



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 01:40 PM BST

PDB ID : 1RY1
EMDB ID: : EMD-1063
Title : Structure of the signal recognition particle interacting with the elongation-arrested ribosome
Authors : Halic, M.; Becker, T.; Pool, M.R.; Spahn, C.M.; Grassucci, R.A.; Frank, J.; Beckmann, R.
Deposited on : 2003-12-19
Resolution : 12.00 Å(reported)

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.

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

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>

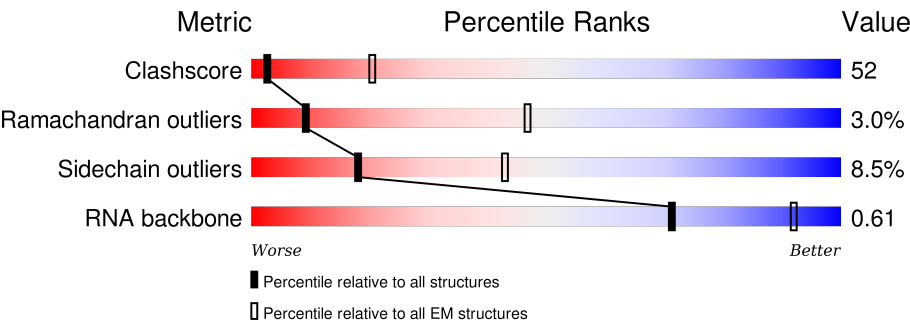
MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : trunk27241

1 Overall quality at a glance i

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

The reported resolution of this entry is 12.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



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

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	E	50	<div><div>22%</div><div>56%</div><div>14%</div><div>6%</div><div>.</div></div>
2	A	128	<div><div>37%</div><div>51%</div><div>13%</div></div>
3	M	27	<div><div>15%</div><div>48%</div><div>15%</div><div>22%</div></div>
4	N	31	<div><div>.</div><div>45%</div><div>29%</div><div>23%</div></div>
5	O	24	<div><div>25%</div><div>54%</div><div>13%</div><div>8%</div></div>
6	P	20	<div><div>10%</div><div>60%</div><div>15%</div><div>10%</div><div>5%</div></div>
7	Q	12	<div><div>8%</div><div>33%</div><div>42%</div><div>17%</div></div>
8	R	12	<div><div>25%</div><div>58%</div><div>17%</div></div>

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Mol	Chain	Length	Quality of chain
9	C	85	<div><div></div><div>29%</div><div>46%</div><div>7%</div><div>•</div><div>16%</div></div>
10	D	106	<div><div></div><div>42%</div><div>25%</div><div>•</div><div>28%</div></div>
11	B	108	<div><div></div><div>41%</div><div>50%</div><div>7%</div><div>••</div></div>
12	U	296	<div><div></div><div>52%</div><div>41%</div><div>6%</div><div>•</div></div>
13	W	109	<div><div></div><div>52%</div><div>40%</div><div>•</div><div>•</div></div>
14	S	18	<div><div></div><div>33%</div><div>67%</div></div>

2 Entry composition [i](#)

There are 14 unique types of molecules in this entry. The entry contains 11794 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called ALU DOMAIN (RNA FRAGMENTS).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	E	49	Total	C	N	O	P	0	0
			1051	466	190	346	49		

- Molecule 2 is a RNA chain called ALU DOMAIN (SRP9, SRP14 + RNA).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	128	Total	C	N	O	P	0	0
			2751	1226	511	886	128		

- Molecule 3 is a RNA chain called fragment of 7S RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	M	27	Total	C	N	O	P	0	0
			585	260	110	188	27		

- Molecule 4 is a RNA chain called RNA (31-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
4	N	31	Total	C	N	O	P	0	0
			649	291	109	218	31		

- Molecule 5 is a RNA chain called RNA (5'-R(P*GP*UP*UP*CP*UP*GP*GP*GP*CP*UP*GP*UP*AP*GP*UP*GP*CP*GP*CP*UP*AP*UP*GP*C)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
5	O	24	Total	C	N	O	P	0	0
			511	227	86	174	24		

- Molecule 6 is a RNA chain called RNA (5'-R(*CP*AP*AP*UP*AP*GP*CP*CP*AP*CP*UP*GP*CP*AP*CP*UP*CP*CP*AP*G)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
6	P	19	Total	C	N	O	P	0	0
			401	180	72	130	19		

- Molecule 7 is a RNA chain called RNA (5'-R(P*CP*GP*AP*UP*CP*GP*GP*GP*UP*GP*UP*C)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Q	12	Total	C	N	O	P	0	0
			257	114	45	86	12		

- Molecule 8 is a RNA chain called RNA (5'-R(P*AP*UP*CP*GP*CP*GP*CP*CP*UP*GP*UP*G)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
8	R	12	Total	C	N	O	P	0	0
			254	113	43	86	12		

- Molecule 9 is a protein called PROTEIN (Signal recognition particle 9 kDa protein).

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	71	Total	C	N	O	S	0	0
			580	369	101	105	5		

- Molecule 10 is a protein called PROTEIN (Signal recognition particle 14 kDa protein).

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	76	Total	C	N	O	S	0	0
			604	382	105	113	4		

- Molecule 11 is a protein called PROTEIN (Signal recognition particle 19 kDa protein).

Mol	Chain	Residues	Atoms					AltConf	Trace
11	B	107	Total	C	N	O	S	0	0
			870	549	159	156	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	13	MET	-	INITIATING METHIONINE	UNP P09132

- Molecule 12 is a protein called Signal recognition particle protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	U	294	Total	C	N	O	S	0	0
			2266	1424	413	423	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U	1	MET	-	INITIATING METHIONINE	UNP O07347

- Molecule 13 is a protein called Signal recognition particle 54 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	W	109	Total	C	N	O	S	0	0
			865	540	150	164	11		

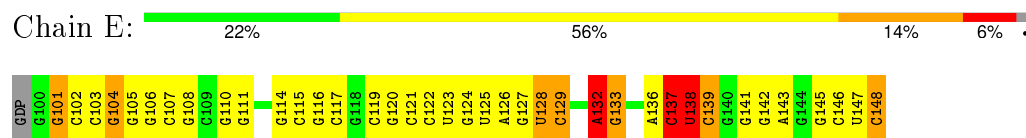
- Molecule 14 is a protein called Rhodopsin.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	S	18	Total	C	N	O	0	0
			150	103	24	23		

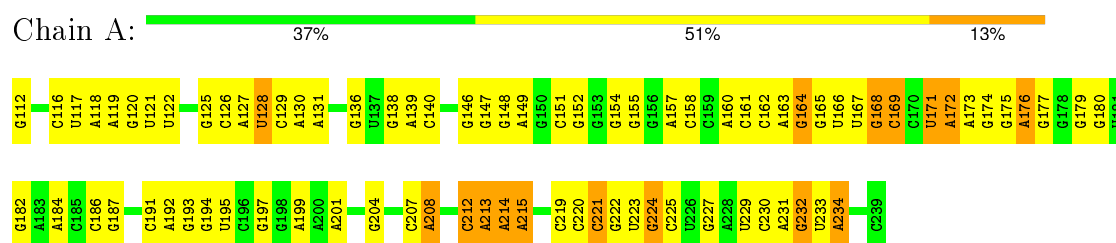
3 Residue-property plots

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.

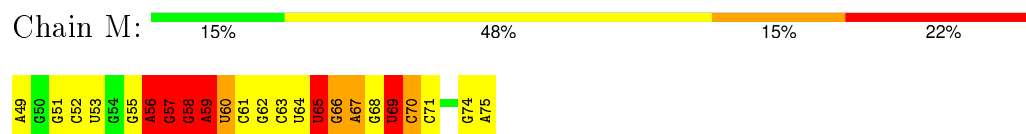
- Molecule 1: ALU DOMAIN (RNA FRAGMENTS)



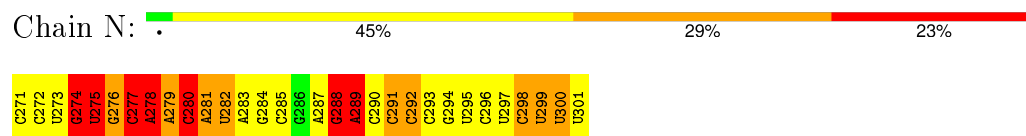
- Molecule 2: ALU DOMAIN (SRP9, SRP14 + RNA)



- Molecule 3: fragment of 7S RNA




- Molecule 4: RNA (31-MER)

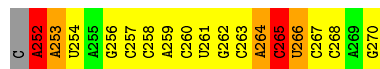


- Molecule 5: RNA (5'-R(P*GP*UP*UP*CP*UP*GP*GP*GP*CP*UP*GP*UP*AP*GP*UP*GP*CP*GP*CP*UP*AP*UP*GP*C)-3')



- Molecule 6: RNA (5'-R(*CP*AP*AP*UP*AP*GP*CP*CP*AP*CP*UP*GP*CP*AP*CP*UP*CP*CP*AP*G)-3')

Chain P: 



- Molecule 7: RNA (5'-R(P*CP*GP*AP*UP*CP*GP*GP*GP*UP*GP*UP*C)-3')

Chain Q: 



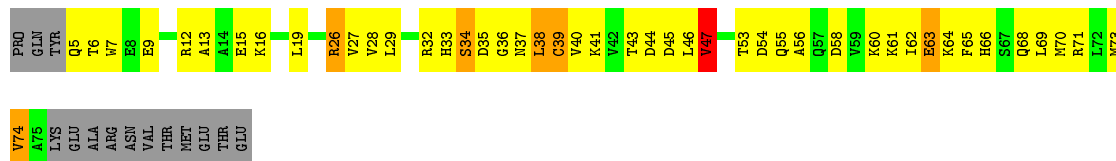
- Molecule 8: RNA (5'-R(P*AP*UP*CP*GP*CP*GP*CP*CP*UP*GP*UP*G)-3')

Chain R: 



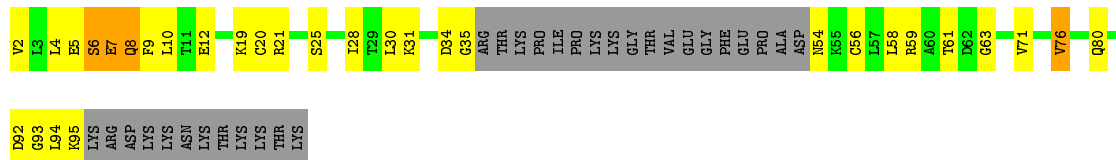
- Molecule 9: PROTEIN (Signal recognition particle 9 kDa protein)

Chain C: 



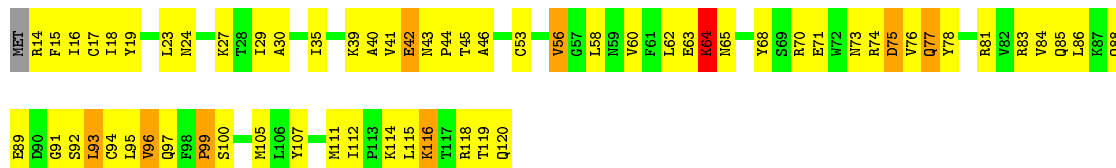
- Molecule 10: PROTEIN (Signal recognition particle 14 kDa protein)

Chain D: 

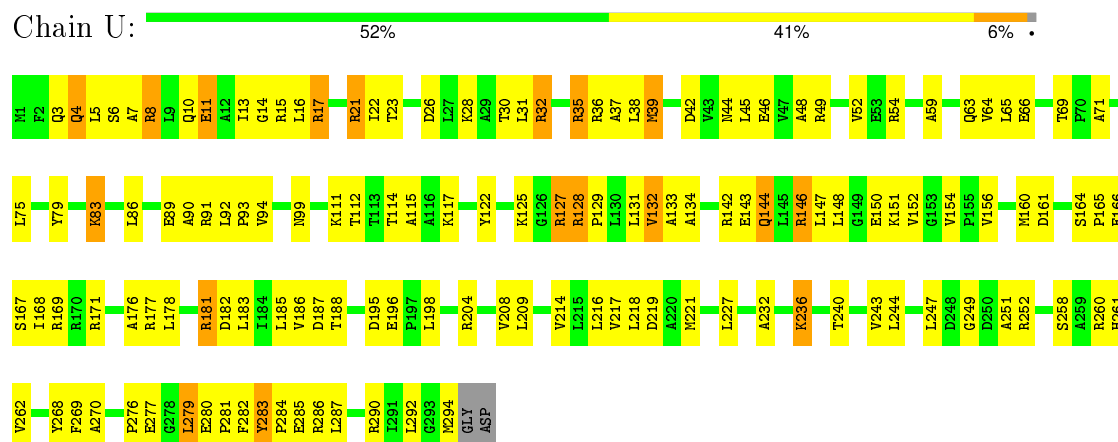


- Molecule 11: PROTEIN (Signal recognition particle 19 kDa protein)

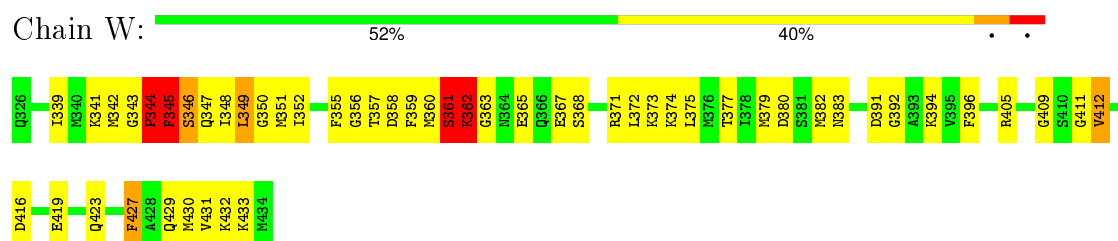
Chain B: 



- Molecule 12: Signal recognition particle protein



- Molecule 13: Signal recognition particle 54 kDa protein



- Molecule 14: Rhodopsin



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	160	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1000	Depositor
Minimum defocus (nm)	10000	Depositor
Maximum defocus (nm)	45000	Depositor
Magnification	51000	Depositor
Image detector	KODAK SO163 FILM	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: CCC

