



## wwPDB/EMDatabank EM Map/Model Validation Summary Report ⓘ

Jun 29, 2019 – 11:17 PM EDT

PDB ID : 6R6P  
EMDB ID: : EMD-4737  
Title : Structure of XBP1u-paused ribosome nascent chain complex (rotated state)  
Authors : Shanmuganathan, V.; Cheng, J.; Berninghausen, O.; Beckmann, R.  
Deposited on : 2019-03-27  
Resolution : 3.10 Å(reported)  
Based on PDB ID : ?

This is a wwPDB/EMDatabank EM Map/Model Validation Summary Report  
for a publicly released PDB/EMDB entry.

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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MolProbity : 4.02b-467  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.3.2

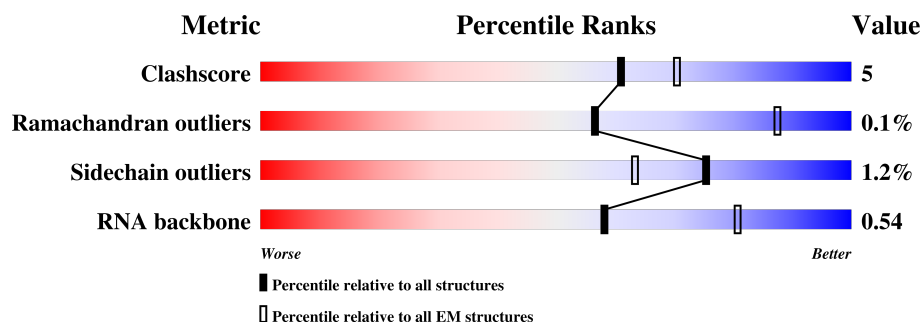
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.10 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.























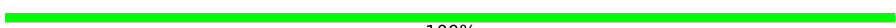

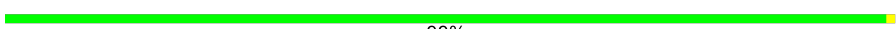


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	136327	1886
Ramachandran outliers	132723	1663
Sidechain outliers	132532	1531
RNA backbone	3747	458

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	5	3662	
2	7	120	
3	8	156	
4	A	244	
5	B	394	
6	C	362	
7	D	292	
8	E	248	

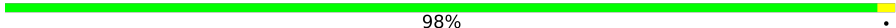
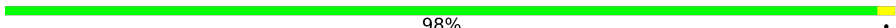
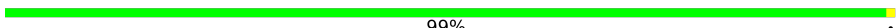
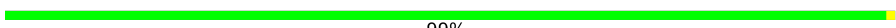
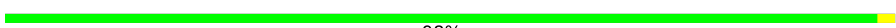








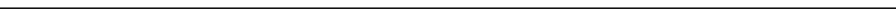





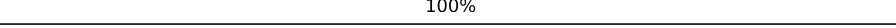
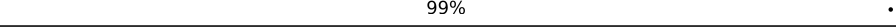
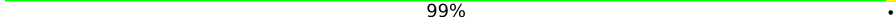
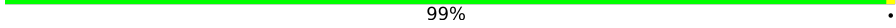
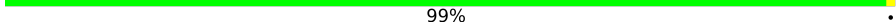
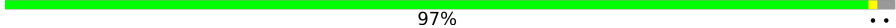
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Mol	Chain	Length	Quality of chain
9	F	225	 80% 20%
10	G	241	 86% 13%
11	H	190	 82% 18%
12	I	213	 77% 19% .
13	J	169	 86% 13% .
14	L	210	 88% 11%
15	M	138	 86% 14%
16	N	203	 83% 16%
17	O	199	 82% 17% .
18	P	153	 84% 15% .
19	Q	187	 89% 11%
20	R	180	 87% 13%
21	S	175	 82% 18%
22	T	159	 84% 16%
23	U	99	 86% 14%
24	V	131	 80% 20%
25	W	63	 86% 13% .
26	X	119	 86% 14%
27	Y	134	 80% 20%
28	Z	135	 82% 17% .
29	a	147	 100%
30	b	75	 99% .
31	c	94	 99% .
32	d	107	 98% .
33	e	128	 99% .



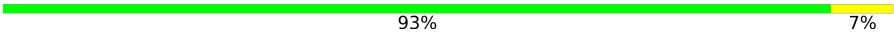




















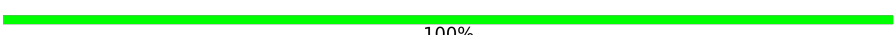

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Mol	Chain	Length	Quality of chain
34	f	109	 98% .
35	g	114	 98% .
36	h	122	 99% .
37	i	102	 99% .
38	j	86	 98% .
39	k	69	 99% .
40	l	50	 94% 6% .
41	m	52	 100% .
42	n	23	 100% .
43	o	104	 96% .
44	p	91	 98% .
45	r	125	 95% . .
46	s	198	 99% .
47	t	163	 98% .
48	1	24	 50% 46% .
49	2	76	 50% 36% 13% .
50	3	75	 68% 28% .
51	K	1698	 60% 33% 7% .
52	q	217	 100% .
53	u	213	 99% .
54	v	221	 99% .
55	x	262	 99% .
56	z	237	 99% .
57	y	189	 97% . .
58	CC	206	 86% 14% .

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Mol	Chain	Length	Quality of chain
59	XX	185	 86% 14%
60	EE	151	 77% 17% • 5%
61	QQ	149	 93% 7%
62	MM	136	 85% 15%
63	UU	142	 85% 13%
64	YY	132	 89% 11%
65	HH	83	 82% 18%
66	TT	129	 84% 16%
67	VV	141	 85% 13%
68	NN	124	 81% 19%
69	ZZ	101	 83% 17%
70	JJ	83	 81% 18%
71	AA	55	 85% 13%
72	DD	228	 85% 15%
73	BB	191	 82% 15%
74	SS	96	 80% 20%
75	RR	117	 87% 13%
76	9	120	 86% 14%
77	II	144	 76% 24%
78	PP	141	 84% 16%
79	GG	100	 75% 25%
80	OO	75	 92% 8%
81	FF	62	 85% 15%
82	w	55	 100%
83	0	68	 79% 19%

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Mol	Chain	Length	Quality of chain
84	6	313	<div><div></div><div>83%</div><div>17%</div></div>
85	4	10	<div><div></div><div>30%</div><div>50%</div><div>20%</div></div>

## 2 Entry composition

There are 87 unique types of molecules in this entry. The entry contains 218067 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 RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	5	3662	Total	C	N	O	P	0	0
			78486	34947	14363	25515	3661		

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 4 is a protein called uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	244	Total	C	N	O	S	0	0
			1868	1171	382	309	6		

- Molecule 5 is a protein called uL3.

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

- Molecule 6 is a protein called uL4.

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

- Molecule 7 is a protein called 60S ribosomal protein L5.

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

- Molecule 8 is a protein called 60S ribosomal protein L6.

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

- Molecule 9 is a protein called uL30.

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

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	175	ALA	THR	conflict	UNP G1SV32
F	185	GLY	ASN	conflict	UNP G1SV32
F	202	ARG	HIS	conflict	UNP G1SV32
F	233	GLU	GLY	conflict	UNP G1SV32

- Molecule 10 is a protein called eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	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 11 is a protein called uL6.

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



- Molecule 12 is a protein called Ribosomal protein L10 (Predicted).

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

- Molecule 13 is a protein called uL5.

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

- Molecule 14 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	L	210	Total	C	N	O	S	0	0
			1703	1065	354	280	4		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	47	ALA	-	insertion	UNP G1TPV0
L	48	PRO	-	insertion	UNP G1TPV0
L	49	ARG	-	insertion	UNP G1TPV0
L	50	PRO	-	insertion	UNP G1TPV0
L	51	ALA	-	insertion	UNP G1TPV0
L	52	SER	-	insertion	UNP G1TPV0
L	53	GLY	-	insertion	UNP G1TPV0
L	54	PRO	-	insertion	UNP G1TPV0
L	55	LEU	-	insertion	UNP G1TPV0

- Molecule 15 is a protein called Ribosomal protein L14.

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

- Molecule 16 is a protein called Ribosomal protein L15.

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

- Molecule 17 is a protein called uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	O	199	Total	C	N	O	S	0	0
			1638	1056	321	256	5		

- Molecule 18 is a protein called uL22.

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

- Molecule 19 is a protein called eL18.

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

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	6	ARG	LEU	conflict	UNP G1TX70
Q	14	ARG	TRP	conflict	UNP G1TX70
Q	23	ILE	MET	conflict	UNP G1TX70
Q	24	TYR	CYS	conflict	UNP G1TX70
Q	38	ARG	HIS	conflict	UNP G1TX70
Q	57	ASN	LYS	conflict	UNP G1TX70
Q	66	MET	VAL	conflict	UNP G1TX70
Q	74	GLY	ASP	conflict	UNP G1TX70
Q	75	ARG	PRO	conflict	UNP G1TX70
Q	77	GLY	ASN	conflict	UNP G1TX70
Q	106	SER	THR	conflict	UNP G1TX70
Q	110	ARG	HIS	conflict	UNP G1TX70
Q	117	GLY	GLU	conflict	UNP G1TX70
Q	124	ASP	HIS	conflict	UNP G1TX70
Q	134	CYS	ARG	conflict	UNP G1TX70
Q	150	ARG	GLN	conflict	UNP G1TX70
Q	172	ARG	GLY	conflict	UNP G1TX70
Q	184	ARG	TRP	conflict	UNP G1TX70

- Molecule 20 is a protein called eL19.

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

- Molecule 21 is a protein called eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	S	175	Total	C	N	O	S	0	0
			1454	925	284	235	10		

- Molecule 22 is a protein called eL21.

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

- Molecule 23 is a protein called Ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	U	99	Total	C	N	O	S	0	0
			808	518	141	147	2		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U	32	GLY	ARG	conflict	UNP G1TSG1
U	36	ALA	GLU	conflict	UNP G1TSG1
U	39	PHE	SER	conflict	UNP G1TSG1
U	54	GLY	ARG	conflict	UNP G1TSG1
U	60	VAL	ALA	conflict	UNP G1TSG1
U	97	ARG	HIS	conflict	UNP G1TSG1

- Molecule 24 is a protein called uL14.

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

- Molecule 25 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	W	63	Total	C	N	O	S	0	0
			528	337	103	85	3		

- Molecule 26 is a protein called uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	X	119	Total	C	N	O	S	0	0
			976	624	183	168	1		

- Molecule 27 is a protein called Ribosomal protein L26.

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

- Molecule 28 is a protein called 60S ribosomal protein L27.

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

- Molecule 29 is a protein called uL15.

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

- Molecule 30 is a protein called 60S ribosomal protein L29.

