18	0
14	O	1638	0	1777	31	0
15	P	1242	0	1269	12	0
16	Q	1506	0	1623	14	0
17	R	1508	0	1664	31	0
18	S	1454	0	1496	14	0
19	T	1298	0	1366	11	0
20	U	808	0	831	5	0
21	V	979	0	1039	5	0
22	W	528	0	541	5	0
23	X	976	0	1053	8	0
24	Y	1115	0	1205	6	0
25	Z	1107	0	1182	16	0
26	a	1162	0	1209	0	0
27	b	609	0	650	0	0
28	c	732	0	769	0	0
29	d	888	0	930	0	0
30	e	1053	0	1147	0	0
31	f	876	0	912	0	0
32	g	906	0	999	0	0
33	h	1013	0	1147	0	0
34	i	830	0	916	0	0
35	j	705	0	738	0	0
36	k	569	0	637	0	0
37	l	444	0	483	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	m	429	0	466	0	0
39	n	222	0	264	0	0
40	o	851	0	921	0	0
41	p	708	0	756	0	0
42	r	1001	0	1060	0	0
43	s	1523	0	1577	0	0
44	t	1238	0	1295	0	0
45	1	125	0	117	3	0
46	2	1616	0	824	18	0
47	3	1593	0	811	79	0
48	5	78486	0	39663	1322	0
49	7	2558	0	1296	27	0
50	8	3314	0	1683	53	0
51	9	36680	0	18529	615	0
52	AA	1642	0	1646	22	0
53	BB	1729	0	1803	15	0
54	CC	1692	0	1780	22	0
55	DD	1764	0	1863	8	0
56	EE	2073	0	2175	45	0
57	FF	1509	0	1562	28	0
58	GG	1923	0	2089	29	0
59	HH	1521	0	1616	20	0
60	II	1686	0	1772	30	0
61	JJ	1525	0	1640	22	0
62	KK	827	0	854	7	0
63	LL	1238	0	1315	17	0
64	MM	958	0	993	3	0
65	NN	1208	0	1294	8	0
66	OO	1016	0	1039	14	0
67	PP	1060	0	1120	13	0
68	QQ	1124	0	1193	11	0
69	RR	1047	0	1103	9	0
70	SS	1139	0	1191	17	0
71	TT	1102	0	1142	11	0
72	UU	821	0	883	6	0
73	VV	636	0	634	9	0
74	WW	1034	0	1080	23	0
75	XX	1098	0	1167	11	0
76	YY	1023	0	1090	11	0
77	ZZ	598	0	656	6	0
78	aa	781	0	828	0	0
79	bb	651	0	672	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	cc	475	0	497	0	0
81	dd	445	0	439	0	0
82	ee	457	0	502	0	0
83	ff	520	0	536	0	0
84	gg	2436	0	2393	0	0
85	hh	257	0	129	0	0
86	ii	3280	0	3326	0	0
87	jj	4543	0	4674	0	0
88	5	146	0	0	0	0
88	7	5	0	0	0	0
88	8	2	0	0	0	0
88	9	34	0	0	0	0
88	B	1	0	0	0	0
88	C	1	0	0	0	0
88	I	1	0	0	0	0
88	LL	1	0	0	0	0
88	P	1	0	0	0	0
88	V	1	0	0	0	0
88	g	1	0	0	0	0
88	hh	1	0	0	0	0
89	aa	1	0	0	0	0
89	dd	1	0	0	0	0
89	ff	1	0	0	0	0
89	g	1	0	0	0	0
89	j	1	0	0	0	0
89	m	1	0	0	0	0
89	o	1	0	0	0	0
89	p	1	0	0	0	0
90	jj	16	0	0	0	0
91	jj	54	0	24	0	0
All	All	226454	0	169855	2802	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

The worst 5 of 2802 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:9:1137:U:O4	51:9:1148:A:N1	1.61	1.34
48:5:976:G:H2'	48:5:977:C:O4'	1.26	1.32
17:R:172:ARG:NH1	51:9:908:A:H5''	1.47	1.29

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:5:2367:A:N1	48:5:2788:U:O4	1.66	1.29
5:E:126:ARG:NH1	48:5:712:C:H1'	1.49	1.27

