



## wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 01:38 PM BST

PDB ID : 2NOQ  
EMDB ID: : EMD-1285  
Title : Structure of ribosome-bound cricket paralysis virus IRES RNA  
Authors : Schuler, M.; Connell, S.R.; Lescoute, A.; Giesebrecht, J.; Dabrowski, M.; Schroeer, B.; Mielke, T.; Penczek, P.A.; Westhof, E.; Spahn, C.M.T.  
Deposited on : 2006-10-26  
Resolution : 7.30 Å(reported)  
Based on PDB ID : 1s1i, 1s1h

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

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

A user guide is available at

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

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

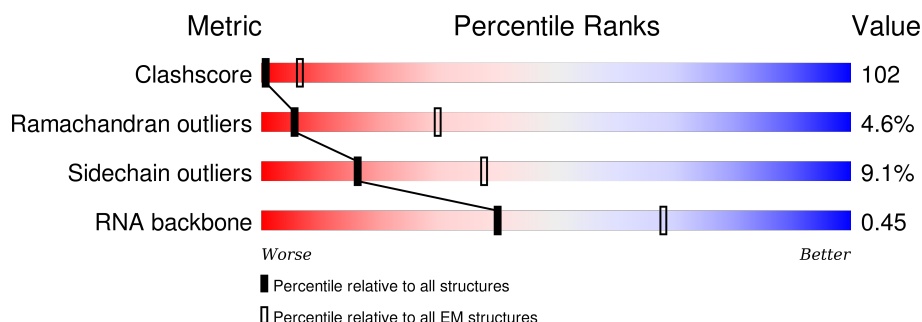
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 7.30 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	A	190	9% 54% 37%
2	B	46	28% 57% 13% .
3	C	13	15% 69% 15%
4	D	15	27% 53% 20%
5	E	53	28% 49% 19% .
6	F	150	27% 65% 8%
7	G	213	23% 71% 6%
8	H	165	13% 61% 22% .

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 10909 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 CrPV IRES.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	190	Total	C	N	O	P	0	0
			4023	1803	692	1338	190		

- Molecule 2 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	46	Total	C	N	O	P	0	0
			986	439	184	318	45		

- Molecule 3 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	13	Total	C	N	O	P	0	0
			276	123	48	93	12		

- Molecule 4 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	15	Total	C	N	O	P	0	0
			319	142	55	107	15		

- Molecule 5 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	53	Total	C	N	O	P	0	0
			1142	508	213	368	53		

- Molecule 6 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	150	Total	C	N	O	S	0	0
			1161	714	229	215	3		

- Molecule 7 is a protein called 60S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	213	Total	C	N	O	S	0	0
			1683	1074	294	306	9		

- Molecule 8 is a protein called 60S ribosomal protein L11-B.

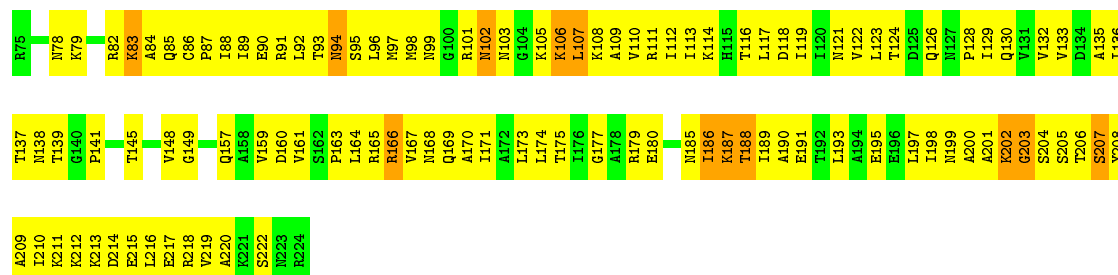
Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	165	Total	C	N	O	S	0	0
			1319	826	247	242	4		





