



Full wwPDB/EMDatabank EM Map/Model Validation Report ⓘ

Nov 22, 2016 – 07:27 PM EST

PDB ID : 5LZU
EMDB ID: : EMD-4132
Title : Structure of the mammalian ribosomal termination complex with accommodated eRF1
Authors : Shao, S.; Murray, J.; Brown, A.; Taunton, J.; Ramakrishnan, V.; Hegde, R.S.
Deposited on : 2016-10-02
Resolution : 3.75 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

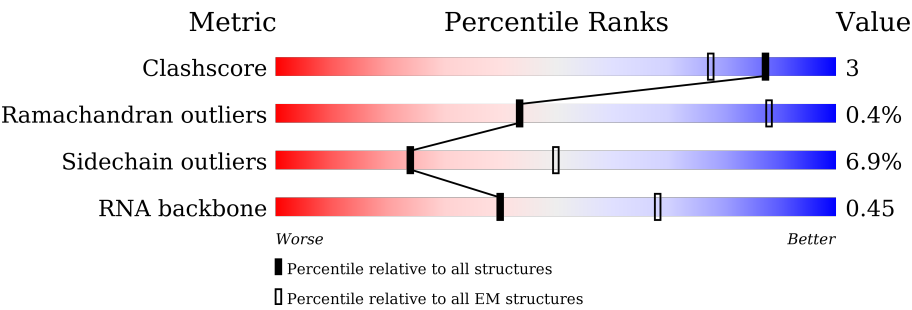
MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
EM map analysis : **NOT EXECUTED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20028320

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.75 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.




















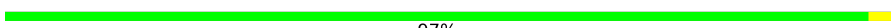







Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686
RNA backbone	3027	244

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	257	<div><div>80%16%..</div></div>
2	B	403	<div><div>85%13%. .</div></div>
3	C	425	<div><div>74%11%15%</div></div>
4	D	297	<div><div>90%7%..</div></div>
5	E	291	<div><div>66%7%.26%</div></div>
6	F	247	<div><div>82%8%.9%</div></div>
7	G	319	<div><div>63%10%27%</div></div>
8	H	192	<div><div>84%15%. .</div></div>



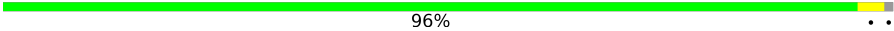
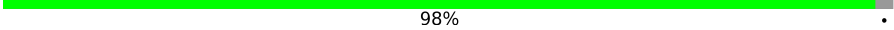



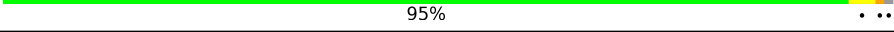



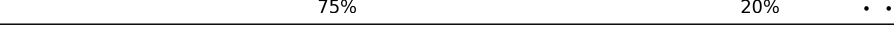







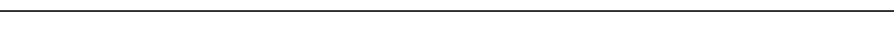

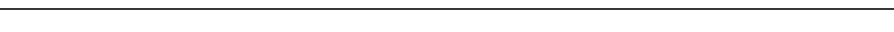
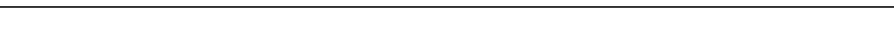


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Mol	Chain	Length	Quality of chain
9	I	214	 88% 7% .
10	J	178	 86% 10% .
11	L	211	 93% 6%
12	M	218	 51% 11% . 37%
13	N	204	 88% 11% .
14	O	203	 79% 16% . .
15	P	184	 74% 8% . 17%
16	Q	188	 87% 12% . .
17	R	196	 78% 13% . 8%
18	S	176	 82% 16% .
19	T	160	 89% 10% .
20	U	128	 70% 6% . 23%
21	V	140	 82% 11% 6%
22	W	157	 63% . 32%
23	X	156	 71% 5% 24%
24	Y	145	 86% 6% 8%
25	Z	136	 91% 8% .
26	a	148	 97% . .
27	b	245	 41% . 58%
28	c	115	 83% . 15%
29	d	125	 79% 6% 14%
30	e	135	 89% 6% 5%
31	f	110	 92% 7% .
32	g	117	 93% . .
33	h	123	 95% . .









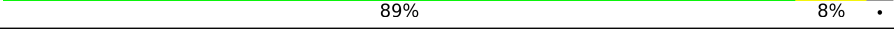

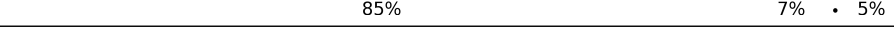
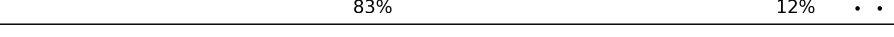

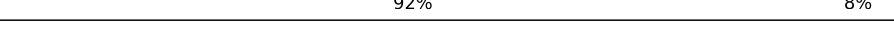


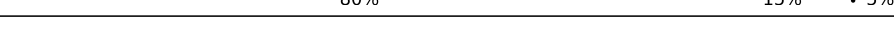

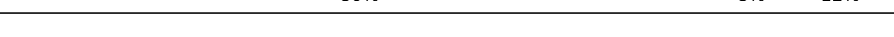






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Mol	Chain	Length	Quality of chain
34	i	105	 94% . .
35	j	97	 82% 6% 11%
36	k	70	 96% . .
37	l	51	 98% .
38	m	102	 48% . 49%
39	n	25	 92% 8%
40	o	106	 92% 7% .
41	p	92	 95% . . .
42	r	137	 85% 6% 9%
43	s	318	 59% . 38%
44	t	165	 90% . 7%
45	2	76	 75% 20% . .
46	3	75	 65% 32% .
47	5	3543	 68% 28% .
48	7	120	 83% 14% .
49	8	156	 67% 28% . .
50	9	1869	 59% 28% . 9%
51	AA	295	 61% 12% . 26%
52	BB	264	 69% 11% . 19%
53	CC	293	 65% 10% 25%
54	DD	243	 82% 11% 6%
55	EE	263	 85% 14% .
56	FF	204	 75% 14% . 9%
57	GG	249	 84% 10% . 5%
58	HH	194	 83% 11% . 5%

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Mol	Chain	Length	Quality of chain
59	II	208	
60	JJ	194	
61	KK	165	
62	LL	158	
63	MM	132	
64	NN	151	
65	OO	168	
66	PP	145	
67	QQ	146	
68	RR	135	
69	SS	152	
70	TT	145	
71	UU	119	
72	VV	83	
73	WW	130	
74	XX	143	
75	YY	130	
76	ZZ	125	
77	aa	115	
78	bb	84	
79	cc	69	
80	dd	56	
81	ee	133	
82	ff	156	
83	gg	317	

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Mol	Chain	Length	Quality of chain
84	hh	15	<div><div></div><div>47%</div><div></div><div>53%</div><div></div></div>
85	ii	459	<div><div></div><div>86%</div><div></div><div>5%</div><div>9%</div><div></div></div>

2 Entry composition i

There are 87 unique types of molecules in this entry. The entry contains 219122 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	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 2 is a protein called uL3.

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 3 is a protein called uL4.

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

There are 47 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	379	VAL	-	expression tag	UNP G1SVW5
C	380	LYS	-	expression tag	UNP G1SVW5
C	381	LYS	-	expression tag	UNP G1SVW5
C	382	PRO	-	expression tag	UNP G1SVW5
C	383	ARG	-	expression tag	UNP G1SVW5
C	384	ALA	-	expression tag	UNP G1SVW5
C	385	VAL	-	expression tag	UNP G1SVW5
C	386	GLY	-	expression tag	UNP G1SVW5
C	387	ILE	-	expression tag	UNP G1SVW5
C	388	LYS	-	expression tag	UNP G1SVW5

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Chain	Residue	Modelled	Actual	Comment	Reference
C	389	GLN	-	expression tag	UNP G1SVW5
C	390	LYS	-	expression tag	UNP G1SVW5
C	391	LYS	-	expression tag	UNP G1SVW5
C	392	LYS	-	expression tag	UNP G1SVW5
C	393	PRO	-	expression tag	UNP G1SVW5
C	394	VAL	-	expression tag	UNP G1SVW5
C	395	VAL	-	expression tag	UNP G1SVW5
C	396	GLY	-	expression tag	UNP G1SVW5
C	397	ARG	-	expression tag	UNP G1SVW5
C	398	LYS	-	expression tag	UNP G1SVW5
C	399	ALA	-	expression tag	UNP G1SVW5
C	400	ALA	-	expression tag	UNP G1SVW5
C	401	ALA	-	expression tag	UNP G1SVW5
C	402	ALA	-	expression tag	UNP G1SVW5
C	403	LYS	-	expression tag	UNP G1SVW5
C	404	LYS	-	expression tag	UNP G1SVW5
C	405	PRO	-	expression tag	UNP G1SVW5
C	406	ALA	-	expression tag	UNP G1SVW5
C	407	ALA	-	expression tag	UNP G1SVW5
C	408	ASP	-	expression tag	UNP G1SVW5
C	409	LYS	-	expression tag	UNP G1SVW5
C	410	LYS	-	expression tag	UNP G1SVW5
C	411	ALA	-	expression tag	UNP G1SVW5
C	412	ALA	-	expression tag	UNP G1SVW5
C	413	ASP	-	expression tag	UNP G1SVW5
C	414	LYS	-	expression tag	UNP G1SVW5
C	415	ARG	-	expression tag	UNP G1SVW5
C	416	ALA	-	expression tag	UNP G1SVW5
C	417	GLY	-	expression tag	UNP G1SVW5
C	418	PRO	-	expression tag	UNP G1SVW5
C	419	GLU	-	expression tag	UNP G1SVW5
C	420	ASP	-	expression tag	UNP G1SVW5
C	421	LYS	-	expression tag	UNP G1SVW5
C	422	LYS	-	expression tag	UNP G1SVW5
C	423	PRO	-	expression tag	UNP G1SVW5
C	424	ALA	-	expression tag	UNP G1SVW5
C	425	ALA	-	expression tag	UNP G1SVW5

- Molecule 4 is a protein called 60S ribosomal protein L5.

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 5 is a protein called 60S ribosomal protein L6.

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

- Molecule 6 is a protein called uL30.

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

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	1	MET	-	initiating methionine	UNP G1SV32
F	2	GLU	-	expression tag	UNP G1SV32
F	3	GLY	-	expression tag	UNP G1SV32
F	4	ALA	-	expression tag	UNP G1SV32
F	5	GLU	-	expression tag	UNP G1SV32

- Molecule 7 is a protein called eL8.

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

There are 78 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	1	MET	-	initiating methionine	UNP G1STW0
G	2	SER	-	expression tag	UNP G1STW0
G	3	SER	-	expression tag	UNP G1STW0
G	4	TYR	-	expression tag	UNP G1STW0
G	5	ARG	-	expression tag	UNP G1STW0
G	6	LEU	-	expression tag	UNP G1STW0
G	7	GLY	-	expression tag	UNP G1STW0
G	8	TYR	-	expression tag	UNP G1STW0
G	9	CYS	-	expression tag	UNP G1STW0

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Chain	Residue	Modelled	Actual	Comment	Reference
G	10	MET	-	expression tag	UNP G1STW0
G	11	LYS	-	expression tag	UNP G1STW0
G	12	GLU	-	expression tag	UNP G1STW0
G	13	GLU	-	expression tag	UNP G1STW0
G	14	ARG	-	expression tag	UNP G1STW0
G	15	HIS	-	expression tag	UNP G1STW0
G	16	ASN	-	expression tag	UNP G1STW0
G	17	LEU	-	expression tag	UNP G1STW0
G	18	VAL	-	expression tag	UNP G1STW0
G	19	LEU	-	expression tag	UNP G1STW0
G	20	CYS	-	expression tag	UNP G1STW0
G	21	LEU	-	expression tag	UNP G1STW0
G	22	TRP	-	expression tag	UNP G1STW0
G	23	SER	-	expression tag	UNP G1STW0
G	24	GLN	-	expression tag	UNP G1STW0
G	25	SER	-	expression tag	UNP G1STW0
G	26	PRO	-	expression tag	UNP G1STW0
G	27	GLY	-	expression tag	UNP G1STW0
G	28	ILE	-	expression tag	UNP G1STW0
G	29	LEU	-	expression tag	UNP G1STW0
G	30	ASN	-	expression tag	UNP G1STW0
G	31	SER	-	expression tag	UNP G1STW0
G	32	LYS	-	expression tag	UNP G1STW0
G	33	CYS	-	expression tag	UNP G1STW0
G	34	LEU	-	expression tag	UNP G1STW0
G	35	TRP	-	expression tag	UNP G1STW0
G	36	PRO	-	expression tag	UNP G1STW0
G	37	PHE	-	expression tag	UNP G1STW0
G	38	THR	-	expression tag	UNP G1STW0
G	39	ASN	-	expression tag	UNP G1STW0
G	40	ILE	-	expression tag	UNP G1STW0
G	41	HIS	-	expression tag	UNP G1STW0
G	42	LEU	-	expression tag	UNP G1STW0
G	43	LEU	-	expression tag	UNP G1STW0
G	44	VAL	-	expression tag	UNP G1STW0
G	45	GLY	-	expression tag	UNP G1STW0
G	46	ALA	-	expression tag	UNP G1STW0
G	47	LEU	-	expression tag	UNP G1STW0
G	48	PRO	-	expression tag	UNP G1STW0
G	49	ARG	-	expression tag	UNP G1STW0
G	50	GLU	-	expression tag	UNP G1STW0
G	51	GLY	-	expression tag	UNP G1STW0

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Chain	Residue	Modelled	Actual	Comment	Reference
G	52	ALA	-	expression tag	UNP G1STW0
G	53	GLY	-	expression tag	UNP G1STW0
G	54	GLY	-	expression tag	UNP G1STW0
G	55	ALA	-	expression tag	UNP G1STW0
G	56	TRP	-	expression tag	UNP G1STW0
G	57	GLY	-	expression tag	UNP G1STW0
G	58	GLY	-	expression tag	UNP G1STW0
G	59	GLY	-	expression tag	UNP G1STW0
G	60	ARG	-	expression tag	UNP G1STW0
G	61	SER	-	expression tag	UNP G1STW0
G	62	GLU	-	expression tag	UNP G1STW0
G	63	GLN	-	expression tag	UNP G1STW0
G	64	LEU	-	expression tag	UNP G1STW0
G	65	PRO	-	expression tag	UNP G1STW0
G	66	THR	-	expression tag	UNP G1STW0
G	67	CYS	-	expression tag	UNP G1STW0
G	68	SER	-	expression tag	UNP G1STW0
G	69	THR	-	expression tag	UNP G1STW0
G	70	THR	-	expression tag	UNP G1STW0
G	71	HIS	-	expression tag	UNP G1STW0
G	72	HIS	-	expression tag	UNP G1STW0
G	73	ASP	-	expression tag	UNP G1STW0
G	74	PHE	-	expression tag	UNP G1STW0
G	75	THR	-	expression tag	UNP G1STW0
G	76	TRP	-	expression tag	UNP G1STW0
G	77	ASP	-	expression tag	UNP G1STW0
G	244	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	205	Total	C	N	O	S	0	0
			1664	1056	321	274	13		

- Molecule 10 is a protein called uL5.

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

- Molecule 11 is a protein called eL13.

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

- Molecule 12 is a protein called eL14.

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

- Molecule 13 is a protein called Ribosomal protein L15.

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

- Molecule 14 is a protein called uL13.

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

- Molecule 15 is a protein called uL22.

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

- Molecule 16 is a protein called eL18.

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

- Molecule 17 is a protein called eL19.

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

- Molecule 18 is a protein called eL20.

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

- Molecule 19 is a protein called eL21.

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

- Molecule 20 is a protein called eL22.

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

- Molecule 21 is a protein called uL14.

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

- Molecule 22 is a protein called eL24.

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

- Molecule 23 is a protein called uL23.

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

- Molecule 24 is a protein called uL24.

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

- Molecule 25 is a protein called 60S ribosomal protein L27.

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

- Molecule 26 is a protein called uL15.

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 27 is a protein called eL29.

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

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
b	227	ALA	-	expression tag	UNP G1SGR6
b	228	PRO	-	expression tag	UNP G1SGR6
b	229	VAL	-	expression tag	UNP G1SGR6
b	230	PRO	-	expression tag	UNP G1SGR6
b	231	ALA	-	expression tag	UNP G1SGR6
b	232	GLN	-	expression tag	UNP G1SGR6
b	233	ALA	-	expression tag	UNP G1SGR6
b	234	PRO	-	expression tag	UNP G1SGR6
b	235	PRO	-	expression tag	UNP G1SGR6
b	236	LYS	-	expression tag	UNP G1SGR6
b	237	GLY	-	expression tag	UNP G1SGR6
b	238	ALA	-	expression tag	UNP G1SGR6
b	239	GLN	-	expression tag	UNP G1SGR6

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Chain	Residue	Modelled	Actual	Comment	Reference
b	240	PRO	-	expression tag	UNP G1SGR6
b	241	PRO	-	expression tag	UNP G1SGR6
b	242	ALA	-	expression tag	UNP G1SGR6
b	243	LYS	-	expression tag	UNP G1SGR6
b	244	ALA	-	expression tag	UNP G1SGR6
b	245	PRO	-	expression tag	UNP G1SGR6

- Molecule 28 is a protein called eL30.

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

- Molecule 29 is a protein called eL31.

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

- Molecule 30 is a protein called eL32.

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

- Molecule 31 is a protein called eL33.

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

- Molecule 32 is a protein called eL34.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
g	117	LYS	-	expression tag	UNP G1U945

- 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 60S ribosomal protein L36.

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 Ribosomal protein L37.

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		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
k	24	LYS	ASN	conflict	UNP G1U001

- Molecule 37 is a protein called eL39.

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

- Molecule 38 is a protein called eL40.

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

- Molecule 39 is a protein called 60s ribosomal protein l41.

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

- Molecule 40 is a protein called eL42.

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

- Molecule 41 is a protein called eL43.

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

- Molecule 42 is a protein called eL28.

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

- Molecule 43 is a protein called uL10.

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

- Molecule 44 is a protein called uL11.

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

- Molecule 45 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	2	76	Total	C	N	O	P	0	0
			1616	723	291	527	75		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
46	3	75	Total	C	N	O	P	0	0
			1593	712	281	526	74		

- Molecule 47 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	5	3543	Total	C	N	O	P	0	0
			75972	33833	13910	24686	3543		

- Molecule 48 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 49 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	8	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 50 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	9	1698	Total	C	N	O	P	0	0
			36249	16180	6508	11864	1697		

- Molecule 51 is a protein called uS2.

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

- Molecule 52 is a protein called 40S ribosomal protein S3a.

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

- Molecule 53 is a protein called uS5.

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

- Molecule 54 is a protein called uS3.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
55	EE	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
EE	25	GLY	SER	conflict	UNP G1TK17
EE	51	ARG	LYS	conflict	UNP G1TK17
EE	78	THR	ALA	conflict	UNP G1TK17
EE	156	VAL	MET	conflict	UNP G1TK17

- Molecule 56 is a protein called uS7.

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

- Molecule 57 is a protein called 40S ribosomal protein S6.

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

- Molecule 58 is a protein called eS7.

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

- Molecule 59 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	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 60 is a protein called Ribosomal protein S9 (Predicted).

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

- Molecule 61 is a protein called eS10.

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

- Molecule 62 is a protein called uS17.

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

- Molecule 63 is a protein called 40S ribosomal protein S12.

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

- Molecule 64 is a protein called uS15.

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

- Molecule 65 is a protein called uS11.

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

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
OO	-16	MET	-	initiating methionine	UNP G1T1F0
OO	-15	LYS	-	expression tag	UNP G1T1F0
OO	-14	ALA	-	expression tag	UNP G1T1F0
OO	-13	ARG	-	expression tag	UNP G1T1F0
OO	-12	ALA	-	expression tag	UNP G1T1F0
OO	-11	LEU	-	expression tag	UNP G1T1F0
OO	-10	SER	-	expression tag	UNP G1T1F0
OO	-9	GLY	-	expression tag	UNP G1T1F0
OO	-8	SER	-	expression tag	UNP G1T1F0
OO	-7	GLY	-	expression tag	UNP G1T1F0
OO	-6	VAL	-	expression tag	UNP G1T1F0
OO	-5	ARG	-	expression tag	UNP G1T1F0

- Molecule 66 is a protein called uS19.

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

- Molecule 67 is a protein called uS9.

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

- Molecule 68 is a protein called eS17.

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

- Molecule 69 is a protein called uS13.

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

- Molecule 70 is a protein called eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	TT	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
TT	119	GLY	TRP	conflict	UNP G1TN62

- Molecule 71 is a protein called uS10.

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

- Molecule 72 is a protein called eS21.

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

- Molecule 73 is a protein called uS8.

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

- Molecule 74 is a protein called uS12.

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

- Molecule 75 is a protein called eS24.

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

- Molecule 76 is a protein called eS25.

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

- Molecule 77 is a protein called eS26.

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

- Molecule 78 is a protein called 40S ribosomal protein S27.

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

- Molecule 79 is a protein called eS28.

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

- Molecule 80 is a protein called uS14.

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

- Molecule 81 is a protein called eS30.

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

- Molecule 82 is a protein called eS31.

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

- Molecule 83 is a protein called RACK1.

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

- Molecule 84 is a RNA chain called mRNA (UGA stop codon).

Mol	Chain	Residues	Atoms					AltConf	Trace
84	hh	15	Total	C	N	O	P	0	0
			317	142	54	106	15		

- Molecule 85 is a protein called Eukaryotic peptide chain release factor subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	ii	418	Total	C	N	O	S	0	0
			3295	2095	561	627	12		

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
ii	-21	MET	-	initiating methionine	UNP P62495
ii	-20	ARG	-	expression tag	UNP P62495
ii	-19	GLY	-	expression tag	UNP P62495
ii	-18	SER	-	expression tag	UNP P62495
ii	-17	HIS	-	expression tag	UNP P62495
ii	-16	HIS	-	expression tag	UNP P62495
ii	-15	HIS	-	expression tag	UNP P62495
ii	-14	HIS	-	expression tag	UNP P62495
ii	-13	HIS	-	expression tag	UNP P62495
ii	-12	HIS	-	expression tag	UNP P62495
ii	-11	GLY	-	expression tag	UNP P62495
ii	-10	MET	-	expression tag	UNP P62495
ii	-9	ALA	-	expression tag	UNP P62495
ii	-8	SER	-	expression tag	UNP P62495
ii	-7	GLU	-	expression tag	UNP P62495
ii	-6	ASN	-	expression tag	UNP P62495
ii	-5	LEU	-	expression tag	UNP P62495
ii	-4	TYR	-	expression tag	UNP P62495
ii	-3	PHE	-	expression tag	UNP P62495
ii	-2	GLN	-	expression tag	UNP P62495
ii	-1	GLY	-	expression tag	UNP P62495
ii	0	SER	-	expression tag	UNP P62495

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

Mol	Chain	Residues	Atoms		AltConf
86	P	1	Total 1	Mg 1	0
86	g	1	Total 1	Mg 1	0
86	j	1	Total 1	Mg 1	0
86	Q	1	Total 1	Mg 1	0
86	e	1	Total 1	Mg 1	0
86	B	1	Total 1	Mg 1	0
86	I	1	Total 1	Mg 1	0
86	V	1	Total 1	Mg 1	0
86	7	5	Total 5	Mg 5	0
86	a	1	Total 1	Mg 1	0
86	5	169	Total 169	Mg 169	0
86	8	3	Total 3	Mg 3	0
86	9	71	Total 71	Mg 71	0
86	hh	1	Total 1	Mg 1	0

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

Mol	Chain	Residues	Atoms		AltConf
87	p	1	Total 1	Zn 1	0
87	g	1	Total 1	Zn 1	0
87	j	1	Total 1	Zn 1	0
87	dd	1	Total 1	Zn 1	0
87	ff	1	Total 1	Zn 1	0
87	aa	1	Total 1	Zn 1	0

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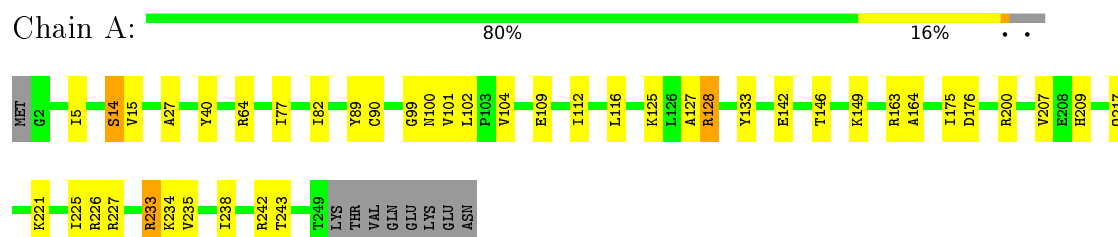
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Mol	Chain	Residues	Atoms		AltConf
87	o	1	Total 1	Zn 1	0
87	m	1	Total 1	Zn 1	0

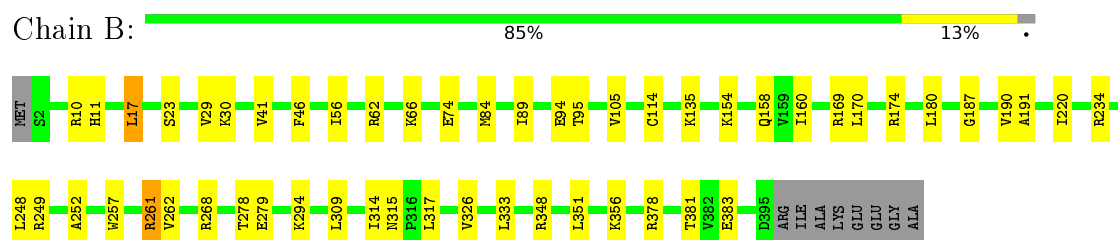
3 Residue-property plots

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.