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

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

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	242/244 (99%)	209 (86%)	28 (12%)	5 (2%)	9	48
2	B	392/394 (100%)	345 (88%)	42 (11%)	5 (1%)	15	58
3	C	360/362 (99%)	322 (89%)	27 (8%)	11 (3%)	5	39
4	D	290/292 (99%)	262 (90%)	25 (9%)	3 (1%)	19	64
5	E	232/248 (94%)	179 (77%)	36 (16%)	17 (7%)	1	15
6	F	223/225 (99%)	204 (92%)	17 (8%)	2 (1%)	21	67
7	G	239/241 (99%)	203 (85%)	31 (13%)	5 (2%)	9	48
8	H	188/190 (99%)	165 (88%)	20 (11%)	3 (2%)	12	53
9	I	200/213 (94%)	181 (90%)	15 (8%)	4 (2%)	9	49
10	J	167/169 (99%)	147 (88%)	13 (8%)	7 (4%)	3	31
11	L	208/210 (99%)	180 (86%)	16 (8%)	12 (6%)	2	21
12	M	136/138 (99%)	123 (90%)	12 (9%)	1 (1%)	26	71
13	N	201/203 (99%)	181 (90%)	20 (10%)	0	100	100
14	O	197/199 (99%)	184 (93%)	12 (6%)	1 (0%)	34	77
15	P	151/153 (99%)	135 (89%)	16 (11%)	0	100	100
16	Q	185/187 (99%)	169 (91%)	14 (8%)	2 (1%)	17	62
17	R	178/180 (99%)	166 (93%)	9 (5%)	3 (2%)	11	52
18	S	173/175 (99%)	157 (91%)	12 (7%)	4 (2%)	8	46

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	T	157/159 (99%)	139 (88%)	15 (10%)	3 (2%)	10	49
20	U	97/99 (98%)	82 (84%)	11 (11%)	4 (4%)	3	32
21	V	129/131 (98%)	115 (89%)	13 (10%)	1 (1%)	24	69
22	W	61/63 (97%)	56 (92%)	4 (7%)	1 (2%)	12	53
23	X	117/119 (98%)	109 (93%)	6 (5%)	2 (2%)	11	52
24	Y	132/134 (98%)	114 (86%)	17 (13%)	1 (1%)	24	69
25	Z	133/135 (98%)	113 (85%)	13 (10%)	7 (5%)	2	23
26	a	145/147 (99%)	122 (84%)	19 (13%)	4 (3%)	6	41
27	b	73/75 (97%)	67 (92%)	5 (7%)	1 (1%)	14	56
28	c	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
29	d	105/107 (98%)	91 (87%)	13 (12%)	1 (1%)	19	64
30	e	126/128 (98%)	115 (91%)	6 (5%)	5 (4%)	4	32
31	f	107/109 (98%)	94 (88%)	8 (8%)	5 (5%)	3	28
32	g	112/114 (98%)	103 (92%)	8 (7%)	1 (1%)	21	67
33	h	120/122 (98%)	107 (89%)	9 (8%)	4 (3%)	5	37
34	i	100/102 (98%)	92 (92%)	6 (6%)	2 (2%)	9	49
35	j	84/86 (98%)	70 (83%)	9 (11%)	5 (6%)	2	20
36	k	67/69 (97%)	56 (84%)	7 (10%)	4 (6%)	2	20
37	l	48/50 (96%)	40 (83%)	7 (15%)	1 (2%)	9	48
38	m	50/52 (96%)	44 (88%)	6 (12%)	0	100	100
39	n	21/23 (91%)	21 (100%)	0	0	100	100
40	o	102/104 (98%)	92 (90%)	7 (7%)	3 (3%)	6	40
41	p	89/91 (98%)	80 (90%)	8 (9%)	1 (1%)	17	62
42	r	123/125 (98%)	102 (83%)	14 (11%)	7 (6%)	2	22
43	s	196/198 (99%)	164 (84%)	22 (11%)	10 (5%)	2	25
44	t	161/163 (99%)	102 (63%)	33 (20%)	26 (16%)	0	2
45	1	13/15 (87%)	11 (85%)	0	2 (15%)	0	3
52	AA	206/208 (99%)	173 (84%)	23 (11%)	10 (5%)	3	26
53	BB	211/213 (99%)	165 (78%)	33 (16%)	13 (6%)	2	19
54	CC	216/218 (99%)	184 (85%)	26 (12%)	6 (3%)	6	41
55	DD	225/227 (99%)	181 (80%)	33 (15%)	11 (5%)	3	26