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	E	0.57	0/1173	0.81	3/1829 (0.2%)
10	D	0.39	0/608	0.66	0/809
11	B	0.46	0/884	0.69	0/1188
12	U	0.27	0/2291	0.50	0/3086
13	W	0.95	2/876 (0.2%)	1.26	8/1165 (0.7%)
14	S	0.55	0/154	0.72	0/208
2	A	0.45	0/3055	0.70	0/4766
3	M	1.23	2/651 (0.3%)	2.01	12/1005 (1.2%)
4	N	2.23	4/721 (0.6%)	2.65	18/1116 (1.6%)
5	O	0.85	0/567	2.75	6/877 (0.7%)
6	P	0.91	0/446	2.33	5/689 (0.7%)
7	Q	2.50	2/284 (0.7%)	3.20	10/436 (2.3%)
8	R	1.31	1/282 (0.4%)	2.53	9/437 (2.1%)
9	C	0.42	0/589	0.66	0/791
All	All	0.89	11/12581 (0.1%)	1.42	71/18402 (0.4%)

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
13	W	0	5
2	A	0	3
All	All	0	8

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	N	288	G	O3'-P	40.60	2.09	1.61
7	Q	110	U	O3'-P	38.67	2.07	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	N	292	C	O3'-P	34.73	2.02	1.61
3	M	74	G	O3'-P	19.79	1.84	1.61
13	W	345	PHE	C-N	-18.39	0.91	1.34
13	W	362	LYS	C-N	17.62	1.64	1.33
8	R	248	U	O3'-P	16.92	1.81	1.61
4	N	275	U	O3'-P	11.13	1.74	1.61
7	Q	103	U	O3'-P	-8.78	1.50	1.61
3	M	56	A	O3'-P	8.32	1.71	1.61
4	N	287	A	O3'-P	-6.69	1.53	1.61

All (71) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	O	92	C	P-O3'-C3'	-65.35	41.28	119.70
4	N	280	C	P-O3'-C3'	-57.26	50.99	119.70
6	P	252	A	P-O3'-C3'	-45.34	65.29	119.70
7	Q	101	G	P-O3'-C3'	-40.29	71.36	119.70
3	M	69	U	O3'-P-O5'	-36.27	35.09	104.00
4	N	275	U	P-O3'-C3'	29.56	155.18	119.70
13	W	362	LYS	C-N-CA	-28.46	62.53	122.30
7	Q	100	C	O3'-P-O5'	28.42	157.99	104.00
7	Q	103	U	O3'-P-O5'	-28.02	50.76	104.00
5	O	83	G	O3'-P-O5'	27.17	155.62	104.00
4	N	277	C	O3'-P-O5'	26.69	154.72	104.00
8	R	248	U	O3'-P-O5'	-26.14	54.33	104.00
6	P	265	C	P-O3'-C3'	-23.34	91.69	119.70
4	N	289	A	O3'-P-O5'	23.21	148.11	104.00
3	M	65	U	P-O3'-C3'	-22.81	92.32	119.70
8	R	248	U	OP1-P-O3'	20.52	150.35	105.20
6	P	264	A	O3'-P-O5'	-20.28	65.47	104.00
8	R	243	G	P-O3'-C3'	18.19	141.53	119.70
5	O	84	C	P-O3'-C3'	-18.09	97.99	119.70
7	Q	110	U	P-O3'-C3'	17.56	140.77	119.70
8	R	250	U	O3'-P-O5'	16.96	136.22	104.00
3	M	59	A	P-O3'-C3'	16.54	139.55	119.70
3	M	57	G	P-O3'-C3'	-15.41	101.21	119.70
8	R	240	A	O3'-P-O5'	-15.27	74.98	104.00
3	M	56	A	O3'-P-O5'	15.12	132.74	104.00
8	R	248	U	P-O3'-C3'	14.34	136.91	119.70
4	N	278	A	O3'-P-O5'	-12.95	79.40	104.00
4	N	274	G	O3'-P-O5'	-11.98	81.25	104.00
7	Q	100	C	OP2-P-O3'	-11.72	79.42	105.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	W	362	LYS	O-C-N	11.68	143.05	123.20
13	W	345	PHE	C-N-CA	11.64	150.81	121.70
13	W	361	SER	CA-C-N	-11.56	91.77	117.20
4	N	288	G	P-O3'-C3'	-11.41	106.00	119.70
5	O	83	G	OP2-P-O3'	-11.23	80.49	105.20
4	N	277	C	OP2-P-O3'	-11.06	80.87	105.20
4	N	288	G	O3'-P-O5'	-10.90	83.29	104.00
3	M	58	G	O3'-P-O5'	-10.66	83.75	104.00
13	W	362	LYS	CA-C-N	-10.53	95.13	116.20
7	Q	100	C	OP1-P-O3'	-10.50	82.11	105.20
5	O	83	G	OP1-P-O3'	-9.85	83.52	105.20
4	N	277	C	OP1-P-O3'	-9.70	83.86	105.20
4	N	287	A	O3'-P-O5'	9.66	122.35	104.00
4	N	289	A	OP2-P-O3'	-9.61	84.07	105.20
5	O	91	G	O3'-P-O5'	9.31	121.70	104.00
7	Q	103	U	OP1-P-O3'	9.18	125.39	105.20
13	W	361	SER	O-C-N	9.15	137.35	122.70
6	P	264	A	OP1-P-O3'	8.83	124.62	105.20
7	Q	110	U	O3'-P-O5'	-8.58	87.69	104.00
3	M	69	U	OP1-P-O3'	8.19	123.22	105.20
8	R	240	A	OP1-P-O3'	8.00	122.80	105.20
3	M	74	G	P-O3'-C3'	-7.97	110.14	119.70
4	N	289	A	OP1-P-O3'	-7.90	87.82	105.20
4	N	278	A	OP1-P-O3'	7.44	121.58	105.20
4	N	274	G	OP1-P-O3'	7.27	121.19	105.20
4	N	277	C	P-O3'-C3'	7.27	128.42	119.70
8	R	250	U	OP2-P-O3'	-6.99	89.81	105.20
4	N	288	G	OP2-P-O3'	6.92	120.42	105.20
3	M	58	G	OP1-P-O3'	6.87	120.32	105.20
3	M	74	G	OP1-P-O3'	6.65	119.84	105.20
13	W	361	SER	C-N-CA	-6.54	105.36	121.70
13	W	344	PRO	O-C-N	-6.54	112.25	122.70
3	M	56	A	OP2-P-O3'	-6.31	91.32	105.20
7	Q	110	U	OP2-P-O3'	6.25	118.96	105.20
7	Q	103	U	OP2-P-O3'	6.21	118.86	105.20
3	M	69	U	OP2-P-O3'	6.01	118.42	105.20
1	E	138	U	N1-C1'-C2'	5.71	121.42	114.00
6	P	264	A	OP2-P-O3'	5.45	117.18	105.20
4	N	298	C	O3'-P-O5'	5.41	114.28	104.00
1	E	137	C	C2'-C3'-O3'	5.36	122.27	113.70
1	E	132	A	C5'-C4'-C3'	-5.26	107.58	116.00
8	R	248	U	OP2-P-O3'	-5.16	93.85	105.20

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	197	G	Sidechain
2	A	201	A	Sidechain
2	A	208	A	Sidechain
13	W	344	PRO	Mainchain,Peptide
13	W	361	SER	Mainchain,Peptide
13	W	362	LYS	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	1051	0	528	84	0
2	A	2751	0	1387	96	0
3	M	585	0	289	99	0
4	N	649	0	330	150	0
5	O	511	0	258	25	0
6	P	401	0	208	108	0
7	Q	257	0	129	83	0
8	R	254	0	128	75	0
9	C	580	0	594	85	0
10	D	604	0	638	34	0
11	B	870	0	901	80	0
12	U	2266	0	2367	226	0
13	W	865	0	865	233	0
14	S	150	0	158	64	0
All	All	11794	0	8780	1071	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 52.

All (1071) 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)
6:P:252:A:C2	8:R:250:U:H2'	1.25	1.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:U:281:PRO:CB	13:W:347:GLN:HG3	1.15	1.61
4:N:274:G:H2'	4:N:275:U:C5	1.11	1.59
12:U:283:TYR:CZ	13:W:360:MET:HE2	1.34	1.58
12:U:283:TYR:CE1	13:W:360:MET:HB2	1.05	1.56
7:Q:104:C:H1'	7:Q:105:G:C8	1.36	1.56
4:N:274:G:C2'	4:N:275:U:C5	1.89	1.54
12:U:283:TYR:HE1	13:W:360:MET:CB	1.19	1.50
13:W:339:ILE:HD11	14:S:54:ILE:CG2	1.36	1.50
6:P:252:A:H5'	7:Q:102:A:N7	1.25	1.49
6:P:263:C:H3'	6:P:265:C:N4	1.21	1.48
6:P:252:A:N3	8:R:250:U:C2	1.80	1.46
4:N:290:C:C2'	4:N:291:C:H5'	1.46	1.46
6:P:252:A:C2	8:R:250:U:C2'	1.95	1.45
13:W:339:ILE:CD1	14:S:54:ILE:CG2	1.91	1.45
12:U:286:ARG:NH2	13:W:360:MET:HB3	1.15	1.44
12:U:283:TYR:OH	13:W:359:PHE:CD2	1.68	1.44
6:P:252:A:N1	8:R:250:U:C2'	1.82	1.43
6:P:252:A:C4	8:R:250:U:C2	2.08	1.41
6:P:252:A:C2	8:R:250:U:C2	2.09	1.39
12:U:281:PRO:HB3	13:W:347:GLN:CG	0.93	1.39
6:P:263:C:C3'	6:P:265:C:H41	1.31	1.39
6:P:264:A:O5'	6:P:265:C:C5	1.75	1.37
12:U:286:ARG:HH21	13:W:360:MET:CB	1.38	1.37
6:P:264:A:O5'	6:P:265:C:H5	1.04	1.36
7:Q:104:C:O2	7:Q:105:G:N7	1.59	1.36
12:U:285:GLU:CD	13:W:359:PHE:HB2	1.44	1.36
4:N:281:A:C8	4:N:281:A:OP2	1.78	1.36
3:M:56:A:C8	9:C:45:ASP:O	1.80	1.35
1:E:105:G:C4'	4:N:290:C:H1'	1.57	1.34
4:N:290:C:H2'	4:N:291:C:C5'	1.57	1.34
1:E:123:U:C2'	3:M:57:G:O2'	1.68	1.34
6:P:252:A:N1	8:R:250:U:H2'	1.04	1.34
12:U:285:GLU:CB	13:W:359:PHE:H	1.41	1.33
6:P:257:C:O3'	6:P:258:C:H5'	1.22	1.30
7:Q:104:C:C1'	7:Q:105:G:C8	2.13	1.30
12:U:283:TYR:CE1	13:W:360:MET:CE	2.15	1.29
6:P:252:A:C5'	7:Q:102:A:N7	1.95	1.28
13:W:423:GLN:NE2	14:S:65:HIS:NE2	1.82	1.28
13:W:372:LEU:HD11	14:S:58:THR:CG2	1.62	1.28
1:E:124:G:P	3:M:57:G:H4'	1.73	1.27
7:Q:104:C:O2'	7:Q:105:G:H8	1.08	1.27

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:124:G:P	3:M:57:G:C4'	2.22	1.27
8:R:250:U:C5'	8:R:251:G:OP2	1.80	1.27
13:W:339:ILE:CD1	14:S:54:ILE:HG23	1.58	1.26
8:R:250:U:H5''	8:R:251:G:OP2	1.13	1.26
1:E:101:G:O2'	3:M:49:A:OP2	1.53	1.24
4:N:288:G:O4'	4:N:288:G:OP2	1.55	1.23
12:U:283:TYR:OH	13:W:360:MET:HE2	1.38	1.23
12:U:283:TYR:CZ	13:W:360:MET:CE	2.21	1.22
13:W:343:GLY:O	13:W:346:SER:HB2	1.05	1.22
6:P:264:A:P	6:P:265:C:C5	2.32	1.22
4:N:271:C:H5'	6:P:270:G:C3'	1.70	1.22
2:A:112:G:N3	7:Q:111:C:O2	1.72	1.22
13:W:423:GLN:HE22	14:S:65:HIS:CD2	1.55	1.22
7:Q:103:U:H3'	7:Q:104:C:C5	1.74	1.21
6:P:252:A:C5	8:R:250:U:O2	1.91	1.21
12:U:281:PRO:HB3	13:W:347:GLN:CB	1.70	1.21
1:E:123:U:H2'	3:M:57:G:O2'	1.24	1.21
13:W:419:GLU:HB3	14:S:65:HIS:CE1	1.76	1.20
7:Q:104:C:C6	7:Q:104:C:OP2	1.94	1.20
6:P:252:A:C4	8:R:250:U:N3	2.10	1.20
13:W:372:LEU:CG	14:S:58:THR:HG23	1.72	1.20
12:U:283:TYR:CE1	13:W:360:MET:HE2	1.74	1.19
13:W:361:SER:O	13:W:362:LYS:HG3	1.43	1.18
4:N:298:C:H5''	4:N:299:U:OP1	1.43	1.18
3:M:57:G:C5'	3:M:58:G:OP1	1.90	1.18
4:N:299:U:C2'	4:N:300:U:O5'	1.92	1.18
12:U:283:TYR:CE1	13:W:360:MET:CB	2.02	1.17
7:Q:104:C:C2'	7:Q:105:G:H8	1.58	1.17
12:U:286:ARG:HH21	13:W:360:MET:CA	1.56	1.16
3:M:57:G:H5''	3:M:58:G:OP1	1.01	1.16
1:E:105:G:H4'	4:N:290:C:C1'	1.74	1.16
12:U:286:ARG:NH2	13:W:360:MET:CB	1.97	1.16
4:N:292:C:O3'	4:N:293:C:P	2.02	1.16
13:W:372:LEU:CD1	14:S:58:THR:HG23	1.76	1.15
6:P:252:A:C2	8:R:250:U:N1	2.13	1.15
1:E:125:U:O2'	4:N:292:C:H4'	1.48	1.14
12:U:283:TYR:CE2	13:W:350:GLY:HA2	1.79	1.14
13:W:427:PHE:CD1	14:S:57:LEU:HD21	1.82	1.14
12:U:285:GLU:CD	13:W:359:PHE:CB	2.16	1.14
6:P:264:A:C8	6:P:265:C:C5	2.35	1.14
6:P:264:A:H8	6:P:265:C:C5	1.65	1.13