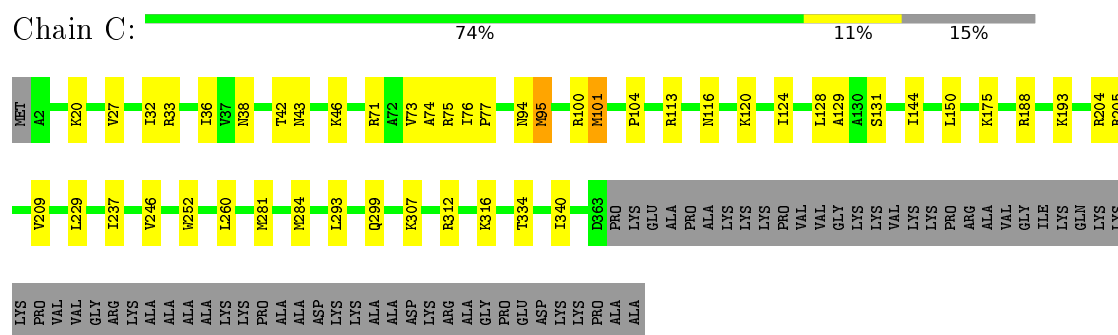
• Molecule 1: uL2



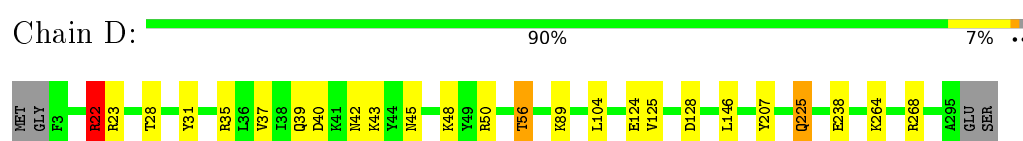
• Molecule 2: uL3



• Molecule 3: uL4

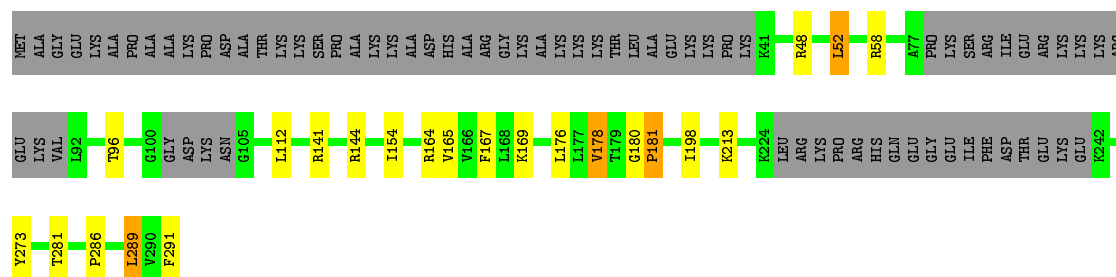


• Molecule 4: 60S ribosomal protein L5

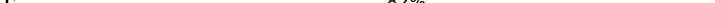


• Molecule 5: 60S ribosomal protein L6

Chain E:  66% 7% 26%



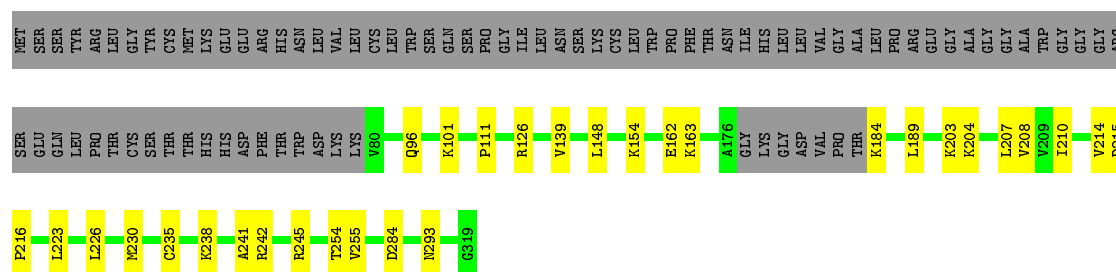
- Molecule 6: uL30

Chain F:  82% 8% 9%



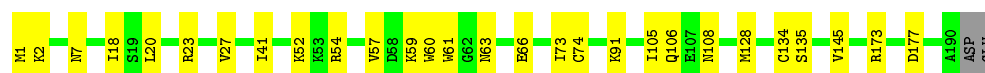
- Molecule 7: eL8

Chain G: 63% 10% 27%

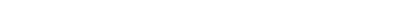


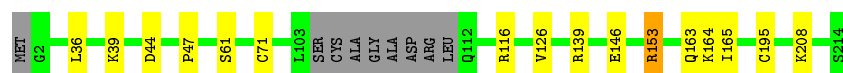
- Molecule 8: uL6

Chain H: 84% 15%



- Molecule 9: uL16

Chain I:  88% 7% .



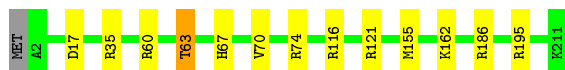
- Molecule 10: uL5

Chain J: 86% 10%



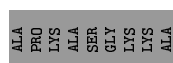
- Molecule 11: eL13

Chain L: 93% 6%



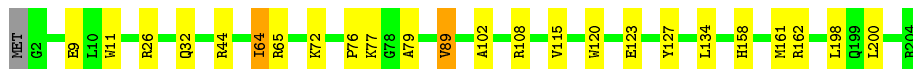
- Molecule 12: eL14

Chain M: 51% 11% 37%



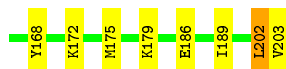
- Molecule 13: Ribosomal protein L15

Chain N: 88% 11%



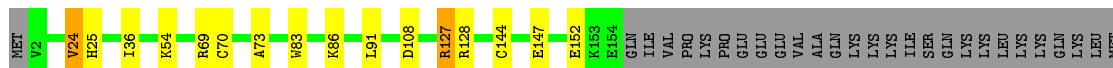
- Molecule 14: uL13

Chain O: 79% 16%



- Molecule 15: uL22

Chain P: 74% 8% 17%



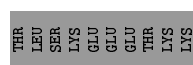
- Molecule 16: eL18

Chain Q: 87% 12%



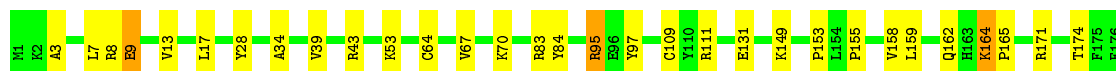
- Molecule 17: eL19

Chain R: 78% 13% 8%



- Molecule 18: eL20

Chain S: 82% 16% 2%



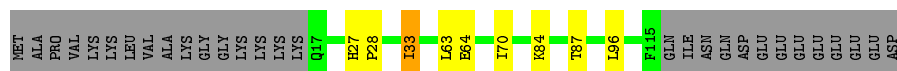
- Molecule 19: eL21

Chain T: 89% 10% 1%



- Molecule 20: eL22

Chain U: 70% 6% 23%



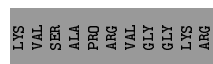
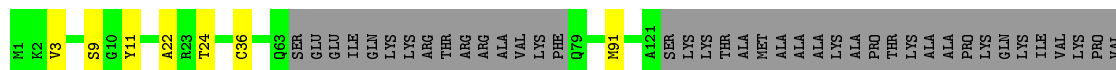
- Molecule 21: uL14

Chain V: 82% 11% 6%



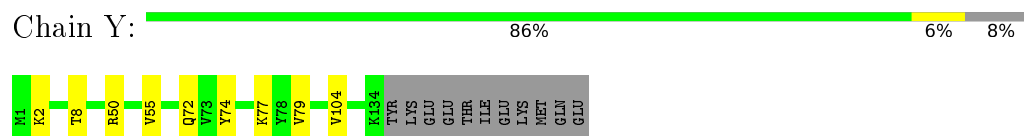
- Molecule 22: eL24

Chain W: 63% 32% 5%

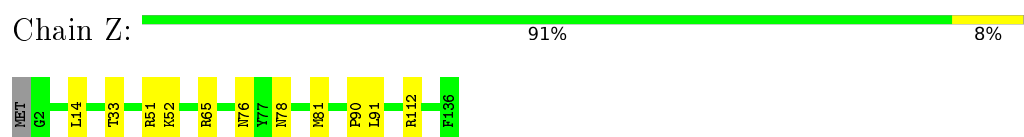


- Molecule 23: uL23

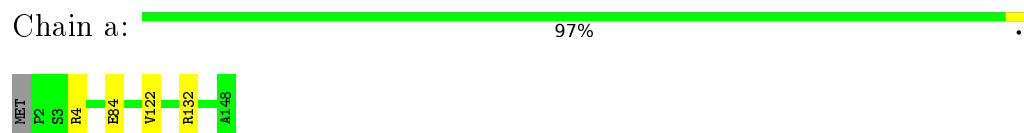
- Molecule 24: uL24



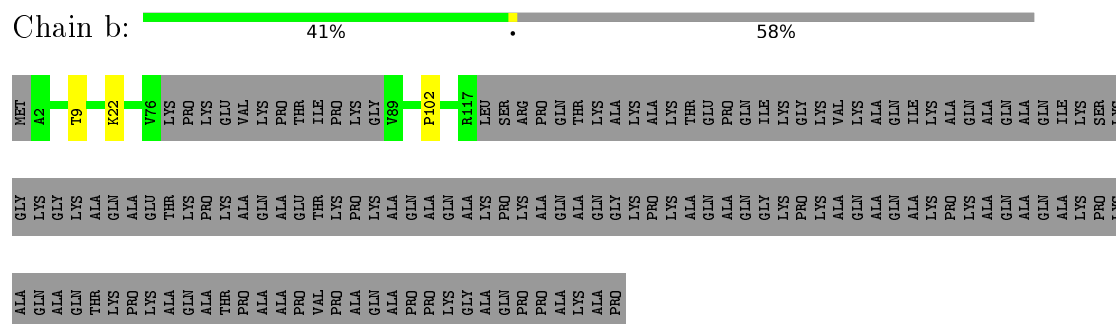
- Molecule 25: 60S ribosomal protein L27



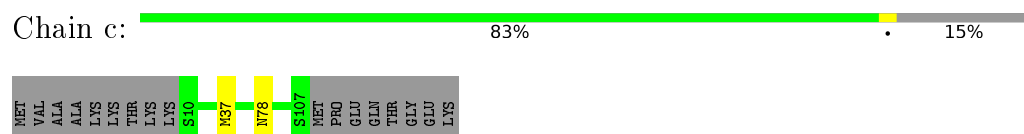
- Molecule 26: uL15



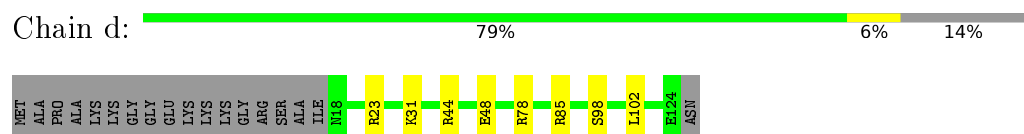
- Molecule 27: eL29




- Molecule 28: eL30

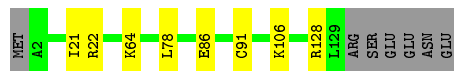


- Molecule 29: eL31




- Molecule 30: eL32

Chain e:  89% 6% 5%



- Molecule 31: eL33

Chain f:  92% 7% .



- Molecule 32: eL34

Chain g:  93% . .



- Molecule 33: uL29

Chain h:  95% . .




- Molecule 34: 60S ribosomal protein L36

Chain i:  94% . .



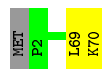
- Molecule 35: Ribosomal protein L37

Chain j:  82% 6% 11%



- Molecule 36: eL38

Chain k:  96% . .



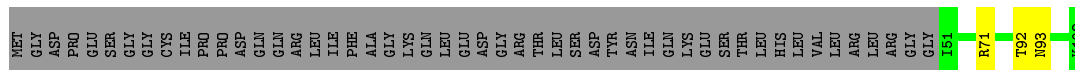
- Molecule 37: eL39

Chain l:  98% .



- Molecule 38: eL40

Chain m: 48% . 49%



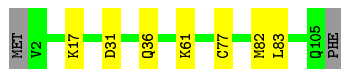
- Molecule 39: 60s ribosomal protein l41

Chain n: 92% 8%



- Molecule 40: eL42

Chain o: 92% 7% .



- Molecule 41: eL43

Chain p: 95% . .



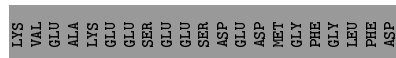
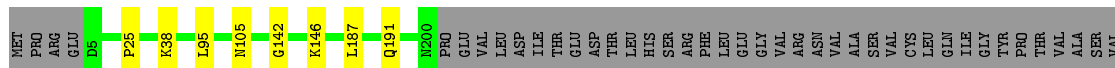
- Molecule 42: eL28

Chain r: 85% 6% 9%




- Molecule 43: uL10

Chain s: 59% . 38%




- Molecule 44: uL11

Chain t:  90% 7%



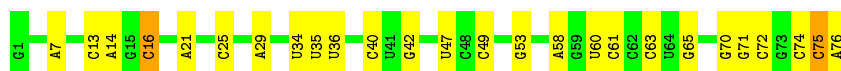
• Molecule 45: P-site tRNA

Chain 2:  75% 20%



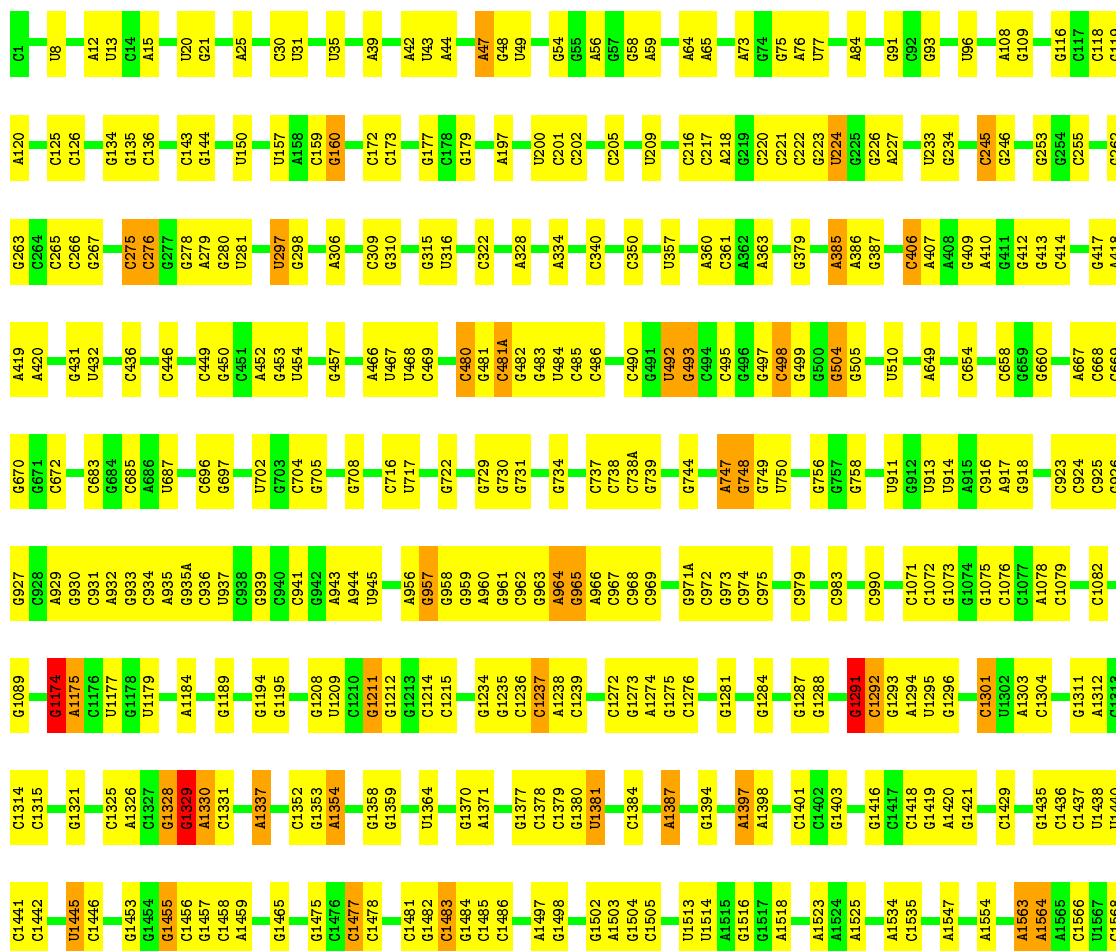
• Molecule 46: E-site tRNA

Chain 3:  65% 32%

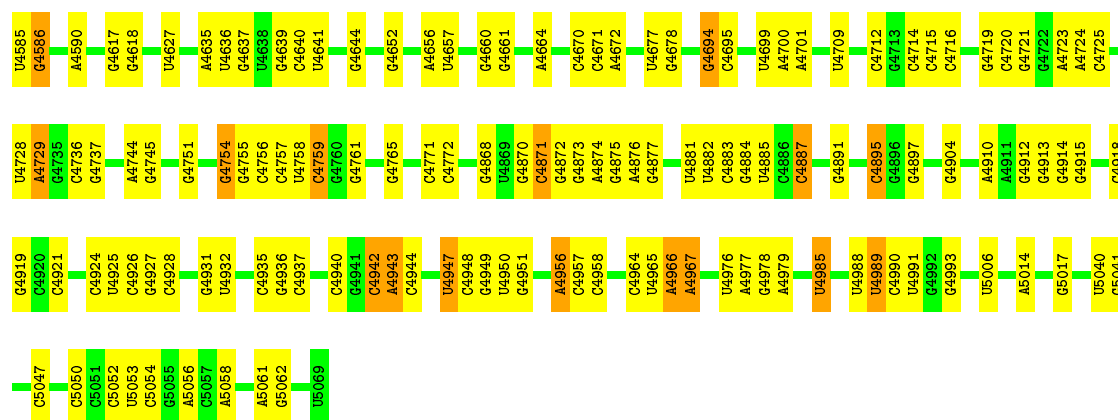


• Molecule 47: 28S ribosomal RNA

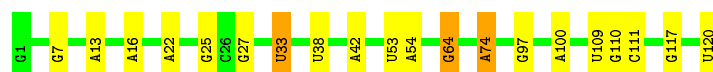
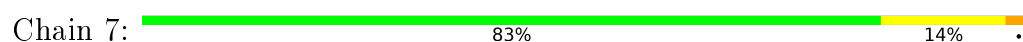
Chain 5:  68% 28%



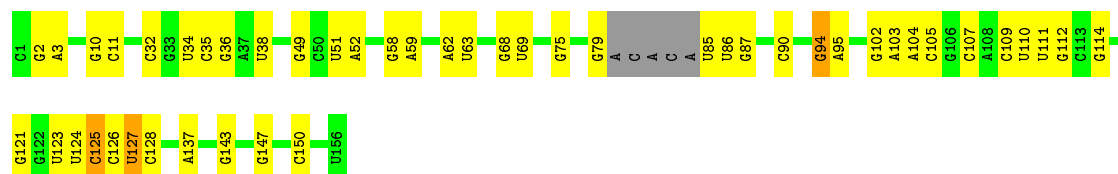
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U4471	C4335	G3819	U3704	C2875	U2740	G2620	C2469	G2331	U2084	A1979	C1856	A1742	U1578
G4475	A4336	G3820	G3710	G2876	A2743	U2625	G2470	G2333	G2085	U1980	A1867	G1750	G1586
C4476	A4339	A3821	A3711	G2884	A2744	U2626	G2471	G2348	A2088	A1983	A1868	G1753	G1590
A4488	G4339	G3822	A3712	G2884	A2745	U2627	G2472	A2349	G2089	A1984	G1869	U1754	U1591
U4495	C4349	A3829	G3722	U2891	A2754	G2638	G2475	A2349	G2090	U1985	U1882	C1755	G1592
G4495	C4350	G3830	A3723	G2896	A2755	U2639	G2476	A2349	G2091	U1986	U1883	U1756	U1596
G4499	U4354	U3831	A3724	G2897	A2756	G2640	G2479	C2351	G2092	C1987	U1883	U1757	
G4500	G4355	U3831	G3725	G2897	A2756	G2641	G2479	C2351	G2093	U1988	U1889		
C4508	G4373	U3838	G3729	C3598	G2760	A2641	G2483	A2363	G2094	G1989	U1889	G1760	
U4509	A4377	G3839	U3730	A3604	U2761	A2647	A2484	G2364	A2095	A1991	A1892	G1761	G1612
A4511	A4378	U3840	U3731	G3605	G2762	U2647	U2485	G2366	G2096	U1992	C1893	G1762	A1613
A4512	A4379	A3845	A3732	C3605	A2763	G2658	C2488	A2367	A2097	C1993	A1897	G1763	G1624
U4513	A4380	U3851	A3733	G3615	U2769	A2660	U2490	U2369	G2098	U1997	U1907	G1768	G1625
A4518	C4387	G3859	C3739	U3616	C2772	U2661	C2491	A2370	G2100		A1908	C1772	G1626
C4519	A4390	A3860	G3740	G3617	C2772	G2663	G2493	A2374	G2102	A2002	G1909	U1773	C1628
G4520	G4391	U3867	A3749	A3621	C2786	G2669	U2495	G2394	A2103	G2003	G1910		A1631
G4524	A4394	A3877	G3753	G3625	U2787	C2670	U2495	A2395	A2105	G2005	U1918	A1776	A1632
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U4531	A4397	G3879	G3755	G3627	A2789	U2676	G2503	G2397	A2107	G2007	C1920	U1781	A1634
C4548	G4401	A3888	A3759	G3628	G2809	G2680	G2506	U2408	G2110	C2011	A1923	C1785	C1635
G4549	A4415	G3889	A3760	U3644	A2806	G2681	A2513	U2409	G2259	A2013	U1930	A1787	G1641
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U4570	U4439	U3914	A3779	G3674	U2829	U2707	G2547	A2418	G2271	G2046	U1947	G1818	A1667
U4572	A4440	G3915	G3780	G3675	U2835	G2710	G2554	A2419	G2272	A2047	G1948	G1819	A1668
G4573	U4441	G3916	A3783	G3685	G2838	G2711	G2555	A2420	G2273	U2048	G1948	U1820	A1669
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G4575	U4445	U3927	U3786	G3690	U2841	C2716	G2566	G2423	A2282	G2053	G1952	U1822	C1676
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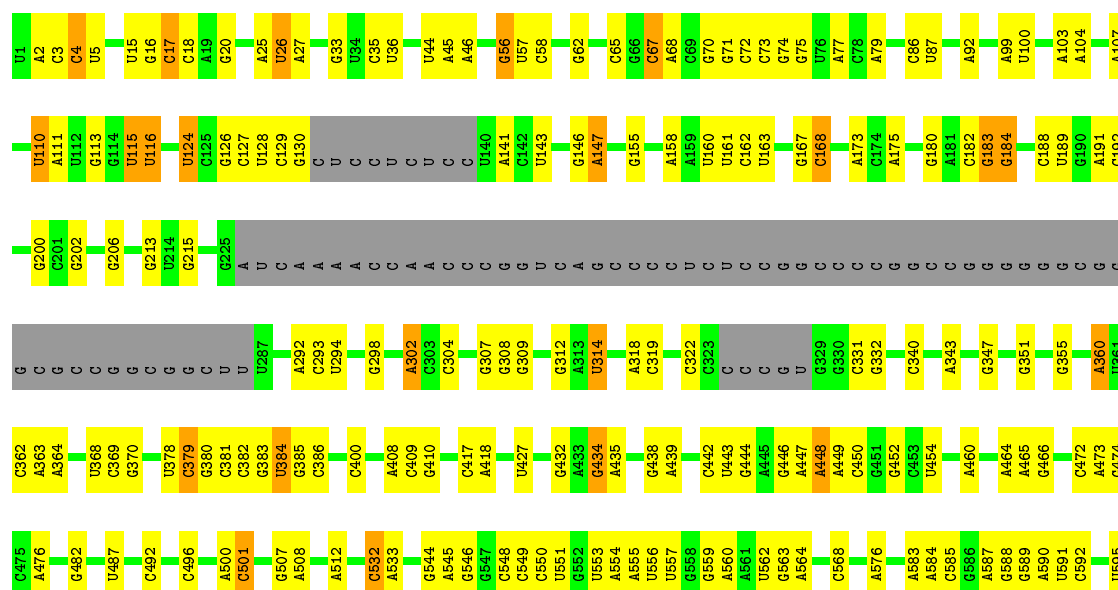
- Molecule 48: 5S ribosomal RNA



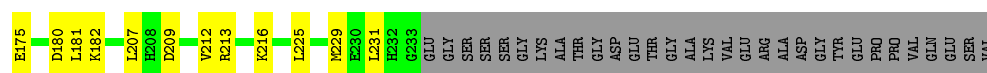
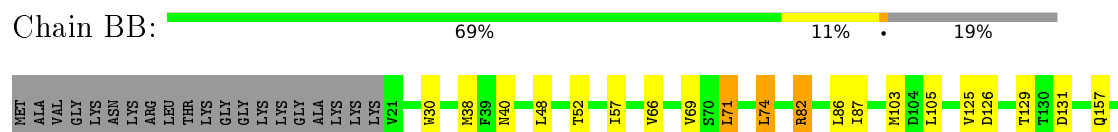
- Molecule 49: 5.8S ribosomal RNA



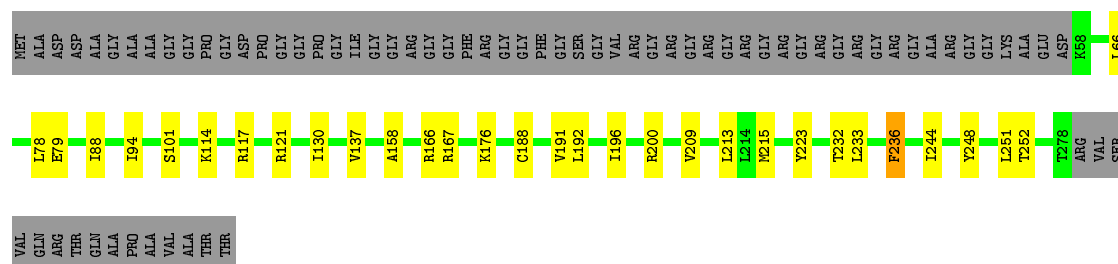
- Molecule 50: 18S ribosomal RNA



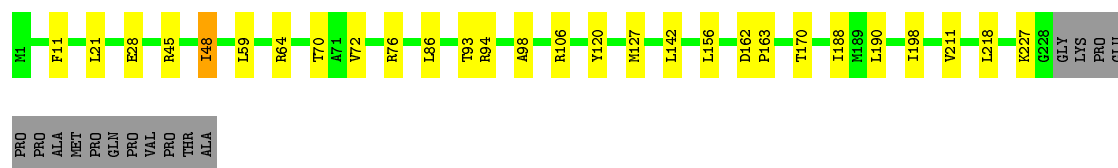
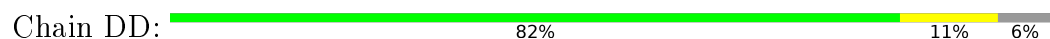
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U505	G906	U905
U506	G907	U906
U507	G908	U907
U508	G909	U908
U509	G910	U909
U510	G911	U910
U511	G912	U911
U512	G913	U912
U513	G914	U913
U514	G915	U914
U515	G916	U915
U516	G917	U916
U517	G918	U917
U518	G919	U918
U519	G920	U919
U520	G921	U920
U521	G922	U921
U522	G923	U922
U523	G924	U923
U524	G925	U924
U525	G926	U925
U526	G927	U926
U527	G928	U927
U528	G929	U928
U529	G930	U929
U530	G931	U930
U531	G932	U931
U532	G933	U932
U533	G934	U933
U534	G935	U934
U535	G936	U935
U536	G937	U936
U537	G938	U937
U538	G939	U938
U539	G940	U939
U540	G941	U940
U541	G942	U941
U542	G943	U942
U543	G944	U943
U544	G945	U944
U545	G946	U945
U546	G947	U946
U547	G948	U947
U548	G949	U948
U549	G950	U949
U550	G951	U950
U551	G952	U951
U552	G953	U952
U553	G954	U953
U554	G955	U954
U555	G956	U955
U556	G957	U956
U557	G958	U957
U558	G959	U958
U559	G960	U959
U560	G961	U960
U561	G962	U961
U562	G963	U962
U563	G964	U963
U564	G965	U964
U565	G966	U965
U566	G967	U966
U567	G968	U967
U568	G969	U968
U569	G970	U969
U570	G971	U970
U571	G972	U971
U572	G973	U972
U573	G974	U973
U574	G975	U974
U575	G976	U975
U576	G977	U976
U577	G978	U977
U578	G979	U978
U579	G980	U979
U580	G981	U980
U581	G982	U981
U582	G983	U982
U583	G984	U983
U584	G985	U984
U585	G986	U985
U586	G987	U986
U587	G988	U987
U588	G989	U988
U589	G990	U989
U590	G991	U990