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
56	EE	260/262 (99%)	200 (77%)	42 (16%)	18 (7%)	1	16
57	FF	189/191 (99%)	160 (85%)	21 (11%)	8 (4%)	3	31
58	GG	235/237 (99%)	198 (84%)	31 (13%)	6 (3%)	7	43
59	HH	187/189 (99%)	148 (79%)	25 (13%)	14 (8%)	1	14
60	II	204/206 (99%)	168 (82%)	28 (14%)	8 (4%)	4	33
61	JJ	183/185 (99%)	153 (84%)	20 (11%)	10 (6%)	2	23
62	KK	96/98 (98%)	65 (68%)	21 (22%)	10 (10%)	1	8
63	LL	150/152 (99%)	125 (83%)	19 (13%)	6 (4%)	4	32
64	MM	122/124 (98%)	87 (71%)	28 (23%)	7 (6%)	2	22
65	NN	148/150 (99%)	126 (85%)	17 (12%)	5 (3%)	5	37
66	OO	134/136 (98%)	99 (74%)	21 (16%)	14 (10%)	1	8
67	PP	125/127 (98%)	107 (86%)	15 (12%)	3 (2%)	7	45
68	QQ	139/141 (99%)	116 (84%)	18 (13%)	5 (4%)	4	35
69	RR	127/129 (98%)	106 (84%)	15 (12%)	6 (5%)	3	28
70	SS	135/137 (98%)	114 (84%)	16 (12%)	5 (4%)	4	35
71	TT	139/141 (99%)	126 (91%)	10 (7%)	3 (2%)	8	47
72	UU	102/104 (98%)	87 (85%)	9 (9%)	6 (6%)	2	21
73	VV	81/83 (98%)	67 (83%)	10 (12%)	4 (5%)	3	26
74	WW	127/129 (98%)	106 (84%)	16 (13%)	5 (4%)	4	33
75	XX	139/141 (99%)	118 (85%)	13 (9%)	8 (6%)	2	21
76	YY	124/126 (98%)	99 (80%)	17 (14%)	8 (6%)	1	18
77	ZZ	73/75 (97%)	59 (81%)	12 (16%)	2 (3%)	6	42
78	aa	96/98 (98%)	73 (76%)	13 (14%)	10 (10%)	1	8
79	bb	81/83 (98%)	61 (75%)	16 (20%)	4 (5%)	3	26
80	cc	59/61 (97%)	47 (80%)	10 (17%)	2 (3%)	5	37
81	dd	51/53 (96%)	45 (88%)	3 (6%)	3 (6%)	2	21
82	ee	55/57 (96%)	40 (73%)	12 (22%)	3 (6%)	2	23
83	ff	58/68 (85%)	50 (86%)	6 (10%)	2 (3%)	5	37
84	gg	311/313 (99%)	269 (86%)	33 (11%)	9 (3%)	6	40
86	ii	414/416 (100%)	380 (92%)	26 (6%)	8 (2%)	10	49
87	jj	568/594 (96%)	513 (90%)	41 (7%)	14 (2%)	7	44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	12492/12709 (98%)	10717 (86%)	1333 (11%)	442 (4%)	8	36

5 of 442 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	196	TRP
3	C	273	LEU
5	E	91	PRO
5	E	95	ASP
5	E	118	PRO