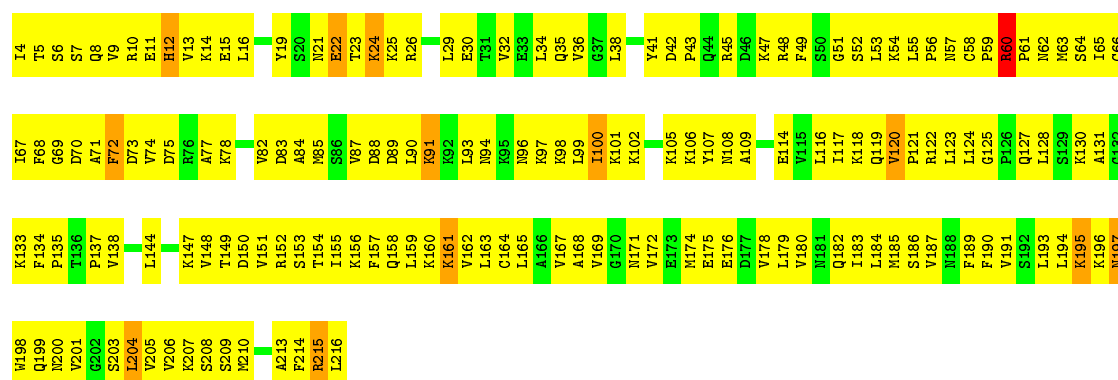
• Molecule 6: 40S ribosomal protein S5

Chain F: 27% 65% 8%



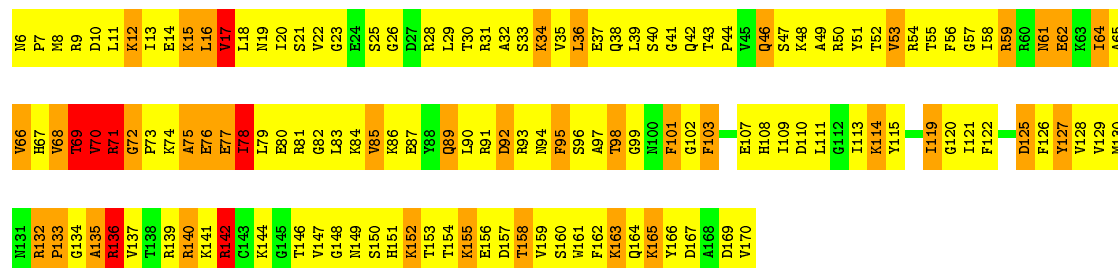
• Molecule 7: 60S ribosomal protein L1

Chain G: 23% 71% 6%



• Molecule 8: 60S ribosomal protein L11-B

Chain H: 13% 61% 22% .



## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI-POLARA G2	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	Not provided	Depositor
Minimum defocus (nm)	100	Depositor
Maximum defocus (nm)	3900	Depositor
Magnification	39000	Depositor
Image detector	KODAK SO163 FILM	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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	1.02	2/4495 (0.0%)	2.56	597/6995 (8.5%)
2	B	0.54	0/1100	0.78	3/1715 (0.2%)
3	C	0.51	0/305	0.79	0/474
4	D	0.47	0/355	0.83	0/551
5	E	1.08	3/1278 (0.2%)	0.94	6/1991 (0.3%)
6	F	1.05	0/1169	1.14	2/1570 (0.1%)
7	G	0.91	0/1707	1.11	1/2289 (0.0%)
8	H	1.20	1/1340 (0.1%)	1.89	20/1797 (1.1%)
All	All	0.98	6/11749 (0.1%)	1.87	629/17382 (3.6%)

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
2	B	0	2
5	E	0	3
8	H	0	1
All	All	0	6

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	E	2160	G	O3'-P	-32.03	1.22	1.61
5	E	2166	G	O3'-P	-11.77	1.47	1.61
1	A	75	U	P-O5'	10.93	1.70	1.59
5	E	2138	G	OP3-P	-6.97	1.52	1.61
1	A	124	C	O3'-P	-5.62	1.54	1.61
8	H	70	VAL	CA-CB	-5.18	1.43	1.54