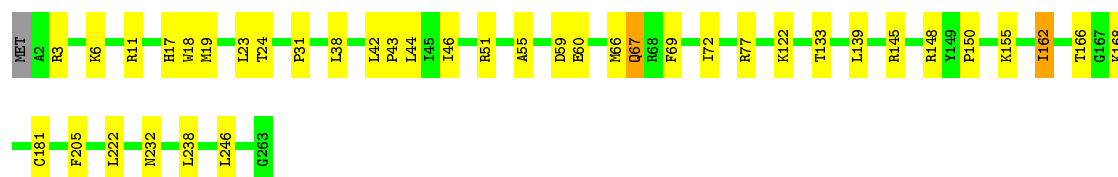
- Molecule 53: uS5



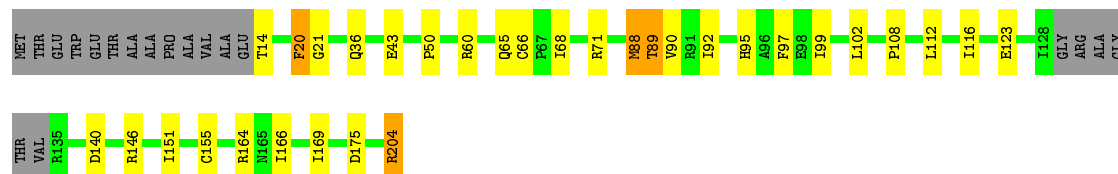
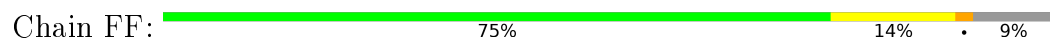
- Molecule 54: uS3




- Molecule 55: 40S ribosomal protein S4



- Molecule 56: uS7




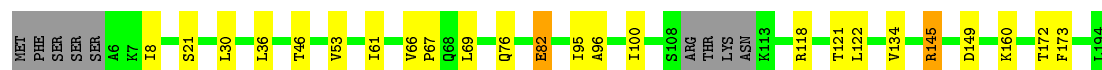
- Molecule 57: 40S ribosomal protein S6

Chain GG:  84% 10% • 5%




- Molecule 58: eS7

Chain HH:  83% 11% • 5%




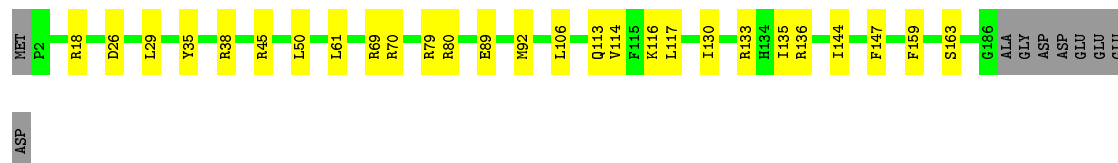
- Molecule 59: 40S ribosomal protein S8

Chain II:  83% 15% •



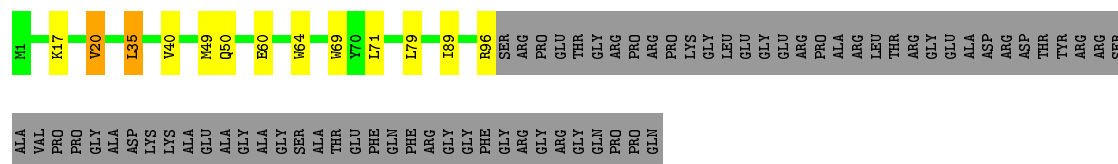
- Molecule 60: Ribosomal protein S9 (Predicted)

Chain JJ:  81% 14% 5%




- Molecule 61: eS10

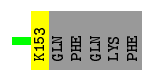
Chain KK:  50% 7% • 42%



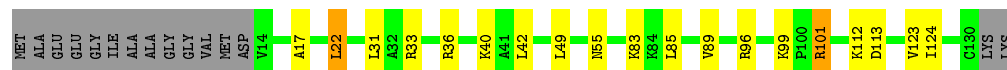
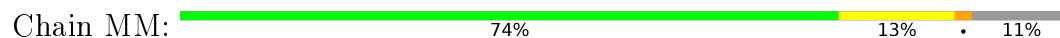
- Molecule 62: uS17

Chain LL:  75% 15% • 9%

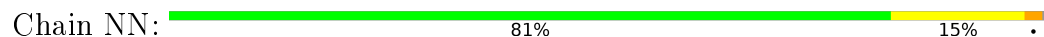




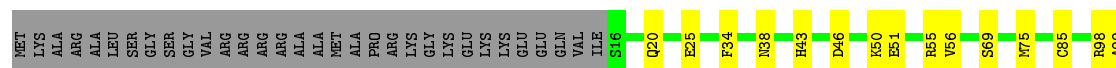
- Molecule 63: 40S ribosomal protein S12



- Molecule 64: uS15



- Molecule 65: uS11



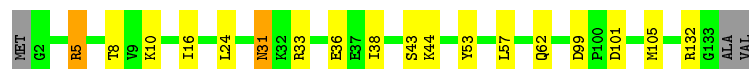
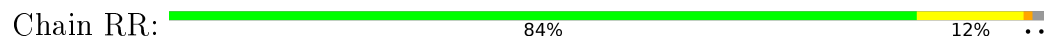
- Molecule 66: uS19



- Molecule 67: uS9

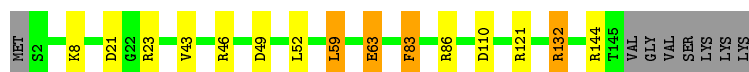


- Molecule 68: eS17

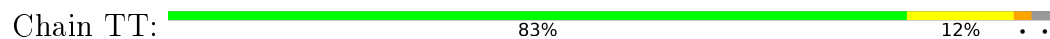


- Molecule 69: uS13

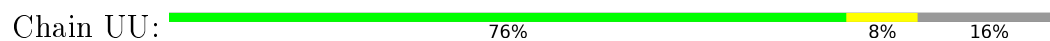




• Molecule 70: eS19



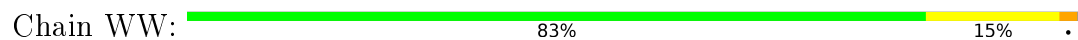
• Molecule 71: uS10



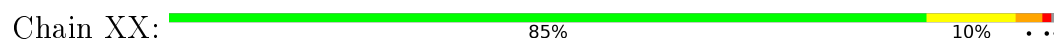
• Molecule 72: eS21



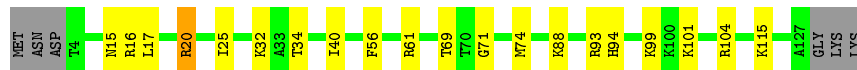
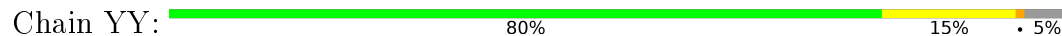
• Molecule 73: uS8



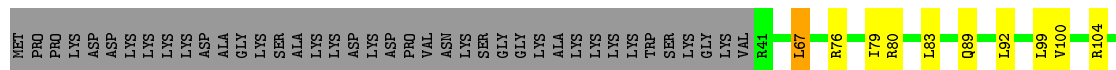
• Molecule 74: uS12

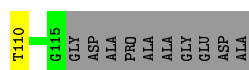


• Molecule 75: eS24

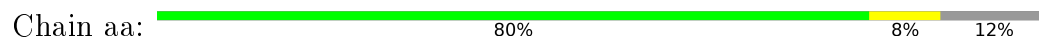


• Molecule 76: eS25





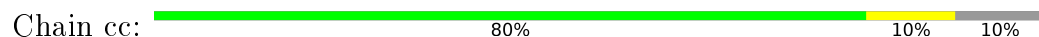
- Molecule 77: eS26



- Molecule 78: 40S ribosomal protein S27



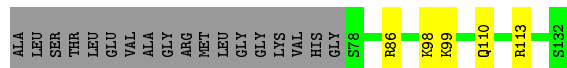
- Molecule 79: eS28



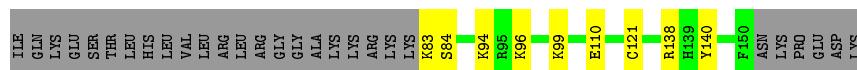
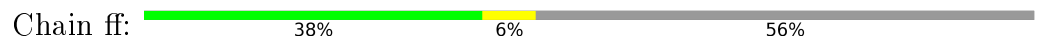
- Molecule 80: uS14



- Molecule 81: eS30



- Molecule 82: eS31



- Molecule 83: RACK1

Chain gg:

94%

..

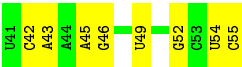


• Molecule 84: mRNA (UGA stop codon)

Chain hh:

47%

53%



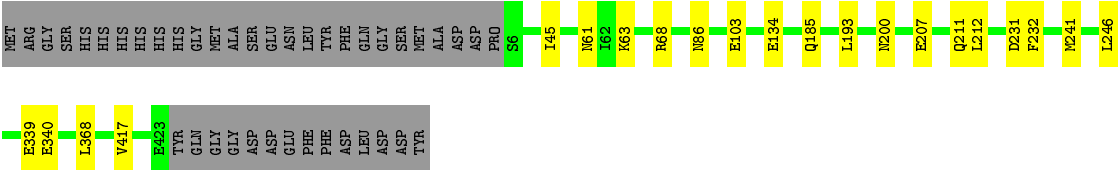
• Molecule 85: Eukaryotic peptide chain release factor subunit 1

Chain ii:

86%

5%

9%



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	13852	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	104478	Depositor
Image detector	Not provided	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	A	0.47	0/1936	0.77	1/2596 (0.0%)
10	J	0.42	0/1385	0.67	1/1852 (0.1%)
11	L	0.55	0/1733	0.78	0/2316
12	M	0.59	1/1158 (0.1%)	0.79	0/1547
13	N	0.51	0/1746	0.79	0/2338
14	O	0.58	0/1662	0.81	2/2222 (0.1%)
15	P	0.53	0/1268	0.73	0/1700
16	Q	0.54	0/1539	0.86	0/2054
17	R	0.59	1/1524 (0.1%)	0.79	1/2013 (0.0%)
18	S	0.53	1/1501 (0.1%)	0.75	0/2012
19	T	0.48	0/1326	0.71	1/1770 (0.1%)
2	B	0.49	0/3240	0.74	1/4339 (0.0%)
20	U	0.42	0/823	0.62	0/1104
21	V	0.50	0/993	0.72	0/1332
22	W	0.42	0/873	0.63	0/1158
23	X	0.45	0/984	0.68	0/1323
24	Y	0.42	0/1132	0.66	0/1504
25	Z	0.46	0/1130	0.65	0/1507
26	a	0.50	0/1191	0.75	0/1590
27	b	0.47	0/861	0.69	0/1138
28	c	0.42	0/771	0.65	0/1034
29	d	0.47	0/903	0.75	0/1216
3	C	0.52	0/2937	0.77	0/3946
30	e	0.49	0/1071	0.77	0/1429
31	f	0.45	0/895	0.77	0/1198
32	g	0.43	0/916	0.73	0/1220
33	h	0.57	0/1021	0.77	1/1348 (0.1%)
34	i	0.45	0/841	0.69	0/1112
35	j	0.57	0/720	0.83	0/952
36	k	0.45	0/575	0.61	0/761
37	l	0.57	0/459	0.76	0/608
38	m	0.49	0/435	0.76	0/575

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
39	n	0.63	0/240	0.91	0/305
4	D	0.55	1/2437 (0.0%)	0.75	1/3264 (0.0%)
40	o	0.50	0/864	0.71	0/1140
41	p	0.55	0/718	0.78	0/953
42	r	0.49	0/1010	0.75	0/1354
43	s	0.44	0/1530	0.58	0/2064
44	t	0.47	0/1173	0.68	0/1579
45	2	0.40	1/1803 (0.1%)	0.72	2/2801 (0.1%)
46	3	0.24	0/1777	0.66	0/2763
47	5	0.39	3/84974 (0.0%)	0.71	22/132512 (0.0%)
48	7	0.38	0/2858	0.66	0/4455
49	8	0.39	0/3581	0.68	0/5577
5	E	0.42	0/1762	0.67	0/2362
50	9	0.34	1/40516 (0.0%)	0.72	12/63102 (0.0%)
51	AA	0.44	0/1747	0.68	0/2374
52	BB	0.40	0/1756	0.66	0/2350
53	CC	0.42	0/1753	0.70	0/2369
54	DD	0.45	0/1796	0.69	0/2417
55	EE	0.44	0/2118	0.73	0/2849
56	FF	0.43	0/1492	0.68	0/2005
57	GG	0.40	0/1946	0.72	0/2590
58	HH	0.41	0/1510	0.64	0/2022
59	II	0.47	0/1715	0.74	2/2287 (0.1%)
6	F	0.56	0/1911	0.76	1/2549 (0.0%)
60	JJ	0.43	0/1550	0.76	0/2069
61	KK	0.45	0/834	0.61	0/1125
62	LL	0.45	0/1195	0.78	0/1597
63	MM	0.44	0/918	0.64	0/1233
64	NN	0.41	0/1226	0.70	0/1649
65	OO	0.41	0/1029	0.80	1/1380 (0.1%)
66	PP	0.42	0/1017	0.74	1/1358 (0.1%)
67	QQ	0.40	0/1146	0.68	0/1534
68	RR	0.43	0/1082	0.65	0/1452
69	SS	0.40	0/1208	0.71	0/1618
7	G	0.47	0/1910	0.70	0/2569
70	TT	0.49	1/1115 (0.1%)	0.69	1/1493 (0.1%)
71	UU	0.51	2/805 (0.2%)	0.70	0/1081
72	VV	0.51	1/643 (0.2%)	0.75	0/860
73	WW	0.46	0/1051	0.74	0/1406
74	XX	0.45	0/1116	0.76	1/1490 (0.1%)
75	YY	0.41	0/1028	0.68	0/1366
76	ZZ	0.39	0/604	0.71	0/810
77	aa	0.43	0/828	0.78	0/1109

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
78	bb	0.41	0/665	0.70	0/891
79	cc	0.52	1/490 (0.2%)	0.72	0/656
8	H	0.41	0/1535	0.66	0/2063
80	dd	0.49	0/470	0.72	0/623
81	ee	0.41	0/447	0.75	0/587
82	ff	0.39	0/567	0.55	0/753
83	gg	0.37	0/2493	0.60	0/3394
84	hh	0.32	0/353	0.74	0/547
85	ii	0.40	0/3345	0.61	0/4492
9	I	0.49	0/1702	0.71	1/2272 (0.0%)
All	All	0.42	14/234908 (0.0%)	0.71	53/344334 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
12	M	0	1
51	AA	0	1
55	EE	0	1
74	XX	0	1
All	All	0	4

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	R	28	GLU	CD-OE2	8.20	1.34	1.25
45	2	20	U	C5'-C4'	7.89	1.60	1.51
18	S	131	GLU	CD-OE2	7.10	1.33	1.25
4	D	238	GLU	CD-OE2	6.30	1.32	1.25
47	5	2411	C	O3'-P	-6.20	1.53	1.61
79	cc	52	GLU	CD-OE1	6.00	1.32	1.25
71	UU	96	GLU	CD-OE1	5.57	1.31	1.25
71	UU	96	GLU	CD-OE2	5.57	1.31	1.25
47	5	4284	C	O3'-P	-5.52	1.54	1.61
72	VV	7	GLU	CD-OE2	5.44	1.31	1.25
70	TT	50	GLU	CD-OE2	5.36	1.31	1.25
12	M	8	GLU	CD-OE2	5.30	1.31	1.25
50	9	432	G	O3'-P	-5.29	1.54	1.61
47	5	4390	A	O3'-P	-5.10	1.55	1.61

All (53) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	22	ARG	NE-CZ-NH1	8.35	124.47	120.30
50	9	1835	A	C2'-C3'-O3'	7.93	126.95	109.50
50	9	1394	G	C2'-C3'-O3'	7.78	126.61	109.50
19	T	32	ARG	NE-CZ-NH1	7.60	124.10	120.30
47	5	1477	C	C2'-C3'-O3'	7.57	126.16	109.50
47	5	1455	G	C2'-C3'-O3'	7.55	126.11	109.50
47	5	2068	C	C4'-C3'-O3'	7.47	127.94	113.00
47	5	1329	G	C2'-C3'-O3'	7.30	125.55	109.50
47	5	1174	G	C2'-C3'-O3'	7.17	125.28	109.50
47	5	2695	A	C2'-C3'-O3'	7.15	125.23	109.50
50	9	110	U	C2'-C3'-O3'	7.13	125.20	109.50
50	9	874	G	C2'-C3'-O3'	6.65	124.34	113.70
47	5	1979	A	C2'-C3'-O3'	6.59	124.25	113.70
65	OO	146	ARG	NE-CZ-NH1	6.54	123.57	120.30
14	O	94	ARG	NE-CZ-NH1	6.53	123.56	120.30
6	F	88	LEU	CA-CB-CG	6.34	129.88	115.30
47	5	406	C	C2'-C3'-O3'	6.27	123.73	113.70
45	2	20(A)	U	N1-C1'-C2'	6.25	122.13	114.00
47	5	3888	G	C2'-C3'-O3'	6.17	123.58	113.70
47	5	3625	G	C2'-C3'-O3'	6.12	123.48	113.70
50	9	1646	C	C2'-C3'-O3'	6.12	123.48	113.70
47	5	1211	G	C2'-C3'-O3'	6.06	123.39	113.70
10	J	75	ARG	NE-CZ-NH1	5.92	123.26	120.30
50	9	434	G	C4'-C3'-O3'	5.87	124.74	113.00
59	II	56	ARG	NE-CZ-NH1	5.84	123.22	120.30
47	5	1445	U	C2'-C3'-O3'	5.80	122.98	113.70
1	A	226	ARG	NE-CZ-NH1	5.73	123.17	120.30
47	5	3697	U	C2'-C3'-O3'	5.70	122.82	113.70
45	2	20	U	C5'-C4'-C3'	5.67	125.08	116.00
47	5	4947	U	C2'-C3'-O3'	5.65	122.74	113.70
50	9	1620	A	N9-C1'-C2'	5.58	121.25	114.00
47	5	47	A	C4'-C3'-O3'	5.54	124.09	113.00
9	I	139	ARG	NE-CZ-NH1	5.54	123.07	120.30
47	5	480	C	C2'-C3'-O3'	5.52	122.53	113.70
33	h	51	ARG	NE-CZ-NH1	5.48	123.04	120.30
47	5	385	A	C4'-C3'-O3'	5.41	123.81	113.00
74	XX	107	ARG	NE-CZ-NH2	5.41	123.00	120.30
47	5	504	G	C2'-C3'-O3'	5.39	122.33	113.70
50	9	532	C	C2'-C3'-O3'	5.37	122.30	113.70
50	9	642	U	C2'-C3'-O3'	5.33	122.23	113.70
2	B	268	ARG	NE-CZ-NH2	5.31	122.95	120.30
50	9	1535	U	N1-C1'-C2'	5.29	120.87	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
70	TT	110	LEU	CA-CB-CG	5.24	127.34	115.30
47	5	1291	G	C2'-C3'-O3'	5.19	122.00	113.70
47	5	275	C	C2'-C3'-O3'	5.16	121.96	113.70
59	II	56	ARG	NE-CZ-NH2	-5.14	117.73	120.30
14	O	12	ARG	NE-CZ-NH1	5.13	122.86	120.30
50	9	1863	A	O4'-C1'-N9	5.13	112.30	108.20
17	R	107	ARG	NE-CZ-NH1	5.11	122.86	120.30
66	PP	37	TYR	CA-CB-CG	5.07	123.03	113.40
47	5	1818	G	C2'-C3'-O3'	5.06	121.80	113.70
47	5	2046	G	C2'-C3'-O3'	5.05	121.78	113.70
50	9	870	A	C4'-C3'-O3'	5.05	123.09	113.00

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
51	AA	42	LYS	Peptide
55	EE	155	LYS	Peptide
12	M	67	SER	Peptide
74	XX	61	GLN	Peptide

5.2 Too-close contacts [i](#)

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	1898	0	1993	18	0
2	B	3172	0	3310	23	0
3	C	2883	0	3053	25	0
4	D	2391	0	2424	12	0
5	E	1729	0	1887	9	0
6	F	1875	0	1995	9	0
7	G	1879	0	2027	11	0
8	H	1516	0	1597	8	0
9	I	1664	0	1712	2	0
10	J	1362	0	1399	6	0
11	L	1702	0	1820	2	0
12	M	1137	0	1211	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	N	1701	0	1749	9	0
14	O	1630	0	1778	21	0
15	P	1242	0	1274	5	0
16	Q	1515	0	1634	9	0
17	R	1508	0	1664	7	0
18	S	1462	0	1508	14	0
19	T	1298	0	1366	5	0
20	U	809	0	833	5	0
21	V	979	0	1039	7	0
22	W	860	0	903	4	0
23	X	967	0	1040	3	0
24	Y	1115	0	1205	2	0
25	Z	1107	0	1182	3	0
26	a	1162	0	1209	0	0
27	b	848	0	920	0	0
28	c	761	0	794	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	998	0	0
33	h	1013	0	1147	0	0
34	i	830	0	916	0	0
35	j	705	0	737	0	0
36	k	569	0	637	0	0
37	l	447	0	480	0	0
38	m	429	0	466	0	0
39	n	239	0	289	0	0
40	o	851	0	920	0	0
41	p	708	0	758	0	0
42	r	994	0	1051	0	0
43	s	1507	0	1564	0	0
44	t	1160	0	1217	0	0
45	2	1616	0	826	36	0
46	3	1593	0	811	3	0
47	5	75972	0	38391	242	0
48	7	2558	0	1296	4	0
49	8	3208	0	1629	9	0
50	9	36249	0	18324	149	0
51	AA	1710	0	1708	13	0
52	BB	1729	0	1803	8	0
53	CC	1716	0	1806	10	0
54	DD	1768	0	1866	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
55	EE	2076	0	2177	18	0
56	FF	1471	0	1522	16	0
57	GG	1923	0	2089	8	0
58	HH	1488	0	1582	8	0
59	II	1686	0	1772	17	0
60	JJ	1525	0	1640	8	0
61	KK	810	0	836	5	0
62	LL	1175	0	1249	9	0
63	MM	908	0	939	4	0
64	NN	1202	0	1289	8	0
65	OO	1016	0	1039	3	0
66	PP	997	0	1045	5	0
67	QQ	1128	0	1195	2	0
68	RR	1068	0	1121	5	0
69	SS	1190	0	1249	4	0
70	TT	1097	0	1132	9	0
71	UU	795	0	862	2	0
72	VV	636	0	637	5	0
73	WW	1034	0	1080	9	0
74	XX	1098	0	1167	12	0
75	YY	1011	0	1083	5	0
76	ZZ	598	0	656	6	0
77	aa	814	0	865	0	0
78	bb	651	0	672	0	0
79	cc	488	0	514	0	0
80	dd	459	0	450	0	0
81	ee	443	0	492	0	0
82	ff	555	0	566	0	0
83	gg	2436	0	2393	0	0
84	hh	317	0	161	0	0
85	ii	3295	0	3334	0	0
86	5	169	0	0	0	0
86	7	5	0	0	0	0
86	8	3	0	0	0	0
86	9	71	0	0	0	0
86	B	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	a	1	0	0	0	0
86	e	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
86	g	1	0	0	0	0
86	hh	1	0	0	0	0
86	j	1	0	0	0	0
87	aa	1	0	0	0	0
87	dd	1	0	0	0	0
87	ff	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	219122	0	163963	773	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 3.