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:P:252:A:C6	8:R:250:U:O2	2.01	1.13
7:Q:110:U:O3'	7:Q:111:C:P	2.07	1.13
6:P:252:A:H1'	8:R:250:U:C4	1.84	1.12
12:U:285:GLU:HB3	13:W:359:PHE:N	1.64	1.11
12:U:285:GLU:CG	13:W:359:PHE:HB2	1.81	1.11
4:N:274:G:N3	4:N:275:U:O4	1.82	1.11
13:W:343:GLY:O	13:W:346:SER:CB	1.97	1.11
13:W:339:ILE:HD13	14:S:54:ILE:HG22	1.31	1.11
4:N:280:C:O2	4:N:281:A:C5'	1.99	1.11
6:P:252:A:O5'	7:Q:102:A:C5	2.04	1.10
6:P:257:C:O3'	6:P:258:C:C5'	1.98	1.10
12:U:281:PRO:CB	13:W:347:GLN:CG	1.90	1.10
4:N:299:U:O2'	4:N:300:U:O5'	1.67	1.10
5:O:98:G:H4'	5:O:99:C:OP1	1.30	1.09
6:P:264:A:C8	6:P:265:C:C6	2.41	1.09
4:N:288:G:O3'	4:N:289:A:P	2.09	1.08
7:Q:104:C:O2'	7:Q:105:G:O5'	1.71	1.08
4:N:271:C:H5'	6:P:270:G:H3'	1.29	1.08
13:W:374:LYS:NZ	14:S:67:LYS:HB3	1.69	1.08
4:N:301:U:C3'	4:N:301:U:OP2	2.00	1.08
6:P:252:A:C5'	7:Q:102:A:C5	2.28	1.07
13:W:427:PHE:CE1	14:S:57:LEU:CD2	2.37	1.07
7:Q:104:C:H3'	7:Q:104:C:P	1.94	1.07
7:Q:104:C:H3'	7:Q:104:C:OP2	1.54	1.06
12:U:285:GLU:HB3	13:W:359:PHE:H	1.17	1.06
3:M:57:G:OP2	9:C:43:THR:HG21	1.53	1.06
6:P:252:A:C4	8:R:250:U:O2	2.03	1.06
12:U:285:GLU:CB	13:W:359:PHE:N	2.18	1.05
1:E:123:U:O3'	3:M:57:G:H4'	1.52	1.05
12:U:285:GLU:CG	13:W:359:PHE:CB	2.32	1.05
13:W:372:LEU:CD1	14:S:58:THR:CG2	2.32	1.05
4:N:301:U:P	4:N:301:U:C3'	2.45	1.05
13:W:423:GLN:CD	14:S:65:HIS:NE2	2.10	1.05
12:U:89:GLU:HB3	13:W:351:MET:C	1.75	1.05
6:P:252:A:P	7:Q:102:A:C8	2.51	1.04
4:N:280:C:C2	4:N:281:A:H5'	1.90	1.04
4:N:280:C:O2	4:N:281:A:H5''	1.54	1.03
6:P:252:A:C2	8:R:250:U:C1'	2.40	1.03
12:U:281:PRO:CB	13:W:347:GLN:CB	2.34	1.03
6:P:265:C:O2'	6:P:266:U:O5'	1.66	1.03
6:P:252:A:H1'	8:R:250:U:O4	1.56	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:W:339:ILE:HD13	14:S:54:ILE:CG2	1.86	1.02
6:P:264:A:OP2	6:P:265:C:C4	2.11	1.02
12:U:283:TYR:CE1	13:W:360:MET:HE3	1.90	1.02
12:U:283:TYR:CE1	13:W:359:PHE:O	2.13	1.02
6:P:265:C:HO2'	6:P:266:U:H6	1.02	1.02
6:P:264:A:OP2	6:P:265:C:C5	2.11	1.02
1:E:105:G:H4'	4:N:290:C:H1'	1.02	1.02
12:U:285:GLU:CB	13:W:359:PHE:HB3	1.90	1.02
9:C:38:LEU:HD12	9:C:39:CYS:H	1.17	1.02
8:R:242:C:H5'	8:R:243:G:OP2	1.61	1.01
4:N:280:C:C2	4:N:281:A:C5'	2.43	1.01
6:P:252:A:N3	8:R:250:U:N3	2.04	1.01
2:A:112:G:C2	7:Q:111:C:O2	2.12	1.01
7:Q:104:C:C2'	7:Q:105:G:C8	2.38	1.01
12:U:283:TYR:CZ	13:W:359:PHE:O	2.13	1.00
4:N:271:C:C5'	6:P:270:G:O3'	2.09	1.00
4:N:281:A:H3'	4:N:281:A:OP2	1.62	1.00
13:W:372:LEU:HD11	14:S:58:THR:HG21	1.39	1.00
12:U:91:ARG:HG2	13:W:351:MET:HB3	1.42	1.00
7:Q:104:C:O3'	7:Q:105:G:P	2.20	0.99
13:W:339:ILE:CD1	14:S:54:ILE:HG22	1.80	0.99
9:C:28:VAL:HG22	9:C:41:LYS:HB3	1.44	0.99
12:U:125:LYS:HE3	13:W:344:PRO:CB	1.91	0.99
12:U:125:LYS:CE	13:W:344:PRO:HB3	1.91	0.99
12:U:283:TYR:OH	13:W:359:PHE:CE2	2.09	0.99
12:U:285:GLU:HG2	13:W:359:PHE:N	1.77	0.99
12:U:285:GLU:CG	13:W:359:PHE:H	1.76	0.98
6:P:264:A:P	6:P:265:C:H5	1.76	0.98
7:Q:103:U:H3'	7:Q:104:C:C6	1.99	0.98
1:E:124:G:OP1	3:M:57:G:C4'	2.10	0.98
6:P:264:A:H3'	6:P:265:C:H6	1.24	0.97
13:W:372:LEU:HD11	14:S:58:THR:HG23	1.30	0.97
13:W:371:ARG:NH2	14:S:63:VAL:HA	1.37	0.96
13:W:372:LEU:CD2	14:S:58:THR:HG23	1.95	0.96
2:A:220:C:H2'	2:A:221:C:H5''	1.45	0.96
8:R:240:A:O3'	8:R:242:C:H5''	1.64	0.95
6:P:252:A:H5'	7:Q:102:A:C5	1.98	0.95
2:A:112:G:C4	7:Q:111:C:O2	2.20	0.95
12:U:285:GLU:HB3	13:W:359:PHE:CA	1.95	0.95
3:M:55:G:H5''	9:C:46:LEU:HD11	1.48	0.95
1:E:124:G:OP1	3:M:57:G:H4'	1.67	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:N:278:A:H2'	4:N:279:A:H5''	1.48	0.94
3:M:55:G:O3'	3:M:56:A:OP1	1.85	0.94
9:C:55:GLN:HA	10:D:95:LYS:HB2	1.49	0.94
4:N:274:G:C2'	4:N:275:U:H5	1.45	0.94
4:N:299:U:H2'	4:N:300:U:O5'	1.68	0.94
6:P:252:A:H2	8:R:250:U:C2'	1.62	0.94
13:W:374:LYS:NZ	14:S:67:LYS:CB	2.27	0.94
12:U:285:GLU:CB	13:W:359:PHE:CB	2.46	0.93
13:W:427:PHE:CE1	14:S:57:LEU:HD21	2.01	0.93
4:N:271:C:H4'	6:P:270:G:O3'	1.67	0.93
12:U:281:PRO:CG	13:W:347:GLN:HB2	1.98	0.93
7:Q:103:U:H3'	7:Q:104:C:H5	1.33	0.93
4:N:281:A:H8	4:N:281:A:OP2	1.36	0.93
11:B:60:VAL:HG23	11:B:83:ARG:O	1.67	0.93
4:N:271:C:C5'	6:P:270:G:C3'	2.46	0.93
8:R:250:U:C4'	8:R:251:G:OP2	2.11	0.93
13:W:427:PHE:CE1	14:S:57:LEU:HD23	2.03	0.93
4:N:274:G:O2'	4:N:275:U:C5	2.20	0.92
1:E:123:U:C2'	3:M:57:G:C2'	2.42	0.92
12:U:89:GLU:HB3	13:W:352:ILE:N	1.52	0.92
13:W:423:GLN:NE2	14:S:65:HIS:CD2	2.28	0.92
12:U:283:TYR:CE2	13:W:350:GLY:CA	2.51	0.92
12:U:281:PRO:CA	13:W:347:GLN:HG3	1.99	0.91
12:U:89:GLU:CB	13:W:352:ILE:N	2.28	0.91
13:W:367:GLU:O	14:S:62:THR:HG21	1.71	0.91
3:M:57:G:P	9:C:26:ARG:NH2	2.44	0.91
2:A:112:G:C2	7:Q:111:C:C2	2.58	0.91
8:R:242:C:H5'	8:R:244:C:H5'	1.53	0.91
12:U:286:ARG:HH22	13:W:360:MET:HB3	1.34	0.90
12:U:125:LYS:HE3	13:W:344:PRO:HB3	0.96	0.90
7:Q:103:U:C3'	7:Q:104:C:C5	2.54	0.90
7:Q:104:C:C3'	7:Q:104:C:OP2	2.18	0.90
6:P:257:C:HO3'	6:P:258:C:H5'	1.10	0.90
12:U:281:PRO:HB3	13:W:347:GLN:CD	1.92	0.89
11:B:64:LYS:HD3	11:B:64:LYS:N	1.88	0.89
2:A:127:A:C2'	2:A:128:U:H5''	2.02	0.89
10:D:61:THR:HG22	10:D:63:GLY:H	1.36	0.89
7:Q:103:U:C3'	7:Q:104:C:C6	2.55	0.89
12:U:285:GLU:CG	13:W:359:PHE:N	2.33	0.89
12:U:89:GLU:CB	13:W:351:MET:C	2.40	0.89
4:N:281:A:C3'	4:N:281:A:OP2	2.21	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:N:280:C:O2	4:N:281:A:H5'	1.68	0.89
12:U:92:LEU:HD12	13:W:348:ILE:N	1.85	0.88
6:P:252:A:C2	8:R:250:U:O2	2.26	0.88
13:W:372:LEU:HD21	14:S:58:THR:HG23	1.55	0.88
4:N:298:C:C5'	4:N:299:U:OP1	2.22	0.88
4:N:299:U:O2'	4:N:300:U:C5'	2.21	0.88
11:B:94:CYS:O	11:B:95:LEU:HD23	1.74	0.88
7:Q:100:C:O2'	7:Q:101:G:P	2.31	0.88
4:N:274:G:C2'	4:N:275:U:C6	2.51	0.88
12:U:283:TYR:CD1	13:W:360:MET:HB2	2.04	0.87
4:N:281:A:P	4:N:281:A:C8	2.67	0.87
5:O:83:G:H1	6:P:266:U:H3	1.22	0.87
12:U:89:GLU:OE1	13:W:352:ILE:HG22	1.73	0.87
6:P:264:A:H5''	6:P:265:C:OP2	1.73	0.87
5:O:84:C:H2'	5:O:86:G:OP2	1.74	0.87
13:W:419:GLU:HB3	14:S:65:HIS:HE1	1.23	0.87
4:N:271:C:C5'	6:P:270:G:H3'	2.04	0.87
2:A:127:A:H2'	2:A:128:U:H5''	1.57	0.87
12:U:268:TYR:O	13:W:347:GLN:NE2	2.06	0.87
3:M:51:G:H1	4:N:295:U:H3	1.22	0.87
3:M:69:U:H3	4:N:276:G:H1	1.22	0.86
5:O:84:C:C2'	5:O:86:G:OP2	2.24	0.86
1:E:122:C:O2	3:M:58:G:N7	2.05	0.86
9:C:5:GLN:HG3	9:C:6:THR:H	1.40	0.86
4:N:282:U:H4'	4:N:282:U:OP2	1.73	0.86
13:W:372:LEU:CG	14:S:58:THR:CG2	2.53	0.86
12:U:90:ALA:N	13:W:350:GLY:O	1.91	0.85
13:W:427:PHE:CD1	14:S:57:LEU:CD2	2.57	0.85
9:C:38:LEU:HD12	9:C:39:CYS:N	1.91	0.85
4:N:271:C:C4'	6:P:270:G:O3'	2.24	0.85
3:M:59:A:O2'	3:M:60:U:C5	2.30	0.85
3:M:55:G:H5''	9:C:46:LEU:CD1	2.06	0.85
4:N:280:C:O2'	4:N:281:A:H3'	1.77	0.85
2:A:184:A:N3	13:W:405:ARG:NH1	2.24	0.85
7:Q:105:G:H1	8:R:248:U:H3	1.22	0.85
13:W:375:LEU:HD11	14:S:61:VAL:HG11	1.57	0.85
4:N:288:G:HO3'	4:N:289:A:P	1.95	0.85
8:R:241:U:O2'	8:R:245:G:H5'	1.76	0.84
7:Q:103:U:H3	8:R:249:G:H1	1.22	0.84
12:U:285:GLU:OE1	13:W:359:PHE:HB2	1.76	0.84
4:N:278:A:O2'	4:N:279:A:P	2.35	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:O:87:U:H3	6:P:262:G:H1	1.22	0.84
12:U:132:VAL:HG13	12:U:186:VAL:HA	1.59	0.84
7:Q:103:U:C5	7:Q:104:C:N4	2.46	0.83
11:B:24:ASN:HD22	11:B:27:LYS:HG3	1.42	0.83
7:Q:104:C:H1'	7:Q:105:G:N7	1.94	0.83
12:U:16:LEU:HD22	12:U:22:ILE:HD12	1.61	0.83
12:U:285:GLU:HB3	13:W:359:PHE:CB	2.06	0.83
7:Q:108:U:H3	8:R:245:G:H1	1.22	0.83
12:U:89:GLU:HB3	13:W:351:MET:O	1.77	0.83
7:Q:109:G:H3'	7:Q:110:U:P	2.18	0.82
3:M:57:G:P	9:C:26:ARG:HH22	2.01	0.82
4:N:274:G:C2	4:N:275:U:O4	2.32	0.82
1:E:127:G:O6	4:N:293:C:P	2.37	0.82
4:N:278:A:O2'	4:N:279:A:O5'	1.96	0.82
12:U:89:GLU:CB	13:W:351:MET:O	2.28	0.82
13:W:419:GLU:OE2	14:S:65:HIS:ND1	2.13	0.81
4:N:278:A:C2'	4:N:279:A:C5'	2.59	0.81
13:W:339:ILE:HD11	14:S:54:ILE:HG23	0.81	0.81
6:P:264:A:O5'	6:P:265:C:C6	2.33	0.81
13:W:339:ILE:HD11	14:S:54:ILE:HG21	1.58	0.81
4:N:288:G:O2'	4:N:289:A:OP2	1.99	0.81
10:D:4:LEU:HD22	10:D:8:GLN:HG2	1.60	0.81
2:A:112:G:C4	7:Q:111:C:C2	2.69	0.81
4:N:278:A:C2'	4:N:279:A:H5''	2.10	0.81
1:E:123:U:O3'	3:M:57:G:C4'	2.25	0.81
11:B:14:ARG:HB3	11:B:14:ARG:NH1	1.96	0.80
6:P:252:A:H1'	8:R:250:U:N3	1.97	0.80
12:U:285:GLU:HB3	13:W:359:PHE:HB3	1.63	0.80
13:W:361:SER:O	13:W:362:LYS:CG	2.27	0.80
13:W:344:PRO:C	13:W:346:SER:N	2.34	0.80
12:U:92:LEU:HD12	13:W:348:ILE:H	1.45	0.80
5:O:98:G:C4'	5:O:99:C:OP1	2.22	0.80
4:N:289:A:O4'	4:N:289:A:OP1	2.00	0.80
8:R:241:U:P	8:R:242:C:H5''	2.22	0.80
