



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 03:07 PM BST

PDB ID : 3JAG
EMDB ID: : EMD-3038
Title : Structure of a mammalian ribosomal termination complex with ABCE1, eRF1(AAQ), and the UAA stop codon
Authors : Brown, A.; Shao, S.; Murray, J.; Hegde, R.S.; Ramakrishnan, V.
Deposited on : 2015-06-10
Resolution : 3.65 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
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>

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

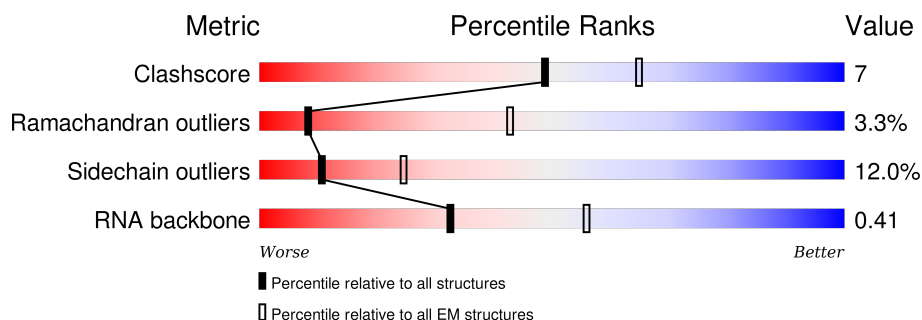
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.65 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 ≥ 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	80% 16% .
2	B	394	81% 17% .
3	C	362	73% 24% .
4	D	292	83% 16% .
5	E	248	67% 24% . 5%
6	F	225	80% 17% .
7	G	241	78% 21% .
8	H	190	82% 16% .












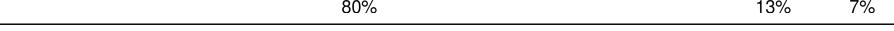

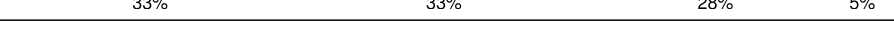





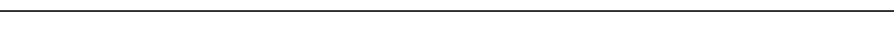

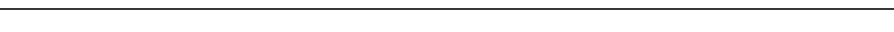
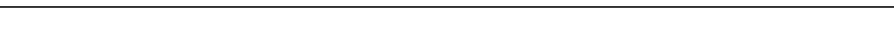


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Mol	Chain	Length	Quality of chain
9	I	213	 70% 20% 5% .
10	J	169	 81% 18% .
11	L	210	 74% 23% .
12	M	138	 73% 25% .
13	N	203	 80% 19% .
14	O	199	 79% 17% .
15	P	153	 87% 12% .
16	Q	187	 82% 17% .
17	R	180	 76% 21% .
18	S	175	 75% 22% . .
19	T	159	 79% 20% .
20	U	99	 83% 15% .
21	V	131	 82% 17% .
22	W	63	 89% 10% .
23	X	119	 85% 14% .
24	Y	134	 81% 16% . .
25	Z	135	 78% 21% .
26	a	147	 88% 12% .
27	b	75	 92% 8%
28	c	94	 88% 12%
29	d	107	 83% 15% .
30	e	128	 84% 16%
31	f	109	 83% 16% .
32	g	114	 88% 12%
33	h	122	 88% 11% .


























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Mol	Chain	Length	Quality of chain
34	i	102	 88% 9% ..
35	j	86	 88% 10% .
36	k	69	 88% 10% .
37	l	50	 80% 20%
38	m	52	 79% 19% .
39	n	23	 87% 13%
40	o	104	 86% 13% .
41	p	91	 93% 7%
42	r	125	 82% 17% .
43	s	198	 90% 9% .
44	t	163	 79% 20% .
45	1	15	 80% 13% 7%
46	2	76	 59% 32% 9%
47	3	75	 33% 33% 28% 5%
48	5	3662	 48% 38% 13% .
49	7	120	 65% 30% 5%
50	8	156	 45% 44% 11%
51	9	1719	 47% 41% 11% .
52	AA	208	 79% 17% .
53	BB	213	 77% 20% ..
54	CC	218	 75% 22% .
55	DD	227	 79% 19% .
56	EE	262	 75% 21% 5%
57	FF	191	 75% 21% .
58	GG	237	 75% 24% .





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Mol	Chain	Length	Quality of chain
59	HH	189	 78% 18% .
60	II	206	 74% 24% .
61	JJ	185	 78% 17% . .
62	KK	98	 68% 30% .
63	LL	152	 80% 17% . .
64	MM	124	 77% 22% .
65	NN	150	 79% 19% .
66	OO	136	 67% 24% 7% .
67	PP	127	 77% 20% .
68	QQ	141	 84% 12% . .
69	RR	129	 80% 16% .
70	SS	137	 78% 18% . .
71	TT	141	 82% 13% 5% .
72	UU	104	 83% 14% .
73	VV	83	 80% 18% .
74	WW	129	 82% 16% .
75	XX	141	 77% 21% .
76	YY	126	 75% 22% .
77	ZZ	75	 84% 16%
78	aa	98	 82% 18%
79	bb	83	 81% 18% .
80	cc	61	 85% 15%
81	dd	53	 81% 19%
82	ee	57	 84% 16%
83	ff	69	 86% 6% 9%

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Mol	Chain	Length	Quality of chain
84	gg	313	 90%10%
85	hh	12	 42%58%
86	ii	416	 91%9%
87	jj	594	 92%5% •

2 Entry composition [i](#)

There are 91 unique types of molecules in this entry. The entry contains 226469 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
			2883	1812	577	480	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	SER	-	EXPRESSION TAG	UNP G1SVW5
C	363	ASP	-	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	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
			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
			1694	1103	287	297	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CC	194	ARG	HIS	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	63	Total	C	N	O	S	0	0
			527	336	99	86	6		

- 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
			256	115	46	83	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	577	Total	C	N	O	S	0	0
			4551	2910	780	830	31		

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

Mol	Chain	Residues	Atoms		AltConf
88	P	1	Total	Mg	0
			1	1	
88	g	1	Total	Mg	0
			1	1	
88	Q	1	Total	Mg	0
			1	1	
88	I	1	Total	Mg	0
			1	1	
88	C	1	Total	Mg	0
			1	1	
88	V	1	Total	Mg	0
			1	1	

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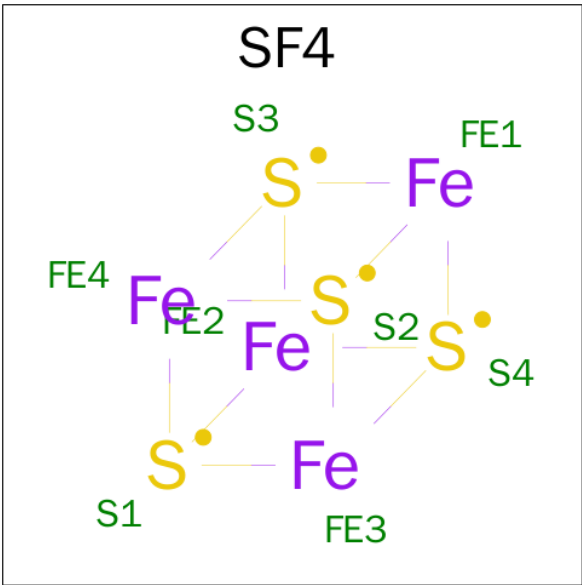
Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
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	35	Total 35	Mg 35	0
88	hh	1	Total 1	Mg 1	0

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

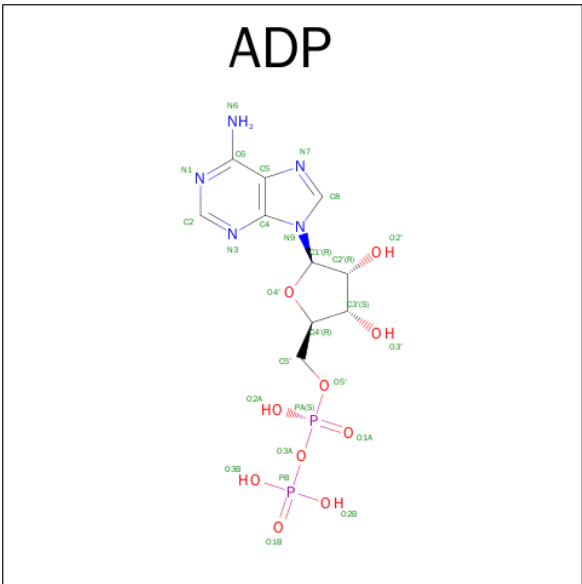
Mol	Chain	Residues	Atoms		AltConf
89	p	1	Total 1	Zn 1	0
89	g	1	Total 1	Zn 1	0
89	j	1	Total 1	Zn 1	0
89	dd	1	Total 1	Zn 1	0
89	ff	1	Total 1	Zn 1	0
89	aa	1	Total 1	Zn 1	0
89	o	1	Total 1	Zn 1	0
89	m	1	Total 1	Zn 1	0

- Molecule 90 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄).



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: C₁₀H₁₅N₅O₁₀P₂).



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

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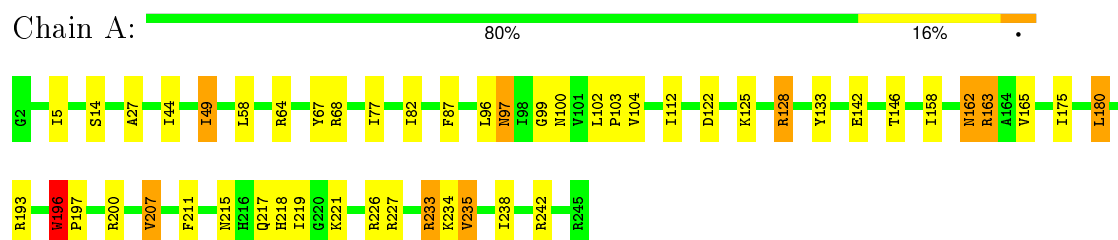
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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
91	jj	1	54	20	10	20	4	0

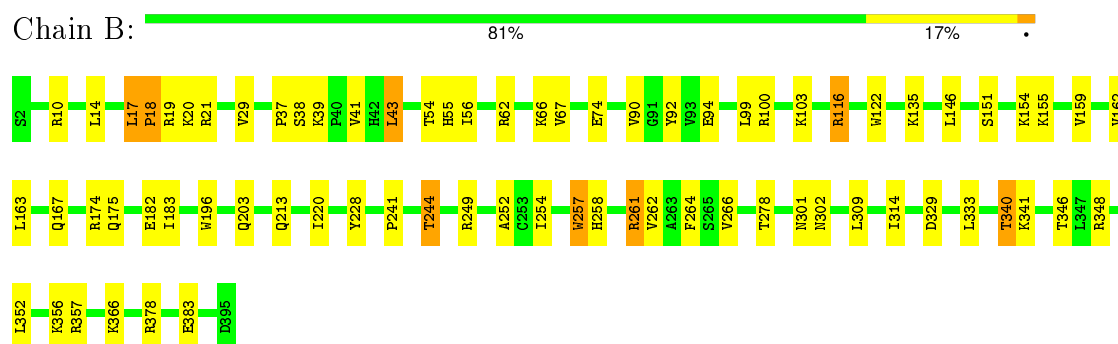
3 Residue-property plots

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.