All (629) bond angle outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	H	46	GLN	CG-CD-OE1	-38.67	44.25	121.60
1	A	111	A	P-O3'-C3'	24.02	148.53	119.70
1	A	101	C	P-O3'-C3'	19.03	142.54	119.70
1	A	124	C	P-O3'-C3'	17.04	140.15	119.70
1	A	93	U	P-O3'-C3'	15.66	138.49	119.70
1	A	155	C	P-O3'-C3'	13.57	135.98	119.70
1	A	94	U	P-O3'-C3'	13.47	135.86	119.70
1	A	96	C	P-O3'-C3'	13.01	135.32	119.70
1	A	177	U	P-O3'-C3'	12.88	135.15	119.70
1	A	150	U	P-O3'-C3'	12.87	135.14	119.70
1	A	94	U	P-O5'-C5'	11.81	139.80	120.90
5	E	2166	G	P-O3'-C3'	-11.11	106.37	119.70
1	A	44	A	OP1-P-O3'	11.09	129.61	105.20
1	A	44	A	P-O3'-C3'	-10.55	107.04	119.70
1	A	112	G	O4'-C1'-N9	10.13	116.31	108.20
1	A	182	A	P-O3'-C3'	9.86	131.53	119.70
8	H	46	GLN	CG-CD-NE2	-9.67	93.49	116.70
8	H	75	ALA	C-N-CA	9.34	145.04	121.70
5	E	2160	G	OP2-P-O3'	-9.28	84.79	105.20
8	H	76	GLU	N-CA-C	-9.25	86.04	111.00
1	A	34	U	P-O3'-C3'	9.13	130.66	119.70
8	H	70	VAL	CA-CB-CG2	-9.06	97.30	110.90
1	A	45	A	OP1-P-OP2	-8.82	106.36	119.60
1	A	103	G	O4'-C1'-N9	8.77	115.22	108.20
5	E	2160	G	P-O3'-C3'	8.60	130.02	119.70
8	H	101	PHE	CB-CA-C	-8.56	93.27	110.40
1	A	113	U	C2-N3-C4	-8.37	121.98	127.00
1	A	45	A	P-O5'-C5'	8.33	134.23	120.90
1	A	129	U	C2-N3-C4	-8.32	122.01	127.00
1	A	44	A	N9-C1'-C2'	-8.24	102.94	112.00
1	A	75	U	N3-C4-C5	8.22	119.53	114.60
1	A	110	U	C2-N3-C4	-8.21	122.07	127.00
1	A	113	U	N3-C4-C5	8.18	119.51	114.60
1	A	154	U	C2-N3-C4	-8.18	122.09	127.00
1	A	129	U	N3-C4-C5	8.17	119.50	114.60
1	A	75	U	C2-N3-C4	-8.14	122.12	127.00
1	A	110	U	N3-C4-C5	8.07	119.44	114.60
1	A	154	U	N3-C4-C5	8.00	119.40	114.60
1	A	127	U	N3-C4-C5	7.98	119.39	114.60
1	A	69	U	C2-N3-C4	-7.97	122.22	127.00
1	A	103	G	P-O5'-C5'	7.96	133.64	120.90
1	A	50	U	C2-N3-C4	-7.93	122.24	127.00
1	A	164	U	N3-C4-C5	7.93	119.36	114.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	66	U	C2-N3-C4	-7.92	122.25	127.00
1	A	98	U	C2-N3-C4	-7.92	122.25	127.00
1	A	185	U	N3-C4-C5	7.91	119.35	114.60
1	A	164	U	C2-N3-C4	-7.90	122.26	127.00
1	A	21	U	C2-N3-C4	-7.89	122.26	127.00
1	A	184	U	C2-N3-C4	-7.89	122.27	127.00
1	A	69	U	N3-C4-C5	7.88	119.33	114.60
1	A	50	U	N3-C4-C5	7.87	119.32	114.60
1	A	66	U	N3-C4-C5	7.87	119.32	114.60
1	A	152	U	C2-N3-C4	-7.86	122.28	127.00
1	A	41	G	P-O3'-C3'	7.85	129.12	119.70
1	A	51	U	C2-N3-C4	-7.85	122.29	127.00
1	A	43	U	C2-N3-C4	-7.84	122.29	127.00
1	A	20	U	C2-N3-C4	-7.84	122.29	127.00
1	A	34	U	C2-N3-C4	-7.84	122.29	127.00
1	A	17	U	C2-N3-C4	-7.84	122.30	127.00
1	A	153	U	C2-N3-C4	-7.84	122.30	127.00
1	A	84	U	C2-N3-C4	-7.83	122.30	127.00
1	A	16	U	C2-N3-C4	-7.83	122.30	127.00
1	A	21	U	N3-C4-C5	7.83	119.30	114.60
1	A	67	U	C2-N3-C4	-7.82	122.31	127.00