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	187/187 (100%)	161 (86%)	26 (14%)	4	23
2	B	336/342 (98%)	291 (87%)	45 (13%)	5	25
3	C	302/302 (100%)	260 (86%)	42 (14%)	4	23
4	D	247/247 (100%)	218 (88%)	29 (12%)	7	30
5	E	208/221 (94%)	185 (89%)	23 (11%)	8	34
6	F	194/195 (100%)	165 (85%)	29 (15%)	4	20
7	G	206/206 (100%)	182 (88%)	24 (12%)	7	30
8	H	169/169 (100%)	148 (88%)	21 (12%)	6	28
9	I	174/180 (97%)	153 (88%)	21 (12%)	6	29
10	J	142/142 (100%)	126 (89%)	16 (11%)	7	32
11	L	176/176 (100%)	145 (82%)	31 (18%)	2	12
12	M	117/117 (100%)	102 (87%)	15 (13%)	5	27
13	N	171/171 (100%)	152 (89%)	19 (11%)	8	34
14	O	171/171 (100%)	144 (84%)	27 (16%)	3	18
15	P	134/134 (100%)	120 (90%)	14 (10%)	9	38
16	Q	163/163 (100%)	145 (89%)	18 (11%)	8	35

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	R	159/159 (100%)	140 (88%)	19 (12%)	6	29
18	S	156/156 (100%)	132 (85%)	24 (15%)	3	19
19	T	139/139 (100%)	122 (88%)	17 (12%)	6	28
20	U	89/89 (100%)	82 (92%)	7 (8%)	15	52
21	V	101/101 (100%)	84 (83%)	17 (17%)	2	14
22	W	55/55 (100%)	50 (91%)	5 (9%)	12	45
23	X	107/107 (100%)	97 (91%)	10 (9%)	11	44
24	Y	124/124 (100%)	107 (86%)	17 (14%)	4	24
25	Z	117/117 (100%)	109 (93%)	8 (7%)	20	59
26	a	119/119 (100%)	107 (90%)	12 (10%)	9	39
27	b	62/62 (100%)	57 (92%)	5 (8%)	15	51
28	c	79/79 (100%)	66 (84%)	13 (16%)	3	15
29	d	98/98 (100%)	82 (84%)	16 (16%)	3	16
30	e	114/114 (100%)	99 (87%)	15 (13%)	5	26
31	f	88/88 (100%)	76 (86%)	12 (14%)	5	24
32	g	98/98 (100%)	83 (85%)	15 (15%)	3	19
33	h	109/109 (100%)	97 (89%)	12 (11%)	8	35
34	i	86/86 (100%)	81 (94%)	5 (6%)	25	65
35	j	73/73 (100%)	62 (85%)	11 (15%)	3	20
36	k	64/64 (100%)	56 (88%)	8 (12%)	6	28
37	l	47/47 (100%)	40 (85%)	7 (15%)	4	20
38	m	48/48 (100%)	39 (81%)	9 (19%)	2	9
39	n	22/22 (100%)	18 (82%)	4 (18%)	2	11
40	o	92/92 (100%)	79 (86%)	13 (14%)	4	22
41	p	74/74 (100%)	68 (92%)	6 (8%)	15	51
42	r	109/109 (100%)	88 (81%)	21 (19%)	2	8
43	s	166/166 (100%)	155 (93%)	11 (7%)	21	61
44	t	136/136 (100%)	128 (94%)	8 (6%)	24	64
45	1	13/13 (100%)	12 (92%)	1 (8%)	16	53
52	AA	174/174 (100%)	152 (87%)	22 (13%)	5	27
53	BB	194/194 (100%)	169 (87%)	25 (13%)	5	26