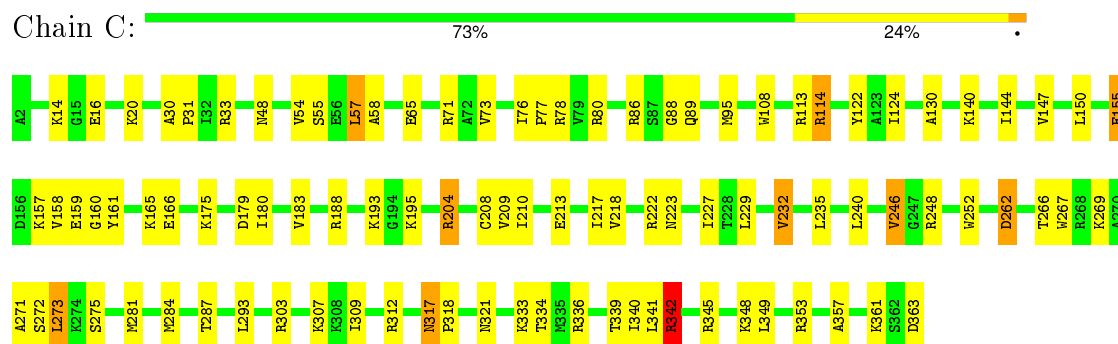
• Molecule 1: uL2



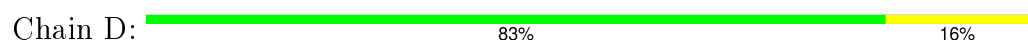
• Molecule 2: uL3

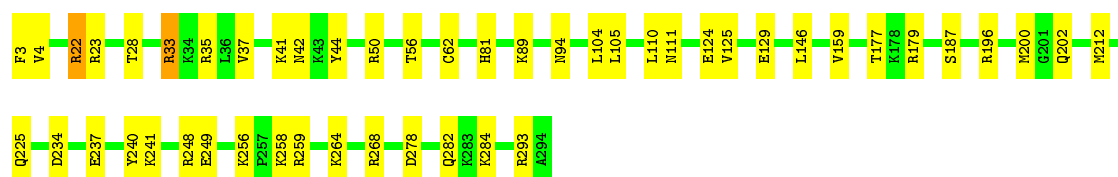


• Molecule 3: uL4

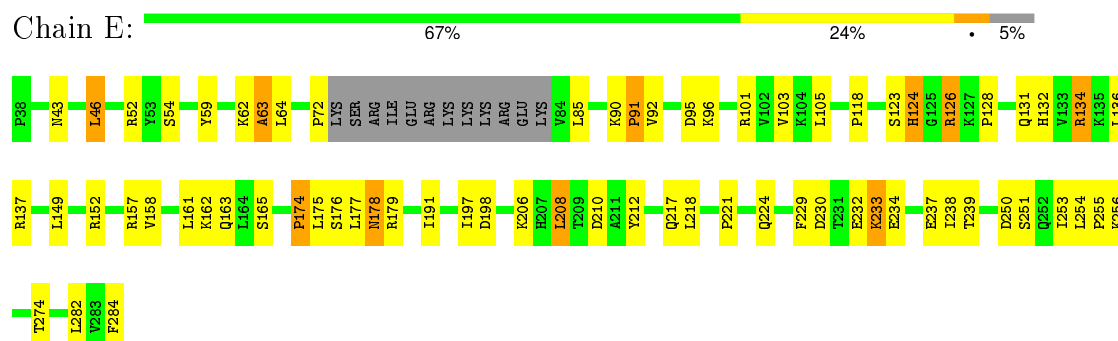


• Molecule 4: uL18

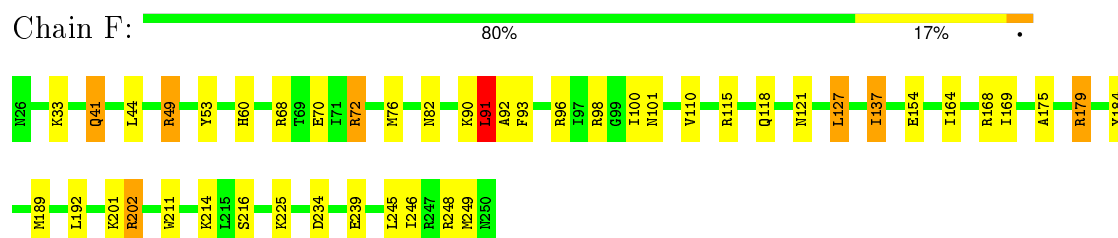




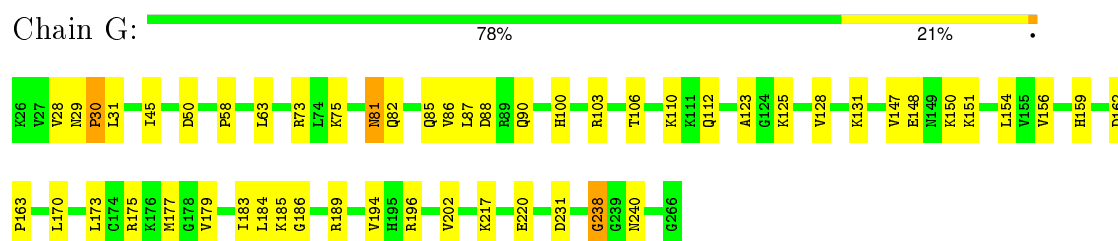
- Molecule 5: eL6



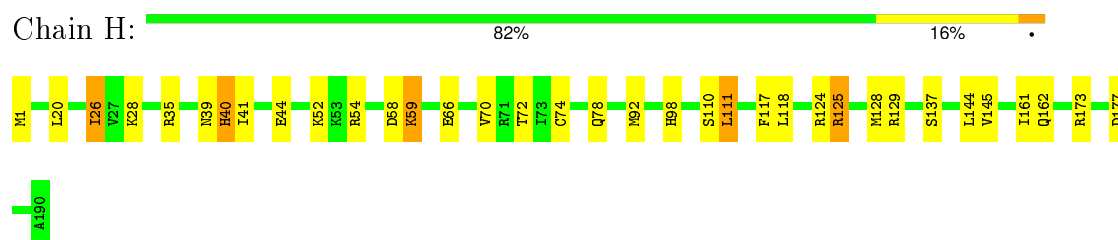
- Molecule 6: uL30



- Molecule 7: eL8

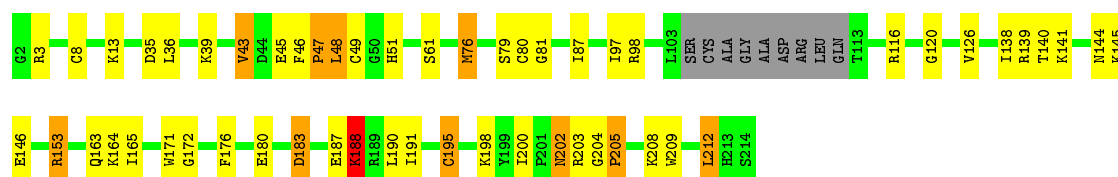


- Molecule 8: uL6



- Molecule 9: uL16





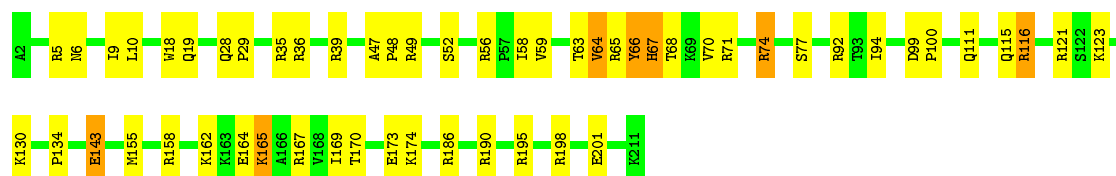
- Molecule 10: uL5

Chain J: 81% 18%



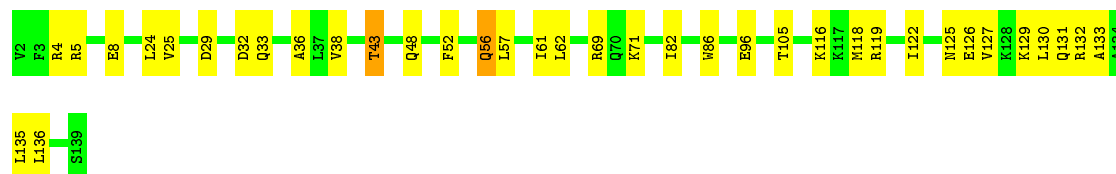
- Molecule 11: eL13

Chain L: 74% 23%



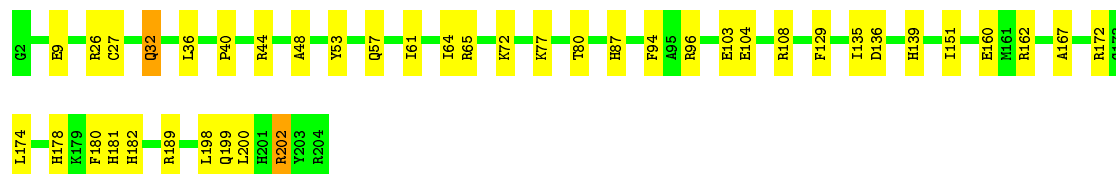
- Molecule 12: eL14

Chain M: 73% 25%



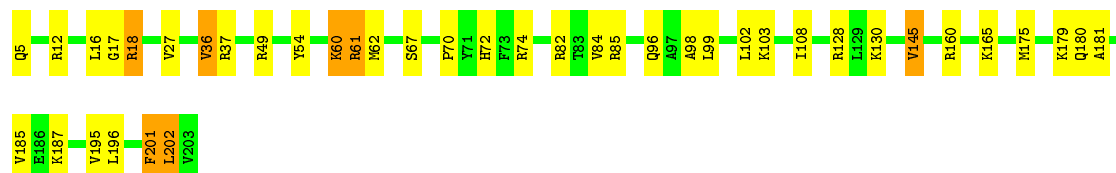
- Molecule 13: eL15

Chain N: 80% 19%




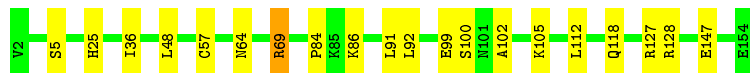
- Molecule 14: uL13

Chain O: 79% 17%




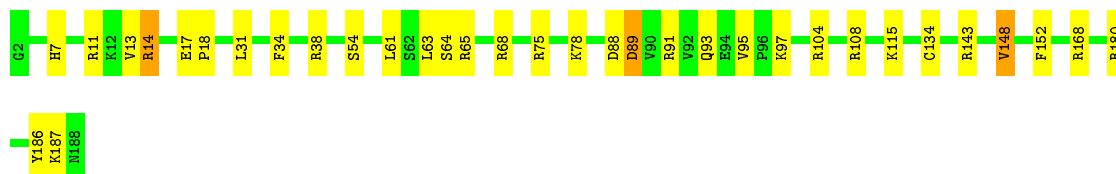
- Molecule 15: uL22

Chain P:  87% 12%



- Molecule 16: eL18

Chain Q:  82% 17%



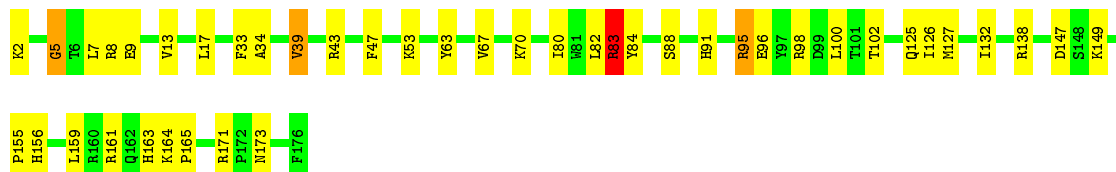
- Molecule 17: eL19

Chain R:  76% 21%




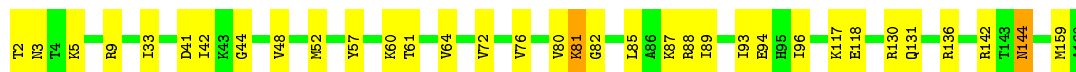
- Molecule 18: eL20

Chain S:  75% 22%




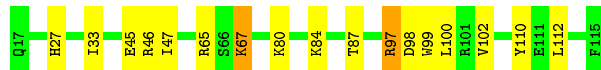
- Molecule 19: eL21

Chain T:  79% 20%

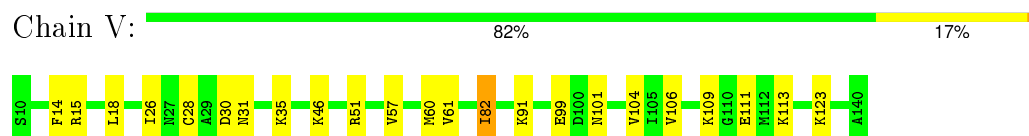


- Molecule 20: eL22

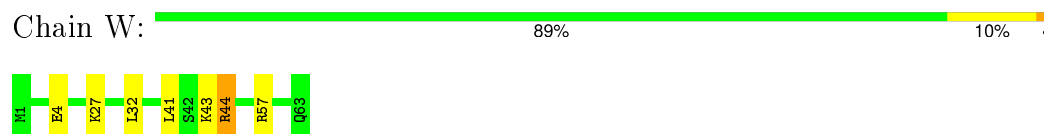
Chain U:  83% 15%



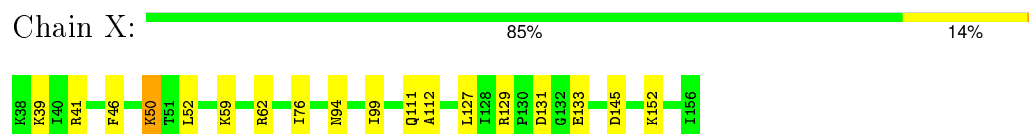
- Molecule 21: uL14



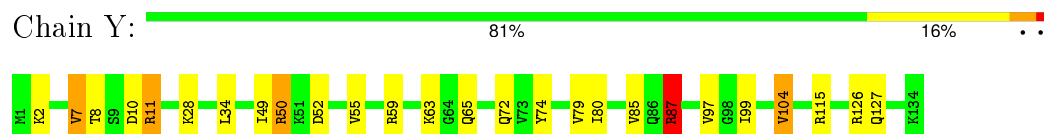
- Molecule 22: eL24



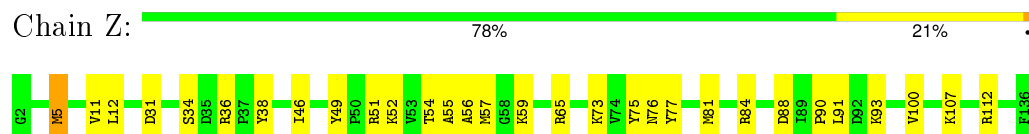
- Molecule 23: uL23



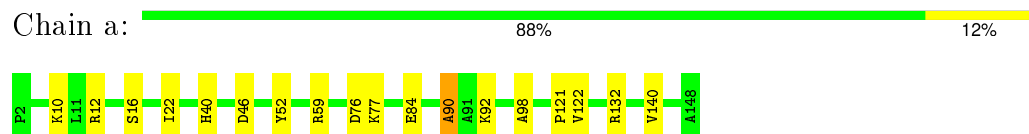
- Molecule 24: uL24



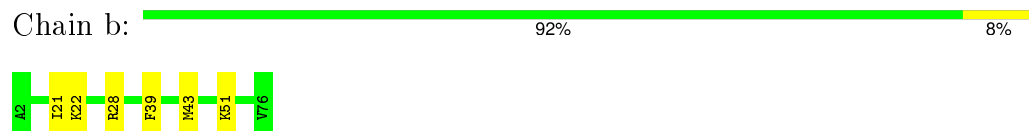
- Molecule 25: eL27



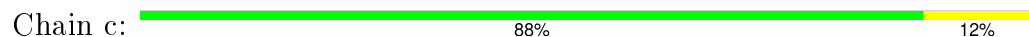
- Molecule 26: uL15



- Molecule 27: eL29



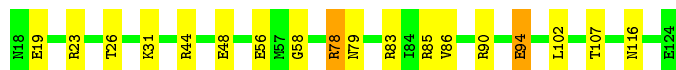
- Molecule 28: eL30





- Molecule 29: eL31

Chain d: 83% 15% .