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

- Molecule 31 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	c	94	Total	C	N	O	S	0	0
			732	465	130	131	6		

- Molecule 32 is a protein called eL31.

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

- Molecule 33 is a protein called eL32.

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

- Molecule 34 is a protein called eL33.

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

- Molecule 35 is a protein called eL34.

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

- Molecule 36 is a protein called uL29.

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

- Molecule 37 is a protein called 60S ribosomal protein L36.

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

- Molecule 38 is a protein called Ribosomal protein L37.

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

- Molecule 39 is a protein called eL38.

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

- Molecule 40 is a protein called ribosomal protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	l	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 41 is a protein called eL40.

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

- Molecule 42 is a protein called 60s ribosomal protein l41.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	n	23	Total	C	N	O	S	0	0
			222	134	61	25	2		

- Molecule 43 is a protein called eL42.

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

- Molecule 44 is a protein called ribosomal protein eL43.

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

- Molecule 45 is a protein called eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	r	125	Total	C	N	O	S	0	0
			1001	621	206	168	6		

- Molecule 46 is a protein called 60S acidic ribosomal protein P0.

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

- Molecule 47 is a protein called Ribosomal protein L12.

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

- Molecule 48 is a protein called X-box-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	1	24	Total	C	N	O	S	0	0
			204	137	35	30	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	255	ALA	SER	conflict	UNP P17861

- Molecule 49 is a RNA chain called A/P-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	2	76	Total	C	N	O	P	0	0
			1614	722	287	530	75		

- Molecule 50 is a RNA chain called P/E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	3	75	Total	C	N	O	P	0	0
			1597	714	287	522	74		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
51	K	1698	Total	C	N	O	P	0	0
			36248	16180	6508	11863	1697		

- Molecule 52 is a protein called uS2.

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

- Molecule 53 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	u	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	v	221	Total	C	N	O	S	0	0
			1716	1111	295	301	9		

- Molecule 55 is a protein called 40S ribosomal protein S4.

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

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
x	25	GLY	SER	conflict	UNP G1TK17
x	51	ARG	LYS	conflict	UNP G1TK17
x	78	THR	ALA	conflict	UNP G1TK17
x	156	VAL	MET	conflict	UNP G1TK17

- Molecule 56 is a protein called 40S ribosomal protein S6.

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

- Molecule 57 is a protein called 40S ribosomal protein S7.

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

- Molecule 58 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	CC	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
CC	47	ARG	GLY	conflict	UNP G1TJW1

- Molecule 59 is a protein called Ribosomal protein S9 (Predicted).

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

- Molecule 60 is a protein called Ribosomal protein S11.

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

- Molecule 61 is a protein called ribosomal protein uS15.

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

- Molecule 62 is a protein called uS11.

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

- Molecule 63 is a protein called Ribosomal protein S16.

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

- Molecule 64 is a protein called eS17.

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

- Molecule 65 is a protein called eS21.

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

- Molecule 66 is a protein called Ribosomal protein S15a.

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

- Molecule 67 is a protein called Ribosomal protein S23.

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

- Molecule 68 is a protein called eS24.

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

- Molecule 69 is a protein called eS26.

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

- Molecule 70 is a protein called 40S ribosomal protein S27.

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

- Molecule 71 is a protein called 40S ribosomal protein S30.

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

- Molecule 72 is a protein called Ribosomal protein S3.

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

- Molecule 73 is a protein called Ribosomal protein S5.

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

- Molecule 74 is a protein called eS10.

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

- Molecule 75 is a protein called 40S ribosomal protein S12.

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

- Molecule 76 is a protein called uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	9	120	Total	C	N	O	S	0	0
			997	635	187	168	7		

- Molecule 77 is a protein called uS13.

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

- Molecule 78 is a protein called eS19.

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 79 is a protein called uS10.

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

- Molecule 80 is a protein called ribosomal protein eS25.

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

- Molecule 81 is a protein called Ribosomal protein S28.

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

- Molecule 82 is a protein called S29.

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

- Molecule 83 is a protein called eS31.

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

- Molecule 84 is a protein called ribosomal protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	6	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	4	10	Total	C	N	O	P	0	0
			211	95	37	69	10		

- Molecule 86 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
86	P	1	Total	Mg	0
			1	1	
86	g	1	Total	Mg	0
			1	1	
86	Q	1	Total	Mg	0
			1	1	
86	e	1	Total	Mg	0
			1	1	
86	I	1	Total	Mg	0
			1	1	
86	V	1	Total	Mg	0
			1	1	
86	7	4	Total	Mg	0
			4	4	
86	5	148	Total	Mg	0
			148	148	
86	8	1	Total	Mg	0
			1	1	

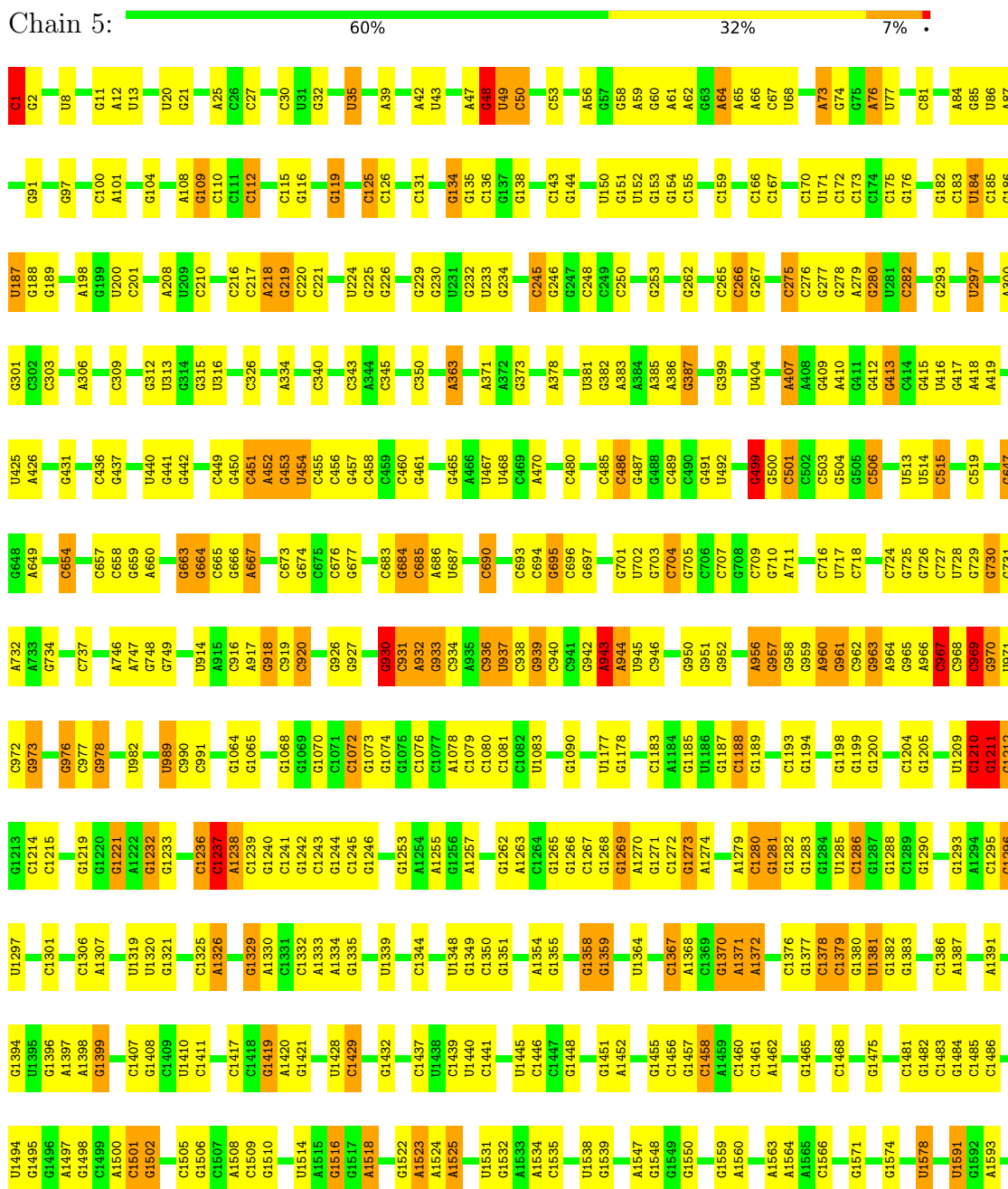
- Molecule 87 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
87	o	1	Total	Zn	0
			1	1	
87	g	1	Total	Zn	0
			1	1	
87	j	1	Total	Zn	0
			1	1	
87	p	1	Total	Zn	0
			1	1	
87	m	1	Total	Zn	0
			1	1	

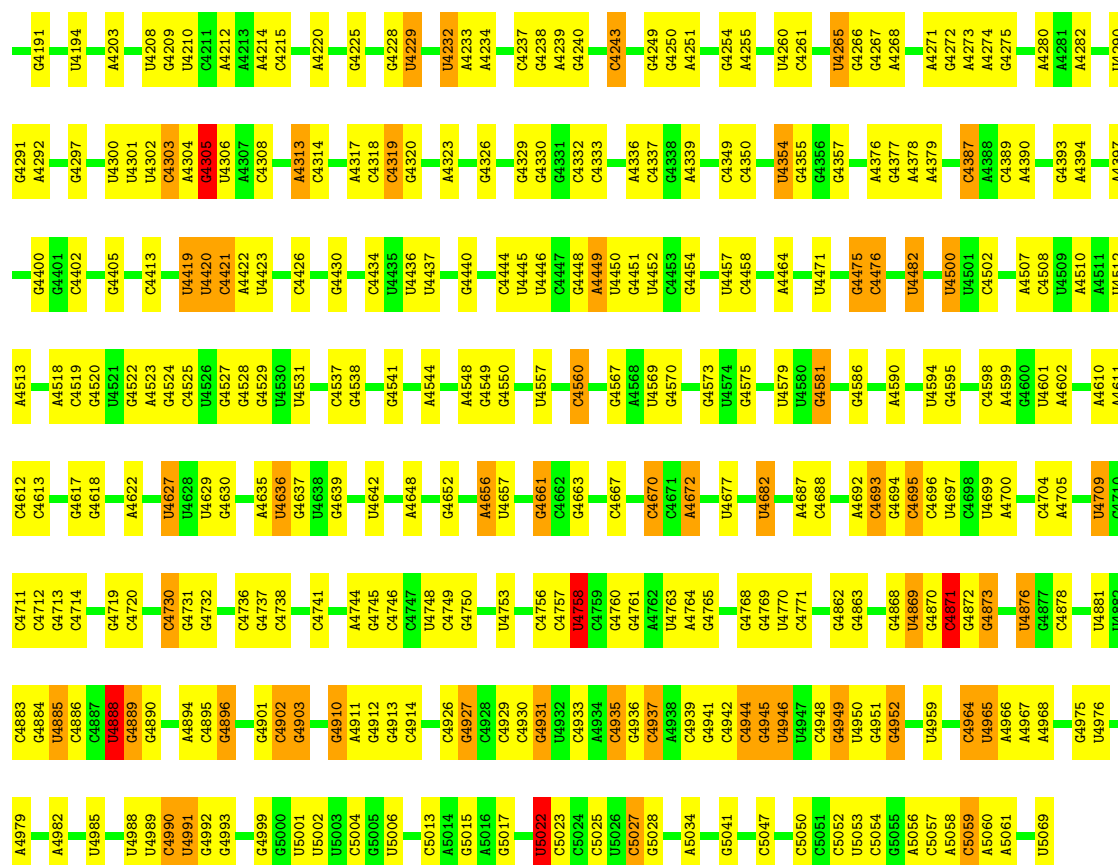
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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: 28S ribosomal RNA