3:M:56:A:N9	9:C:45:ASP:O	2.13	0.79
4:N:279:A:H4'	4:N:280:C:OP2	1.82	0.79
7:Q:100:C:O2'	7:Q:101:G:H5'	1.82	0.79
12:U:281:PRO:HB2	13:W:347:GLN:HG3	1.56	0.79
12:U:283:TYR:CZ	13:W:359:PHE:CD2	2.69	0.79
1:E:104:G:N2	3:M:57:G:N2	2.29	0.79
12:U:283:TYR:OH	13:W:359:PHE:CG	2.34	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:U:285:GLU:OE1	13:W:355:PHE:C	2.21	0.79
5:O:84:C:N3	5:O:86:G:OP1	2.06	0.79
3:M:57:G:H5''	3:M:58:G:P	2.22	0.79
4:N:278:A:C3'	4:N:279:A:C5'	2.59	0.79
6:P:252:A:N9	8:R:250:U:N3	2.31	0.78
4:N:278:A:C2'	4:N:279:A:O5'	2.32	0.78
8:R:240:A:C5	8:R:242:C:N3	2.43	0.78
4:N:277:C:H4'	4:N:278:A:OP2	1.83	0.78
2:A:220:C:C2'	2:A:221:C:H5''	2.14	0.78
4:N:288:G:C2'	4:N:289:A:P	2.72	0.77
9:C:70:MET:HB2	10:D:30:LEU:HD21	1.65	0.77
14:S:52:PHE:HB3	14:S:53:PRO:HD3	1.65	0.77
12:U:6:SER:O	12:U:10:GLN:HG2	1.84	0.77
1:E:122:C:C6	3:M:58:G:O6	2.22	0.77
8:R:242:C:H5'	8:R:244:C:C5'	2.14	0.77
13:W:344:PRO:O	13:W:346:SER:N	2.18	0.77
7:Q:103:U:H2'	7:Q:104:C:C6	2.20	0.77
7:Q:104:C:N1	7:Q:104:C:OP2	2.17	0.77
4:N:288:G:N3	4:N:288:G:H2'	2.00	0.77
6:P:263:C:H3'	6:P:265:C:C4	2.16	0.77
6:P:252:A:N1	8:R:250:U:O2	2.18	0.76
3:M:70:C:O2'	3:M:71:C:C5	2.39	0.76
3:M:56:A:O2'	3:M:57:G:P	2.44	0.76
6:P:264:A:H3'	6:P:265:C:C6	2.15	0.76
3:M:70:C:O2'	3:M:71:C:H5	1.66	0.76
12:U:290:ARG:HD2	13:W:362:LYS:H	1.50	0.76
12:U:91:ARG:CG	13:W:351:MET:HB3	2.13	0.76
3:M:59:A:O2'	3:M:60:U:H5	1.68	0.76
12:U:285:GLU:OE1	13:W:355:PHE:CB	2.34	0.76
6:P:265:C:O2'	6:P:266:U:C5'	2.33	0.76
3:M:55:G:O3'	9:C:46:LEU:HG	1.86	0.76
9:C:53:THR:HG21	9:C:58:ASP:HB2	1.67	0.76
12:U:79:TYR:HE1	13:W:358:ASP:CG	1.90	0.75
12:U:290:ARG:HG3	13:W:361:SER:HB3	1.66	0.75
12:U:42:ASP:HB2	12:U:252:ARG:HH11	1.49	0.75
2:A:175:G:H3'	2:A:176:A:H5'	1.68	0.75
4:N:278:A:H2'	4:N:279:A:C5'	2.16	0.75
4:N:282:U:C4'	4:N:282:U:OP2	2.33	0.75
12:U:283:TYR:CD2	13:W:350:GLY:HA3	2.22	0.75
4:N:290:C:H2'	4:N:291:C:H5'	0.77	0.75
13:W:371:ARG:NH1	14:S:63:VAL:C	2.37	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:W:339:ILE:CD1	14:S:54:ILE:HG21	2.14	0.75
9:C:56:ALA:HB2	10:D:95:LYS:O	1.87	0.75
6:P:264:A:C8	6:P:265:C:C4	2.74	0.75
3:M:57:G:OP1	9:C:26:ARG:NH2	2.18	0.75
1:E:124:G:O4'	3:M:57:G:H2'	1.86	0.75
3:M:57:G:OP2	9:C:43:THR:CG2	2.34	0.75
12:U:31:LEU:HD22	12:U:52:VAL:HG23	1.67	0.75
1:E:124:G:OP1	3:M:57:G:O4'	2.04	0.74
7:Q:109:G:O3'	7:Q:110:U:P	2.44	0.74
4:N:281:A:H2'	4:N:282:U:OP1	1.87	0.74
11:B:14:ARG:HB3	11:B:14:ARG:CZ	2.17	0.74
2:A:127:A:H2'	2:A:128:U:C5'	2.17	0.74
13:W:371:ARG:NH2	14:S:63:VAL:CA	2.29	0.74
7:Q:104:C:O2'	7:Q:105:G:C8	1.97	0.74
12:U:89:GLU:OE1	13:W:352:ILE:CG2	2.21	0.74
7:Q:104:C:C6	7:Q:104:C:P	2.81	0.73
4:N:282:U:H4'	4:N:283:A:OP2	1.87	0.73
3:M:69:U:H5''	3:M:70:C:OP2	1.88	0.73
3:M:55:G:O2'	3:M:56:A:O4'	2.05	0.73
12:U:32:ARG:O	12:U:36:ARG:HG3	1.88	0.73
4:N:282:U:H2'	4:N:283:A:C8	2.23	0.73
12:U:285:GLU:CA	13:W:359:PHE:H	2.02	0.73
13:W:375:LEU:HD11	14:S:61:VAL:CG1	2.19	0.73
3:M:57:G:O4'	9:C:26:ARG:NH2	2.21	0.73
4:N:290:C:H2'	4:N:291:C:C4'	2.18	0.73
4:N:288:G:H21	4:N:289:A:H5'	1.53	0.73
12:U:285:GLU:HG2	13:W:359:PHE:HB2	1.71	0.73
1:E:132:A:O2'	1:E:133:G:H8	1.72	0.73
13:W:372:LEU:CD1	14:S:58:THR:HG21	2.11	0.72
2:A:117:U:H3	2:A:234:A:H61	1.37	0.72
4:N:278:A:O2'	4:N:279:A:OP1	2.08	0.72
12:U:283:TYR:HE2	13:W:350:GLY:HA2	1.48	0.72
2:A:148:G:H4'	11:B:15:PHE:O	1.89	0.72
12:U:285:GLU:OE1	13:W:355:PHE:HB2	1.88	0.72
1:E:123:U:H4'	3:M:57:G:O3'	1.88	0.71
12:U:283:TYR:CD2	13:W:350:GLY:CA	2.73	0.71
4:N:281:A:N9	4:N:281:A:OP2	2.23	0.71
7:Q:103:U:C3'	7:Q:104:C:H6	2.03	0.71
8:R:241:U:O3'	8:R:244:C:H4'	1.89	0.71
3:M:58:G:H1'	4:N:280:C:N4	2.06	0.71
13:W:423:GLN:OE1	14:S:65:HIS:NE2	2.22	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:N:281:A:C2'	4:N:282:U:OP1	2.39	0.71
4:N:274:G:O2'	4:N:275:U:C6	2.38	0.71
8:R:240:A:C6	8:R:242:C:N3	2.59	0.70
13:W:372:LEU:HG	14:S:58:THR:HG23	1.71	0.70
7:Q:109:G:C3'	7:Q:110:U:P	2.79	0.70
12:U:14:GLY:HA2	12:U:17:ARG:HH21	1.56	0.70
9:C:28:VAL:CG2	9:C:41:LYS:HB3	2.19	0.70
7:Q:103:U:C2'	7:Q:104:C:C6	2.74	0.70
12:U:283:TYR:OH	13:W:360:MET:CE	2.28	0.70
2:A:151:C:OP1	2:A:204:G:H4'	1.90	0.70
1:E:129:C:OP1	10:D:2:VAL:HG23	1.92	0.70
13:W:371:ARG:HH12	14:S:63:VAL:C	1.94	0.70
12:U:283:TYR:HE1	13:W:360:MET:CG	2.01	0.70
8:R:242:C:C5'	8:R:244:C:H5'	2.21	0.69
3:M:67:A:O3'	3:M:68:G:P	2.50	0.69
6:P:252:A:C1'	8:R:250:U:N3	2.55	0.69
6:P:252:A:H2	8:R:250:U:C3'	2.03	0.69
11:B:73:ASN:ND2	11:B:75:ASP:H	1.89	0.69
12:U:285:GLU:OE1	13:W:355:PHE:O	2.10	0.69
5:O:92:C:OP2	5:O:93:G:H8	1.75	0.69
12:U:169:ARG:HG3	12:U:209:LEU:HD13	1.73	0.69
12:U:8:ARG:HG2	12:U:37:ALA:CB	2.23	0.69
6:P:252:A:O5'	7:Q:102:A:N7	2.16	0.69
13:W:374:LYS:HZ1	14:S:67:LYS:HB3	1.55	0.69
2:A:130:A:H2'	2:A:131:A:C8	2.26	0.69
4:N:282:U:O2	4:N:282:U:H2'	1.90	0.69
2:A:125:G:H1	2:A:225:C:H42	1.39	0.69
1:E:123:U:H4'	3:M:58:G:P	2.34	0.68
4:N:282:U:C2'	4:N:283:A:H8	1.95	0.68
8:R:241:U:O2'	8:R:244:C:O3'	2.11	0.68
9:C:15:GLU:O	9:C:19:LEU:HG	1.92	0.68
12:U:285:GLU:CD	13:W:359:PHE:HB3	2.13	0.68
12:U:89:GLU:CA	13:W:352:ILE:N	2.56	0.68
2:A:175:G:H1	2:A:221:C:H42	1.42	0.68
13:W:339:ILE:CG1	14:S:54:ILE:CG2	2.71	0.68
4:N:290:C:C2'	4:N:291:C:C5'	2.37	0.68
7:Q:110:U:O3'	7:Q:111:C:H5'	1.94	0.68
3:M:65:U:H4'	3:M:66:G:OP1	1.89	0.68
4:N:288:G:C3'	4:N:289:A:P	2.82	0.68
6:P:252:A:C1'	8:R:250:U:H3	2.08	0.67
12:U:35:ARG:HH21	12:U:49:ARG:HD2	1.58	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:154:G:O2'	2:A:155:G:H5'	1.93	0.67
11:B:93:LEU:N	11:B:93:LEU:HD23	2.08	0.67
7:Q:104:C:C2	7:Q:105:G:N7	2.57	0.67
1:E:122:C:P	9:C:32:ARG:HH21	2.17	0.67
4:N:282:U:C4'	4:N:283:A:OP2	2.42	0.67
6:P:264:A:OP2	6:P:265:C:N4	2.27	0.67
1:E:123:U:C4'	3:M:57:G:O3'	2.43	0.67
1:E:123:U:H5'	3:M:58:G:C8	2.30	0.67
11:B:15:PHE:CE1	11:B:85:GLN:HB2	2.30	0.67
8:R:248:U:H2'	8:R:249:G:C8	2.29	0.66
13:W:419:GLU:CB	14:S:65:HIS:HE1	2.06	0.66
3:M:66:G:H2'	3:M:67:A:OP2	1.96	0.66
2:A:127:A:O2'	2:A:128:U:H5''	1.93	0.66
2:A:215:A:O5'	2:A:215:A:H8	1.78	0.66
5:O:97:U:O3'	5:O:98:G:P	2.53	0.66
9:C:5:GLN:HG3	9:C:6:THR:N	2.09	0.66
13:W:361:SER:C	13:W:362:LYS:HG3	2.13	0.65
11:B:14:ARG:HG2	11:B:14:ARG:O	1.95	0.65
12:U:268:TYR:HD1	13:W:351:MET:HE3	1.60	0.65
12:U:286:ARG:O	13:W:361:SER:CB	2.44	0.65
6:P:265:C:O2'	6:P:266:U:H6	1.73	0.65
13:W:372:LEU:HG	14:S:58:THR:CG2	2.23	0.65
7:Q:103:U:C3'	7:Q:104:C:H5	2.03	0.65
2:A:157:A:H2'	2:A:158:C:C6	2.32	0.65
2:A:157:A:H2'	2:A:158:C:H6	1.62	0.65
12:U:131:LEU:HB2	12:U:156:VAL:HG22	1.79	0.65
12:U:17:ARG:N	12:U:71:ALA:HB2	2.12	0.65
1:E:123:U:H4'	3:M:58:G:O5'	1.97	0.65
13:W:349:LEU:HD22	13:W:359:PHE:HE2	1.62	0.65
1:E:126:A:N7	4:N:293:C:C5'	2.61	0.64
12:U:286:ARG:HB2	13:W:360:MET:O	1.97	0.64
1:E:123:U:O3'	3:M:57:G:C3'	2.45	0.64
7:Q:100:C:O2'	7:Q:101:G:C5'	2.44	0.64
8:R:241:U:OP2	8:R:242:C:H3'	1.98	0.64
11:B:88:GLN:HE21	11:B:92:SER:HB2	1.63	0.64
11:B:60:VAL:HG23	11:B:83:ARG:C	2.18	0.64
4:N:271:C:H5'	6:P:270:G:C5'	2.28	0.64
2:A:148:G:O2'	11:B:83:ARG:NH2	2.31	0.63
1:E:148:C:C5'	1:E:148:C:H6	2.11	0.63
2:A:139:A:H2'	2:A:140:C:H6	1.63	0.63
11:B:76:VAL:HG13	11:B:77:GLN:N	2.14	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:U:44:ASN:OD1	12:U:46:GLU:HB3	1.98	0.63
12:U:285:GLU:HG2	13:W:359:PHE:CB	2.24	0.63
13:W:341:LYS:O	13:W:345:PHE:CD1	2.52	0.63
12:U:260:ARG:HH21	12:U:261:HIS:HB2	1.63	0.63
10:D:76:VAL:O	10:D:80:GLN:HG3	1.99	0.63
13:W:419:GLU:CB	14:S:65:HIS:CE1	2.68	0.63
9:C:74:VAL:HG11	10:D:76:VAL:HG11	1.81	0.63
7:Q:104:C:H1'	7:Q:105:G:N9	2.08	0.63
12:U:112:THR:HG21	12:U:144:GLN:CD	2.18	0.63
4:N:282:U:H2'	4:N:283:A:H8	1.58	0.62
2:A:149:A:H4'	11:B:17:CYS:SG	2.39	0.62
12:U:281:PRO:HB2	13:W:347:GLN:HA	1.79	0.62
12:U:285:GLU:HB2	13:W:359:PHE:HB3	1.79	0.62
1:E:121:C:O2'	1:E:122:C:H5'	1.99	0.62
2:A:117:U:H3	2:A:234:A:N6	1.98	0.62
1:E:123:U:O3'	3:M:57:G:O3'	2.17	0.62
1:E:105:G:C5'	4:N:290:C:H1'	2.29	0.62
1:E:114:G:O2'	1:E:115:C:H5'	2.00	0.62
6:P:252:A:P	7:Q:102:A:N9	2.72	0.62
3:M:70:C:O3'	3:M:71:C:P	2.57	0.62
12:U:283:TYR:CD1	13:W:359:PHE:O	2.53	0.62
11:B:107:TYR:CZ	11:B:111:MET:HG3	2.35	0.62
1:E:105:G:O4'	4:N:290:C:H1'	2.00	0.61
4:N:288:G:O2'	4:N:289:A:P	2.58	0.61
4:N:278:A:C3'	4:N:279:A:H5''	2.30	0.61
12:U:285:GLU:C	13:W:359:PHE:N	2.52	0.61
1:E:125:U:O2'	4:N:292:C:C4'	2.38	0.61
13:W:344:PRO:O	13:W:346:SER:HB3	1.99	0.61
10:D:4:LEU:HD22	10:D:8:GLN:CG	2.29	0.61