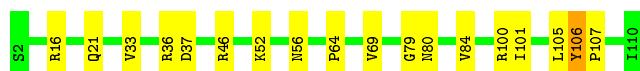
- Molecule 30: eL32

Chain e: 84% 16%



- Molecule 31: eL33

Chain f: 83% 16% .



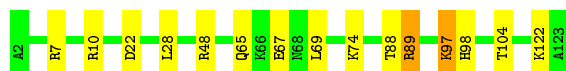
- Molecule 32: eL34

Chain g: 88% 12%



- Molecule 33: uL29

Chain h: 88% 11% .



- Molecule 34: eL36

Chain i: 88% 9% ..




- Molecule 35: eL37

Chain j: 88% 10% .




- Molecule 36: eL38

Chain k:  88% 10%




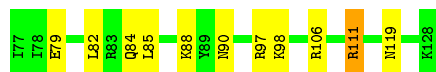
- Molecule 37: eL39

Chain l:  80% 20%




- Molecule 38: eL40

Chain m:  79% 19%




- Molecule 39: eL41

Chain n:  87% 13%



- Molecule 40: eL42

Chain o:  86% 13%




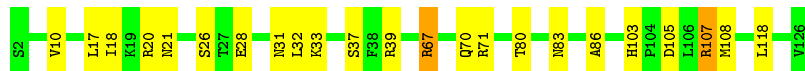
- Molecule 41: eL43

Chain p:  93% 7%



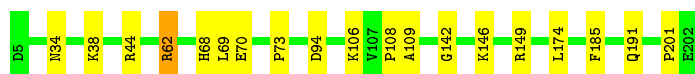
- Molecule 42: eL28

Chain r:  82% 17%

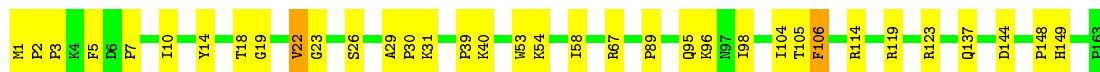
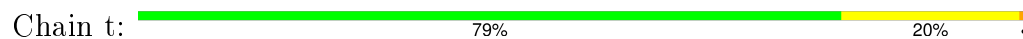


- Molecule 43: uL10

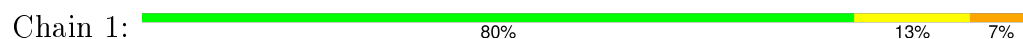
Chain s:  90% 9%



- Molecule 44: uL11



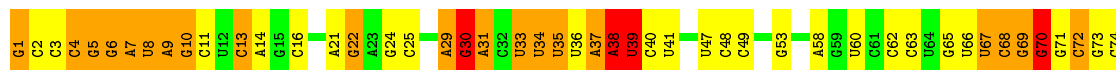
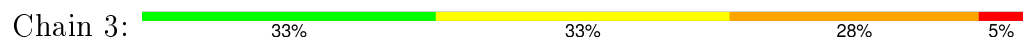
- Molecule 45: peptide



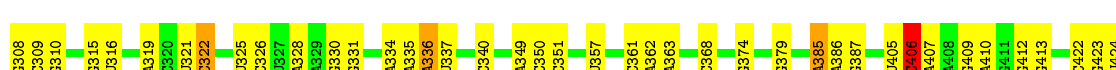
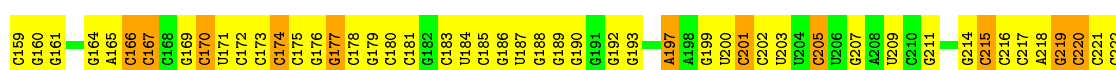
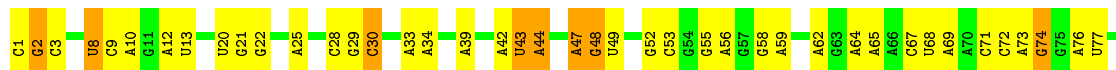
- Molecule 46: tRNA(Val)



- Molecule 47: tRNA(Lys)