1	A	98	U	N3-C4-C5	7.82	119.29	114.60
1	A	46	U	C2-N3-C4	-7.82	122.31	127.00
1	A	23	U	C2-N3-C4	-7.81	122.31	127.00
1	A	143	U	C2-N3-C4	-7.81	122.31	127.00
1	A	151	U	C2-N3-C4	-7.81	122.31	127.00
1	A	177	U	C2-N3-C4	-7.80	122.32	127.00
1	A	193	U	C2-N3-C4	-7.79	122.33	127.00
1	A	34	U	N3-C4-C5	7.79	119.27	114.60
1	A	35	U	C2-N3-C4	-7.78	122.33	127.00
1	A	63	U	C2-N3-C4	-7.78	122.33	127.00
1	A	160	U	C2-N3-C4	-7.78	122.33	127.00
1	A	68	U	C2-N3-C4	-7.77	122.34	127.00
1	A	60	U	C2-N3-C4	-7.77	122.34	127.00
1	A	11	U	C2-N3-C4	-7.77	122.34	127.00
1	A	74	U	C2-N3-C4	-7.76	122.34	127.00
1	A	42	U	C2-N3-C4	-7.76	122.34	127.00
1	A	159	U	C2-N3-C4	-7.76	122.34	127.00
1	A	145	U	C2-N3-C4	-7.76	122.35	127.00
1	A	93	U	C2-N3-C4	-7.75	122.35	127.00
1	A	86	U	C2-N3-C4	-7.75	122.35	127.00
1	A	33	U	C2-N3-C4	-7.75	122.35	127.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	67	U	N3-C4-C5	7.75	119.25	114.60
1	A	150	U	C2-N3-C4	-7.75	122.35	127.00
1	A	141	U	C2-N3-C4	-7.74	122.36	127.00
1	A	143	U	N3-C4-C5	7.74	119.24	114.60
1	A	32	U	C2-N3-C4	-7.73	122.36	127.00
1	A	14	U	C2-N3-C4	-7.73	122.36	127.00
1	A	63	U	N3-C4-C5	7.73	119.24	114.60
1	A	9	U	C2-N3-C4	-7.73	122.36	127.00
1	A	88	U	C2-N3-C4	-7.73	122.36	127.00
1	A	184	U	N3-C4-C5	7.73	119.23	114.60
1	A	42	U	N3-C4-C5	7.72	119.23	114.60
1	A	92	U	C2-N3-C4	-7.72	122.37	127.00
1	A	160	U	N3-C4-C5	7.72	119.23	114.60
1	A	20	U	N3-C4-C5	7.72	119.23	114.60
1	A	151	U	N3-C4-C5	7.71	119.23	114.60
1	A	193	U	N3-C4-C5	7.71	119.23	114.60
1	A	43	U	N3-C4-C5	7.71	119.23	114.60
1	A	71	U	C2-N3-C4	-7.71	122.37	127.00
1	A	65	U	C2-N3-C4	-7.71	122.37	127.00
1	A	73	U	C2-N3-C4	-7.71	122.38	127.00
1	A	127	U	C2-N3-C4	-7.71	122.38	127.00
1	A	150	U	N3-C4-C5	7.70	119.22	114.60
1	A	87	U	C2-N3-C4	-7.70	122.38	127.00
1	A	99	U	N3-C4-C5	7.70	119.22	114.60
1	A	93	U	N3-C4-C5	7.70	119.22	114.60
1	A	60	U	N3-C4-C5	7.69	119.21	114.60
1	A	51	U	N3-C4-C5	7.69	119.21	114.60
1	A	57	U	C2-N3-C4	-7.69	122.39	127.00
1	A	99	U	C2-N3-C4	-7.69	122.39	127.00
1	A	152	U	N3-C4-C5	7.69	119.21	114.60
1	A	57	U	N3-C4-C5	7.68	119.21	114.60
1	A	84	U	N3-C4-C5	7.68	119.21	114.60
1	A	153	U	N3-C4-C5	7.68	119.21	114.60
1	A	33	U	N3-C4-C5	7.67	119.20	114.60
1	A	46	U	N3-C4-C5	7.67	119.20	114.60
1	A	159	U	N3-C4-C5	7.67	119.20	114.60
1	A	32	U	N3-C4-C5	7.67	119.20	114.60
1	A	167	U	C2-N3-C4	-7.67	122.40	127.00
1	A	65	U	N3-C4-C5	7.66	119.20	114.60
1	A	80	U	N3-C4-C5	7.66	119.20	114.60
1	A	86	U	N3-C4-C5	7.66	119.19	114.60
1	A	141	U	N3-C4-C5	7.66	119.19	114.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	17	U	N3-C4-C5	7.66	119.19	114.60
1	A	71	U	N3-C4-C5	7.66	119.19	114.60
1	A	68	U	N3-C4-C5	7.65	119.19	114.60
1	A	177	U	N3-C4-C5	7.64	119.19	114.60
