



Full wwPDB/EMDatabank EM Map/Model Validation Report ⓘ

Sep 10, 2019 – 09:50 AM EDT

PDB ID : 6PPF
EMDB ID: : EMD-20435
Title : Bacterial 45SRbgA ribosomal particle class B
Authors : Ortega, J.; Seffouh, A.; Jain, N.; Jahagirdar, D.; Basu, K.; Razi, A.; Ni, X.;
Guarne, A.; Britton, R.A.
Deposited on : 2019-07-06
Resolution : 3.40 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

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

with specific help available everywhere you see the ⓘ symbol.

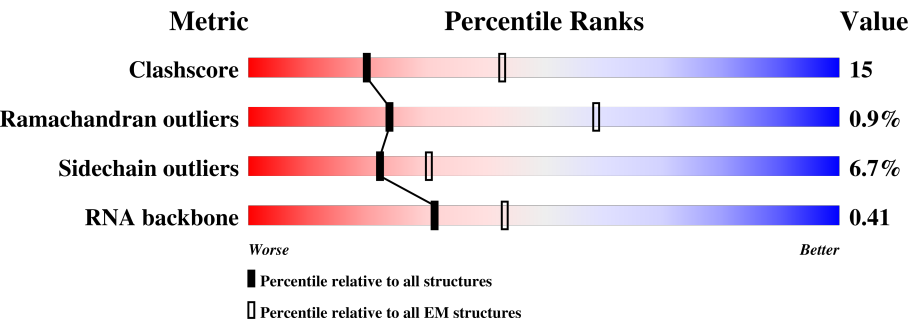
MolProbity : 4.02b-467
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : 2.4

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 3.40 Å.

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













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

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

Mol	Chain	Length	Quality of chain
1	A	2927	<div><div>45%</div><div>31%</div><div>8%</div><div>•</div><div>16%</div></div>
2	B	119	<div><div>36%</div><div>43%</div><div>15%</div><div>6%</div></div>
3	C	277	<div><div>51%</div><div>26%</div><div>•</div><div>20%</div></div>
4	D	209	<div><div>47%</div><div>25%</div><div>7%</div><div>•</div><div>20%</div></div>
5	E	207	<div><div>56%</div><div>35%</div><div>•</div><div>6%</div></div>
6	J	145	<div><div>66%</div><div>27%</div><div>•</div><div>•</div><div>•</div></div>
7	K	122	<div><div>66%</div><div>34%</div><div>•</div></div>
8	L	145	<div><div>56%</div><div>28%</div><div>•</div><div>12%</div></div>

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Mol	Chain	Length	Quality of chain
9	N	120	 86% 13% .
10	O	120	 51% 32% . 13%
11	P	115	 61% 27% . 10%
12	Q	118	 58% 33% 7% ..
13	R	102	 48% 41% . . 6%
14	S	113	 74% 21% . .
15	T	95	 53% 38% . 7%
16	U	103	 68% 21% 6% 5%
17	V	94	 32% 40% 5% 22%
18	Z	59	 73% 25% .
19	b	59	 81% 10% 8%
20	Y	66	 79% 18% . .
21	d	44	 100%

2 Entry composition

There are 22 unique types of molecules in this entry. The entry contains 71835 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 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2471	Total	C	N	O	P	0	0
			53094	23688	9835	17100	2471		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	112	Total	C	N	O	P	0	0
			2395	1068	435	780	112		

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	221	Total	C	N	O	S	0	0
			1684	1047	326	307	4		

- Molecule 4 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	167	Total	C	N	O	S	0	0
			1265	802	220	240	3		

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	194	Total	C	N	O	S	0	0
			1484	937	270	275	2		

- Molecule 6 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	J	141	Total	C	N	O	S	0	0
			1119	708	205	201	5		

- Molecule 7 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	K	122	Total	C	N	O	S	0	0
			920	571	173	172	4		

- Molecule 8 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L	128	Total	C	N	O	S	0	0
			952	594	179	177	2		

- Molecule 9 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	N	119	Total	C	N	O	S	0	0
			953	583	186	180	4		

- Molecule 10 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	O	104	Total	C	N	O	0	0
			791	492	157	142		

- Molecule 11 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	P	103	Total	C	N	O	0	0
			846	540	162	144		

- Molecule 12 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	Q	117	Total	C	N	O	S	0	0
			940	591	189	156	4		

- Molecule 13 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	R	96	Total	C	N	O	0	0
			758	485	134	139		

- Molecule 14 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	S	109	Total	C	N	O	S	0	0
			842	525	164	150	3		

- Molecule 15 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	T	88	Total	C	N	O	S	0	0
			707	441	131	132	3		

- Molecule 16 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	U	98	Total	C	N	O	S	0	0
			739	464	138	134	3		

- Molecule 17 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	V	73	Total	C	N	O		0	0
			555	344	106	105			

- Molecule 18 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Z	58	Total	C	N	O	S	0	0
			455	281	89	84	1		

- Molecule 19 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	b	54	Total	C	N	O	S	0	0
			426	262	86	71	7		

- Molecule 20 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Y	65	Total	C	N	O	S	0	0
			530	328	102	98	2		

- Molecule 21 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	d	44	Total	C	N	O	S	0	0
			367	222	89	54	2		

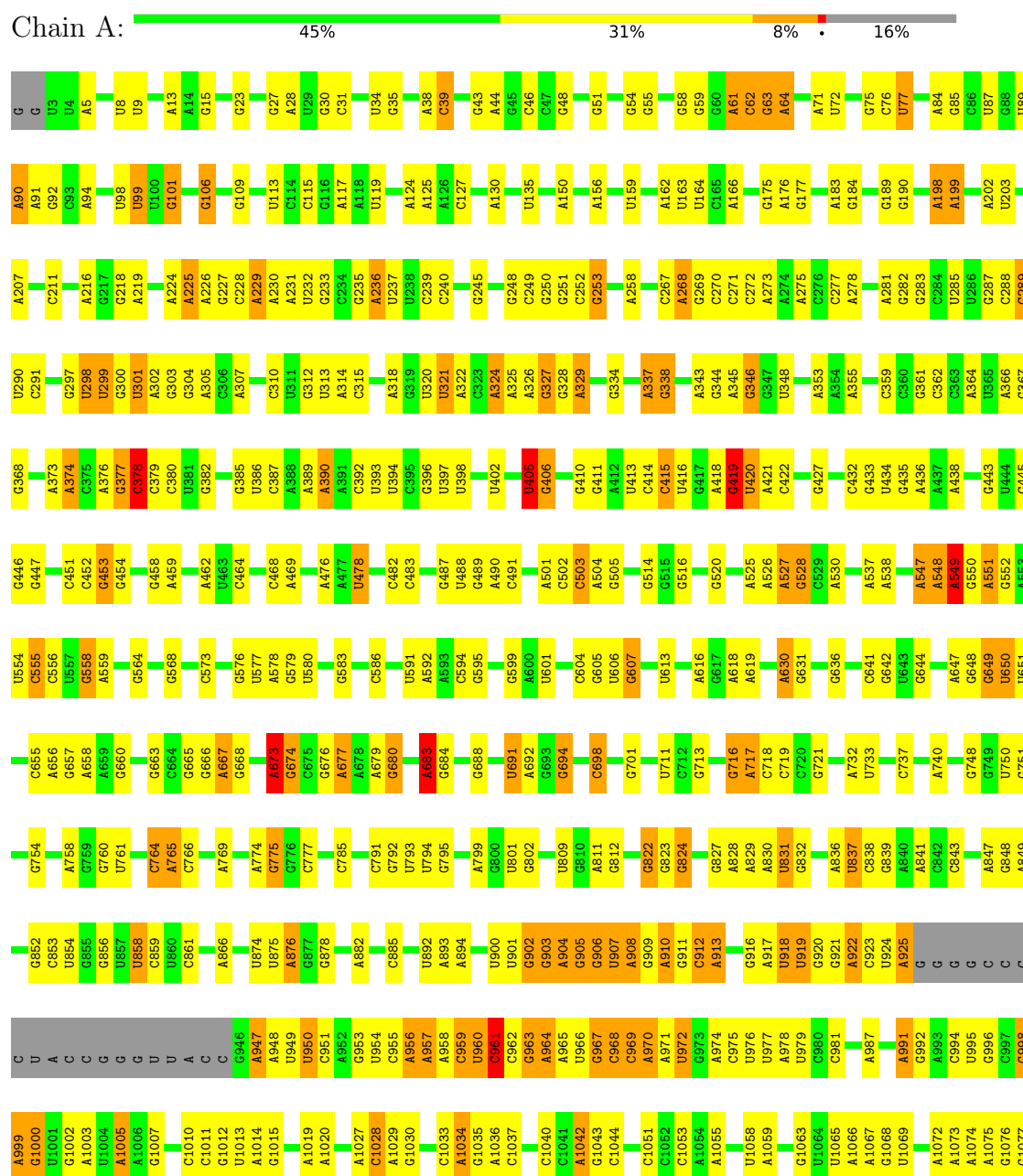
- Molecule 22 is water.

Mol	Chain	Residues	Atoms		AltConf
22	A	13	Total	O	0
			13	13	

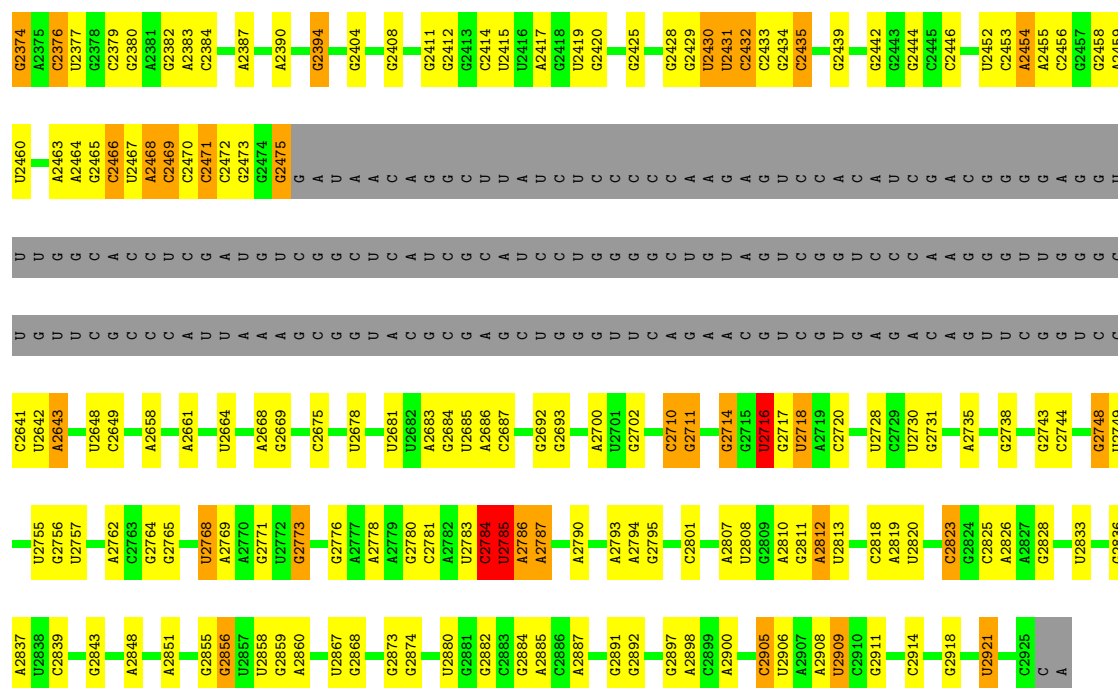
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

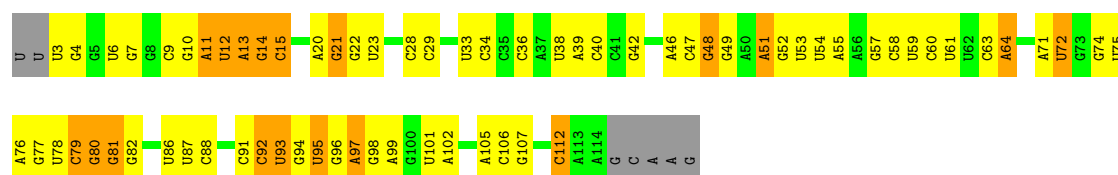
• Molecule 1: 23S rRNA



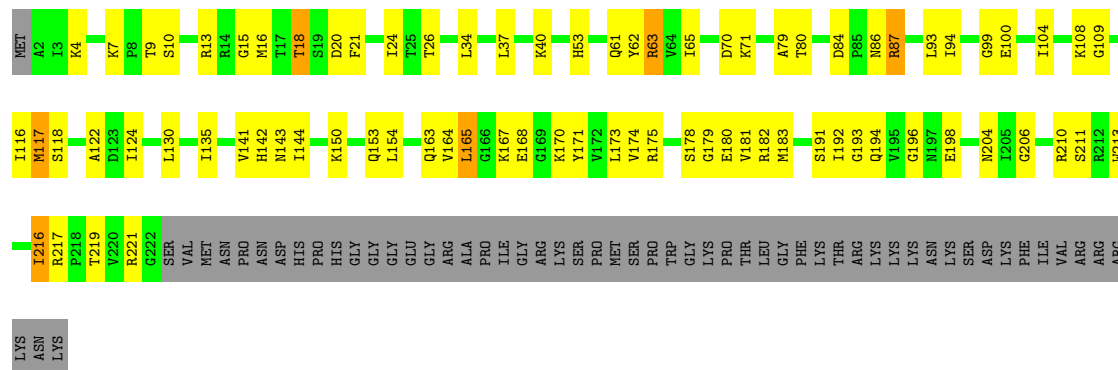


- Molecule 2: 5S rRNA

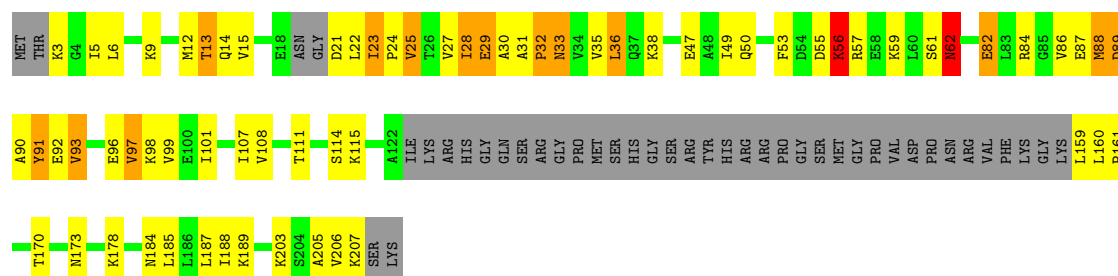


- Molecule 3: 50S ribosomal protein L2



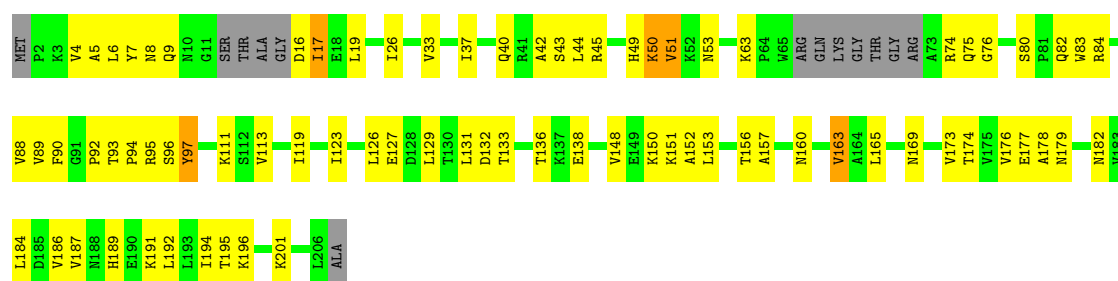
- Molecule 4: 50S ribosomal protein L3





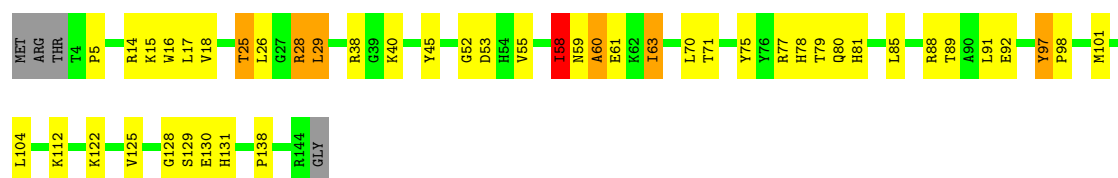
• Molecule 5: 50S ribosomal protein L4

Chain E: 56% 35% 6%



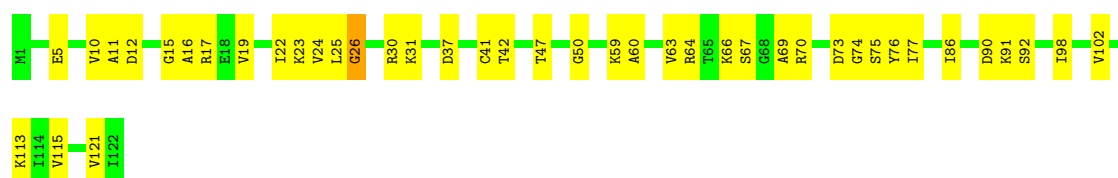
• Molecule 6: 50S ribosomal protein L13

Chain J: 66% 27%



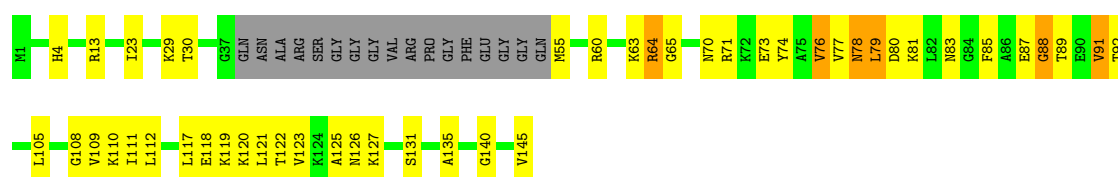
• Molecule 7: 50S ribosomal protein L14

Chain K: 66% 34%




• Molecule 8: 50S ribosomal protein L15

Chain L: 56% 28% 12%



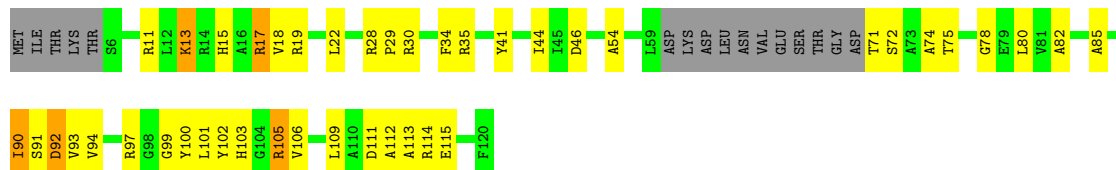
- Molecule 9: 50S ribosomal protein L17

Chain N:  86% 13%



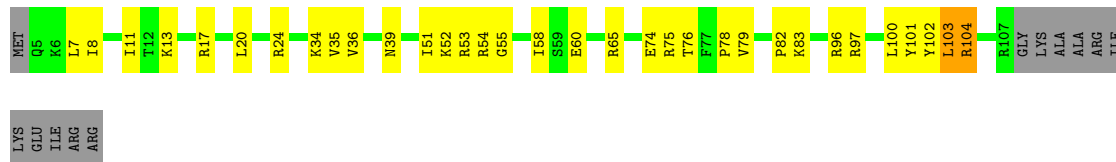
- Molecule 10: 50S ribosomal protein L18

Chain O:  51% 32% 13%




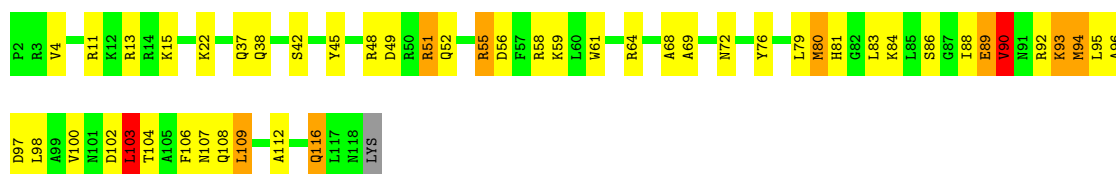
- Molecule 11: 50S ribosomal protein L19

Chain P:  61% 27% 10%



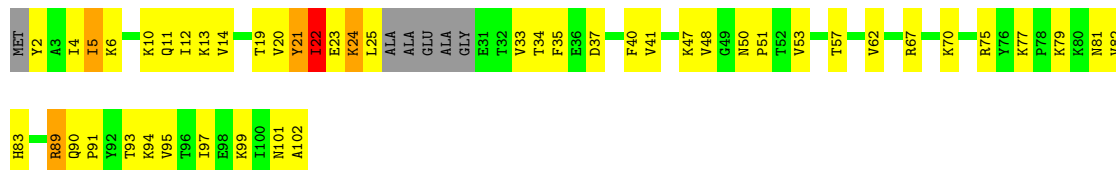
- Molecule 12: 50S ribosomal protein L20

Chain Q:  58% 33% 7%



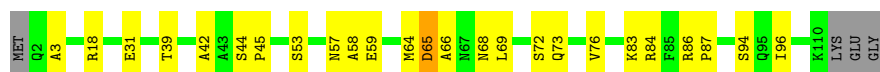
- Molecule 13: 50S ribosomal protein L21

Chain R:  48% 41% 6%



- Molecule 14: 50S ribosomal protein L22

Chain S:  74% 21%



- Molecule 15: 50S ribosomal protein L23

Chain T: 53% 38% 7%



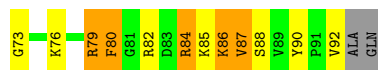
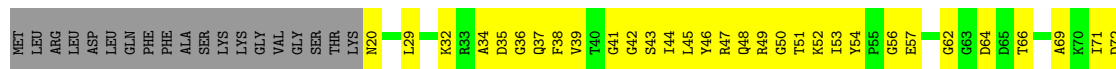
- Molecule 16: 50S ribosomal protein L24

Chain U: 68% 21% 6% 5%



- Molecule 17: 50S ribosomal protein L27

Chain V: 32% 40% 5% 22%



- Molecule 18: 50S ribosomal protein L30

Chain Z: 73% 25% 2%



- Molecule 19: 50S ribosomal protein L32

Chain b: 81% 10% 8%



- Molecule 20: 50S ribosomal protein L29

Chain Y: 79% 18% 3%



- Molecule 21: 50S ribosomal protein L34

Chain d:  100%

There are no outlier residues recorded for this chain.

4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	546297	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor

5 Model quality

5.1 Standard geometry

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	0.77	0/59472	1.00	137/92759 (0.1%)
10	O	0.24	0/799	0.67	3/1070 (0.3%)
11	P	0.35	0/859	0.52	0/1152
12	Q	0.39	0/952	0.63	2/1266 (0.2%)
13	R	0.39	0/768	0.67	2/1029 (0.2%)
14	S	0.34	0/851	0.50	0/1146
15	T	0.36	0/713	0.46	0/951
16	U	0.34	0/748	0.51	0/1000
17	V	0.20	0/563	0.33	0/753
18	Z	0.33	0/457	0.54	0/613
19	b	0.34	0/433	0.45	0/574
2	B	0.33	0/2678	0.94	3/4174 (0.1%)
20	Y	0.31	0/531	0.47	0/707
21	d	0.39	0/370	0.49	0/483
3	C	0.33	0/1709	0.53	2/2296 (0.1%)
4	D	0.35	0/1276	0.64	3/1709 (0.2%)
5	E	0.32	0/1501	0.60	4/2025 (0.2%)
6	J	0.36	0/1142	0.60	2/1537 (0.1%)
7	K	0.33	0/927	0.54	0/1245
8	L	0.29	0/961	0.78	7/1281 (0.5%)
9	N	0.40	0/960	0.54	0/1284
All	All	0.69	0/78670	0.94	165/119054 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
12	Q	0	1
4	D	0	1
All	All	0	2

There are no bond length outliers.