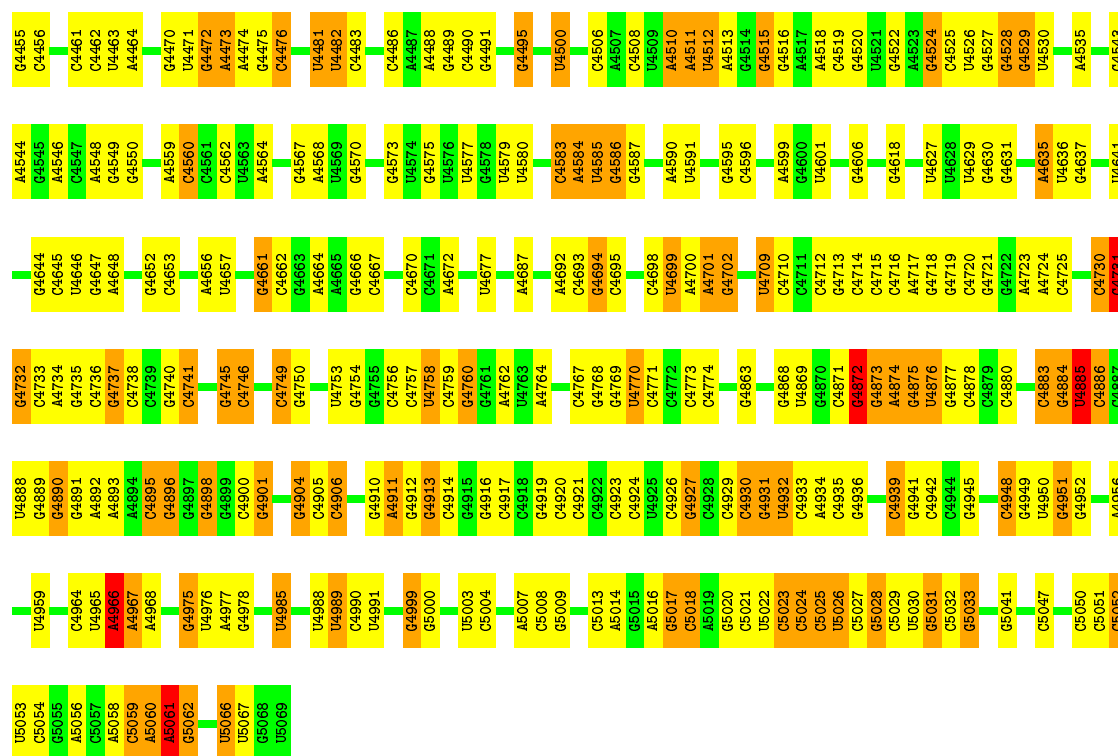


- Molecule 48: 28S ribosomal RNA



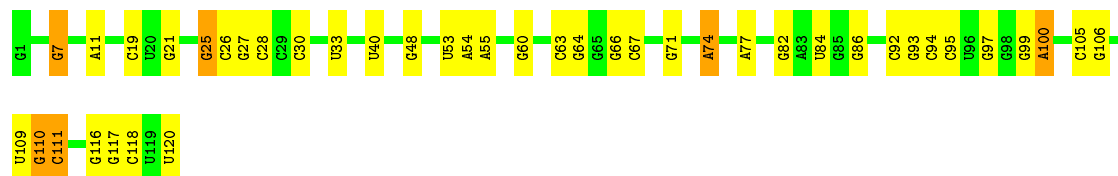
G2058	U1986	G1904	G1815	U1725	A1631	G1429	G1360	G1271	G1194	G994	G930	G703	U513	A429
G2059	C1987	A1907	G1818	U1726	A1632	C1430	G1361	C1272	G1195	C995	C931	C704	U514	A430
C2062	G1989	G1910	G1819	C1732	A1633	C1431	G1362	G1273	G1196	G1048	A932	C705	C515	G431
G2064	A1991	G1911	G1820	G1734	C1635	G1432	G1363	A1274	C1197	C1049	G933	C706	C516	A432
G2065	U1992	G1912	G1821	U1735	U1636	A1517	G1365	C1275	G1198	C1050	A935	C707	C517	A433
C2067	C1993	C1913	U1822	U1735	A1637	G1435	G1366	C1276	G1199	C1051	C936	A711	G518	A434
C2068	G1994	U1918	G1823	G1739	A1638	C1436	G1367	C1277	G1203	G1064	U937	C712	C519	C446
C2069	G1995	A1825	A1825	C1740	C1640	C1439	G1369	A1278	C1204	G1065	C938	G715	G642	C447
A2069	C1996	G1826	G1826	G1741	G1641	C1440	G1370	G1281	C1205	G1066	G939	C716	G643	G448
U2070	U1997	C1827	C1827	A1742	A1642	C1441	A1371	G1282	G1206	G1067	C940	U717	G645	C449
A2071	A1998	C1828	C1828	A1742	A1643	C1442	A1372	G1283	G1207	G1068	C941	C718	G646	C450
C2072	A1999	G1829	G1829	A1746	G1654	U1445	A1373	G1284	U1209	G1070	A943		G647	C451
C2073	G2000	G1830	G1830	U1747	C1655	C1446	G1374	U1285	G1210	C1071	A944	G721	A649	A452
G2076	G2001	G1831	G1831	U1748	C1655	C1447	C1375	C1286	G1211	C1072	U945	G722	A649	G453
G2077	A2002	C1832	C1832	U1749	U1656	C1447	C1376	G1287	G1212	C1073	C946	A723	U454	U454
C2078	G2003	G1833	G1833	G1750	A1656	G1448	C1377	G1288	G1213	G1074	C947	C724	G654	C455
G2079	U2004	U1834	U1834	A1751	C1661	C1449	C1378		G1214	G1075	C948	G725	G655	C458
G2080	G2005	G1835	G1835	G1752	C1662	C1450	C1379	G1291	G1215	C1076		G726	C656	C462
C2083	U2006	G1836	G1836	G1753	C1663		G1380	C1292	G1219	C1081	G951	C727	C657	
C2084	G2007	A1837	A1837	U1754	G1663	G1454	U1381	G1293	G1220	C1082	G952	U728	G663	G465
G2085	U2008	A1838	A1838	C1755	G1667	G1455	G1382	A1294	G1221	C1083	C953	G729	G664	A466
G2086	A2009	U1839	U1839	U1756	A1668	C1456	G1383	C1295	G1222	U1084	A956	G730	G665	U467
C2087	A2010	G1840	G1840	U1757	G1670	G1457	C1384	G1296	A1222	C1085	C957		G666	U468
A2088	C2011	G1842	G1842	G1758	U1671	C1464	A1387	U1297	G1232	C1086	G958	A733	G667	U469
G2089	G2016	G1846	G1846	G1759	U1672	G1465	G1388	C1301	G1233	C1087	G959	C737	C674	U470
U2090	A2017	C1847	C1847	G1760	U1673	G1466	G1390	U1302	G1234	C1088	G960	G742	C675	A471
C2091	C2018	C1848	C1848	G1761	U1673	C1467	G1391	A1303	G1235	C1089	A961	G743	G670	C472
G2092	C2019	G1854	G1854	G1762	C1676	C1468	G1394	C1304	G1236	C1090	G962	G744	C671	C473
A2093	U2020	G1855	G1855	G1764	U1677		A1397	C1308	G1238	C1093	G963	G745	C672	
G2094	G2021	C1856	C1856	U1765	C1678	C1472	A1398	C1309	G1239	C1097	A964	G746	C673	G476
A2095	C2022	A1857	A1857	C1767	A1679	U1473	C1399	G1474	G1240	C1098	G965	A747	C674	G479
C2096	G2023	G1867	G1867	U1768	A1682	G1475	G1400	C1313	G1242	C1099	G966	G748	C676	C480
U2097	G2024	U1868	U1868	G1771	U1683	C1476	C1401	G1243	G1243	U1100	C968	G749	G677	G483
A2100	A2025	G1869	G1869	C1772	A1684	C1477		A1322	G1244	C1167	C969	U750	C678	G487
C2107	A2026	G1872	G1872	A1776	G1685	C1478	G1404	C1326	G1245	G1170	G970	G751	C679	G488
G2108	U2027	C1873	C1873	C1777	C1686		C1405	A1327	G1246	G1171	U971	G752	G682	G489
C2109	A2028	A1874	A1874	U1777	U1687	C1481	G1406	G1327	U1247	C1172	C972		C683	U484
G2110	G2034	G1878	G1878	A1780	G1688	G1482	C1407	G1328	C1248	C1175	G973	U911	G684	C485
G2111	C2035	C1879	C1879	U1781	G1689	C1483	C1408	G1329	G1249	A1175	C974	U912	C685	C486
G2112	A2043	U1882	U1882	U1782	G1690	C1484	C1409	A1330	C1252	C1176	C975	U913	G686	G487
G2113	U2044	U1883	U1883	C1783	G1691	C1486	U1410	C1332	G1255	U1177	G976	U914	A686	G488
G2114	G2045	G1885	G1885	A1787	C1692	G1489	G1411	C1337	A1256	C1181	G977	A915	U687	C489
G2115	A2046	G1886	G1886	U1798	C1694	A1601	C1412	A1337	G1256	C1182	C978	A917	U688	G497
G2117	U2048	A1891	A1891	G1799	C1695	U1602	C1413	U1339	G1256	C1183	U982	U918	C690	C498
G2118	C2049	G1898	G1898	U1800	G1696	C1497	G1415	C1340	G1259	A1184	C983	C920	C693	G500
G2119	G2050	C1894	C1894	U1800	G1697	C1498	C1416	C1344	G1262	C1185	C984	C921	C694	C501
C2120	C2051	A1894	A1894	A1804	C1718	A1500	C1417	C1344	G1263	U1186	C985	C922	G695	C502
G2121	G2052	U1980	U1980	A1805	C1719	C1501	C1418	C1344	C1264	C1187	C986	C923	C696	C503
G2122	C2053	A1897	A1897	A1805	C1720	G1502	C1420	G1353	G1265	C1188	C987	C924	G697	G504
C2123	U2054	C1898	C1898	G1721	G1721	A1503	G1421	A1354	G1266	C1189	U989	C925	G698	C505
G2124	G2055	A1983	A1983	U1722	A1722	G1504	G1422	C1357	C1267	C1190	C990	G926	C699	C506
C2125	C2056	C1984	C1984	A1723	A1723	C1505	U1423	C1357	G1268	C1191	C991	G927	G700	A509
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U4372	G4276	C4171	G4106	A3905	U3814	A3719	A3624	G2847	G2756	G2673	C2583	C2505	G2483	G2314	C2127
A4376	A4280	G4182	G4107	A3906	G3815	G3722	G3625	G2855	A2757	A2676	G2586	G2506	G2424	G2315	G2128
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A4378	A4282	G4184	G4109	U3912	G3817	A3724	G3627	A2858	G2759	G2681	A2511	A2512	A2428	G2323	G2130
A4379	G4283	G4185	C4110	G3913	U3818	G3725	G3628	G2859	U2761	G2682	C2589	A2513	A2429	C2324	C2131
A4380	C4284	G4186	C4111	U3914	G3819	A3726	A3630	G2862	G2762	C2683	C2594	G2514	G2433	C2325	G2245
C4387	G4285	U4187	U4112	U3915	U3822	A3728	A3635	G2863	A2763	G2686	A2601	G2515	G2434	G2328	G2246
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G4391	G4287	G4115	G4114	A3917	A3824	U3730	A3642	U2874	G2768	G2688	A2517	G2517	G2436	G2331	C2248
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G4297	G4289	U4117	U4118	C3919	U3832	A3733	U3644	G2889	C2770	U2691	G2607	C2520	C2441	G2333	G2251
U4394	U4301	A4203	C4119	U3925	C3834	G3735	U3645	G2890	G2771	G2692	G2608	G2521	C2442	C2334	G2252
U4395	C4302	C4207	U4120	C3926	C3835	G3740	U3646	C2891	G2772	U2693	G2609	G2522	C2443	C2335	G2253
C4398	A4303	U4208	G4121	U3927	A3836	G3741	A3647	U2891	G2773	G2694	G2610	U2524	C2444	C2336	G2254
G4399	A4304	G4209	G4122	G3930	C3837	A3742	A3648	G2896	C2774	A2695	G2611	U2527	C2445	C2337	C2255
G4400	G4305	U4210	C4123	G3933	U3838	A3743	A3649	G2897	C2775	A2696	G2612	G2528	C2446	C2338	C2256
U4404	U4306	G4211	G4124	G3938	G3839	G3744	G3659	G2898	G2776	A2697	G2613	G2529	C2447	G2339	C2257
U4405	A4307	C4212	C4125	G3939	U3840	G3750	G3660	G2899	C2777	G2698	C2614	U2530	C2448	C2340	G2258
G4408	A4311	A4213	C4126	G3940	U3841	G3751	A3662	G2900	C2778	G2699	C2615	U2531	C2449	G2341	G2259
C4409	U4312	G4216	A4128	U3941	C3842	G3752	A3663	G2901	U2782	C2703	G2616	U2532	C2450	G2342	G2260
A4410	A4313	G4217	G4129	A3942	G3843	G3753	G3664	C2902	A2783	G2704	G2617	U2533	C2451	G2343	G2261
G4411	C4314	U4218	C4130	A3943	U3844	G3754	G3665	G2903	A2784	G2705	G2618	U2534	C2452	G2344	A2263
C4412	C4315	A4219	G4131	G3944	C3845	G3755	G3666	G2904	A2785	G2706	G2619	C2540	C2453	U2350	G2264
G4413	A4317	C4221	C4132	G3945	C3846	A3756	G3667	G2905	A2786	G2707	G2620	C2541	C2454	C2351	G2265
U4416	C4318	G4225	G4133	U4070	G3847	G3757	G3668	G2906	U2787	G2708	G2621	C2542	C2455	U2352	U2267
G4417	A4319	G4226	C4134	U4071	C3848	A3758	G3669	G2907	U2788	C2709	G2622	C2543	C2456	G2353	U2268
G4418	G4320	G4227	C4135	U4072	G3849	A3759	G3670	G2908	U2789	A2789	G2623	C2544	C2457	G2354	A2268
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A4420	A4325	U4429	G4137	C4074	U3851	A3761	U3680	G3586	C2791	G2712	C2625	C2546	C2459	G2361	G2270
C4421	G4326	C4232	G4138	U4075	G3852	G3762	G3681	G3587	A2792	G2713	C2626	C2547	C2460	A2362	C2271
A4422	C4327	U4233	C4139	G4076	C3853	A3763	G3682	G3588	C2793	G2714	G2627	C2548	C2461	G2363	G2272
U4423	G4328	A4234	G4140	U4077	G3854	A3764	G3683	G3589	A2794	G2715	U2632	C2549	C2462	G2364	C2273
A4424	C4329	G4235	C4141	C4080	C3855	A3765	G3684	G3590	A2795	G2716	U2633	C2550	C2463	A2365	C2274
G4425	G4330	G4236	C4142	G4081	C3856	G3766	G3685	G3591	A2796	G2717	G2634	C2551	C2464	A2366	A2275
C4426	G4331	G4237	G4143	U4082	G3857	G3767	G3686	G3592	A2797	G2718	G2635	C2552	C2465	U2367	C2276
U4431	C4332	G4238	G4144	G4083	A3876	G3768	A3692	G3593	A2798	G2719	G2636	C2553	C2466	U2368	C2277
C4432	C4333	A4239	C4145	A4084	A3877	G3769	G3696	G3594	G2800	G2720	G2637	C2554	C2467	A2369	A2278
G4433	A4334	G4240	G4146	G4085	A3878	G3770	U3697	G3595	A2801	G2721	G2638	C2555	C2468	U2370	G2279
C4434	C4335	C4241	C4147	G4086	A3879	G3771	G3698	G3596	G2802	G2722	U2639	C2556	C2469	A2371	A2282
U4438	A4336	G4242	G4148	G4087	G3880	A3772	C3699	G3597	G2803	G2723	G2640	C2557	C2470	A2372	G2289
C4439	C4337	U4243	C4149	C4088	C3881	G3773	U3699	G3598	C2814	U2724	G2641	C2558	C2471	A2373	G2290
U4440	G4338	G4244	G4150	G4089	G3882	A3774	G3699	G3599	C2815	G2725	G2642	C2559	C2472	A2374	G2291
A4441	C4339	A4245	C4151	G4090	G3883	G3775	G3699	G3600	A2816	G2726	G2643	C2560	C2473	A2382	G2288
C4442	A4340	G4246	C4152	G4091	C3884	G3776	G3699	G3601	C2817	G2727	G2644	C2561	C2474	G2391	C2290
U4443	U4341	G4247	C4153	G4092	G3885	A3777	G3699	G3602	A2818	U2728	G2645	C2562	C2475	C2392	G2295
G4444	C4342	U4248	G4154	G4093	C3886	G3778	G3699	G3603	U2820	U2729	G2646	C2563	C2476	A2395	G2296
U4445	A4343	C4249	C4155	G4094	C3887	G3779	G3699	G3604	U2821	G2730	C2647	C2564	C2477	A2396	G2297
C4446	C4344	G4250	C4156	G4095	C3888	A3780	G3699	G3605	U2822	U2731	G2648	C2565	C2478	A2397	G2298
U4447	U4345	A4251	C4157	G4096	C3889	G3781	G3699	G3606	U2823	G2732	C2649	C2566	C2479	A2400	G2299
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U4450	U4348	C4254	C4160	G4099	C3892	G3784	G3699	G3609	U2826	U2735	G2652	C2569	C2482	C2410	C2302
C4453	A4349	G4255	C4161	G4100	U3893	G3785	G3699	G3610	U2827	G2736	G2653	C2570	C2483	A2417	C2311
G4454	C4350	U4256	G4162	G4101	C3894	G3786	G3699	G3611	U2828	U2737	G2654	C2571	C2484	C2422	U2312
U4455	U4351	A4257	C4163	G4102	C3895	A3787	G3699	G3612	U2829	G2738	G2655	C2572	C2485	G2423	U2313
C4456	C4352	G4258	C4164	G4103	C3896	G3788	G3699	G3613	U2830	U2739	G2656	C2573	C2486	C2424	A2314
U4457	A4353	U4259	C4165	G4104	G3897	G3789	G3699	G3614	U2831	G2740	G2657	C2574	C2487	C2425	G2315
U4458	C4354	C4260	C4166	G4105	C3898	A3790	G3699	G3615	U2832	G2741	G2658	C2575	C2488	C2426	G2316
U4459	U4355	A4261	C4167	G4106	C3899	G3791	G3699	G3616	U2833	G2742	G2659	C2576	C2489	C2427	U2317
C4463	A4356	G4262	C4168	G4107	G3900	G3792	G3699	G3617	U2834	G2743	G2660	C2577	C2490	C2428	A2318
G4464	C4357	U4263	C4169	G4108	C3901	G3793	G3699	G3618	U2835	G2744	G2661	C2578	C2491	C2429	G2319
U4465	U4358	C4264	C4170	G4109	G3902	G3794	G3699	G3619	U2836	G2745	G2662	C2579	C2492	C2430	G2320
C4466	A4359	A4265	C4171	G4110	C3903	G3795	G3699	G3620	U2837	G2746	G2663	C2580	C2493	C2431	G2321
U4467	C4360	G4266	C4172	G4111	G3904	G3796	G3699	G3621	U2838	G2747	G2664	C2581	C2494	C2432	G2322
G4468	U4361	U4267	C4173	G4112	C3905	G3797	G3699	G3622	U2839	G2748	G2665	C2582	C2495	C2433	G2323
U4469	C4362	C4268	C4174	G4113	G3906	G3798	G3699	G3623	U2840	G2749	G2666	C2583	C2496	C2434	G2324
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C4471	C4364	G4270	C4176	G4115	G3908	G3799	G3699	G3625	U2842	G2751	G2668	C2585	C2498	C2436	G2326
U4472	U4365	U4271	C4177	G4116	C3909	G3800	G3699	G3626	U2843	G2752	G2669	C2586	C2499	C2437	G2327
G4473	A4366	G4272	C4178	G4117	G3910	G3801	G3699	G3627	U2844	G2753	G2670	C2587	C2500	C2438	G2328
U4474	C4367	A4273	C4179	G4118	C3911	G3802	G3699	G3628	U2845	G2754	G2671	C2588	C2501	C2439	G2329
C4475	U4368	U4274	C4180	G4119	G3912	G3803	G3699	G3629	U2846	G2755	G2672	C2589	C2502	C2440	G2330
U4476	A4369	C4275	C4181	G4120	C3913	G3804	G3699	G3630	U2847	G2756	G2673	C2590	C2503	C2441	G2331
G4477	C4370	G4276	C4182	G4121	G3914	G3805	G3699	G3631	U2848	G2757	G2674	C2591	C2504	C2442	G2332
U4478	U4371	U4277	C4183	G4122	G3915	G3806	G3699	G3632	U2849	G2758	G2675	C2592	C2505	C2443	G2333
C4479	A4372	C4278	C4184	G4123	G3916	G3807	G3699	G3633	U2850	G2759	G2676	C2593	C2506	C2444	G2334
U4480	C4373	A4279	C4185	G4124	G3917	G3808	G3699	G3634	U2851	G2760	G2677	C2594	C2507	C2445	G2335
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U4482	A4375	U4281	C4187	G4126	G3919	G3810	G3699	G3636	U2853	G2762	G2679	C2596	C2509	C2447	G2337
C4483	C4376	C4282	C4188	G4127	G3920	G3811	G3699	G3637	U2854	G2763	G2680	C2597	C2510	C2448	G2338
U4484	U4377	G4283	C4189	G4128	G3921	G3812	G3699	G3638	U2855	G2764	G2681	C2598	C2511	C2449	G2339