G4097	A4098	G4099	G4104	G4107	C4114	C4115	C4116	U4117	C4119	C4120	C4121	G4124	C4125	C4126	C4128	C4134	C4135	G4143	C4144	C4145	C4146	C4149	G4150	C4151	C4158	C4162	U4163	C4164	C4165	C4166	A4170	C4171	C4172	C4173	C4174	C4175	C4176	C4177	C4180	C4181	C4182	C4183	C4184	C4185	C4187	C4188	C4189	C4190	G4094	G4095	G4096		
G3889	U3889	U3892	U3893	U3894	G3897	G3898	G3899	G3900	A3901	A3905	A3906	A3907	A3908	A3909	U3915	G3916	A3917	G3918	C3919	C3926	U3927	A3928	G3932	G3933	G3938	G3939	A3943	G3946	U4067	U4068	U4069	U4070	U4071	C4072	A4073	G4076	G4084	A4085	G4086	U4087	C4088	C4089	C4090	G4094	G4095	G4096							
A3766	C3767	C3771	U3772	U3773	C3774	G3777	U3778	A3784	U3785	U3786	A3799	U3802	G3809	C3810	G3811	C3812	U3813	U3814	A3817	U3818	C3819	G3823	U3838	U3839	U3840	C3843	U3853	U3854	C3855	U3856	A3860	A3861	A3862	A3865	G3868	U3869	C3870	A3871	A3876	U3877	C3878	C3879	C3882										
A3643	A3646	A3647	A3648	A3649	C3650	U3657	A3662	C3667	C3670	U3671	C3672	C3673	U3680	C3683	G3686	A3687	U3688	G3689	A3692	U3697	C3698	C3700	G3705	U3709	C3710	C3711	C3712	C3713	C3714	U3721	A2725	C2726	U2730	C2735	C2736	C2737	C2738	C2739	U2740	U2741	G2742	A2745											
G2848	A2849	G2855	C2856	A2857	C2860	C2867	C2890	U2891	G2897	C2898	G2903	U2904	G2905	C2909	C2910	G3592	C3593	C3594	C3595	A3596	G3597	C3598	A3599	C3602	G3603	A3604	C3605	A3611	C3621	C3622	C3623	A3624	G3625	G3626	C3741	A3748	A3760	C3761	G3765														
A3766	C3767	C3771	U3772	U3773	C3774	G3777	U3778	A3784	U3785	U3786	A3799	U3802	G3809	C3810	G3811	C3812	U3813	U3814	A3817	U3818	C3819	G3823	U3838	U3839	U3840	C3843	U3853	U3854	C3855	U3856	A3860	A3861	A3862	A3865	G3868	U3869	C3870	A3871	A3876	U3877	C3878	C3879	C3882										
G3889	U3889	U3892	U3893	U3894	G3897	G3898	G3899	G3900	A3901	A3905	A3906	A3907	A3908	A3909	U3915	G3916	A3917	G3918	C3919	C3926	U3927	A3928	G3932	G3933	G3938	G3939	A3943	G3946	U4067	U4068	U4069	U4070	U4071	C4072	A4073	G4076	G4084	A4085	G4086	U4087	C4088	C4089	C4090	G4094	G4095	G4096							
G4097	A4098	G4099	G4104	G4107	C4114	C4115	C4116	U4117	C4119	C4120	C4121	G4124	C4125	C4126	C4128	C4134	C4135	G4143	C4144	C4145	C4146	C4149	G4150	C4151	C4158	C4162	U4163	C4164	C4165	C4166	A4170	C4171	C4172	C4173	C4174	C4175	C4176	C4177	C4180	C4181	C4182	C4183	C4184	C4185	C4187	C4188	C4189	C4190	G4094	G4095	G4096		
C1694	C1698	A1699	C1718	A1719	C1720	G1721	G1724	U1725	U1726	U1727	U1728	A1729	U1730	C1731	G1734	U1735	C1740	G1741	A1742	A1743	U1754	C1755	U1756	U1757	G1758	C1759	G1760	G1761	G1764	A1765	C1768	G1769	C1772	A1775	A1776	C1777	A1780	U1781	A1786	A1787	U1790	U1791	U1792	A1793	A1794	C1795	G1796	C1797					
G1799	A1802	G1803	A1804	A1805	C1806	C1807	C1812	G1815	C1816	U1817	G1818	A1819	C1820	G1821	U1822	C1829	G1833	U1834	G1835	G1836	G1840	C1847	U1848	A1850	G1853	G1854	G1855	C1859	G1864	G1865	U1866	G1869	C1881	U1882	G1886	G1887	A1888	U1889	C1890	C1891	U1892	C1893	C1894	A1895	C1896								
A1897	U1906	A1907	A1908	G1909	G1910	C1914	U1915	U1916	U1917	U1918	G1919	C1920	C1921	G1922	A1923	C1924	G1925	A1928	A1929	U1930	C1931	C1935	C1936	A1939	G1940	A1941	A1942	A1943	U1949	U1957	A1958	U1959	A1960	G1961	A1962	C1963	A1964	G1965	C1966	A1967	G1968	G1969	C1970	C1971	C1972	U1973	U1974	G1975	C1976	C1977			
C1978	A1979	U1980	G1981	G1982	A1983	U1984	G1985	U1986	C1987	G1988	A1991	U1992	C1993	C1994	U1997	G2001	A2002	G2003	G2007	U2008	A2009	A2010	C2011	U2015	C2016	A2017	U2020	C2021	C2022	C2023	A2026	A2029	A2030	A2041	U2044	G2045	G2046	A2047	U2048	G2052	C2053	G2055	G2056	C2062	G2063	G2064	G2065	G2066					
A2069	C2072	C2083	C2084	G2085	C2088	U2090	C2091	G2092	U2093	G2094	A2095	C2096	U2097	C2101	A2105	G2106	C2107	G2108	G2109	C2110	G2111	C2112	G2113	C2114	G2115	C2116	G2117	C2118	C2119	G2120	C2121	G2122	C2123	G2124	C2125	G2126	C2127	C2247	C2248	C2249	C2250	G2251	C2252	A2253	C2254	C2255	C2256	C2257	C2258	G2259	C2260	G2261	G2262
A2263	C2264	G2265	C2266	U2267	A2268	C2274	A2279	C2280	U2281	U2282	G2283	A2289	C2295	G2296	A2300	G2301	G2306	G2309	C2310	C2311	U2312	A2313	C2314	G2315	C2316	G2322	U2329	C2330	C2331	C2332	C2333	C2334	C2335	C2336	C2337	C2338	G2345	G2348	A2349	U2350	C2351	U2352	A2360	G2361	U2362	U2386							
G2387	A2395	A2396	G2407	C2410	C2411	A2412	A2417	G2421	C2422	U2425	G2433	A2438	G2439	U2440	U2447	G2448	A2449	G2450	U2454	G2457	C2458	G2459	A2460	G2461	C2462	C2465	G2466	U2467	U2468	C2469	C2470	G2471	C2478	G2479	C2480	G2481	U2485	G2486	G2487	C2488	G2489	U2490											
C2491	C2498	C2499	G2502	G2503	C2504	G2505	G2506	A2513	C2514	G2515	A2516	G2517	C2520	G2521	G2522	C2526	A2527	G2528	A2529	U2530	C2531	C2532	A2537	G2544	U2545	G2546	G2547	C2548	G2549	A2553	U2554	G2557	C2560	C2568	G2569	U2570	U2575	C2572	A2573	G2574	U2575	C2581	A2582	C2583	A2587	C2588							
C2589	G2609	G2610	A2611	G2618	G2638	A2647	U2661	G2662	G2663	C2669	C2670	G2681	G2686	U2687	G2688	G2694	A2695	A2696	A2697	G2698	C2699	C2704	G2705	G2706	C2709	C2710	G2711	G2712	C2713	C2714	U2721	A2725	C2726	U2730	C2735	C2736	C2737	C2738	C2739	U2740	U2741	G2742	A2745										
A2746	C2749	C2750	C2751	C2752	C2753	C2754	A2757	C2758	C2759	U2761	C2762	U2763	A2766	U2767	C2768	C2770	C2777	C2778	C2786	A2787	C2788	A2789	U2790	C2794	A2798	A2806	G2811	A2812	A2813	C2814	U2819	C2820	U2826	G2827	U2828	A2833	C2834	A2835	U2839	G2842	A2845												
G2848	A2849	G2855	C2856	A2857	C2860	C2867	C2890	U2891	G2897	C2898	G2903	U2904	G2905	C2909	C2910	G3592	C3593	C3594	C3595	A3596	G3597	C3598	A3599	C3602	G3603	A3604	C3605	A3611	C3621	C3622	C3623	A3624	G3625	G3626	C3741	A3748	A3760	C3761	G3765														
A3643	A3646	A3647	A3648	A3649	C3650	U3657	A3662	C3667	C3670	U3671	C3672	C3673	U3680	C3683	G3686	A3687	U3688	G3689	A3692	U3697	C3698	C3700	G3705	U3709	C3710	C3711	C3712	C3713	C3714	U3721	A2725	C2726	U2730	C2735	C2736	C2737	C2738	C2739	U2740	U2741	G2742	A2745											
A3766	C3767	C3771	U3772	U3773	C3774	G3777	U3778	A3784	U3785	U3786	A3799	U3802	G3809	C3810	G3811	C3812	U3813	U3814	A3817	U3818	C3819	G3823	U3838	U3839	U3840	C3843	U3853	U3854	C3855	U3856	A3860	A3861	A3862	A3865	G3868	U3869	C3870	A3871	A3876	U3877	C3878	C3879	C3882										
G3889	U3889	U3892	U3893	U3894	G3897	G3898	G3899	G3900	A3901	A3905	A3906	A3907	A3908	A3909	U3915	G3916	A3917	G3918	C3919	C3926	U3927	A3928	G3932	G3933	G3938	G3939	A3943	G3946	U4067	U4068	U4069	U4070	U4071	C4072	A4073	G4076	G4084	A4085	G4086	U4087	C4088	C4089	C4090	G4094	G4095	G4096							
G4097	A4098	G4099	G4104	G4107	C4114	C4115	C4116	U4117	C4119	C4120	C4121	G4124	C4125	C4126	C4128	C4134	C4135	G4143	C4144	C4145	C4146	C4149	G4150	C4151	C4158	C4162	U4163	C4164	C4165	C4166	A4170	C4171	C4172	C4173	C4174	C4175	C4176	C4177	C4180	C4181	C4182	C4183	C4184	C4185	C4187	C4188	C4189	C4190	G4094	G4095	G4096		
U1596	G1597	C1598	A1599	A1600	A1601	U1602	C1607	G1612	A1613	A1621	G1624	G1625	C1628	A1631	A1632	G1633	A1634	A1635	U1636	A1637	A1638	U1639	C1640	G1641	C1645	A1646	U1649	A1650	G1651	C1654	C1655	U1656	U1660	C1661	A1669	G1670	U1671	C1676	U1677	G1680	C1686	U1691	C1692	U1693									
C1694	C1698	A1699	C1718	A1719	C1720	G1721	G1724	U1725	U1726	U1727	U1728	A1729	U1730	C1731	G1734	U1735	C1740	G1741	A1742	A1743	U1754	C1755	U1756	U1757	G1758	C1759	G1760	G1761	G1764	A1765	C1768	G1769	C1772	A1775	A1776	C1777	A1780	U1781	A1786	A1787	U1790	U1791	U1792	A1793	A1794	C1795	G1796	C1797					
G1799	A1802	G1803	A1804	A1805	C1806	C1807	C1812	G1815	C1816	U1817	G1818	A1819	C1820	G1821	U1822	C1829	G1833	U1834	G1835	G1836	G1840	C1847	U1848	A1850	G1853	G1854	G1855	C1859	G1864	G1865	U1866	G1869	C1881	U1882	G1886	G1887	A1888	U1889	C1890	C1891	U1892	C1893	C1894	A1895	C1896								
A1897	U1906	A1907	A1908	G1909	G1910	C1914	U1915	U1916	U1917	U1918	G1919	C1920	C1921	G1922	A1923	C1924	G1925	A1928	A1929	U1930	C1931	C1935	C1936	A1939	G1940	A1941	A1942	A1943	U1949	U19																							