All (165) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	Q	103	LEU	CB-CA-C	15.54	139.72	110.20
1	A	1433	U	C2-N1-C1'	12.62	132.85	117.70
10	O	90	ILE	CB-CA-C	-12.23	87.14	111.60
8	L	85	PHE	CB-CA-C	-12.23	85.95	110.40
1	A	961	C	N1-C2-O2	11.32	125.69	118.90
8	L	63	LYS	CB-CA-C	-10.57	89.27	110.40
1	A	1433	U	N1-C2-O2	10.38	130.07	122.80
4	D	56	LYS	CB-CA-C	-10.24	89.93	110.40
13	R	22	ILE	CB-CA-C	-9.78	92.04	111.60
4	D	62	ASN	CB-CA-C	-9.62	91.17	110.40
1	A	961	C	N3-C2-O2	-9.35	115.36	121.90
1	A	2905	C	N1-C2-O2	9.18	124.41	118.90
6	J	15	LYS	CB-CA-C	8.99	128.38	110.40
1	A	961	C	C2-N1-C1'	8.98	128.68	118.80
1	A	1433	U	N3-C2-O2	-8.95	115.94	122.20
5	E	84	ARG	CB-CA-C	-8.83	92.74	110.40
1	A	1433	U	C6-N1-C1'	-8.81	108.86	121.20
1	A	1281	C	C2-N1-C1'	8.61	128.27	118.80
10	O	90	ILE	N-CA-C	8.45	133.80	111.00
1	A	1148	C	N1-C2-O2	8.35	123.91	118.90
1	A	2905	C	N3-C2-O2	-8.12	116.22	121.90
1	A	89	U	C2-N1-C1'	8.12	127.44	117.70
1	A	2905	C	C2-N1-C1'	8.05	127.65	118.80
1	A	89	U	N1-C2-O2	7.99	128.39	122.80
8	L	105	LEU	CB-CA-C	7.75	124.93	110.20
1	A	716	G	C4-N9-C1'	7.68	136.48	126.50
1	A	1281	C	N1-C2-O2	7.46	123.38	118.90
1	A	89	U	N3-C2-O2	-7.41	117.02	122.20
1	A	1030	G	C4-N9-C1'	7.32	136.01	126.50
1	A	1030	G	N3-C4-N9	7.22	130.33	126.00
1	A	1069	U	N1-C2-O2	7.17	127.82	122.80
1	A	2785	U	P-O3'-C3'	7.11	128.23	119.70
1	A	1030	G	N3-C4-C5	-7.05	125.08	128.60
1	A	1069	U	N3-C2-O2	-7.01	117.29	122.20
1	A	1107	U	P-O3'-C3'	7.00	128.10	119.70
6	J	60	ALA	CB-CA-C	7.00	120.60	110.10
1	A	1281	C	N3-C2-O2	-6.96	117.03	121.90
1	A	961	C	C6-N1-C2	-6.85	117.56	120.30
5	E	90	PHE	CB-CA-C	-6.83	96.75	110.40
1	A	1069	U	C2-N1-C1'	6.73	125.78	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1216	C	C6-N1-C2	-6.61	117.66	120.30
1	A	683	A	P-O3'-C3'	6.61	127.63	119.70
1	A	1433	U	C5-C6-N1	6.60	126.00	122.70
1	A	2346	C	N1-C2-O2	6.59	122.86	118.90
1	A	1712	G	O4'-C1'-N9	6.58	113.47	108.20
1	A	716	G	C8-N9-C1'	-6.58	118.45	127.00
1	A	1216	C	C5-C6-N1	6.54	124.27	121.00
1	A	1652	C	P-O3'-C3'	6.53	127.54	119.70
1	A	2905	C	C6-N1-C2	-6.50	117.70	120.30
1	A	1539	C	N1-C2-O2	6.48	122.79	118.90
1	A	1245	G	P-O3'-C3'	6.48	127.47	119.70
8	L	78	ASN	CB-CA-C	6.45	123.31	110.40
1	A	1148	C	C2-N1-C1'	6.45	125.89	118.80
1	A	482	C	C2-N1-C1'	6.45	125.89	118.80
5	E	84	ARG	N-CA-C	6.42	128.33	111.00
1	A	1148	C	N3-C2-O2	-6.40	117.42	121.90
1	A	1281	C	C6-N1-C2	-6.32	117.77	120.30
1	A	1515	C	C2-N1-C1'	6.29	125.72	118.80
1	A	1030	G	C8-N9-C1'	-6.29	118.83	127.00
1	A	1246	G	O4'-C1'-N9	6.26	113.21	108.20
12	Q	103	LEU	C-N-CA	6.25	137.32	121.70
1	A	1519	C	O5'-P-OP1	6.24	118.19	110.70
1	A	717	A	P-O3'-C3'	6.22	127.17	119.70
1	A	2716	U	P-O3'-C3'	6.11	127.04	119.70
1	A	422	C	N1-C2-O2	6.06	122.53	118.90
1	A	310	C	N1-C2-O2	6.05	122.53	118.90
1	A	1028	C	N1-C2-O2	6.04	122.53	118.90
1	A	419	G	P-O3'-C3'	6.04	126.94	119.70
1	A	961	C	C6-N1-C1'	-6.02	113.58	120.80
1	A	1368	U	N3-C2-O2	-6.02	117.99	122.20
3	C	170	LYS	CB-CA-C	-5.99	98.42	110.40
1	A	1600	G	O4'-C1'-N9	5.98	112.98	108.20
1	A	90	A	P-O3'-C3'	5.94	126.83	119.70
1	A	1203	G	C4-N9-C1'	5.92	134.19	126.50
1	A	1148	C	C6-N1-C2	-5.89	117.95	120.30
1	A	2909	U	N3-C2-O2	-5.89	118.08	122.20
1	A	1246	G	C4-N9-C1'	5.88	134.14	126.50
1	A	327	G	N3-C4-N9	5.87	129.52	126.00
1	A	1351	U	P-O3'-C3'	5.86	126.74	119.70
1	A	1527	C	P-O3'-C3'	5.86	126.73	119.70
1	A	1491	A	C2-N3-C4	5.83	113.51	110.60
1	A	1353	C	C6-N1-C2	-5.80	117.98	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1169	C	N1-C2-O2	5.79	122.38	118.90
1	A	2376	C	O4'-C1'-N1	5.79	112.83	108.20
1	A	719	C	C6-N1-C2	-5.73	118.01	120.30
8	L	118	GLU	N-CA-C	5.72	126.45	111.00
1	A	1577	C	N1-C2-O2	5.71	122.33	118.90
1	A	1339	A	P-O3'-C3'	5.71	126.55	119.70
1	A	1281	C	C6-N1-C1'	-5.71	113.95	120.80
1	A	405	U	P-O3'-C3'	5.70	126.54	119.70
1	A	2454	A	P-O3'-C3'	5.67	126.51	119.70
1	A	1683	C	C6-N1-C2	-5.67	118.03	120.30
4	D	56	LYS	N-CA-C	-5.66	95.71	111.00
1	A	1134	A	C4-N9-C1'	5.66	136.49	126.30
1	A	482	C	N1-C2-O2	5.64	122.29	118.90
1	A	732	A	C4-N9-C1'	5.64	136.45	126.30
1	A	1033	C	N1-C2-O2	5.59	122.25	118.90
1	A	392	C	N1-C2-O2	5.54	122.22	118.90
1	A	698	C	N1-C2-O2	5.52	122.21	118.90
1	A	478	U	N3-C2-O2	-5.51	118.34	122.20
1	A	1353	C	N1-C2-O2	5.50	122.20	118.90
1	A	2334	U	P-O3'-C3'	5.46	126.25	119.70
1	A	1577	C	N3-C2-O2	-5.46	118.08	121.90
8	L	105	LEU	N-CA-C	-5.45	96.28	111.00
1	A	991	A	C2-N3-C4	5.44	113.32	110.60
1	A	1327	U	C2-N1-C1'	5.43	124.21	117.70
2	B	48	G	O4'-C1'-N9	5.41	112.53	108.20
5	E	90	PHE	N-CA-C	5.38	125.52	111.00
1	A	1028	C	N3-C2-O2	-5.37	118.14	121.90
1	A	1246	G	C8-N9-C1'	-5.36	120.03	127.00
1	A	77	U	N1-C2-O2	5.36	126.55	122.80
1	A	327	G	C4-N9-C1'	5.36	133.46	126.50
1	A	1577	C	C6-N1-C2	-5.35	118.16	120.30
1	A	732	A	N7-C8-N9	5.34	116.47	113.80
13	R	22	ILE	N-CA-C	-5.34	96.59	111.00
1	A	1450	C	N1-C2-O2	5.33	122.10	118.90
3	C	170	LYS	N-CA-C	5.33	125.40	111.00
1	A	908	A	C2'-C3'-O3'	5.32	122.21	113.70
1	A	478	U	C2-N1-C1'	5.32	124.08	117.70
8	L	118	GLU	CB-CA-C	-5.32	99.77	110.40
1	A	1651	G	N7-C8-N9	5.31	115.76	113.10
1	A	1539	C	N3-C2-O2	-5.31	118.18	121.90
2	B	48	G	C4-N9-C1'	-5.30	119.61	126.50
1	A	549	A	P-O3'-C3'	5.28	126.04	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	89	U	C6-N1-C1'	-5.27	113.82	121.20
1	A	2801	C	C6-N1-C2	-5.27	118.19	120.30
1	A	2784	C	P-O3'-C3'	5.23	125.98	119.70
1	A	1180	C	N1-C2-O2	5.23	122.04	118.90
1	A	2801	C	N3-C2-O2	-5.22	118.24	121.90
1	A	2905	C	C6-N1-C1'	-5.22	114.53	120.80
1	A	837	U	P-O3'-C3'	5.22	125.96	119.70
1	A	719	C	C5-C6-N1	5.21	123.61	121.00
1	A	1649	C	C6-N1-C2	-5.20	118.22	120.30
1	A	667	A	P-O3'-C3'	5.20	125.94	119.70
1	A	717	A	OP2-P-O3'	5.19	116.62	105.20
1	A	1771	C	N1-C2-O2	5.19	122.01	118.90
10	O	80	LEU	CA-CB-CG	5.18	127.22	115.30
1	A	77	U	N3-C2-O2	-5.16	118.59	122.20
1	A	1327	U	N3-C2-O2	-5.16	118.59	122.20
1	A	1327	U	N1-C2-O2	5.16	126.41	122.80
1	A	2909	U	N1-C2-O2	5.13	126.39	122.80
1	A	673	A	O4'-C1'-N9	5.13	112.30	108.20
1	A	478	U	N1-C2-O2	5.12	126.39	122.80
1	A	327	G	N3-C4-C5	-5.12	126.04	128.60
1	A	1382	G	C4-N9-C1'	5.10	133.13	126.50
1	A	1485	A	O4'-C1'-N9	5.10	112.28	108.20
1	A	99	U	N1-C2-O2	5.10	126.37	122.80
1	A	1784	A	P-O3'-C3'	5.09	125.81	119.70
1	A	1491	A	N1-C6-N6	-5.09	115.55	118.60
1	A	2801	C	N1-C2-O2	5.09	121.95	118.90
1	A	1714	A	C4-N9-C1'	5.08	135.45	126.30
2	B	112	C	N1-C2-O2	5.08	121.94	118.90
1	A	378	C	C6-N1-C2	-5.07	118.27	120.30
1	A	649	G	P-O3'-C3'	5.07	125.78	119.70
1	A	327	G	C8-N9-C1'	-5.06	120.42	127.00
1	A	972	U	O4'-C1'-N1	5.06	112.25	108.20
1	A	2812	A	P-O3'-C3'	5.06	125.77	119.70
1	A	1244	A	O4'-C1'-N9	5.05	112.24	108.20
1	A	2823	C	N1-C2-O2	5.05	121.93	118.90
1	A	464	C	N1-C2-O2	5.04	121.92	118.90
1	A	1203	G	C8-N9-C1'	-5.04	120.45	127.00
1	A	2351	A	P-O3'-C3'	5.03	125.74	119.70
1	A	1771	C	C6-N1-C2	-5.02	118.29	120.30
1	A	1169	C	N3-C2-O2	-5.02	118.39	121.90
1	A	229	A	P-O3'-C3'	5.01	125.72	119.70

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	D	56	LYS	Peptide
12	Q	103	LEU	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	53094	0	26707	695	0
2	B	2395	0	1212	52	0
3	C	1684	0	1754	81	0
4	D	1265	0	1332	102	0
5	E	1484	0	1565	80	0
6	J	1119	0	1159	47	0
7	K	920	0	977	54	0
8	L	952	0	1002	104	0
9	N	953	0	983	12	0
10	O	791	0	824	39	0
11	P	846	0	902	54	0
12	Q	940	0	1005	123	0
13	R	758	0	801	97	0
14	S	842	0	899	27	0
15	T	707	0	751	35	0
16	U	739	0	790	41	0
17	V	555	0	540	81	0
18	Z	455	0	491	12	0
19	b	426	0	445	0	0
20	Y	530	0	568	20	0
21	d	367	0	410	0	0
22	A	13	0	0	0	0
All	All	71835	0	45117	1512	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 15.

All (1512) 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)
12:Q:61:TRP:CZ2	12:Q:94:MET:HB2	1.27	1.60
12:Q:95:LEU:HD22	13:R:11:GLN:CB	1.28	1.57
1:A:901:U:H2'	1:A:902:G:C8	1.36	1.56
1:A:2465:G:H2'	1:A:2466:C:C5'	1.38	1.52
12:Q:95:LEU:CD2	13:R:11:GLN:HB3	1.30	1.52
12:Q:109:LEU:HA	13:R:47:LYS:NZ	1.24	1.48
1:A:673:A:N6	8:L:112:LEU:HD13	1.17	1.40
12:Q:95:LEU:HD21	13:R:4:ILE:CG2	1.52	1.38
5:E:51:VAL:CG2	5:E:92:PRO:HD2	1.54	1.37
4:D:31:ALA:HB3	4:D:53:PHE:CD1	1.58	1.37
4:D:31:ALA:HB3	4:D:53:PHE:CE1	1.59	1.34
3:C:94:ILE:HD12	3:C:104:ILE:CD1	1.58	1.34
3:C:4:LYS:CE	3:C:20:ASP:OD1	1.74	1.34
1:A:2465:G:C2'	1:A:2466:C:C5'	2.06	1.33
3:C:94:ILE:CD1	3:C:104:ILE:HD12	1.56	1.33
1:A:913:A:C6	1:A:961:C:H5	1.47	1.32
1:A:970:A:O2'	17:V:37:GLN:CG	1.79	1.30
1:A:970:A:O2'	17:V:37:GLN:CD	1.70	1.30
4:D:185:LEU:HD12	11:P:11:ILE:CD1	1.62	1.29
4:D:31:ALA:CB	4:D:53:PHE:CE1	2.14	1.28
1:A:1077:G:N2	1:A:1170:C:C2	2.04	1.26
1:A:2465:G:C2'	1:A:2466:C:H5'	1.64	1.26
12:Q:61:TRP:CZ2	12:Q:94:MET:CB	2.19	1.25
12:Q:108:GLN:OE1	13:R:47:LYS:HB2	1.24	1.25
1:A:1807:U:C2	1:A:1816:A:N1	2.05	1.25
7:K:73:ASP:OD2	11:P:83:LYS:HE2	1.32	1.25
1:A:901:U:C2'	1:A:902:G:C8	2.18	1.25
8:L:77:VAL:HG13	8:L:81:LYS:CG	1.67	1.25
1:A:1807:U:O2	1:A:1816:A:N1	1.68	1.24
12:Q:61:TRP:CE2	12:Q:94:MET:HB2	1.72	1.24
1:A:2360:G:O2'	17:V:51:THR:HG22	1.32	1.24
12:Q:61:TRP:CH2	12:Q:94:MET:HB2	1.72	1.24
4:D:31:ALA:CB	4:D:53:PHE:HE1	1.48	1.23
1:A:905:G:H4'	1:A:2298:A:OP2	1.39	1.23
1:A:970:A:C1'	17:V:37:GLN:HE21	1.51	1.22
3:C:4:LYS:HE3	3:C:20:ASP:OD1	1.06	1.22
1:A:970:A:O2'	17:V:37:GLN:HG2	1.36	1.20
1:A:2428:G:N1	1:A:2429:G:C6	1.98	1.20
1:A:901:U:H2'	1:A:902:G:N7	1.55	1.20
8:L:120:LYS:C	8:L:121:LEU:HD12	1.61	1.19
3:C:150:LYS:HD3	3:C:153:GLN:NE2	1.58	1.19
12:Q:108:GLN:CD	13:R:47:LYS:HB2	1.61	1.18