All (773) 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)
45:2:20:U:C1'	45:2:20(A):U:H1'	1.32	1.56
45:2:20:U:C2'	45:2:20(A):U:C1'	1.75	1.55
45:2:20:U:C3'	45:2:20(A):U:C3'	1.77	1.50
45:2:20:U:H2'	45:2:20(A):U:C2'	1.34	1.50
45:2:20:U:C2'	45:2:20(A):U:H1'	1.09	1.39
47:5:3914:U:O4	47:5:4378:A:N1	1.56	1.38
45:2:20:U:H3'	45:2:20(A):U:C3'	0.85	1.33
50:9:1137:U:O4	50:9:1148:A:N1	1.65	1.29
45:2:20:U:H2'	45:2:20(A):U:O2'	1.33	1.28
45:2:20:U:C2'	45:2:20(A):U:C2'	1.95	1.27
47:5:2367:A:N1	47:5:2788:U:O4	1.71	1.22
50:9:1137:U:C4	50:9:1148:A:N1	2.09	1.20
45:2:20:U:C3'	45:2:20(A):U:O3'	1.91	1.17
45:2:20:U:H2'	45:2:20(A):U:C1'	1.57	1.13
45:2:20:U:H3'	45:2:20(A):U:C2'	1.66	1.11
45:2:20:U:C3'	45:2:20(A):U:C2'	2.07	1.10
45:2:20:U:O4'	45:2:20(A):U:O2	1.73	1.06
45:2:20:U:H3'	45:2:20(A):U:O3'	1.57	0.98
45:2:20:U:O3'	45:2:20(A):U:O3'	1.82	0.96
50:9:1137:U:O4	50:9:1148:A:C2	2.18	0.95
45:2:20:U:C2'	45:2:20(A):U:O2'	2.04	0.92
45:2:20:U:O4'	45:2:20(A):U:C2	2.24	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:2:20:U:C1'	45:2:20(A):U:C1'	2.26	0.86
47:5:3914:U:H3	47:5:4378:A:N6	1.74	0.85
47:5:2367:A:N6	47:5:2788:U:N3	2.26	0.82
47:5:3914:U:C4	47:5:4378:A:N1	2.48	0.80
47:5:3914:U:O4	47:5:4378:A:C2	2.35	0.79
47:5:4579:U:H2'	47:5:4580:U:C6	2.18	0.78
45:2:20:U:H2'	45:2:20(A):U:HO2'	1.48	0.77
1:A:225:ILE:HD12	1:A:233:ARG:CZ	2.14	0.77
50:9:1407:U:H2'	50:9:1408:U:C6	2.20	0.77
50:9:1137:U:O4	50:9:1148:A:C6	2.38	0.76
47:5:3914:U:N3	47:5:4378:A:N6	2.31	0.76
4:D:22:ARG:NH1	4:D:28:THR:OG1	2.19	0.74
47:5:2395:A:O2'	47:5:2806:A:N3	2.17	0.74
47:5:2367:A:H61	47:5:2788:U:H3	1.34	0.73
50:9:1091:C:HO2'	73:WW:2:VAL:N	1.87	0.72
47:5:2367:A:N1	47:5:2788:U:C4	2.57	0.71
17:R:74:ARG:NH2	47:5:2891:U:OP2	2.23	0.71
47:5:2367:A:N6	47:5:2788:U:H3	1.86	0.71
61:KK:35:LEU:HD13	61:KK:40:VAL:HG21	1.72	0.70
3:C:101:MET:SD	3:C:104:PRO:HA	2.31	0.70
55:EE:122:LYS:HG2	55:EE:162:ILE:HD11	1.73	0.69
45:2:20:U:C6	45:2:20(A):U:C6	2.81	0.69
47:5:1986:U:C2	47:5:2006:U:O4	2.46	0.69
14:O:18:ARG:NH1	47:5:2053:C:O3'	2.26	0.69
47:5:1986:U:O2	47:5:2006:U:O4	2.11	0.68
50:9:1438:A:H2'	50:9:1439:A:C8	2.29	0.68
47:5:1986:U:O2	47:5:2006:U:C4	2.47	0.68
47:5:1986:U:H2'	47:5:2007:G:O6	1.94	0.68
47:5:3766:A:N1	50:9:1827:U:O2'	2.23	0.68
55:EE:122:LYS:CG	55:EE:162:ILE:HD11	2.25	0.67
60:JJ:35:TYR:CD2	60:JJ:106:LEU:HD23	2.29	0.67
50:9:1137:U:C4	50:9:1148:A:C6	2.83	0.67
50:9:980:A:H2'	50:9:981:A:C8	2.31	0.66
47:5:4579:U:O2	47:5:4580:U:C2	2.49	0.66
4:D:146:LEU:HD12	47:5:4323:A:C2	2.31	0.65
47:5:2013:A:C2	47:5:2014:C:C2	2.85	0.65
50:9:945:U:H2'	50:9:946:U:C6	2.31	0.65
45:2:20:U:C2	45:2:20(A):U:C2	2.85	0.65
14:O:72:HIS:N	47:5:4586:G:OP1	2.24	0.65
50:9:1533:A:OP2	56:FF:164:ARG:NH2	2.30	0.65
56:FF:68:ILE:HD12	56:FF:112:LEU:HD22	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
76:ZZ:79:ILE:HB	76:ZZ:83:LEU:HD12	1.79	0.64
50:9:1130:G:H2'	50:9:1130:G:N3	2.11	0.64
1:A:27:ALA:O	1:A:128:ARG:NH2	2.31	0.63
3:C:38:ASN:O	3:C:42:THR:HG23	1.99	0.63
50:9:298:G:OP1	55:EE:133:THR:O	2.16	0.63
47:5:3654:G:O2'	47:5:3693:U:OP1	2.11	0.62
50:9:1611:G:OP2	69:SS:121:ARG:NH1	2.32	0.62
50:9:384:U:O4	59:II:5:ARG:NH2	2.33	0.62
6:F:227:VAL:HA	18:S:39:VAL:HG12	1.82	0.62
47:5:1986:U:C4	47:5:2013:A:N6	2.68	0.61
2:B:174:ARG:NH1	47:5:4985:U:O2	2.33	0.61
47:5:1964:A:C6	47:5:4694:G:C6	2.89	0.61
47:5:4723:A:H2'	47:5:4724:A:C8	2.35	0.61
50:9:640:A:H2'	50:9:641:A:C8	2.36	0.61
50:9:124:U:OP1	55:EE:148:ARG:NE	2.34	0.60
10:J:128:LEU:HD11	10:J:130:PHE:CE1	2.37	0.60
55:EE:55:ALA:HB1	55:EE:60:GLU:HB2	1.84	0.60
51:AA:60:LEU:HD13	51:AA:159:ILE:HD11	1.84	0.60
12:M:24:LEU:HD11	12:M:86:TRP:CG	2.38	0.59
47:5:3811:G:O2'	47:5:3814:U:OP2	2.21	0.59
63:MM:22:LEU:HD11	63:MM:89:VAL:HA	1.85	0.59
21:V:98:PHE:CD1	22:W:22:ALA:HB3	2.37	0.58
47:5:4887:C:H6	47:5:4887:C:H5''	1.68	0.58
47:5:747:A:H4'	47:5:748:G:OP1	2.03	0.58
3:C:334:THR:HG21	6:F:50:TYR:OH	2.03	0.58
75:YY:34:THR:HG23	75:YY:69:THR:HG21	1.85	0.58
51:AA:104:THR:O	51:AA:107:THR:HG23	2.02	0.58
54:DD:11:PHE:CE2	71:UU:84:ILE:HD11	2.39	0.58
4:D:39:GLN:HG2	4:D:48:LYS:HB2	1.86	0.58
3:C:73:VAL:O	47:5:2350:U:C4	2.57	0.57
52:BB:66:VAL:HG22	52:BB:87:ILE:HG22	1.86	0.57
8:H:41:ILE:HG21	8:H:73:ILE:HD11	1.86	0.57
50:9:1220:A:N6	50:9:1221:G:C6	2.73	0.57
14:O:12:ARG:O	18:S:171:ARG:NH2	2.37	0.57
73:WW:75:ILE:HD11	73:WW:93:LEU:HD11	1.86	0.57
47:5:2007:G:C2	47:5:2013:A:N6	2.73	0.57
63:MM:22:LEU:HD21	63:MM:89:VAL:HG23	1.85	0.57
18:S:164:LYS:HB3	18:S:165:PRO:HD3	1.87	0.57
50:9:925:G:N2	64:NN:48:SER:OG	2.37	0.57
53:CC:251:LEU:HD23	72:VV:23:ILE:HG23	1.87	0.57
19:T:87:LYS:NZ	47:5:4301:U:OP2	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:5:1964:A:C5	47:5:4694:G:C6	2.93	0.56
55:EE:31:PRO:HG2	55:EE:38:LEU:HD12	1.87	0.56
50:9:1117:C:O2'	50:9:1118:C:O4'	2.24	0.56
8:H:61:TRP:CZ3	12:M:33:GLN:HG2	2.39	0.56
45:2:20:U:N1	45:2:20(A):U:C2	2.74	0.56
50:9:507:G:OP2	75:YY:104:ARG:NH2	2.38	0.56
47:5:3690:U:O2'	47:5:3817:A:N3	2.32	0.56
51:AA:33:GLN:HB3	51:AA:154:LEU:HD12	1.87	0.56
45:2:20:U:C1'	45:2:20(A):U:N1	2.69	0.56
45:2:16:C:O4'	45:2:16:C:O2	2.24	0.56
14:O:27:VAL:HG12	14:O:98:ALA:HB1	1.86	0.56
47:5:4548:A:H5'	47:5:4549:G:OP1	2.05	0.56
50:9:1599:U:H2'	56:FF:166:ILE:HD11	1.87	0.55
68:RR:16:ILE:HG22	68:RR:24:LEU:HD11	1.87	0.55
50:9:183:G:O2'	50:9:184:G:O5'	2.23	0.55
47:5:1483:C:O4'	47:5:1483:C:O2	2.22	0.55
5:E:281:THR:OG1	47:5:4754:G:N7	2.40	0.55
50:9:115:U:H2'	50:9:116:U:C6	2.41	0.55
18:S:97:TYR:CZ	18:S:109:CYS:HA	2.42	0.55
47:5:21:G:O6	49:8:36:G:C6	2.60	0.55
47:5:222:C:H2'	47:5:223:G:O4'	2.06	0.55
50:9:1589:A:N3	50:9:1653:U:O2'	2.36	0.55
1:A:14:SER:OG	1:A:15:VAL:N	2.39	0.55
50:9:1593:C:OP2	76:ZZ:104:ARG:NH2	2.40	0.55
56:FF:102:LEU:HD22	76:ZZ:110:THR:HG21	1.89	0.55
57:GG:63:MET:N	57:GG:63:MET:SD	2.75	0.55
15:P:70:CYS:SG	15:P:73:ALA:N	2.80	0.55
47:5:2505:C:O4'	47:5:2505:C:O2	2.24	0.55
21:V:82:ILE:HD12	21:V:104:VAL:HG13	1.87	0.55
47:5:1381:U:O2	47:5:1381:U:H5''	2.07	0.55
18:S:3:ALA:O	18:S:111:ARG:NH1	2.40	0.55
62:LL:37:TYR:CE2	62:LL:51:ILE:HG23	2.41	0.54
4:D:42:ASN:HD21	19:T:69:GLN:HE22	1.54	0.54
47:5:4942:C:H4'	47:5:4943:A:OP1	2.08	0.54
50:9:1489:A:H4'	50:9:1490:G:OP2	2.07	0.54
72:VV:55:ILE:HD11	72:VV:69:ILE:CG1	2.38	0.54
74:XX:128:VAL:HG11	74:XX:133:LEU:HD21	1.90	0.54
50:9:501:C:C2'	50:9:501:C:O2	2.56	0.54
12:M:97:ALA:HB2	14:O:203:VAL:HB	1.89	0.54
47:5:2627:C:O2	47:5:2627:C:O4'	2.24	0.54
50:9:1351:G:O2'	50:9:1378:A:N1	2.29	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:9:427:U:O4'	50:9:427:U:O2	2.26	0.54
47:5:3810:C:O4'	47:5:3810:C:O2	2.25	0.54
7:G:189:LEU:HD22	7:G:255:VAL:CG1	2.38	0.54
24:Y:55:VAL:HG13	24:Y:104:VAL:HG13	1.90	0.54
47:5:224:U:O2	47:5:224:U:O4'	2.26	0.53
50:9:1315:U:O2	50:9:1315:U:O4'	2.26	0.53
16:Q:67:ILE:HD12	16:Q:96:PRO:HD2	1.88	0.53
50:9:1139:C:O2	50:9:1139:C:O4'	2.24	0.53
1:A:207:VAL:HG11	47:5:1633:G:C6	2.44	0.53
47:5:4989:U:O2	47:5:4989:U:O4'	2.27	0.53
50:9:823:U:O2	50:9:823:U:O4'	2.26	0.53
54:DD:11:PHE:CZ	71:UU:84:ILE:HD11	2.43	0.53
54:DD:72:VAL:HG23	61:KK:20:VAL:HG21	1.90	0.53
45:2:20:U:C4'	45:2:20(A):U:O2	2.56	0.53
50:9:1137:U:N3	50:9:1148:A:N6	2.56	0.53
50:9:501:C:H2'	50:9:501:C:O2	2.08	0.53
54:DD:70:THR:HG22	54:DD:86:LEU:HD13	1.90	0.53
45:2:20:U:O2'	45:2:20(A):U:O2'	2.26	0.53
47:5:2408:U:O4'	47:5:2409:U:C5	2.62	0.53
47:5:245:C:O2	47:5:245:C:O4'	2.25	0.52
50:9:1364:U:O4'	50:9:1364:U:O2	2.28	0.52
50:9:943:U:OP2	52:BB:216:LYS:NZ	2.40	0.52
2:B:41:VAL:HA	2:B:187:GLY:HA3	1.91	0.52
2:B:252:ALA:HB1	47:5:4524:G:N3	2.25	0.52
47:5:2265:G:O2'	47:5:2266:C:OP1	2.24	0.52
47:5:3724:A:N6	47:5:3725:G:C6	2.77	0.52
50:9:1653:U:H2'	50:9:1654:G:C8	2.45	0.52
45:2:74:C:OP2	47:5:4548:A:N3	2.43	0.52
53:CC:196:ILE:HB	53:CC:223:TYR:HB2	1.90	0.52
14:O:84:VAL:HG11	14:O:102:LEU:HD22	1.92	0.52
50:9:1129:G:C6	50:9:1130:G:O6	2.63	0.52
62:LL:60:CYS:SG	62:LL:63:THR:N	2.79	0.52
12:M:51:PRO:HG2	12:M:54:CYS:SG	2.50	0.52
47:5:2733:C:H2'	47:5:2734:U:O4'	2.09	0.52
55:EE:44:LEU:HD13	55:EE:72:ILE:HD11	1.92	0.52
54:DD:21:LEU:HD21	54:DD:48:ILE:HD11	1.92	0.51
46:3:16:C:O2	46:3:16:C:O4'	2.24	0.51
50:9:92:A:C6	50:9:446:G:C6	2.97	0.51
58:HH:69:LEU:HG	58:HH:96:ALA:HB2	1.91	0.51
64:NN:125:LEU:HD22	64:NN:129:TYR:CE2	2.45	0.51
76:ZZ:99:LEU:HD23	76:ZZ:100:VAL:N	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:M:11:ARG:HD2	12:M:57:LEU:HD12	1.91	0.51
47:5:2412:A:C2	47:5:2433:G:C2	2.99	0.51
2:B:249:ARG:NH2	47:5:3845:A:OP2	2.44	0.51
50:9:887:U:O4'	50:9:887:U:O2	2.28	0.51
56:FF:99:ILE:HG23	76:ZZ:67:LEU:HD21	1.92	0.51
50:9:146:G:O2'	50:9:147:A:O5'	2.24	0.51
3:C:299:GLN:NE2	47:5:2089:G:OP1	2.44	0.51
54:DD:21:LEU:CD2	54:DD:48:ILE:HD11	2.41	0.51
47:5:1802:A:O2'	47:5:1837:A:OP1	2.28	0.51
74:XX:61:GLN:HB3	74:XX:62:PRO:CD	2.40	0.51
49:8:125:C:O4'	49:8:125:C:O2	2.28	0.51
73:WW:30:CYS:N	73:WW:59:GLY:O	2.44	0.51
50:9:1036:A:N3	50:9:1844:U:O2'	2.40	0.51
56:FF:89:THR:HA	56:FF:92:ILE:HD12	1.93	0.51
50:9:1272:C:O2'	50:9:1274:G:N2	2.44	0.51
59:II:117:TYR:CD1	59:II:156:ALA:HB2	2.45	0.51
3:C:316:LYS:NZ	47:5:1281:G:OP1	2.41	0.50
14:O:18:ARG:NH2	47:5:2057:A:OP1	2.44	0.50
45:2:20:U:C1'	45:2:20(A):U:C2	2.94	0.50
45:2:20:U:C5'	45:2:20(A):U:O2	2.60	0.50
62:LL:37:TYR:CG	62:LL:51:ILE:HG12	2.46	0.50
50:9:1587:G:H1	70:TT:74:SER:HG	1.55	0.50
47:5:2763:U:O2	47:5:2763:U:O4'	2.29	0.50
47:5:3648:A:C4	47:5:3785:A:C6	2.99	0.50
5:E:154:ILE:HB	5:E:198:ILE:HB	1.93	0.50
73:WW:104:LEU:HD12	73:WW:104:LEU:O	2.12	0.50
22:W:9:SER:OG	22:W:36:CYS:SG	2.68	0.50
15:P:127:ARG:NH2	47:5:2422:C:OP1	2.45	0.50
47:5:1634:A:C6	47:5:1635:C:C4	2.99	0.50
47:5:2368:A:C2	47:5:2788:U:C5	3.00	0.50
47:5:3648:A:H1'	47:5:3785:A:N6	2.26	0.50
1:A:89:TYR:HB2	1:A:100:ASN:HD21	1.75	0.50
1:A:104:VAL:CG1	1:A:146:THR:HG21	2.42	0.50
6:F:88:LEU:HD22	6:F:89:ALA:N	2.26	0.50
59:II:113:TYR:CE2	59:II:121:LEU:HD23	2.46	0.50
62:LL:120:VAL:HG22	62:LL:145:VAL:HG11	1.94	0.50
10:J:33:LEU:HD21	10:J:70:VAL:HB	1.94	0.50
25:Z:51:ARG:HB2	25:Z:65:ARG:HD2	1.94	0.50
2:B:114:CYS:SG	2:B:180:LEU:HD11	2.51	0.50
50:9:1444:U:O2'	50:9:1580:A:N1	2.44	0.49
50:9:443:U:H2'	50:9:444:G:O4'	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:5:498:C:O2	47:5:498:C:O4'	2.27	0.49
50:9:1719:A:N6	50:9:1814:G:O2'	2.44	0.49
51:AA:89:LYS:HB3	51:AA:202:TYR:CZ	2.47	0.49
3:C:293:LEU:HD22	16:Q:34:PHE:CD2	2.47	0.49
4:D:56:THR:HG22	48:7:27:G:P	2.52	0.49
12:M:36:ALA:HB2	12:M:52:PHE:CE1	2.47	0.49
13:N:120:TRP:NE1	13:N:123:GLU:OE1	2.45	0.49
75:YY:15:ASN:HB2	75:YY:20:ARG:HG3	1.94	0.49
50:9:1714:U:H2'	50:9:1715:A:C8	2.47	0.49
64:NN:33:VAL:HG21	64:NN:66:VAL:HG11	1.93	0.49
66:PP:56:LEU:HD13	66:PP:78:THR:HG21	1.93	0.49
21:V:82:ILE:HG22	21:V:83:ARG:HG3	1.95	0.49
47:5:2439:G:C6	47:5:2440:U:C4	3.01	0.49
47:5:3653:A:N6	47:5:3691:G:O2'	2.46	0.49
53:CC:176:LYS:O	53:CC:200:ARG:NH1	2.45	0.49
47:5:4525:C:H2'	47:5:4526:U:O4'	2.12	0.49
51:AA:180:ARG:HG2	51:AA:195:TRP:CE3	2.47	0.49
54:DD:98:ALA:HA	54:DD:188:ILE:HD12	1.94	0.49
47:5:3816:A:O2'	47:5:3819:G:N3	2.46	0.49
50:9:56:G:C6	50:9:57:U:C4	3.01	0.49
5:E:167:PHE:CE1	5:E:176:LEU:HD22	2.48	0.49
13:N:76:PRO:O	13:N:79:ALA:HB3	2.12	0.49
50:9:1298:G:C4	66:PP:79:HIS:CE1	3.00	0.49
21:V:39:ILE:HG23	21:V:61:VAL:CG2	2.43	0.49
47:5:1311:G:H2'	47:5:1312:A:O4'	2.13	0.49
50:9:830:A:H2'	50:9:831:G:O4'	2.12	0.49
50:9:974:C:HO2'	65:OO:43:HIS:HD1	1.60	0.49
1:A:112:ILE:HG23	1:A:133:TYR:CD2	2.48	0.49
3:C:209:VAL:HB	3:C:229:LEU:HD13	1.95	0.49
9:I:61:SER:HA	9:I:126:VAL:HG23	1.94	0.49
73:WW:52:ILE:HG22	73:WW:61:ILE:HG12	1.95	0.49
50:9:439:A:O2'	50:9:1799:G:H4'	2.13	0.49
50:9:314:U:H2'	50:9:314:U:O2	2.13	0.49
74:XX:51:VAL:HG13	74:XX:70:VAL:CG1	2.42	0.49
47:5:4236:G:C2	47:5:4289:U:O2	2.65	0.49
5:E:48:ARG:O	47:5:1883:G:O2'	66.01	0.49
59:II:36:THR:HG21	59:II:179:PRO:HB2	1.95	0.49
47:5:1662:C:H2'	47:5:1663:C:C6	2.48	0.49
50:9:853:C:O2	50:9:853:C:O4'	2.26	0.49
51:AA:161:ILE:HG22	51:AA:163:CYS:SG	2.53	0.49
15:P:54:LYS:HA	15:P:83:TRP:CD1	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
75:YY:56:PHE:CD1	75:YY:94:HIS:NE2	2.81	0.49
50:9:1700:C:C2	50:9:1834:A:N6	2.80	0.48
3:C:95:MET:SD	3:C:95:MET:N	2.74	0.48
47:5:2367:A:C2	47:5:2788:U:O4	2.58	0.48
50:9:1020:A:N7	64:NN:70:LYS:NZ	2.60	0.48
69:SS:43:VAL:HG21	69:SS:83:PHE:CZ	2.48	0.48
50:9:1667:U:H2'	50:9:1668:U:C6	2.48	0.48
55:EE:139:LEU:HD12	55:EE:150:PRO:HB3	1.95	0.48
70:TT:39:LEU:HD13	70:TT:47:PRO:CG	2.44	0.48
55:EE:11:ARG:HH22	55:EE:24:THR:HG1	1.61	0.48
56:FF:112:LEU:C	56:FF:112:LEU:HD23	2.34	0.48
50:9:1587:G:N1	70:TT:74:SER:OG	2.43	0.48
7:G:139:VAL:HG11	7:G:238:LYS:HG3	1.96	0.48
50:9:67:C:C6	57:GG:162:LEU:HD23	2.48	0.48
58:HH:134:VAL:HG12	58:HH:173:PHE:CE2	2.49	0.48
13:N:158:HIS:HB3	13:N:161:MET:HG2	1.95	0.48
47:5:1960:A:C8	47:5:1960:A:OP1	2.67	0.48
47:5:4723:A:C2	47:5:4724:A:C6	3.02	0.48
56:FF:14:THR:O	56:FF:14:THR:HG23	2.14	0.48
56:FF:88:MET:HE1	56:FF:92:ILE:HD11	1.96	0.48
47:5:1986:U:H2'	47:5:2007:G:C6	2.48	0.48
47:5:1990:A:H3'	47:5:1991:A:H5''	1.96	0.48
3:C:116:ASN:O	3:C:120:LYS:HG3	2.13	0.48
5:E:180:GLY:O	5:E:181:PRO:C	2.52	0.48
47:5:3652:A:C2	47:5:3653:A:N1	2.82	0.48
50:9:1228:A:H2'	50:9:1229:G:C8	2.47	0.48
50:9:4:C:O2'	60:JJ:18:ARG:NH1	2.46	0.48
4:D:39:GLN:OE1	4:D:43:LYS:HG3	2.14	0.48
58:HH:145:ARG:HA	73:WW:51:GLU:HB2	1.95	0.48
17:R:70:ARG:HE	17:R:75:HIS:HB2	1.79	0.48
47:5:3723:A:C2	47:5:3724:A:C6	3.01	0.48
50:9:1551:U:O2	50:9:1551:U:O4'	2.30	0.48
47:5:1352:C:H2'	47:5:1353:G:O4'	2.14	0.47
50:9:1707:U:H2'	50:9:1708:C:O4'	2.14	0.47
55:EE:18:TRP:CE3	55:EE:46:ILE:CD1	2.97	0.47
6:F:131:MET:O	6:F:134:ILE:HG22	2.14	0.47
1:A:77:ILE:HD13	1:A:128:ARG:HB2	1.95	0.47
21:V:99:GLU:HB3	22:W:24:THR:HG23	1.96	0.47
45:2:74:C:OP2	47:5:4548:A:C4	2.66	0.47
47:5:1590:C:H3'	47:5:1591:U:H4'	1.96	0.47
58:HH:118:ARG:O	58:HH:121:THR:HG22	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:27:GLY:HA2	10:J:68:ILE:HG23	1.95	0.47
50:9:1624:U:O2	50:9:1624:U:O4'	2.32	0.47
8:H:134:CYS:SG	8:H:135:SER:N	2.88	0.47
48:7:16:A:C2	48:7:64:G:C2	3.02	0.47
50:9:1834:A:N3	50:9:1834:A:H2'	2.29	0.47
51:AA:147:LEU:HD13	51:AA:161:ILE:HB	1.96	0.47
47:5:1840:G:O2'	47:5:1841:C:H5'	2.14	0.47
47:5:2268:A:H4'	47:5:2269:C:H5'	1.96	0.47
47:5:3696:C:C4	47:5:3697:U:C4	3.03	0.47
47:5:3723:A:H2'	47:5:3724:A:C8	2.49	0.47
50:9:1012:A:H2'	50:9:1013:U:O4'	2.15	0.47
54:DD:162:ASP:N	54:DD:163:PRO:CD	2.78	0.47
14:O:51:LYS:O	14:O:55:LEU:HG	2.14	0.47
47:5:1237:C:O2	47:5:1237:C:O4'	2.33	0.47
47:5:1667:A:N1	47:5:2281:U:OP2	2.48	0.47
47:5:957:G:N7	47:5:958:G:C6	2.83	0.47
50:9:944:A:C5	50:9:945:U:C5	3.03	0.47
50:9:1834:A:C2	50:9:1836:G:C4	3.03	0.47
3:C:76:ILE:HG22	3:C:77:PRO:HD2	1.96	0.47
14:O:68:ARG:NH2	47:5:4564:A:OP1	2.48	0.47
53:CC:166:ARG:HB2	53:CC:248:TYR:CG	2.49	0.47
65:OO:98:ARG:NH1	65:OO:99:ALA:O	2.48	0.47
18:S:34:ALA:HB1	18:S:39:VAL:HG23	1.97	0.47
47:5:1804:A:N6	47:5:1833:G:O4'	2.47	0.47
50:9:1190:A:H2'	50:9:1191:C:O4'	2.14	0.47
12:M:34:ASN:OD1	12:M:34:ASN:N	2.48	0.47
74:XX:82:THR:O	74:XX:118:VAL:HG13	2.15	0.47
74:XX:105:PHE:CG	74:XX:112:VAL:HG21	2.50	0.46
2:B:378:ARG:HD3	22:W:11:TYR:CD2	2.50	0.46
8:H:18:ILE:HG22	8:H:27:VAL:HG22	1.98	0.46
13:N:198:LEU:HD13	13:N:200:LEU:HD21	1.97	0.46
47:5:2035:C:C4	47:5:2036:C:C4	3.04	0.46
47:5:3749:C:C5	47:5:3750:G:C8	3.03	0.46
49:8:10:G:C6	49:8:11:C:C4	3.02	0.46
50:9:1303:C:O2	50:9:1303:C:O4'	2.30	0.46
50:9:1530:U:H2'	50:9:1531:A:O4'	2.15	0.46
50:9:1834:A:N3	50:9:1834:A:C2'	2.78	0.46
50:9:183:G:O2'	50:9:183:G:N3	2.48	0.46
11:L:60:ARG:NH1	11:L:70:VAL:HG22	2.30	0.46
16:Q:13:VAL:HG23	47:5:1691:G:C8	2.50	0.46
50:9:1046:U:H2'	50:9:1047:C:O4'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:9:584:A:C6	50:9:585:C:C4	3.03	0.46
47:5:1978:C:H3'	47:5:1979:A:H5''	1.97	0.46
58:HH:30:LEU:HD22	58:HH:82:GLU:HG2	1.97	0.46
14:O:43:ILE:HD11	14:O:138:LEU:HD13	1.96	0.46
51:AA:63:ARG:HE	72:VV:78:ILE:HG23	1.80	0.46
50:9:1581:C:OP2	50:9:1582:C:N4	2.47	0.46
47:5:1337:A:C2	47:5:2349:A:C2	3.04	0.46
47:5:3621:A:H2'	47:5:3622:C:O4'	2.16	0.46
47:5:716:C:H2'	47:5:717:U:O4'	2.16	0.46
4:D:207:TYR:CE1	48:7:33:U:C6	3.04	0.46
50:9:1835:A:HO2'	50:9:1836:G:P	2.39	0.46
53:CC:130:ILE:HG22	53:CC:158:ALA:HB1	1.96	0.46
56:FF:116:ILE:HD12	56:FF:151:ILE:HG13	1.98	0.46
18:S:164:LYS:HB3	18:S:165:PRO:CD	2.45	0.46
47:5:1612:G:C2'	47:5:1612:G:N3	2.79	0.46
47:5:1889:U:O4	47:5:1939:A:N6	2.49	0.46
55:EE:67:GLN:HB3	55:EE:69:PHE:CZ	2.50	0.46
74:XX:4:CYS:O	74:XX:4:CYS:SG	2.74	0.46
74:XX:67:ARG:NH2	74:XX:114:ASP:OD2	2.49	0.46
47:5:4966:A:H2'	47:5:4967:A:C8	2.51	0.46
50:9:980:A:C2	50:9:981:A:C6	3.04	0.46
2:B:257:TRP:CE2	47:5:4518:A:N7	2.84	0.46
17:R:23:TRP:CH2	17:R:25:ASP:HA	2.51	0.46
18:S:9:GLU:HB3	18:S:67:VAL:HG13	1.98	0.46
21:V:13:LYS:O	47:5:4617:G:O2'	2.33	0.46
14:O:18:ARG:HH11	47:5:2054:U:P	2.39	0.46
47:5:2744:A:C6	47:5:2745:A:C6	3.04	0.46
49:8:10:G:C5	49:8:11:C:C5	3.03	0.46
50:9:1021:U:O4'	50:9:1022:U:C2	2.69	0.46
50:9:168:C:OP1	57:GG:131:ARG:NH2	2.49	0.46
50:9:17:C:H2'	50:9:18:C:C6	2.50	0.46
13:N:108:ARG:NH2	47:5:54:G:O2'	2.47	0.45
52:BB:30:TRP:CH2	52:BB:48:LEU:HD23	2.51	0.45
4:D:31:TYR:CE1	4:D:35:ARG:NH2	2.84	0.45
59:II:11:ARG:NH1	59:II:15:GLY:O	2.49	0.45
68:RR:53:TYR:CE2	68:RR:57:LEU:HD11	2.52	0.45
47:5:4232:U:H4'	47:5:4233:A:O5'	2.17	0.45
50:9:1149:A:H2'	50:9:1149:A:N3	2.32	0.45
50:9:874:G:N2	50:9:875:A:C4	2.84	0.45
54:DD:48:ILE:HG23	54:DD:86:LEU:HD12	1.98	0.45
18:S:95:ARG:NH2	47:5:1951:G:O2'	2.48	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:5:4724:A:C6	47:5:4725:C:C4	3.04	0.45
47:5:4758:U:O4'	47:5:4758:U:O2	2.33	0.45
56:FF:97:PHE:CD2	56:FF:108:PRO:HB2	2.51	0.45
54:DD:211:VAL:HG22	68:RR:38:ILE:O	2.17	0.45
47:5:1960:A:H4'	47:5:1961:G:OP2	2.17	0.45
47:5:4510:A:C6	47:5:4511:A:C2	3.04	0.45
52:BB:69:VAL:HG11	52:BB:74:LEU:HD13	1.99	0.45
4:D:40:ASP:OD1	4:D:40:ASP:N	2.50	0.45
50:9:846:G:H2'	55:EE:19:MET:HE2	1.98	0.45
14:O:168:TYR:CE2	14:O:172:LYS:HD2	2.50	0.45
47:5:419:A:C6	47:5:420:A:C6	3.05	0.45
47:5:4238:G:H2'	47:5:4239:A:C8	2.51	0.45
47:5:4966:A:C2	47:5:4967:A:C2	3.05	0.45
50:9:658:U:O4	50:9:1165:G:H2'	2.17	0.45
50:9:1543:U:OP2	70:TT:62:ARG:NH1	2.49	0.45
50:9:442:C:C2	50:9:452:G:N2	2.85	0.45
7:G:207:LEU:HD23	7:G:208:VAL:N	2.31	0.45
11:L:116:ARG:NH1	11:L:155:MET:O	2.50	0.45
47:5:1964:A:N7	47:5:4694:G:C4	2.84	0.45
2:B:11:HIS:NE2	47:5:4458:C:OP1	2.50	0.45
74:XX:57:VAL:HG11	74:XX:115:ILE:HG22	1.99	0.45
47:5:2363:A:C2	47:5:3860:A:C4	3.05	0.45
50:9:1045:U:H2'	50:9:1046:U:O4'	2.16	0.45
50:9:1742:C:H2'	50:9:1743:G:O4'	2.17	0.45
8:H:60:TRP:CD2	18:S:153:PRO:CD	3.00	0.45
17:R:60:ARG:NH1	17:R:63:CYS:SG	2.90	0.45
47:5:1387:A:C6	47:5:1397:A:C8	3.04	0.45
47:5:4390:A:H2'	47:5:4391:G:O4'	2.17	0.45
50:9:183:G:C2'	50:9:183:G:N3	2.79	0.45
2:B:160:ILE:HD12	2:B:190:VAL:HG13	1.98	0.45
59:II:99:ASN:HA	59:II:174:CYS:SG	2.56	0.45
14:O:54:TYR:CD1	14:O:145:VAL:HG21	2.52	0.45
45:2:20:U:C5'	45:2:20(A):U:C2	3.00	0.45
47:5:2088:A:O2'	47:5:2089:G:OP2	2.28	0.45
47:5:4744:A:N1	47:5:4956:A:N1	2.64	0.45
50:9:1610:G:OP2	69:SS:132:ARG:NH1	2.48	0.45
15:P:24:VAL:HG23	15:P:144:CYS:SG	2.57	0.45
47:5:1669:A:N3	47:5:1852:U:O2'	2.47	0.44
47:5:3829:G:C2	47:5:3830:A:C8	3.05	0.44
50:9:1130:G:O2'	50:9:1131:G:P	2.75	0.44
50:9:1605:G:C6	50:9:1606:G:N1	2.85	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:9:932:G:C2'	50:9:934:G:OP2	2.65	0.44
50:9:973:C:C5	50:9:974:C:C5	3.05	0.44
51:AA:145:ILE:HG12	51:AA:159:ILE:CG2	2.47	0.44
47:5:1986:U:N3	47:5:2013:A:N6	2.65	0.44
50:9:1735:A:C4	50:9:1800:A:C2	3.04	0.44
50:9:378:U:H2'	50:9:379:C:O4'	2.17	0.44
47:5:1869:G:C4	47:5:3877:A:C2	3.05	0.44
47:5:2006:U:C4	47:5:2007:G:C8	3.05	0.44
47:5:4212:A:C2	47:5:4218:U:C5	3.05	0.44
3:C:73:VAL:O	47:5:2350:U:C5	2.70	0.44
57:GG:5:ILE:HD12	57:GG:16:ILE:HD13	1.98	0.44
59:II:80:ASP:OD1	59:II:81:VAL:N	2.51	0.44
20:U:63:LEU:HD23	20:U:64:GLU:N	2.32	0.44
45:2:20:U:N1	45:2:20(A):U:N1	2.64	0.44
2:B:249:ARG:N	47:5:2838:G:OP1	2.42	0.44
4:D:23:ARG:NH2	47:5:4280:A:OP2	2.48	0.44
2:B:234:ARG:NH2	47:5:4566:U:O2'	2.50	0.44
47:5:4635:A:C2	47:5:4664:A:C5	3.05	0.44
47:5:4759:C:O2	47:5:4759:C:O4'	2.36	0.44
50:9:360:A:C2	50:9:363:A:C8	3.05	0.44
47:5:2841:G:H3'	47:5:2842:G:H5''	2.00	0.44
2:B:317:LEU:HD21	2:B:381:THR:HA	1.99	0.44
13:N:64:ILE:HD11	13:N:102:ALA:HA	1.99	0.44
47:5:2428:A:C6	47:5:2789:A:C5	3.05	0.44
49:8:94:G:H5'	49:8:94:G:C8	2.52	0.44
50:9:1678:A:C6	50:9:1679:A:N6	2.86	0.44
1:A:90:CYS:HB2	1:A:101:VAL:HG13	1.99	0.44
50:9:302:A:H1'	59:II:73:THR:HG23	2.00	0.44
10:J:24:ILE:HG21	10:J:36:ALA:HB1	2.00	0.44
12:M:24:LEU:HD11	12:M:86:TRP:CD2	2.52	0.44
47:5:2397:G:C8	47:5:2399:G:C8	3.05	0.44
50:9:5:U:C2	50:9:20:G:N2	2.86	0.44
58:HH:61:ILE:HD11	58:HH:95:ILE:HD12	1.98	0.44
59:II:113:TYR:OH	59:II:156:ALA:O	2.34	0.44
72:VV:55:ILE:HD11	72:VV:69:ILE:HG12	1.99	0.44
47:5:1632:A:H2'	47:5:1632:A:N3	2.33	0.44
50:9:1130:G:O2'	50:9:1131:G:O5'	2.35	0.44
50:9:26:U:C2	50:9:27:A:C8	3.06	0.44
51:AA:162:PRO:C	51:AA:163:CYS:SG	2.96	0.44
47:5:1174:G:C2'	47:5:1175:A:O5'	2.66	0.44
47:5:2625:U:C4	47:5:2626:U:C4	3.06	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:5:1965:G:H4'	47:5:4695:C:H1'	2.00	0.44
50:9:16:G:H2'	50:9:17:C:C6	2.52	0.44
50:9:448:A:C2	59:II:26:LYS:HG3	2.53	0.44
50:9:943:U:H2'	50:9:944:A:O4'	2.18	0.44
47:5:1089:G:C4	47:5:1208:G:N2	2.86	0.43
47:5:2090:U:C4	47:5:2265:G:C5	3.05	0.43
47:5:1964:A:N7	47:5:4694:G:C5	2.86	0.43
50:9:824:C:C2	60:JJ:144:ILE:HD13	2.52	0.43
69:SS:59:LEU:HD12	69:SS:63:GLU:OE2	2.18	0.43
21:V:30:ASP:N	21:V:30:ASP:OD1	2.50	0.43
25:Z:14:LEU:HD22	25:Z:81:MET:HB2	2.00	0.43
47:5:1563:A:O2'	47:5:1564:A:O4'	2.36	0.43
47:5:1907:A:N6	47:5:1908:A:N1	2.66	0.43
47:5:4288:C:O2'	47:5:4321:U:OP1	2.32	0.43
50:9:1673:U:H2'	50:9:1674:G:O4'	2.17	0.43
50:9:600:G:C2	50:9:601:G:C8	3.06	0.43
60:JJ:136:ARG:NH1	60:JJ:159:PHE:O	2.47	0.43
16:Q:33:ARG:HG2	16:Q:48:LEU:HD11	1.99	0.43
47:5:4871:C:O4'	47:5:4871:C:O2	2.36	0.43
3:C:43:ASN:O	3:C:46:LYS:HB2	2.19	0.43
53:CC:88:ILE:HG21	53:CC:94:ILE:CD1	2.48	0.43
47:5:2094:C:O4'	47:5:2094:C:O2	2.33	0.43
53:CC:191:VAL:HG11	53:CC:236:PHE:HA	2.01	0.43
4:D:42:ASN:HD21	19:T:69:GLN:NE2	2.16	0.43
14:O:48:TYR:CD2	47:5:1930:U:C6	3.06	0.43
16:Q:67:ILE:HD13	16:Q:98:LEU:HD11	1.99	0.43
47:5:2640:G:N2	47:5:2641:A:N3	2.66	0.43
47:5:160:G:N2	47:5:276:C:O2	2.52	0.43
47:5:2786:C:H5'	47:5:2787:A:C8	2.54	0.43
50:9:1096:G:C6	50:9:1097:G:C5	3.06	0.43
52:BB:52:THR:HG23	52:BB:57:ILE:HA	2.01	0.43
60:JJ:130:ILE:HG12	60:JJ:135:ILE:HD11	2.01	0.43
16:Q:186:TYR:CD2	47:5:4307:A:H4'	2.54	0.43
20:U:27:HIS:N	20:U:28:PRO:HD2	2.34	0.43
47:5:1330:A:C6	47:5:1331:C:C4	3.06	0.43
47:5:3867:A:C6	47:5:3868:G:C6	3.07	0.43
47:5:4640:C:C4	47:5:4641:U:C4	3.07	0.43
47:5:4714:C:C5	47:5:4715:C:C5	3.07	0.43
47:5:4729:A:O4'	47:5:4966:A:C8	2.72	0.43
50:9:1123:C:C4	50:9:1124:C:C5	3.07	0.43
50:9:1207:G:C6	50:9:1837:G:C6	3.06	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:33:ARG:HD2	3:C:36:ILE:HD12	2.00	0.43
4:D:225:GLN:N	4:D:225:GLN:OE1	2.52	0.43
9:I:153:ARG:HA	9:I:165:ILE:HD11	2.00	0.43
14:O:122:ALA:HB2	18:S:162:GLN:HB3	1.99	0.43
46:3:75:C:O2	46:3:75:C:O4'	2.32	0.43
2:B:29:VAL:HG13	2:B:348:ARG:HD3	2.01	0.43
6:F:92:ILE:HG21	6:F:246:MET:HE1	2.00	0.43
7:G:96:GLN:O	47:5:4124:G:N2	2.51	0.43
10:J:18:ARG:HG3	10:J:135:GLY:HA3	2.01	0.43
13:N:115:VAL:HG22	13:N:134:LEU:HD21	2.01	0.43
47:5:1291:G:O2'	47:5:1292:C:OP1	2.27	0.43
1:A:175:ILE:HD12	1:A:176:ASP:N	2.34	0.43
2:B:46:PHE:HA	2:B:84:MET:HE1	2.01	0.43
3:C:204:ARG:NH1	3:C:205:ARG:O	2.52	0.43
74:XX:51:VAL:HG22	74:XX:70:VAL:HG11	2.01	0.43
25:Z:76:ASN:HB3	25:Z:78:ASN:OD1	2.19	0.43
47:5:1381:U:O4'	47:5:1381:U:O2	2.36	0.43
50:9:1298:G:O2'	50:9:1299:A:O5'	2.37	0.43
50:9:1718:G:C6	50:9:1814:G:C6	3.07	0.43
50:9:86:C:N4	50:9:87:U:C4	2.87	0.43
3:C:128:LEU:O	3:C:131:SER:OG	2.23	0.43
56:FF:88:MET:CE	56:FF:92:ILE:HD11	2.48	0.43
7:G:241:ALA:O	7:G:245:ARG:N	2.51	0.43
57:GG:61:PHE:CE1	57:GG:96:SER:HB3	2.54	0.43
2:B:261:ARG:HB2	14:O:64:THR:HG21	2.01	0.43
66:PP:103:ASN:HB2	66:PP:120:SER:HB2	2.00	0.43
18:S:158:VAL:O	18:S:158:VAL:HG13	2.18	0.43
20:U:33:ILE:HD12	20:U:96:LEU:HD22	2.01	0.43
73:WW:55:ASP:O	73:WW:57:ARG:N	2.52	0.43
7:G:214:VAL:HG23	47:5:150:U:C4	2.54	0.43
47:5:4423:U:O2	47:5:4423:U:O4'	2.35	0.43
50:9:1144:A:H2'	50:9:1145:A:C8	2.54	0.43
8:H:7:ASN:N	8:H:7:ASN:OD1	2.52	0.43
12:M:80:ALA:O	12:M:85:LYS:NZ	2.52	0.43
13:N:11:TRP:CE3	13:N:44:ARG:NH2	2.87	0.43
2:B:56:ILE:HG22	2:B:74:GLU:HB3	2.01	0.42
56:FF:50:PRO:HG2	56:FF:90:VAL:HG13	2.01	0.42
57:GG:108:VAL:HG12	57:GG:109:LEU:N	2.33	0.42
13:N:65:ARG:HD3	13:N:127:TYR:CD1	2.54	0.42
14:O:9:LEU:O	14:O:36:VAL:HG12	2.19	0.42
50:9:1407:U:O2	50:9:1408:U:C2	2.72	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:9:688:U:O2	58:HH:122:LEU:HG	2.19	0.42
5:E:164:ARG:HD2	5:E:273:TYR:CZ	2.53	0.42
50:9:92:A:O4'	55:EE:3:ARG:NH1	2.52	0.42
68:RR:5:ARG:HB2	68:RR:10:LYS:HE2	2.01	0.42
45:2:20:U:H5'	45:2:20(A):U:O2	2.19	0.42
47:5:1818:G:O2'	47:5:1819:G:OP1	2.21	0.42
47:5:2097:A:OP1	47:5:2107:A:N6	2.52	0.42
47:5:4075:U:O2'	47:5:4076:G:P	2.77	0.42
47:5:737:C:C2	47:5:927:G:C2	3.07	0.42
50:9:1518:C:O2	50:9:1518:C:O4'	2.35	0.42
53:CC:209:VAL:HG21	53:CC:233:LEU:HD13	2.01	0.42
55:EE:31:PRO:HG3	55:EE:43:PRO:HG3	2.01	0.42
60:JJ:114:VAL:HG21	60:JJ:135:ILE:CD1	2.49	0.42
12:M:122:ILE:HD13	14:O:189:ILE:HG22	2.01	0.42
20:U:84:LYS:HA	20:U:87:THR:HG22	2.00	0.42
75:YY:25:ILE:N	75:YY:71:GLY:O	2.52	0.42
47:5:1668:A:C4	47:5:2282:A:C2	3.07	0.42
47:5:4378:A:O2'	47:5:4379:A:H2'	2.20	0.42
47:5:974:C:C4	47:5:975:C:C4	3.08	0.42
2:B:315:ASN:OD1	2:B:326:VAL:N	2.52	0.42
6:F:88:LEU:HD21	6:F:121:PHE:CD1	2.54	0.42
47:5:1089:G:C2	47:5:1208:G:C2	3.07	0.42
47:5:1328:G:C6	47:5:1329:G:C6	3.08	0.42
50:9:1459:G:C6	50:9:1460:C:C4	3.07	0.42
47:5:2013:A:N3	47:5:2014:C:C6	2.88	0.42
47:5:297:U:C2	47:5:298:G:C8	3.06	0.42
47:5:481(A):C:O4'	47:5:481(A):C:O2	2.38	0.42
52:BB:71:LEU:HD12	52:BB:82:ARG:HB3	2.02	0.42
6:F:189:LEU:O	6:F:189:LEU:HD23	2.19	0.42
7:G:111:PRO:CD	23:X:46:PHE:HD2	2.33	0.42
57:GG:18:VAL:HG21	57:GG:41:LEU:HD23	2.01	0.42
64:NN:110:ASP:O	64:NN:114:ARG:HG2	2.20	0.42
47:5:1957:U:O4	47:5:2026:A:N1	2.53	0.42
47:5:4305:G:N3	47:5:4305:G:C2'	2.82	0.42
50:9:953:C:H2'	50:9:954:U:O4'	2.19	0.42
2:B:94:GLU:HB2	2:B:158:GLN:HG3	2.02	0.42
2:B:220:ILE:HG12	2:B:278:THR:HG23	2.02	0.42
6:F:89:ALA:HB2	6:F:124:LEU:HD21	2.01	0.42
59:II:194:GLU:HA	62:LL:10:TYR:CE2	2.55	0.42
60:JJ:113:GLN:O	60:JJ:117:LEU:HD13	2.19	0.42
64:NN:67:THR:OG1	64:NN:69:ASN:O	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:5:1321:G:C6	47:5:3876:A:C2	3.08	0.42
47:5:2438:A:C2	47:5:2441:C:C5	3.07	0.42
47:5:2368:A:N1	47:5:2788:U:C5	2.87	0.42
47:5:4895:C:O2	47:5:4895:C:C2'	2.68	0.42
50:9:15:U:H2'	50:9:16:G:O4'	2.20	0.42
50:9:979:C:C4	50:9:980:A:N7	2.88	0.42
1:A:225:ILE:HD12	1:A:233:ARG:NH1	2.35	0.42
1:A:234:LYS:HG2	1:A:238:ILE:HD12	2.01	0.42
2:B:169:ARG:HH12	2:B:170:LEU:HD21	1.85	0.42
62:LL:89:ARG:NH1	62:LL:91:ASP:OD2	2.49	0.42
70:TT:30:VAL:HG12	70:TT:53:PHE:CD1	2.54	0.42
47:5:1301:C:O2	47:5:1301:C:O4'	2.34	0.42
47:5:1563:A:O2'	47:5:1564:A:O5'	2.34	0.42
47:5:1633:G:H5'	47:5:1634:A:OP1	2.19	0.42
47:5:4119:C:O4'	47:5:4119:C:O2	2.37	0.42
53:CC:66:LEU:HD13	53:CC:66:LEU:C	2.40	0.42
54:DD:72:VAL:HG23	61:KK:20:VAL:CG2	2.50	0.42
12:M:6:PHE:O	12:M:11:ARG:NE	2.53	0.42
64:NN:3:ARG:CB	64:NN:6:ALA:HB3	2.50	0.42
50:9:1566:G:N7	70:TT:101:ARG:NH2	2.67	0.42
76:ZZ:83:LEU:HD13	76:ZZ:83:LEU:C	2.40	0.42
47:5:1855:G:C6	47:5:1856:C:C4	3.08	0.42
50:9:1336:C:H2'	50:9:1337:C:O4'	2.20	0.42
50:9:107:A:C2	50:9:355:G:C2	3.08	0.42
55:EE:166:THR:HG23	55:EE:168:LYS:HB2	2.02	0.42
59:II:48:VAL:HG11	59:II:54:LYS:HG3	2.01	0.42
63:MM:17:ALA:C	63:MM:124:ILE:HD11	2.40	0.42
7:G:101:LYS:HB3	23:X:42:THR:HG23	2.02	0.42
7:G:111:PRO:HD3	23:X:46:PHE:HD2	1.85	0.42
47:5:1986:U:C2'	47:5:2007:G:O6	2.67	0.41
47:5:1961:G:O2'	47:5:2025:A:N6	2.53	0.41
47:5:2418:A:C5	47:5:2419:C:C5	3.08	0.41
47:5:4887:C:C5'	47:5:4887:C:H6	2.32	0.41
51:AA:57:LYS:HE2	72:VV:70:LEU:HD23	2.02	0.41
55:EE:122:LYS:O	55:EE:162:ILE:HD12	2.19	0.41
16:Q:85:THR:HA	16:Q:104:ARG:O	2.19	0.41
47:5:1964:A:C6	47:5:4694:G:O6	2.73	0.41
19:T:2:THR:N	47:5:4220:A:OP2	2.53	0.41
47:5:492:U:HO2'	47:5:493:G:P	2.43	0.41
50:9:35:C:H2'	50:9:36:U:C6	2.55	0.41
50:9:380:G:H1'	59:II:5:ARG:NE	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:BB:129:THR:OG1	52:BB:131:ASP:O	2.36	0.41
3:C:252:TRP:CZ3	3:C:260:LEU:HD11	2.55	0.41
7:G:215:ASP:HB3	7:G:216:PRO:HD3	2.02	0.41
12:M:119:ARG:HH11	14:O:202:LEU:HD21	1.86	0.41
12:M:36:ALA:HB2	12:M:52:PHE:CZ	2.54	0.41
18:S:13:VAL:HA	18:S:28:TYR:O	2.20	0.41
45:2:20(A):U:O2'	45:2:21:A:H5''	2.20	0.41
47:5:3700:C:O2'	47:5:3774:A:N3	2.50	0.41
47:5:4089:G:C2	47:5:4161:G:C2	3.08	0.41
50:9:1118:C:H2'	50:9:1119:A:C8	2.55	0.41
3:C:252:TRP:CH2	3:C:260:LEU:HD11	2.55	0.41
8:H:91:LYS:HG2	8:H:145:VAL:HG22	2.03	0.41
59:II:194:GLU:HA	62:LL:10:TYR:CD2	2.55	0.41
62:LL:61:PRO:HA	62:LL:66:VAL:HG13	2.02	0.41
45:2:33:U:OP2	67:QQ:146:ARG:NH2	2.53	0.41
47:5:1835:G:O2'	47:5:1836:G:OP2	2.32	0.41
45:2:74:C:OP2	47:5:4548:A:C2	2.73	0.41
50:9:845:G:H2'	50:9:846:G:O4'	2.20	0.41
51:AA:61:ALA:CB	51:AA:161:ILE:HD11	2.51	0.41
74:XX:67:ARG:HG2	74:XX:115:ILE:HD12	2.02	0.41
47:5:1314:C:C2	47:5:1315:C:C5	3.08	0.41
47:5:1627:G:C5	47:5:1628:C:C4	3.09	0.41
47:5:2046:G:C2	47:5:2047:A:C2	3.08	0.41
10:J:63:ARG:NH2	49:8:58:G:N7	130.04	0.41
3:C:27:VAL:HG11	3:C:128:LEU:HD13	2.03	0.41
59:II:60:LEU:HD23	59:II:185:ALA:HB2	2.02	0.41
61:KK:49:MET:HB3	61:KK:69:TRP:CE2	2.55	0.41
14:O:28:LEU:HD11	14:O:88:LEU:HD23	2.01	0.41
66:PP:17:TYR:CE1	66:PP:37:TYR:HB3	2.55	0.41
6:F:97:ILE:HD11	16:Q:4:ASP:CG	2.41	0.41
49:8:127:U:C4	49:8:128:C:C5	3.08	0.41
49:8:68:G:H2'	49:8:69:U:O4'	2.21	0.41
50:9:1596:U:H2'	50:9:1597:C:O4'	2.20	0.41
1:A:40:TYR:CE1	47:5:4117:U:C4	3.08	0.41
51:AA:24:HIS:HB3	51:AA:51:LEU:HD11	2.02	0.41
52:BB:103:MET:CE	52:BB:212:VAL:HG23	2.51	0.41
59:II:36:THR:HG23	59:II:96:LEU:HB2	2.03	0.41
68:RR:31:ASN:C	68:RR:31:ASN:HD22	2.24	0.41
47:5:2290:C:O4'	47:5:2321:G:C2	2.74	0.41
50:9:1391:C:H2'	50:9:1392:U:O4'	2.21	0.41
3:C:94:ASN:HA	3:C:100:ARG:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:9:1679:A:H3'	56:FF:60:ARG:HD2	2.03	0.41
18:S:53:LYS:NZ	48:7:74:A:O2'	2.53	0.41
47:5:1354:A:N6	47:5:1503:A:O4'	2.54	0.41
47:5:3703:G:C6	47:5:3704:U:C4	3.09	0.41
47:5:76:A:H2'	47:5:77:U:O4'	2.21	0.41
50:9:1130:G:C2'	50:9:1130:G:N3	2.82	0.41
50:9:302:A:H1'	59:II:73:THR:CG2	2.50	0.41
1:A:116:LEU:HA	1:A:164:ALA:HB2	2.03	0.41
3:C:32:ILE:HD13	3:C:129:ALA:HB3	2.02	0.41
56:FF:123:GLU:OE1	56:FF:204:ARG:NH1	2.54	0.41
57:GG:41:LEU:HD22	57:GG:41:LEU:C	2.41	0.41
73:WW:90:GLN:OE1	73:WW:117:ARG:NH2	2.54	0.41
47:5:2415:U:C4	47:5:2416:G:C6	3.09	0.41
47:5:297:U:H2'	47:5:298:G:O4'	2.21	0.41
1:A:227:ARG:NH2	47:5:3659:G:O2'	2.53	0.41
46:3:70:G:HO2'	47:5:3740:G:HO2'	1.68	0.41
47:5:1591:U:N3	47:5:4555:U:OP1	2.49	0.41
50:9:1078:C:O2	50:9:1078:C:H2'	2.21	0.41
50:9:1260:A:C6	50:9:1619:A:C6	3.08	0.41
50:9:604:A:C6	50:9:605:A:N1	2.89	0.41
3:C:237:ILE:HD12	3:C:237:ILE:H	1.86	0.41
54:DD:48:ILE:CG2	54:DD:86:LEU:HD12	2.51	0.41
60:JJ:135:ILE:HG22	60:JJ:159:PHE:HA	2.03	0.41
63:MM:101:ARG:HA	63:MM:101:ARG:CZ	2.50	0.41
64:NN:98:VAL:HG11	64:NN:115:LEU:HB2	2.03	0.41
17:R:45:ILE:HG12	17:R:50:ILE:HD11	2.01	0.41
17:R:99:MET:SD	17:R:99:MET:N	2.94	0.41
70:TT:6:VAL:HG22	70:TT:65:TYR:CE1	2.55	0.41
74:XX:51:VAL:HG13	74:XX:70:VAL:HG13	2.03	0.41
47:5:1384:C:O2'	47:5:1505:C:OP1	2.37	0.41
47:5:2081:C:H2'	47:5:2082:G:O4'	2.21	0.41
47:5:2395:A:C4'	47:5:2395:A:OP1	2.67	0.41
47:5:4499:G:N1	47:5:4500:U:O2	2.53	0.41
50:9:1057:C:O2	50:9:1057:C:O4'	2.38	0.41
50:9:1095:U:O2	50:9:1151:G:N2	2.54	0.41
2:B:89:ILE:HD11	2:B:105:VAL:HB	2.03	0.41
53:CC:166:ARG:HB2	53:CC:248:TYR:CD1	2.56	0.41
3:C:340:ILE:HG21	5:E:52:LEU:HD12	2.03	0.41
62:LL:37:TYR:CD2	62:LL:51:ILE:HG23	2.56	0.41
47:5:1513:U:H2'	47:5:1514:U:O4'	2.21	0.41
47:5:3732:A:C2	47:5:3733:A:C4	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:5:2809:G:O2'	47:5:4644:G:OP1	2.34	0.41
50:9:1444:U:H2'	50:9:1445:U:C6	2.56	0.41
7:G:210:ILE:HG12	7:G:254:THR:HG22	2.03	0.41
8:H:2:LYS:NZ	8:H:63:ASN:OD1	2.53	0.41
19:T:62:GLY:HA3	19:T:76:VAL:HG12	2.03	0.41
70:TT:14:PHE:CZ	70:TT:134:ILE:HD11	2.56	0.41
74:XX:61:GLN:O	74:XX:63:ASN:N	2.54	0.41
47:5:4562:C:H2'	47:5:4563:U:O4'	2.22	0.40
47:5:964:A:H2'	47:5:965:G:O4'	2.21	0.40
49:8:102:G:OP2	49:8:104:A:O2'	2.24	0.40
50:9:1190:A:N3	50:9:1714:U:O2'	2.44	0.40
2:B:154:LYS:HD2	2:B:191:ALA:CB	2.52	0.40
2:B:30:LYS:HG3	47:5:4716:C:OP2	2.21	0.40
5:E:165:VAL:HG11	5:E:178:VAL:HG13	2.03	0.40
17:R:17:CYS:HB3	17:R:52:ARG:CZ	2.52	0.40
47:5:1337:A:C2	47:5:2349:A:N1	2.88	0.40
47:5:419:A:N1	47:5:420:A:C2	2.90	0.40
47:5:4508:C:H2'	47:5:4509:U:O4'	2.21	0.40
47:5:4579:U:H2'	47:5:4580:U:N1	2.34	0.40
47:5:4977:A:H2'	47:5:4978:G:O4'	2.21	0.40
61:KK:71:LEU:HD21	61:KK:79:LEU:HD12	2.03	0.40
15:P:108:ASP:N	15:P:152:GLU:OE2	2.54	0.40
70:TT:39:LEU:HD13	70:TT:47:PRO:HG2	2.03	0.40
47:5:1653:A:H2'	47:5:1655:C:C4	2.57	0.40
47:5:1964:A:C5	47:5:4694:G:C5	3.09	0.40
47:5:3729:U:H2'	47:5:3730:U:C6	2.56	0.40
47:5:4415:A:N6	47:5:4427:G:O2'	2.53	0.40
14:O:74:ARG:NH2	47:5:4712:C:OP1	2.54	0.40
50:9:1034:A:C6	50:9:1082:A:C4	3.09	0.40
50:9:1121:G:C6	50:9:1122:A:C5	3.10	0.40
1:A:82:ILE:HD11	1:A:99:GLY:CA	2.51	0.40
5:E:286:PRO:HA	5:E:289:LEU:CD2	2.52	0.40
55:EE:122:LYS:HG3	55:EE:162:ILE:HD11	1.99	0.40
56:FF:20:PHE:C	56:FF:20:PHE:CD1	2.94	0.40
12:M:10:GLY:HA2	12:M:64:PHE:CE1	2.56	0.40
66:PP:15:PHE:CE1	66:PP:109:PRO:HB3	2.56	0.40
16:Q:89:ASP:OD1	16:Q:91:ARG:N	2.54	0.40
20:U:70:ILE:N	20:U:70:ILE:HD12	2.36	0.40
47:5:4188:U:H2'	47:5:4189:U:C6	2.57	0.40
3:C:33:ARG:CD	3:C:36:ILE:HD12	2.51	0.40
67:QQ:34:VAL:HG21	67:QQ:84:ILE:HD12	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:5:30:C:C4	47:5:31:U:C4	3.10	0.40
47:5:3820:G:C6	47:5:3821:A:C5	3.10	0.40
47:5:3876:A:O2'	47:5:3877:A:P	2.80	0.40
1:A:207:VAL:HG12	47:5:3919:C:C5'	2.52	0.40
47:5:4448:G:H4'	47:5:4449:A:OP2	2.22	0.40
50:9:1056:U:H2'	50:9:1057:C:O4'	2.21	0.40
1:A:90:CYS:CB	1:A:101:VAL:HG13	2.51	0.40
3:C:74:ALA:O	3:C:75:ARG:CB	2.70	0.40
55:EE:11:ARG:NH2	55:EE:24:THR:OG1	2.50	0.40
58:HH:66:VAL:N	58:HH:67:PRO:CD	2.84	0.40
65:OO:43:HIS:CD2	65:OO:55:ARG:HB2	2.57	0.40
73:WW:28:ARG:HB2	73:WW:29:PRO:HD3	2.03	0.40
24:Y:77:LYS:HB2	24:Y:79:VAL:HG12	2.03	0.40