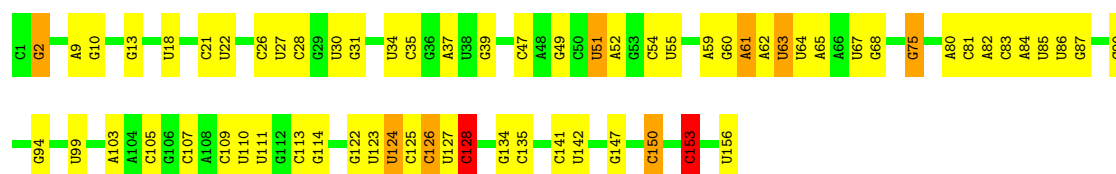
- Molecule 2: 5S ribosomal RNA

Chain 7:  73% 20% 7%



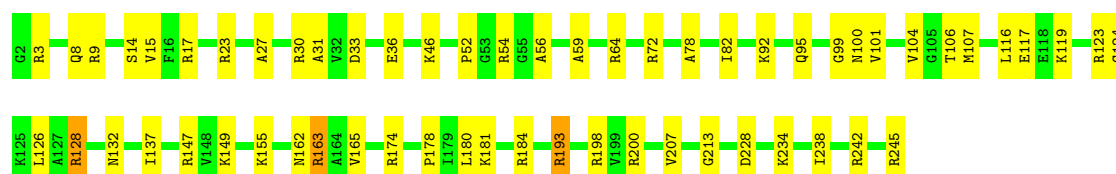
- Molecule 3: 5.8S ribosomal RNA

Chain 8:  58% 36% 5%



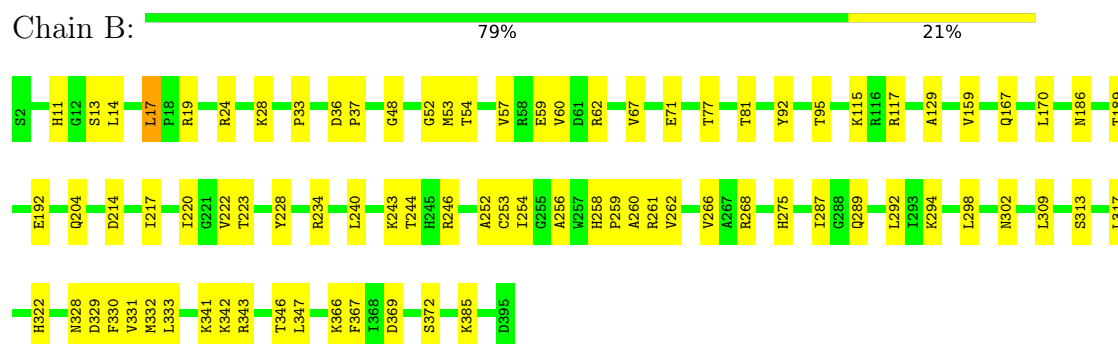
- Molecule 4: uL2

Chain A:  76% 23%

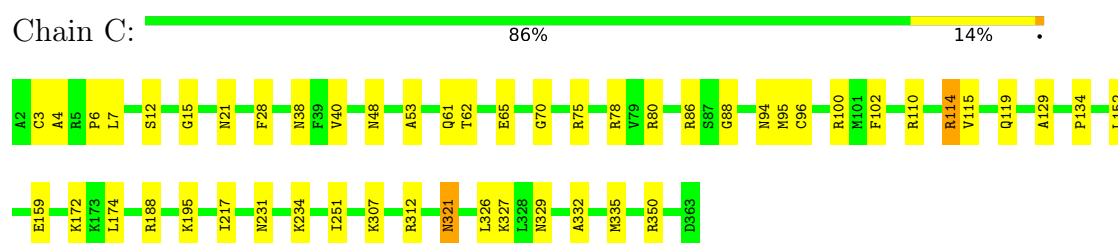




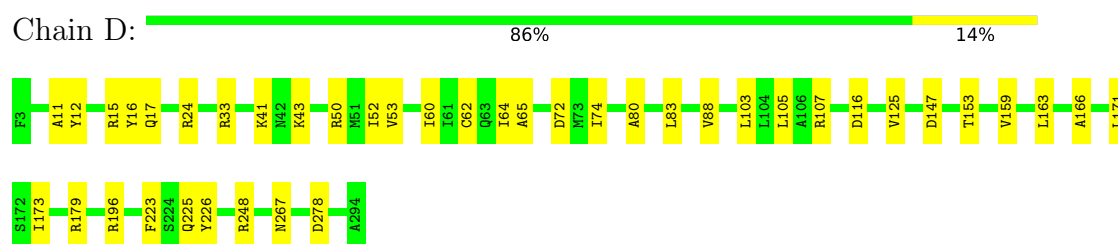
- Molecule 5: uL3



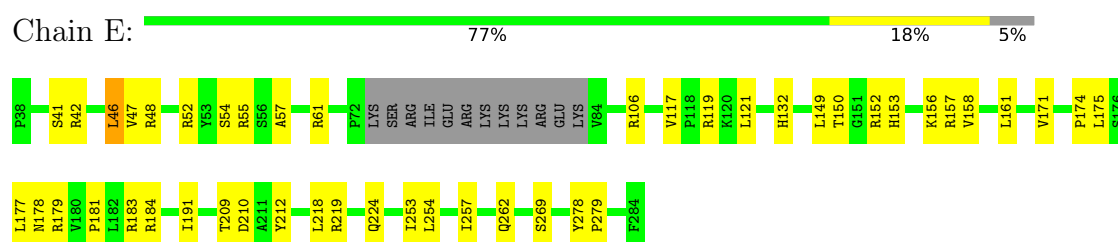
- Molecule 6: uL4



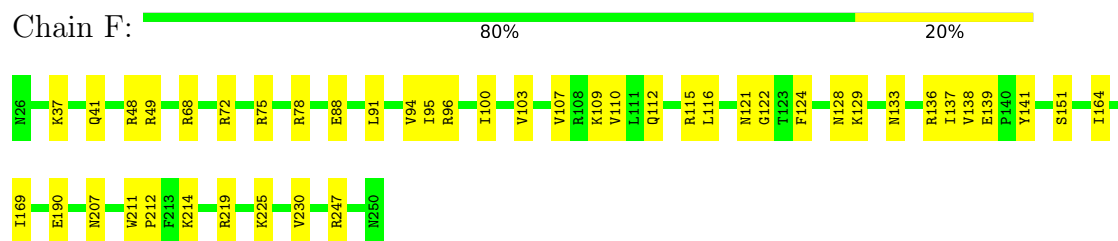
- Molecule 7: 60S ribosomal protein L5



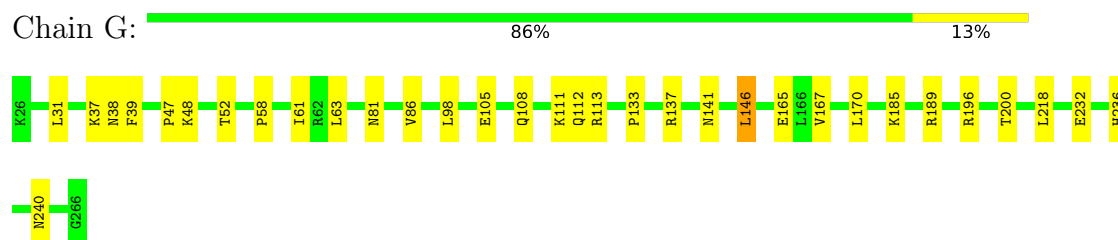
- Molecule 8: 60S ribosomal protein L6



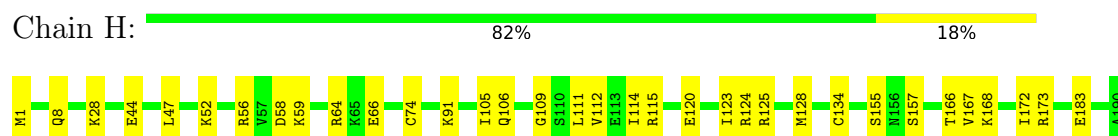
- Molecule 9: uL30



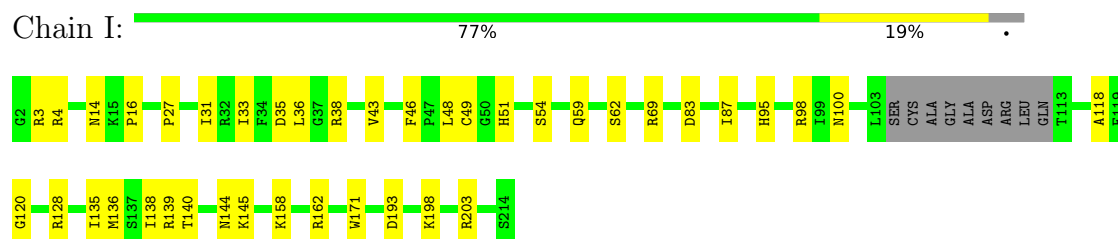
- Molecule 10: eL8



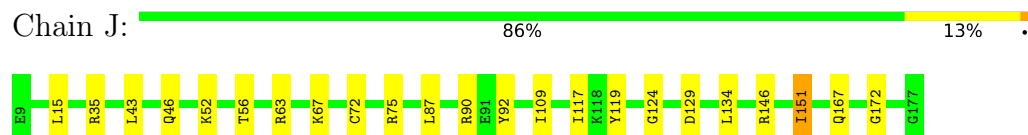
- Molecule 11: uL6



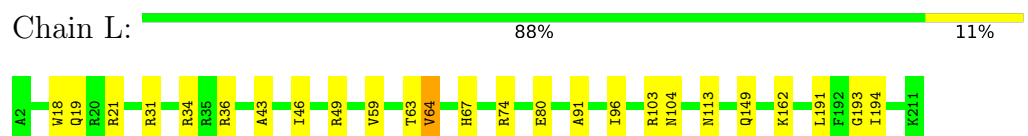
- Molecule 12: Ribosomal protein L10 (Predicted)



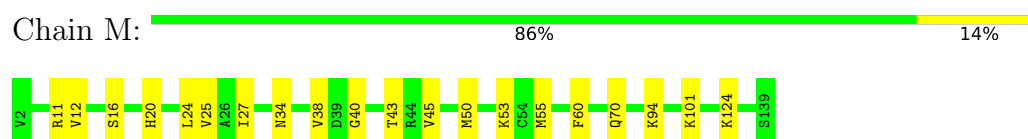
- Molecule 13: uL5



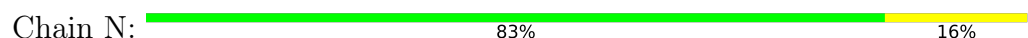
- Molecule 14: 60S ribosomal protein L13

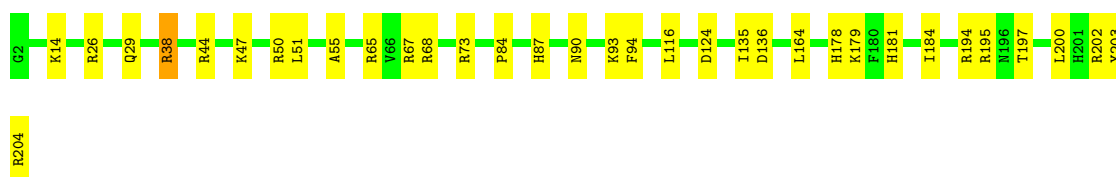


- Molecule 15: Ribosomal protein L14



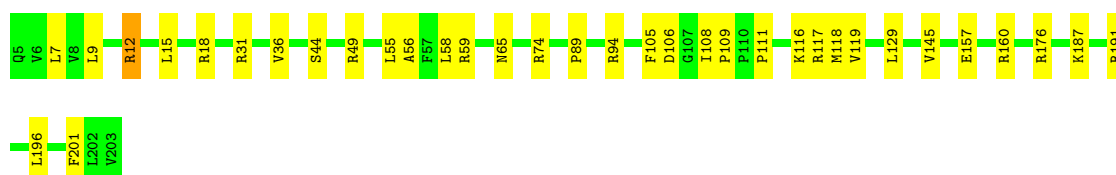
- Molecule 16: Ribosomal protein L15





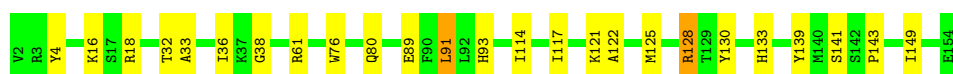
- Molecule 17: uL13

Chain O: 82% 17%



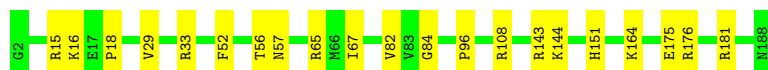
- Molecule 18: uL22

Chain P: 84% 15%



- Molecule 19: eL18

Chain Q: 89% 11%



- Molecule 20: eL19

Chain R: 87% 13%



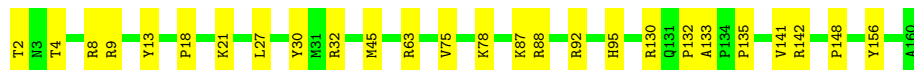
- Molecule 21: eL20

Chain S: 82% 18%




- Molecule 22: eL21

Chain T: 84% 16%




- Molecule 23: Ribosomal protein L22

Chain U:  86% 14%




- Molecule 24: uL14

Chain V:  80% 20%