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1805:G:O6	1:A:1817:C:N4	1.73	1.18
12:Q:92:ARG:N	13:R:11:GLN:OE1	1.76	1.18
1:A:1805:G:C6	1:A:1817:C:N4	2.11	1.17
8:L:88:GLY:HA3	8:L:121:LEU:HA	1.23	1.17
1:A:673:A:C6	8:L:112:LEU:HD13	1.79	1.17
8:L:88:GLY:CA	8:L:121:LEU:HG	1.74	1.16
10:O:11:ARG:HD3	10:O:100:TYR:CE1	1.80	1.16
1:A:2360:G:O2'	17:V:51:THR:CG2	1.92	1.16
1:A:673:A:N6	8:L:112:LEU:CD1	2.09	1.16
4:D:14:GLN:HB3	11:P:58:ILE:HG21	1.28	1.15
8:L:120:LYS:O	8:L:121:LEU:HD12	1.47	1.14
1:A:61:A:H2'	1:A:62:C:C6	1.82	1.14
1:A:906:G:N1	1:A:963:G:N7	1.94	1.14
12:Q:108:GLN:OE1	13:R:47:LYS:CB	1.94	1.14
5:E:51:VAL:HG21	5:E:92:PRO:CD	1.78	1.13
1:A:2465:G:C2'	1:A:2466:C:H5''	1.72	1.13
1:A:580:U:O2'	12:Q:49:ASP:OD2	1.65	1.13
1:A:913:A:C6	1:A:961:C:C5	2.36	1.13
8:L:74:TYR:HB3	8:L:108:GLY:O	1.44	1.13
8:L:76:VAL:CG2	8:L:112:LEU:HG	1.79	1.12
1:A:1805:G:N1	1:A:1817:C:N4	1.98	1.12
4:D:185:LEU:CD1	11:P:11:ILE:HD11	1.79	1.12
1:A:1805:G:H1	1:A:1817:C:N4	1.46	1.12
1:A:2124:A:N6	1:A:2223:U:O4	1.81	1.11
17:V:54:TYR:CD2	17:V:84:ARG:HD3	1.85	1.11
2:B:75:U:O2	2:B:97:A:N6	1.81	1.10
16:U:6:GLY:HA2	16:U:23:ILE:HB	1.16	1.10
1:A:2465:G:O2'	1:A:2466:C:H5''	1.50	1.10
4:D:22:LEU:HD12	7:K:74:GLY:HA3	1.14	1.10
1:A:2428:G:N1	1:A:2429:G:C5	2.19	1.09
1:A:970:A:C1'	17:V:37:GLN:NE2	2.16	1.09
1:A:1807:U:N3	1:A:1816:A:N1	2.00	1.09
1:A:63:G:O6	15:T:10:ARG:NH1	1.83	1.08
4:D:31:ALA:HB2	4:D:53:PHE:HE1	1.18	1.08
1:A:677:A:OP1	8:L:64:ARG:NH1	1.85	1.08
8:L:88:GLY:HA3	8:L:121:LEU:CA	1.84	1.08
1:A:970:A:H1'	17:V:37:GLN:HE21	1.18	1.07
4:D:33:ASN:HB2	4:D:97:VAL:HG13	1.29	1.07
16:U:9:VAL:HG23	16:U:70:PRO:HA	1.34	1.07
7:K:115:VAL:HG13	7:K:121:VAL:HG21	1.13	1.06
1:A:2124:A:N1	1:A:2223:U:N3	2.00	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:61:A:N7	1:A:62:C:C4	2.24	1.06
1:A:1077:G:N2	1:A:1170:C:O2	1.87	1.06
7:K:25:LEU:CD1	7:K:59:LYS:HE3	1.84	1.06
8:L:77:VAL:HG13	8:L:81:LYS:HG2	1.36	1.06
13:R:5:ILE:H	13:R:5:ILE:HD12	1.20	1.06
8:L:91:VAL:HB	8:L:122:THR:O	1.54	1.05
1:A:913:A:N1	1:A:961:C:N4	2.04	1.05
12:Q:95:LEU:HD21	13:R:4:ILE:HG21	1.11	1.05
1:A:61:A:N7	1:A:62:C:N4	2.03	1.05
12:Q:109:LEU:CA	13:R:47:LYS:NZ	2.19	1.05
1:A:2465:G:N2	1:A:2466:C:H1'	1.70	1.05
1:A:377:G:O2'	1:A:378:C:H6	1.36	1.05
1:A:1080:G:O6	1:A:1168:G:N1	1.90	1.04
3:C:84:ASP:OD2	3:C:87:ARG:HG2	1.55	1.04
1:A:994:C:H2'	1:A:995:U:C6	1.93	1.04
12:Q:90:VAL:O	13:R:11:GLN:NE2	1.89	1.04
1:A:901:U:N3	1:A:902:G:O6	1.91	1.04
7:K:25:LEU:HD11	7:K:59:LYS:CE	1.88	1.04
1:A:61:A:C8	1:A:62:C:C5	2.45	1.04
1:A:970:A:O2'	17:V:37:GLN:NE2	1.91	1.03
1:A:61:A:C8	1:A:62:C:C4	2.47	1.03
12:Q:96:ALA:O	12:Q:100:VAL:HG23	1.58	1.03
1:A:907:U:C2	1:A:2297:A:H1'	1.93	1.03
1:A:2428:G:C2	1:A:2429:G:C4	2.48	1.02
10:O:22:LEU:HD21	10:O:94:VAL:CG1	1.90	1.02
1:A:673:A:C6	8:L:112:LEU:CD1	2.41	1.02
12:Q:61:TRP:CH2	12:Q:94:MET:CB	2.41	1.02
4:D:98:LYS:HG2	4:D:99:VAL:H	1.23	1.01
1:A:1526:G:N2	1:A:1558:G:H22	1.55	1.01
15:T:43:VAL:HG13	15:T:47:PHE:CD2	1.95	1.01
13:R:25:LEU:HD11	13:R:33:VAL:HG11	1.41	1.01
6:J:61:GLU:HG3	6:J:98:PRO:HG2	1.41	1.01
1:A:2383:A:O2'	17:V:44:ILE:HG12	1.60	1.00
8:L:88:GLY:CA	8:L:121:LEU:HA	1.91	1.00
2:B:77:G:N2	2:B:94:G:H22	1.59	1.00
17:V:54:TYR:CE2	17:V:84:ARG:HD3	1.96	1.00
11:P:100:LEU:HB3	11:P:103:LEU:HD23	1.41	0.99
1:A:1044:C:H5''	12:Q:84:LYS:NZ	1.77	0.99
1:A:775:G:H5'	3:C:13:ARG:NH2	1.76	0.99
1:A:916:G:H2'	1:A:917:A:C8	1.97	0.99
2:B:77:G:H22	2:B:94:G:H22	1.05	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:98:LYS:HE3	4:D:184:ASN:OD1	1.61	0.99
8:L:76:VAL:HG21	8:L:112:LEU:HG	1.43	0.99
7:K:25:LEU:HD11	7:K:59:LYS:HE3	1.02	0.99
1:A:1080:G:C6	1:A:1168:G:C2	2.50	0.99
5:E:192:LEU:HD13	5:E:194:ILE:HD11	1.42	0.99
1:A:2429:G:N1	1:A:2446:C:N3	2.09	0.98
3:C:13:ARG:HG2	3:C:16:MET:SD	2.01	0.98
16:U:46:LYS:HG2	16:U:47:PRO:HD2	1.45	0.98
1:A:2465:G:C2	1:A:2466:C:C1'	2.47	0.98
10:O:22:LEU:HD21	10:O:94:VAL:HG11	0.98	0.98
1:A:1806:U:H3	1:A:1816:A:N6	1.61	0.97
10:O:22:LEU:CD2	10:O:94:VAL:HG11	1.94	0.97
1:A:377:G:O2'	1:A:378:C:C6	2.13	0.97
10:O:11:ARG:HD3	10:O:100:TYR:CZ	2.00	0.97
1:A:61:A:H2'	1:A:62:C:H6	1.25	0.97
16:U:16:ASP:OD2	16:U:38:VAL:CG1	2.12	0.96
11:P:100:LEU:HB3	11:P:103:LEU:CD2	1.93	0.96
1:A:913:A:N1	1:A:961:C:C5	2.33	0.96
4:D:173:ASN:HD21	4:D:207:LYS:HE2	1.31	0.96
2:B:77:G:H22	2:B:94:G:N2	1.64	0.96
5:E:6:LEU:HD21	5:E:17:ILE:HD13	1.44	0.96
14:S:86:ARG:HB2	14:S:96:ILE:HD11	1.46	0.96
4:D:22:LEU:CD1	7:K:74:GLY:HA3	1.96	0.95
17:V:76:LYS:HD2	17:V:90:TYR:CD2	2.00	0.95
14:S:65:ASP:HB3	14:S:68:ASN:HB2	1.47	0.95
12:Q:109:LEU:CA	13:R:47:LYS:HZ1	1.75	0.95
8:L:109:VAL:H	8:L:126:ASN:HD22	1.15	0.95
12:Q:108:GLN:OE1	13:R:47:LYS:CG	2.15	0.95
3:C:150:LYS:CD	3:C:153:GLN:NE2	2.30	0.95
1:A:2444:G:O3'	8:L:65:GLY:HA2	1.68	0.94
17:V:29:LEU:HD21	17:V:49:ARG:NH1	1.82	0.94
4:D:31:ALA:HB3	4:D:53:PHE:HD1	1.30	0.94
3:C:211:SER:O	3:C:216:ILE:HB	1.66	0.93
1:A:970:A:C2'	17:V:37:GLN:NE2	2.32	0.93
1:A:580:U:C2'	12:Q:49:ASP:OD2	2.15	0.93
1:A:994:C:H2'	1:A:995:U:C5	2.02	0.93
1:A:1807:U:O2	1:A:1816:A:C2	2.21	0.93
4:D:29:GLU:OE1	11:P:7:LEU:HD22	1.69	0.93
1:A:2711:G:C8	4:D:12:MET:HG2	2.04	0.93
1:A:1806:U:H3	1:A:1816:A:H62	1.04	0.92
7:K:115:VAL:HG13	7:K:121:VAL:CG2	1.99	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:677:A:H5'	8:L:64:ARG:HD3	1.49	0.92
8:L:88:GLY:CA	8:L:121:LEU:CG	2.47	0.92
14:S:86:ARG:HB2	14:S:96:ILE:CD1	1.98	0.92
17:V:73:GLY:HA2	17:V:92:VAL:HG23	1.48	0.92
7:K:22:ILE:HD11	7:K:42:THR:HG23	1.49	0.92
1:A:1526:G:N2	1:A:1558:G:H1	1.68	0.92
13:R:62:VAL:HG22	13:R:95:VAL:HG22	1.49	0.92
1:A:2384:C:O4'	17:V:44:ILE:HG13	1.69	0.92
1:A:2359:G:H21	17:V:50:GLY:CA	1.83	0.92
1:A:848:G:O6	5:E:53:ASN:ND2	2.03	0.92
1:A:673:A:H62	8:L:112:LEU:HD13	1.18	0.92
6:J:14:ARG:NH1	6:J:122:LYS:HZ1	1.67	0.91
12:Q:86:SER:HA	12:Q:116:GLN:HG3	1.52	0.91
1:A:1080:G:C6	1:A:1168:G:N2	2.39	0.91
3:C:4:LYS:HE3	3:C:20:ASP:CG	1.91	0.91
16:U:16:ASP:OD2	16:U:38:VAL:HG13	1.70	0.90
1:A:970:A:C4'	17:V:37:GLN:NE2	2.35	0.90
6:J:58:ILE:CG2	6:J:129:SER:HA	2.00	0.90
1:A:2428:G:C2	1:A:2429:G:C5	2.58	0.90
1:A:61:A:C5	1:A:62:C:C4	2.59	0.90
1:A:963:G:O2'	1:A:964:A:O4'	1.88	0.90
12:Q:108:GLN:OE1	13:R:47:LYS:HD2	1.72	0.90
12:Q:95:LEU:CD2	13:R:4:ILE:CG2	2.47	0.90
4:D:31:ALA:HB2	4:D:53:PHE:CE1	1.97	0.90
5:E:6:LEU:HD11	5:E:17:ILE:HG23	1.54	0.90
5:E:49:HIS:HD2	5:E:92:PRO:HB2	1.35	0.90
16:U:46:LYS:CG	16:U:47:PRO:CD	2.49	0.90
1:A:2428:G:C6	1:A:2429:G:C5	2.45	0.89
5:E:51:VAL:CG2	5:E:92:PRO:CD	2.41	0.89
16:U:46:LYS:CG	16:U:47:PRO:HD2	2.01	0.89
5:E:51:VAL:HG21	5:E:92:PRO:HD2	0.90	0.89
1:A:2290:C:N3	1:A:2291:U:O4	2.05	0.89
3:C:150:LYS:HD3	3:C:153:GLN:HE22	1.37	0.89
8:L:77:VAL:CG1	8:L:81:LYS:HB2	2.03	0.89
12:Q:95:LEU:CD2	13:R:4:ILE:HG21	1.98	0.89
1:A:530:A:H4'	16:U:45:SER:O	1.71	0.89
2:B:81:G:N2	2:B:92:C:O2	2.04	0.89
4:D:35:VAL:HG21	4:D:91:TYR:HD1	1.36	0.89
2:B:76:A:N6	2:B:96:G:N2	2.21	0.89
16:U:6:GLY:CA	16:U:23:ILE:HB	2.03	0.89
4:D:185:LEU:CD1	11:P:11:ILE:CD1	2.45	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:Q:108:GLN:NE2	13:R:47:LYS:HB2	1.88	0.88
1:A:970:A:O4'	17:V:37:GLN:NE2	2.07	0.88
16:U:6:GLY:HA2	16:U:23:ILE:CB	2.01	0.88
1:A:2360:G:HO2'	17:V:51:THR:HG22	1.33	0.88
1:A:1076:G:O6	1:A:1171:G:N2	2.06	0.88
6:J:18:VAL:HG13	6:J:58:ILE:HD11	1.53	0.88
8:L:88:GLY:HA3	8:L:121:LEU:CG	2.04	0.88
11:P:20:LEU:HD22	11:P:79:VAL:CG1	2.04	0.88
5:E:126:LEU:HD13	5:E:129:LEU:HD13	1.55	0.88
17:V:56:GLY:HA3	17:V:87:VAL:O	1.74	0.88
1:A:1076:G:C6	1:A:1171:G:N2	2.42	0.88
12:Q:95:LEU:HD23	13:R:11:GLN:OE1	1.74	0.88
1:A:1526:G:H21	1:A:1558:G:H22	1.20	0.87
1:A:61:A:C8	1:A:62:C:N4	2.43	0.87
1:A:2290:C:H2'	1:A:2291:U:C6	2.08	0.87
6:J:14:ARG:NH1	6:J:122:LYS:NZ	2.22	0.87
1:A:61:A:C2'	1:A:62:C:C6	2.56	0.87
8:L:74:TYR:HB3	8:L:108:GLY:C	1.93	0.87
12:Q:109:LEU:CD2	13:R:47:LYS:HE3	2.05	0.87
7:K:115:VAL:CG1	7:K:121:VAL:HG21	2.02	0.86
1:A:1526:G:H22	1:A:1558:G:H1	0.87	0.86
5:E:6:LEU:HD21	5:E:17:ILE:CD1	2.05	0.86
8:L:120:LYS:CB	8:L:140:GLY:O	2.24	0.86
1:A:2465:G:N2	1:A:2466:C:C1'	2.38	0.86
1:A:2465:G:H2'	1:A:2466:C:H5'	0.87	0.86
11:P:20:LEU:HD22	11:P:79:VAL:HG11	1.57	0.86
8:L:77:VAL:HG13	8:L:81:LYS:HG3	1.56	0.86
10:O:82:ALA:HB2	10:O:113:ALA:HB1	1.57	0.86
1:A:2228:A:C6	1:A:2254:A:C6	2.64	0.86
1:A:2465:G:N3	1:A:2466:C:O4'	2.09	0.86
8:L:88:GLY:N	8:L:121:LEU:HG	1.90	0.86
4:D:14:GLN:HB3	11:P:58:ILE:CG2	2.04	0.86
6:J:16:TRP:O	6:J:17:LEU:HD23	1.76	0.86
8:L:74:TYR:CB	8:L:108:GLY:O	2.24	0.85
1:A:1043:G:OP1	12:Q:93:LYS:HD3	1.75	0.85
1:A:913:A:N6	1:A:961:C:H5	1.73	0.85
8:L:77:VAL:CG1	8:L:81:LYS:CG	2.51	0.85
14:S:44:SER:N	14:S:45:PRO:HD2	1.90	0.85
1:A:673:A:N7	8:L:112:LEU:HD12	1.90	0.85
1:A:1526:G:N2	1:A:1558:G:N2	2.24	0.85
3:C:16:MET:HB3	3:C:206:GLY:HA3	1.58	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:R:21:TYR:HB3	13:R:93:THR:O	1.77	0.85
8:L:88:GLY:HA3	8:L:121:LEU:CB	2.06	0.85
17:V:47:ARG:HB3	17:V:66:THR:HG22	1.58	0.85
14:S:59:GLU:OE1	14:S:64:MET:O	1.94	0.85
1:A:2428:G:N1	1:A:2429:G:N1	2.23	0.85
1:A:2290:C:H2'	1:A:2291:U:C5	2.11	0.84
1:A:673:A:C5	8:L:112:LEU:HD12	2.12	0.84
5:E:8:ASN:HB2	5:E:127:GLU:OE2	1.77	0.84
1:A:2669:G:H5''	6:J:77:ARG:NH1	1.92	0.84
7:K:73:ASP:OD2	11:P:83:LYS:CE	2.23	0.84
12:Q:86:SER:HA	12:Q:116:GLN:CG	2.07	0.84
5:E:132:ASP:OD2	5:E:133:THR:HG23	1.78	0.84
14:S:86:ARG:CB	14:S:96:ILE:HD11	2.07	0.84
1:A:1806:U:N3	1:A:1816:A:N6	2.24	0.84
1:A:299:U:O2'	1:A:303:G:H1'	1.77	0.84
12:Q:108:GLN:OE1	13:R:47:LYS:CD	2.26	0.84
1:A:61:A:N9	1:A:62:C:C5	2.46	0.84
12:Q:109:LEU:HA	13:R:47:LYS:HZ2	1.06	0.84
1:A:906:G:H1'	1:A:907:U:H5	1.43	0.83
3:C:163:GLN:O	3:C:174:VAL:HG13	1.76	0.83
12:Q:95:LEU:CD2	13:R:11:GLN:CB	2.13	0.83
1:A:970:A:C4'	17:V:37:GLN:HE22	1.89	0.83
12:Q:109:LEU:HA	13:R:47:LYS:HZ1	1.04	0.83
1:A:377:G:HO2'	1:A:378:C:H6	0.96	0.83
5:E:49:HIS:CD2	5:E:92:PRO:HB2	2.13	0.83
4:D:185:LEU:HD12	11:P:11:ILE:HD11	0.87	0.83
7:K:22:ILE:HD11	7:K:42:THR:CG2	2.09	0.83
1:A:2429:G:C2	1:A:2446:C:N3	2.39	0.83
7:K:75:SER:OG	11:P:75:ARG:NH1	2.10	0.83
11:P:52:LYS:HD2	11:P:101:TYR:OH	1.78	0.83
1:A:925:A:N3	1:A:925:A:H5''	1.93	0.83
5:E:6:LEU:HG	5:E:17:ILE:HG12	1.61	0.83
1:A:2432:C:N3	1:A:2444:G:C2	2.47	0.82
1:A:913:A:N1	1:A:961:C:C4	2.47	0.82
6:J:25:THR:HG23	6:J:28:ARG:HB2	1.61	0.82
1:A:2307:A:H5''	17:V:20:ASN:ND2	1.94	0.82
1:A:1125:C:C4	1:A:1126:A:N7	2.47	0.82
12:Q:76:TYR:CZ	12:Q:80:MET:HG2	2.14	0.82
11:P:100:LEU:CB	11:P:103:LEU:HD21	2.09	0.82
12:Q:95:LEU:CD2	13:R:11:GLN:CG	2.58	0.82
1:A:2096:G:N1	1:A:2473:G:C6	2.48	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2101:G:N1	1:A:2466:C:O2	2.12	0.82
1:A:994:C:C4	1:A:995:U:O4	2.33	0.82
1:A:1044:C:H5''	12:Q:84:LYS:HZ2	1.44	0.81
1:A:907:U:O2	1:A:2297:A:C8	2.33	0.81
1:A:916:G:C2'	1:A:917:A:C8	2.63	0.81
5:E:4:VAL:HG21	5:E:123:ILE:HD11	1.62	0.81
17:V:29:LEU:HD21	17:V:49:ARG:CZ	2.10	0.81
1:A:673:A:C5	8:L:112:LEU:CD1	2.63	0.81
12:Q:95:LEU:HD21	13:R:4:ILE:HG23	1.62	0.80
1:A:2096:G:C6	1:A:2473:G:C6	2.69	0.80
3:C:4:LYS:NZ	3:C:20:ASP:OD1	2.14	0.80
6:J:14:ARG:CZ	6:J:122:LYS:HZ1	1.93	0.80
20:Y:14:ILE:HG12	20:Y:57:ILE:HD13	1.61	0.80
4:D:25:VAL:HG12	4:D:188:ILE:O	1.80	0.80
7:K:25:LEU:CD1	7:K:59:LYS:CE	2.52	0.80
1:A:2465:G:HO2'	1:A:2466:C:H5''	1.44	0.80
1:A:902:G:H22	1:A:970:A:H2	1.26	0.79
4:D:31:ALA:CB	4:D:53:PHE:CD1	2.50	0.79
8:L:88:GLY:CA	8:L:121:LEU:CB	2.61	0.79
8:L:88:GLY:HA3	8:L:121:LEU:HG	1.61	0.79
16:U:16:ASP:CG	16:U:38:VAL:HG13	2.02	0.79
1:A:2359:G:H21	17:V:50:GLY:HA2	1.47	0.79
1:A:902:G:N2	1:A:970:A:H2	1.81	0.79
8:L:120:LYS:C	8:L:121:LEU:CD1	2.47	0.79
1:A:1044:C:H5''	12:Q:84:LYS:HZ1	1.47	0.79
15:T:47:PHE:CG	15:T:90:ILE:HD13	2.16	0.79
1:A:2297:A:N3	1:A:2297:A:H5''	1.97	0.79
16:U:46:LYS:HG3	16:U:47:PRO:HD3	1.64	0.79
3:C:18:THR:CG2	3:C:210:ARG:HH22	1.95	0.79
15:T:13:ILE:HD13	20:Y:34:THR:HG23	1.64	0.78
1:A:605:G:HO2'	12:Q:45:TYR:HH	1.18	0.78
16:U:9:VAL:HG23	16:U:70:PRO:CA	2.12	0.78
1:A:1818:A:OP1	3:C:221:ARG:HG3	1.83	0.78
15:T:30:VAL:HG12	15:T:31:ASP:N	1.98	0.78
1:A:2465:G:C2	1:A:2466:C:H1'	2.17	0.78
8:L:77:VAL:CG1	8:L:81:LYS:CB	2.61	0.78
1:A:2290:C:C2	1:A:2291:U:C4	2.71	0.78
4:D:35:VAL:HG21	4:D:91:TYR:CD1	2.16	0.78
11:P:100:LEU:CB	11:P:103:LEU:CD2	2.62	0.78
12:Q:86:SER:HB2	12:Q:116:GLN:CB	2.14	0.78
1:A:1197:A:O3'	12:Q:81:HIS:HB2	1.84	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:61:A:H3'	1:A:62:C:C5	2.18	0.77
17:V:47:ARG:CB	17:V:66:THR:HG22	2.13	0.77
20:Y:14:ILE:HG12	20:Y:57:ILE:CD1	2.14	0.77
5:E:51:VAL:HG23	5:E:92:PRO:HD2	1.65	0.77
8:L:109:VAL:H	8:L:126:ASN:ND2	1.80	0.77
1:A:913:A:C2	1:A:961:C:N4	2.53	0.77
6:J:61:GLU:CG	6:J:98:PRO:HG2	2.14	0.76
1:A:64:A:C8	1:A:64:A:OP2	2.38	0.76
11:P:100:LEU:HB2	11:P:103:LEU:HD21	1.65	0.76
5:E:148:VAL:HG22	5:E:191:LYS:HD3	1.66	0.76
1:A:2383:A:O2'	17:V:44:ILE:CG1	2.34	0.76
16:U:49:GLN:NE2	16:U:49:GLN:HA	2.00	0.76
4:D:98:LYS:CE	4:D:184:ASN:OD1	2.33	0.76
2:B:93:U:H2'	2:B:94:G:H5'	1.68	0.76
3:C:150:LYS:CD	3:C:153:GLN:HE21	1.97	0.76
12:Q:76:TYR:CE1	12:Q:80:MET:HG2	2.21	0.76
1:A:530:A:H5''	16:U:46:LYS:CD	2.16	0.76
17:V:76:LYS:HD2	17:V:90:TYR:HD2	1.51	0.76
5:E:42:ALA:O	5:E:45:ARG:HG2	1.86	0.76
17:V:45:LEU:HD21	17:V:87:VAL:HG11	1.67	0.75
13:R:47:LYS:HG2	13:R:48:VAL:H	1.51	0.75
15:T:13:ILE:CD1	20:Y:34:THR:HG23	2.17	0.75
1:A:2664:U:O2'	4:D:82:GLU:OE2	2.03	0.75
1:A:1807:U:O4	1:A:1815:A:N1	2.19	0.75
13:R:5:ILE:H	13:R:5:ILE:CD1	1.98	0.75
1:A:970:A:H4'	17:V:37:GLN:HE22	1.50	0.75
8:L:74:TYR:HD1	8:L:108:GLY:N	1.84	0.75
8:L:76:VAL:HG22	8:L:112:LEU:HG	1.66	0.75
1:A:902:G:N2	1:A:970:A:C2	2.52	0.75
2:B:11:A:OP2	2:B:11:A:H4'	1.87	0.75
1:A:2711:G:C2	4:D:24:PRO:HG3	2.22	0.75
5:E:148:VAL:HG11	5:E:152:ALA:HB2	1.68	0.75
8:L:125:ALA:O	8:L:145:VAL:HG13	1.87	0.75
1:A:901:U:C3'	1:A:902:G:C8	2.70	0.74
1:A:970:A:HO2'	17:V:37:GLN:HG2	1.51	0.74
1:A:2122:G:H21	1:A:2227:A:H62	1.35	0.74
1:A:2098:G:O6	1:A:2471:C:N4	2.20	0.74
5:E:6:LEU:CD2	5:E:17:ILE:CD1	2.65	0.74
17:V:54:TYR:CD2	17:V:84:ARG:CD	2.69	0.74
5:E:126:LEU:CD1	5:E:129:LEU:HD13	2.17	0.74
7:K:70:ARG:HH11	7:K:70:ARG:HG2	1.51	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:673:A:H62	8:L:112:LEU:CD1	1.87	0.74
12:Q:109:LEU:HD23	13:R:47:LYS:HE3	1.69	0.74
1:A:905:G:C4'	1:A:2298:A:OP2	2.28	0.74
8:L:77:VAL:HG11	8:L:81:LYS:HB2	1.67	0.74
2:B:80:G:H4'	2:B:80:G:OP1	1.87	0.74
8:L:74:TYR:HD1	8:L:108:GLY:CA	2.00	0.74
8:L:91:VAL:CB	8:L:122:THR:O	2.34	0.74
17:V:76:LYS:HD2	17:V:90:TYR:CE2	2.23	0.74
1:A:677:A:H5'	8:L:64:ARG:CD	2.17	0.73
2:B:71:A:H2'	2:B:72:U:H5'	1.70	0.73
8:L:79:LEU:HD21	8:L:117:LEU:HG	1.70	0.73
12:Q:61:TRP:CE2	12:Q:94:MET:CB	2.59	0.73
12:Q:58:ARG:NH1	12:Q:93:LYS:HE2	2.03	0.73
4:D:47:GLU:HG2	4:D:88:MET:CE	2.19	0.73
11:P:74:GLU:OE1	11:P:104:ARG:HD3	1.88	0.73
4:D:98:LYS:HG2	4:D:99:VAL:N	2.03	0.73
8:L:88:GLY:HA2	8:L:121:LEU:HG	1.68	0.73
4:D:98:LYS:CG	4:D:99:VAL:H	2.01	0.73
1:A:1080:G:C5	1:A:1168:G:N2	2.56	0.73
1:A:996:G:N1	1:A:1014:A:N1	2.36	0.73
16:U:46:LYS:CG	16:U:47:PRO:HD3	2.18	0.73
3:C:13:ARG:HA	3:C:16:MET:HG2	1.70	0.72
8:L:79:LEU:CD1	8:L:117:LEU:HD21	2.19	0.72
1:A:916:G:C3'	1:A:917:A:C8	2.72	0.72
4:D:35:VAL:CG2	4:D:91:TYR:CD1	2.72	0.72
1:A:2099:G:C2	1:A:2471:C:N3	2.57	0.72
1:A:1080:G:O6	1:A:1168:G:C2	2.40	0.72
1:A:2465:G:C2	1:A:2466:C:O4'	2.42	0.72
1:A:970:A:OP1	1:A:970:A:H4'	1.89	0.72
1:A:1197:A:H4'	12:Q:81:HIS:CD2	2.24	0.72
1:A:901:U:C2	1:A:902:G:C6	2.77	0.72
6:J:58:ILE:HG22	6:J:129:SER:HA	1.72	0.72
1:A:61:A:H3'	1:A:62:C:H5	1.53	0.72
12:Q:112:ALA:HB3	13:R:47:LYS:HZ3	1.54	0.72
10:O:92:ASP:OD1	10:O:92:ASP:N	2.23	0.71
1:A:907:U:N3	1:A:2297:A:H1'	2.04	0.71
2:B:76:A:N6	2:B:96:G:H21	1.87	0.71
16:U:46:LYS:HG2	16:U:47:PRO:CD	2.17	0.71
11:P:100:LEU:O	11:P:103:LEU:HG	1.91	0.71
4:D:25:VAL:CG1	4:D:188:ILE:O	2.38	0.71
6:J:88:ARG:CZ	6:J:97:TYR:OH	2.39	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:R:47:LYS:HG2	13:R:48:VAL:N	2.06	0.71