2:A:120:G:N2	2:A:230:C:O2	2.32	0.61
3:M:65:U:O2	3:M:65:U:O4'	2.16	0.61
2:A:195:U:O4'	13:W:411:GLY:HA3	1.99	0.61
2:A:139:A:H2'	2:A:140:C:C6	2.35	0.61
1:E:138:U:H4'	1:E:139:C:OP2	2.01	0.61
1:E:137:C:H3'	1:E:137:C:O2	2.01	0.61
6:P:252:A:N3	8:R:250:U:N1	2.32	0.61
9:C:53:THR:HG22	9:C:54:ASP:N	2.15	0.61
1:E:122:C:O2'	1:E:123:U:H5'	2.01	0.60
3:M:55:G:O2'	9:C:45:ASP:HB2	2.01	0.60
4:N:279:A:O2'	4:N:280:C:OP2	2.14	0.60
12:U:21:ARG:NH1	12:U:66:GLU:HA	2.15	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:N:271:C:C4'	6:P:270:G:C3'	2.79	0.60
12:U:79:TYR:CE1	13:W:358:ASP:CG	2.73	0.60
10:D:4:LEU:HD11	10:D:12:GLU:HG3	1.83	0.60
13:W:344:PRO:O	13:W:346:SER:CB	2.50	0.60
9:C:5:GLN:CG	9:C:6:THR:H	2.11	0.60
12:U:48:ALA:O	12:U:52:VAL:HG12	2.00	0.60
12:U:59:ALA:O	12:U:64:VAL:HG13	2.02	0.60
4:N:288:G:C2'	4:N:289:A:OP2	2.49	0.60
2:A:193:G:N1	13:W:409:GLY:O	2.32	0.60
6:P:252:A:O5'	7:Q:102:A:C4	2.53	0.60
8:R:240:A:C6	8:R:242:C:C2	2.69	0.60
12:U:285:GLU:HG2	13:W:359:PHE:CA	2.32	0.60
1:E:110:G:C2'	1:E:111:G:H5'	2.31	0.60
3:M:55:G:O3'	9:C:46:LEU:CG	2.50	0.60
9:C:12:ARG:CG	9:C:13:ALA:N	2.65	0.60
3:M:55:G:O3'	9:C:46:LEU:CD1	2.50	0.60
8:R:242:C:H5'	8:R:243:G:P	2.42	0.59
1:E:126:A:N7	4:N:293:C:H5''	2.17	0.59
2:A:233:U:H2'	2:A:234:A:H5''	1.84	0.59
4:N:290:C:C2	4:N:291:C:O4'	2.55	0.59
11:B:73:ASN:HD21	11:B:75:ASP:H	1.50	0.59
9:C:46:LEU:O	9:C:47:VAL:HG13	2.02	0.59
13:W:372:LEU:HD21	14:S:58:THR:HA	1.85	0.59
1:E:132:A:O2'	1:E:133:G:C8	2.50	0.59
10:D:19:LYS:O	10:D:19:LYS:HG2	2.01	0.59
11:B:73:ASN:HD21	11:B:75:ASP:CB	2.16	0.59
7:Q:103:U:C6	7:Q:104:C:C5	2.91	0.59
12:U:92:LEU:HB2	13:W:348:ILE:CG1	2.33	0.59
6:P:264:A:N7	6:P:265:C:C2	2.71	0.59
7:Q:103:U:C2'	7:Q:104:C:C5	2.86	0.59
14:S:51:GLY:O	14:S:55:ASN:HB2	2.01	0.59
7:Q:104:C:O2'	7:Q:105:G:P	2.60	0.59
4:N:277:C:O2'	4:N:278:A:OP2	2.14	0.58
1:E:141:G:O2'	1:E:142:G:H5'	2.03	0.58
4:N:288:G:N3	4:N:288:G:C2'	2.66	0.58
2:A:212:C:H4'	2:A:213:A:OP1	2.03	0.58
4:N:271:C:C4'	6:P:270:G:H3'	2.33	0.58
12:U:281:PRO:HG2	13:W:347:GLN:HB2	1.84	0.58
2:A:112:G:C5	7:Q:111:C:C2	2.91	0.58
12:U:285:GLU:CG	13:W:359:PHE:CA	2.81	0.58
6:P:264:A:H8	6:P:265:C:C4	2.17	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:214:A:H5'	2:A:215:A:P	2.43	0.58
8:R:243:G:OP2	8:R:244:C:C5'	2.51	0.58
4:N:271:C:H5'	6:P:270:G:C4'	2.31	0.58
9:C:29:LEU:HD11	9:C:38:LEU:HD11	1.86	0.58
12:U:42:ASP:HB2	12:U:252:ARG:NH1	2.18	0.58
12:U:35:ARG:NE	12:U:49:ARG:HG3	2.19	0.58
8:R:241:U:H5'	8:R:242:C:OP1	2.03	0.58
1:E:101:G:O2'	3:M:49:A:P	2.61	0.58
2:A:128:U:H6	2:A:128:U:H5'	1.68	0.58
12:U:22:ILE:HG12	12:U:23:THR:N	2.18	0.58
12:U:8:ARG:HG2	12:U:37:ALA:HB2	1.86	0.58
2:A:163:A:O5'	2:A:163:A:H8	1.87	0.58
6:P:252:A:N1	8:R:250:U:C1'	2.62	0.57
4:N:288:G:H21	4:N:289:A:C5'	2.15	0.57
7:Q:100:C:H4'	7:Q:101:G:OP1	2.02	0.57
1:E:132:A:HO2'	1:E:133:G:H8	1.47	0.57
11:B:73:ASN:ND2	11:B:75:ASP:N	2.51	0.57
5:O:92:C:OP2	5:O:93:G:C8	2.55	0.57
1:E:110:G:O2'	1:E:111:G:H5'	2.04	0.57
11:B:112:ILE:HG23	11:B:115:LEU:HD12	1.87	0.57
7:Q:104:C:C3'	7:Q:104:C:P	2.71	0.57
12:U:283:TYR:CE2	13:W:359:PHE:O	2.54	0.57
3:M:67:A:O2'	3:M:68:G:OP2	2.21	0.57
11:B:77:GLN:HG2	11:B:77:GLN:O	2.05	0.57
9:C:32:ARG:O	9:C:32:ARG:HG2	2.04	0.57
3:M:56:A:C8	9:C:46:LEU:HG	2.38	0.57
9:C:12:ARG:HG2	9:C:13:ALA:H	1.68	0.57
12:U:167:SER:O	12:U:171:ARG:HG3	2.04	0.57
7:Q:104:C:C1'	7:Q:104:C:OP2	2.53	0.57
12:U:286:ARG:NH2	13:W:360:MET:CA	2.38	0.57
4:N:277:C:C4'	4:N:278:A:OP2	2.48	0.57
13:W:371:ARG:CA	14:S:62:THR:HG23	1.91	0.57
9:C:53:THR:HG21	9:C:58:ASP:CB	2.34	0.57
12:U:86:LEU:HD13	12:U:287:LEU:HB2	1.87	0.57
13:W:379:MET:HA	13:W:382:MET:HG3	1.87	0.57
1:E:105:G:H5'	4:N:290:C:O2'	2.05	0.57
7:Q:110:U:O3'	7:Q:111:C:C5'	2.53	0.57
2:A:233:U:H3'	2:A:234:A:H5'	1.86	0.57
6:P:252:A:N1	8:R:250:U:O2'	2.37	0.57
13:W:391:ASP:HB3	13:W:394:LYS:HZ2	1.70	0.57
6:P:252:A:OP2	7:Q:102:A:C8	2.58	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:Q:100:C:HO2'	7:Q:101:G:P	2.25	0.56
4:N:281:A:C1'	4:N:281:A:OP2	2.53	0.56
2:A:171:U:C3'	2:A:172:A:H5''	2.35	0.56
12:U:279:LEU:HG	12:U:280:GLU:N	2.20	0.56
11:B:86:LEU:HD13	11:B:99:PRO:O	2.05	0.56
9:C:12:ARG:HG2	9:C:13:ALA:N	2.20	0.56
12:U:69:THR:HG23	12:U:69:THR:O	2.06	0.56
9:C:29:LEU:HD13	9:C:40:VAL:HG22	1.87	0.56
3:M:56:A:C8	3:M:56:A:OP1	2.59	0.56
3:M:56:A:N7	9:C:46:LEU:HG	2.21	0.56
1:E:148:C:H5''	1:E:148:C:H6	1.70	0.56
3:M:56:A:H8	9:C:45:ASP:O	1.75	0.55
3:M:55:G:H2'	3:M:56:A:N9	2.20	0.55
11:B:60:VAL:CG2	11:B:84:VAL:HG12	2.35	0.55
9:C:7:TRP:CD1	9:C:61:LYS:HD3	2.42	0.55
12:U:283:TYR:CE1	13:W:360:MET:CG	2.83	0.55
6:P:264:A:C5'	6:P:265:C:OP2	2.51	0.55
3:M:67:A:O2'	3:M:68:G:P	2.64	0.55
13:W:375:LEU:CD1	14:S:61:VAL:HG11	2.33	0.55
12:U:128:ARG:HH11	12:U:181:ARG:NH2	2.05	0.55
8:R:242:C:C5'	8:R:243:G:OP2	2.45	0.55
2:A:112:G:C5	7:Q:111:C:N1	2.73	0.55
9:C:13:ALA:O	9:C:16:LYS:HB3	2.05	0.55
4:N:274:G:H2'	4:N:275:U:C4	2.17	0.55
4:N:290:C:O2'	4:N:291:C:H5'	2.00	0.55
12:U:281:PRO:HG3	13:W:347:GLN:HB2	1.85	0.55
2:A:112:G:N1	7:Q:111:C:C2	2.75	0.55
11:B:62:LEU:HD12	11:B:81:ARG:O	2.07	0.55
6:P:252:A:P	7:Q:102:A:N7	2.80	0.55
1:E:106:G:N2	3:M:58:G:C6	2.75	0.55
2:A:220:C:H2'	2:A:221:C:C5'	2.29	0.55
12:U:4:GLN:HB3	12:U:251:ALA:O	2.07	0.55
9:C:5:GLN:O	9:C:9:GLU:N	2.34	0.55
13:W:429:GLN:O	13:W:432:LYS:HG2	2.06	0.55
1:E:105:G:O4'	4:N:290:C:O2	2.25	0.54
7:Q:110:U:HO3'	7:Q:111:C:P	2.25	0.54
2:A:220:C:C3'	2:A:221:C:H5''	2.36	0.54
11:B:116:LYS:N	11:B:116:LYS:HD2	2.23	0.54
12:U:290:ARG:HD2	13:W:362:LYS:N	2.20	0.54
4:N:299:U:O2'	4:N:300:U:P	2.65	0.54
12:U:8:ARG:HG2	12:U:37:ALA:HB1	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:U:283:TYR:CD1	13:W:360:MET:O	2.60	0.54
1:E:125:U:OP2	10:D:59:ARG:NH2	2.41	0.54
3:M:57:G:H2'	3:M:57:G:N3	2.20	0.54
11:B:64:LYS:NZ	11:B:65:ASN:H	2.06	0.54
2:A:127:A:C2'	2:A:128:U:C5'	2.79	0.54
11:B:73:ASN:HD21	11:B:75:ASP:N	2.06	0.54
1:E:102:C:O2'	1:E:103:C:H5'	2.08	0.54
6:P:257:C:O3'	6:P:258:C:P	2.65	0.54
3:M:57:G:C4'	3:M:58:G:OP1	2.55	0.54
5:O:92:C:C5	5:O:94:C:OP2	2.61	0.54
12:U:281:PRO:CB	13:W:347:GLN:CA	2.87	0.53
12:U:35:ARG:NH2	12:U:49:ARG:HH11	2.05	0.53
7:Q:103:U:C6	7:Q:104:C:H5	2.26	0.53
3:M:57:G:OP2	9:C:26:ARG:NH2	2.41	0.53
2:A:172:A:H2	2:A:225:C:H1'	1.73	0.53
2:A:130:A:H2'	2:A:131:A:H8	1.72	0.53
2:A:195:U:H4'	13:W:411:GLY:O	2.08	0.53
12:U:269:PHE:CE2	13:W:347:GLN:OE1	2.62	0.53
9:C:65:PHE:CZ	9:C:69:LEU:HD11	2.44	0.53
6:P:252:A:N3	8:R:250:U:C4	2.76	0.53
2:A:233:U:H3'	2:A:234:A:C5'	2.39	0.53
2:A:208:A:H1'	13:W:380:ASP:O	2.08	0.53
11:B:76:VAL:HG13	11:B:77:GLN:H	1.71	0.53
11:B:116:LYS:O	11:B:120:GLN:HG2	2.09	0.53
12:U:83:LYS:CE	13:W:356:GLY:O	2.57	0.53
1:E:105:G:O2'	1:E:106:G:H5'	2.08	0.53
13:W:341:LYS:O	13:W:345:PHE:CE1	2.62	0.53
7:Q:109:G:O3'	7:Q:110:U:OP2	2.27	0.53
12:U:134:ALA:HB3	12:U:188:THR:HA	1.90	0.53
12:U:91:ARG:HG2	13:W:351:MET:CB	2.28	0.53
10:D:30:LEU:HD13	10:D:58:LEU:HD13	1.90	0.53
2:A:164:G:OP2	2:A:164:G:H8	1.92	0.53
13:W:361:SER:C	13:W:362:LYS:CG	2.67	0.52
12:U:112:THR:O	12:U:115:ALA:HB3	2.10	0.52
9:C:32:ARG:NH2	10:D:25:SER:OG	2.42	0.52
6:P:252:A:HO2'	6:P:253:A:H8	1.58	0.52
4:N:290:C:C3'	4:N:291:C:H5'	2.33	0.52
4:N:271:C:H5''	6:P:270:G:O3'	2.04	0.52
4:N:301:U:OP1	4:N:301:U:C3'	2.56	0.52
4:N:274:G:N2	4:N:275:U:O4	2.42	0.52
11:B:60:VAL:HB	11:B:84:VAL:HG12	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:D:61:THR:HG22	10:D:63:GLY:N	2.16	0.52
11:B:112:ILE:C	11:B:114:LYS:H	2.13	0.52
12:U:92:LEU:HB2	13:W:348:ILE:HG13	1.91	0.52
12:U:285:GLU:OE2	13:W:359:PHE:CB	2.56	0.52
4:N:280:C:C2	4:N:281:A:H5''	2.28	0.52
3:M:57:G:H8	9:C:26:ARG:HH22	1.58	0.52
13:W:371:ARG:HH22	14:S:63:VAL:HA	1.60	0.52
11:B:64:LYS:HZ3	11:B:65:ASN:HB2	1.73	0.52
10:D:7:GLU:O	10:D:8:GLN:C	2.47	0.52
11:B:71:GLU:OE2	11:B:78:TYR:HD2	1.92	0.52
11:B:41:VAL:CG1	11:B:42:GLU:N	2.72	0.52
12:U:247:LEU:CD1	12:U:270:ALA:HB1	2.39	0.52
12:U:285:GLU:C	13:W:359:PHE:H	2.10	0.52
11:B:88:GLN:O	11:B:91:GLY:N	2.42	0.52
6:P:252:A:O5'	7:Q:102:A:C8	2.60	0.52
7:Q:104:C:OP1	7:Q:104:C:H3'	2.09	0.52
8:R:243:G:OP2	8:R:244:C:H5''	2.10	0.51
3:M:67:A:HO2'	3:M:68:G:P	2.32	0.51
10:D:5:GLU:O	10:D:6:SER:C	2.48	0.51
10:D:92:ASP:O	10:D:92:ASP:OD1	2.27	0.51
9:C:40:VAL:HG21	9:C:62:ILE:HG23	1.91	0.51
9:C:70:MET:CB	10:D:30:LEU:HD21	2.38	0.51
10:D:34:ASP:CG	10:D:35:GLY:H	2.13	0.51
10:D:56:CYS:SG	10:D:71:VAL:HB	2.50	0.51