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	246/257 (96%)	216 (88%)	28 (11%)	2 (1%)	24	70
2	B	392/403 (97%)	364 (93%)	27 (7%)	1 (0%)	46	83
3	C	360/425 (85%)	335 (93%)	24 (7%)	1 (0%)	46	83
4	D	291/297 (98%)	277 (95%)	13 (4%)	1 (0%)	46	83
5	E	208/291 (72%)	194 (93%)	13 (6%)	1 (0%)	34	77
6	F	223/247 (90%)	213 (96%)	9 (4%)	1 (0%)	39	80
7	G	229/319 (72%)	216 (94%)	13 (6%)	0	100	100
8	H	188/192 (98%)	174 (93%)	14 (7%)	0	100	100
9	I	201/214 (94%)	185 (92%)	15 (8%)	1 (0%)	34	77
10	J	168/178 (94%)	158 (94%)	10 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	L	208/211 (99%)	198 (95%)	8 (4%)	2 (1%)	19	66
12	M	136/218 (62%)	123 (90%)	12 (9%)	1 (1%)	26	72
13	N	201/204 (98%)	187 (93%)	13 (6%)	1 (0%)	34	77
14	O	197/203 (97%)	186 (94%)	8 (4%)	3 (2%)	13	59
15	P	151/184 (82%)	141 (93%)	10 (7%)	0	100	100
16	Q	185/188 (98%)	172 (93%)	12 (6%)	1 (0%)	34	77
17	R	178/196 (91%)	170 (96%)	8 (4%)	0	100	100
18	S	174/176 (99%)	164 (94%)	9 (5%)	1 (1%)	30	75
19	T	157/160 (98%)	143 (91%)	13 (8%)	1 (1%)	30	75
20	U	97/128 (76%)	88 (91%)	9 (9%)	0	100	100
21	V	129/140 (92%)	114 (88%)	15 (12%)	0	100	100
22	W	102/157 (65%)	97 (95%)	4 (4%)	1 (1%)	19	66
23	X	116/156 (74%)	109 (94%)	7 (6%)	0	100	100
24	Y	132/145 (91%)	124 (94%)	8 (6%)	0	100	100
25	Z	133/136 (98%)	126 (95%)	4 (3%)	3 (2%)	8	51
26	a	145/148 (98%)	133 (92%)	12 (8%)	0	100	100
27	b	100/245 (41%)	94 (94%)	5 (5%)	1 (1%)	19	66
28	c	96/115 (84%)	90 (94%)	6 (6%)	0	100	100
29	d	105/125 (84%)	92 (88%)	13 (12%)	0	100	100
30	e	126/135 (93%)	119 (94%)	7 (6%)	0	100	100
31	f	107/110 (97%)	99 (92%)	6 (6%)	2 (2%)	10	55
32	g	112/117 (96%)	104 (93%)	8 (7%)	0	100	100
33	h	120/123 (98%)	112 (93%)	8 (7%)	0	100	100
34	i	100/105 (95%)	93 (93%)	7 (7%)	0	100	100
35	j	84/97 (87%)	74 (88%)	10 (12%)	0	100	100
36	k	67/70 (96%)	65 (97%)	2 (3%)	0	100	100
37	l	48/51 (94%)	44 (92%)	4 (8%)	0	100	100
38	m	50/102 (49%)	48 (96%)	2 (4%)	0	100	100
39	n	23/25 (92%)	23 (100%)	0	0	100	100
40	o	102/106 (96%)	99 (97%)	2 (2%)	1 (1%)	19	66
41	p	89/92 (97%)	80 (90%)	7 (8%)	2 (2%)	8	52