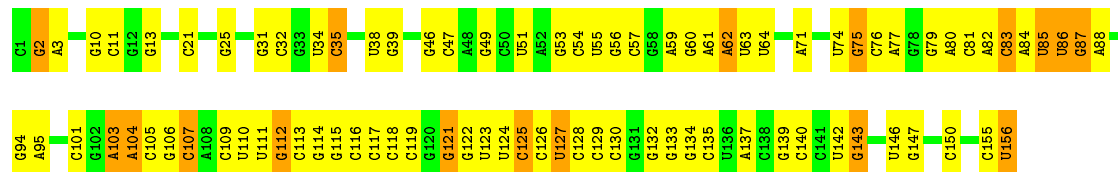
• Molecule 49: 5S ribosomal RNA

Chain 7: 65% 30% 5%



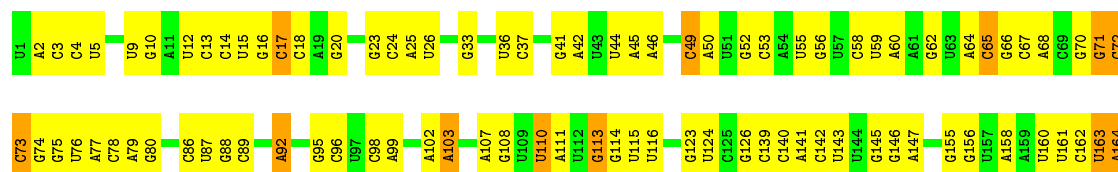
• Molecule 50: 5.8S ribosomal RNA

Chain 8: 45% 44% 11%

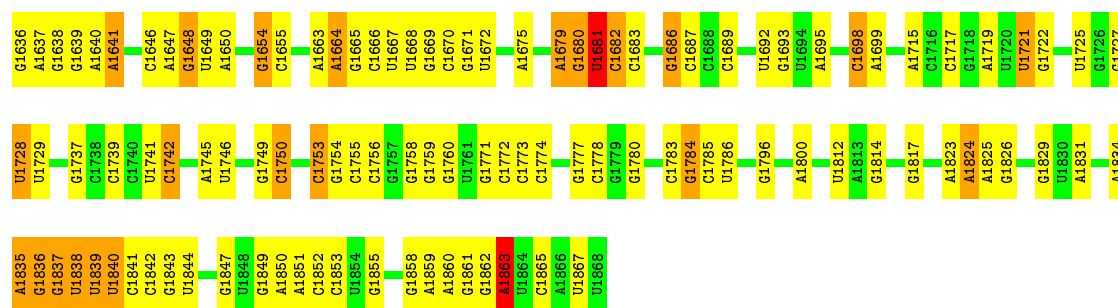


• Molecule 51: 18S ribosomal RNA

Chain 9: 47% 41% 11%

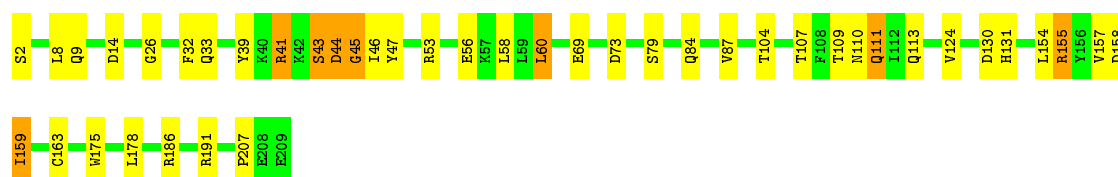


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G1488	A1489	G1490	U1494	G1495	G1498	U1499	G1500	C1501	G1507	A1508	U1509	G1510	G1516	G1517	C1518	U1519	G1520	C1521	A1522	C1523	G1524	C1525	G1526	C1527	G1528	C1529	U1530	A1531	G1532	A1533	G1534	U1535	G1536	A1537	C1538	G1541	C1542	U1543	C1544	G1545	G1546	C1547	A1548	U1551	G1552	C1553	U1554	U1555	A1556	C1557	C1558	C1559	U1560																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
C1416	C1417	C1418	C1419	G1420	A1421	G1422	C1423	G1424	G1425	G1426	C1427	U1432	C1433	C1434	C1437	A1438	A1439	C1440	U1441	U1442	C1443	C1444	U1445	G1446	C1447	A1448	G1449	A1452	C1453	G1454	G1455	G1456	G1459	G1460	U1461	U1462	U1463	C1464	G1465	G1466	C1467	G1473	G1475	A1476	A1477	U1478	G1481	G1482	A1483	A1486	A1487																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
G1318	G1321	G1322	G1330	C1331	A1332	C1333	G1334	G1335	C1336	U1342	U1343	U1344	U1347	G1348	G1351	U1364	U1371	U1372	C1373	C1374	G1375	A1378	C1384	G1385	A1386	G1387	G1393	G1394	A1395	U1396	U1397	G1398	U1399	A1400	A1401	A1402	C1403	A1404	A1405	G1406	U1407	U1408	A1409	C1410	G1411	C1412	G1413	A1414	C1415																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
A1251	C1252	A1253	C1254	G1255	G1256	G1257	A1258	A1259	A1260	A1265	C1266	C1267	C1268	G1269	G1270	C1271	G1274	G1275	A1276	G1280	G1281	A1282	G1283	A1284	G1285	G1286	A1287	U1288	U1289	G1290	A1291	C1292	A1293	C1294	A1295	G1298	A1299	U1300	A1301	C1302	U1303	C1304	C1305	U1306	U1307	U1308	C1309	U1310	C1311	G1312	A1313	U1314	U1315	C1317																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
G1166	G1167	G1168	G1169	A1170	G1175	C1180	A1181	A1190	C1191	A1194	A1195	A1196	G1197	G1198	A1199	A1200	G1207	A1208	G1209	A1210	G1211	G1212	G1213	G1214	C1215	C1216	A1217	C1218	G1219	A1220	G1221	G1224	G1227	A1228	G1229	C1230	C1231	G1232	G1233	C1234	G1235	G1236	C1237	A1240	A1241	U1242	U1243	C1247	A1250																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
G1097	C1098	G1099	A1100	U1101	G1102	C1103	G1104	G1105	G1108	G1109	G1110	U1111	U1112	A1113	U1114	U1115	C1116	C1117	C1118	U1119	U1120	A1121	A1122	C1125	G1126	C1127	G1128	G1129	G1130	G1131	A1132	A1133	G1134	C1135	U1136	U1137	C1138	G1139	G1140	G1141	G1142	A1143	A1144	A1145	C1146	C1147	A1148	A1149	A1150	C1153	U1154	G1157	G1158	G1165																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
A990	G991	A992	G993	C994	G995	A996	A997	A998	C1000	C1007	A1008	U1016	U1017	A1023	A1028	G1033	A1034	A1035	A1036	G1037	U1038	C1039	G1040	G1041	G1044	U1045	U1046	C1047	G1048	A1049	A1055	U1056	C1057	A1058	G1059	A1060	C1063	U1067	A1083	A1084	C1085	G1086	A1087	U1088	G1089	C1090	G1096																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
G901	G902	A903	A908	G909	G910	C911	C912	A913	U914	G915	A916	U917	A920	G921	A930	G931	G932	C933	C934	C935	G936	G937	C940	A941	U943	A944	U945	U946	G947	C948	G949	C950	C953	G956	U960	G961	A962	A963	A964	G970	G971	A980	U987	U988	C979	G982	G985	U986	U987	G989																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
A854	A855	G856	G859	U862	G863	A864	G865	U866	U867	A868	A869	A870	A871	A872	C873	G874	U878	G883	G884	G885	G886	G887	C888	C889	C890	G893	G894	G895	G896	G897	G898	G899	G900	G901	G902	U900	A810	A811	A812	G821	U822	U823	U824	A827	G828	C829	G830	G831	G832	C833	C834	C835	A837	G838	G839	U868	U869	G870	G871	G872	G873	G874	U875	G876	G877	G878	G879	G880	U887	U888	C889	G892	G895	U896	U897	U898	G899	G900	A903																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
G798	U799	U800	A810	A811	A812	G821	U822	U823	C824	A827	G828	C829	G830	G831	G832	C833	C834	C835	A837	G838	G839	C840	G841	C842	C843	G844	U845	G846	A847	C848	G849	C853	G856	U868	U869	G870	G871	G872	G873	G874	U875	G876	C877	G878	C879	G880	U887	U888	C889	G892	G895	U896	U897	U898	G899	G900	A903																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
A654	A655	G656	G659	U662	G663	A664	G665	U666	U667	A668	A669	A670	A671	A672	C673	G674	U678	G683	G684	U688	U689	G696	G697	G698	G730	G731	U732	U733	C734	C735	G736	G737	C738	C746	U747	U748	U749	G750	G751	G752	C753	G768	G769	C770	C771	C772	C773	C774	C775	C776	C777	C778	C779	C780	C781	C782	C783	C784	C785	C786	C787	C788	C789	C790	C791	C792	C793	C794	C795	C796	C797	C798	C799	C800	C801	C802	C803	C804	C805	C806	C807	C808	C809	C810	C811	C812	C813	C814	C815	C816	C817	C818	C819	C820	C821	C822	C823	C824	C825	C826	C827	C828	C829	C830	C831	C832	C833	C834	C835	C836	C837	C838	C839	C840	C841	C842	C843	C844	C845	C846	C847	C848	C849	C850	C851	C852	C853	C854	C855	C856	C857	C858	C859	C860	C861	C862	C863	C864	C865	C866	C867	C868	C869	C870	C871	C872	C873	C874	C875	C876	C877	C878	C879	C880	C881	C882	C883	C884	C885	C886	C887	C888	C889	C890	C891	C892	C893	C894	C895	C896	C897	C898	C899	C900	C901	C902	C903	C904	C905	C906	C907	C908	C909	C910	C911	C912	C913	C914	C915	C916	C917	C918	C919	C920	C921	C922	C923	C924	C925	C926	C927	C928	C929	C930	C931	C932	C933	C934	C935	C936	C937	C938	C939	C940	C941	C942	C943	C944	C945	C946	C947	C948	C949	C950	C951	C952	C953	C954	C955	C956	C957	C958	C959	C960	C961	C962	C963	C964	C965	C966	C967	C968	C969	C970	C971	C972	C973	C974	C975	C976	C977	C978	C979	C980	C981	C982	C983	C984	C985	C986	C987	C988	C989	C990	C991	C992	C993	C994	C995	C996	C997	C998	C999	C1000	C1001	C1002	C1003	C1004	C1005	C1006	C1007	C1008	C1009	C1010	C1011	C1012	C1013	C1014	C1015	C1016	C1017	C1018	C1019	C1020	C1021	C1022	C1023	C1024	C1025	C1026	C1027	C1028	C1029	C1030	C1031	C1032	C1033	C1034	C1035	C1036	C1037	C1038	C1039	C1040	C1041	C1042	C1043	C1044	C1045	C1046	C1047	C1048	C1049	C1050	C1051	C1052	C1053	C1054	C1055	C1056	C1057	C1058	C1059	C1060	C1061	C1062	C1063	C1064	C1065	C1066	C1067	C1068	C1069	C1070	C1071	C1072	C1073	C1074	C1075	C1076	C1077	C1078	C1079	C1080	C1081	C1082	C1083	C1084	C1085	C1086	C1087	C1088	C1089	C1090	C1091	C1092	C1093	C1094	C1095	C1096	C1097	C1098	C1099	C1100	C1101	C1102	C1103	C1104	C1105	C1106	C1107	C1108	C1109	C1110	C1111	C1112	C1113	C1114	C1115	C1116	C1117	C1118	C1119	C1120	C1121	C1122	C1123	C1124	C1125	C1126	C1127	C1128	C1129	C1130	C1131	C1132	C1133	C1134	C1135	C1136	C1137	C1138	C1139	C1140	C1141	C1142	C1143	C1144	C1145	C1146	C1147	C1148	C1149	C1150	C1151	C1152	C1153	C1154	C1155	C1156	C1157	C1158	C1159	C1160	C1161	C1162	C1163	C1164	C1165	C1166	C1167	C1168	C1169	C1170	C1171	C1172	C1173	C1174	C1175	C1176	C1177	C1178	C1179	C1180	C1181	C1182	C1183	C1184	C1185	C1186	C1187	C1188	C1189	C1190	C1191	C1192	C1193	C1194	C1195	C1196	C1197	C1198	C1199	C1200	C1201	C1202	C1203	C1204	C1205	C1206	C1207	C1208	C1209	C1210	C1211	C1212	C1213	C1214	C1215	C1216	C1217	C1218	C1219	C1220	C1221	C1222	C1223	C1224	C1225	C1226	C1227	C1228	C1229	C1230	C1231	C1232	C1233	C1234	C1235	C1236	C1237	C1238	C1239	C1240	C1241	C1242	C1243	C1244	C1245	C1246	C1247	C1248	C1249	C1250	C1251	C1252	C1253	C1254	C1255	C1256	C1257	C1258	C1259	C1260	C1261	C1262	C1263	C1264	C1265	C1266	C1267	C1268	C1269	C1270	C1271	C1272	C1273	C1274	C1275	C1276	C1277	C1278	C1279	C1280	C1281	C1282	C1283	C1284	C1285	C1286	C1287	C1288	C1289	C1290	C1291	C1292	C1293	C1294	C1295	C1296	C1297	C1298	C1299	C1300	C1301	C1302	C1303	C1304	C1305	C1306	C1307	C1308	C1309	C1310	C1311	C1312	C1313	C1314	C1315	C1316	C1317	C1318	C1319	C1320	C1321	C1322	C1323	C1324	C1325	C1326	C1327	C1328	C1329	C1330	C1331	C1332	C1333	C1334	C1335	C1336	C1337	C1338	C1339	C1340	C1341	C1342	C1343	C1344	C1345	C1346	C1347	C1348	C1349	C1350	C1351	C1352	C1353	C1354	C1355	C1356	C1357	C1358	C1359	C1360	C1361	C1362	C1363	C1364	C1365	C1366	C1367	C1368	C1369	C1370	C1371	C1372	C1373	C1374	C1375	C1376	C1377	C1378	C1379	C1380	C1381	C1382	C1383	C1384	C1385	C1386	C1387	C1388	C1389	C1390	C1391	C1392	C1393	C1394	C1395	C1396	C1397	C1398	C1399	C1400	C1401	C1402	C1403	C1404	C1405	C1406	C1407	C1408	C1409	C1410	C1411	C1412	C1413	C1414	C1415	C1416	C1417	C1418	C1419	C1420	C1421	C1422	C1423	C1424	C1425	C1426	C1427	C1428	C1429	C1430	C1431	C1432	C1433	C1434	C1435	C1436	C1437	C1438	C1439	C1440	C1441	C1442	C1443	C1444	C1445	C1446	C1447	C1448	C1449	C1450	C1451	C1452	C1453	C1454	C1455	C1456	C1457	C1458	C1459	C1460	C1461	C1462	C1463	C1464	C1465	C1466	C1467	C1468	C1469	C1470	C1471	C1472	C1473	C1474	C1475	C1476	C1477	C1478	C1479	C1480	C1481	C1482	C1483	C1484	C1485	C1486	C1487	C1488	C1489	C1490	C1491	C1492	C1493	C1494	C1495	C1496	C1497	C1498	C1499	C1500	C1501	C1502	C1503	C1504	C1505	C1506	C1507	C1508	C1509	C1510	C1511	C1512	C1513	C1