1:A:2122:G:H1	1:A:2225:C:H42	1.39	0.70
1:A:2836:G:OP1	4:D:62:ASN:HB3	1.91	0.70
12:Q:72:ASN:ND2	12:Q:107:ASN:OD1	2.24	0.70
1:A:2290:C:C2	1:A:2291:U:C5	2.79	0.70
3:C:71:LYS:O	3:C:118:SER:OG	2.09	0.70
11:P:79:VAL:HG12	11:P:79:VAL:O	1.91	0.70
7:K:73:ASP:CG	11:P:83:LYS:HE2	2.10	0.70
4:D:9:LYS:HA	4:D:28:ILE:HA	1.72	0.70
1:A:2394:G:OP1	17:V:62:GLY:HA2	1.91	0.70
3:C:150:LYS:CE	3:C:153:GLN:HE21	2.04	0.70
12:Q:109:LEU:HD22	13:R:47:LYS:HE3	1.73	0.70
2:B:12:U:H2'	2:B:12:U:OP1	1.91	0.70
10:O:101:LEU:O	10:O:103:HIS:N	2.25	0.70
1:A:2228:A:N6	1:A:2254:A:C5	2.59	0.70
2:B:77:G:N2	2:B:94:G:N2	2.30	0.70
5:E:6:LEU:CD2	5:E:17:ILE:HD13	2.21	0.70
8:L:120:LYS:CB	8:L:140:GLY:C	2.60	0.70
10:O:34:PHE:HB3	10:O:41:TYR:HB2	1.74	0.70
2:B:91:C:C4	2:B:92:C:N4	2.59	0.69
4:D:173:ASN:ND2	4:D:207:LYS:HE2	2.04	0.69
4:D:9:LYS:CA	4:D:28:ILE:HG23	2.21	0.69
17:V:54:TYR:CE2	17:V:84:ARG:NH1	2.54	0.69
1:A:903:G:H2'	1:A:903:G:N3	2.06	0.69
15:T:43:VAL:CG1	15:T:47:PHE:CD2	2.75	0.69
15:T:43:VAL:CG1	15:T:47:PHE:HD2	2.05	0.69
1:A:907:U:C2	1:A:2297:A:C1'	2.72	0.69
1:A:1042:A:O2'	12:Q:92:ARG:NE	2.15	0.69
1:A:2428:G:N2	1:A:2429:G:C4	2.60	0.69
1:A:996:G:C6	1:A:1014:A:N1	2.61	0.69
1:A:906:G:C5	1:A:963:G:O6	2.45	0.69
1:A:1520:A:H61	1:A:1564:C:H42	1.40	0.69
5:E:177:GLU:HG3	5:E:179:ASN:H	1.58	0.69
12:Q:109:LEU:CA	13:R:47:LYS:HZ2	1.94	0.69
8:L:83:ASN:O	8:L:83:ASN:OD1	2.10	0.68
17:V:80:PHE:HB2	17:V:84:ARG:HG2	1.74	0.68
10:O:75:THR:HG23	10:O:109:LEU:CD2	2.23	0.68
12:Q:95:LEU:HD23	13:R:11:GLN:CD	2.12	0.68
15:T:43:VAL:HG13	15:T:47:PHE:HD2	1.50	0.68
1:A:996:G:N1	1:A:1014:A:C2	2.60	0.68
6:J:78:HIS:ND1	6:J:79:THR:O	2.26	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2297:A:N3	1:A:2297:A:H3'	2.08	0.68
1:A:911:G:N2	1:A:960:U:H3	1.91	0.68
1:A:2468:A:N3	1:A:2468:A:H2'	2.07	0.68
4:D:32:PRO:HB3	4:D:96:GLU:OE1	1.94	0.68
1:A:2122:G:N2	1:A:2226:U:O2	2.27	0.68
1:A:1526:G:N2	1:A:1558:G:N1	2.35	0.67
1:A:580:U:H2'	12:Q:49:ASP:OD2	1.94	0.67
1:A:901:U:C2'	1:A:902:G:N7	2.40	0.67
2:B:11:A:O2'	2:B:13:A:H2'	1.93	0.67
4:D:57:ARG:HD2	4:D:59:LYS:HB3	1.75	0.67
10:O:11:ARG:HG2	10:O:99:GLY:HA3	1.77	0.67
1:A:298:U:OP1	1:A:298:U:H4'	1.95	0.67
1:A:2465:G:C3'	1:A:2466:C:H5'	2.23	0.67
3:C:84:ASP:OD2	3:C:87:ARG:CG	2.37	0.67
4:D:13:THR:CG2	11:P:8:ILE:CG2	2.72	0.67
12:Q:58:ARG:HH12	12:Q:93:LYS:HE2	1.58	0.67
2:B:71:A:C2'	2:B:72:U:H5'	2.24	0.67
7:K:10:VAL:HG21	7:K:16:ALA:HB3	1.77	0.67
1:A:2428:G:N2	1:A:2429:G:N3	2.42	0.67
5:E:6:LEU:CG	5:E:17:ILE:HG12	2.25	0.67
1:A:2428:G:N1	1:A:2429:G:C4	2.61	0.67
1:A:2898:A:HO2'	9:N:2:SER:N	1.93	0.67
20:Y:9:LEU:HB3	20:Y:12:ALA:HB3	1.75	0.66
2:B:93:U:O5'	2:B:93:U:H6	1.79	0.66
4:D:28:ILE:HD11	4:D:188:ILE:HD12	1.76	0.66
1:A:1807:U:N3	1:A:1816:A:C6	2.62	0.66
1:A:2359:G:N2	17:V:50:GLY:HA2	2.11	0.66
1:A:906:G:C2	1:A:963:G:N7	2.63	0.66
1:A:1842:C:OP1	3:C:40:LYS:NZ	2.29	0.66
1:A:1820:A:N6	1:A:1857:G:O2'	2.28	0.66
8:L:74:TYR:CD1	8:L:108:GLY:HA3	2.31	0.66
1:A:1081:U:H6	1:A:1081:U:O5'	1.79	0.66
1:A:2226:U:H6	1:A:2226:U:O5'	1.79	0.66
6:J:58:ILE:HG22	6:J:128:GLY:O	1.95	0.66
6:J:89:THR:OG1	6:J:92:GLU:HB2	1.94	0.66
8:L:79:LEU:HD11	8:L:117:LEU:HD21	1.78	0.66
1:A:2096:G:O6	1:A:2473:G:O6	2.13	0.66
6:J:29:LEU:HG	6:J:29:LEU:O	1.94	0.66
1:A:995:U:H6	1:A:995:U:O5'	1.78	0.66
1:A:2415:U:O2'	17:V:64:ASP:OD1	2.13	0.66
15:T:47:PHE:CD1	15:T:90:ILE:HD13	2.31	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:R:5:ILE:N	13:R:5:ILE:HD12	2.03	0.65
13:R:21:TYR:CB	13:R:93:THR:O	2.42	0.65
1:A:1076:G:C6	1:A:1171:G:C2	2.84	0.65
1:A:2292:C:H6	1:A:2292:C:O5'	1.79	0.65
1:A:607:G:H21	12:Q:37:GLN:HE22	1.43	0.65
1:A:901:U:H2'	1:A:902:G:C5	2.30	0.65
1:A:2228:A:C5	1:A:2254:A:C6	2.84	0.65
1:A:530:A:H5''	16:U:46:LYS:HD2	1.78	0.65
14:S:44:SER:N	14:S:45:PRO:CD	2.59	0.65
16:U:38:VAL:HG12	16:U:39:ASN:N	2.12	0.65
3:C:171:TYR:HB2	3:C:183:MET:CE	2.25	0.65
16:U:9:VAL:HG22	16:U:69:MET:O	1.95	0.65
1:A:1042:A:HO2'	12:Q:92:ARG:HE	1.41	0.65
7:K:75:SER:HG	11:P:75:ARG:HH12	1.42	0.65
12:Q:61:TRP:CZ2	12:Q:94:MET:CG	2.80	0.65
12:Q:95:LEU:HD22	13:R:11:GLN:CG	2.16	0.65
6:J:58:ILE:HG21	6:J:129:SER:HA	1.79	0.65
13:R:2:TYR:CD2	13:R:13:LYS:HE2	2.32	0.65
10:O:29:PRO:O	10:O:93:VAL:HG23	1.97	0.64
1:A:906:G:C6	1:A:963:G:N7	2.66	0.64
5:E:8:ASN:CB	5:E:127:GLU:OE2	2.45	0.64
1:A:530:A:H5''	16:U:46:LYS:HD3	1.79	0.64
1:A:304:G:N2	1:A:415:C:N3	2.46	0.64
12:Q:61:TRP:CH2	12:Q:94:MET:HB3	2.31	0.64
1:A:2225:C:H6	1:A:2225:C:O5'	1.81	0.64
1:A:2374:G:H5'	1:A:2376:C:H5'	1.79	0.64
4:D:87:GLU:OE1	4:D:87:GLU:HA	1.97	0.64
5:E:177:GLU:HG3	5:E:178:ALA:N	2.12	0.64
1:A:910:A:OP1	1:A:910:A:H4'	1.97	0.64
1:A:965:A:H8	1:A:965:A:O5'	1.80	0.64
8:L:126:ASN:O	8:L:145:VAL:CG1	2.46	0.64
8:L:77:VAL:HG13	8:L:81:LYS:CB	2.25	0.64
1:A:604:C:O2'	12:Q:48:ARG:NH1	2.31	0.64
16:U:6:GLY:HA3	16:U:23:ILE:O	1.97	0.64
12:Q:94:MET:HG2	12:Q:94:MET:O	1.98	0.64
1:A:61:A:C5	1:A:62:C:N3	2.66	0.64
1:A:999:A:N1	1:A:1011:C:N3	2.45	0.64
2:B:77:G:O5'	2:B:77:G:H8	1.80	0.64
1:A:2295:A:C4'	1:A:2296:A:OP2	2.46	0.64
2:B:92:C:O5'	2:B:92:C:H6	1.81	0.64
15:T:30:VAL:CG1	15:T:31:ASP:N	2.61	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:906:G:H1'	1:A:907:U:C5	2.31	0.63
13:R:11:GLN:O	13:R:12:ILE:HG13	1.97	0.63
1:A:1077:G:H8	1:A:1077:G:O5'	1.81	0.63
1:A:912:C:H42	1:A:956:A:H62	1.46	0.63
1:A:913:A:N6	1:A:961:C:C5	2.59	0.63
1:A:994:C:C2	1:A:995:U:C4	2.87	0.63
8:L:74:TYR:CD1	8:L:108:GLY:CA	2.82	0.63
15:T:49:VAL:HG13	15:T:87:SER:OG	1.98	0.63
12:Q:109:LEU:HA	13:R:47:LYS:CE	2.24	0.63
1:A:2757:U:OP1	7:K:70:ARG:CD	2.47	0.63
1:A:61:A:C2'	1:A:62:C:H6	2.02	0.63
17:V:54:TYR:HE2	17:V:84:ARG:HH11	1.40	0.63
1:A:1494:G:H1	1:A:1509:C:H42	1.45	0.63
1:A:2465:G:C3'	1:A:2466:C:C5'	2.76	0.63
7:K:63:VAL:HG13	7:K:102:VAL:HG13	1.80	0.63
8:L:88:GLY:CA	8:L:121:LEU:CA	2.60	0.63
1:A:2465:G:C2	1:A:2466:C:N1	2.66	0.63
1:A:2039:G:H5'	14:S:42:ALA:HB2	1.81	0.63
4:D:13:THR:HG22	11:P:8:ILE:CG2	2.27	0.62
17:V:56:GLY:CA	17:V:87:VAL:O	2.44	0.62
1:A:2432:C:C2	1:A:2444:G:N2	2.67	0.62
4:D:25:VAL:HG13	4:D:189:LYS:HA	1.81	0.62
5:E:148:VAL:HG13	5:E:191:LYS:HD2	1.80	0.62
1:A:224:A:H1'	1:A:236:A:H1'	1.81	0.62
14:S:44:SER:H	14:S:45:PRO:HD2	1.63	0.62
16:U:46:LYS:CB	16:U:47:PRO:CD	2.76	0.62
1:A:2307:A:H5''	17:V:20:ASN:HD22	1.62	0.62
1:A:1078:A:H8	1:A:1078:A:O5'	1.81	0.62
1:A:901:U:C4	1:A:902:G:O6	2.52	0.62
1:A:922:A:N7	1:A:923:C:N4	2.47	0.62
11:P:17:ARG:HG2	11:P:17:ARG:HH11	1.65	0.62
1:A:2757:U:H5''	7:K:70:ARG:HE	1.63	0.62
8:L:88:GLY:HA2	8:L:121:LEU:CB	2.29	0.62
1:A:1076:G:O6	1:A:1171:G:C2	2.52	0.62
1:A:916:G:O3'	1:A:917:A:H8	1.83	0.62
12:Q:88:ILE:O	13:R:51:PRO:HD3	1.85	0.62
1:A:922:A:H3'	1:A:923:C:C5	2.35	0.62
1:A:910:A:N6	1:A:960:U:O4	2.31	0.62
15:T:66:VAL:O	15:T:66:VAL:HG12	2.00	0.62
1:A:917:A:H8	1:A:917:A:P	2.23	0.61
10:O:75:THR:HG23	10:O:109:LEU:HG	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2093:C:O5'	1:A:2093:C:H6	1.82	0.61
1:A:2465:G:C4	1:A:2466:C:C6	2.89	0.61
1:A:904:A:C2	1:A:967:G:O6	2.54	0.61
3:C:171:TYR:HB2	3:C:183:MET:HE1	1.83	0.61
1:A:1263:G:N7	13:R:70:LYS:NZ	2.49	0.61
12:Q:95:LEU:HD23	13:R:11:GLN:CG	2.30	0.61
13:R:47:LYS:CG	13:R:48:VAL:H	2.13	0.61
1:A:921:G:O5'	1:A:921:G:H8	1.83	0.61
1:A:996:G:C2	1:A:1014:A:C2	2.88	0.61
1:A:901:U:C2	1:A:902:G:O6	2.54	0.61
1:A:2290:C:N3	1:A:2291:U:C4	2.69	0.61
6:J:14:ARG:HG2	6:J:52:GLY:O	1.99	0.61
20:Y:14:ILE:HD11	20:Y:57:ILE:CG2	2.30	0.61
1:A:2228:A:N6	1:A:2254:A:C6	2.68	0.60
4:D:111:THR:HG22	4:D:170:THR:HG23	1.83	0.60
7:K:63:VAL:HG12	7:K:64:ARG:HG3	1.83	0.60
1:A:677:A:P	8:L:64:ARG:NH1	2.73	0.60
1:A:644:G:N2	1:A:650:U:OP1	2.33	0.60
1:A:907:U:H3	1:A:2297:A:H8	1.49	0.60
4:D:13:THR:CG2	11:P:8:ILE:HG23	2.30	0.60
1:A:325:A:N1	1:A:402:U:O2'	2.35	0.60
1:A:458:G:OP2	1:A:2435:C:O2'	2.19	0.60
4:D:36:LEU:HB2	4:D:50:GLN:O	2.02	0.60
1:A:2757:U:H5''	7:K:70:ARG:NE	2.16	0.60
1:A:907:U:C2	1:A:2297:A:C8	2.90	0.60
5:E:174:THR:O	5:E:174:THR:HG23	2.02	0.60
12:Q:92:ARG:HB2	13:R:11:GLN:HB2	1.83	0.60
12:Q:90:VAL:C	13:R:11:GLN:HE22	1.97	0.60
1:A:925:A:H8	1:A:947:A:N1	2.00	0.60
1:A:2307:A:OP2	17:V:20:ASN:ND2	2.35	0.60
1:A:2360:G:O2'	17:V:51:THR:HG23	1.99	0.60
1:A:917:A:C8	1:A:917:A:P	2.95	0.60
14:S:53:SER:O	14:S:57:ASN:ND2	2.35	0.60
1:A:2383:A:C2'	17:V:44:ILE:HG12	2.32	0.60
1:A:910:A:N1	1:A:960:U:O4	2.34	0.59
1:A:922:A:H2	1:A:949:U:H3	1.49	0.59
5:E:19:LEU:HD12	5:E:19:LEU:N	2.16	0.59
1:A:1482:G:H21	1:A:1562:A:H8	1.50	0.59
1:A:2095:C:H2'	1:A:2096:G:C8	2.37	0.59
1:A:996:G:O5'	1:A:996:G:H8	1.85	0.59
2:B:75:U:C4	2:B:96:G:N2	2.70	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2749:U:OP1	11:P:54:ARG:NH1	2.36	0.59
1:A:503:C:H2'	15:T:69:TYR:HE1	1.66	0.59
8:L:110:LYS:HG3	8:L:127:LYS:HB2	1.84	0.59
1:A:969:C:O2	17:V:34:ALA:HB2	2.03	0.59
12:Q:51:ARG:HG3	12:Q:51:ARG:HH11	1.66	0.59
17:V:39:VAL:HG13	17:V:43:SER:OG	2.03	0.59
20:Y:6:ILE:O	20:Y:60:ARG:NH2	2.36	0.59
4:D:9:LYS:HA	4:D:28:ILE:HG23	1.83	0.59
11:P:36:VAL:HG12	11:P:36:VAL:O	2.01	0.59
5:E:5:ALA:HA	5:E:16:ASP:HA	1.83	0.59
12:Q:86:SER:HB2	12:Q:116:GLN:HB2	1.84	0.59
1:A:1197:A:H4'	12:Q:81:HIS:CG	2.37	0.59
1:A:998:G:O6	1:A:1012:G:C2	2.33	0.59
1:A:1082:G:H2'	1:A:1083:G:C8	2.37	0.59
3:C:53:HIS:HA	3:C:217:ARG:HB2	1.85	0.59
7:K:24:VAL:HG11	7:K:30:ARG:HD2	1.83	0.59
1:A:998:G:N2	1:A:2296:A:H1'	2.18	0.58
4:D:93:VAL:O	4:D:93:VAL:HG12	2.01	0.58
8:L:77:VAL:HG11	8:L:81:LYS:CB	2.30	0.58
12:Q:95:LEU:HD11	13:R:4:ILE:HG23	1.83	0.58
1:A:903:G:H1'	17:V:35:ASP:HB2	1.85	0.58
17:V:47:ARG:HB3	17:V:66:THR:CG2	2.33	0.58
1:A:1578:G:N2	1:A:1587:U:OP2	2.34	0.58
1:A:2773:G:OP2	1:A:2784:C:N4	2.36	0.58
4:D:185:LEU:CD1	11:P:11:ILE:HD12	2.32	0.58
7:K:70:ARG:NH1	7:K:70:ARG:HG2	2.15	0.58
12:Q:86:SER:CA	12:Q:116:GLN:CG	2.81	0.58
4:D:114:SER:OG	4:D:115:LYS:N	2.36	0.58
12:Q:94:MET:O	12:Q:98:LEU:HD13	2.04	0.58
1:A:2228:A:C6	1:A:2254:A:C5	2.91	0.58
3:C:142:HIS:ND1	3:C:193:GLY:O	2.37	0.58
1:A:2039:G:H5''	14:S:42:ALA:HB3	1.86	0.58
1:A:1087:U:O2'	1:A:1160:G:N2	2.36	0.58
10:O:29:PRO:O	10:O:93:VAL:CG2	2.51	0.58
1:A:963:G:H2'	1:A:964:A:H5''	1.84	0.58
7:K:30:ARG:NH1	7:K:37:ASP:OD1	2.37	0.58
1:A:2669:G:H5''	6:J:77:ARG:HH11	1.69	0.58
10:O:78:GLY:HA3	10:O:109:LEU:CD2	2.34	0.58
12:Q:68:ALA:HB1	12:Q:106:PHE:CE2	2.38	0.58
1:A:1075:A:H2'	1:A:1076:G:H5'	1.85	0.58
1:A:1231:G:H2'	1:A:1232:G:H8	1.69	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1257:C:OP1	12:Q:15:LYS:NZ	2.36	0.58
1:A:2472:C:H6	1:A:2472:C:O5'	1.85	0.58
11:P:51:ILE:HG22	11:P:52:LYS:HG3	1.85	0.58
1:A:61:A:C3'	1:A:62:C:C5	2.85	0.58
1:A:957:A:O2'	1:A:2293:C:O3'	2.16	0.58
9:N:22:THR:HG21	9:N:67:ARG:H	1.68	0.58
16:U:46:LYS:CB	16:U:47:PRO:HD2	2.34	0.58
1:A:1845:A:N6	1:A:2242:U:O4	2.37	0.57
1:A:916:G:C3'	1:A:917:A:H8	2.16	0.57
3:C:150:LYS:HE2	3:C:153:GLN:HE21	1.67	0.57
1:A:1077:G:C2	1:A:1170:C:N3	2.72	0.57
1:A:1585:A:H62	1:A:1586:G:H21	1.52	0.57
4:D:9:LYS:CB	4:D:28:ILE:HG23	2.35	0.57
8:L:23:ILE:HG12	13:R:81:ASN:HB3	1.86	0.57
8:L:79:LEU:HD11	8:L:117:LEU:HD11	1.85	0.57
13:R:5:ILE:CD1	13:R:14:VAL:HB	2.35	0.57
1:A:2428:G:N1	1:A:2429:G:C2	2.69	0.57
8:L:88:GLY:C	8:L:121:LEU:HA	2.24	0.57
10:O:71:THR:OG1	10:O:72:SER:N	2.36	0.57
1:A:2359:G:N2	17:V:50:GLY:CA	2.63	0.57
7:K:23:LYS:HG2	7:K:24:VAL:N	2.18	0.57
13:R:67:ARG:HB3	13:R:89:ARG:HH11	1.70	0.57
1:A:1094:A:OP2	1:A:1156:G:N2	2.38	0.57
1:A:673:A:O2'	1:A:674:G:O4'	2.22	0.57
1:A:848:G:C6	5:E:53:ASN:ND2	2.60	0.57
1:A:2295:A:N6	1:A:2302:A:OP2	2.36	0.57
17:V:41:GLY:N	17:V:72:ASP:OD1	2.30	0.57
1:A:1558:G:H8	1:A:1558:G:O5'	1.87	0.57
1:A:61:A:C2'	1:A:62:C:C5	2.88	0.57
4:D:35:VAL:CG2	4:D:91:TYR:HD1	2.10	0.57
11:P:34:LYS:O	11:P:83:LYS:NZ	2.37	0.57
12:Q:92:ARG:HD3	13:R:11:GLN:CD	2.25	0.57
1:A:299:U:OP1	1:A:299:U:H4'	2.05	0.57
1:A:761:U:N3	1:A:764:C:OP2	2.37	0.57
1:A:852:G:N2	1:A:876:A:OP1	2.38	0.57
14:S:86:ARG:HB2	14:S:96:ILE:HD12	1.82	0.57
1:A:2092:C:N4	1:A:2475:G:O6	2.37	0.57
1:A:61:A:C4	1:A:62:C:C5	2.92	0.57
4:D:96:GLU:O	4:D:97:VAL:C	2.42	0.57
5:E:50:LYS:HG3	5:E:50:LYS:O	2.04	0.57
7:K:73:ASP:CG	11:P:83:LYS:CD	2.73	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2874:G:O2'	1:A:2891:G:N2	2.37	0.56
3:C:210:ARG:HA	3:C:213:TRP:HB2	1.87	0.56
11:P:13:LYS:HG2	11:P:13:LYS:O	2.05	0.56
1:A:2295:A:H4'	1:A:2296:A:OP2	2.04	0.56
1:A:364:A:N3	5:E:169:ASN:ND2	2.53	0.56
2:B:76:A:O5'	2:B:76:A:H8	1.87	0.56
2:B:13:A:H3'	2:B:14:G:H8	1.70	0.56
2:B:75:U:O4	2:B:96:G:C2	2.58	0.56
4:D:47:GLU:CG	4:D:88:MET:CE	2.82	0.56
1:A:2307:A:C5'	17:V:20:ASN:ND2	2.67	0.56
1:A:2365:A:H61	17:V:51:THR:HG21	1.69	0.56
3:C:18:THR:CG2	3:C:210:ARG:NH2	2.68	0.56
1:A:1513:U:H3	1:A:1572:G:H1	1.54	0.56
12:Q:38:GLN:O	12:Q:42:SER:HB3	2.05	0.56
1:A:1433:U:H4'	1:A:1648:A:H4'	1.88	0.56
1:A:1807:U:C2	1:A:1816:A:C6	2.91	0.56
1:A:2095:C:O5'	1:A:2095:C:H6	1.88	0.56
1:A:906:G:C6	1:A:963:G:O6	2.58	0.56
3:C:37:LEU:HD22	3:C:62:TYR:HB2	1.87	0.56
10:O:29:PRO:C	10:O:93:VAL:HG23	2.26	0.56
1:A:1335:A:OP1	1:A:2738:G:O2'	2.23	0.56
4:D:107:ILE:HG22	4:D:205:ALA:CB	2.36	0.56
8:L:74:TYR:CA	8:L:108:GLY:O	2.53	0.56
20:Y:14:ILE:HD11	20:Y:57:ILE:HG23	1.88	0.56
18:Z:18:ASP:N	18:Z:18:ASP:OD1	2.38	0.56
5:E:51:VAL:HG11	5:E:88:VAL:HG11	1.88	0.56
1:A:2874:G:O6	11:P:24:ARG:NH2	2.39	0.56
3:C:13:ARG:HA	3:C:16:MET:CG	2.35	0.56
13:R:47:LYS:CG	13:R:48:VAL:N	2.69	0.56
1:A:1526:G:N2	1:A:1558:G:C2	2.68	0.56
1:A:2433:C:H2'	1:A:2434:G:O4'	2.06	0.56
17:V:79:ARG:HA	17:V:85:LYS:HA	1.87	0.56
3:C:194:GLN:NE2	3:C:198:GLU:OE1	2.39	0.56
7:K:23:LYS:HG2	7:K:24:VAL:H	1.70	0.56
1:A:84:A:N6	1:A:101:G:O2'	2.39	0.55
2:B:91:C:C5	2:B:92:C:N4	2.74	0.55
3:C:53:HIS:ND1	3:C:219:THR:HG22	2.21	0.55
1:A:2669:G:H5''	6:J:77:ARG:HH12	1.68	0.55
8:L:117:LEU:HD12	8:L:135:ALA:O	2.04	0.55
11:P:79:VAL:CG1	11:P:79:VAL:O	2.53	0.55
14:S:18:ARG:NH1	14:S:76:VAL:O	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2096:G:N1	1:A:2473:G:C5	2.73	0.55
1:A:2768:U:H2'	1:A:2769:A:H8	1.72	0.55
1:A:996:G:N1	1:A:1014:A:C6	2.74	0.55
1:A:1326:A:H5'	9:N:107:ARG:HD2	1.88	0.55
1:A:2641:C:O2'	1:A:2643:A:N6	2.40	0.55
11:P:20:LEU:HD22	11:P:79:VAL:HG12	1.84	0.55
18:Z:47:ILE:HG21	18:Z:56:VAL:HG21	1.87	0.55
1:A:894:A:H62	1:A:979:U:H3	1.53	0.55
1:A:1082:G:H2'	1:A:1083:G:H8	1.70	0.55
1:A:630:A:H62	1:A:1291:A:H2	1.55	0.55
1:A:1292:G:OP2	12:Q:13:ARG:NH2	2.34	0.55
1:A:2810:A:H5''	1:A:2811:G:H5'	1.89	0.55
1:A:925:A:N3	1:A:925:A:H3'	2.21	0.55
10:O:78:GLY:HA3	10:O:109:LEU:HD21	1.87	0.55
1:A:559:A:O2'	12:Q:11:ARG:NH2	2.40	0.55
2:B:71:A:C5	2:B:72:U:C4	2.95	0.55
4:D:13:THR:HG21	4:D:27:VAL:HG21	1.89	0.55
8:L:117:LEU:HD12	8:L:135:ALA:C	2.27	0.55
17:V:32:LYS:CB	17:V:45:LEU:O	2.55	0.55
1:A:2757:U:OP1	7:K:70:ARG:HD3	2.06	0.55
1:A:2776:G:N1	1:A:2785:U:OP1	2.39	0.55
1:A:2094:C:H5''	1:A:2281:G:H1'	1.88	0.55
1:A:304:G:H1	1:A:414:C:H42	1.55	0.55
1:A:549:A:N3	1:A:551:A:O2'	2.37	0.55
2:B:77:G:H1	2:B:94:G:H1	1.54	0.55
4:D:107:ILE:HG23	4:D:173:ASN:HA	1.89	0.55
1:A:1140:U:O2'	1:A:1144:A:N6	2.41	0.55
1:A:2336:G:O4'	1:A:2337:G:N2	2.40	0.55
1:A:925:A:H8	1:A:947:A:C6	2.24	0.55
17:V:57:GLU:HB2	17:V:88:SER:HB2	1.89	0.55
1:A:901:U:N3	1:A:902:G:C6	2.73	0.54
1:A:1491:A:H62	1:A:1512:G:H22	1.55	0.54
1:A:1807:U:N3	1:A:1816:A:N6	2.56	0.54
1:A:2326:C:H2'	1:A:2327:A:H8	1.72	0.54
2:B:81:G:C2	2:B:92:C:O2	2.60	0.54
4:D:25:VAL:CG1	4:D:188:ILE:C	2.75	0.54
9:N:104:LEU:HD11	9:N:116:ILE:HG13	1.89	0.54
16:U:38:VAL:CG1	16:U:39:ASN:N	2.71	0.54
1:A:1010:C:O2'	1:A:2302:A:N3	2.37	0.54
1:A:1178:U:H5''	6:J:85:LEU:HD11	1.89	0.54
1:A:2882:G:N2	1:A:2885:A:OP2	2.31	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:901:U:C3'	1:A:902:G:H8	2.16	0.54
6:J:91:LEU:HD23	6:J:91:LEU:O	2.07	0.54
11:P:65:ARG:NE	11:P:104:ARG:HG2	2.22	0.54
12:Q:86:SER:CB	12:Q:116:GLN:CG	2.86	0.54
1:A:72:U:OP2	20:Y:54:LYS:NZ	2.40	0.54
1:A:1816:A:H3'	1:A:1817:C:H5''	1.88	0.54
1:A:2098:G:H1	1:A:2471:C:N4	2.03	0.54