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	r	122/137 (89%)	112 (92%)	9 (7%)	1 (1%)	24	70
43	s	194/318 (61%)	177 (91%)	15 (8%)	2 (1%)	19	66
44	t	149/165 (90%)	135 (91%)	13 (9%)	1 (1%)	26	72
51	AA	215/295 (73%)	196 (91%)	18 (8%)	1 (0%)	34	77
52	BB	211/264 (80%)	202 (96%)	9 (4%)	0	100	100
53	CC	219/293 (75%)	206 (94%)	12 (6%)	1 (0%)	34	77
54	DD	226/243 (93%)	213 (94%)	11 (5%)	2 (1%)	21	68
55	EE	260/263 (99%)	239 (92%)	21 (8%)	0	100	100
56	FF	181/204 (89%)	169 (93%)	11 (6%)	1 (1%)	30	75
57	GG	235/249 (94%)	226 (96%)	8 (3%)	1 (0%)	39	80
58	HH	181/194 (93%)	171 (94%)	10 (6%)	0	100	100
59	II	204/208 (98%)	186 (91%)	17 (8%)	1 (0%)	34	77
60	JJ	183/194 (94%)	175 (96%)	6 (3%)	2 (1%)	17	65
61	KK	94/165 (57%)	88 (94%)	5 (5%)	1 (1%)	17	65
62	LL	139/158 (88%)	126 (91%)	12 (9%)	1 (1%)	26	72
63	MM	115/132 (87%)	105 (91%)	10 (9%)	0	100	100
64	NN	147/151 (97%)	136 (92%)	11 (8%)	0	100	100
65	OO	134/168 (80%)	122 (91%)	10 (8%)	2 (2%)	13	59
66	PP	118/145 (81%)	109 (92%)	9 (8%)	0	100	100
67	QQ	140/146 (96%)	130 (93%)	10 (7%)	0	100	100
68	RR	130/135 (96%)	122 (94%)	8 (6%)	0	100	100
69	SS	142/152 (93%)	135 (95%)	7 (5%)	0	100	100
70	TT	139/145 (96%)	130 (94%)	9 (6%)	0	100	100
71	UU	98/119 (82%)	87 (89%)	11 (11%)	0	100	100
72	VV	81/83 (98%)	75 (93%)	6 (7%)	0	100	100
73	WW	127/130 (98%)	119 (94%)	8 (6%)	0	100	100
74	XX	139/143 (97%)	130 (94%)	6 (4%)	3 (2%)	8	52
75	YY	122/130 (94%)	113 (93%)	9 (7%)	0	100	100
76	ZZ	73/125 (58%)	70 (96%)	3 (4%)	0	100	100
77	aa	99/115 (86%)	88 (89%)	11 (11%)	0	100	100
78	bb	81/84 (96%)	73 (90%)	7 (9%)	1 (1%)	16	63

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
79	cc	60/69 (87%)	58 (97%)	2 (3%)	0	100	100
80	dd	53/56 (95%)	52 (98%)	1 (2%)	0	100	100
81	ee	53/133 (40%)	50 (94%)	3 (6%)	0	100	100
82	ff	66/156 (42%)	60 (91%)	6 (9%)	0	100	100
83	gg	311/317 (98%)	286 (92%)	25 (8%)	0	100	100
85	ii	410/459 (89%)	394 (96%)	16 (4%)	0	100	100
All	All	11927/13834 (86%)	11108 (93%)	770 (6%)	49 (0%)	43	80

All (49) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
42	r	11	ARG
74	XX	61	GLN
74	XX	62	PRO
11	L	17	ASP
18	S	155	PRO
25	Z	52	LYS
25	Z	91	LEU
27	b	102	PRO
43	s	142	GLY
51	AA	159	ILE
54	DD	48	ILE
56	FF	21	GLY
59	II	3	ILE
62	LL	66	VAL
65	OO	20	GLN
74	XX	86	PRO
1	A	14	SER
11	L	63	THR
16	Q	14	ARG
25	Z	90	PRO
1	A	127	ALA
2	B	17	LEU
14	O	186	GLU
40	o	77	CYS
44	t	54	LYS
54	DD	93	THR
61	KK	64	TRP
9	I	47	PRO
13	N	89	VAL

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Mol	Chain	Res	Type
14	O	89	PRO
31	f	106	TYR
41	p	9	GLY
57	GG	135	PRO
60	JJ	92	MET
60	JJ	147	PHE
65	OO	143	LYS
3	C	71	ARG
5	E	181	PRO
41	p	8	VAL
53	CC	232	THR
78	bb	20	LYS
22	W	3	VAL
6	F	196	VAL
14	O	146	GLY
31	f	107	PRO
43	s	25	PRO
12	M	19	PRO
4	D	125	VAL
19	T	74	ILE

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	190/199 (96%)	173 (91%)	17 (9%)	12	50
2	B	342/348 (98%)	324 (95%)	18 (5%)	28	69
3	C	302/347 (87%)	287 (95%)	15 (5%)	30	70
4	D	247/250 (99%)	235 (95%)	12 (5%)	31	70
5	E	190/251 (76%)	179 (94%)	11 (6%)	25	66
6	F	196/215 (91%)	184 (94%)	12 (6%)	23	65
7	G	200/272 (74%)	185 (92%)	15 (8%)	17	57
8	H	169/171 (99%)	154 (91%)	15 (9%)	12	50

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	I	175/181 (97%)	164 (94%)	11 (6%)	22	64
10	J	143/149 (96%)	138 (96%)	5 (4%)	43	78
11	L	175/176 (99%)	167 (95%)	8 (5%)	33	72
12	M	117/161 (73%)	109 (93%)	8 (7%)	20	61
13	N	171/172 (99%)	163 (95%)	8 (5%)	32	72
14	O	171/173 (99%)	160 (94%)	11 (6%)	22	63
15	P	134/163 (82%)	125 (93%)	9 (7%)	20	62
16	Q	164/165 (99%)	154 (94%)	10 (6%)	23	65
17	R	159/175 (91%)	144 (91%)	15 (9%)	11	47
18	S	157/157 (100%)	143 (91%)	14 (9%)	12	50
19	T	139/140 (99%)	130 (94%)	9 (6%)	21	63
20	U	89/114 (78%)	88 (99%)	1 (1%)	80	92
21	V	101/107 (94%)	94 (93%)	7 (7%)	19	60
22	W	86/126 (68%)	85 (99%)	1 (1%)	78	91
23	X	106/134 (79%)	100 (94%)	6 (6%)	25	67
24	Y	124/135 (92%)	119 (96%)	5 (4%)	38	75
25	Z	117/118 (99%)	115 (98%)	2 (2%)	68	89
26	a	119/120 (99%)	115 (97%)	4 (3%)	44	79
27	b	84/184 (46%)	82 (98%)	2 (2%)	57	84
28	c	84/98 (86%)	82 (98%)	2 (2%)	57	84
29	d	98/110 (89%)	90 (92%)	8 (8%)	14	53
30	e	114/121 (94%)	106 (93%)	8 (7%)	19	60
31	f	88/89 (99%)	82 (93%)	6 (7%)	20	61
32	g	98/100 (98%)	93 (95%)	5 (5%)	29	70
33	h	109/110 (99%)	105 (96%)	4 (4%)	41	77
34	i	86/89 (97%)	83 (96%)	3 (4%)	43	78
35	j	73/80 (91%)	67 (92%)	6 (8%)	14	53
36	k	64/65 (98%)	62 (97%)	2 (3%)	47	80
37	l	47/48 (98%)	47 (100%)	0	100	100
38	m	48/90 (53%)	45 (94%)	3 (6%)	22	64
39	n	24/24 (100%)	22 (92%)	2 (8%)	14	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	o	92/94 (98%)	86 (94%)	6 (6%)	21	63
41	p	74/75 (99%)	71 (96%)	3 (4%)	37	75
42	r	108/121 (89%)	101 (94%)	7 (6%)	21	63
43	s	164/258 (64%)	158 (96%)	6 (4%)	41	77
44	t	126/137 (92%)	122 (97%)	4 (3%)	46	79
51	AA	180/245 (74%)	162 (90%)	18 (10%)	9	44
52	BB	194/231 (84%)	174 (90%)	20 (10%)	9	42
53	CC	187/225 (83%)	172 (92%)	15 (8%)	15	54
54	DD	190/202 (94%)	174 (92%)	16 (8%)	14	53
55	EE	224/225 (100%)	207 (92%)	17 (8%)	16	56
56	FF	158/170 (93%)	143 (90%)	15 (10%)	11	46
57	GG	207/218 (95%)	189 (91%)	18 (9%)	13	51
58	HH	165/174 (95%)	153 (93%)	12 (7%)	17	58
59	II	178/180 (99%)	167 (94%)	11 (6%)	23	64
60	JJ	161/168 (96%)	147 (91%)	14 (9%)	13	51
61	KK	87/136 (64%)	80 (92%)	7 (8%)	15	54
62	LL	130/142 (92%)	116 (89%)	14 (11%)	8	41
63	MM	99/108 (92%)	83 (84%)	16 (16%)	3	21
64	NN	130/131 (99%)	115 (88%)	15 (12%)	7	37
65	OO	106/130 (82%)	91 (86%)	15 (14%)	4	29
66	PP	109/130 (84%)	97 (89%)	12 (11%)	8	39
67	QQ	117/121 (97%)	108 (92%)	9 (8%)	16	56
68	RR	119/121 (98%)	107 (90%)	12 (10%)	9	43
69	SS	125/132 (95%)	112 (90%)	13 (10%)	9	42
70	TT	111/115 (96%)	101 (91%)	10 (9%)	12	49
71	UU	92/107 (86%)	84 (91%)	8 (9%)	13	51
72	VV	67/67 (100%)	66 (98%)	1 (2%)	72	90
73	WW	112/113 (99%)	104 (93%)	8 (7%)	18	59
74	XX	113/115 (98%)	107 (95%)	6 (5%)	28	69
75	YY	107/112 (96%)	95 (89%)	12 (11%)	7	38
76	ZZ	66/103 (64%)	61 (92%)	5 (8%)	16	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
77	aa	88/98 (90%)	79 (90%)	9 (10%)	9	43
78	bb	75/76 (99%)	68 (91%)	7 (9%)	11	48
79	cc	55/62 (89%)	49 (89%)	6 (11%)	8	40
80	dd	48/49 (98%)	46 (96%)	2 (4%)	36	74
81	ee	46/106 (43%)	41 (89%)	5 (11%)	8	40
82	ff	61/140 (44%)	52 (85%)	9 (15%)	4	26
83	gg	272/275 (99%)	258 (95%)	14 (5%)	29	70
85	ii	360/394 (91%)	339 (94%)	21 (6%)	25	66
All	All	10403/11733 (89%)	9685 (93%)	718 (7%)	24	60

All (718) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	ILE
1	A	64	ARG
1	A	102	LEU
1	A	109	GLU
1	A	125	LYS
1	A	128	ARG
1	A	142	GLU
1	A	149	LYS
1	A	163	ARG
1	A	200	ARG
1	A	209	HIS
1	A	217	GLN
1	A	221	LYS
1	A	233	ARG
1	A	235	VAL
1	A	242	ARG
1	A	243	THR
2	B	10	ARG
2	B	17	LEU
2	B	23	SER
2	B	62	ARG
2	B	66	LYS
2	B	95	THR
2	B	135	LYS
2	B	248	LEU
2	B	261	ARG

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Mol	Chain	Res	Type
2	B	262	VAL
2	B	279	GLU
2	B	294	LYS
2	B	309	LEU
2	B	314	ILE
2	B	333	LEU
2	B	351	LEU
2	B	356	LYS
2	B	383	GLU
3	C	20	LYS
3	C	95	MET
3	C	101	MET
3	C	113	ARG
3	C	124	ILE
3	C	144	ILE
3	C	150	LEU
3	C	175	LYS
3	C	188	ARG
3	C	193	LYS
3	C	246	VAL
3	C	281	MET
3	C	284	MET
3	C	307	LYS
3	C	312	ARG
4	D	22	ARG
4	D	37	VAL
4	D	45	ASN
4	D	50	ARG
4	D	56	THR
4	D	89	LYS
4	D	104	LEU
4	D	124	GLU
4	D	128	ASP
4	D	225	GLN
4	D	264	LYS
4	D	268	ARG
5	E	52	LEU
5	E	58	ARG
5	E	96	THR
5	E	112	LEU
5	E	141	ARG
5	E	144	ARG

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Mol	Chain	Res	Type
5	E	169	LYS
5	E	178	VAL
5	E	213	LYS
5	E	289	LEU
5	E	291	PHE
6	F	30	LYS
6	F	46	ARG
6	F	65	ARG
6	F	67	GLU
6	F	88	LEU
6	F	128	SER
6	F	134	ILE
6	F	151	GLU
6	F	187	GLU
6	F	198	LYS
6	F	245	ARG
6	F	246	MET
7	G	126	ARG
7	G	148	LEU
7	G	154	LYS
7	G	162	GLU
7	G	163	LYS
7	G	184	LYS
7	G	203	LYS
7	G	204	LYS
7	G	223	LEU
7	G	226	LEU
7	G	230	MET
7	G	235	CYS
7	G	242	ARG
7	G	284	ASP
7	G	293	ASN
8	H	1	MET
8	H	20	LEU
8	H	23	ARG
8	H	52	LYS
8	H	54	ARG
8	H	57	VAL
8	H	59	LYS
8	H	66	GLU
8	H	74	CYS
8	H	105	ILE

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Mol	Chain	Res	Type
8	H	106	GLN
8	H	108	ASN
8	H	128	MET
8	H	173	ARG
8	H	177	ASP
9	I	36	LEU
9	I	39	LYS
9	I	44	ASP
9	I	71	CYS
9	I	116	ARG
9	I	146	GLU
9	I	153	ARG
9	I	163	GLN
9	I	164	LYS
9	I	195	CYS
9	I	208	LYS
10	J	16	ARG
10	J	28	GLU
10	J	81	GLU
10	J	113	ILE
10	J	175	LEU
11	L	35	ARG
11	L	63	THR
11	L	67	HIS
11	L	74	ARG
11	L	121	ARG
11	L	162	LYS
11	L	186	ARG
11	L	195	ARG
12	M	8	GLU
12	M	32	ASP
12	M	37	LEU
12	M	56	GLN
12	M	61	ILE
12	M	96	GLU
12	M	105	THR
12	M	119	ARG
13	N	9	GLU
13	N	26	ARG
13	N	32	GLN
13	N	64	ILE
13	N	72	LYS

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Mol	Chain	Res	Type
13	N	77	LYS
13	N	89	VAL
13	N	162	ARG
14	O	18	ARG
14	O	49	ARG
14	O	74	ARG
14	O	82	ARG
14	O	128	ARG
14	O	130	LYS
14	O	140	ARG
14	O	145	VAL
14	O	175	MET
14	O	179	LYS
14	O	202	LEU
15	P	24	VAL
15	P	25	HIS
15	P	36	ILE
15	P	69	ARG
15	P	86	LYS
15	P	91	LEU
15	P	127	ARG
15	P	128	ARG
15	P	147	GLU
16	Q	5	ILE
16	Q	20	SER
16	Q	42	THR
16	Q	61	LEU
16	Q	63	LEU
16	Q	75	ARG
16	Q	91	ARG
16	Q	97	LYS
16	Q	115	LYS
16	Q	143	ARG
17	R	8	LYS
17	R	36	ASN
17	R	40	GLN
17	R	50	ILE
17	R	89	MET
17	R	98	ARG
17	R	99	MET
17	R	103	ARG
17	R	106	LEU

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Mol	Chain	Res	Type
17	R	113	LYS
17	R	122	SER
17	R	133	LYS
17	R	138	LEU
17	R	176	ARG
17	R	178	GLN
18	S	7	LEU
18	S	8	ARG
18	S	9	GLU
18	S	17	LEU
18	S	43	ARG
18	S	64	CYS
18	S	70	LYS
18	S	83	ARG
18	S	84	TYR
18	S	95	ARG
18	S	149	LYS
18	S	159	LEU
18	S	164	LYS
18	S	174	THR
19	T	5	LYS
19	T	33	ILE
19	T	60	LYS
19	T	96	ILE
19	T	117	LYS
19	T	142	ARG
19	T	144	ASN
19	T	146	LYS
19	T	159	MET
20	U	33	ILE
21	V	15	ARG
21	V	18	LEU
21	V	35	LYS
21	V	60	MET
21	V	91	LYS
21	V	109	LYS
21	V	123	LYS
22	W	91	MET
23	X	39	LYS
23	X	41	ARG
23	X	53	ARG
23	X	59	LYS