1	A	79	U	C2-N3-C4	-7.64	122.41	127.00
1	A	23	U	N3-C4-C5	7.64	119.18	114.60
1	A	79	U	N3-C4-C5	7.63	119.18	114.60
1	A	11	U	N3-C4-C5	7.63	119.18	114.60
1	A	16	U	N3-C4-C5	7.62	119.17	114.60
1	A	35	U	N3-C4-C5	7.62	119.17	114.60
1	A	167	U	N3-C4-C5	7.62	119.17	114.60
1	A	27	U	C2-N3-C4	-7.61	122.43	127.00
1	A	87	U	N3-C4-C5	7.61	119.17	114.60
1	A	145	U	N3-C4-C5	7.61	119.17	114.60
1	A	73	U	N3-C4-C5	7.61	119.17	114.60
1	A	186	U	N3-C4-C5	7.61	119.16	114.60
1	A	14	U	N3-C4-C5	7.60	119.16	114.60
1	A	9	U	N3-C4-C5	7.60	119.16	114.60
1	A	80	U	C2-N3-C4	-7.58	122.45	127.00
1	A	185	U	C2-N3-C4	-7.57	122.46	127.00
1	A	88	U	N3-C4-C5	7.55	119.13	114.60
1	A	92	U	N3-C4-C5	7.54	119.12	114.60
1	A	74	U	N3-C4-C5	7.54	119.12	114.60
1	A	106	U	C2-N3-C4	-7.53	122.48	127.00
1	A	27	U	N3-C4-C5	7.53	119.12	114.60
6	F	203	GLY	N-CA-C	-7.49	94.38	113.10
1	A	106	U	N3-C4-C5	7.42	119.05	114.60
1	A	186	U	C2-N3-C4	-7.39	122.56	127.00
1	A	97	G	O4'-C1'-N9	7.38	114.10	108.20
8	H	76	GLU	CB-CA-C	-7.37	95.66	110.40
1	A	138	C	P-O3'-C3'	7.36	128.53	119.70
1	A	190	U	C2-N3-C4	-7.34	122.60	127.00
5	E	2160	G	O3'-P-O5'	7.32	117.91	104.00
1	A	190	U	N3-C4-C5	7.31	118.99	114.60
1	A	148	G	P-O3'-C3'	7.25	128.40	119.70
8	H	127	TYR	CB-CG-CD2	-7.24	116.66	121.00
1	A	106	U	P-O3'-C3'	7.18	128.32	119.70
1	A	81	A	N1-C2-N3	-7.15	125.72	129.30
1	A	96	C	O4'-C1'-N1	7.13	113.91	108.20
1	A	32	U	P-O3'-C3'	7.01	128.11	119.70
1	A	41	G	O4'-C1'-N9	6.99	113.79	108.20
1	A	73	U	P-O3'-C3'	6.99	128.08	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	59	G	O4'-C1'-N9	6.98	113.79	108.20
1	A	94	U	N3-C4-C5	6.95	118.77	114.60
1	A	94	U	OP1-P-OP2	-6.94	109.19	119.60
1	A	125	A	OP1-P-OP2	-6.94	109.19	119.60
5	E	2150	A	N9-C1'-C2'	6.91	122.99	114.00
1	A	132	A	N1-C2-N3	-6.91	125.85	129.30
8	H	46	GLN	OE1-CD-NE2	6.88	137.73	121.90
1	A	72	A	P-O3'-C3'	6.76	127.81	119.70
1	A	90	G	C5-C6-N1	6.74	114.87	111.50
1	A	81	A	O4'-C1'-N9	6.74	113.59	108.20
1	A	38	G	C5-C6-N1	6.72	114.86	111.50
1	A	156	A	P-O3'-C3'	6.71	127.75	119.70
1	A	165	A	N1-C2-N3	-6.70	125.95	129.30
1	A	77	G	C5-C6-N1	6.66	114.83	111.50
8	H	101	PHE	N-CA-CB	6.65	122.56	110.60
1	A	56	G	C5-C6-N1	6.64	114.82	111.50
1	A	128	A	N1-C2-N3	-6.63	125.98	129.30
1	A	134	G	C5-C6-N1	6.60	114.80	111.50
1	A	169	G	C5-C6-N1	6.57	114.78	111.50
1	A	78	G	C5-C6-N1	6.55	114.77	111.50
1	A	132	A	P-O3'-C3'	6.49	127.49	119.70
1	A	22	G	C5-C6-N1	6.46	114.73	111.50
1	A	48	A	N1-C2-N3	-6.42	126.09	129.30
1	A	133	G	C5-C6-N1	6.40	114.70	111.50
1	A	40	G	C5-C6-N1	6.40	114.70	111.50
1	A	161	A	N1-C2-N3	-6.40	126.10	129.30
1	A	112	G	C5-C6-N1	6.39	114.70	111.50
1	A	151	U	OP1-P-OP2	-6.38	110.04	119.60
1	A	36	G	C5-C6-N1	6.38	114.69	111.50