2:A:112:G:C6	7:Q:111:C:C2	2.98	0.51
12:U:152:VAL:HG23	12:U:154:VAL:HG23	1.92	0.51
7:Q:103:U:C2'	7:Q:104:C:H6	2.18	0.51
8:R:250:U:H4'	8:R:251:G:OP2	2.06	0.51
3:M:55:G:H2'	3:M:56:A:C1'	2.40	0.51
3:M:55:G:O3'	9:C:46:LEU:HD12	2.09	0.51
9:C:40:VAL:CG2	9:C:62:ILE:HG23	2.40	0.51
11:B:93:LEU:H	11:B:93:LEU:HD23	1.75	0.51
4:N:281:A:OP2	4:N:281:A:C4'	2.58	0.51
12:U:22:ILE:CG1	12:U:26:ASP:HB2	2.40	0.51
2:A:199:A:H8	2:A:199:A:OP1	1.93	0.51
1:E:121:C:H5''	9:C:32:ARG:HH22	1.76	0.51
11:B:56:VAL:HG21	11:B:107:TYR:CE2	2.45	0.51
12:U:270:ALA:HB2	12:U:282:PHE:HD1	1.76	0.51
12:U:196:GLU:OE1	12:U:196:GLU:HA	2.11	0.51
2:A:121:U:H2'	2:A:122:U:C6	2.46	0.51
12:U:92:LEU:HB2	13:W:348:ILE:HG12	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:U:283:TYR:HH	13:W:360:MET:HE2	1.69	0.51
13:W:339:ILE:CG1	14:S:54:ILE:HG21	2.40	0.51
11:B:15:PHE:CZ	11:B:85:GLN:HB2	2.45	0.50
2:A:125:G:H1	2:A:225:C:N4	2.08	0.50
9:C:33:HIS:CD2	10:D:21:ARG:HG3	2.46	0.50
12:U:22:ILE:HG12	12:U:26:ASP:HB2	1.92	0.50
12:U:128:ARG:HH11	12:U:181:ARG:HH22	1.59	0.50
4:N:271:C:H4'	6:P:270:G:HO3'	1.76	0.50
2:A:136:G:N3	2:A:214:A:H2	2.09	0.50
1:E:119:C:O2'	1:E:120:G:H5'	2.12	0.50
12:U:93:PRO:HG3	12:U:268:TYR:CD2	2.46	0.50
4:N:280:C:O3'	4:N:281:A:C8	2.64	0.50
4:N:282:U:OP2	4:N:283:A:OP2	2.29	0.50
7:Q:104:C:O2'	7:Q:105:G:C5'	2.58	0.50
10:D:28:ILE:HA	10:D:59:ARG:O	2.11	0.50
11:B:68:TYR:CE2	11:B:70:ARG:HB2	2.46	0.50
12:U:268:TYR:CD1	13:W:351:MET:HE3	2.45	0.50
6:P:263:C:C3'	6:P:265:C:N4	2.15	0.50
12:U:13:ILE:HD13	12:U:75:LEU:HD12	1.93	0.50
8:R:248:U:C3'	8:R:249:G:H8	2.24	0.50
3:M:58:G:H1'	4:N:280:C:H41	1.75	0.50
1:E:127:G:C6	4:N:293:C:P	3.05	0.50
1:E:147:U:H2'	1:E:148:C:H5''	1.94	0.50
1:E:105:G:H4'	4:N:290:C:O4'	2.12	0.50
11:B:60:VAL:CG2	11:B:83:ARG:O	2.52	0.50
13:W:349:LEU:HD22	13:W:359:PHE:CE2	2.45	0.50
7:Q:104:C:C2'	7:Q:104:C:OP2	2.59	0.49
8:R:240:A:O3'	8:R:242:C:C5'	2.50	0.49
1:E:126:A:N7	4:N:293:C:P	2.83	0.49
7:Q:103:U:H2'	7:Q:104:C:H6	1.74	0.49
12:U:281:PRO:HB3	13:W:347:GLN:HG3	0.53	0.49
4:N:280:C:O2'	4:N:281:A:C3'	2.44	0.49
4:N:288:G:P	4:N:288:G:O4'	2.65	0.49
13:W:394:LYS:HB3	13:W:394:LYS:NZ	2.27	0.49
12:U:281:PRO:CB	13:W:347:GLN:HA	2.43	0.49
2:A:175:G:H1	2:A:221:C:N4	2.08	0.49
2:A:231:A:H5''	2:A:232:G:OP2	2.12	0.49
12:U:214:VAL:HB	12:U:240:THR:HG23	1.95	0.49
12:U:258:SER:O	12:U:262:VAL:HG23	2.13	0.49
12:U:281:PRO:CG	13:W:347:GLN:CB	2.68	0.49
2:A:125:G:H2'	2:A:126:C:C6	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:B:64:LYS:HZ3	11:B:65:ASN:H	1.61	0.49
11:B:14:ARG:CB	11:B:14:ARG:CZ	2.88	0.49
6:P:252:A:H2	8:R:250:U:H3'	1.78	0.49
9:C:44:ASP:HB3	9:C:47:VAL:HG23	1.95	0.49
13:W:392:GLY:O	13:W:396:PHE:HD1	1.95	0.49
12:U:285:GLU:HG3	13:W:356:GLY:O	2.13	0.49
12:U:83:LYS:HE2	13:W:356:GLY:O	2.13	0.49
12:U:92:LEU:HG	13:W:347:GLN:HG2	1.36	0.49
3:M:55:G:C2'	3:M:56:A:O4'	2.61	0.49
3:M:52:C:H2'	3:M:53:U:C6	2.48	0.49
5:O:96:A:H2'	5:O:97:U:C6	2.48	0.49
1:E:142:G:O2'	1:E:143:A:H5'	2.12	0.49
8:R:247:C:H2'	8:R:248:U:C6	2.48	0.48
10:D:4:LEU:HD13	10:D:8:GLN:HG3	1.95	0.48
1:E:145:G:O2'	1:E:146:C:H5'	2.13	0.48
13:W:373:LYS:O	13:W:377:THR:HG23	2.13	0.48
14:S:57:LEU:O	14:S:61:VAL:HG23	2.14	0.48
10:D:4:LEU:HB3	10:D:8:GLN:HB3	1.95	0.48
5:O:94:C:H2'	5:O:95:U:C6	2.49	0.48
3:M:68:G:H2'	3:M:69:U:C6	2.48	0.48
12:U:227:LEU:HB3	12:U:262:VAL:HG11	1.95	0.48
7:Q:107:G:H2'	7:Q:108:U:C6	2.49	0.48
8:R:249:G:H2'	8:R:250:U:C6	2.49	0.48
5:O:86:G:H2'	5:O:87:U:C6	2.49	0.48
4:N:272:C:H2'	4:N:273:U:C6	2.49	0.48
11:B:64:LYS:HD3	11:B:64:LYS:H	1.71	0.48
2:A:172:A:H2	2:A:225:C:C1'	2.26	0.48
5:O:79:C:H2'	5:O:80:U:C6	2.49	0.48
4:N:282:U:O4	4:N:283:A:N6	2.46	0.48
4:N:288:G:C4'	4:N:288:G:OP2	2.57	0.48
4:N:296:C:H2'	4:N:297:U:C6	2.49	0.48
5:O:89:G:H2'	5:O:90:U:C6	2.49	0.48
1:E:107:C:O2'	1:E:108:G:H5'	2.12	0.48
8:R:240:A:C5	8:R:242:C:C4	3.02	0.48
5:O:84:C:C1'	5:O:86:G:OP2	2.62	0.48
4:N:294:G:H2'	4:N:295:U:C6	2.48	0.48
6:P:260:C:H2'	6:P:261:U:C6	2.49	0.48
12:U:285:GLU:OE2	13:W:359:PHE:HB3	2.14	0.48
12:U:8:ARG:HA	12:U:11:GLU:OE1	2.13	0.48
12:U:122:TYR:O	12:U:127:ARG:HB2	2.13	0.48
12:U:129:PRO:HA	12:U:183:LEU:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:P:267:C:H2'	6:P:268:C:C6	2.49	0.48
6:P:256:G:H2'	6:P:257:C:C6	2.49	0.48
5:O:93:G:H2'	5:O:94:C:C6	2.49	0.48
12:U:21:ARG:HH11	12:U:66:GLU:HA	1.78	0.48
12:U:177:ARG:NH2	12:U:178:LEU:HD21	2.28	0.48
12:U:114:THR:HG21	12:U:243:VAL:HG11	1.96	0.48
6:P:253:A:H2'	6:P:254:U:C6	2.48	0.48
4:N:276:G:H2'	4:N:277:C:C6	2.49	0.48
11:B:29:ILE:HG22	11:B:30:ALA:N	2.29	0.48
7:Q:102:A:H2'	7:Q:103:U:C6	2.48	0.47
2:A:192:A:H2'	2:A:193:G:O4'	2.13	0.47
7:Q:104:C:P	7:Q:104:C:H6	2.32	0.47
4:N:295:U:H2'	4:N:296:C:C6	2.49	0.47
12:U:79:TYR:HE1	13:W:358:ASP:CB	2.26	0.47
1:E:148:C:C5'	1:E:148:C:C6	2.96	0.47
5:O:79:C:H2'	5:O:80:U:H6	1.79	0.47
3:M:63:C:H2'	3:M:64:U:C6	2.48	0.47
2:A:224:G:H8	2:A:224:G:H5'	1.79	0.47
2:A:165:G:N7	2:A:176:A:C6	2.82	0.47
9:C:5:GLN:O	9:C:9:GLU:HB2	2.14	0.47
5:O:94:C:H2'	5:O:95:U:H6	1.79	0.47
12:U:134:ALA:HB3	12:U:187:ASP:O	2.14	0.47
3:M:63:C:H2'	3:M:64:U:H6	1.79	0.47
9:C:34:SER:O	9:C:36:GLY:N	2.47	0.47
6:P:267:C:H2'	6:P:268:C:H6	1.80	0.47
3:M:70:C:HO2'	3:M:71:C:H5	1.53	0.47
11:B:62:LEU:HD12	11:B:63:GLU:N	2.30	0.47
2:A:160:A:H2'	2:A:161:C:C6	2.49	0.47
2:A:160:A:H2'	2:A:161:C:O4'	2.14	0.47
8:R:246:C:H2'	8:R:247:C:C6	2.49	0.47
6:P:266:U:H2'	6:P:267:C:C6	2.49	0.47
4:N:276:G:H2'	4:N:277:C:H6	1.80	0.47
5:O:93:G:H2'	5:O:94:C:H6	1.80	0.47
6:P:257:C:O3'	6:P:258:C:O5'	2.29	0.47
4:N:271:C:H2'	4:N:272:C:C6	2.49	0.47
3:M:52:C:H2'	3:M:53:U:H6	1.79	0.47
9:C:34:SER:C	9:C:36:GLY:N	2.65	0.47
8:R:245:G:H2'	8:R:246:C:H6	1.80	0.47
6:P:262:G:H2'	6:P:263:C:C6	2.49	0.47
9:C:32:ARG:HG3	9:C:32:ARG:HH11	1.79	0.47
4:N:291:C:H2'	4:N:292:C:C6	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:N:295:U:H2'	4:N:296:C:H6	1.80	0.47
4:N:294:G:H2'	4:N:295:U:H6	1.79	0.47
4:N:296:C:H2'	4:N:297:U:H6	1.79	0.47
4:N:297:U:H2'	4:N:298:C:H6	1.80	0.47
11:B:73:ASN:HD21	11:B:75:ASP:HB3	1.80	0.47
12:U:208:VAL:HG12	12:U:209:LEU:HD22	1.96	0.47
5:O:89:G:H2'	5:O:90:U:H6	1.80	0.47
6:P:259:A:H2'	6:P:260:C:C6	2.49	0.47
3:M:62:G:H2'	3:M:63:C:C6	2.49	0.47
4:N:284:G:H2'	4:N:285:C:C6	2.49	0.47
7:Q:102:A:H2'	7:Q:103:U:H6	1.79	0.47
7:Q:107:G:H2'	7:Q:108:U:H6	1.80	0.47
1:E:121:C:C2'	1:E:122:C:H5'	2.43	0.47
4:N:272:C:H2'	4:N:273:U:H6	1.80	0.47
9:C:5:GLN:O	9:C:9:GLU:CB	2.63	0.47
9:C:53:THR:CG2	9:C:54:ASP:N	2.78	0.47
12:U:221:MET:HE3	12:U:249:GLY:HA3	1.96	0.47
4:N:271:C:H2'	4:N:272:C:H6	1.80	0.47
6:P:253:A:H2'	6:P:254:U:H6	1.79	0.47
5:O:96:A:H2'	5:O:97:U:H6	1.79	0.47
8:R:245:G:H2'	8:R:246:C:C6	2.49	0.46
8:R:246:C:H2'	8:R:247:C:H6	1.80	0.46
12:U:284:PRO:HD2	13:W:350:GLY:O	2.15	0.46
6:P:252:A:O2'	6:P:253:A:H8	1.98	0.46
6:P:262:G:H2'	6:P:263:C:H6	1.80	0.46
4:N:297:U:H2'	4:N:298:C:C6	2.49	0.46
3:M:60:U:H2'	3:M:61:C:C6	2.49	0.46
12:U:247:LEU:HD12	12:U:270:ALA:HB1	1.98	0.46
2:A:146:G:C6	2:A:147:G:C5	3.03	0.46
2:A:167:U:H2'	2:A:168:G:O4'	2.15	0.46
12:U:90:ALA:HB1	13:W:347:GLN:O	2.16	0.46
3:M:55:G:O3'	3:M:56:A:P	2.73	0.46
3:M:68:G:H2'	3:M:69:U:H6	1.79	0.46
4:N:290:C:C3'	4:N:291:C:C5'	2.93	0.46
3:M:62:G:H2'	3:M:63:C:H6	1.80	0.46
12:U:216:LEU:HD21	12:U:218:LEU:HD21	1.98	0.46
7:Q:104:C:O2	7:Q:105:G:C5	2.59	0.46
8:R:241:U:OP2	8:R:242:C:H5''	2.15	0.46
5:O:86:G:H2'	5:O:87:U:H6	1.79	0.46
4:N:291:C:H2'	4:N:292:C:H6	1.80	0.46
6:P:259:A:H2'	6:P:260:C:H6	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:116:G:H2'	1:E:117:C:H5'	1.98	0.46
12:U:286:ARG:O	13:W:361:SER:HB2	2.14	0.46
6:P:256:G:H2'	6:P:257:C:H6	1.80	0.46
2:A:116:C:H2'	2:A:117:U:C6	2.50	0.46
12:U:11:GLU:O	12:U:15:ARG:HB2	2.15	0.46
9:C:61:LYS:HE2	9:C:61:LYS:HB3	1.71	0.46
12:U:176:ALA:HA	12:U:181:ARG:CG	2.45	0.46
3:M:51:G:H2'	3:M:52:C:C6	2.50	0.46
10:D:30:LEU:HD12	10:D:31:LYS:H	1.79	0.46
2:A:207:C:C4	2:A:208:A:N7	2.84	0.46
4:N:284:G:H2'	4:N:285:C:H6	1.80	0.46
2:A:125:G:H2'	2:A:126:C:H6	1.81	0.46
2:A:171:U:H3'	2:A:172:A:H5''	1.96	0.46
12:U:283:TYR:CE2	13:W:359:PHE:CD2	3.03	0.46
11:B:76:VAL:C	11:B:78:TYR:N	2.70	0.46
6:P:260:C:H2'	6:P:261:U:H6	1.80	0.46
8:R:247:C:H2'	8:R:248:U:H6	1.79	0.46
12:U:83:LYS:HE3	13:W:356:GLY:O	2.16	0.46
3:M:60:U:H2'	3:M:61:C:H6	1.80	0.46
8:R:249:G:H2'	8:R:250:U:H6	1.80	0.45
11:B:35:ILE:HD11	11:B:40:ALA:HA	1.98	0.45
6:P:266:U:H2'	6:P:267:C:H6	1.80	0.45