1:A:77:U:OP1	20:Y:52:ARG:NH2	2.40	0.54
8:L:121:LEU:N	8:L:121:LEU:HD12	2.18	0.54
12:Q:92:ARG:HB2	13:R:11:GLN:OE1	2.07	0.54
1:A:970:A:H4'	17:V:37:GLN:NE2	2.10	0.54
1:A:2336:G:H4'	1:A:2337:G:H5''	1.89	0.54
3:C:144:ILE:HB	3:C:154:LEU:HD12	1.89	0.54
5:E:152:ALA:O	5:E:189:HIS:ND1	2.41	0.54
11:P:55:GLY:HA2	11:P:60:GLU:HA	1.90	0.54
1:A:113:U:O2'	15:T:33:ARG:NH1	2.40	0.54
1:A:2353:U:H5''	1:A:2354:G:H5''	1.90	0.54
3:C:141:VAL:HA	3:C:191:SER:O	2.08	0.54
7:K:60:ALA:HB2	7:K:86:ILE:HD12	1.90	0.54
1:A:1246:G:H1'	1:A:1247:G:H5'	1.90	0.54
1:A:1519:C:H42	1:A:1565:U:H3	1.55	0.54
1:A:453:G:H1	1:A:468:C:H42	1.53	0.54
1:A:1209:G:OP1	13:R:24:LYS:HG2	2.08	0.54
1:A:419:G:N2	1:A:420:U:O4	2.38	0.54
2:B:22:G:H22	2:B:57:G:H1	1.56	0.54
8:L:76:VAL:HG21	8:L:112:LEU:CG	2.28	0.54
12:Q:86:SER:CB	12:Q:116:GLN:CB	2.85	0.54
5:E:157:ALA:O	5:E:201:LYS:NZ	2.37	0.54
1:A:1177:G:O2'	1:A:1179:A:N7	2.39	0.53
1:A:1765:G:N2	1:A:1768:A:OP2	2.41	0.53
3:C:108:LYS:HB2	3:C:196:GLY:HA2	1.91	0.53
5:E:192:LEU:HD13	5:E:194:ILE:CD1	2.28	0.53
16:U:5:LYS:O	16:U:23:ILE:HD12	2.07	0.53
1:A:999:A:C2	1:A:1011:C:C2	2.97	0.53
1:A:1526:G:H22	1:A:1558:G:N2	1.97	0.53
4:D:22:LEU:HD11	11:P:78:PRO:HG3	1.88	0.53
4:D:47:GLU:CG	4:D:88:MET:HE3	2.39	0.53
1:A:2757:U:OP1	7:K:70:ARG:HD2	2.09	0.53
8:L:74:TYR:HD1	8:L:108:GLY:HA3	1.69	0.53
1:A:1582:U:O4	1:A:1585:A:N6	2.40	0.53
13:R:21:TYR:HA	13:R:93:THR:O	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:V:76:LYS:CD	17:V:90:TYR:CD2	2.84	0.53
1:A:1131:A:O2'	1:A:1150:C:O2	2.25	0.53
1:A:2467:U:H6	1:A:2467:U:H3'	1.74	0.53
5:E:113:VAL:HG11	5:E:186:VAL:HG23	1.89	0.53
1:A:994:C:N3	1:A:995:U:C4	2.76	0.53
4:D:33:ASN:HB2	4:D:97:VAL:CG1	2.19	0.53
8:L:55:MET:O	8:L:60:ARG:NH1	2.40	0.53
1:A:901:U:C2	1:A:902:G:C5	2.97	0.53
2:B:101:U:H2'	2:B:102:A:H8	1.72	0.53
11:P:17:ARG:HG2	11:P:17:ARG:NH1	2.22	0.53
12:Q:64:ARG:HB2	12:Q:97:ASP:OD2	2.08	0.53
16:U:48:THR:HG23	16:U:50:ALA:H	1.74	0.53
1:A:2469:C:O2	1:A:2469:C:H2'	2.08	0.53
2:B:75:U:C5	2:B:96:G:N2	2.76	0.53
10:O:35:ARG:HH22	10:O:105:ARG:NH2	2.07	0.53
16:U:16:ASP:CG	16:U:38:VAL:CG1	2.69	0.53
1:A:1103:A:N6	1:A:1134:A:OP2	2.42	0.53
1:A:2094:C:H5''	1:A:2281:G:C1'	2.38	0.53
1:A:389:A:O2'	1:A:390:A:N7	2.33	0.53
1:A:911:G:N2	1:A:960:U:N3	2.57	0.53
6:J:53:ASP:OD1	6:J:53:ASP:N	2.41	0.53
1:A:1012:G:H1'	1:A:2296:A:N1	2.24	0.53
1:A:968:C:O2	1:A:968:C:H2'	2.08	0.53
1:A:2357:A:N6	1:A:2415:U:O4	2.42	0.52
3:C:150:LYS:CD	3:C:153:GLN:HE22	2.10	0.52
6:J:88:ARG:NH1	6:J:97:TYR:OH	2.43	0.52
8:L:77:VAL:CG1	8:L:81:LYS:HG2	2.24	0.52
12:Q:86:SER:HA	12:Q:116:GLN:HG2	1.89	0.52
1:A:106:G:H1'	1:A:337:A:H8	1.74	0.52
1:A:2434:G:N2	1:A:2442:G:O6	2.43	0.52
13:R:21:TYR:CA	13:R:93:THR:O	2.57	0.52
1:A:673:A:H62	8:L:112:LEU:HB3	1.75	0.52
1:A:911:G:H22	1:A:960:U:H3	1.55	0.52
15:T:47:PHE:HB3	15:T:90:ILE:CD1	2.39	0.52
1:A:925:A:C8	1:A:947:A:C6	2.98	0.52
1:A:947:A:H3'	1:A:948:A:C2	2.44	0.52
6:J:18:VAL:CG1	6:J:58:ILE:HD11	2.34	0.52
9:N:110:ASP:OD1	9:N:110:ASP:N	2.42	0.52
13:R:62:VAL:HG22	13:R:95:VAL:CG2	2.31	0.52
1:A:1526:G:H21	1:A:1558:G:N2	1.95	0.52
1:A:329:A:H61	1:A:398:U:H3	1.57	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:948:A:N3	1:A:948:A:C5'	2.73	0.52
6:J:75:TYR:OH	6:J:101:MET:HG3	2.09	0.52
10:O:29:PRO:HG2	10:O:93:VAL:HG23	1.90	0.52
15:T:30:VAL:CG1	15:T:31:ASP:H	2.22	0.52
1:A:1102:G:N1	1:A:1149:A:N7	2.58	0.52
1:A:2289:C:HO2'	1:A:2417:A:HO2'	1.58	0.52
1:A:676:G:N2	1:A:679:A:OP2	2.40	0.52
6:J:38:ARG:NH2	6:J:45:TYR:OH	2.43	0.52
1:A:1587:U:H2'	1:A:1588:A:H8	1.74	0.52
1:A:2686:A:N6	1:A:2693:G:O2'	2.43	0.52
10:O:75:THR:HG23	10:O:109:LEU:CG	2.39	0.52
13:R:21:TYR:HB3	13:R:93:THR:C	2.28	0.52
12:Q:88:ILE:CG1	13:R:50:ASN:HA	2.40	0.52
1:A:2898:A:O2'	9:N:2:SER:N	2.43	0.52
1:A:680:G:N7	8:L:71:ARG:NH2	2.58	0.52
2:B:74:G:O5'	2:B:74:G:H8	1.93	0.52
10:O:75:THR:HG23	10:O:109:LEU:HD23	1.92	0.52
16:U:64:HIS:HD2	16:U:66:SER:H	1.58	0.52
1:A:1518:G:H1	1:A:1566:G:H1	1.57	0.52
1:A:688:G:N1	1:A:691:U:OP2	2.42	0.52
3:C:167:LYS:HG3	3:C:167:LYS:O	2.10	0.52
4:D:13:THR:HG21	11:P:8:ILE:HG23	1.92	0.52
1:A:827:G:H21	1:A:830:A:H62	1.58	0.52
4:D:206:VAL:O	4:D:206:VAL:HG12	2.09	0.52
8:L:77:VAL:O	8:L:78:ASN:C	2.48	0.52
12:Q:112:ALA:HB3	13:R:47:LYS:NZ	2.23	0.52
12:Q:86:SER:HB2	12:Q:116:GLN:HB3	1.90	0.52
8:L:111:ILE:HD12	8:L:123:VAL:HG11	1.91	0.51
13:R:33:VAL:HG12	13:R:34:THR:N	2.25	0.51
16:U:5:LYS:O	16:U:23:ILE:HB	2.10	0.51
1:A:995:U:C2	1:A:1015:G:N2	2.79	0.51
1:A:2465:G:N1	1:A:2466:C:C2	2.78	0.51
1:A:904:A:N1	1:A:967:G:O6	2.43	0.51
1:A:919:U:H2'	1:A:920:G:C8	2.45	0.51
1:A:922:A:O2'	1:A:950:U:O2	2.28	0.51
3:C:124:ILE:O	3:C:124:ILE:HG22	2.10	0.51
3:C:211:SER:O	3:C:216:ILE:CB	2.51	0.51
14:S:83:LYS:O	14:S:84:ARG:NH1	2.44	0.51
15:T:47:PHE:CB	15:T:90:ILE:HD13	2.41	0.51
1:A:301:U:H3'	1:A:301:U:H6	1.75	0.51
5:E:37:ILE:HD11	5:E:187:VAL:HG11	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:V:39:VAL:CG1	17:V:43:SER:OG	2.57	0.51
1:A:605:G:O2'	12:Q:45:TYR:OH	1.99	0.51
1:A:2024:U:O2'	7:K:31:LYS:HD2	2.11	0.51
15:T:30:VAL:HG12	15:T:31:ASP:H	1.73	0.51
1:A:1379:U:OP2	15:T:59:TYR:OH	2.28	0.51
1:A:343:A:HO2'	1:A:362:C:HO2'	1.56	0.51
3:C:173:LEU:HD11	3:C:181:VAL:HG12	1.91	0.51
3:C:178:SER:OG	3:C:180:GLU:OE2	2.28	0.51
5:E:40:GLN:OE1	5:E:182:ASN:ND2	2.43	0.51
13:R:82:VAL:O	13:R:83:HIS:ND1	2.43	0.51
17:V:79:ARG:HD3	17:V:79:ARG:N	2.25	0.51
1:A:2063:U:O2'	1:A:2064:G:O4'	2.28	0.51
5:E:8:ASN:ND2	5:E:127:GLU:OE2	2.43	0.51
1:A:1521:G:H22	1:A:1563:G:H1	1.58	0.51
1:A:2297:A:N3	1:A:2297:A:C3'	2.73	0.51
1:A:830:A:H2'	1:A:831:U:H4'	1.91	0.51
5:E:177:GLU:CG	5:E:178:ALA:N	2.73	0.51
5:E:6:LEU:HD21	5:E:17:ILE:CG1	2.40	0.51
16:U:8:LYS:O	16:U:71:LEU:HB2	2.10	0.51
1:A:1074:A:OP2	1:A:1172:A:N6	2.35	0.51
1:A:1577:C:H41	1:A:1578:G:H21	1.59	0.51
3:C:62:TYR:HA	3:C:86:ASN:HD21	1.76	0.51
6:J:29:LEU:CD2	6:J:63:ILE:HD13	2.41	0.51
7:K:17:ARG:HH21	7:K:47:THR:HB	1.76	0.51
12:Q:76:TYR:CZ	12:Q:80:MET:CG	2.89	0.51
12:Q:61:TRP:CZ2	12:Q:94:MET:HG3	2.45	0.51
1:A:1214:U:O4	1:A:1221:A:N6	2.44	0.51
3:C:108:LYS:HG2	3:C:109:GLY:N	2.26	0.51
3:C:171:TYR:HB2	3:C:183:MET:HE3	1.92	0.51
4:D:23:ILE:HG21	4:D:189:LYS:NZ	2.25	0.51
4:D:107:ILE:HG22	4:D:205:ALA:HB2	1.92	0.51
8:L:88:GLY:HA2	8:L:121:LEU:CG	2.31	0.51
1:A:2096:G:H3'	1:A:2097:U:H4'	1.93	0.50
11:P:17:ARG:HH21	11:P:82:PRO:HA	1.77	0.50
1:A:1101:G:N2	1:A:1150:C:O2	2.39	0.50
1:A:2291:U:H2'	1:A:2292:C:C6	2.46	0.50
1:A:5:A:N6	1:A:2921:U:O4	2.43	0.50
1:A:61:A:C3'	1:A:62:C:C6	2.95	0.50
2:B:3:U:H2'	2:B:4:G:H8	1.76	0.50
3:C:13:ARG:HA	3:C:16:MET:SD	2.51	0.50
5:E:6:LEU:CD2	5:E:17:ILE:HG12	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:J:75:TYR:OH	6:J:101:MET:CG	2.59	0.50
6:J:55:VAL:HG23	6:J:55:VAL:O	2.12	0.50
12:Q:109:LEU:HD23	13:R:47:LYS:CE	2.39	0.50
13:R:57:THR:HG23	13:R:101:ASN:HD22	1.77	0.50
1:A:2428:G:C5	1:A:2429:G:C5	2.97	0.50
1:A:2098:G:C6	1:A:2471:C:N4	2.79	0.50
1:A:954:U:C4	1:A:955:C:N4	2.80	0.50
11:P:34:LYS:NZ	11:P:82:PRO:O	2.44	0.50
1:A:1818:A:C6	1:A:1819:C:N3	2.80	0.50
1:A:198:A:H5'	1:A:199:A:H4'	1.94	0.50
4:D:5:ILE:HB	4:D:33:ASN:HD21	1.75	0.50
5:E:51:VAL:CG2	5:E:92:PRO:CG	2.89	0.50
5:E:63:LYS:NZ	5:E:74:ARG:O	2.42	0.50
7:K:19:VAL:HG13	7:K:41:CYS:HB3	1.93	0.50
1:A:2290:C:C4	1:A:2291:U:O4	2.65	0.50
1:A:2297:A:N3	1:A:2297:A:C5'	2.73	0.50
1:A:528:G:H1	1:A:555:C:H42	1.58	0.50
15:T:35:ASN:HB2	15:T:38:GLU:HG3	1.94	0.50
18:Z:23:VAL:HA	18:Z:26:LEU:HD12	1.92	0.50
1:A:1053:C:OP1	6:J:40:LYS:NZ	2.42	0.50
2:B:91:C:H2'	2:B:92:C:C6	2.47	0.50
6:J:125:VAL:O	6:J:125:VAL:HG13	2.12	0.50
1:A:1182:G:H2'	1:A:1183:G:H8	1.76	0.50
1:A:2293:C:H6	1:A:2293:C:O5'	1.95	0.50
1:A:268:A:H2'	1:A:269:G:H4'	1.93	0.50
1:A:61:A:H3'	1:A:62:C:C6	2.47	0.50
1:A:970:A:HO2'	17:V:37:GLN:CG	2.08	0.50
1:A:225:A:H62	1:A:235:G:H21	1.60	0.50
15:T:65:ARG:HB3	15:T:70:THR:HG22	1.94	0.50
16:U:39:ASN:HB3	16:U:61:ALA:HB3	1.93	0.50
17:V:51:THR:HG23	17:V:51:THR:O	2.10	0.50
1:A:1555:A:H1'	1:A:1556:A:C8	2.46	0.49
1:A:1574:G:N1	1:A:1592:A:OP2	2.36	0.49
8:L:79:LEU:HD11	8:L:117:LEU:CG	2.42	0.49
1:A:2836:G:H5'	4:D:62:ASN:HB3	1.95	0.49
4:D:96:GLU:HG2	4:D:96:GLU:O	2.12	0.49
4:D:98:LYS:CG	4:D:99:VAL:N	2.71	0.49
12:Q:51:ARG:HG3	12:Q:51:ARG:NH1	2.26	0.49
1:A:1259:G:OP1	12:Q:22:LYS:NZ	2.46	0.49
1:A:916:G:H1	1:A:955:C:H42	1.59	0.49
4:D:9:LYS:HB3	4:D:28:ILE:HG23	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:126:LEU:HD13	5:E:129:LEU:CD1	2.34	0.49
1:A:2757:U:C5'	7:K:70:ARG:HE	2.26	0.49
8:L:121:LEU:N	8:L:121:LEU:CD1	2.73	0.49
15:T:57:MET:SD	15:T:78:LYS:HE2	2.52	0.49
1:A:1125:C:N4	1:A:1126:A:N7	2.61	0.49
1:A:1077:G:C2	1:A:1170:C:O2	2.61	0.49
1:A:2472:C:H2'	1:A:2473:G:C8	2.48	0.49
1:A:2714:G:OP2	11:P:52:LYS:NZ	2.43	0.49
20:Y:14:ILE:HD11	20:Y:57:ILE:HG12	1.95	0.49
1:A:2291:U:O5'	1:A:2291:U:H6	1.96	0.49
1:A:2359:G:H21	17:V:50:GLY:HA3	1.73	0.49
2:B:64:A:H61	2:B:105:A:H2'	1.77	0.49
8:L:78:ASN:C	8:L:80:ASP:H	2.14	0.49
12:Q:92:ARG:H	13:R:11:GLN:CD	1.94	0.49
1:A:1528:U:H4'	1:A:1529:G:H5'	1.95	0.49
13:R:4:ILE:HG22	13:R:4:ILE:O	2.13	0.49
16:U:49:GLN:NE2	16:U:49:GLN:CA	2.75	0.49
1:A:2228:A:H2'	1:A:2228:A:N3	2.28	0.49
4:D:47:GLU:HG2	4:D:88:MET:SD	2.53	0.49
8:L:88:GLY:HA2	8:L:121:LEU:HB3	1.93	0.49
10:O:111:ASP:HA	10:O:114:ARG:HB2	1.94	0.49
1:A:2295:A:OP1	1:A:2302:A:N6	2.41	0.49
1:A:994:C:N3	1:A:995:U:O4	2.45	0.49
4:D:55:ASP:N	4:D:55:ASP:OD1	2.45	0.49
13:R:5:ILE:HD13	13:R:14:VAL:CG2	2.42	0.49
17:V:54:TYR:HE2	17:V:84:ARG:NH1	2.04	0.49
5:E:97:TYR:N	5:E:97:TYR:CD1	2.81	0.48
1:A:2096:G:C6	1:A:2473:G:N1	2.80	0.48
2:B:98:G:H2'	2:B:99:A:O4'	2.13	0.48
3:C:117:MET:HB3	3:C:122:ALA:HB1	1.94	0.48
17:V:49:ARG:NH1	17:V:64:ASP:OD2	2.46	0.48
1:A:1585:A:N6	1:A:1587:U:O2	2.46	0.48
1:A:2430:U:H2'	1:A:2431:U:C6	2.49	0.48
17:V:54:TYR:HD2	17:V:84:ARG:HD3	1.66	0.48
1:A:2094:C:H2'	1:A:2095:C:C6	2.48	0.48
1:A:2028:C:O2'	1:A:2716:U:O2	2.31	0.48
1:A:925:A:C5'	1:A:925:A:N3	2.73	0.48
2:B:80:G:C6	2:B:93:U:O2	2.66	0.48
3:C:21:PHE:HB3	3:C:24:ILE:HD12	1.95	0.48
15:T:47:PHE:HB3	15:T:90:ILE:HD13	1.95	0.48
1:A:1801:G:O6	1:A:2005:C:N4	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2037:C:H2'	1:A:2038:G:H8	1.78	0.48
5:E:19:LEU:CD1	5:E:19:LEU:N	2.76	0.48
1:A:1815:A:OP2	1:A:1815:A:H2'	2.14	0.48
1:A:2433:C:H6	1:A:2433:C:O5'	1.97	0.48
1:A:583:G:N2	1:A:601:U:O4	2.45	0.48
10:O:11:ARG:CD	10:O:100:TYR:CZ	2.85	0.48
1:A:1618:A:OP1	3:C:61:GLN:NE2	2.47	0.48
1:A:2432:C:N3	1:A:2444:G:N2	2.61	0.48
3:C:94:ILE:CD1	3:C:104:ILE:CD1	2.45	0.48
4:D:108:VAL:HG13	4:D:203:LYS:O	2.13	0.48
16:U:6:GLY:CA	16:U:23:ILE:O	2.61	0.48
1:A:2471:C:H3'	1:A:2471:C:H6	1.79	0.48
1:A:760:G:H21	1:A:765:A:H2	1.61	0.48
1:A:828:A:OP1	3:C:217:ARG:NH1	2.47	0.48
8:L:91:VAL:O	8:L:91:VAL:HG12	2.14	0.48
12:Q:68:ALA:CB	12:Q:106:PHE:CE2	2.96	0.48
17:V:37:GLN:O	17:V:39:VAL:HG23	2.14	0.48
1:A:953:G:O5'	1:A:953:G:H8	1.96	0.48
12:Q:61:TRP:CZ3	12:Q:94:MET:HB2	2.41	0.48
12:Q:108:GLN:HE22	13:R:47:LYS:HB2	1.72	0.48
20:Y:14:ILE:CG1	20:Y:57:ILE:CD1	2.88	0.48
1:A:1614:A:OP1	3:C:210:ARG:NH1	2.47	0.48
3:C:70:ASP:OD1	3:C:70:ASP:N	2.45	0.48
1:A:1546:G:H21	3:C:99:GLY:HA3	1.79	0.48
12:Q:86:SER:CA	12:Q:116:GLN:HG2	2.44	0.48
12:Q:86:SER:CB	12:Q:116:GLN:HG2	2.43	0.48
15:T:20:LEU:HD22	15:T:25:LYS:HD2	1.96	0.48
5:E:26:ILE:CD1	5:E:111:LYS:HD3	2.44	0.47
10:O:93:VAL:HG13	10:O:93:VAL:O	2.13	0.47
1:A:1205:U:H2'	1:A:1206:G:H8	1.79	0.47
1:A:1557:G:H2'	1:A:1558:G:C8	2.49	0.47
1:A:283:G:N2	1:A:289:C:O2	2.35	0.47
3:C:7:LYS:O	3:C:9:THR:HG23	2.15	0.47
4:D:33:ASN:O	4:D:96:GLU:HA	2.14	0.47
1:A:911:G:N2	1:A:960:U:O4	2.41	0.47
2:B:80:G:C6	2:B:93:U:C2	3.03	0.47
7:K:115:VAL:O	7:K:115:VAL:HG12	2.13	0.47
13:R:25:LEU:HD12	13:R:25:LEU:O	2.14	0.47
1:A:1000:G:N2	1:A:1010:C:C2	2.82	0.47
1:A:1149:A:OP2	1:A:1150:C:N4	2.38	0.47
1:A:1660:C:OP2	1:A:1662:C:N4	2.41	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2122:G:H21	1:A:2227:A:N6	2.07	0.47
1:A:2325:U:O2	1:A:2366:G:N2	2.48	0.47
1:A:2444:G:O3'	8:L:65:GLY:CA	2.53	0.47
1:A:2039:G:C5'	14:S:42:ALA:CB	2.93	0.47
1:A:999:A:N1	1:A:1011:C:C2	2.82	0.47
3:C:34:LEU:CD2	3:C:63:ARG:HG3	2.44	0.47
5:E:150:LYS:HG2	5:E:151:LYS:H	1.80	0.47
10:O:112:ALA:O	10:O:115:GLU:HG3	2.14	0.47
10:O:28:ARG:HG2	10:O:91:SER:OG	2.15	0.47
12:Q:69:ALA:HB2	12:Q:79:LEU:HD22	1.96	0.47
1:A:1782:G:OP1	11:P:96:ARG:NH1	2.47	0.47
3:C:150:LYS:HD3	3:C:153:GLN:HE21	1.52	0.47
4:D:47:GLU:HG3	4:D:88:MET:HE3	1.96	0.47
8:L:78:ASN:C	8:L:80:ASP:N	2.67	0.47
10:O:82:ALA:HB2	10:O:113:ALA:CB	2.39	0.47
15:T:9:LYS:HB3	15:T:9:LYS:HE2	1.70	0.47
1:A:1516:A:H62	1:A:1568:G:H8	1.61	0.47
1:A:2099:G:N3	1:A:2471:C:N3	2.63	0.47
1:A:2432:C:C2	1:A:2444:G:C2	3.02	0.47
1:A:923:C:O5'	1:A:923:C:H6	1.98	0.47
13:R:6:LYS:HB3	13:R:37:ASP:OD2	2.14	0.47
1:A:2383:A:HO2'	17:V:44:ILE:H	1.58	0.47
17:V:48:GLN:N	17:V:48:GLN:OE1	2.48	0.47
1:A:1076:G:H2'	1:A:1077:G:C8	2.50	0.47
1:A:913:A:C2	1:A:961:C:C4	3.00	0.47
2:B:15:C:N4	2:B:106:C:O2	2.47	0.47
3:C:26:THR:OG1	3:C:80:THR:HG21	2.14	0.47
5:E:160:ASN:HB3	5:E:163:VAL:HG12	1.95	0.47
5:E:4:VAL:HG21	5:E:123:ILE:CD1	2.39	0.47
12:Q:83:LEU:HD22	12:Q:89:GLU:CD	2.35	0.47
1:A:1065:U:H3	1:A:1188:A:H62	1.63	0.47
1:A:1560:U:H6	1:A:1560:U:H5''	1.79	0.47
1:A:1818:A:C6	1:A:1819:C:C4	3.03	0.47
8:L:79:LEU:HD11	8:L:117:LEU:CD2	2.43	0.47
2:B:6:U:O3'	10:O:30:ARG:NH2	2.48	0.47
1:A:2429:G:O5'	1:A:2429:G:H8	1.98	0.47
1:A:760:G:N2	1:A:764:C:OP2	2.48	0.47
1:A:999:A:H1'	1:A:2295:A:OP2	2.15	0.47
10:O:82:ALA:HA	10:O:85:ALA:HB3	1.95	0.47
1:A:822:G:OP1	1:A:824:G:O2'	2.33	0.47
1:A:948:A:N3	1:A:948:A:H5''	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:94:G:H2'	2:B:95:U:C6	2.49	0.47
3:C:79:ALA:C	3:C:80:THR:HG23	2.35	0.47
1:A:1240:U:H1'	12:Q:4:VAL:HG22	1.97	0.47
1:A:1365:U:H3	1:A:1693:C:HO2'	1.63	0.46
1:A:2322:C:O3'	10:O:97:ARG:NH2	2.47	0.46
1:A:683:A:OP1	8:L:131:SER:OG	2.28	0.46
1:A:999:A:N6	1:A:1011:C:N4	2.63	0.46
3:C:53:HIS:HB3	3:C:217:ARG:O	2.15	0.46
8:L:79:LEU:CD2	8:L:117:LEU:HG	2.43	0.46
15:T:3:ASP:HB3	15:T:4:PRO:HD2	1.97	0.46
1:A:1774:A:H3'	1:A:1775:G:H8	1.80	0.46
4:D:25:VAL:HG12	4:D:188:ILE:C	2.34	0.46
5:E:7:TYR:HB2	5:E:126:LEU:HD23	1.97	0.46
7:K:10:VAL:HG12	7:K:11:ALA:N	2.30	0.46
13:R:5:ILE:HD13	13:R:14:VAL:HG21	1.97	0.46
1:A:2228:A:N7	1:A:2254:A:N6	2.63	0.46
1:A:61:A:C4	1:A:62:C:C6	3.04	0.46
1:A:61:A:C4	1:A:62:C:C4	3.03	0.46
16:U:38:VAL:CG1	16:U:39:ASN:H	2.29	0.46
1:A:1460:G:H22	1:A:1630:G:H2'	1.81	0.46
1:A:1496:G:H1	1:A:1507:U:H3	1.63	0.46
1:A:2106:A:N3	1:A:2463:A:O2'	2.45	0.46
5:E:160:ASN:HB3	5:E:163:VAL:CG1	2.46	0.46
13:R:19:THR:O	13:R:19:THR:OG1	2.25	0.46
13:R:90:GLN:NE2	13:R:91:PRO:O	2.41	0.46
20:Y:10:THR:HG22	20:Y:60:ARG:NH1	2.30	0.46
1:A:2880:U:H3	1:A:2887:A:H61	1.64	0.46
12:Q:61:TRP:CE2	12:Q:94:MET:CA	2.99	0.46
18:Z:47:ILE:HD13	18:Z:56:VAL:CG2	2.45	0.46
1:A:740:A:O2'	1:A:1392:A:N3	2.41	0.46
3:C:15:GLY:O	3:C:204:ASN:ND2	2.48	0.46
4:D:56:LYS:O	4:D:56:LYS:HG3	2.16	0.46
5:E:93:THR:CG2	5:E:94:PRO:HD2	2.46	0.46
8:L:111:ILE:CD1	8:L:123:VAL:HG11	2.44	0.46
1:A:1077:G:C2	1:A:1170:C:C2	2.93	0.46
1:A:1818:A:H8	1:A:1818:A:O5'	1.98	0.46
1:A:505:G:O2'	1:A:516:G:O6	2.33	0.46
1:A:2855:G:H5'	4:D:57:ARG:HH21	1.81	0.46
4:D:5:ILE:HB	4:D:33:ASN:ND2	2.30	0.46
7:K:10:VAL:HG21	7:K:16:ALA:CB	2.45	0.46
7:K:73:ASP:CG	11:P:83:LYS:CE	2.78	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:Q:95:LEU:HD23	13:R:11:GLN:CB	2.30	0.46
15:T:34:ALA:O	15:T:77:ARG:NH1	2.49	0.46
1:A:2124:A:N1	1:A:2223:U:C4	2.80	0.46
1:A:907:U:N3	1:A:2297:A:H8	2.12	0.46
1:A:453:G:H2'	1:A:454:G:H8	1.80	0.46
5:E:6:LEU:HD11	5:E:17:ILE:CG2	2.36	0.46
1:A:1198:C:H5'	12:Q:81:HIS:HB2	1.97	0.46
14:S:86:ARG:O	14:S:94:SER:OG	2.34	0.46
1:A:2294:U:C5	1:A:2295:A:O2'	2.66	0.46
7:K:10:VAL:HG12	7:K:12:ASP:H	1.81	0.46
7:K:22:ILE:CD1	7:K:42:THR:HG23	2.34	0.46
10:O:44:ILE:HD12	10:O:54:ALA:HB3	1.97	0.46
10:O:74:ALA:O	10:O:78:GLY:N	2.49	0.46