1	A	115	G	C5-C6-N1	6.37	114.69	111.50
1	A	178	A	N1-C2-N3	-6.37	126.12	129.30
1	A	109	C	O4'-C1'-N1	6.36	113.29	108.20
1	A	113	U	OP1-P-OP2	-6.36	110.07	119.60
1	A	102	A	OP1-P-OP2	-6.35	110.07	119.60
1	A	103	G	C5-C6-N1	6.34	114.67	111.50
1	A	114	G	C5-C6-N1	6.34	114.67	111.50
1	A	117	A	N1-C2-N3	-6.32	126.14	129.30
1	A	128	A	O4'-C1'-N9	6.30	113.24	108.20
1	A	31	A	N1-C2-N3	-6.30	126.15	129.30
2	B	533	A	C2'-C3'-O3'	6.28	123.74	113.70
1	A	30	A	N1-C2-N3	-6.27	126.16	129.30
1	A	163	G	C5-C6-N1	6.27	114.63	111.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	H	70	VAL	CB-CA-C	-6.26	99.51	111.40
1	A	28	A	N1-C2-N3	-6.26	126.17	129.30
1	A	58	A	N1-C2-N3	-6.24	126.18	129.30
1	A	85	A	N1-C2-N3	-6.24	126.18	129.30
1	A	11	U	O4'-C1'-N1	6.22	113.18	108.20
1	A	173	A	N1-C2-N3	-6.21	126.19	129.30
1	A	39	A	N1-C2-N3	-6.20	126.20	129.30
1	A	64	A	N1-C2-N3	-6.20	126.20	129.30
1	A	89	A	N1-C2-N3	-6.20	126.20	129.30
1	A	47	A	N1-C2-N3	-6.19	126.20	129.30
1	A	104	G	C5-C6-N1	6.19	114.59	111.50
1	A	13	A	N1-C2-N3	-6.18	126.21	129.30
1	A	135	A	N1-C2-N3	-6.18	126.21	129.30
1	A	136	A	N1-C2-N3	-6.18	126.21	129.30
1	A	158	A	N1-C2-N3	-6.18	126.21	129.30
1	A	26	A	N1-C2-N3	-6.17	126.21	129.30
1	A	45	A	N1-C2-N3	-6.17	126.21	129.30
1	A	171	A	N1-C2-N3	-6.17	126.21	129.30
8	H	76	GLU	N-CA-CB	6.17	121.70	110.60
1	A	5	A	N1-C2-N3	-6.17	126.22	129.30
1	A	52	A	N1-C2-N3	-6.16	126.22	129.30
1	A	172	A	N1-C2-N3	-6.16	126.22	129.30
1	A	8	A	N1-C2-N3	-6.14	126.23	129.30
1	A	82	G	C5-C6-N1	6.13	114.56	111.50
1	A	24	A	N1-C2-N3	-6.13	126.24	129.30
1	A	181	A	N1-C2-N3	-6.13	126.24	129.30
1	A	6	A	N1-C2-N3	-6.12	126.24	129.30
1	A	106	U	O4'-C1'-N1	6.12	113.10	108.20
1	A	125	A	N1-C2-N3	-6.12	126.24	129.30
6	F	188	THR	C-N-CA	6.12	136.99	121.70
8	H	136	ARG	N-CA-C	-6.11	94.50	111.00
1	A	179	A	N1-C2-N3	-6.11	126.25	129.30
1	A	72	A	N1-C2-N3	-6.09	126.26	129.30
1	A	73	U	O4'-C1'-N1	6.08	113.07	108.20
1	A	49	A	N1-C2-N3	-6.08	126.26	129.30
1	A	107	G	OP1-P-OP2	-6.06	110.51	119.60
1	A	4	A	N1-C2-N3	-6.06	126.27	129.30
1	A	7	A	N1-C2-N3	-6.06	126.27	129.30
1	A	44	A	N1-C2-N3	-6.05	126.27	129.30
1	A	25	A	N1-C2-N3	-6.05	126.28	129.30
1	A	54	A	N1-C2-N3	-6.05	126.28	129.30
1	A	126	A	N1-C2-N3	-6.04	126.28	129.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	55	A	N1-C2-N3	-6.03	126.28	129.30
1	A	82	G	OP1-P-OP2	-6.03	110.55	119.60
1	A	183	A	N1-C2-N3	-6.03	126.29	129.30
1	A	37	A	N1-C2-N3	-6.02	126.29	129.30
1	A	92	U	O4'-C1'-N1	6.02	113.02	108.20
1	A	174	A	N1-C2-N3	-6.02	126.29	129.30
8	H	77	GLU	C-N-CA	6.00	136.69	121.70
1	A	77	G	C6-N1-C2	-5.98	121.51	125.10
1	A	111	A	N1-C2-N3	-5.96	126.32	129.30
1	A	124	C	N3-C4-C5	-5.96	119.52	121.90