- Molecule 25: Ribosomal protein L24

Chain W:  86% 13% .




- Molecule 26: uL23

Chain X:  86% 14%




- Molecule 27: Ribosomal protein L26

Chain Y:  80% 20%



- Molecule 28: 60S ribosomal protein L27

Chain Z:  82% 17% .



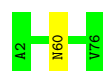
- Molecule 29: uL15

Chain a:  100%

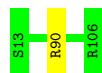
There are no outlier residues recorded for this chain.

- Molecule 30: 60S ribosomal protein L29

Chain b:  99% .



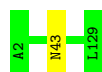
## • Molecule 31: eL30

Chain c:  99% .

## • Molecule 32: eL31

Chain d:  98% .

## • Molecule 33: eL32

Chain e:  99% .

## • Molecule 34: eL33

Chain f:  98% .

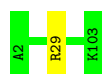
## • Molecule 35: eL34

Chain g:  98% .

## • Molecule 36: uL29

Chain h:  99% .

## • Molecule 37: 60S ribosomal protein L36

Chain i:  99% .

## • Molecule 38: Ribosomal protein L37

Chain j:  98% .



- Molecule 39: eL38

Chain k: 99%



- Molecule 40: ribosomal protein eL39

Chain l: 94%



- Molecule 41: eL40

Chain m: 100%

There are no outlier residues recorded for this chain.

- Molecule 42: 60s ribosomal protein l41

Chain n: 100%

There are no outlier residues recorded for this chain.

- Molecule 43: eL42

Chain o: 96%



- Molecule 44: ribosomal protein eL43

Chain p: 98%



- Molecule 45: eL28

Chain r: 95%



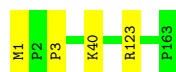
- Molecule 46: 60S acidic ribosomal protein P0

Chain s:  99% .



- Molecule 47: Ribosomal protein L12

Chain t:  98% .



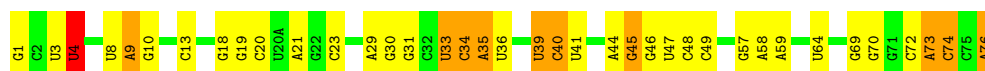
- Molecule 48: X-box-binding protein 1

Chain 1:  50% 46% .



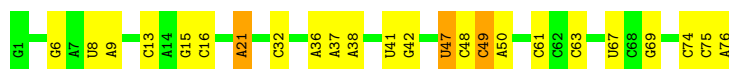
- Molecule 49: A/P-tRNA

Chain 2:  50% 36% 13% .