1:A:1160:G:H2'	1:A:1161:A:C8	2.51	0.45
1:A:2867:U:H3	1:A:2900:A:H61	1.64	0.45
6:J:60:ALA:O	6:J:98:PRO:HB2	2.16	0.45
9:N:9:THR:OG1	9:N:10:SER:N	2.49	0.45
15:T:58:ASN:N	15:T:58:ASN:OD1	2.49	0.45
1:A:1365:U:HO2'	1:A:2039:G:HO2'	1.63	0.45
1:A:858:U:O2'	1:A:1290:G:O2'	2.25	0.45
1:A:1080:G:N1	1:A:1168:G:C2	2.84	0.45
1:A:910:A:N6	1:A:911:G:H1	2.14	0.45
3:C:71:LYS:NZ	3:C:100:GLU:OE2	2.37	0.45
8:L:77:VAL:HG12	8:L:78:ASN:O	2.16	0.45
13:R:67:ARG:HH21	13:R:89:ARG:HB3	1.81	0.45
14:S:86:ARG:HB3	14:S:96:ILE:HD11	1.95	0.45
2:B:63:C:H41	2:B:106:C:H2'	1.81	0.45
6:J:5:PRO:HA	12:Q:98:LEU:HD11	1.98	0.45
6:J:79:THR:HG23	6:J:81:HIS:H	1.82	0.45
12:Q:61:TRP:CE2	12:Q:94:MET:HA	2.52	0.45
14:S:44:SER:OG	14:S:45:PRO:HD3	2.16	0.45
1:A:2092:C:H2'	1:A:2093:C:C6	2.51	0.45
1:A:353:A:N7	1:A:374:A:N6	2.65	0.45
1:A:580:U:O2'	12:Q:49:ASP:CG	2.48	0.45
11:P:102:TYR:C	11:P:102:TYR:CD1	2.90	0.45
17:V:73:GLY:CA	17:V:92:VAL:HG23	2.34	0.45
1:A:2228:A:C5	1:A:2254:A:N1	2.83	0.45
1:A:965:A:O2'	2:B:79:C:C1'	2.65	0.45
4:D:23:ILE:CG2	4:D:189:LYS:HZ2	2.29	0.45
8:L:71:ARG:HG2	8:L:73:GLU:CD	2.36	0.45
1:A:2467:U:C6	1:A:2467:U:C3'	3.00	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:249:C:N4	1:A:250:G:O6	2.50	0.45
1:A:956:A:H3'	1:A:959:C:H41	1.82	0.45
5:E:40:GLN:O	5:E:40:GLN:NE2	2.50	0.45
14:S:72:SER:OG	14:S:73:GLN:N	2.49	0.45
16:U:29:LYS:HG2	16:U:30:LYS:HG3	1.98	0.45
1:A:1015:G:H5''	18:Z:20:ARG:HH21	1.82	0.45
1:A:1814:A:H8	1:A:1814:A:OP2	1.99	0.45
1:A:2349:A:O2'	1:A:2362:A:N6	2.50	0.45
1:A:910:A:C6	1:A:960:U:O4	2.69	0.45
10:O:15:HIS:CE1	10:O:19:ARG:CG	2.99	0.45
1:A:1673:G:H2'	1:A:1674:G:H8	1.82	0.45
1:A:2290:C:O2	1:A:2291:U:C4	2.69	0.45
12:Q:109:LEU:CB	13:R:47:LYS:HZ1	2.27	0.45
1:A:1783:C:OP1	11:P:97:ARG:NE	2.46	0.45
1:A:1815:A:H1'	1:A:1816:A:C1'	2.47	0.45
1:A:2098:G:N1	1:A:2471:C:N4	2.65	0.45
1:A:250:G:O2'	1:A:253:G:O6	2.35	0.45
5:E:131:LEU:HD11	5:E:163:VAL:HA	1.98	0.45
1:A:1322:G:N2	1:A:1325:A:OP2	2.50	0.44
1:A:2686:A:OP2	1:A:2687:C:N4	2.49	0.44
1:A:760:G:O2'	1:A:765:A:N6	2.44	0.44
1:A:911:G:OP2	1:A:911:G:C8	2.71	0.44
4:D:3:LYS:HB2	4:D:101:ILE:HD12	1.99	0.44
4:D:49:ILE:HD13	4:D:91:TYR:CE2	2.52	0.44
7:K:23:LYS:CG	7:K:24:VAL:H	2.30	0.44
8:L:109:VAL:O	8:L:125:ALA:HB1	2.17	0.44
1:A:2428:G:C5	1:A:2429:G:N7	2.86	0.44
3:C:173:LEU:HD11	3:C:181:VAL:CG1	2.46	0.44
5:E:6:LEU:HD23	5:E:17:ILE:CD1	2.47	0.44
7:K:23:LYS:CG	7:K:24:VAL:N	2.81	0.44
12:Q:88:ILE:HG12	13:R:50:ASN:HA	1.99	0.44
1:A:1491:A:H62	1:A:1512:G:H1	1.65	0.44
1:A:1601:A:N6	1:A:1603:U:O2	2.50	0.44
14:S:86:ARG:CB	14:S:96:ILE:CD1	2.77	0.44
1:A:970:A:C2'	17:V:37:GLN:HE21	2.06	0.44
1:A:1125:C:N3	1:A:1126:A:N7	2.65	0.44
1:A:2383:A:O2'	17:V:44:ILE:N	2.24	0.44
1:A:721:G:H5''	5:E:76:GLY:H	1.83	0.44
3:C:150:LYS:CG	3:C:153:GLN:NE2	2.81	0.44
6:J:79:THR:OG1	6:J:80:GLN:N	2.49	0.44
16:U:9:VAL:HG22	16:U:69:MET:C	2.38	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:364:A:H2'	5:E:136:THR:HG21	2.00	0.44
1:A:61:A:C3'	1:A:62:C:H5	2.24	0.44
4:D:35:VAL:HG22	4:D:91:TYR:CD1	2.49	0.44
1:A:2224:U:H2'	1:A:2225:C:C6	2.53	0.44
1:A:2710:C:OP2	4:D:115:LYS:NZ	2.34	0.44
13:R:41:VAL:HG21	13:R:102:ALA:HA	2.00	0.44
1:A:2444:G:H4'	8:L:65:GLY:HA2	2.00	0.44
6:J:58:ILE:H	6:J:58:ILE:HG12	1.60	0.44
12:Q:100:VAL:HG12	12:Q:100:VAL:O	2.17	0.44
12:Q:108:GLN:HE22	13:R:47:LYS:N	2.16	0.44
1:A:1242:U:H2'	1:A:1243:A:C8	2.53	0.44
1:A:774:A:O2'	1:A:775:G:O4'	2.36	0.44
6:J:18:VAL:HG23	6:J:138:PRO:HB2	2.00	0.44
6:J:75:TYR:CZ	6:J:101:MET:HG3	2.53	0.44
13:R:25:LEU:CD2	13:R:35:PHE:HE1	2.31	0.44
16:U:10:MET:HE3	16:U:11:VAL:H	1.83	0.44
3:C:164:VAL:C	3:C:165:LEU:HG	2.38	0.44
5:E:26:ILE:HD12	5:E:111:LYS:HB3	1.99	0.44
12:Q:86:SER:OG	12:Q:116:GLN:HG2	2.18	0.44
12:Q:109:LEU:HD21	13:R:40:PHE:HE2	1.83	0.44
1:A:2224:U:O5'	1:A:2224:U:H6	2.01	0.43
1:A:971:A:H4'	17:V:36:GLY:O	2.18	0.43
13:R:21:TYR:HE2	13:R:94:LYS:HE3	1.83	0.43
1:A:1034:A:H5''	18:Z:11:SER:HB3	2.00	0.43
1:A:1818:A:O5'	1:A:1818:A:C8	2.71	0.43
1:A:337:A:O2'	1:A:338:G:O4'	2.37	0.43
1:A:969:C:O2	17:V:34:ALA:CB	2.65	0.43
3:C:130:LEU:HD11	3:C:135:ILE:HG12	2.00	0.43
4:D:13:THR:HG21	4:D:27:VAL:CG2	2.48	0.43
13:R:21:TYR:CD2	13:R:94:LYS:HG3	2.53	0.43
3:C:53:HIS:CB	3:C:217:ARG:O	2.66	0.43
5:E:8:ASN:CG	5:E:127:GLU:OE2	2.56	0.43
7:K:91:LYS:HE3	7:K:113:LYS:HB2	2.00	0.43
11:P:51:ILE:HD11	11:P:103:LEU:HD11	2.00	0.43
18:Z:9:LYS:HD3	18:Z:9:LYS:HA	1.74	0.43
1:A:1075:A:C2'	1:A:1076:G:H5'	2.47	0.43
5:E:156:THR:HG23	5:E:195:THR:HG21	1.99	0.43
8:L:109:VAL:N	8:L:126:ASN:ND2	2.59	0.43
9:N:55:ASP:HB3	9:N:58:ALA:H	1.84	0.43
12:Q:61:TRP:CD2	12:Q:94:MET:HB2	2.43	0.43
1:A:1182:G:H2'	1:A:1183:G:C8	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1380:U:O2'	15:T:55:ASN:ND2	2.52	0.43
1:A:1676:G:N2	1:A:1679:A:OP2	2.49	0.43
1:A:237:U:H3	1:A:476:A:H61	1.66	0.43
1:A:320:U:H5''	1:A:321:U:H2'	2.00	0.43
1:A:64:A:H8	1:A:64:A:OP2	1.95	0.43
1:A:916:G:H3'	1:A:917:A:C8	2.52	0.43
1:A:998:G:N2	1:A:2296:A:C1'	2.81	0.43
3:C:79:ALA:O	3:C:80:THR:CG2	2.66	0.43
5:E:6:LEU:CD2	5:E:17:ILE:CG1	2.96	0.43
12:Q:56:ASP:O	12:Q:59:LYS:N	2.51	0.43
20:Y:14:ILE:CG1	20:Y:57:ILE:HD13	2.40	0.43
1:A:1084:A:H2'	1:A:1085:G:C8	2.54	0.43
1:A:324:A:H2'	1:A:325:A:C8	2.53	0.43
3:C:79:ALA:O	3:C:80:THR:HG23	2.18	0.43
6:J:26:LEU:HB2	6:J:63:ILE:HG21	2.00	0.43
12:Q:61:TRP:CZ3	12:Q:94:MET:CB	2.98	0.43
13:R:48:VAL:HG13	13:R:53:VAL:HG23	2.00	0.43
2:B:81:G:H4'	18:Z:52:HIS:CD2	2.53	0.43
1:A:1491:A:N6	1:A:1512:G:H1	2.16	0.43
6:J:104:LEU:HA	6:J:104:LEU:HD12	1.91	0.43
8:L:70:ASN:OD1	8:L:70:ASN:N	2.51	0.43
1:A:1364:C:O2	14:S:86:ARG:NH2	2.52	0.43
1:A:995:U:H2'	1:A:996:G:C8	2.54	0.43
7:K:15:GLY:HA3	7:K:50:GLY:HA3	2.00	0.43
8:L:126:ASN:O	8:L:145:VAL:HG11	2.18	0.43
15:T:22:THR:OG1	15:T:23:GLU:OE2	2.35	0.43
1:A:1366:C:O2'	9:N:108:ARG:NH1	2.49	0.43
1:A:1479:G:N2	1:A:1609:C:O2	2.43	0.43
1:A:1012:G:O2'	1:A:2296:A:C6	2.68	0.43
3:C:13:ARG:CG	3:C:16:MET:SD	2.91	0.43
12:Q:55:ARG:HG2	12:Q:55:ARG:H	1.69	0.43
1:A:1133:G:O6	1:A:1148:C:N4	2.51	0.43
1:A:1424:A:O2'	1:A:1435:U:O2	2.35	0.43
1:A:2095:C:O2	1:A:2473:G:N2	2.51	0.43
1:A:2778:A:N6	1:A:2783:U:O2	2.52	0.43
1:A:916:G:H2'	1:A:917:A:N7	2.31	0.43
5:E:40:GLN:O	5:E:40:GLN:HG3	2.19	0.43
7:K:76:TYR:O	11:P:76:THR:HG22	2.19	0.43
13:R:5:ILE:HD11	13:R:14:VAL:HB	2.00	0.43
1:A:1012:G:H1'	1:A:2296:A:C2	2.54	0.42
1:A:1575:A:C5	1:A:1576:G:H1'	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2466:C:H5'	1:A:2466:C:H6	1.84	0.42
4:D:23:ILE:CG2	4:D:189:LYS:NZ	2.81	0.42
5:E:80:SER:OG	5:E:83:TRP:CD1	2.71	0.42
12:Q:86:SER:CB	12:Q:116:GLN:HB2	2.47	0.42
15:T:85:ALA:O	15:T:86:ASP:HB2	2.19	0.42
1:A:1818:A:C5	1:A:1819:C:C4	3.07	0.42
1:A:2839:C:H42	1:A:2911:G:H1	1.68	0.42
3:C:65:ILE:HD12	3:C:87:ARG:CZ	2.49	0.42
14:S:65:ASP:O	14:S:69:LEU:HG	2.19	0.42
15:T:89:GLU:HG2	15:T:89:GLU:O	2.19	0.42
1:A:2383:A:C2'	17:V:44:ILE:CG1	2.95	0.42
1:A:2094:C:O5'	1:A:2094:C:H6	2.02	0.42
1:A:2856:G:O2'	1:A:2909:U:OP1	2.33	0.42
1:A:903:G:C2'	1:A:903:G:N3	2.78	0.42
1:A:910:A:C6	1:A:911:G:N1	2.87	0.42
5:E:148:VAL:HA	5:E:191:LYS:NZ	2.34	0.42
5:E:33:VAL:O	5:E:33:VAL:HG12	2.19	0.42
6:J:70:LEU:HA	6:J:70:LEU:HD23	1.89	0.42
13:R:97:ILE:HA	13:R:97:ILE:HD13	1.86	0.42
17:V:29:LEU:HD11	17:V:49:ARG:CZ	2.49	0.42
1:A:1417:A:O2'	1:A:1419:G:N7	2.48	0.42
1:A:2301:U:H3'	1:A:2301:U:H6	1.83	0.42
1:A:27:G:N2	1:A:558:G:H2'	2.34	0.42
3:C:79:ALA:N	3:C:93:LEU:O	2.38	0.42
4:D:160:LEU:HD22	4:D:161:PRO:HD2	2.00	0.42
7:K:69:ALA:HB3	7:K:77:ILE:HG22	2.01	0.42
8:L:29:LYS:HE3	8:L:30:THR:HG23	2.00	0.42
9:N:24:LEU:HD13	9:N:30:ILE:HG12	2.02	0.42
10:O:13:LYS:HB3	10:O:13:LYS:HE2	1.32	0.42
13:R:67:ARG:HE	13:R:89:ARG:HE	1.68	0.42
20:Y:14:ILE:HG12	20:Y:57:ILE:HD11	1.97	0.42
1:A:405:U:H2'	1:A:406:G:C8	2.54	0.42
2:B:71:A:C3'	2:B:72:U:H5'	2.49	0.42
11:P:65:ARG:CZ	11:P:104:ARG:HA	2.50	0.42
12:Q:15:LYS:HD3	12:Q:15:LYS:HA	1.86	0.42
1:A:1317:G:H5'	9:N:20:LEU:HD21	2.00	0.42
1:A:1365:U:N3	1:A:1693:C:O2'	2.52	0.42
1:A:1529:G:H3'	1:A:1530:G:H8	1.85	0.42
1:A:2101:G:C2	1:A:2466:C:O2	2.72	0.42
1:A:2471:C:C3'	1:A:2471:C:C6	3.03	0.42
1:A:965:A:HO2'	2:B:79:C:C1'	2.33	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:J:14:ARG:NH1	6:J:122:LYS:HZ3	2.11	0.42
15:T:89:GLU:OE1	15:T:89:GLU:N	2.52	0.42
20:Y:21:LEU:HA	20:Y:21:LEU:HD23	1.87	0.42
1:A:2111:A:H3'	1:A:2112:G:C8	2.55	0.42
1:A:2467:U:C6	1:A:2467:U:H3'	2.54	0.42
16:U:91:VAL:HG12	16:U:92:ARG:N	2.33	0.42
20:Y:18:VAL:CG2	20:Y:53:MET:HE3	2.49	0.42
1:A:861:C:O2'	1:A:1264:G:N2	2.53	0.42
1:A:2099:G:H2'	1:A:2100:A:H8	1.85	0.42
1:A:2473:G:H8	1:A:2473:G:O5'	2.03	0.42
1:A:39:C:H42	1:A:487:G:H1	1.68	0.42
5:E:126:LEU:O	5:E:196:LYS:N	2.53	0.42
1:A:1696:G:H3'	9:N:35:THR:HG21	2.02	0.42
1:A:2228:A:C5	1:A:2254:A:N6	2.87	0.42
1:A:694:G:O2'	1:A:2380:G:OP1	2.29	0.42
1:A:917:A:O5'	1:A:917:A:C8	2.72	0.42
4:D:6:LEU:HD12	4:D:6:LEU:O	2.19	0.42
5:E:184:LEU:HA	5:E:187:VAL:HG12	2.02	0.42
1:A:1036:A:H2	13:R:75:ARG:HH22	1.67	0.42
17:V:54:TYR:O	17:V:86:LYS:HA	2.19	0.42
1:A:907:U:N3	1:A:2297:A:C8	2.86	0.42
1:A:677:A:O5'	8:L:64:ARG:CZ	2.67	0.42
1:A:918:U:H5''	1:A:918:U:H6	1.85	0.42
1:A:1829:C:OP2	3:C:182:ARG:NH2	2.53	0.42
8:L:74:TYR:HA	8:L:108:GLY:O	2.20	0.42
1:A:2472:C:O5'	1:A:2472:C:C6	2.70	0.41
1:A:304:G:H2'	1:A:305:A:H8	1.84	0.41
1:A:775:G:H5'	3:C:13:ARG:HH21	1.73	0.41
4:D:99:VAL:HG21	4:D:184:ASN:HB3	2.01	0.41
6:J:78:HIS:CE1	6:J:79:THR:O	2.72	0.41
11:P:53:ARG:HA	11:P:53:ARG:HD2	1.83	0.41
13:R:22:ILE:O	13:R:93:THR:HB	2.20	0.41
1:A:2786:A:H3'	1:A:2787:A:H5''	2.02	0.41
1:A:373:A:H61	16:U:15:LYS:HB2	1.85	0.41
1:A:547:A:N7	1:A:548:A:N6	2.68	0.41
1:A:925:A:C3'	1:A:925:A:N3	2.82	0.41
2:B:71:A:C5	2:B:72:U:C5	3.08	0.41
5:E:51:VAL:CG2	5:E:92:PRO:HG2	2.50	0.41
10:O:75:THR:OG1	10:O:105:ARG:HG2	2.20	0.41
1:A:1093:G:H3'	1:A:1156:G:H22	1.85	0.41
4:D:25:VAL:HG13	4:D:188:ILE:C	2.40	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:35:VAL:HG22	4:D:91:TYR:CE1	2.55	0.41
1:A:2855:G:H5'	4:D:57:ARG:NH2	2.35	0.41
5:E:6:LEU:HD23	5:E:17:ILE:HD11	2.02	0.41
3:C:117:MET:HG3	3:C:122:ALA:HB2	2.02	0.41
4:D:25:VAL:HG13	4:D:189:LYS:CA	2.48	0.41
10:O:17:ARG:HG2	10:O:18:VAL:N	2.35	0.41
17:V:42:GLY:N	17:V:69:ALA:O	2.50	0.41
1:A:1814:A:N7	1:A:1815:A:N6	2.66	0.41
1:A:2039:G:H5'	14:S:42:ALA:CB	2.47	0.41
14:S:3:ALA:HB2	14:S:58:ALA:HB2	2.03	0.41
17:V:79:ARG:H	17:V:79:ARG:HD3	1.85	0.41
1:A:1000:G:N2	1:A:1010:C:O2	2.54	0.41
1:A:1577:C:C4	1:A:1578:G:H1'	2.56	0.41
1:A:1711:G:OP1	7:K:66:LYS:NZ	2.41	0.41
1:A:346:G:N1	1:A:359:C:O2	2.45	0.41
2:B:36:C:H4'	10:O:103:HIS:CE1	2.56	0.41
8:L:108:GLY:HA2	8:L:126:ASN:ND2	2.35	0.41
1:A:2467:U:O5'	1:A:2467:U:C6	2.74	0.41
1:A:301:U:C3'	1:A:301:U:C6	3.03	0.41
1:A:911:G:N2	1:A:960:U:C4	2.86	0.41
4:D:111:THR:CG2	4:D:170:THR:HG23	2.51	0.41
4:D:56:LYS:HB2	4:D:57:ARG:H	1.73	0.41
6:J:131:HIS:O	6:J:131:HIS:CG	2.74	0.41
7:K:77:ILE:HG23	7:K:77:ILE:O	2.19	0.41
12:Q:100:VAL:HA	12:Q:106:PHE:HB2	2.02	0.41
17:V:29:LEU:HD11	17:V:49:ARG:NE	2.36	0.41
20:Y:10:THR:HG22	20:Y:60:ARG:HH11	1.86	0.41
18:Z:8:LEU:HG	18:Z:28:LEU:HD13	2.01	0.41
1:A:1087:U:HO2'	1:A:1160:G:N2	2.19	0.41
1:A:2039:G:H5''	14:S:42:ALA:CB	2.50	0.41
1:A:2069:U:OP2	6:J:112:LYS:NZ	2.43	0.41
1:A:277:C:H2'	1:A:278:A:C8	2.56	0.41
1:A:655:C:H2'	1:A:656:A:H8	1.86	0.41
3:C:142:HIS:CE1	3:C:193:GLY:O	2.74	0.41
3:C:9:THR:OG1	3:C:10:SER:N	2.54	0.41
5:E:119:ILE:HG13	5:E:119:ILE:H	1.71	0.41
20:Y:18:VAL:HG23	20:Y:53:MET:HE3	2.02	0.41
1:A:1279:C:H2'	1:A:1280:G:C8	2.56	0.41
1:A:1673:G:H2'	1:A:1674:G:C8	2.56	0.41
1:A:2298:A:OP1	1:A:2298:A:C8	2.74	0.41
1:A:2465:G:C5	1:A:2466:C:C6	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:875:U:O2'	1:A:878:G:O6	2.39	0.41
2:B:29:C:H1'	2:B:51:A:H61	1.86	0.41
2:B:93:U:C2'	2:B:94:G:H5'	2.46	0.41
3:C:216:ILE:HG22	3:C:216:ILE:O	2.20	0.41
7:K:24:VAL:HG12	7:K:26:GLY:H	1.86	0.41
8:L:79:LEU:HD11	8:L:117:LEU:CD1	2.48	0.41
1:A:1044:C:C5'	12:Q:84:LYS:HZ1	2.24	0.41
14:S:59:GLU:CD	14:S:66:ALA:HB2	2.41	0.41
14:S:86:ARG:HD3	14:S:87:PRO:HD2	2.03	0.41
1:A:1002:G:O2'	1:A:1005:A:N6	2.53	0.41
1:A:1313:A:H62	1:A:1691:A:H2'	1.84	0.41
1:A:2718:U:P	1:A:2748:G:H1	2.44	0.41
1:A:273:A:OP2	1:A:297:G:N1	2.44	0.41
1:A:641:C:H2'	1:A:642:G:H8	1.85	0.41
4:D:25:VAL:HG13	4:D:188:ILE:O	2.18	0.41
16:U:6:GLY:HA2	16:U:23:ILE:CA	2.50	0.41
1:A:1245:G:H5'	8:L:4:HIS:HE1	1.86	0.41
1:A:1297:C:H5'	5:E:75:GLN:HE21	1.86	0.41
1:A:912:C:N4	1:A:956:A:H62	2.17	0.41
4:D:13:THR:HG22	11:P:8:ILE:HG21	2.00	0.41
4:D:30:ALA:HB3	4:D:184:ASN:O	2.21	0.41
4:D:178:LYS:HB2	4:D:187:LEU:HD12	2.03	0.41
5:E:153:LEU:HD23	5:E:174:THR:HG23	2.03	0.41
8:L:13:ARG:HA	8:L:13:ARG:HD3	1.94	0.41
1:A:1075:A:N7	1:A:1076:G:N7	2.69	0.40
1:A:1403:G:N2	1:A:1406:A:OP2	2.40	0.40
1:A:2297:A:C2	1:A:2297:A:OP1	2.74	0.40
1:A:2300:G:OP2	1:A:2300:G:C8	2.74	0.40
1:A:2353:U:H1'	1:A:2366:G:H5''	2.03	0.40
1:A:907:U:C2	1:A:2297:A:H8	2.37	0.40
1:A:910:A:H62	1:A:959:C:H42	1.68	0.40
20:Y:9:LEU:HB3	20:Y:12:ALA:CB	2.47	0.40
1:A:999:A:C2	1:A:1011:C:O2	2.73	0.40
1:A:299:U:O2	1:A:416:U:O2	2.39	0.40
1:A:453:G:H2'	1:A:454:G:C8	2.56	0.40
1:A:525:A:N7	1:A:527:A:N6	2.67	0.40
1:A:916:G:H3'	1:A:917:A:N7	2.36	0.40
2:B:75:U:O4	2:B:96:G:N3	2.54	0.40
6:J:26:LEU:HA	6:J:29:LEU:HD23	2.04	0.40
13:R:79:LYS:HA	13:R:79:LYS:HD3	1.96	0.40
15:T:54:VAL:HG22	15:T:81:VAL:HG22	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1040:C:O2'	13:R:10:LYS:NZ	2.52	0.40
1:A:1131:A:O3'	1:A:1150:C:O2'	2.39	0.40
1:A:1714:A:H8	7:K:5:GLU:HB3	1.86	0.40
1:A:958:A:H1'	1:A:2293:C:H4'	2.04	0.40
1:A:549:A:H8	1:A:549:A:H2'	1.79	0.40
1:A:61:A:C6	1:A:62:C:N3	2.88	0.40
3:C:142:HIS:HD2	3:C:143:ASN:HB2	1.86	0.40
4:D:56:LYS:HE3	4:D:61:SER:HB3	2.02	0.40
10:O:15:HIS:CE1	10:O:19:ARG:HG2	2.56	0.40
13:R:77:LYS:HB3	13:R:77:LYS:HE3	1.92	0.40
13:R:79:LYS:HE3	13:R:79:LYS:HB2	1.92	0.40
18:Z:5:GLU:HB2	18:Z:57:LYS:HB3	2.03	0.40
1:A:1125:C:N4	1:A:1126:A:H62	2.20	0.40
1:A:1132:A:O2'	1:A:1149:A:N1	2.54	0.40
1:A:1444:C:H2'	1:A:1445:A:C8	2.57	0.40
1:A:189:G:H2'	1:A:190:G:H8	1.87	0.40
1:A:801:U:H2'	1:A:802:G:H8	1.85	0.40
1:A:970:A:H2'	1:A:971:A:O4'	2.22	0.40
2:B:21:G:H1	2:B:58:C:H42	1.70	0.40
3:C:175:ARG:HD2	3:C:179:GLY:HA2	2.03	0.40
5:E:131:LEU:CD1	5:E:163:VAL:HA	2.52	0.40
5:E:165:LEU:HD23	5:E:165:LEU:HA	1.90	0.40
7:K:12:ASP:HB3	7:K:98:ILE:HG12	2.04	0.40
8:L:79:LEU:CD1	8:L:117:LEU:CD2	2.95	0.40
18:Z:40:ASN:OD1	18:Z:41:ALA:N	2.55	0.40
18:Z:47:ILE:HD13	18:Z:56:VAL:HG21	2.04	0.40
1:A:1572:G:O2'	1:A:1573:C:O5'	2.37	0.40
1:A:1012:G:H4'	1:A:2296:A:N6	2.36	0.40
1:A:364:A:H4'	1:A:366:A:N7	2.37	0.40
1:A:421:A:H62	1:A:447:G:H21	1.69	0.40
1:A:750:U:O4	1:A:751:G:N2	2.55	0.40
2:B:76:A:P	2:B:76:A:H8	2.45	0.40
4:D:89:ASP:HB3	4:D:90:ALA:H	1.59	0.40
7:K:90:ASP:HB3	7:K:92:SER:H	1.85	0.40
13:R:99:LYS:HE3	13:R:101:ASN:HD21	1.85	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	
3	C	219/277 (79%)	199 (91%)	20 (9%)	0	100	100
4	D	161/209 (77%)	138 (86%)	20 (12%)	3 (2%)	9	42
5	E	188/207 (91%)	159 (85%)	28 (15%)	1 (0%)	31	69
6	J	139/145 (96%)	122 (88%)	14 (10%)	3 (2%)	7	39
7	K	120/122 (98%)	110 (92%)	9 (8%)	1 (1%)	21	60
8	L	124/145 (86%)	115 (93%)	6 (5%)	3 (2%)	6	37
9	N	117/120 (98%)	107 (92%)	10 (8%)	0	100	100
10	O	100/120 (83%)	92 (92%)	7 (7%)	1 (1%)	17	56
11	P	101/115 (88%)	92 (91%)	9 (9%)	0	100	100
12	Q	115/118 (98%)	110 (96%)	4 (4%)	1 (1%)	19	58
13	R	92/102 (90%)	77 (84%)	15 (16%)	0	100	100
14	S	107/113 (95%)	100 (94%)	7 (6%)	0	100	100
15	T	86/95 (90%)	79 (92%)	7 (8%)	0	100	100
16	U	94/103 (91%)	82 (87%)	9 (10%)	3 (3%)	4	31
17	V	71/94 (76%)	62 (87%)	8 (11%)	1 (1%)	12	48
18	Z	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
19	b	52/59 (88%)	47 (90%)	4 (8%)	1 (2%)	9	42
20	Y	63/66 (96%)	58 (92%)	5 (8%)	0	100	100
21	d	42/44 (96%)	42 (100%)	0	0	100	100
All	All	2047/2313 (88%)	1844 (90%)	185 (9%)	18 (1%)	24	58