9:C:44:ASP:HB3	9:C:47:VAL:CG2	2.46	0.45
8:R:242:C:C5'	8:R:243:G:P	3.04	0.45
13:W:374:LYS:CD	14:S:67:LYS:C	2.81	0.45
11:B:75:ASP:OD1	11:B:76:VAL:N	2.47	0.45
12:U:21:ARG:HD2	12:U:65:LEU:O	2.16	0.45
6:P:264:A:C8	6:P:265:C:N1	2.82	0.45
3:M:56:A:OP1	3:M:56:A:H8	1.98	0.45
11:B:43:ASN:C	11:B:118:ARG:HH22	2.20	0.45
3:M:57:G:H8	9:C:26:ARG:NH2	2.14	0.45
13:W:372:LEU:HD21	14:S:58:THR:CG2	2.35	0.45
3:M:51:G:H2'	3:M:52:C:H6	1.80	0.45
9:C:5:GLN:CG	9:C:6:THR:N	2.76	0.45
2:A:229:U:H2'	2:A:230:C:C6	2.51	0.45
1:E:105:G:C4'	4:N:290:C:C1'	2.49	0.45
13:W:344:PRO:C	13:W:346:SER:CB	2.85	0.45
2:A:168:G:H3'	2:A:169:C:H5'	1.99	0.45
12:U:133:ALA:HB1	12:U:142:ARG:HA	1.99	0.45
12:U:269:PHE:CE2	13:W:347:GLN:NE2	2.85	0.45
1:E:105:G:C2'	1:E:106:G:H5'	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:B:24:ASN:ND2	11:B:27:LYS:HG3	2.22	0.45
14:S:52:PHE:CB	14:S:53:PRO:HD3	2.40	0.45
1:E:148:C:H5''	1:E:148:C:C6	2.50	0.45
2:A:223:U:C2'	2:A:224:G:H5''	2.47	0.45
2:A:223:U:H2'	2:A:224:G:H5''	1.98	0.45
4:N:282:U:C4	4:N:283:A:N6	2.84	0.45
13:W:427:PHE:O	13:W:431:VAL:HG23	2.17	0.45
4:N:288:G:H2'	4:N:289:A:OP2	2.16	0.45
9:C:37:ASN:CA	10:D:94:LEU:HD11	2.47	0.45
12:U:195:ASP:HB3	12:U:198:LEU:HB3	1.97	0.45
13:W:344:PRO:O	13:W:345:PHE:C	2.53	0.45
12:U:143:GLU:OE2	12:U:146:ARG:NH1	2.50	0.45
13:W:339:ILE:HG12	14:S:54:ILE:HG21	1.99	0.44
13:W:423:GLN:NE2	14:S:61:VAL:HG13	2.32	0.44
9:C:29:LEU:CD1	9:C:38:LEU:HD11	2.46	0.44
11:B:116:LYS:CD	11:B:116:LYS:N	2.80	0.44
2:A:166:U:H2'	2:A:167:U:O4'	2.17	0.44
12:U:111:LYS:HA	12:U:217:VAL:HG21	2.00	0.44
6:P:252:A:P	7:Q:102:A:C4	3.10	0.44
8:R:242:C:C5'	8:R:244:C:C5'	2.89	0.44
4:N:279:A:O2'	4:N:280:C:P	2.75	0.44
4:N:279:A:C4'	4:N:280:C:OP2	2.57	0.44
12:U:132:VAL:HG11	12:U:186:VAL:HG22	1.99	0.44
11:B:76:VAL:O	11:B:78:TYR:N	2.50	0.44
12:U:144:GLN:O	12:U:148:LEU:HG	2.17	0.44
8:R:243:G:OP2	8:R:244:C:H5'	2.17	0.44
9:C:26:ARG:HG2	9:C:26:ARG:HH11	1.82	0.44
3:M:55:G:C5'	9:C:46:LEU:HD11	2.32	0.44
3:M:66:G:C2'	3:M:67:A:OP2	2.55	0.44
12:U:131:LEU:O	12:U:156:VAL:HA	2.17	0.44
2:A:163:A:H2'	2:A:164:G:N9	2.32	0.44
3:M:65:U:O5'	3:M:65:U:O2	2.35	0.44
1:E:128:U:C2	1:E:129:C:C5	3.05	0.44
12:U:164:SER:O	12:U:168:ILE:HG13	2.17	0.44
9:C:32:ARG:NH1	9:C:32:ARG:HG3	2.33	0.44
9:C:68:GLN:O	9:C:71:ARG:N	2.50	0.44
12:U:89:GLU:HB2	13:W:351:MET:O	2.17	0.44
9:C:29:LEU:CD1	9:C:40:VAL:HG22	2.47	0.44
6:P:252:A:C1'	8:R:250:U:C4	2.76	0.44
12:U:16:LEU:HD21	12:U:30:THR:OG1	2.18	0.44
11:B:76:VAL:CG1	11:B:77:GLN:N	2.80	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:138:G:H2'	2:A:139:A:H8	1.83	0.44
8:R:248:U:C2'	8:R:249:G:C8	3.01	0.44
3:M:55:G:C5'	9:C:46:LEU:CD1	2.88	0.44
2:A:117:U:H2'	2:A:118:A:C8	2.53	0.44
4:N:292:C:C3'	4:N:293:C:P	3.01	0.43
13:W:368:SER:O	14:S:62:THR:OG1	2.36	0.43
11:B:93:LEU:N	11:B:93:LEU:CD2	2.77	0.43
2:A:162:C:H2'	2:A:163:A:C8	2.52	0.43
13:W:347:GLN:O	13:W:351:MET:HG3	2.18	0.43
12:U:89:GLU:C	13:W:351:MET:O	2.32	0.43
10:D:7:GLU:O	10:D:10:LEU:N	2.47	0.43
11:B:73:ASN:ND2	11:B:74:ARG:N	2.67	0.43
12:U:90:ALA:O	13:W:348:ILE:O	2.36	0.43
12:U:128:ARG:NH1	12:U:181:ARG:HH22	2.16	0.43
2:A:186:C:O5'	2:A:186:C:H6	2.01	0.43
2:A:179:G:N2	2:A:180:G:H1'	2.33	0.43
12:U:283:TYR:CZ	13:W:359:PHE:C	2.90	0.43
4:N:288:G:H2'	4:N:289:A:P	2.53	0.43
2:A:221:C:H2'	2:A:222:G:O4'	2.18	0.43
11:B:96:VAL:HG23	11:B:97:GLN:N	2.33	0.43
1:E:121:C:H5''	9:C:32:ARG:NH2	2.33	0.43
13:W:427:PHE:CZ	14:S:57:LEU:HD23	2.52	0.43
11:B:15:PHE:O	11:B:83:ARG:NH2	2.52	0.43
2:A:117:U:H2'	2:A:118:A:H8	1.83	0.43
11:B:88:GLN:HG3	11:B:92:SER:O	2.18	0.43
2:A:160:A:H2'	2:A:161:C:H6	1.84	0.43
13:W:344:PRO:HB2	13:W:345:PHE:H	1.69	0.43
9:C:27:VAL:CG1	10:D:30:LEU:HB3	2.49	0.43
11:B:42:GLU:HG3	11:B:43:ASN:N	2.34	0.43
12:U:5:LEU:HD11	12:U:38:LEU:HD23	2.00	0.43
1:E:124:G:O4'	3:M:57:G:C2'	2.54	0.42
10:D:7:GLU:O	10:D:9:PHE:N	2.52	0.42
12:U:17:ARG:HE	12:U:17:ARG:HB2	1.37	0.42
5:O:92:C:H5	5:O:94:C:OP2	2.00	0.42
12:U:7:ALA:O	12:U:11:GLU:HG3	2.19	0.42
11:B:116:LYS:H	11:B:116:LYS:HE3	1.83	0.42
12:U:285:GLU:CG	13:W:356:GLY:O	2.67	0.42
9:C:27:VAL:HG13	10:D:30:LEU:HB3	2.00	0.42
9:C:70:MET:HE2	10:D:30:LEU:HD13	2.01	0.42
9:C:46:LEU:C	9:C:47:VAL:HG22	2.39	0.42
13:W:423:GLN:OE1	14:S:65:HIS:CD2	2.71	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:223:U:H2'	2:A:224:G:C5'	2.49	0.42
2:A:127:A:H2'	2:A:128:U:H5'	1.99	0.42
1:E:138:U:O2	1:E:138:U:C2'	2.67	0.42
12:U:283:TYR:CE2	13:W:359:PHE:HD2	2.38	0.42
13:W:339:ILE:HG12	14:S:54:ILE:CG2	2.49	0.42
3:M:55:G:C4'	9:C:46:LEU:HD12	2.50	0.42
11:B:16:ILE:HG12	11:B:84:VAL:HG22	2.02	0.42
12:U:227:LEU:HD13	12:U:262:VAL:HB	2.01	0.42
13:W:430:MET:HA	13:W:433:LYS:HB3	2.00	0.42
1:E:126:A:N7	4:N:293:C:H5'	2.34	0.42
2:A:171:U:H3'	2:A:172:A:C5'	2.49	0.42
2:A:195:U:C4'	13:W:411:GLY:HA3	2.50	0.42
11:B:53:CYS:O	11:B:58:LEU:HB2	2.19	0.42
12:U:219:ASP:OD1	12:U:219:ASP:C	2.58	0.42
9:C:63:GLU:C	9:C:63:GLU:CD	2.78	0.42
11:B:24:ASN:HD22	11:B:27:LYS:CG	2.22	0.42
11:B:19:TYR:CE2	11:B:81:ARG:HD3	2.55	0.42
11:B:45:THR:O	11:B:46:ALA:C	2.56	0.42
12:U:132:VAL:HG12	12:U:185:LEU:O	2.20	0.42
11:B:107:TYR:O	11:B:111:MET:HG2	2.19	0.42
8:R:240:A:C8	8:R:242:C:C5	3.08	0.42
11:B:56:VAL:HG12	11:B:56:VAL:O	2.20	0.42
12:U:79:TYR:HA	12:U:292:LEU:HD11	2.02	0.42
11:B:88:GLN:O	11:B:89:GLU:C	2.58	0.42
11:B:41:VAL:HG12	11:B:42:GLU:N	2.34	0.42
11:B:94:CYS:C	11:B:95:LEU:HD23	2.38	0.41
9:C:5:GLN:OE1	9:C:5:GLN:HA	2.20	0.41
1:E:110:G:H2'	1:E:111:G:H5'	2.02	0.41
9:C:37:ASN:N	10:D:94:LEU:HD11	2.34	0.41
9:C:63:GLU:O	9:C:66:HIS:HB3	2.20	0.41
13:W:412:VAL:HG22	13:W:416:ASP:OD2	2.20	0.41
4:N:271:C:H5'	6:P:270:G:O5'	2.20	0.41
12:U:31:LEU:HB3	12:U:52:VAL:CG2	2.51	0.41
2:A:182:G:H21	2:A:215:A:H62	1.67	0.41
2:A:171:U:H5'	2:A:172:A:OP2	2.20	0.41
12:U:260:ARG:NH2	12:U:261:HIS:HB2	2.31	0.41
12:U:285:GLU:CD	13:W:355:PHE:HB2	2.39	0.41
11:B:60:VAL:CB	11:B:84:VAL:HG12	2.49	0.41
12:U:35:ARG:O	12:U:39:MET:CG	2.69	0.41
12:U:147:LEU:O	12:U:150:GLU:HB3	2.21	0.41
6:P:264:A:N7	6:P:265:C:C4	2.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:124:G:O3'	3:M:57:G:C5	2.71	0.41
1:E:104:G:C2	3:M:57:G:N2	2.87	0.41
11:B:116:LYS:CE	11:B:116:LYS:H	2.34	0.41
11:B:23:LEU:HB2	11:B:44:PRO:HG3	2.01	0.41
12:U:269:PHE:CZ	13:W:347:GLN:OE1	2.73	0.41
2:A:118:A:H2'	2:A:119:A:H5'	2.02	0.41
2:A:193:G:H2'	2:A:194:G:O4'	2.21	0.41
12:U:117:LYS:HD2	12:U:279:LEU:HB2	2.01	0.41
10:D:5:GLU:O	10:D:7:GLU:N	2.54	0.41
1:E:114:G:C2'	1:E:115:C:H5'	2.49	0.41
12:U:281:PRO:CB	13:W:347:GLN:CD	2.70	0.41
12:U:59:ALA:HB1	12:U:64:VAL:HG11	2.02	0.41
11:B:99:PRO:HB2	11:B:100:SER:H	1.59	0.41
9:C:65:PHE:O	9:C:69:LEU:HG	2.21	0.41
11:B:18:ILE:HD12	11:B:105:MET:HG2	2.02	0.41
12:U:232:ALA:O	12:U:236:LYS:HD2	2.21	0.41
1:E:105:G:O4'	4:N:290:C:C2	2.74	0.41
11:B:16:ILE:CG1	11:B:84:VAL:HG22	2.51	0.41
2:A:233:U:C3'	2:A:234:A:C5'	2.98	0.41
12:U:35:ARG:CZ	12:U:49:ARG:HG3	2.51	0.41
8:R:243:G:P	8:R:244:C:H5'	2.61	0.41
1:E:105:G:C5'	4:N:290:C:O2'	2.69	0.41
13:W:342:MET:O	13:W:345:PHE:HB2	2.21	0.41
12:U:79:TYR:O	13:W:357:THR:HG23	2.21	0.40
1:E:148:C:H5'	1:E:148:C:H6	1.86	0.40
1:E:138:U:O2	1:E:138:U:H2'	2.19	0.40
9:C:69:LEU:O	9:C:73:MET:HG3	2.21	0.40
8:R:240:A:H5''	8:R:241:U:H3'	2.04	0.40
12:U:283:TYR:HB3	12:U:286:ARG:HB3	2.02	0.40
2:A:151:C:H2'	2:A:152:G:H8	1.86	0.40
11:B:76:VAL:CG1	11:B:77:GLN:H	2.34	0.40
12:U:276:PRO:HD2	12:U:277:GLU:OE2	2.21	0.40
12:U:285:GLU:OE1	13:W:355:PHE:CA	2.69	0.40
12:U:283:TYR:HD1	13:W:360:MET:O	2.04	0.40
1:E:116:G:C2'	1:E:117:C:H5'	2.51	0.40
9:C:60:LYS:O	9:C:64:LYS:HG3	2.20	0.40
12:U:165:PRO:HD2	12:U:166:GLU:OE1	2.21	0.40
12:U:89:GLU:O	13:W:351:MET:O	2.39	0.40
12:U:269:PHE:CE2	13:W:347:GLN:CD	2.95	0.40
3:M:69:U:C5'	3:M:70:C:OP2	2.63	0.40
2:A:172:A:C2	2:A:225:C:H1'	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:124:G:O3'	3:M:57:G:C8	2.75	0.40
2:A:126:C:H2'	2:A:127:A:O4'	2.21	0.40
12:U:35:ARG:O	12:U:39:MET:HG3	2.21	0.40
11:B:119:THR:O	11:B:120:GLN:OXT	2.40	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	C	69/85 (81%)	57 (83%)	9 (13%)	3 (4%)	3	34
10	D	72/106 (68%)	63 (88%)	5 (7%)	4 (6%)	2	28
11	B	105/108 (97%)	87 (83%)	11 (10%)	7 (7%)	1	24
12	U	292/296 (99%)	273 (94%)	18 (6%)	1 (0%)	46	83
13	W	107/109 (98%)	100 (94%)	2 (2%)	5 (5%)	3	32
14	S	16/18 (89%)	14 (88%)	2 (12%)	0	100	100
All	All	661/722 (92%)	594 (90%)	47 (7%)	20 (3%)	9	42