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
54	CC	183/183 (100%)	155 (85%)	28 (15%)	3	19
55	DD	190/190 (100%)	168 (88%)	22 (12%)	7	31
56	EE	223/223 (100%)	183 (82%)	40 (18%)	2	11
57	FF	161/161 (100%)	126 (78%)	35 (22%)	1	6
58	GG	207/207 (100%)	179 (86%)	28 (14%)	5	25
59	HH	169/169 (100%)	151 (89%)	18 (11%)	8	36
60	II	178/178 (100%)	155 (87%)	23 (13%)	5	26
61	JJ	161/161 (100%)	141 (88%)	20 (12%)	6	28
62	KK	89/89 (100%)	76 (85%)	13 (15%)	4	21
63	LL	136/136 (100%)	110 (81%)	26 (19%)	2	9
64	MM	104/104 (100%)	85 (82%)	19 (18%)	2	10
65	NN	130/130 (100%)	108 (83%)	22 (17%)	2	14
66	OO	106/106 (100%)	81 (76%)	25 (24%)	1	4
67	PP	116/116 (100%)	98 (84%)	18 (16%)	3	18
68	QQ	117/117 (100%)	102 (87%)	15 (13%)	5	27
69	RR	117/117 (100%)	102 (87%)	15 (13%)	5	27
70	SS	119/119 (100%)	100 (84%)	19 (16%)	3	17
71	TT	112/112 (100%)	94 (84%)	18 (16%)	3	17
72	UU	94/94 (100%)	79 (84%)	15 (16%)	3	17
73	VV	67/67 (100%)	61 (91%)	6 (9%)	12	46
74	WW	112/112 (100%)	99 (88%)	13 (12%)	7	31
75	XX	113/113 (100%)	94 (83%)	19 (17%)	2	14
76	YY	108/108 (100%)	88 (82%)	20 (18%)	2	10
77	ZZ	66/66 (100%)	59 (89%)	7 (11%)	8	37
78	aa	85/85 (100%)	77 (91%)	8 (9%)	11	43
79	bb	75/75 (100%)	62 (83%)	13 (17%)	2	13
80	cc	54/54 (100%)	44 (82%)	10 (18%)	2	10
81	dd	47/47 (100%)	40 (85%)	7 (15%)	4	20
82	ee	47/47 (100%)	39 (83%)	8 (17%)	2	14
83	ff	58/61 (95%)	57 (98%)	1 (2%)	68	89
84	gg	272/272 (100%)	250 (92%)	22 (8%)	15	51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
86	ii	358/358 (100%)	324 (90%)	34 (10%)	11	42
87	jj	506/522 (97%)	487 (96%)	19 (4%)	40	76
All	All	10889/10934 (100%)	9508 (87%)	1381 (13%)	10	27

5 of 1381 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
34	i	33	LEU
53	BB	212	VAL
79	bb	72	ARG
36	k	37	ARG
42	r	70	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
5	E	217	GLN
7	G	29	ASN
42	r	103	HIS

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
46	2	74/76 (97%)	20 (27%)	1 (1%)
47	3	72/75 (96%)	36 (50%)	7 (9%)
48	5	3645/3662 (99%)	1179 (32%)	269 (7%)
49	7	119/120 (99%)	19 (15%)	1 (0%)
50	8	155/156 (99%)	52 (33%)	6 (3%)
51	9	1711/1719 (99%)	608 (35%)	129 (7%)
85	hh	11/12 (91%)	7 (63%)	0
All	All	5787/5820 (99%)	1921 (33%)	413 (7%)

5 of 1921 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
46	2	7	G
46	2	8	U
46	2	9	A
46	2	13	U

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Mol	Chain	Res	Type
46	2	16	C

5 of 413 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
48	5	2505	C
48	5	4124	G
51	9	1438	A
48	5	2587	A
48	5	3670	C

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

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 207 ligands modelled in this entry, 203 are monoatomic - leaving 4 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	SF4	jj	600	87	0,12,12	0.00	-	0,24,24	0.00	-
90	SF4	jj	601	87	0,12,12	0.00	-	0,24,24	0.00	-
91	ADP	jj	602	-	24,29,29	1.07	1 (4%)	23,45,45	1.92	1 (4%)
91	ADP	jj	603	-	24,29,29	1.08	2 (8%)	23,45,45	1.91	1 (4%)

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	SF4	jj	600	87	-	0/0/48/48	0/6/5/5
90	SF4	jj	601	87	-	0/0/48/48	0/6/5/5
91	ADP	jj	602	-	-	0/12/32/32	0/3/3/3
91	ADP	jj	603	-	-	0/12/32/32	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
91	jj	603	ADP	C2-N3	2.06	1.35	1.32
91	jj	602	ADP	C5-C4	3.28	1.47	1.40
91	jj	603	ADP	C5-C4	3.34	1.48	1.40

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
91	jj	602	ADP	N3-C2-N1	-7.73	122.80	128.87
91	jj	603	ADP	N3-C2-N1	-7.72	122.81	128.87

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.