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	O	102	TYR
4	D	93	VAL

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Mol	Chain	Res	Type
6	J	59	ASN
7	K	26	GLY
12	Q	90	VAL
19	b	50	ASN
5	E	9	GLN
8	L	79	LEU
16	U	8	LYS
16	U	54	GLY
17	V	38	PHE
6	J	63	ILE
16	U	47	PRO
4	D	32	PRO
4	D	97	VAL
8	L	91	VAL
6	J	58	ILE
8	L	88	GLY

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	
3	C	177/225 (79%)	168 (95%)	9 (5%)	26	61
4	D	135/170 (79%)	115 (85%)	20 (15%)	3	17
5	E	162/170 (95%)	148 (91%)	14 (9%)	11	41
6	J	120/123 (98%)	113 (94%)	7 (6%)	22	58
7	K	101/101 (100%)	100 (99%)	1 (1%)	78	89
8	L	98/109 (90%)	92 (94%)	6 (6%)	20	56
9	N	99/100 (99%)	99 (100%)	0	100	100
10	O	78/93 (84%)	71 (91%)	7 (9%)	10	39
11	P	91/100 (91%)	87 (96%)	4 (4%)	31	66
12	Q	96/97 (99%)	83 (86%)	13 (14%)	4	20
13	R	82/84 (98%)	75 (92%)	7 (8%)	12	42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	S	90/93 (97%)	87 (97%)	3 (3%)	41	73
15	T	79/85 (93%)	74 (94%)	5 (6%)	20	55
16	U	82/87 (94%)	78 (95%)	4 (5%)	27	63
17	V	54/74 (73%)	44 (82%)	10 (18%)	2	8
18	Z	52/53 (98%)	52 (100%)	0	100	100
19	b	48/53 (91%)	43 (90%)	5 (10%)	8	32
20	Y	56/57 (98%)	55 (98%)	1 (2%)	62	83
21	d	39/39 (100%)	39 (100%)	0	100	100
All	All	1739/1913 (91%)	1623 (93%)	116 (7%)	22	53