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	C	34	SER
9	C	47	VAL
10	D	6	SER
11	B	42	GLU
11	B	75	ASP
13	W	344	PRO
13	W	345	PHE
13	W	362	LYS

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Mol	Chain	Res	Type
10	D	7	GLU
10	D	8	GLN
11	B	99	PRO
13	W	346	SER
12	U	21	ARG
9	C	35	ASP
11	B	64	LYS
11	B	77	GLN
10	D	93	GLY
13	W	363	GLY
11	B	56	VAL
11	B	96	VAL

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	
9	C	64/77 (83%)	58 (91%)	6 (9%)	11	42
10	D	69/96 (72%)	66 (96%)	3 (4%)	35	70
11	B	96/97 (99%)	92 (96%)	4 (4%)	36	70
12	U	233/234 (100%)	202 (87%)	31 (13%)	5	28
13	W	96/96 (100%)	91 (95%)	5 (5%)	29	65
14	S	17/17 (100%)	17 (100%)	0	100	100
All	All	575/617 (93%)	526 (92%)	49 (8%)	18	48

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
9	C	26	ARG
9	C	38	LEU
9	C	39	CYS
9	C	47	VAL
9	C	63	GLU
9	C	74	VAL

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Mol	Chain	Res	Type
10	D	20	CYS
10	D	54	ASN
10	D	76	VAL
11	B	39	LYS
11	B	64	LYS
11	B	93	LEU
11	B	116	LYS
12	U	3	GLN
12	U	4	GLN
12	U	8	ARG
12	U	11	GLU
12	U	17	ARG
12	U	28	LYS
12	U	32	ARG
12	U	35	ARG
12	U	39	MET
12	U	45	LEU
12	U	54	ARG
12	U	63	GLN
12	U	83	LYS
12	U	94	VAL
12	U	99	ASN
12	U	127	ARG
12	U	128	ARG
12	U	132	VAL
12	U	144	GLN
12	U	146	ARG
12	U	151	LYS
12	U	160	MET
12	U	161	ASP
12	U	181	ARG
12	U	182	ASP
12	U	204	ARG
12	U	236	LYS
12	U	244	LEU
12	U	279	LEU
12	U	283	TYR
12	U	294	MET
13	W	349	LEU
13	W	365	GLU
13	W	383	ASN
13	W	412	VAL

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Mol	Chain	Res	Type
13	W	427	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
10	D	85	ASN
11	B	24	ASN
11	B	59	ASN
11	B	65	ASN
11	B	73	ASN
11	B	88	GLN
12	U	3	GLN
13	W	383	ASN
13	W	385	GLN
13	W	423	GLN
13	W	429	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	E	48/50 (96%)	11 (22%)	2 (4%)
2	A	127/128 (99%)	22 (17%)	1 (0%)
3	M	24/27 (88%)	8 (33%)	3 (12%)
4	N	28/31 (90%)	12 (42%)	9 (32%)
5	O	22/24 (91%)	4 (18%)	1 (4%)
6	P	18/20 (90%)	2 (11%)	2 (11%)
7	Q	10/12 (83%)	4 (40%)	2 (20%)
8	R	11/12 (91%)	6 (54%)	3 (27%)
All	All	288/304 (94%)	69 (23%)	23 (7%)

All (69) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	E	101	G
1	E	104	G
1	E	128	U
1	E	129	C
1	E	132	A
1	E	133	G
1	E	136	A

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Mol	Chain	Res	Type
1	E	137	C
1	E	138	U
1	E	139	C
1	E	148	C
2	A	128	U
2	A	129	C
2	A	164	G
2	A	168	G
2	A	169	C
2	A	171	U
2	A	172	A
2	A	173	A
2	A	174	G
2	A	176	A
2	A	177	G
2	A	187	G
2	A	191	C
2	A	213	A
2	A	214	A
2	A	215	A
2	A	219	C
2	A	221	C
2	A	224	G
2	A	227	G
2	A	232	G
2	A	234	A
3	M	57	G
3	M	58	G
3	M	59	A
3	M	60	U
3	M	66	G
3	M	67	A
3	M	70	C
3	M	75	A
4	N	275	U
4	N	276	G
4	N	278	A
4	N	279	A
4	N	280	C
4	N	281	A
4	N	282	U
4	N	288	G

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Mol	Chain	Res	Type
4	N	289	A
4	N	291	C
4	N	299	U
4	N	300	U
5	O	77	U
5	O	84	C
5	O	92	C
5	O	99	C
6	P	253	A
6	P	266	U
7	Q	101	G
7	Q	102	A
7	Q	104	C
7	Q	111	C
8	R	241	U
8	R	242	C
8	R	243	G
8	R	244	C
8	R	249	G
8	R	251	G

All (23) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	E	136	A
1	E	137	C
2	A	212	C
3	M	56	A
3	M	65	U
3	M	69	U
4	N	274	G
4	N	275	U
4	N	277	C
4	N	278	A
4	N	279	A
4	N	280	C
4	N	281	A
4	N	288	G
4	N	299	U
5	O	98	G
6	P	252	A
6	P	265	C

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Mol	Chain	Res	Type
7	Q	100	C
7	Q	101	G
8	R	242	C
8	R	243	G
8	R	248	U

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	CCC	A	239	8,2	16,25,26	0.95	0	20,38,41	2.19	4 (20%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	CCC	A	239	8,2	-	0/3/35/36	0/3/3/3

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	239	CCC	O2C-PC-O2'	-7.43	95.19	108.46
2	A	239	CCC	O2C-PC-O3'	-2.90	103.29	108.46
2	A	239	CCC	O3'-C3'-C2'	3.26	111.24	105.03
2	A	239	CCC	O2'-C2'-C3'	4.07	112.79	105.03

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.