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Mol	Chain	Res	Type
23	X	63	LYS
23	X	111	GLN
24	Y	2	LYS
24	Y	8	THR
24	Y	50	ARG
24	Y	72	GLN
24	Y	74	TYR
25	Z	33	THR
25	Z	112	ARG
26	a	4	ARG
26	a	84	GLU
26	a	122	VAL
26	a	132	ARG
27	b	9	THR
27	b	22	LYS
28	c	37	MET
28	c	78	ASN
29	d	23	ARG
29	d	31	LYS
29	d	44	ARG
29	d	48	GLU
29	d	78	ARG
29	d	85	ARG
29	d	98	SER
29	d	102	LEU
30	e	21	ILE
30	e	22	ARG
30	e	64	LYS
30	e	78	LEU
30	e	86	GLU
30	e	91	CYS
30	e	106	LYS
30	e	128	ARG
31	f	16	ARG
31	f	33	VAL
31	f	52	LYS
31	f	69	VAL
31	f	90	SER
31	f	101	ILE
32	g	26	PRO
32	g	54	ARG
32	g	60	ARG

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Mol	Chain	Res	Type
32	g	66	ARG
32	g	114	GLN
33	h	15	GLU
33	h	28	LEU
33	h	67	GLU
33	h	82	ASP
34	i	77	VAL
34	i	86	LYS
34	i	89	GLU
35	j	3	LYS
35	j	6	SER
35	j	11	ARG
35	j	20	ARG
35	j	58	THR
35	j	59	THR
36	k	69	LEU
36	k	70	LYS
38	m	71	ARG
38	m	92	THR
38	m	93	ASN
39	n	1	MET
39	n	13	LEU
40	o	17	LYS
40	o	31	ASP
40	o	36	GLN
40	o	61	LYS
40	o	82	MET
40	o	83	LEU
41	p	8	VAL
41	p	24	LYS
41	p	84	ARG
42	r	8	MET
42	r	20	ARG
42	r	32	LEU
42	r	67	ARG
42	r	80	THR
42	r	115	SER
42	r	118	LEU
43	s	38	LYS
43	s	95	LEU
43	s	105	ASN
43	s	146	LYS

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Mol	Chain	Res	Type
43	s	187	LEU
43	s	191	GLN
44	t	37	LEU
44	t	98	ILE
44	t	133	LEU
44	t	137	GLN
51	AA	5	LEU
51	AA	12	GLU
51	AA	25	LEU
51	AA	32	PHE
51	AA	50	ASN
51	AA	56	GLU
51	AA	58	LEU
51	AA	59	LEU
51	AA	60	LEU
51	AA	111	GLN
51	AA	122	LEU
51	AA	132	GLN
51	AA	135	THR
51	AA	136	GLU
51	AA	155	ARG
51	AA	170	SER
51	AA	178	LEU
51	AA	198	MET
52	BB	38	MET
52	BB	40	ASN
52	BB	71	LEU
52	BB	74	LEU
52	BB	82	ARG
52	BB	86	LEU
52	BB	105	LEU
52	BB	125	VAL
52	BB	126	ASP
52	BB	157	GLN
52	BB	175	GLU
52	BB	180	ASP
52	BB	181	LEU
52	BB	182	LYS
52	BB	207	LEU
52	BB	209	ASP
52	BB	213	ARG
52	BB	225	LEU

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Mol	Chain	Res	Type
52	BB	229	MET
52	BB	231	LEU
53	CC	78	LEU
53	CC	79	GLU
53	CC	101	SER
53	CC	114	LYS
53	CC	117	ARG
53	CC	121	ARG
53	CC	137	VAL
53	CC	167	ARG
53	CC	188	CYS
53	CC	192	LEU
53	CC	213	LEU
53	CC	215	MET
53	CC	236	PHE
53	CC	244	ILE
53	CC	252	THR
54	DD	28	GLU
54	DD	45	ARG
54	DD	59	LEU
54	DD	64	ARG
54	DD	76	ARG
54	DD	94	ARG
54	DD	106	ARG
54	DD	120	TYR
54	DD	127	MET
54	DD	142	LEU
54	DD	156	LEU
54	DD	170	THR
54	DD	190	LEU
54	DD	198	ILE
54	DD	218	LEU
54	DD	227	LYS
55	EE	6	LYS
55	EE	17	HIS
55	EE	23	LEU
55	EE	42	LEU
55	EE	51	ARG
55	EE	59	ASP
55	EE	66	MET
55	EE	67	GLN
55	EE	77	ARG

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Mol	Chain	Res	Type
55	EE	145	ARG
55	EE	162	ILE
55	EE	181	CYS
55	EE	205	PHE
55	EE	222	LEU
55	EE	232	ASN
55	EE	238	LEU
55	EE	246	LEU
56	FF	20	PHE
56	FF	36	GLN
56	FF	43	GLU
56	FF	65	GLN
56	FF	66	CYS
56	FF	71	ARG
56	FF	88	MET
56	FF	89	THR
56	FF	95	HIS
56	FF	140	ASP
56	FF	146	ARG
56	FF	155	CYS
56	FF	169	ILE
56	FF	175	ASP
56	FF	204	ARG
57	GG	12	CYS
57	GG	39	ASP
57	GG	41	LEU
57	GG	63	MET
57	GG	64	LYS
57	GG	67	VAL
57	GG	72	ARG
57	GG	103	ASP
57	GG	116	LYS
57	GG	135	PRO
57	GG	171	THR
57	GG	178	ARG
57	GG	183	ARG
57	GG	190	ARG
57	GG	216	ARG
57	GG	217	MET
57	GG	230	LYS
57	GG	235	SER
58	HH	8	ILE

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Mol	Chain	Res	Type
58	HH	21	SER
58	HH	36	LEU
58	HH	46	THR
58	HH	53	VAL
58	HH	76	GLN
58	HH	82	GLU
58	HH	100	ILE
58	HH	145	ARG
58	HH	149	ASP
58	HH	160	LYS
58	HH	172	THR
59	II	12	ARG
59	II	19	LYS
59	II	23	LYS
59	II	26	LYS
59	II	45	THR
59	II	100	CYS
59	II	130	THR
59	II	161	LEU
59	II	178	ARG
59	II	182	CYS
59	II	203	LYS
60	JJ	26	ASP
60	JJ	29	LEU
60	JJ	38	ARG
60	JJ	45	ARG
60	JJ	50	LEU
60	JJ	61	LEU
60	JJ	69	ARG
60	JJ	70	ARG
60	JJ	79	ARG
60	JJ	80	ARG
60	JJ	89	GLU
60	JJ	116	LYS
60	JJ	133	ARG
60	JJ	163	SER
61	KK	17	LYS
61	KK	20	VAL
61	KK	35	LEU
61	KK	50	GLN
61	KK	60	GLU
61	KK	89	ILE

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Mol	Chain	Res	Type
61	KK	96	ARG
62	LL	16	ILE
62	LL	20	LYS
62	LL	40	ILE
62	LL	42	LEU
62	LL	49	GLU
62	LL	56	ILE
62	LL	69	ARG
62	LL	85	THR
62	LL	110	SER
62	LL	121	GLN
62	LL	126	VAL
62	LL	132	ARG
62	LL	134	LEU
62	LL	153	LYS
63	MM	22	LEU
63	MM	31	LEU
63	MM	33	ARG
63	MM	36	ARG
63	MM	40	LYS
63	MM	42	LEU
63	MM	49	LEU
63	MM	55	ASN
63	MM	83	LYS
63	MM	85	LEU
63	MM	96	ARG
63	MM	99	LYS
63	MM	101	ARG
63	MM	112	LYS
63	MM	113	ASP
63	MM	123	VAL
64	NN	3	ARG
64	NN	20	ARG
64	NN	27	LYS
64	NN	55	ARG
64	NN	60	VAL
64	NN	75	LEU
64	NN	78	LYS
64	NN	84	LEU
64	NN	86	GLU
64	NN	94	LYS
64	NN	107	LYS

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Mol	Chain	Res	Type
64	NN	110	ASP
64	NN	120	SER
64	NN	125	LEU
64	NN	132	LYS
65	OO	25	GLU
65	OO	34	PHE
65	OO	38	ASN
65	OO	46	ASP
65	OO	50	LYS
65	OO	51	GLU
65	OO	56	VAL
65	OO	69	SER
65	OO	75	MET
65	OO	85	CYS
65	OO	128	ARG
65	OO	131	ASP
65	OO	146	ARG
65	OO	150	ARG
65	OO	151	LEU
66	PP	13	ARG
66	PP	14	LYS
66	PP	15	PHE
66	PP	37	TYR
66	PP	42	ARG
66	PP	44	ARG
66	PP	55	SER
66	PP	65	LYS
66	PP	78	THR
66	PP	83	MET
66	PP	108	LYS
66	PP	130	ARG
67	QQ	31	LEU
67	QQ	41	MET
67	QQ	47	LEU
67	QQ	60	LYS
67	QQ	67	ASP
67	QQ	90	LYS
67	QQ	123	ASP
67	QQ	127	CYS
67	QQ	140	ARG
68	RR	5	ARG
68	RR	8	THR

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Mol	Chain	Res	Type
68	RR	31	ASN
68	RR	33	ARG
68	RR	36	GLU
68	RR	43	SER
68	RR	44	LYS
68	RR	62	GLN
68	RR	99	ASP
68	RR	101	ASP
68	RR	105	MET
68	RR	132	ARG
69	SS	8	LYS
69	SS	21	ASP
69	SS	23	ARG
69	SS	46	ARG
69	SS	49	ASP
69	SS	52	LEU
69	SS	59	LEU
69	SS	63	GLU
69	SS	83	PHE
69	SS	86	ARG
69	SS	110	ASP
69	SS	132	ARG
69	SS	144	ARG
70	TT	62	ARG
70	TT	74	SER
70	TT	102	ARG
70	TT	108	GLU
70	TT	110	LEU
70	TT	121	ARG
70	TT	123	LEU
70	TT	124	THR
70	TT	131	LEU
70	TT	142	LYS
71	UU	25	THR
71	UU	56	MET
71	UU	64	THR
71	UU	79	ARG
71	UU	90	ASP
71	UU	95	SER
71	UU	106	ILE
71	UU	111	GLU
72	VV	12	TYR

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Mol	Chain	Res	Type
73	WW	23	ARG
73	WW	36	ARG
73	WW	51	GLU
73	WW	72	CYS
73	WW	85	ASP
73	WW	92	ASN
73	WW	103	VAL
73	WW	104	LEU
74	XX	4	CYS
74	XX	64	SER
74	XX	67	ARG
74	XX	98	ASP
74	XX	105	PHE
74	XX	115	ILE
75	YY	16	ARG
75	YY	17	LEU
75	YY	20	ARG
75	YY	32	LYS
75	YY	40	ILE
75	YY	61	ARG
75	YY	74	MET
75	YY	88	LYS
75	YY	93	ARG
75	YY	99	LYS
75	YY	101	LYS
75	YY	115	LYS
76	ZZ	67	LEU
76	ZZ	76	ARG
76	ZZ	80	ARG
76	ZZ	89	GLN
76	ZZ	92	LEU
77	aa	21	ILE
77	aa	23	CYS
77	aa	41	ILE
77	aa	44	ILE
77	aa	55	GLU
77	aa	57	SER
77	aa	67	LEU
77	aa	74	CYS
77	aa	100	ARG
78	bb	17	ARG
78	bb	42	LYS

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Mol	Chain	Res	Type
78	bb	60	SER
78	bb	64	CYS
78	bb	78	SER
78	bb	80	ARG
78	bb	81	ARG
79	cc	26	GLN
79	cc	27	CYS
79	cc	31	ARG
79	cc	40	ARG
79	cc	44	ARG
79	cc	60	GLU
80	dd	4	GLN
80	dd	36	LEU
81	ee	86	ARG
81	ee	98	LYS
81	ee	99	LYS
81	ee	110	GLN
81	ee	113	ARG
82	ff	83	LYS
82	ff	84	SER
82	ff	94	LYS
82	ff	96	LYS
82	ff	99	LYS
82	ff	110	GLU
82	ff	121	CYS
82	ff	138	ARG
82	ff	140	TYR
83	gg	17	TRP
83	gg	20	GLN
83	gg	36	ARG
83	gg	47	ARG
83	gg	79	LEU
83	gg	87	LEU
83	gg	113	PHE
83	gg	119	GLN
83	gg	198	VAL
83	gg	207	CYS
83	gg	273	GLU
83	gg	289	LEU
83	gg	298	LEU
83	gg	306	LEU
85	ii	45	ILE

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Mol	Chain	Res	Type
85	ii	61	ASN
85	ii	63	LYS
85	ii	68	ARG
85	ii	86	ASN
85	ii	103	GLU
85	ii	134	GLU
85	ii	185	GLN
85	ii	193	LEU
85	ii	200	ASN
85	ii	207	GLU
85	ii	211	GLN
85	ii	212	LEU
85	ii	231	ASP
85	ii	232	PHE
85	ii	241	MET
85	ii	246	LEU
85	ii	339	GLU
85	ii	340	GLU
85	ii	368	LEU
85	ii	417	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (36) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	100	ASN
1	A	140	ASN
2	B	245	HIS
3	C	310	HIS
6	F	79	ASN
7	G	135	GLN
7	G	194	ASN
7	G	248	HIS
8	H	42	ASN
8	H	78	GLN
12	M	20	HIS
13	N	196	ASN
14	O	180	GLN
14	O	184	ASN
15	P	56	GLN
15	P	133	HIS
16	Q	57	ASN
18	S	163	HIS

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Mol	Chain	Res	Type
19	T	69	GLN
31	f	24	HIS
34	i	20	ASN
40	o	19	GLN
43	s	34	ASN
44	t	100	HIS
44	t	147	HIS
52	BB	179	ASN
55	EE	36	HIS
58	HH	193	GLN
59	II	35	ASN
69	SS	125	HIS
70	TT	42	HIS
74	XX	77	ASN
85	ii	180	HIS
85	ii	185	GLN
85	ii	200	ASN
85	ii	265	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
45	2	73/76 (96%)	15 (20%)	1 (1%)
46	3	72/75 (96%)	25 (34%)	2 (2%)
47	5	3515/3543 (99%)	893 (25%)	175 (4%)
48	7	119/120 (99%)	17 (14%)	2 (1%)
49	8	150/156 (96%)	36 (24%)	8 (5%)
50	9	1671/1869 (89%)	436 (26%)	70 (4%)
84	hh	14/15 (93%)	8 (57%)	0
All	All	5614/5854 (95%)	1430 (25%)	258 (4%)

All (1430) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
45	2	8	U
45	2	9	A
45	2	13	U
45	2	16	C
45	2	19	G
45	2	21	A
45	2	46	G

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Mol	Chain	Res	Type
45	2	47	U
45	2	49	C
45	2	60	A
45	2	61	C
45	2	64	G
45	2	67	G
45	2	72	C
45	2	75	C
46	3	7	A
46	3	13	C
46	3	14	A
46	3	16	C
46	3	21	A
46	3	25	C
46	3	29	A
46	3	34	U
46	3	35	U
46	3	36	U
46	3	40	C
46	3	42	G
46	3	47	U
46	3	49	C
46	3	53	G
46	3	58	A
46	3	60	U
46	3	61	C
46	3	63	C
46	3	65	G
46	3	71	G
46	3	72	C
46	3	74	C
46	3	75	C
46	3	76	A
47	5	8	U
47	5	12	A
47	5	13	U
47	5	15	A
47	5	25	A
47	5	35	U
47	5	39	A
47	5	42	A
47	5	43	U

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Mol	Chain	Res	Type
47	5	44	A
47	5	48	G
47	5	49	U
47	5	56	A
47	5	58	G
47	5	59	A
47	5	64	A
47	5	65	A
47	5	73	A
47	5	75	G
47	5	84	A
47	5	91	G
47	5	93	G
47	5	96	U
47	5	108	A
47	5	109	G
47	5	116	G
47	5	118	C
47	5	119	G
47	5	120	A
47	5	126	C
47	5	134	G
47	5	135	G
47	5	136	C
47	5	143	C
47	5	144	G
47	5	157	U
47	5	159	C
47	5	160	G
47	5	172	C
47	5	173	C
47	5	177	G
47	5	179	G
47	5	197	A
47	5	200	U
47	5	201	C
47	5	202	C
47	5	205	C
47	5	209	U
47	5	216	C
47	5	217	C
47	5	218	A

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Mol	Chain	Res	Type
47	5	220	C
47	5	221	C
47	5	224	U
47	5	226	G
47	5	227	A
47	5	233	U
47	5	234	G
47	5	245	C
47	5	246	G
47	5	253	G
47	5	255	C
47	5	262	G
47	5	263	G
47	5	266	C
47	5	267	G
47	5	276	C
47	5	279	A
47	5	280	G
47	5	281	U
47	5	297	U
47	5	306	A
47	5	309	C
47	5	310	G
47	5	315	G
47	5	316	U
47	5	322	C
47	5	328	A
47	5	334	A
47	5	340	C
47	5	350	C
47	5	357	U
47	5	360	A
47	5	361	C
47	5	363	A
47	5	379	G
47	5	386	A
47	5	387	G
47	5	407	A
47	5	409	G
47	5	410	A
47	5	412	G
47	5	413	G

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Mol	Chain	Res	Type
47	5	414	C
47	5	418	A
47	5	431	G
47	5	432	U
47	5	436	C
47	5	446	C
47	5	449	C
47	5	450	G
47	5	452	A
47	5	453	G
47	5	454	U
47	5	457	G
47	5	466	A
47	5	467	U
47	5	468	U
47	5	469	C
47	5	481	G
47	5	481(A)	C
47	5	482	G
47	5	483	G
47	5	484	U
47	5	485	C
47	5	486	C
47	5	490	C
47	5	492	U
47	5	493	G
47	5	495	C
47	5	497	G
47	5	498	C
47	5	499	G
47	5	505	G
47	5	510	U
47	5	649	A
47	5	654	C
47	5	658	C
47	5	660	G
47	5	667	A
47	5	668	C
47	5	669	C
47	5	670	G
47	5	672	C
47	5	683	C

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Mol	Chain	Res	Type
47	5	685	C
47	5	687	U
47	5	696	C
47	5	697	G
47	5	702	U
47	5	704	C
47	5	705	G
47	5	708	G
47	5	722	G
47	5	729	G
47	5	730	G
47	5	731	G
47	5	734	G
47	5	738	C
47	5	738(A)	C
47	5	739	G
47	5	744	G
47	5	747	A
47	5	748	G
47	5	749	G
47	5	750	U
47	5	756	G
47	5	758	G
47	5	911	U
47	5	913	U
47	5	914	U
47	5	917	A
47	5	918	G
47	5	923	C
47	5	924	C
47	5	925	C
47	5	926	G
47	5	929	A
47	5	931	C
47	5	932	A
47	5	933	G
47	5	934	C
47	5	935	A
47	5	935(A)	G
47	5	936	C
47	5	937	U
47	5	939	G

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Mol	Chain	Res	Type
47	5	941	C
47	5	943	A
47	5	944	A
47	5	945	U
47	5	956	A
47	5	957	G
47	5	959	G
47	5	960	A
47	5	961	G
47	5	962	C
47	5	963	G
47	5	964	A
47	5	965	G
47	5	966	A
47	5	967	C
47	5	968	C
47	5	969	C
47	5	972	C
47	5	973	G
47	5	979	C
47	5	983	C
47	5	990	C
47	5	1072	C
47	5	1073	G
47	5	1075	G
47	5	1076	C
47	5	1078	A
47	5	1079	C
47	5	1082	C
47	5	1174	G
47	5	1175	A
47	5	1177	U
47	5	1179	U
47	5	1184	A
47	5	1189	G
47	5	1194	G
47	5	1195	G
47	5	1211	G
47	5	1212	G
47	5	1214	C
47	5	1215	C
47	5	1234	G

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Mol	Chain	Res	Type
47	5	1235	G
47	5	1236	C
47	5	1237	C
47	5	1238	A
47	5	1239	C
47	5	1272	C
47	5	1273	G
47	5	1274	A
47	5	1275	G
47	5	1276	C
47	5	1284	G
47	5	1287	G
47	5	1288	G
47	5	1292	C
47	5	1293	G
47	5	1295	U
47	5	1296	G
47	5	1301	C
47	5	1303	A
47	5	1304	C
47	5	1326	A
47	5	1328	G
47	5	1330	A
47	5	1337	A
47	5	1354	A
47	5	1359	G
47	5	1364	U
47	5	1370	G
47	5	1371	A
47	5	1377	G
47	5	1378	C
47	5	1379	C
47	5	1381	U
47	5	1387	A
47	5	1394	G
47	5	1397	A
47	5	1398	A
47	5	1401	C
47	5	1403	G
47	5	1416	G
47	5	1418	C
47	5	1419	G

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Mol	Chain	Res	Type
47	5	1420	A
47	5	1421	G
47	5	1429	C
47	5	1435	G
47	5	1436	C
47	5	1437	C
47	5	1438	U
47	5	1441	C
47	5	1442	C
47	5	1445	U
47	5	1446	C
47	5	1453	G
47	5	1456	C
47	5	1457	G
47	5	1458	C
47	5	1459	A
47	5	1465	G
47	5	1475	G
47	5	1477	C
47	5	1478	C
47	5	1482	G
47	5	1483	C
47	5	1484	G
47	5	1485	C
47	5	1486	C
47	5	1497	A
47	5	1498	G
47	5	1502	G
47	5	1504	G
47	5	1516	G
47	5	1518	A
47	5	1523	A
47	5	1525	A
47	5	1534	A
47	5	1535	C
47	5	1547	A
47	5	1554	A
47	5	1563	A
47	5	1564	A
47	5	1566	C
47	5	1568	C
47	5	1574	G

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Mol	Chain	Res	Type
47	5	1578	U
47	5	1586	G
47	5	1591	U
47	5	1592	G
47	5	1596	U
47	5	1612	G
47	5	1613	A
47	5	1624	G
47	5	1625	G
47	5	1628	C
47	5	1631	A
47	5	1633	G
47	5	1634	A
47	5	1640	C
47	5	1641	G
47	5	1654	G
47	5	1656	U
47	5	1661	C
47	5	1670	G
47	5	1676	C
47	5	1677	U
47	5	1678	C
47	5	1679	A
47	5	1691	G
47	5	1724	G
47	5	1726	U
47	5	1734	G
47	5	1735	U
47	5	1740	C
47	5	1741	G
47	5	1742	A
47	5	1750	G
47	5	1753	G
47	5	1755	C
47	5	1756	U
47	5	1757	U
47	5	1760	G
47	5	1761	G
47	5	1763	C
47	5	1764	G
47	5	1768	C
47	5	1772	C

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Mol	Chain	Res	Type
47	5	1773	U
47	5	1776	A
47	5	1780	A
47	5	1781	U
47	5	1785	C
47	5	1787	A
47	5	1799	G
47	5	1800	U
47	5	1804	A
47	5	1805	A
47	5	1818	G
47	5	1819	G
47	5	1821	G
47	5	1822	U
47	5	1823	G
47	5	1828	C
47	5	1833	G
47	5	1834	U
47	5	1835	G
47	5	1836	G
47	5	1837	A
47	5	1842	G
47	5	1855	G
47	5	1867	A
47	5	1869	G
47	5	1882	U
47	5	1893	C
47	5	1897	A
47	5	1910	G
47	5	1918	U
47	5	1920	C
47	5	1921	C
47	5	1922	G
47	5	1923	A
47	5	1931	C
47	5	1933	G
47	5	1941	A
47	5	1948	G
47	5	1952	G
47	5	1957	U
47	5	1959	U
47	5	1960	A

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Mol	Chain	Res	Type
47	5	1961	G
47	5	1962	A
47	5	1963	C
47	5	1967	A
47	5	1976	G
47	5	1977	C
47	5	1978	C
47	5	1979	A
47	5	1980	U
47	5	1983	A
47	5	1984	A
47	5	1986	U
47	5	1987	C
47	5	1988	G
47	5	1991	A
47	5	1993	C
47	5	1997	U
47	5	2001	G
47	5	2002	A
47	5	2003	G
47	5	2004	U
47	5	2005	G
47	5	2007	G
47	5	2008	U
47	5	2011	C
47	5	2024	G
47	5	2026	A
47	5	2034	G
47	5	2046	G
47	5	2047	A
47	5	2048	U
47	5	2052	G
47	5	2055	G
47	5	2056	G
47	5	2062	C
47	5	2064	G
47	5	2069	A
47	5	2070	U
47	5	2084	U
47	5	2085	G
47	5	2089	G
47	5	2090	U

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Mol	Chain	Res	Type
47	5	2092	G
47	5	2093	G
47	5	2094	C
47	5	2095	A
47	5	2097	A
47	5	2098	G
47	5	2100	G
47	5	2101	A
47	5	2102	G
47	5	2104	A
47	5	2105	A
47	5	2106	G
47	5	2107	A
47	5	2108	G
47	5	2110	G
47	5	2259	G
47	5	2260	C
47	5	2262	G
47	5	2266	C
47	5	2267	U
47	5	2268	A
47	5	2269	C
47	5	2270	G
47	5	2274	C
47	5	2275	G
47	5	2277	C
47	5	2278	G
47	5	2279	A
47	5	2289	C
47	5	2300	A
47	5	2301	G
47	5	2313	A
47	5	2314	G
47	5	2331	G
47	5	2333	G
47	5	2348	G
47	5	2351	C
47	5	2364	G
47	5	2366	A
47	5	2370	A
47	5	2374	A
47	5	2395	A

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Mol	Chain	Res	Type
47	5	2396	A
47	5	2399	G
47	5	2416	G
47	5	2417	A
47	5	2422	C
47	5	2424	G
47	5	2425	U
47	5	2428	A
47	5	2429	A
47	5	2433	G
47	5	2441	C
47	5	2447	U
47	5	2450	G
47	5	2467	U
47	5	2468	U
47	5	2469	C
47	5	2471	G
47	5	2475	G
47	5	2479	G
47	5	2483	G
47	5	2485	U
47	5	2488	C
47	5	2489	C
47	5	2490	U
47	5	2491	C
47	5	2493	G
47	5	2495	U
47	5	2503	G
47	5	2504	C
47	5	2505	C
47	5	2506	G
47	5	2513	A
47	5	2521	G
47	5	2530	U
47	5	2537	A
47	5	2546	G
47	5	2547	G
47	5	2553	A
47	5	2554	U
47	5	2555	G
47	5	2564	G
47	5	2566	G

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Mol	Chain	Res	Type
47	5	2571	C
47	5	2575	U
47	5	2583	C
47	5	2587	A
47	5	2601	A
47	5	2618	G
47	5	2620	G
47	5	2627	C
47	5	2638	G
47	5	2640	G
47	5	2647	A
47	5	2658	G
47	5	2660	A
47	5	2661	U
47	5	2662	G
47	5	2663	G
47	5	2669	C
47	5	2670	C
47	5	2673	G
47	5	2676	A
47	5	2680	G
47	5	2681	G
47	5	2686	G
47	5	2687	U
47	5	2688	G
47	5	2689	C
47	5	2694	G
47	5	2695	A
47	5	2696	A
47	5	2707	U
47	5	2708	U
47	5	2709	C
47	5	2710	C
47	5	2711	G
47	5	2712	G
47	5	2716	C
47	5	2719	C
47	5	2721	G
47	5	2725	A
47	5	2726	G
47	5	2735	G
47	5	2740	U