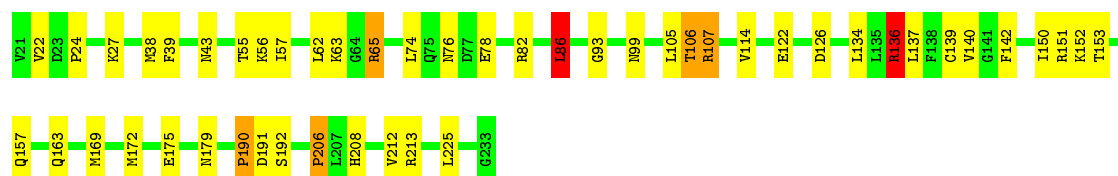
- Molecule 52: uS2

Chain AA: 79% 17%



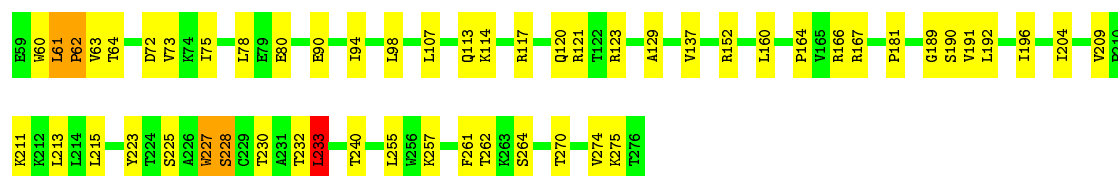
- Molecule 53: eS1

Chain BB: 77% 20%



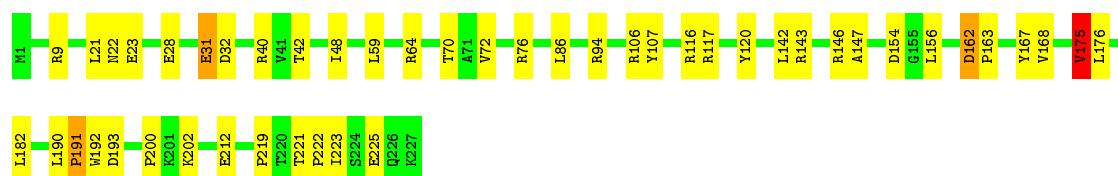
- Molecule 54: uS5

Chain CC: 75% 22%




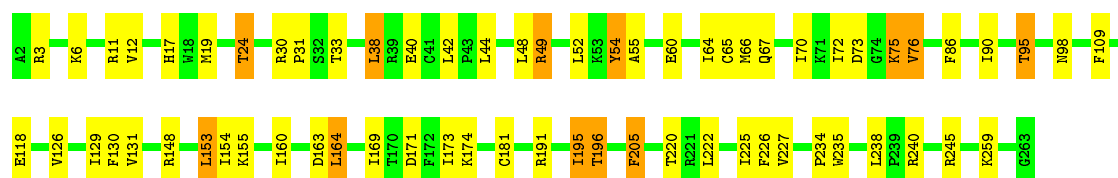
- Molecule 55: uS3

Chain DD: 79% 19%




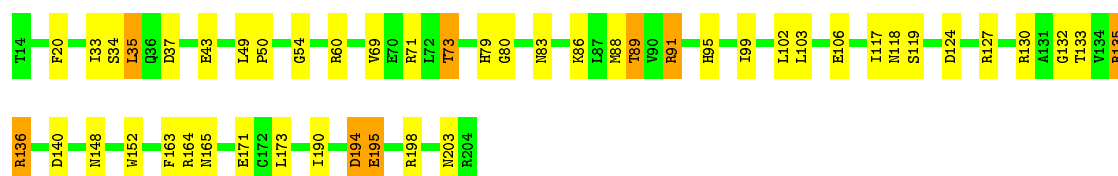
- Molecule 56: eS4

Chain EE: 




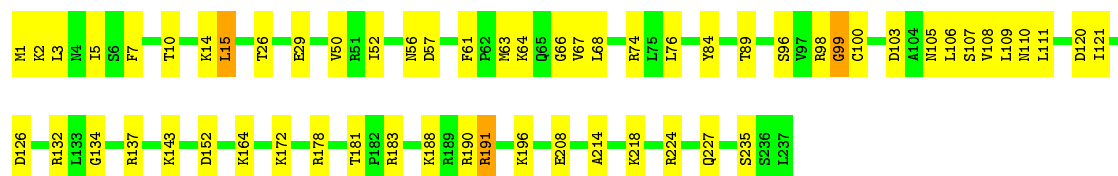
• Molecule 57: uS7

Chain FF: 




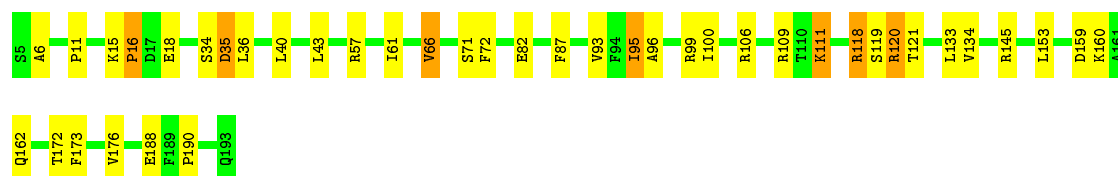
• Molecule 58: eS6

Chain GG: 



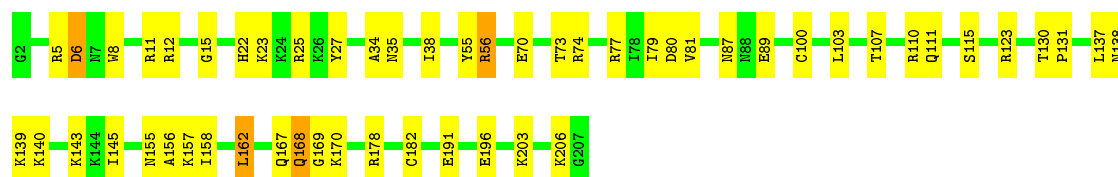
• Molecule 59: eS7

Chain HH: 




• Molecule 60: eS8

Chain II: 



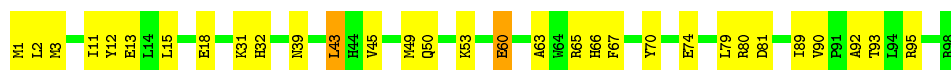
• Molecule 61: uS4

Chain JJ: 



- Molecule 62: eS10

Chain KK: 68% 30% .



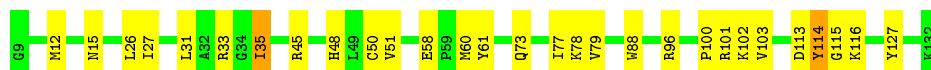
- Molecule 63: uS17

Chain LL: 80% 17% . .



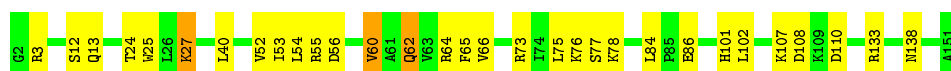
- Molecule 64: eS12

Chain MM: 77% 22% .



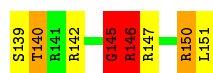
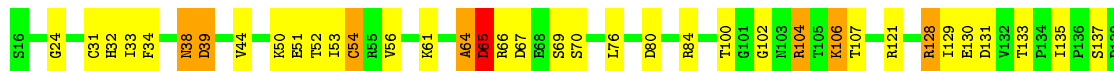
- Molecule 65: uS15

Chain NN: 79% 19% .



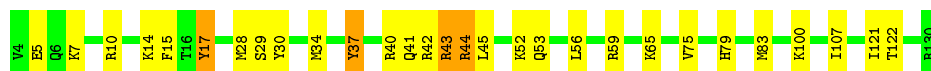
- Molecule 66: uS11

Chain OO: 67% 24% 7% .




- Molecule 67: uS19

Chain PP: 77% 20% .




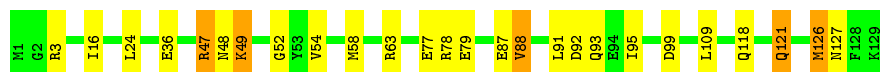
- Molecule 68: uS9

Chain QQ:  84% 12% ..




- Molecule 69: eS17

Chain RR:  80% 16% .




- Molecule 70: uS13

Chain SS:  78% 18% ..




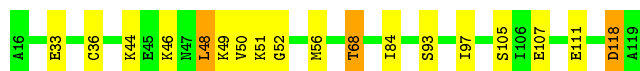
- Molecule 71: eS19

Chain TT:  82% 13% 5%




- Molecule 72: uS10

Chain UU:  83% 14% .




- Molecule 73: eS21

Chain VV:  80% 18% .




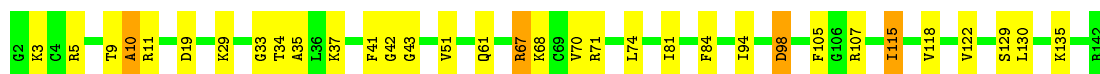
- Molecule 74: uS8

Chain WW:  82% 16% .



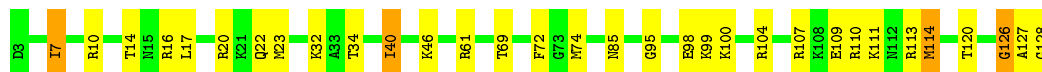
- Molecule 75: uS12

Chain XX:  77% 21% .



- Molecule 76: eS24

Chain YY: 75% 22%



- Molecule 77: eS25

Chain ZZ: 84% 16%



- Molecule 78: eS26

Chain aa: 82% 18%



- Molecule 79: eS27

Chain bb: 81% 18%



- Molecule 80: eS28

Chain cc: 85% 15%



- Molecule 81: uS14

Chain dd: 81% 19%




- Molecule 82: eS30

Chain ee: 84% 16%



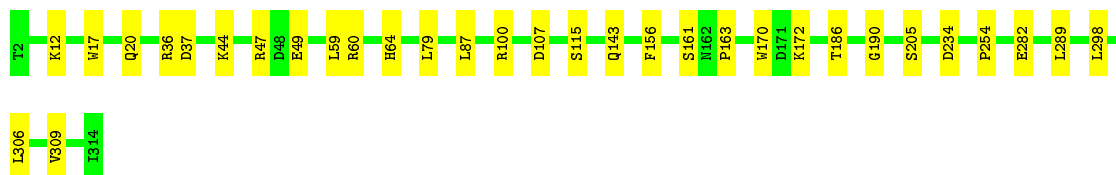
- Molecule 83: eS31

Chain ff:  86% 6% 9%



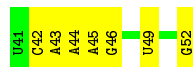
- Molecule 84: RACK1

Chain gg:  90% 10%



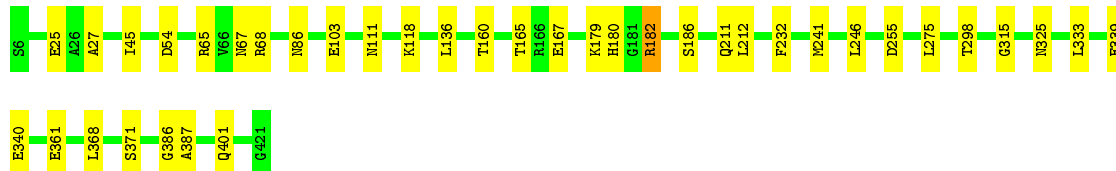
- Molecule 85: mRNA

Chain hh:  42% 58%



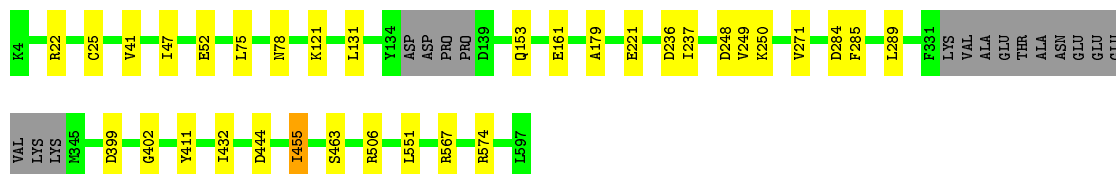
- Molecule 86: eRF1

Chain ii:  91% 9%



- Molecule 87: ABCE1

Chain jj:  92% 5% .