1	A	134	G	C6-N1-C2	-5.96	121.52	125.10
1	A	139	C	OP1-P-OP2	-5.96	110.66	119.60
1	A	182	A	N1-C2-N3	-5.96	126.32	129.30
1	A	179	A	OP1-P-OP2	-5.95	110.67	119.60
1	A	90	G	C6-N1-C2	-5.93	121.54	125.10
1	A	181	A	O4'-C1'-N9	5.93	112.95	108.20
1	A	35	U	OP1-P-OP2	-5.93	110.70	119.60
1	A	38	G	C6-N1-C2	-5.93	121.54	125.10
1	A	95	A	N1-C2-N3	-5.92	126.34	129.30
1	A	50	U	OP1-P-OP2	-5.92	110.72	119.60
1	A	44	A	P-O5'-C5'	5.92	130.37	120.90
1	A	177	U	O4'-C1'-N1	5.91	112.93	108.20
2	B	509	A	C2'-C3'-O3'	5.91	123.15	113.70
1	A	139	C	P-O3'-C3'	5.90	126.78	119.70
1	A	104	G	OP1-P-OP2	-5.89	110.76	119.60
1	A	123	A	N1-C2-N3	-5.89	126.36	129.30
1	A	47	A	O4'-C1'-N9	5.89	112.91	108.20
1	A	33	U	OP1-P-OP2	-5.87	110.80	119.60
1	A	42	U	OP1-P-OP2	-5.86	110.81	119.60
1	A	75	U	C5-C4-O4	-5.86	122.39	125.90
1	A	183	A	OP1-P-OP2	-5.85	110.82	119.60
1	A	161	A	C5-C6-N1	-5.84	114.78	117.70
1	A	187	A	N1-C2-N3	-5.84	126.38	129.30
1	A	170	A	N1-C2-N3	-5.84	126.38	129.30
1	A	16	U	O4'-C1'-N1	5.84	112.87	108.20
1	A	76	A	N1-C2-N3	-5.83	126.39	129.30
1	A	107	G	O4'-C1'-N9	5.83	112.86	108.20
1	A	74	U	O4'-C1'-N1	5.82	112.86	108.20
1	A	56	G	C6-N1-C2	-5.81	121.61	125.10
1	A	120	C	O4'-C1'-N1	5.81	112.85	108.20
1	A	31	A	O4'-C1'-N9	5.79	112.84	108.20
1	A	180	G	O4'-C1'-N9	5.79	112.84	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	58	A	O4'-C1'-N9	5.79	112.83	108.20
1	A	102	A	N1-C2-N3	-5.79	126.41	129.30
1	A	186	U	OP1-P-OP2	-5.78	110.93	119.60
1	A	169	G	C6-N1-C2	-5.76	121.64	125.10
1	A	140	C	OP1-P-OP2	-5.76	110.96	119.60
1	A	149	G	OP1-P-OP2	-5.76	110.96	119.60
1	A	131	C	N3-C4-C5	-5.76	119.60	121.90
1	A	145	U	O4'-C1'-N1	5.74	112.79	108.20
1	A	78	G	C6-N1-C2	-5.73	121.66	125.10
1	A	112	G	OP1-P-OP2	-5.73	111.00	119.60
1	A	117	A	O4'-C1'-N9	5.73	112.78	108.20
1	A	133	G	C6-N1-C2	-5.72	121.67	125.10
1	A	80	U	OP1-P-OP2	-5.72	111.03	119.60
1	A	90	G	O4'-C1'-N9	5.71	112.77	108.20
1	A	102	A	C5-C6-N1	-5.71	114.85	117.70
1	A	97	G	C5-C6-N1	5.70	114.35	111.50
1	A	159	U	O4'-C1'-N1	5.70	112.76	108.20
1	A	161	A	C6-N1-C2	5.70	122.02	118.60
1	A	129	U	OP1-P-OP2	-5.69	111.07	119.60
1	A	150	U	OP1-P-OP2	-5.68	111.08	119.60
1	A	156	A	N1-C2-N3	-5.68	126.46	129.30
1	A	18	G	O4'-C1'-N9	5.67	112.74	108.20
1	A	22	G	C6-N1-C2	-5.67	121.70	125.10
1	A	12	G	C5-C6-N1	5.67	114.34	111.50
8	H	95	PHE	N-CA-CB	5.67	120.81	110.60
1	A	167	U	OP1-P-OP2	-5.67	111.10	119.60
1	A	126	A	OP1-P-OP2	-5.66	111.11	119.60
1	A	118	G	C5-C6-N1	5.64	114.32	111.50
1	A	146	G	C5-C6-N1	5.64	114.32	111.50
1	A	99	U	OP1-P-OP2	-5.64	111.14	119.60
1	A	58	A	C5-C6-N1	-5.63	114.88	117.70
1	A	105	A	N1-C2-N3	-5.63	126.48	129.30
1	A	190	U	O4'-C1'-N1	5.63	112.70	108.20
1	A	126	A	C5-C6-N1	-5.62	114.89	117.70