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Mol	Chain	Res	Type
47	5	2743	A
47	5	2754	G
47	5	2755	A
47	5	2760	G
47	5	2761	U
47	5	2763	U
47	5	2764	A
47	5	2769	U
47	5	2772	C
47	5	2787	A
47	5	2788	U
47	5	2789	A
47	5	2790	U
47	5	2794	C
47	5	2795	A
47	5	2798	A
47	5	2806	A
47	5	2807	A
47	5	2814	C
47	5	2819	U
47	5	2826	U
47	5	2827	G
47	5	2828	U
47	5	2829	U
47	5	2835	A
47	5	2838	G
47	5	2842	G
47	5	2855	G
47	5	2857	A
47	5	2858	A
47	5	2862	G
47	5	2864	A
47	5	2875	C
47	5	2876	G
47	5	2884	G
47	5	2896	G
47	5	2897	G
47	5	3598	C
47	5	3604	A
47	5	3605	C
47	5	3615	G
47	5	3617	G

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Mol	Chain	Res	Type
47	5	3625	G
47	5	3626	G
47	5	3630	A
47	5	3635	A
47	5	3644	U
47	5	3646	A
47	5	3662	A
47	5	3673	C
47	5	3674	G
47	5	3685	C
47	5	3692	A
47	5	3696	C
47	5	3698	G
47	5	3711	A
47	5	3712	A
47	5	3722	G
47	5	3729	U
47	5	3733	A
47	5	3739	C
47	5	3740	G
47	5	3748	A
47	5	3750	G
47	5	3753	G
47	5	3755	G
47	5	3759	A
47	5	3760	A
47	5	3763	A
47	5	3772	U
47	5	3773	U
47	5	3774	A
47	5	3776	G
47	5	3777	G
47	5	3778	U
47	5	3780	G
47	5	3783	A
47	5	3784	A
47	5	3786	U
47	5	3810	C
47	5	3811	G
47	5	3812	C
47	5	3814	U
47	5	3817	A

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Mol	Chain	Res	Type
47	5	3819	G
47	5	3822	U
47	5	3831	U
47	5	3838	U
47	5	3839	G
47	5	3840	U
47	5	3851	U
47	5	3859	G
47	5	3867	A
47	5	3876	A
47	5	3877	A
47	5	3878	C
47	5	3879	G
47	5	3889	G
47	5	3897	G
47	5	3898	G
47	5	3901	A
47	5	3905	A
47	5	3906	A
47	5	3907	G
47	5	3908	A
47	5	3915	U
47	5	3916	G
47	5	3927	U
47	5	3939	G
47	5	3943	A
47	5	4067	U
47	5	4069	U
47	5	4076	G
47	5	4084	G
47	5	4085	A
47	5	4086	G
47	5	4088	C
47	5	4099	G
47	5	4100	C
47	5	4116	C
47	5	4117	U
47	5	4119	C
47	5	4120	U
47	5	4121	G
47	5	4122	G
47	5	4125	C

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Mol	Chain	Res	Type
47	5	4127	A
47	5	4150	G
47	5	4158	C
47	5	4162	C
47	5	4163	U
47	5	4166	G
47	5	4171	C
47	5	4183	G
47	5	4184	G
47	5	4190	U
47	5	4191	G
47	5	4205	A
47	5	4212	A
47	5	4213	A
47	5	4218	U
47	5	4219	A
47	5	4225	G
47	5	4229	U
47	5	4232	U
47	5	4233	A
47	5	4237	C
47	5	4251	A
47	5	4255	A
47	5	4257	A
47	5	4258	C
47	5	4265	U
47	5	4267	G
47	5	4268	A
47	5	4271	A
47	5	4273	A
47	5	4281	A
47	5	4291	G
47	5	4297	G
47	5	4304	A
47	5	4305	G
47	5	4306	U
47	5	4314	C
47	5	4317	A
47	5	4318	C
47	5	4319	C
47	5	4326	G
47	5	4329	G

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Mol	Chain	Res	Type
47	5	4330	G
47	5	4332	C
47	5	4335	C
47	5	4336	A
47	5	4339	A
47	5	4349	C
47	5	4350	C
47	5	4354	U
47	5	4355	G
47	5	4373	G
47	5	4377	G
47	5	4378	A
47	5	4379	A
47	5	4380	A
47	5	4387	C
47	5	4394	A
47	5	4395	U
47	5	4396	A
47	5	4398	C
47	5	4401	G
47	5	4415	A
47	5	4419	U
47	5	4421	C
47	5	4422	A
47	5	4437	U
47	5	4438	U
47	5	4440	G
47	5	4441	A
47	5	4444	C
47	5	4448	G
47	5	4449	A
47	5	4450	U
47	5	4453	C
47	5	4464	A
47	5	4471	U
47	5	4475	G
47	5	4476	C
47	5	4488	A
47	5	4495	G
47	5	4500	U
47	5	4510	A
47	5	4511	A

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Mol	Chain	Res	Type
47	5	4512	U
47	5	4513	A
47	5	4519	C
47	5	4520	G
47	5	4524	G
47	5	4531	U
47	5	4548	A
47	5	4549	G
47	5	4560	C
47	5	4563	U
47	5	4567	G
47	5	4570	G
47	5	4573	G
47	5	4575	G
47	5	4578	G
47	5	4581	G
47	5	4584	A
47	5	4585	U
47	5	4586	G
47	5	4590	A
47	5	4618	G
47	5	4627	U
47	5	4636	U
47	5	4637	G
47	5	4639	G
47	5	4652	G
47	5	4656	A
47	5	4657	U
47	5	4660	G
47	5	4661	G
47	5	4670	C
47	5	4672	A
47	5	4677	U
47	5	4678	G
47	5	4694	G
47	5	4700	A
47	5	4701	A
47	5	4709	U
47	5	4719	G
47	5	4720	C
47	5	4721	G
47	5	4728	U

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Mol	Chain	Res	Type
47	5	4729	A
47	5	4736	C
47	5	4737	G
47	5	4745	G
47	5	4751	G
47	5	4754	G
47	5	4755	G
47	5	4756	C
47	5	4757	C
47	5	4759	C
47	5	4761	G
47	5	4765	G
47	5	4771	C
47	5	4772	C
47	5	4868	G
47	5	4870	G
47	5	4871	C
47	5	4872	G
47	5	4873	G
47	5	4874	A
47	5	4875	G
47	5	4876	A
47	5	4877	G
47	5	4881	U
47	5	4882	U
47	5	4883	C
47	5	4885	U
47	5	4887	C
47	5	4891	G
47	5	4895	C
47	5	4897	G
47	5	4904	G
47	5	4910	A
47	5	4912	G
47	5	4913	G
47	5	4914	G
47	5	4915	G
47	5	4918	C
47	5	4919	G
47	5	4921	C
47	5	4924	C
47	5	4925	U

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Mol	Chain	Res	Type
47	5	4926	C
47	5	4927	G
47	5	4928	C
47	5	4931	G
47	5	4932	U
47	5	4935	C
47	5	4937	C
47	5	4940	C
47	5	4943	A
47	5	4944	C
47	5	4947	U
47	5	4948	C
47	5	4949	G
47	5	4950	U
47	5	4951	G
47	5	4956	A
47	5	4957	C
47	5	4958	C
47	5	4964	C
47	5	4965	U
47	5	4966	A
47	5	4967	A
47	5	4976	U
47	5	4979	A
47	5	4985	U
47	5	4988	U
47	5	4989	U
47	5	4990	C
47	5	4991	U
47	5	4993	G
47	5	5006	U
47	5	5014	A
47	5	5017	G
47	5	5040	U
47	5	5041	G
47	5	5047	C
47	5	5050	C
47	5	5052	C
47	5	5053	U
47	5	5054	C
47	5	5056	A
47	5	5058	A

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Mol	Chain	Res	Type
47	5	5061	A
47	5	5062	G
48	7	7	G
48	7	13	A
48	7	22	A
48	7	25	G
48	7	33	U
48	7	38	U
48	7	42	A
48	7	53	U
48	7	54	A
48	7	64	G
48	7	74	A
48	7	97	G
48	7	100	A
48	7	110	G
48	7	111	C
48	7	117	G
48	7	120	U
49	8	2	G
49	8	3	A
49	8	32	C
49	8	34	U
49	8	35	C
49	8	38	U
49	8	49	G
49	8	52	A
49	8	59	A
49	8	62	A
49	8	63	U
49	8	75	G
49	8	79	G
49	8	86	U
49	8	87	G
49	8	90	C
49	8	94	G
49	8	95	A
49	8	103	A
49	8	105	C
49	8	107	C
49	8	109	C
49	8	110	U

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Mol	Chain	Res	Type
49	8	111	U
49	8	112	G
49	8	114	G
49	8	121	G
49	8	123	U
49	8	124	U
49	8	125	C
49	8	126	C
49	8	127	U
49	8	137	A
49	8	143	G
49	8	147	G
49	8	150	C
50	9	2	A
50	9	3	C
50	9	4	C
50	9	17	C
50	9	25	A
50	9	26	U
50	9	33	G
50	9	44	U
50	9	45	A
50	9	46	A
50	9	56	G
50	9	58	C
50	9	62	G
50	9	65	C
50	9	67	C
50	9	68	A
50	9	70	G
50	9	71	G
50	9	73	C
50	9	74	G
50	9	75	G
50	9	77	A
50	9	79	A
50	9	99	A
50	9	100	U
50	9	103	A
50	9	104	A
50	9	110	U
50	9	111	A

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Mol	Chain	Res	Type
50	9	113	G
50	9	115	U
50	9	116	U
50	9	124	U
50	9	126	G
50	9	127	C
50	9	128	U
50	9	129	C
50	9	130	G
50	9	141	A
50	9	143	U
50	9	147	A
50	9	155	G
50	9	158	A
50	9	161	U
50	9	162	C
50	9	163	U
50	9	167	G
50	9	168	C
50	9	173	A
50	9	175	A
50	9	180	G
50	9	182	C
50	9	183	G
50	9	184	G
50	9	188	C
50	9	189	U
50	9	191	A
50	9	192	C
50	9	200	G
50	9	202	G
50	9	206	G
50	9	213	G
50	9	215	G
50	9	292	A
50	9	294	U
50	9	302	A
50	9	304	C
50	9	307	G
50	9	308	G
50	9	309	G
50	9	312	G

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Mol	Chain	Res	Type
50	9	314	U
50	9	318	A
50	9	319	C
50	9	322	C
50	9	331	C
50	9	332	G
50	9	340	C
50	9	343	A
50	9	347	G
50	9	351	G
50	9	360	A
50	9	362	C
50	9	364	A
50	9	368	U
50	9	370	G
50	9	379	C
50	9	381	C
50	9	382	C
50	9	383	G
50	9	384	U
50	9	385	G
50	9	386	C
50	9	400	C
50	9	408	A
50	9	409	C
50	9	410	G
50	9	417	C
50	9	418	A
50	9	434	G
50	9	435	A
50	9	438	G
50	9	448	A
50	9	449	A
50	9	450	C
50	9	454	U
50	9	460	A
50	9	464	A
50	9	465	A
50	9	466	G
50	9	472	C
50	9	473	A
50	9	474	G

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Mol	Chain	Res	Type
50	9	476	A
50	9	482	G
50	9	487	U
50	9	492	C
50	9	496	C
50	9	500	A
50	9	501	C
50	9	508	A
50	9	512	A
50	9	532	C
50	9	533	A
50	9	544	G
50	9	545	A
50	9	546	G
50	9	548	C
50	9	549	C
50	9	550	C
50	9	551	U
50	9	554	A
50	9	555	A
50	9	556	U
50	9	557	U
50	9	559	G
50	9	560	A
50	9	562	U
50	9	563	G
50	9	564	A
50	9	568	C
50	9	576	A
50	9	583	A
50	9	587	A
50	9	588	G
50	9	589	G
50	9	590	A
50	9	591	U
50	9	592	C
50	9	595	U
50	9	597	G
50	9	598	G
50	9	604	A
50	9	606	G
50	9	607	U

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Mol	Chain	Res	Type
50	9	608	C
50	9	614	C
50	9	620	G
50	9	621	C
50	9	628	A
50	9	629	A
50	9	631	U
50	9	637	U
50	9	643	A
50	9	644	G
50	9	659	G
50	9	660	C
50	9	663	C
50	9	664	A
50	9	668	A
50	9	669	A
50	9	670	A
50	9	671	A
50	9	672	A
50	9	673	G
50	9	678	U
50	9	684	G
50	9	688	U
50	9	689	U
50	9	732	U
50	9	733	C
50	9	752	G
50	9	753	C
50	9	754	G
50	9	798	G
50	9	811	A
50	9	812	A
50	9	821	G
50	9	822	U
50	9	830	A
50	9	834	C
50	9	847	A
50	9	861	A
50	9	868	G
50	9	869	A
50	9	870	A
50	9	871	U

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Mol	Chain	Res	Type
50	9	872	A
50	9	873	G
50	9	874	G
50	9	875	A
50	9	877	C
50	9	878	G
50	9	885	U
50	9	890	U
50	9	892	U
50	9	902	G
50	9	913	A
50	9	914	U
50	9	920	A
50	9	922	A
50	9	930	C
50	9	933	G
50	9	934	G
50	9	943	U
50	9	955	A
50	9	971	G
50	9	985	G
50	9	990	A
50	9	992	A
50	9	999	G
50	9	1017	U
50	9	1023	A
50	9	1030	A
50	9	1041	G
50	9	1044	G
50	9	1060	A
50	9	1061	U
50	9	1062	A
50	9	1067	C
50	9	1078	C
50	9	1083	A
50	9	1085	C
50	9	1089	G
50	9	1099	G
50	9	1100	A
50	9	1111	U
50	9	1114	U
50	9	1115	U

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Mol	Chain	Res	Type
50	9	1116	C
50	9	1117	C
50	9	1118	C
50	9	1120	U
50	9	1121	G
50	9	1131	G
50	9	1132	C
50	9	1133	A
50	9	1138	C
50	9	1139	C
50	9	1144	A
50	9	1148	A
50	9	1149	A
50	9	1150	A
50	9	1153	C
50	9	1154	U
50	9	1165	G
50	9	1166	G
50	9	1195	A
50	9	1207	G
50	9	1208	A
50	9	1211	G
50	9	1213	C
50	9	1215	C
50	9	1221	G
50	9	1224	G
50	9	1227	G
50	9	1240	A
50	9	1242	U
50	9	1251	A
50	9	1253	A
50	9	1254	C
50	9	1256	G
50	9	1257	G
50	9	1259	A
50	9	1265	A
50	9	1266	C
50	9	1268	C
50	9	1271	C
50	9	1274	G
50	9	1275	G
50	9	1281	G

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Mol	Chain	Res	Type
50	9	1284	A
50	9	1285	G
50	9	1286	G
50	9	1287	A
50	9	1289	U
50	9	1293	A
50	9	1298	G
50	9	1299	A
50	9	1300	U
50	9	1301	A
50	9	1302	G
50	9	1303	C
50	9	1307	U
50	9	1308	U
50	9	1313	A
50	9	1314	U
50	9	1316	C
50	9	1321	G
50	9	1322	G
50	9	1330	G
50	9	1331	C
50	9	1341	C
50	9	1342	U
50	9	1348	G
50	9	1354	G
50	9	1369	A
50	9	1371	U
50	9	1372	U
50	9	1375	G
50	9	1376	A
50	9	1378	A
50	9	1382	A
50	9	1395	C
50	9	1396	A
50	9	1397	U
50	9	1401	A
50	9	1402	A
50	9	1404	U
50	9	1406	G
50	9	1410	C
50	9	1424	G
50	9	1428	G

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Mol	Chain	Res	Type
50	9	1429	G
50	9	1439	A
50	9	1449	G
50	9	1454	A
50	9	1458	G
50	9	1459	G
50	9	1462	U
50	9	1463	U
50	9	1466	G
50	9	1473	G
50	9	1475	G
50	9	1476	A
50	9	1477	U
50	9	1478	U
50	9	1480	A
50	9	1490	G
50	9	1494	U
50	9	1495	G
50	9	1497	G
50	9	1498	A
50	9	1509	U
50	9	1510	G
50	9	1521	C
50	9	1522	A
50	9	1531	A
50	9	1533	A
50	9	1536	G
50	9	1539	U
50	9	1544	C
50	9	1545	A
50	9	1548	G
50	9	1552	G
50	9	1553	C
50	9	1555	U
50	9	1556	A
50	9	1557	C
50	9	1560	U
50	9	1570	G
50	9	1574	C
50	9	1575	G
50	9	1580	A
50	9	1581	C

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Mol	Chain	Res	Type
50	9	1582	C
50	9	1585	U
50	9	1586	U
50	9	1587	G
50	9	1588	A
50	9	1589	A
50	9	1600	G
50	9	1601	A
50	9	1602	U
50	9	1604	G
50	9	1621	U
50	9	1623	A
50	9	1625	U
50	9	1637	A
50	9	1638	G
50	9	1639	G
50	9	1641	A
50	9	1647	A
50	9	1648	G
50	9	1654	G
50	9	1661	A
50	9	1664	A
50	9	1665	G
50	9	1671	G
50	9	1680	G
50	9	1682	C
50	9	1683	C
50	9	1686	G
50	9	1689	C
50	9	1695	A
50	9	1698	C
50	9	1699	A
50	9	1703	C
50	9	1715	A
50	9	1721	U
50	9	1722	G
50	9	1726	G
50	9	1728	U
50	9	1729	U
50	9	1730	U
50	9	1737	G
50	9	1744	G

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Mol	Chain	Res	Type
50	9	1745	A
50	9	1753	C
50	9	1757	G
50	9	1758	G
50	9	1760	G
50	9	1772	C
50	9	1783	C
50	9	1785	C
50	9	1800	A
50	9	1801	A
50	9	1823	A
50	9	1824	A
50	9	1825	A
50	9	1826	G
50	9	1829	G
50	9	1831	A
50	9	1835	A
50	9	1836	G
50	9	1838	U
50	9	1849	G
50	9	1851	A
50	9	1852	C
50	9	1861	G
50	9	1862	G
50	9	1863	A
50	9	1865	C
50	9	1866	A
50	9	1867	U
50	9	1869	A
84	hh	42	C
84	hh	43	A
84	hh	45	A
84	hh	46	G
84	hh	49	U
84	hh	52	G
84	hh	54	U
84	hh	55	C

All (258) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
45	2	20(A)	U

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Mol	Chain	Res	Type
46	3	7	A
46	3	74	C
47	5	12	A
47	5	20	U
47	5	47	A
47	5	48	G
47	5	64	A
47	5	119	G
47	5	125	C
47	5	134	G
47	5	135	G
47	5	143	C
47	5	159	C
47	5	209	U
47	5	217	C
47	5	226	G
47	5	245	C
47	5	265	C
47	5	275	C
47	5	278	G
47	5	385	A
47	5	406	C
47	5	409	G
47	5	417	G
47	5	449	C
47	5	453	G
47	5	466	A
47	5	480	C
47	5	481(A)	C
47	5	484	U
47	5	485	C
47	5	492	U
47	5	497	G
47	5	498	C
47	5	504	G
47	5	669	C
47	5	696	C
47	5	729	G
47	5	738(A)	C
47	5	747	A
47	5	748	G
47	5	913	U

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Mol	Chain	Res	Type
47	5	916	C
47	5	924	C
47	5	930	G
47	5	933	G
47	5	935(A)	G
47	5	936	C
47	5	956	A
47	5	959	G
47	5	963	G
47	5	966	A
47	5	968	C
47	5	969	C
47	5	971(A)	G
47	5	1071	C
47	5	1072	C
47	5	1174	G
47	5	1209	U
47	5	1211	G
47	5	1214	C
47	5	1236	C
47	5	1238	A
47	5	1287	G
47	5	1291	G
47	5	1294	A
47	5	1295	U
47	5	1325	C
47	5	1329	G
47	5	1358	G
47	5	1370	G
47	5	1378	C
47	5	1380	G
47	5	1420	A
47	5	1440	U
47	5	1445	U
47	5	1455	G
47	5	1477	C
47	5	1481	C
47	5	1484	G
47	5	1485	C
47	5	1534	A
47	5	1563	A
47	5	1633	G

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Mol	Chain	Res	Type
47	5	1654	G
47	5	1678	C
47	5	1733	G
47	5	1734	G
47	5	1740	C
47	5	1804	A
47	5	1818	G
47	5	1833	G
47	5	1834	U
47	5	1835	G
47	5	1892	A
47	5	1910	G
47	5	1921	C
47	5	1935	C
47	5	1947	U
47	5	1960	A
47	5	1979	A
47	5	1983	A
47	5	1986	U
47	5	2001	G
47	5	2025	A
47	5	2046	G
47	5	2068	C
47	5	2088	A
47	5	2089	G
47	5	2100	G
47	5	2265	G
47	5	2266	C
47	5	2278	G
47	5	2313	A
47	5	2369	U
47	5	2394	G
47	5	2396	A
47	5	2398	U
47	5	2425	U
47	5	2428	A
47	5	2467	U
47	5	2468	U
47	5	2474	G
47	5	2475	G
47	5	2490	U
47	5	2502	A

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Mol	Chain	Res	Type
47	5	2529	A
47	5	2546	G
47	5	2661	U
47	5	2695	A
47	5	2724	G
47	5	2754	G
47	5	2794	C
47	5	3625	G
47	5	3673	C
47	5	3697	U
47	5	3710	G
47	5	3809	G
47	5	3876	A
47	5	3878	C
47	5	3888	G
47	5	3904	G
47	5	4075	U
47	5	4076	G
47	5	4084	G
47	5	4119	C
47	5	4121	G
47	5	4124	G
47	5	4162	C
47	5	4170	A
47	5	4204	C
47	5	4232	U
47	5	4254	G
47	5	4266	G
47	5	4272	G
47	5	4378	A
47	5	4395	U
47	5	4448	G
47	5	4449	A
47	5	4463	U
47	5	4488	A
47	5	4572	U
47	5	4583	C
47	5	4656	A
47	5	4671	C
47	5	4699	U
47	5	4719	G
47	5	4871	C

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Mol	Chain	Res	Type
47	5	4872	G
47	5	4876	A
47	5	4884	G
47	5	4925	U
47	5	4936	G
47	5	4942	C
47	5	4947	U
47	5	4965	U
47	5	4966	A
48	7	13	A
48	7	109	U
49	8	2	G
49	8	34	U
49	8	51	U
49	8	85	U
49	8	86	U
49	8	94	G
49	8	110	U
49	8	124	U
50	9	2	A
50	9	72	C
50	9	110	U
50	9	126	G
50	9	160	U
50	9	182	C
50	9	293	C
50	9	369	C
50	9	434	G
50	9	447	A
50	9	448	A
50	9	465	A
50	9	473	A
50	9	474	G
50	9	500	A
50	9	532	C
50	9	553	U
50	9	555	A
50	9	559	G
50	9	563	G
50	9	591	U
50	9	620	G
50	9	642	U

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Mol	Chain	Res	Type
50	9	656	G
50	9	670	A
50	9	688	U
50	9	752	G
50	9	821	G
50	9	861	A
50	9	868	G
50	9	869	A
50	9	870	A
50	9	872	A
50	9	874	G
50	9	1016	U
50	9	1114	U
50	9	1115	U
50	9	1137	U
50	9	1138	C
50	9	1165	G
50	9	1253	A
50	9	1264	C
50	9	1274	G
50	9	1284	A
50	9	1286	G
50	9	1313	A
50	9	1330	G
50	9	1394	G
50	9	1395	C
50	9	1396	A
50	9	1476	A
50	9	1489	A
50	9	1493	C
50	9	1497	G
50	9	1519	U
50	9	1520	G
50	9	1585	U
50	9	1636	G
50	9	1637	A
50	9	1646	C
50	9	1664	A
50	9	1665	G
50	9	1679	A
50	9	1721	U
50	9	1744	G

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Mol	Chain	Res	Type
50	9	1824	A
50	9	1835	A
50	9	1837	G
50	9	1867	U
50	9	1868	U

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 266 ligands modelled in this entry, 266 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
47	5	29
50	9	15
85	ii	3

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Mol	Chain	Number of breaks
45	2	3
46	3	2
44	t	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	2113:G	O3'	2258:C	P	41.35
1	5	1252:C	O3'	1271:G	P	35.75
1	5	1219:G	O3'	1233:G	P	22.89
1	5	3948:C	O3'	4065:G	P	19.77
1	5	1406(C):G	O3'	1411:C	P	18.60
1	5	990:C	O3'	1064:G	P	18.45
1	5	523:C	O3'	638:G	P	18.02
1	5	4138:C	O3'	4146:G	P	18.00
1	5	4101:C	O3'	4107:G	P	17.49
1	5	4777:C	O3'	4859:C	P	16.69
1	5	760:G	O3'	904:C	P	15.23
1	5	5022:U	O3'	5028:G	P	14.88
1	5	1696:C	O3'	1720:C	P	14.26
1	5	182:G	O3'	189:G	P	13.98
1	5	1364:U	O3'	1368:A	P	13.96
1	5	2901:G	O3'	3597:G	P	13.23
1	5	4729:A	O3'	4735:G	P	10.07
1	5	512:U	O3'	515:C	P	9.81
1	5	1180:C	O3'	1183:C	P	8.91
1	2	19:G	O3'	20:U	P	7.20
1	2	20:U	O3'	20(A):U	P	6.67
1	5	500:G	O3'	504:G	P	6.41
1	5	1100:U	O3'	1168:G	P	5.86
1	3	19:G	O3'	20:U	P	5.64
1	5	1239:C	O3'	1244:G	P	5.34
1	9	689:U	O3'	690:G	P	5.09
1	9	322:C	O3'	323:C	P	5.07
1	9	1412:C	O3'	1413:G	P	5.02
1	9	1410:C	O3'	1411:G	P	4.96
1	9	1411:G	O3'	1412:C	P	4.83
1	5	4740:G	O3'	4743:G	P	4.80
1	3	16:C	O3'	18:U	P	4.79
1	9	798:G	O3'	799:U	P	4.51
1	9	304:C	O3'	305:U	P	4.34
1	9	309:G	O3'	310:C	P	4.34
1	2	16:C	O3'	18:G	P	4.32

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	170:C	O3'	171:U	P	3.68
1	9	902:G	O3'	903:A	P	3.46
1	5	4899:G	O3'	4902:C	P	3.43
1	9	886:A	O3'	887:U	P	3.35
1	5	1438:U	O3'	1440:U	P	3.31
1	9	1295:A	O3'	1296:U	P	3.30
1	9	903:A	O3'	904:A	P	3.26
1	5	267:G	O3'	268:G	P	3.23
1	9	1413:G	O3'	1414:A	P	3.16
1	9	1414:A	O3'	1415:C	P	3.14
1	5	751:G	O3'	752:G	P	3.13
1	9	1406:G	O3'	1407:U	P	3.09
1	t	124:GLU	C	125:LEU	N	3.07
1	5	5020:G	O3'	5021:C	P	3.06
1	ii	144:SER	C	145:LYS	N	2.68
1	ii	324:GLU	C	325:ASN	N	2.67
1	ii	374:LEU	C	375:LEU	N	2.52