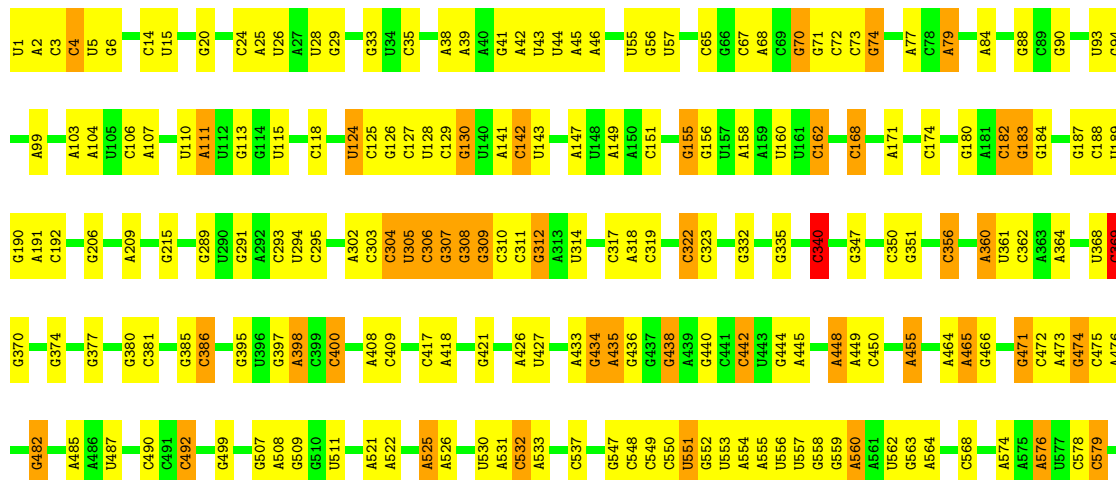
- Molecule 50: P/E-tRNA

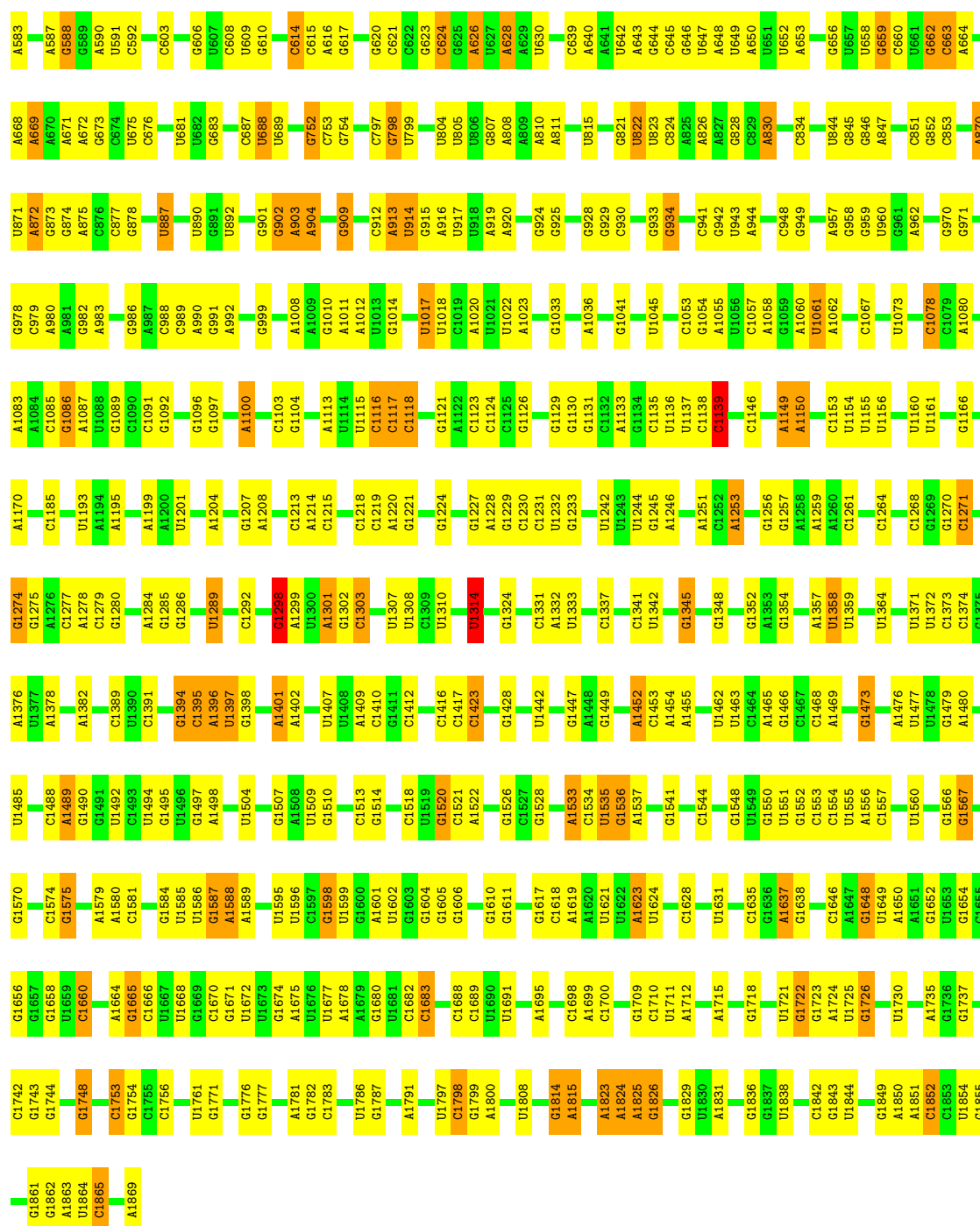
Chain 3:  68% 28% .



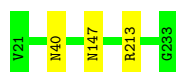
- Molecule 51: 18S rRNA

Chain K:  60% 33% 7% .









- Molecule 54: uS5

Chain v: 99%



- Molecule 55: 40S ribosomal protein S4

Chain x: 99%



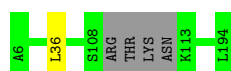
- Molecule 56: 40S ribosomal protein S6

Chain z: 99%



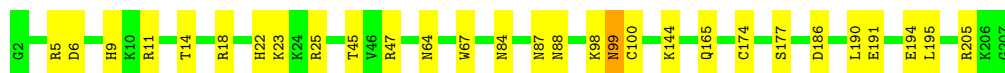
- Molecule 57: 40S ribosomal protein S7

Chain y: 97%



- Molecule 58: 40S ribosomal protein S8

Chain CC: 86%



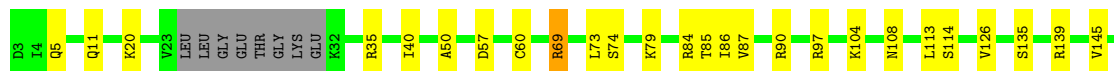
- Molecule 59: Ribosomal protein S9 (Predicted)

Chain XX: 86%



- Molecule 60: Ribosomal protein S11

Chain EE: 77%


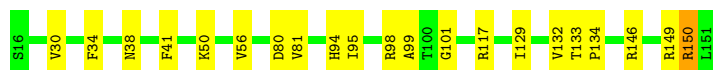


K153


- Molecule 61: ribosomal protein uS15

Chain QQ:  93% 7%

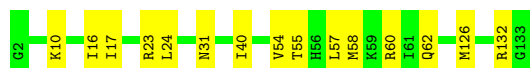

- Molecule 62: uS11

Chain MM:  85% 15%




- Molecule 63: Ribosomal protein S16

Chain UU:  85% 13%


- Molecule 64: eS17

Chain YY:  89% 11%



- Molecule 65: eS21

Chain HH:  82% 18%



- Molecule 66: Ribosomal protein S15a

Chain TT:  84% 16%


- Molecule 67: Ribosomal protein S23


Chain VV:  85% 13%

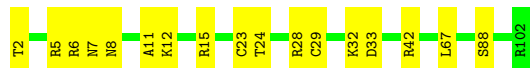

- Molecule 68: eS24

Chain NN:  81% 19%




- Molecule 69: eS26

Chain ZZ:  83% 17%



- Molecule 70: 40S ribosomal protein S27

Chain JJ:  81% 18%




- Molecule 71: 40S ribosomal protein S30

Chain AA:  85% 13%




- Molecule 72: Ribosomal protein S3

Chain DD:  85% 15%




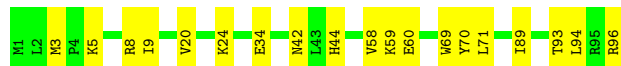
- Molecule 73: Ribosomal protein S5

Chain BB:  82% 15%




- Molecule 74: eS10

Chain SS:  80% 20%




- Molecule 75: 40S ribosomal protein S12

Chain RR:  87% 13%




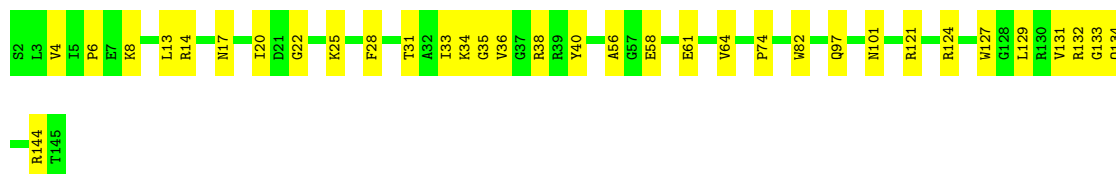
- Molecule 76: uS14

Chain 9:  86% 14%




- Molecule 77: uS13

Chain II:  76% 24%




- Molecule 78: eS19

Chain PP:  84% 16%



- Molecule 79: uS10

Chain GG:  75% 25%



- Molecule 80: ribosomal protein eS25

Chain OO:  92% 8%



- Molecule 81: Ribosomal protein S28

Chain FF:  85% 15%




- Molecule 82: S29

Chain w:  100%


There are no outlier residues recorded for this chain.

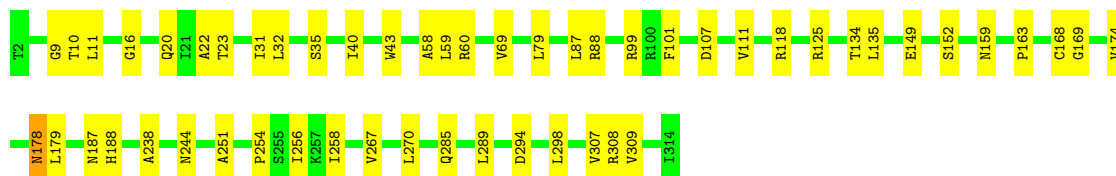
- Molecule 83: eS31

Chain 0:  79% 19%



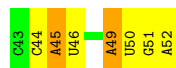
- Molecule 84: ribosomal protein RACK1

Chain 6:  83% 17%



- Molecule 85: mRNA

Chain 4:  30% 50% 20%



## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	94923	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	28	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	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

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	5	0.31	1/87794 (0.0%)	1.05	383/136953 (0.3%)
10	G	0.27	0/1967	0.55	1/2647 (0.0%)
11	H	0.27	0/1535	0.54	0/2063
12	I	0.27	0/1693	0.49	0/2260
13	J	0.27	0/1376	0.56	0/1841
14	L	0.27	0/1734	0.53	0/2317
15	M	0.27	0/1158	0.52	0/1547
16	N	0.27	0/1746	0.51	0/2338
17	O	0.28	0/1671	0.51	0/2234
18	P	0.33	0/1268	0.53	1/1700 (0.1%)
19	Q	0.25	0/1530	0.53	0/2041
2	7	0.28	0/2858	0.99	6/4455 (0.1%)
20	R	0.27	0/1524	0.54	0/2013
21	S	0.27	0/1493	0.51	0/2002
22	T	0.27	0/1326	0.49	0/1770
23	U	0.27	0/822	0.53	0/1103
24	V	0.28	0/993	0.56	0/1332
25	W	0.27	0/541	0.50	0/720
26	X	0.25	0/993	0.51	0/1334
27	Y	0.26	0/1132	0.50	0/1504
28	Z	0.28	0/1130	0.55	1/1507 (0.1%)
29	a	0.29	0/1191	0.51	0/1590
3	8	0.32	0/3701	1.06	10/5766 (0.2%)
30	b	0.25	0/619	0.46	0/818
31	c	0.28	0/742	0.51	0/996
32	d	0.28	0/903	0.51	0/1216
33	e	0.27	0/1071	0.49	0/1429
34	f	0.27	0/895	0.58	0/1198
35	g	0.26	0/916	0.55	0/1220
36	h	0.26	0/1021	0.51	0/1348
37	i	0.26	0/841	0.52	0/1112
38	j	0.26	0/720	0.51	0/952