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	49979	Depositor
Resolution determination method	FSC 0.143	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TITAN KRIOS, FEI TITAN KRIOS	Depositor
Voltage (kV)	300, 300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30, 30	Depositor
Minimum defocus (nm)	2000, 2000	Depositor
Maximum defocus (nm)	3600, 3600	Depositor
Magnification	59000, 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	0.47	0/1906	0.78	0/2556
10	J	0.43	0/1376	0.75	1/1841 (0.1%)
11	L	0.42	0/1734	0.80	0/2317
12	M	0.44	0/1158	0.74	0/1547
13	N	0.46	0/1746	0.79	0/2338
14	O	0.48	1/1671 (0.1%)	0.79	0/2234
15	P	0.49	0/1268	0.75	0/1700
16	Q	0.43	0/1530	0.81	0/2041
17	R	0.43	0/1524	0.80	3/2013 (0.1%)
18	S	0.48	0/1493	0.85	3/2002 (0.1%)
19	T	0.40	0/1326	0.70	0/1770
2	B	0.47	0/3216	0.77	2/4311 (0.0%)
20	U	0.40	0/822	0.64	0/1103
21	V	0.45	0/993	0.74	0/1332
22	W	0.47	0/541	0.81	1/720 (0.1%)
23	X	0.45	0/993	0.71	0/1334
24	Y	0.44	0/1132	0.79	1/1504 (0.1%)
25	Z	0.41	0/1130	0.71	0/1507
26	a	0.45	0/1191	0.77	0/1590
27	b	0.45	0/619	0.72	0/818
28	c	0.38	0/742	0.66	0/996
29	d	0.44	0/903	0.82	1/1216 (0.1%)
3	C	0.48	0/2937	0.81	6/3946 (0.2%)
30	e	0.52	0/1071	0.84	0/1429
31	f	0.48	0/895	0.87	0/1198
32	g	0.46	0/916	0.79	1/1220 (0.1%)
33	h	0.39	0/1021	0.75	1/1348 (0.1%)
34	i	0.53	1/841 (0.1%)	1.85	7/1112 (0.6%)
35	j	0.50	0/720	0.91	2/952 (0.2%)
36	k	0.39	0/575	0.68	0/761
37	l	0.49	0/454	0.83	0/599
38	m	0.41	0/435	0.79	0/575

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
39	n	0.46	0/223	0.89	0/284
4	D	0.40	0/2432	0.70	1/3257 (0.0%)
40	o	0.42	0/864	0.74	0/1140
41	p	0.46	0/718	0.72	0/953
42	r	0.49	0/1017	0.79	0/1364
43	s	0.38	0/1547	0.59	0/2088
44	t	0.41	0/1257	0.70	0/1697
45	1	0.48	0/129	0.61	0/173
46	2	0.26	0/1805	0.71	0/2809
47	3	0.39	1/1777 (0.1%)	0.97	8/2763 (0.3%)
48	5	0.39	2/87790 (0.0%)	0.78	87/136937 (0.1%)
49	7	0.32	0/2858	0.67	0/4455
5	E	0.46	0/1936	0.81	2/2600 (0.1%)
50	8	0.39	0/3701	0.73	0/5766
51	9	0.33	1/41013 (0.0%)	0.78	43/63919 (0.1%)
52	AA	0.41	0/1679	0.68	0/2283
53	BB	0.40	0/1756	0.76	4/2350 (0.2%)
54	CC	0.40	0/1732	0.75	2/2347 (0.1%)
55	DD	0.41	0/1792	0.72	0/2412
56	EE	0.38	0/2115	0.74	1/2843 (0.0%)
57	FF	0.42	1/1531 (0.1%)	0.74	2/2059 (0.1%)
58	GG	0.43	0/1946	0.75	0/2590
59	HH	0.40	0/1544	0.69	1/2068 (0.0%)
6	F	0.45	0/1905	0.75	1/2539 (0.0%)
60	II	0.44	0/1715	0.76	0/2287
61	JJ	0.44	0/1550	0.85	5/2069 (0.2%)
62	KK	0.41	0/851	0.72	0/1147
63	LL	0.44	0/1259	0.75	0/1684
64	MM	0.45	0/968	0.64	0/1296
65	NN	0.44	0/1232	0.75	0/1656
66	OO	0.41	0/1029	0.84	1/1380 (0.1%)
67	PP	0.43	0/1079	0.75	1/1437 (0.1%)
68	QQ	0.37	0/1142	0.73	1/1528 (0.1%)
69	RR	0.38	0/1060	0.70	0/1421
7	G	0.42	0/1967	0.75	2/2647 (0.1%)
70	SS	0.41	0/1157	0.83	2/1548 (0.1%)
71	TT	0.39	0/1120	0.77	2/1499 (0.1%)
72	UU	0.37	0/831	0.69	0/1115
73	VV	0.39	0/645	0.74	0/865
74	WW	0.44	0/1051	0.75	0/1406
75	XX	0.38	0/1116	0.74	0/1490
76	YY	0.40	0/1040	0.72	0/1382
77	ZZ	0.38	0/604	0.74	0/810

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
78	aa	0.39	0/794	0.76	0/1065
79	bb	0.39	0/665	0.64	0/891
8	H	0.40	0/1535	0.74	1/2063 (0.0%)
80	cc	0.36	0/478	0.76	0/640
81	dd	0.41	0/455	0.81	1/603 (0.2%)
82	ee	0.38	0/462	0.74	0/607
83	ff	0.41	0/538	0.61	0/713
84	gg	0.35	0/2493	0.63	0/3394
85	hh	0.32	0/286	0.74	0/443
86	ii	0.38	0/3333	0.62	1/4483 (0.0%)
87	jj	0.43	1/4633 (0.0%)	0.61	2/6249 (0.0%)
9	I	0.40	0/1693	0.68	1/2260 (0.0%)
All	All	0.40	8/242727 (0.0%)	0.77	201/355704 (0.1%)

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	1
17	R	0	1
18	S	0	3
2	B	0	2
24	Y	0	1
26	a	0	2
3	C	0	2
31	f	0	2
34	i	0	3
38	m	0	1
42	r	0	1
5	E	0	1
51	9	0	3
52	AA	0	2
56	EE	0	2
57	FF	0	1
59	HH	0	1
66	OO	0	1
68	QQ	0	1
70	SS	0	1
71	TT	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
72	UU	0	1
73	VV	0	1
74	WW	0	1
75	XX	0	1
86	ii	0	2
9	I	0	2
All	All	0	42

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
87	jj	121	LYS	CE-NZ	13.88	1.83	1.49
34	i	91	SER	C-N	-9.54	1.12	1.34
51	9	1306	U	O3'-P	-7.59	1.52	1.61
48	5	957	G	O3'-P	6.93	1.69	1.61
47	3	41	U	C3'-C2'	6.36	1.59	1.52

The worst 5 of 201 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	i	92	SER	CA-C-N	-33.35	43.83	117.20
34	i	91	SER	O-C-N	-30.40	74.06	122.70
34	i	92	SER	C-N-CA	-30.10	46.45	121.70
47	3	70	G	N9-C1'-C2'	-11.69	98.81	114.00
48	5	3753	G	N9-C1'-C2'	-11.37	99.22	114.00

There are no chirality outliers.

5 of 42 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
3	C	339	THR	Peptide
3	C	48	ASN	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	19	0
2	B	3148	0	3267	30	0
3	C	2883	0	3053	41	0
4	D	2386	0	2419	23	0
5	E	1898	0	2035	34	0
6	F	1870	0	1994	18	0
7	G	1934	0	2087	36	0
8	H	1516	0	1597	10	0
9	I	1655	0	1704	36	0
10	J	1353	0	1386	16	0
11	L	1703	0	1820	22	0
12	M	1137	0	1211	23	0
13	N	1701	0	1749	16	0
14	O	1638	0	1777	23	0
15	P	1242	0	1274	5	0
16	Q	1506	0	1623	10	0
17	R	1508	0	1664	34	0
18	S	1454	0	1496	11	0
19	T	1298	0	1366	11	0
20	U	808	0	831	3	0
21	V	979	0	1039	3	0
22	W	528	0	541	3	0
23	X	976	0	1053	6	0
24	Y	1115	0	1205	6	0
25	Z	1107	0	1182	11	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	1000	0	0
33	h	1013	0	1147	0	0
34	i	830	0	914	0	0
35	j	705	0	737	0	0
36	k	569	0	637	0	0
37	l	444	0	483	0	0
38	m	429	0	467	0	0
39	n	222	0	264	0	0
40	o	851	0	921	0	0
41	p	708	0	757	0	0
42	r	1001	0	1060	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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	15	0
47	3	1593	0	811	111	0
48	5	78486	0	39661	1252	0
49	7	2558	0	1296	26	0
50	8	3314	0	1683	48	0
51	9	36680	0	18530	603	0
52	AA	1642	0	1646	14	0
53	BB	1729	0	1803	9	0
54	CC	1694	0	1782	35	0
55	DD	1764	0	1863	8	0
56	EE	2073	0	2175	22	0
57	FF	1509	0	1563	34	0
58	GG	1923	0	2089	20	0
59	HH	1521	0	1616	14	0
60	II	1686	0	1772	30	0
61	JJ	1525	0	1640	18	0
62	KK	827	0	854	5	0
63	LL	1238	0	1315	11	0
64	MM	958	0	993	3	0
65	NN	1208	0	1294	6	0
66	OO	1016	0	1039	13	0
67	PP	1060	0	1120	12	0
68	QQ	1124	0	1193	6	0
69	RR	1047	0	1103	17	0
70	SS	1139	0	1191	11	0
71	TT	1102	0	1142	11	0
72	UU	821	0	883	1	0
73	VV	636	0	634	4	0
74	WW	1034	0	1080	5	0
75	XX	1098	0	1167	11	0
76	YY	1023	0	1090	7	0
77	ZZ	598	0	656	3	0
78	aa	781	0	828	0	0
79	bb	651	0	672	0	0
80	cc	475	0	497	0	0
81	dd	445	0	439	0	0
82	ee	457	0	502	0	0
83	ff	527	0	545	0	0
84	gg	2436	0	2393	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
85	hh	256	0	129	0	0
86	ii	3280	0	3326	0	0
87	jj	4551	0	4687	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	35	0	0	0	0
88	C	1	0	0	0	0
88	I	1	0	0	0	0
88	P	1	0	0	0	0
88	Q	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	226469	0	169875	2584	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 7.

The worst 5 of 2584 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)
61:JJ:121:LYS:NZ	61:JJ:121:LYS:CE	1.49	1.39
57:FF:194:ASP:O	57:FF:198:ARG:HG3	1.28	1.33
48:5:976:G:H2'	48:5:977:C:O4'	1.26	1.30
7:G:29:ASN:OD1	7:G:30:PRO:HD3	1.30	1.28
48:5:4213:A:N1	48:5:4218:U:O4	1.66	1.26

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	242/244 (99%)	215 (89%)	23 (10%)	4 (2%)	11	57
2	B	392/394 (100%)	354 (90%)	33 (8%)	5 (1%)	15	61
3	C	360/362 (99%)	322 (89%)	30 (8%)	8 (2%)	8	52
4	D	290/292 (99%)	263 (91%)	25 (9%)	2 (1%)	26	72
5	E	232/248 (94%)	179 (77%)	34 (15%)	19 (8%)	1	17
6	F	223/225 (99%)	206 (92%)	16 (7%)	1 (0%)	39	80
7	G	239/241 (99%)	206 (86%)	25 (10%)	8 (3%)	5	44
8	H	188/190 (99%)	170 (90%)	16 (8%)	2 (1%)	17	65
9	I	200/213 (94%)	181 (90%)	14 (7%)	5 (2%)	7	49
10	J	167/169 (99%)	144 (86%)	15 (9%)	8 (5%)	3	32
11	L	208/210 (99%)	182 (88%)	15 (7%)	11 (5%)	2	29
12	M	136/138 (99%)	124 (91%)	12 (9%)	0	100	100
13	N	201/203 (99%)	186 (92%)	15 (8%)	0	100	100
14	O	197/199 (99%)	190 (96%)	7 (4%)	0	100	100
15	P	151/153 (99%)	141 (93%)	9 (6%)	1 (1%)	26	72
16	Q	185/187 (99%)	172 (93%)	11 (6%)	2 (1%)	17	65
17	R	178/180 (99%)	166 (93%)	10 (6%)	2 (1%)	17	65
18	S	173/175 (99%)	158 (91%)	11 (6%)	4 (2%)	8	52
19	T	157/159 (99%)	139 (88%)	15 (10%)	3 (2%)	10	55
20	U	97/99 (98%)	84 (87%)	8 (8%)	5 (5%)	2	30
21	V	129/131 (98%)	116 (90%)	12 (9%)	1 (1%)	24	70
22	W	61/63 (97%)	57 (93%)	4 (7%)	0	100	100
23	X	117/119 (98%)	111 (95%)	5 (4%)	1 (1%)	21	68
24	Y	132/134 (98%)	115 (87%)	15 (11%)	2 (2%)	13	59
25	Z	133/135 (98%)	114 (86%)	13 (10%)	6 (4%)	3	34