All (116) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	18	THR
3	C	63	ARG
3	C	87	ARG
3	C	116	ILE
3	C	117	MET
3	C	165	LEU
3	C	168	GLU
3	C	192	ILE
3	C	216	ILE
4	D	13	THR
4	D	15	VAL
4	D	21	ASP
4	D	23	ILE
4	D	25	VAL
4	D	28	ILE
4	D	29	GLU
4	D	33	ASN
4	D	36	LEU
4	D	38	LYS
4	D	56	LYS
4	D	62	ASN
4	D	82	GLU
4	D	84	ARG
4	D	86	VAL
4	D	88	MET
4	D	89	ASP

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Mol	Chain	Res	Type
4	D	91	TYR
4	D	92	GLU
4	D	159	LEU
5	E	17	ILE
5	E	43	SER
5	E	44	LEU
5	E	50	LYS
5	E	51	VAL
5	E	82	GLN
5	E	89	VAL
5	E	95	ARG
5	E	96	SER
5	E	97	TYR
5	E	138	GLU
5	E	163	VAL
5	E	173	VAL
5	E	176	VAL
6	J	25	THR
6	J	28	ARG
6	J	29	LEU
6	J	58	ILE
6	J	71	THR
6	J	97	TYR
6	J	130	GLU
7	K	67	SER
8	L	64	ARG
8	L	76	VAL
8	L	87	GLU
8	L	89	THR
8	L	92	THR
8	L	119	LYS
10	O	13	LYS
10	O	17	ARG
10	O	46	ASP
10	O	90	ILE
10	O	92	ASP
10	O	105	ARG
10	O	106	VAL
11	P	35	VAL
11	P	39	ASN
11	P	103	LEU
11	P	104	ARG

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Mol	Chain	Res	Type
12	Q	51	ARG
12	Q	52	GLN
12	Q	55	ARG
12	Q	80	MET
12	Q	89	GLU
12	Q	90	VAL
12	Q	93	LYS
12	Q	94	MET
12	Q	102	ASP
12	Q	103	LEU
12	Q	104	THR
12	Q	109	LEU
12	Q	116	GLN
13	R	5	ILE
13	R	20	VAL
13	R	21	TYR
13	R	22	ILE
13	R	23	GLU
13	R	24	LYS
13	R	89	ARG
14	S	31	GLU
14	S	39	THR
14	S	65	ASP
15	T	65	ARG
15	T	68	ARG
15	T	76	ARG
15	T	87	SER
15	T	88	LYS
16	U	9	VAL
16	U	10	MET
16	U	46	LYS
16	U	49	GLN
17	V	46	TYR
17	V	52	LYS
17	V	53	ILE
17	V	71	ILE
17	V	79	ARG
17	V	80	PHE
17	V	82	ARG
17	V	84	ARG
17	V	86	LYS
17	V	87	VAL

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Mol	Chain	Res	Type
19	b	35	GLU
19	b	36	MET
19	b	37	LYS
19	b	52	LYS
19	b	53	ASP
20	Y	9	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	86	ASN
3	C	153	GLN
4	D	14	GLN
4	D	33	ASN
4	D	120	GLN
5	E	49	HIS
6	J	59	ASN
7	K	13	ASN
8	L	4	HIS
8	L	78	ASN
8	L	83	ASN
8	L	126	ASN
10	O	15	HIS
10	O	49	ASN
10	O	103	HIS
11	P	32	HIS
12	Q	37	GLN
13	R	81	ASN
14	S	60	HIS
15	T	35	ASN
15	T	55	ASN
16	U	49	GLN
16	U	64	HIS
17	V	20	ASN
17	V	37	GLN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2458/2927 (83%)	792 (32%)	50 (2%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	111/119 (93%)	45 (40%)	3 (2%)
All	All	2569/3046 (84%)	837 (32%)	53 (2%)

All (837) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	8	U
1	A	9	U
1	A	13	A
1	A	15	G
1	A	23	G
1	A	28	A
1	A	30	G
1	A	31	C
1	A	34	U
1	A	35	G
1	A	38	A
1	A	39	C
1	A	43	G
1	A	44	A
1	A	46	C
1	A	48	G
1	A	51	G
1	A	54	G
1	A	55	G
1	A	59	G
1	A	61	A
1	A	63	G
1	A	64	A
1	A	71	A
1	A	75	G
1	A	76	C
1	A	85	G
1	A	87	U
1	A	90	A
1	A	91	A
1	A	92	G
1	A	94	A
1	A	98	U
1	A	99	U
1	A	101	G
1	A	106	G

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Mol	Chain	Res	Type
1	A	109	G
1	A	115	C
1	A	117	A
1	A	119	U
1	A	124	A
1	A	125	A
1	A	127	C
1	A	130	A
1	A	135	U
1	A	150	A
1	A	156	A
1	A	159	U
1	A	162	A
1	A	163	U
1	A	164	U
1	A	166	A
1	A	176	A
1	A	177	G
1	A	183	A
1	A	184	G
1	A	198	A
1	A	199	A
1	A	202	A
1	A	203	U
1	A	207	A
1	A	211	C
1	A	216	A
1	A	218	G
1	A	219	A
1	A	225	A
1	A	226	A
1	A	227	G
1	A	228	C
1	A	230	A
1	A	231	A
1	A	232	U
1	A	233	G
1	A	236	A
1	A	239	C
1	A	240	C
1	A	245	G
1	A	248	G

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Mol	Chain	Res	Type
1	A	251	G
1	A	252	C
1	A	253	G
1	A	258	A
1	A	267	C
1	A	268	A
1	A	270	C
1	A	272	C
1	A	275	A
1	A	281	A
1	A	282	G
1	A	285	U
1	A	287	G
1	A	289	C
1	A	290	U
1	A	291	C
1	A	298	U
1	A	299	U
1	A	300	G
1	A	301	U
1	A	302	A
1	A	307	A
1	A	312	G
1	A	313	U
1	A	314	A
1	A	315	C
1	A	318	A
1	A	321	U
1	A	322	A
1	A	324	A
1	A	326	A
1	A	327	G
1	A	328	G
1	A	329	A
1	A	334	G
1	A	337	A
1	A	338	G
1	A	344	G
1	A	345	A
1	A	346	G
1	A	348	U
1	A	355	A

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Mol	Chain	Res	Type
1	A	361	G
1	A	367	G
1	A	368	G
1	A	374	A
1	A	376	A
1	A	378	C
1	A	379	C
1	A	380	C
1	A	382	G
1	A	385	G
1	A	386	U
1	A	387	C
1	A	390	A
1	A	393	U
1	A	394	U
1	A	396	G
1	A	397	U
1	A	405	U
1	A	406	G
1	A	410	G
1	A	411	G
1	A	413	U
1	A	415	C
1	A	418	A
1	A	419	G
1	A	420	U
1	A	427	G
1	A	432	C
1	A	433	G
1	A	434	U
1	A	435	G
1	A	436	A
1	A	438	A
1	A	443	G
1	A	445	C
1	A	446	G
1	A	451	C
1	A	452	C
1	A	453	G
1	A	459	A
1	A	462	A
1	A	469	A

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Mol	Chain	Res	Type
1	A	478	U
1	A	483	C
1	A	488	U
1	A	489	G
1	A	490	A
1	A	491	C
1	A	501	A
1	A	502	C
1	A	503	C
1	A	504	A
1	A	514	G
1	A	520	G
1	A	526	A
1	A	527	A
1	A	528	G
1	A	537	A
1	A	538	A
1	A	547	A
1	A	548	A
1	A	550	G
1	A	551	A
1	A	552	G
1	A	554	U
1	A	555	C
1	A	556	C
1	A	558	G
1	A	564	G
1	A	568	G
1	A	573	C
1	A	576	G
1	A	577	U
1	A	578	A
1	A	579	G
1	A	586	C
1	A	591	U
1	A	592	A
1	A	594	C
1	A	595	G
1	A	599	G
1	A	606	U
1	A	607	G
1	A	613	U

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Mol	Chain	Res	Type
1	A	616	A
1	A	618	A
1	A	619	A
1	A	630	A
1	A	631	G
1	A	636	G
1	A	647	A
1	A	648	G
1	A	649	G
1	A	650	U
1	A	651	U
1	A	657	G
1	A	658	A
1	A	660	G
1	A	663	G
1	A	665	G
1	A	666	G
1	A	668	G
1	A	673	A
1	A	674	G
1	A	677	A
1	A	680	G
1	A	683	A
1	A	684	G
1	A	691	U
1	A	692	A
1	A	694	G
1	A	698	C
1	A	701	G
1	A	711	U
1	A	713	G
1	A	716	G
1	A	717	A
1	A	718	C
1	A	733	U
1	A	737	C
1	A	748	G
1	A	754	G
1	A	758	A
1	A	764	C
1	A	765	A
1	A	766	C

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Mol	Chain	Res	Type
1	A	769	A
1	A	775	G
1	A	777	C
1	A	785	C
1	A	791	C
1	A	792	G
1	A	793	U
1	A	794	U
1	A	795	G
1	A	799	A
1	A	809	U
1	A	811	A
1	A	812	G
1	A	822	G
1	A	823	G
1	A	824	G
1	A	829	A
1	A	831	U
1	A	832	G
1	A	836	A
1	A	837	U
1	A	838	C
1	A	839	G
1	A	841	A
1	A	843	C
1	A	847	A
1	A	849	A
1	A	853	C
1	A	854	U
1	A	856	G
1	A	858	U
1	A	859	C
1	A	866	A
1	A	874	U
1	A	876	A
1	A	882	A
1	A	885	C
1	A	892	U
1	A	893	A
1	A	900	U
1	A	902	G
1	A	903	G

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Mol	Chain	Res	Type
1	A	904	A
1	A	905	G
1	A	906	G
1	A	907	U
1	A	908	A
1	A	909	G
1	A	910	A
1	A	912	C
1	A	913	A
1	A	918	U
1	A	919	U
1	A	922	A
1	A	924	U
1	A	925	A
1	A	947	A
1	A	950	U
1	A	951	C
1	A	956	A
1	A	957	A
1	A	959	C
1	A	960	U
1	A	961	C
1	A	962	C
1	A	963	G
1	A	964	A
1	A	966	U
1	A	967	G
1	A	968	C
1	A	969	C
1	A	970	A
1	A	972	U
1	A	974	A
1	A	975	C
1	A	976	U
1	A	977	U
1	A	978	A
1	A	981	C
1	A	987	A
1	A	991	A
1	A	992	G
1	A	998	G
1	A	999	A

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Mol	Chain	Res	Type
1	A	1000	G
1	A	1003	A
1	A	1005	A
1	A	1007	G
1	A	1013	U
1	A	1019	A
1	A	1020	A
1	A	1027	A
1	A	1028	C
1	A	1029	A
1	A	1034	A
1	A	1035	G
1	A	1037	C
1	A	1042	A
1	A	1051	C
1	A	1055	A
1	A	1058	U
1	A	1059	A
1	A	1063	G
1	A	1067	A
1	A	1068	G
1	A	1072	A
1	A	1073	A
1	A	1079	U
1	A	1080	G
1	A	1083	G
1	A	1091	U
1	A	1093	G
1	A	1096	A
1	A	1097	A
1	A	1100	A
1	A	1102	G
1	A	1103	A
1	A	1104	U
1	A	1106	U
1	A	1107	U
1	A	1108	G
1	A	1109	G
1	A	1128	U
1	A	1130	A
1	A	1131	A
1	A	1133	G

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Mol	Chain	Res	Type
1	A	1135	G
1	A	1136	U
1	A	1138	C
1	A	1139	G
1	A	1141	A
1	A	1142	A
1	A	1148	C
1	A	1150	C
1	A	1151	U
1	A	1158	G
1	A	1168	G
1	A	1172	A
1	A	1178	U
1	A	1179	A
1	A	1180	C
1	A	1181	C
1	A	1183	G
1	A	1185	G
1	A	1187	U
1	A	1188	A
1	A	1189	A
1	A	1193	U
1	A	1194	A
1	A	1201	A
1	A	1202	A
1	A	1209	G
1	A	1215	U
1	A	1222	A
1	A	1223	C
1	A	1227	G
1	A	1246	G
1	A	1247	G
1	A	1248	C
1	A	1251	U
1	A	1252	G
1	A	1258	A
1	A	1260	A
1	A	1274	U
1	A	1276	G
1	A	1278	G
1	A	1286	A
1	A	1287	A

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Mol	Chain	Res	Type
1	A	1288	G
1	A	1289	U
1	A	1290	G
1	A	1291	A
1	A	1293	A
1	A	1295	U
1	A	1296	G
1	A	1305	A
1	A	1311	G
1	A	1312	A
1	A	1313	A
1	A	1314	A
1	A	1315	G
1	A	1327	U
1	A	1333	C
1	A	1339	A
1	A	1340	A
1	A	1341	U
1	A	1344	C
1	A	1345	U
1	A	1346	A
1	A	1352	U
1	A	1359	G
1	A	1360	A
1	A	1363	G
1	A	1364	C
1	A	1366	C
1	A	1375	A
1	A	1376	G
1	A	1377	G
1	A	1384	C
1	A	1388	A
1	A	1391	U
1	A	1404	A
1	A	1405	A
1	A	1409	C
1	A	1414	G
1	A	1417	A
1	A	1418	U
1	A	1423	A
1	A	1424	A
1	A	1425	C

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Mol	Chain	Res	Type
1	A	1427	G
1	A	1428	G
1	A	1432	A
1	A	1434	A
1	A	1435	U
1	A	1436	U
1	A	1439	U
1	A	1441	U
1	A	1442	A
1	A	1448	U
1	A	1450	C
1	A	1455	C
1	A	1456	A
1	A	1459	U
1	A	1460	G
1	A	1462	G
1	A	1464	A
1	A	1473	A
1	A	1474	C
1	A	1481	G
1	A	1483	A
1	A	1488	G
1	A	1494	G
1	A	1495	C
1	A	1496	G
1	A	1498	U
1	A	1499	A
1	A	1500	U
1	A	1501	U
1	A	1503	G
1	A	1504	A
1	A	1506	A
1	A	1507	U
1	A	1513	U
1	A	1519	C
1	A	1520	A
1	A	1521	G
1	A	1524	A
1	A	1528	U
1	A	1529	G
1	A	1530	G
1	A	1539	C

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Mol	Chain	Res	Type
1	A	1540	A
1	A	1543	U
1	A	1544	C
1	A	1554	U
1	A	1555	A
1	A	1556	A
1	A	1558	G
1	A	1560	U
1	A	1561	G
1	A	1563	G
1	A	1564	C
1	A	1569	A
1	A	1572	G
1	A	1573	C
1	A	1576	G
1	A	1577	C
1	A	1579	A
1	A	1581	A
1	A	1582	U
1	A	1585	A
1	A	1586	G
1	A	1596	U
1	A	1607	C
1	A	1608	A
1	A	1613	C
1	A	1615	A
1	A	1617	A
1	A	1626	U
1	A	1629	C
1	A	1631	A
1	A	1632	G
1	A	1634	U
1	A	1638	A
1	A	1639	G
1	A	1640	G
1	A	1651	G
1	A	1652	C
1	A	1653	A
1	A	1655	A
1	A	1660	C
1	A	1667	A
1	A	1681	U

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Mol	Chain	Res	Type
1	A	1684	U
1	A	1685	A
1	A	1688	G
1	A	1689	U
1	A	1692	U
1	A	1693	C
1	A	1696	G
1	A	1697	A
1	A	1698	G
1	A	1699	A
1	A	1712	G
1	A	1717	C
1	A	1718	G
1	A	1719	G
1	A	1720	C
1	A	1724	A
1	A	1726	G
1	A	1727	A
1	A	1735	A
1	A	1739	C
1	A	1740	G
1	A	1743	A
1	A	1744	G
1	A	1745	A
1	A	1746	A
1	A	1747	G
1	A	1752	G
1	A	1755	C
1	A	1757	G
1	A	1758	U
1	A	1759	U
1	A	1762	G
1	A	1769	G
1	A	1771	C
1	A	1774	A
1	A	1776	A
1	A	1778	A
1	A	1779	G
1	A	1780	C
1	A	1781	C
1	A	1782	G
1	A	1785	G

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Mol	Chain	Res	Type
1	A	1791	A
1	A	1792	G
1	A	1793	G
1	A	1794	C
1	A	1802	A
1	A	1803	C
1	A	1805	G
1	A	1815	A
1	A	1817	C
1	A	1828	G
1	A	1829	C
1	A	1831	A
1	A	1835	C
1	A	1844	A
1	A	1848	A
1	A	1858	A
1	A	1861	C
1	A	2004	G
1	A	2005	C
1	A	2006	A
1	A	2010	A
1	A	2011	U
1	A	2016	G
1	A	2018	A
1	A	2020	U
1	A	2021	G
1	A	2022	U
1	A	2024	U
1	A	2026	A
1	A	2033	G
1	A	2052	A
1	A	2059	A
1	A	2064	G
1	A	2065	C
1	A	2068	G
1	A	2072	C
1	A	2080	A
1	A	2084	C
1	A	2086	G
1	A	2092	C
1	A	2096	G
1	A	2097	U

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Mol	Chain	Res	Type
1	A	2098	G
1	A	2109	G
1	A	2111	A
1	A	2112	G
1	A	2116	G
1	A	2121	U
1	A	2122	G
1	A	2123	A
1	A	2124	A
1	A	2125	U
1	A	2222	C
1	A	2224	U
1	A	2227	A
1	A	2232	G
1	A	2233	C
1	A	2239	U
1	A	2240	U
1	A	2241	A
1	A	2246	G
1	A	2254	A
1	A	2255	C
1	A	2267	G
1	A	2268	G
1	A	2274	U
1	A	2285	G
1	A	2288	G
1	A	2295	A
1	A	2296	A
1	A	2297	A
1	A	2298	A
1	A	2299	G
1	A	2300	G
1	A	2308	G
1	A	2312	C
1	A	2325	U
1	A	2326	C
1	A	2328	G
1	A	2334	U
1	A	2335	U
1	A	2336	G
1	A	2337	G
1	A	2338	A

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Mol	Chain	Res	Type
1	A	2339	A
1	A	2340	A
1	A	2343	A
1	A	2344	U
1	A	2345	U
1	A	2346	C
1	A	2347	G
1	A	2348	C
1	A	2349	A
1	A	2351	A
1	A	2352	G
1	A	2356	A
1	A	2363	C
1	A	2364	A
1	A	2374	G
1	A	2377	U
1	A	2379	C
1	A	2382	G
1	A	2387	A
1	A	2390	A
1	A	2394	G
1	A	2404	G
1	A	2408	G
1	A	2411	G
1	A	2412	G
1	A	2414	C
1	A	2419	U
1	A	2420	G
1	A	2425	G
1	A	2430	U
1	A	2431	U
1	A	2432	C
1	A	2435	C
1	A	2439	G
1	A	2452	U
1	A	2453	C
1	A	2454	A
1	A	2455	A
1	A	2456	C
1	A	2458	G
1	A	2459	A
1	A	2460	U

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Mol	Chain	Res	Type
1	A	2464	A
1	A	2466	C
1	A	2468	A
1	A	2469	C
1	A	2470	C
1	A	2471	C
1	A	2475	G
1	A	2642	U
1	A	2643	A
1	A	2648	U
1	A	2649	C
1	A	2658	A
1	A	2661	A
1	A	2668	A
1	A	2675	C
1	A	2678	U
1	A	2681	U
1	A	2683	A
1	A	2684	G
1	A	2685	U
1	A	2692	G
1	A	2700	A
1	A	2702	G
1	A	2710	C
1	A	2711	G
1	A	2714	G
1	A	2717	G
1	A	2718	U
1	A	2720	C
1	A	2728	U
1	A	2730	U
1	A	2731	G
1	A	2735	A
1	A	2743	G
1	A	2744	C
1	A	2748	G
1	A	2755	U
1	A	2756	G
1	A	2762	A
1	A	2764	G
1	A	2765	G
1	A	2768	U

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Mol	Chain	Res	Type
1	A	2771	G
1	A	2773	G
1	A	2780	G
1	A	2781	C
1	A	2784	C
1	A	2785	U
1	A	2786	A
1	A	2787	A
1	A	2790	A
1	A	2793	A
1	A	2794	A
1	A	2795	G
1	A	2807	A
1	A	2808	U
1	A	2813	U
1	A	2818	C
1	A	2819	A
1	A	2820	U
1	A	2823	C
1	A	2825	C
1	A	2826	A
1	A	2828	G
1	A	2833	U
1	A	2837	A
1	A	2843	G
1	A	2848	A
1	A	2851	A
1	A	2856	G
1	A	2858	U
1	A	2859	G
1	A	2860	A
1	A	2868	G
1	A	2873	G
1	A	2884	G
1	A	2892	G
1	A	2897	G
1	A	2905	C
1	A	2906	U
1	A	2908	A
1	A	2914	C
1	A	2918	G
1	A	2921	U

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Mol	Chain	Res	Type
2	B	7	G
2	B	9	C
2	B	10	G
2	B	11	A
2	B	12	U
2	B	13	A
2	B	14	G
2	B	15	C
2	B	20	A
2	B	21	G
2	B	23	U
2	B	28	C
2	B	33	U
2	B	34	C
2	B	38	U
2	B	39	A
2	B	40	C
2	B	42	G
2	B	46	A
2	B	48	G
2	B	49	G
2	B	51	A
2	B	52	G
2	B	53	U
2	B	54	U
2	B	55	A
2	B	59	U
2	B	60	C
2	B	61	U
2	B	64	A
2	B	72	U
2	B	78	U
2	B	79	C
2	B	80	G
2	B	81	G
2	B	82	G
2	B	86	U
2	B	87	U
2	B	88	C
2	B	92	C
2	B	93	U
2	B	95	U

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Mol	Chain	Res	Type
2	B	97	A
2	B	107	G
2	B	112	C

All (53) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	43	G
1	A	58	G
1	A	62	C
1	A	63	G
1	A	90	A
1	A	163	U
1	A	175	G
1	A	183	A
1	A	229	A
1	A	267	C
1	A	271	C
1	A	288	C
1	A	377	G
1	A	405	U
1	A	419	G
1	A	527	A
1	A	537	A
1	A	549	A
1	A	649	G
1	A	667	A
1	A	683	A
1	A	717	A
1	A	837	U
1	A	908	A
1	A	962	C
1	A	1066	A
1	A	1103	A
1	A	1107	U
1	A	1245	G
1	A	1250	G
1	A	1339	A
1	A	1351	U
1	A	1362	G
1	A	1438	C
1	A	1455	C

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Mol	Chain	Res	Type
1	A	1527	C
1	A	1595	U
1	A	1630	G
1	A	1652	C
1	A	1779	G
1	A	1784	A
1	A	2267	G
1	A	2295	A
1	A	2334	U
1	A	2351	A
1	A	2454	A
1	A	2716	U
1	A	2784	C
1	A	2785	U
1	A	2812	A
2	B	47	C
2	B	54	U
2	B	59	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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.