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
39	k	0.30	0/575	0.70	1/761 (0.1%)
4	A	0.29	0/1906	0.55	0/2556
40	l	0.26	0/454	0.47	0/599
41	m	0.28	0/435	0.54	0/575
42	n	0.25	0/223	0.45	0/284
43	o	0.27	0/864	0.59	0/1140
44	p	0.26	0/718	0.54	0/953
45	r	0.29	0/1017	0.67	1/1364 (0.1%)
46	s	0.27	0/1547	0.52	0/2088
47	t	0.32	0/1257	0.65	0/1697
48	1	0.50	0/216	0.56	0/298
49	2	0.28	0/1802	0.95	6/2804 (0.2%)
5	B	0.27	0/3216	0.55	2/4311 (0.0%)
50	3	0.27	0/1783	1.00	3/2773 (0.1%)
51	K	0.29	1/40530 (0.0%)	1.04	165/63160 (0.3%)
52	q	0.26	0/1747	0.50	0/2374
53	u	0.25	0/1756	0.53	0/2350
54	v	0.27	0/1753	0.51	0/2369
55	x	0.25	0/2118	0.51	0/2849
56	z	0.25	0/1946	0.48	0/2590
57	y	0.26	0/1510	0.52	1/2022 (0.0%)
58	CC	0.25	0/1715	0.49	0/2287
59	XX	0.25	0/1550	0.50	0/2069
6	C	0.26	0/2937	0.51	0/3946
60	EE	0.26	0/1195	0.50	0/1597
61	QQ	0.25	0/1226	0.46	0/1649
62	MM	0.26	0/1029	0.51	0/1380
63	UU	0.26	0/1146	0.50	0/1534
64	YY	0.24	0/1082	0.46	0/1452
65	HH	0.27	0/643	0.52	0/860
66	TT	0.27	0/1051	0.51	0/1406
67	VV	0.26	0/1116	0.53	0/1490
68	NN	0.26	0/1028	0.48	0/1366
69	ZZ	0.26	0/828	0.49	0/1109
7	D	0.26	0/2432	0.50	0/3257
70	JJ	0.25	0/665	0.48	0/891
71	AA	0.26	0/447	0.46	0/587
72	DD	0.27	0/1796	0.54	0/2417
73	BB	0.26	0/1492	0.49	0/2005
74	SS	0.27	0/834	0.55	0/1125
75	RR	0.26	0/918	0.56	0/1233
76	9	0.26	0/1017	0.50	0/1358
77	II	0.27	0/1208	0.53	0/1618



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >2	RMSZ	# Z  >2
78	PP	0.26	0/1115	0.50	0/1493
79	GG	0.25	0/805	0.50	0/1081
8	E	0.26	0/1936	0.61	1/2600 (0.0%)
80	OO	0.24	0/604	0.51	0/810
81	FF	0.24	0/490	0.48	0/656
82	w	0.26	0/470	0.46	0/623
83	0	0.25	0/567	0.48	0/753
84	6	0.25	0/2493	0.53	0/3394
85	4	0.45	0/235	1.14	1/363 (0.3%)
9	F	0.28	0/1905	0.51	0/2539
All	All	0.29	2/234252 (0.0%)	0.89	583/344191 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
20	R	0	1
21	S	0	1
23	U	0	1
34	f	0	1
5	B	0	2
67	VV	0	2
76	9	0	2
All	All	0	10

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	5	967	C	N3-C4	-5.24	1.30	1.33
51	K	1520	G	N9-C4	5.10	1.42	1.38

The worst 5 of 583 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5	961	G	N1-C6-O6	-19.59	108.15	119.90
1	5	967	C	N3-C4-N4	-19.03	104.68	118.00
1	5	967	C	C5-C4-N4	16.73	131.91	120.20
1	5	961	G	C5-C6-O6	13.97	136.98	128.60
1	5	931	C	N1-C2-O2	13.86	127.22	118.90

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	B	17	LEU	Peptide
5	B	258	HIS	Peptide
20	R	18	GLY	Peptide
21	S	164	LYS	Peptide
23	U	27	HIS	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	5	78486	0	39654	540	0
2	7	2558	0	1296	17	0
3	8	3314	0	1683	26	0
4	A	1868	0	1959	43	0
5	B	3148	0	3267	53	0
6	C	2883	0	3053	37	0
7	D	2386	0	2419	30	0
8	E	1898	0	2035	32	0
9	F	1870	0	1994	35	0
10	G	1934	0	2087	22	0
11	H	1516	0	1597	20	0
12	I	1655	0	1704	25	0
13	J	1353	0	1386	14	0
14	L	1703	0	1820	21	0
15	M	1137	0	1211	15	0
16	N	1701	0	1749	30	0
17	O	1638	0	1777	24	0
18	P	1242	0	1274	17	0
19	Q	1506	0	1623	15	0
20	R	1508	0	1664	17	0
21	S	1454	0	1496	24	0
22	T	1298	0	1366	21	0
23	U	808	0	831	8	0
24	V	979	0	1039	17	0
25	W	528	0	541	8	0
26	X	976	0	1053	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	Y	1115	0	1205	19	0
28	Z	1107	0	1182	13	0
29	a	1162	0	1209	0	0
30	b	609	0	650	0	0
31	c	732	0	769	0	0
32	d	888	0	930	0	0
33	e	1053	0	1147	0	0
34	f	876	0	912	0	0
35	g	906	0	998	0	0
36	h	1013	0	1147	0	0
37	i	830	0	916	0	0
38	j	705	0	737	0	0
39	k	569	0	637	0	0
40	l	444	0	483	0	0
41	m	429	0	465	0	0
42	n	222	0	264	0	0
43	o	851	0	921	0	0
44	p	708	0	757	0	0
45	r	1001	0	1060	0	0
46	s	1523	0	1577	0	0
47	t	1238	0	1295	0	0
48	1	204	0	193	24	0
49	2	1614	0	821	26	0
50	3	1597	0	813	6	0
51	K	36248	0	18309	300	0
52	q	1710	0	1708	0	0
53	u	1729	0	1803	0	0
54	v	1716	0	1806	0	0
55	x	2076	0	2177	0	0
56	z	1923	0	2089	0	0
57	y	1488	0	1582	0	0
58	CC	1686	0	1772	22	0
59	XX	1525	0	1640	18	0
60	EE	1175	0	1249	16	0
61	QQ	1202	0	1289	7	0
62	MM	1016	0	1039	14	0
63	UU	1128	0	1195	16	0
64	YY	1068	0	1121	10	0
65	HH	636	0	637	7	0
66	TT	1034	0	1080	15	0
67	VV	1098	0	1167	20	0
68	NN	1011	0	1083	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
69	ZZ	814	0	867	14	0
70	JJ	651	0	672	11	0
71	AA	443	0	492	6	0
72	DD	1768	0	1866	20	0
73	BB	1471	0	1522	20	0
74	SS	810	0	836	11	0
75	RR	908	0	939	8	0
76	9	997	0	1045	12	0
77	II	1190	0	1249	24	0
78	PP	1097	0	1132	15	0
79	GG	795	0	862	15	0
80	OO	598	0	656	7	0
81	FF	488	0	514	8	0
82	w	459	0	452	0	0
83	0	555	0	567	10	0
84	6	2436	0	2393	34	0
85	4	211	0	108	7	0
86	5	148	0	0	0	0
86	7	4	0	0	0	0
86	8	1	0	0	0	0
86	I	1	0	0	0	0
86	P	1	0	0	0	0
86	Q	1	0	0	0	0
86	V	1	0	0	0	0
86	e	1	0	0	0	0
86	g	1	0	0	0	0
87	g	1	0	0	0	0
87	j	1	0	0	0	0
87	m	1	0	0	0	0
87	o	1	0	0	0	0
87	p	1	0	0	0	0
All	All	218067	0	161584	1484	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 5.

The worst 5 of 1484 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:K:1096:G:H1	51:K:1136:U:H3	1.07	1.02
51:K:1452:A:H61	51:K:1473:G:H21	1.02	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:5:2017:A:C8	1:5:2017:A:H5'	1.99	0.97
51:K:1726:G:H1	51:K:1808:U:H3	0.99	0.96
1:5:2017:A:H8	1:5:2017:A:H5'	1.30	0.94