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	a	145/147 (99%)	124 (86%)	16 (11%)	5 (3%)	5	44
27	b	73/75 (97%)	66 (90%)	6 (8%)	1 (1%)	14	60
28	c	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
29	d	105/107 (98%)	90 (86%)	13 (12%)	2 (2%)	10	55
30	e	126/128 (98%)	117 (93%)	6 (5%)	3 (2%)	7	51
31	f	107/109 (98%)	93 (87%)	9 (8%)	5 (5%)	3	33
32	g	112/114 (98%)	107 (96%)	5 (4%)	0	100	100
33	h	120/122 (98%)	108 (90%)	8 (7%)	4 (3%)	5	44
34	i	100/102 (98%)	85 (85%)	11 (11%)	4 (4%)	4	38
35	j	84/86 (98%)	73 (87%)	10 (12%)	1 (1%)	16	63
36	k	67/69 (97%)	57 (85%)	7 (10%)	3 (4%)	3	34
37	l	48/50 (96%)	40 (83%)	4 (8%)	4 (8%)	1	16
38	m	50/52 (96%)	46 (92%)	4 (8%)	0	100	100
39	n	21/23 (91%)	21 (100%)	0	0	100	100
40	o	102/104 (98%)	89 (87%)	10 (10%)	3 (3%)	6	47
41	p	89/91 (98%)	79 (89%)	10 (11%)	0	100	100
42	r	123/125 (98%)	100 (81%)	18 (15%)	5 (4%)	3	37
43	s	196/198 (99%)	162 (83%)	24 (12%)	10 (5%)	2	30
44	t	161/163 (99%)	100 (62%)	34 (21%)	27 (17%)	0	4
45	1	13/15 (87%)	10 (77%)	1 (8%)	2 (15%)	0	5
52	AA	206/208 (99%)	174 (84%)	23 (11%)	9 (4%)	3	34
53	BB	211/213 (99%)	172 (82%)	25 (12%)	14 (7%)	1	24
54	CC	216/218 (99%)	187 (87%)	22 (10%)	7 (3%)	5	45
55	DD	225/227 (99%)	187 (83%)	29 (13%)	9 (4%)	4	38
56	EE	260/262 (99%)	215 (83%)	29 (11%)	16 (6%)	2	26
57	FF	189/191 (99%)	163 (86%)	18 (10%)	8 (4%)	3	36
58	GG	235/237 (99%)	205 (87%)	27 (12%)	3 (1%)	15	61
59	HH	187/189 (99%)	153 (82%)	22 (12%)	12 (6%)	2	25
60	II	204/206 (99%)	171 (84%)	26 (13%)	7 (3%)	5	44
61	JJ	183/185 (99%)	156 (85%)	20 (11%)	7 (4%)	4	39
62	KK	96/98 (98%)	64 (67%)	21 (22%)	11 (12%)	0	9

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
63	LL	150/152 (99%)	131 (87%)	14 (9%)	5 (3%)	5	44
64	MM	122/124 (98%)	85 (70%)	29 (24%)	8 (7%)	1	24
65	NN	148/150 (99%)	126 (85%)	16 (11%)	6 (4%)	3	37
66	OO	134/136 (98%)	104 (78%)	15 (11%)	15 (11%)	0	9
67	PP	125/127 (98%)	111 (89%)	11 (9%)	3 (2%)	7	51
68	QQ	139/141 (99%)	116 (84%)	17 (12%)	6 (4%)	3	35
69	RR	127/129 (98%)	108 (85%)	14 (11%)	5 (4%)	4	38
70	SS	135/137 (98%)	116 (86%)	11 (8%)	8 (6%)	2	27
71	TT	139/141 (99%)	128 (92%)	8 (6%)	3 (2%)	8	52
72	UU	102/104 (98%)	88 (86%)	8 (8%)	6 (6%)	2	27
73	VV	81/83 (98%)	70 (86%)	7 (9%)	4 (5%)	3	32
74	WW	127/129 (98%)	110 (87%)	10 (8%)	7 (6%)	2	29
75	XX	139/141 (99%)	125 (90%)	10 (7%)	4 (3%)	6	47
76	YY	124/126 (98%)	102 (82%)	15 (12%)	7 (6%)	2	28
77	ZZ	73/75 (97%)	59 (81%)	12 (16%)	2 (3%)	6	48
78	aa	96/98 (98%)	78 (81%)	9 (9%)	9 (9%)	1	14
79	bb	81/83 (98%)	66 (82%)	9 (11%)	6 (7%)	1	20
80	cc	59/61 (97%)	48 (81%)	10 (17%)	1 (2%)	11	57
81	dd	51/53 (96%)	44 (86%)	6 (12%)	1 (2%)	9	54
82	ee	55/57 (96%)	40 (73%)	13 (24%)	2 (4%)	4	41
83	ff	59/69 (86%)	51 (86%)	6 (10%)	2 (3%)	5	44
84	gg	311/313 (99%)	269 (86%)	33 (11%)	9 (3%)	6	47
86	ii	414/416 (100%)	383 (92%)	25 (6%)	6 (1%)	14	60
87	jj	569/594 (96%)	518 (91%)	40 (7%)	11 (2%)	10	55
All	All	12494/12710 (98%)	10874 (87%)	1202 (10%)	418 (3%)	8	44

5 of 418 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	196	TRP
5	E	91	PRO
5	E	95	ASP
5	E	118	PRO
5	E	175	LEU

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%)	160 (86%)	27 (14%)	4	27
2	B	336/342 (98%)	301 (90%)	35 (10%)	9	43
3	C	302/302 (100%)	260 (86%)	42 (14%)	4	29
4	D	247/247 (100%)	222 (90%)	25 (10%)	9	44
5	E	208/221 (94%)	184 (88%)	24 (12%)	7	37
6	F	194/195 (100%)	166 (86%)	28 (14%)	4	27
7	G	206/206 (100%)	183 (89%)	23 (11%)	7	39
8	H	169/169 (100%)	149 (88%)	20 (12%)	6	36
9	I	174/180 (97%)	155 (89%)	19 (11%)	8	41
10	J	142/142 (100%)	130 (92%)	12 (8%)	13	53
11	L	176/176 (100%)	147 (84%)	29 (16%)	3	20
12	M	117/117 (100%)	100 (86%)	17 (14%)	4	27
13	N	171/171 (100%)	151 (88%)	20 (12%)	7	36
14	O	171/171 (100%)	148 (86%)	23 (14%)	5	30
15	P	134/134 (100%)	121 (90%)	13 (10%)	10	46
16	Q	163/163 (100%)	141 (86%)	22 (14%)	5	30
17	R	159/159 (100%)	139 (87%)	20 (13%)	5	32
18	S	156/156 (100%)	133 (85%)	23 (15%)	4	26
19	T	139/139 (100%)	123 (88%)	16 (12%)	7	37
20	U	89/89 (100%)	81 (91%)	8 (9%)	12	50
21	V	101/101 (100%)	84 (83%)	17 (17%)	2	19
22	W	55/55 (100%)	50 (91%)	5 (9%)	12	50
23	X	107/107 (100%)	96 (90%)	11 (10%)	9	43
24	Y	124/124 (100%)	106 (86%)	18 (14%)	4	27
25	Z	117/117 (100%)	110 (94%)	7 (6%)	24	66
26	a	119/119 (100%)	107 (90%)	12 (10%)	9	44

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	b	62/62 (100%)	57 (92%)	5 (8%)	15	54
28	c	79/79 (100%)	68 (86%)	11 (14%)	4	29
29	d	98/98 (100%)	81 (83%)	17 (17%)	2	17
30	e	114/114 (100%)	97 (85%)	17 (15%)	4	26
31	f	88/88 (100%)	76 (86%)	12 (14%)	5	30
32	g	98/98 (100%)	85 (87%)	13 (13%)	5	31
33	h	109/109 (100%)	97 (89%)	12 (11%)	8	40
34	i	86/86 (100%)	79 (92%)	7 (8%)	15	54
35	j	73/73 (100%)	64 (88%)	9 (12%)	6	34
36	k	64/64 (100%)	58 (91%)	6 (9%)	11	48
37	l	47/47 (100%)	41 (87%)	6 (13%)	5	32
38	m	48/48 (100%)	37 (77%)	11 (23%)	1	8
39	n	22/22 (100%)	19 (86%)	3 (14%)	5	30
40	o	92/92 (100%)	79 (86%)	13 (14%)	4	28
41	p	74/74 (100%)	68 (92%)	6 (8%)	15	54
42	r	109/109 (100%)	90 (83%)	19 (17%)	2	17
43	s	166/166 (100%)	156 (94%)	10 (6%)	24	66
44	t	136/136 (100%)	126 (93%)	10 (7%)	17	58
45	1	13/13 (100%)	13 (100%)	0	100	100
52	AA	174/174 (100%)	154 (88%)	20 (12%)	7	37
53	BB	194/194 (100%)	166 (86%)	28 (14%)	4	27
54	CC	184/184 (100%)	161 (88%)	23 (12%)	6	33
55	DD	190/190 (100%)	160 (84%)	30 (16%)	3	23
56	EE	223/223 (100%)	191 (86%)	32 (14%)	4	28
57	FF	161/161 (100%)	138 (86%)	23 (14%)	4	28
58	GG	207/207 (100%)	177 (86%)	30 (14%)	4	27
59	HH	169/169 (100%)	153 (90%)	16 (10%)	11	47
60	II	178/178 (100%)	155 (87%)	23 (13%)	5	32
61	JJ	161/161 (100%)	140 (87%)	21 (13%)	5	32
62	KK	89/89 (100%)	76 (85%)	13 (15%)	4	27
63	LL	136/136 (100%)	119 (88%)	17 (12%)	6	33

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
64	MM	104/104 (100%)	87 (84%)	17 (16%)	3	20
65	NN	130/130 (100%)	112 (86%)	18 (14%)	4	29
66	OO	106/106 (100%)	81 (76%)	25 (24%)	1	7
67	PP	116/116 (100%)	98 (84%)	18 (16%)	3	24
68	QQ	117/117 (100%)	104 (89%)	13 (11%)	8	40
69	RR	117/117 (100%)	104 (89%)	13 (11%)	8	40
70	SS	119/119 (100%)	100 (84%)	19 (16%)	3	22
71	TT	112/112 (100%)	98 (88%)	14 (12%)	6	33
72	UU	94/94 (100%)	82 (87%)	12 (13%)	5	32
73	VV	67/67 (100%)	59 (88%)	8 (12%)	6	35
74	WW	112/112 (100%)	102 (91%)	10 (9%)	12	51
75	XX	113/113 (100%)	98 (87%)	15 (13%)	5	31
76	YY	108/108 (100%)	87 (81%)	21 (19%)	2	12
77	ZZ	66/66 (100%)	58 (88%)	8 (12%)	6	34
78	aa	85/85 (100%)	76 (89%)	9 (11%)	8	42
79	bb	75/75 (100%)	64 (85%)	11 (15%)	4	26
80	cc	54/54 (100%)	46 (85%)	8 (15%)	4	26
81	dd	47/47 (100%)	39 (83%)	8 (17%)	2	18
82	ee	47/47 (100%)	40 (85%)	7 (15%)	4	26
83	ff	59/62 (95%)	57 (97%)	2 (3%)	44	79
84	gg	272/272 (100%)	249 (92%)	23 (8%)	13	53
86	ii	358/358 (100%)	328 (92%)	30 (8%)	14	53
87	jj	507/522 (97%)	486 (96%)	21 (4%)	37	76
All	All	10892/10936 (100%)	9583 (88%)	1309 (12%)	11	35

5 of 1309 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
33	h	28	LEU
53	BB	105	LEU
79	bb	84	HIS
34	i	103	LYS
42	r	10	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
5	E	217	GLN
12	M	131	GLN
80	cc	40	HIS
86	ii	325	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
46	2	74/76 (97%)	22 (29%)	1 (1%)
47	3	72/75 (96%)	36 (50%)	13 (18%)
48	5	3645/3662 (99%)	1161 (31%)	270 (7%)
49	7	119/120 (99%)	19 (15%)	1 (0%)
50	8	155/156 (99%)	47 (30%)	6 (3%)
51	9	1710/1719 (99%)	559 (32%)	113 (6%)
85	hh	11/12 (91%)	7 (63%)	0
All	All	5786/5820 (99%)	1851 (31%)	404 (6%)

5 of 1851 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
46	2	5	C
46	2	7	G
46	2	8	U
46	2	9	A
46	2	13	U

5 of 404 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
48	5	2398	U
48	5	3810	C
51	9	1396	A
48	5	2475	G
48	5	2760	G

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

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	1.93	1 (4%)
91	ADP	jj	603	-	24,29,29	1.08	2 (8%)	23,45,45	1.90	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	2.02	1.35	1.32
91	jj	603	ADP	C5-C4	3.28	1.47	1.40
91	jj	602	ADP	C5-C4	3.31	1.48	1.40

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
91	jj	602	ADP	N3-C2-N1	-7.77	122.77	128.87
91	jj	603	ADP	N3-C2-N1	-7.64	122.87	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.