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	
4	A	242/244 (99%)	222 (92%)	20 (8%)	0	100	100
5	B	392/394 (100%)	370 (94%)	21 (5%)	1 (0%)	43	77
6	C	360/362 (99%)	338 (94%)	22 (6%)	0	100	100
7	D	290/292 (99%)	273 (94%)	17 (6%)	0	100	100
8	E	232/248 (94%)	195 (84%)	37 (16%)	0	100	100
9	F	223/225 (99%)	216 (97%)	7 (3%)	0	100	100
10	G	239/241 (99%)	213 (89%)	26 (11%)	0	100	100
11	H	188/190 (99%)	174 (93%)	14 (7%)	0	100	100
12	I	200/213 (94%)	192 (96%)	8 (4%)	0	100	100
13	J	167/169 (99%)	155 (93%)	12 (7%)	0	100	100
14	L	208/210 (99%)	190 (91%)	17 (8%)	1 (0%)	31	68
15	M	136/138 (99%)	128 (94%)	8 (6%)	0	100	100
16	N	201/203 (99%)	190 (94%)	11 (6%)	0	100	100
17	O	197/199 (99%)	191 (97%)	6 (3%)	0	100	100
18	P	151/153 (99%)	145 (96%)	6 (4%)	0	100	100
19	Q	185/187 (99%)	176 (95%)	9 (5%)	0	100	100
20	R	178/180 (99%)	170 (96%)	8 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	S	173/175 (99%)	164 (95%)	8 (5%)	1 (1%)	27	64
22	T	157/159 (99%)	147 (94%)	10 (6%)	0	100	100
23	U	97/99 (98%)	90 (93%)	7 (7%)	0	100	100
24	V	129/131 (98%)	120 (93%)	9 (7%)	0	100	100
25	W	61/63 (97%)	58 (95%)	3 (5%)	0	100	100
26	X	117/119 (98%)	113 (97%)	4 (3%)	0	100	100
27	Y	132/134 (98%)	126 (96%)	6 (4%)	0	100	100
28	Z	133/135 (98%)	122 (92%)	9 (7%)	2 (2%)	11	43
29	a	145/147 (99%)	136 (94%)	9 (6%)	0	100	100
30	b	73/75 (97%)	68 (93%)	5 (7%)	0	100	100
31	c	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
32	d	105/107 (98%)	101 (96%)	4 (4%)	0	100	100
33	e	126/128 (98%)	122 (97%)	4 (3%)	0	100	100
34	f	107/109 (98%)	99 (92%)	8 (8%)	0	100	100
35	g	112/114 (98%)	110 (98%)	2 (2%)	0	100	100
36	h	120/122 (98%)	113 (94%)	7 (6%)	0	100	100
37	i	100/102 (98%)	92 (92%)	8 (8%)	0	100	100
38	j	84/86 (98%)	79 (94%)	5 (6%)	0	100	100
39	k	67/69 (97%)	59 (88%)	8 (12%)	0	100	100
40	l	48/50 (96%)	44 (92%)	4 (8%)	0	100	100
41	m	50/52 (96%)	50 (100%)	0	0	100	100
42	n	21/23 (91%)	21 (100%)	0	0	100	100
43	o	102/104 (98%)	94 (92%)	7 (7%)	1 (1%)	17	53
44	p	89/91 (98%)	84 (94%)	5 (6%)	0	100	100
45	r	123/125 (98%)	110 (89%)	11 (9%)	2 (2%)	11	41
46	s	196/198 (99%)	178 (91%)	18 (9%)	0	100	100
47	t	161/163 (99%)	124 (77%)	36 (22%)	1 (1%)	27	64
48	l	22/24 (92%)	21 (96%)	1 (4%)	0	100	100
52	q	215/217 (99%)	204 (95%)	11 (5%)	0	100	100
53	u	211/213 (99%)	199 (94%)	12 (6%)	0	100	100
54	v	219/221 (99%)	213 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
55	x	260/262 (99%)	247 (95%)	13 (5%)	0	100	100
56	z	235/237 (99%)	232 (99%)	3 (1%)	0	100	100
57	y	181/189 (96%)	172 (95%)	9 (5%)	0	100	100
58	CC	204/206 (99%)	189 (93%)	15 (7%)	0	100	100
59	XX	183/185 (99%)	178 (97%)	5 (3%)	0	100	100
60	EE	139/151 (92%)	131 (94%)	8 (6%)	0	100	100
61	QQ	147/149 (99%)	146 (99%)	1 (1%)	0	100	100
62	MM	134/136 (98%)	127 (95%)	7 (5%)	0	100	100
63	UU	140/142 (99%)	135 (96%)	5 (4%)	0	100	100
64	YY	130/132 (98%)	124 (95%)	6 (5%)	0	100	100
65	HH	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
66	TT	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
67	VV	139/141 (99%)	134 (96%)	4 (3%)	1 (1%)	24	61
68	NN	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
69	ZZ	99/101 (98%)	90 (91%)	9 (9%)	0	100	100
70	JJ	81/83 (98%)	79 (98%)	2 (2%)	0	100	100
71	AA	53/55 (96%)	52 (98%)	1 (2%)	0	100	100
72	DD	226/228 (99%)	221 (98%)	5 (2%)	0	100	100
73	BB	181/191 (95%)	170 (94%)	11 (6%)	0	100	100
74	SS	94/96 (98%)	88 (94%)	6 (6%)	0	100	100
75	RR	115/117 (98%)	106 (92%)	9 (8%)	0	100	100
76	9	118/120 (98%)	110 (93%)	8 (7%)	0	100	100
77	II	142/144 (99%)	129 (91%)	13 (9%)	0	100	100
78	PP	139/141 (99%)	133 (96%)	6 (4%)	0	100	100
79	GG	98/100 (98%)	96 (98%)	2 (2%)	0	100	100
80	OO	73/75 (97%)	70 (96%)	3 (4%)	0	100	100
81	FF	60/62 (97%)	60 (100%)	0	0	100	100
82	w	53/55 (96%)	53 (100%)	0	0	100	100
83	0	66/68 (97%)	61 (92%)	5 (8%)	0	100	100
84	6	311/313 (99%)	289 (93%)	22 (7%)	0	100	100
All	All	11507/11712 (98%)	10831 (94%)	666 (6%)	10 (0%)	56	85

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
14	L	64	VAL
67	VV	62	PRO
43	o	97	LYS
45	r	19	LYS
45	r	21	ASN

### 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	
4	A	187/187 (100%)	182 (97%)	5 (3%)	48	78
5	B	336/342 (98%)	334 (99%)	2 (1%)	87	94
6	C	302/302 (100%)	297 (98%)	5 (2%)	63	85
7	D	247/247 (100%)	247 (100%)	0	100	100
8	E	208/221 (94%)	206 (99%)	2 (1%)	78	91
9	F	194/195 (100%)	194 (100%)	0	100	100
10	G	206/206 (100%)	201 (98%)	5 (2%)	52	80
11	H	169/169 (100%)	167 (99%)	2 (1%)	74	89
12	I	174/180 (97%)	171 (98%)	3 (2%)	63	85
13	J	142/142 (100%)	140 (99%)	2 (1%)	69	88
14	L	176/176 (100%)	174 (99%)	2 (1%)	76	90
15	M	117/117 (100%)	117 (100%)	0	100	100
16	N	171/171 (100%)	170 (99%)	1 (1%)	87	94
17	O	171/171 (100%)	165 (96%)	6 (4%)	39	73
18	P	134/134 (100%)	133 (99%)	1 (1%)	85	94
19	Q	163/163 (100%)	163 (100%)	0	100	100
20	R	159/159 (100%)	157 (99%)	2 (1%)	71	88
21	S	156/156 (100%)	156 (100%)	0	100	100
22	T	139/139 (100%)	138 (99%)	1 (1%)	85	94

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	U	89/89 (100%)	89 (100%)	0	100	100
24	V	101/101 (100%)	100 (99%)	1 (1%)	78	91
25	W	55/55 (100%)	54 (98%)	1 (2%)	62	85
26	X	107/107 (100%)	106 (99%)	1 (1%)	81	92
27	Y	124/124 (100%)	123 (99%)	1 (1%)	83	93
28	Z	117/117 (100%)	116 (99%)	1 (1%)	81	92
29	a	119/119 (100%)	119 (100%)	0	100	100
30	b	62/62 (100%)	61 (98%)	1 (2%)	65	87
31	c	79/79 (100%)	78 (99%)	1 (1%)	71	88
32	d	98/98 (100%)	96 (98%)	2 (2%)	58	83
33	e	114/114 (100%)	113 (99%)	1 (1%)	81	92
34	f	88/88 (100%)	87 (99%)	1 (1%)	76	90
35	g	98/98 (100%)	96 (98%)	2 (2%)	58	83
36	h	109/109 (100%)	108 (99%)	1 (1%)	81	92
37	i	86/86 (100%)	85 (99%)	1 (1%)	74	89
38	j	73/73 (100%)	71 (97%)	2 (3%)	48	78
39	k	64/64 (100%)	64 (100%)	0	100	100
40	l	47/47 (100%)	44 (94%)	3 (6%)	19	52
41	m	48/48 (100%)	48 (100%)	0	100	100
42	n	22/22 (100%)	22 (100%)	0	100	100
43	o	92/92 (100%)	89 (97%)	3 (3%)	41	74
44	p	74/74 (100%)	72 (97%)	2 (3%)	48	78
45	r	109/109 (100%)	105 (96%)	4 (4%)	37	71
46	s	166/166 (100%)	165 (99%)	1 (1%)	87	94
47	t	136/136 (100%)	133 (98%)	3 (2%)	55	81
48	l	22/22 (100%)	21 (96%)	1 (4%)	30	65
52	q	180/181 (99%)	179 (99%)	1 (1%)	87	94
53	u	194/194 (100%)	191 (98%)	3 (2%)	67	87
54	v	187/187 (100%)	185 (99%)	2 (1%)	76	90
55	x	224/224 (100%)	222 (99%)	2 (1%)	81	92
56	z	207/207 (100%)	205 (99%)	2 (1%)	78	91

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
57	y	165/169 (98%)	165 (100%)	0	100	100
58	CC	178/178 (100%)	175 (98%)	3 (2%)	63	85
59	XX	161/161 (100%)	158 (98%)	3 (2%)	60	84
60	EE	130/136 (96%)	127 (98%)	3 (2%)	53	80
61	QQ	130/130 (100%)	129 (99%)	1 (1%)	83	93
62	MM	106/106 (100%)	104 (98%)	2 (2%)	60	84
63	UU	117/117 (100%)	114 (97%)	3 (3%)	49	78
64	YY	119/119 (100%)	119 (100%)	0	100	100
65	HH	67/67 (100%)	66 (98%)	1 (2%)	67	87
66	TT	112/112 (100%)	112 (100%)	0	100	100
67	VV	113/113 (100%)	113 (100%)	0	100	100
68	NN	107/107 (100%)	106 (99%)	1 (1%)	81	92
69	ZZ	88/88 (100%)	88 (100%)	0	100	100
70	JJ	75/75 (100%)	74 (99%)	1 (1%)	71	88
71	AA	46/46 (100%)	44 (96%)	2 (4%)	32	66
72	DD	190/190 (100%)	185 (97%)	5 (3%)	49	78
73	BB	158/161 (98%)	158 (100%)	0	100	100
74	SS	87/87 (100%)	86 (99%)	1 (1%)	76	90
75	RR	99/99 (100%)	98 (99%)	1 (1%)	78	91
76	9	109/109 (100%)	108 (99%)	1 (1%)	81	92
77	II	125/125 (100%)	124 (99%)	1 (1%)	83	93
78	PP	111/111 (100%)	110 (99%)	1 (1%)	81	92
79	GG	92/92 (100%)	91 (99%)	1 (1%)	76	90
80	OO	66/66 (100%)	66 (100%)	0	100	100
81	FF	55/55 (100%)	54 (98%)	1 (2%)	62	85
82	w	48/48 (100%)	48 (100%)	0	100	100
83	0	61/61 (100%)	60 (98%)	1 (2%)	65	87
84	6	272/272 (100%)	270 (99%)	2 (1%)	85	94
All	All	10029/10069 (100%)	9911 (99%)	118 (1%)	75	89

5 of 118 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
37	i	29	ARG
45	r	31	ASN
75	RR	33	ARG
38	j	20	ARG
43	o	9	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 110 such sidechains are listed below:

Mol	Chain	Res	Type
32	d	30	HIS
45	r	21	ASN
73	BB	114	ASN
33	e	52	GLN
35	g	112	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	3649/3662 (99%)	841 (23%)	72 (1%)
2	7	119/120 (99%)	16 (13%)	0
3	8	155/156 (99%)	40 (25%)	1 (0%)
49	2	74/76 (97%)	23 (31%)	1 (1%)
50	3	72/75 (96%)	13 (18%)	1 (1%)
51	K	1686/1698 (99%)	352 (20%)	22 (1%)
85	4	9/10 (90%)	4 (44%)	0
All	All	5764/5797 (99%)	1289 (22%)	97 (1%)

5 of 1289 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	5	2	G
1	5	8	U
1	5	11	G
1	5	12	A
1	5	13	U

5 of 97 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	5	2257	C
1	5	4170	A

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Mol	Chain	Res	Type
51	K	870	A
1	5	2262	G
1	5	2695	A

## 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 164 ligands modelled in this entry, 164 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	5	12
51	K	11
50	3	2
49	2	1

The worst 5 of 26 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	K	697:G	O3'	729:C	P	18.34
1	K	756:C	O3'	788:G	P	17.89
1	K	1761:U	O3'	1771:G	P	17.79
1	5	4776:G	O3'	4859:C	P	17.38
1	5	757:G	O3'	906:C	P	17.23