1	A	10	G	C5-C6-N1	5.60	114.30	111.50
1	A	132	A	C6-N1-C2	5.60	121.96	118.60
1	A	71	U	O4'-C1'-N1	5.59	112.67	108.20
1	A	73	U	OP1-P-OP2	-5.59	111.21	119.60
1	A	191	G	C5-C6-N1	5.59	114.29	111.50
1	A	70	G	C5-C6-N1	5.59	114.29	111.50
1	A	157	G	OP1-P-OP2	-5.58	111.23	119.60
1	A	182	A	OP1-P-OP2	-5.58	111.23	119.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	40	G	C6-N1-C2	-5.58	121.75	125.10
1	A	149	G	C5-C6-N1	5.57	114.28	111.50
1	A	18	G	C5-C6-N1	5.57	114.28	111.50
1	A	94	U	C2-N3-C4	-5.56	123.66	127.00
1	A	165	A	C6-N1-C2	5.56	121.94	118.60
1	A	74	U	P-O5'-C5'	5.56	129.79	120.90
1	A	41	G	C5-C6-N1	5.54	114.27	111.50
1	A	91	C	N3-C4-C5	-5.54	119.68	121.90
2	B	533	A	N9-C1'-C2'	5.54	121.20	114.00
1	A	59	G	C5-C6-N1	5.53	114.27	111.50
1	A	61	G	C5-C6-N1	5.53	114.27	111.50
1	A	181	A	OP1-P-OP2	-5.53	111.31	119.60
1	A	36	G	C6-N1-C2	-5.52	121.79	125.10
1	A	115	G	C6-N1-C2	-5.52	121.79	125.10
1	A	168	C	O4'-C1'-N1	5.52	112.61	108.20
1	A	157	G	C5-C6-N1	5.52	114.26	111.50
1	A	128	A	C6-N1-C2	5.52	121.91	118.60
1	A	26	A	O4'-C1'-N9	5.51	112.61	108.20
1	A	162	G	C5-C6-N1	5.51	114.25	111.50
1	A	166	G	C5-C6-N1	5.51	114.25	111.50
1	A	130	C	N3-C4-C5	-5.50	119.70	121.90
1	A	48	A	C5-C6-N1	-5.49	114.95	117.70
1	A	76	A	OP1-P-OP2	-5.49	111.36	119.60
1	A	121	C	N3-C4-C5	-5.49	119.70	121.90
1	A	180	G	C5-C6-N1	5.49	114.24	111.50
1	A	85	A	O4'-C1'-N9	5.48	112.58	108.20
1	A	104	G	C6-N1-C2	-5.47	121.81	125.10
1	A	163	G	C6-N1-C2	-5.47	121.82	125.10
1	A	129	U	C5-C4-O4	-5.47	122.62	125.90
1	A	163	G	OP1-P-OP2	-5.47	111.39	119.60
1	A	74	U	O3'-P-O5'	-5.47	93.61	104.00
1	A	107	G	C5-C6-N1	5.47	114.23	111.50
1	A	148	G	C5-C6-N1	5.46	114.23	111.50
1	A	44	A	C5-C6-N1	-5.46	114.97	117.70
1	A	137	G	C5-C6-N1	5.46	114.23	111.50
1	A	144	C	N3-C4-C5	-5.46	119.72	121.90
1	A	95	A	C5-C6-N1	-5.46	114.97	117.70
1	A	128	A	P-O5'-C5'	5.46	129.63	120.90
1	A	184	U	OP1-P-OP2	-5.46	111.41	119.60
1	A	135	A	C5-C6-N1	-5.45	114.97	117.70
1	A	155	C	OP1-P-OP2	-5.45	111.43	119.60
1	A	13	A	O4'-C1'-N9	5.45	112.56	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	62	C	OP1-P-OP2	-5.45	111.43	119.60
1	A	79	U	O4'-C1'-N1	5.45	112.56	108.20
1	A	165	A	C5-C6-N1	-5.45	114.98	117.70
1	A	114	G	C6-N1-C2	-5.44	121.84	125.10
1	A	39	A	O4'-C1'-N9	5.43	112.55	108.20
1	A	46	U	P-O3'-C3'	-5.43	113.18	119.70
1	A	192	C	O4'-C1'-N1	5.43	112.54	108.20
1	A	48	A	C6-N1-C2	5.42	121.86	118.60
1	A	147	C	N3-C4-C5	-5.42	119.73	121.90
1	A	188	C	OP1-P-OP2	-5.42	111.47	119.60
1	A	182	A	C5-C6-N1	-5.42	114.99	117.70
1	A	59	G	P-O3'-C3'	5.42	126.20	119.70
1	A	113	U	C5-C4-O4	-5.42	122.65	125.90
5	E	2166	G	OP2-P-O3'	5.42	117.12	105.20
1	A	138	C	N3-C4-C5	-5.41	119.74	121.90
1	A	8	A	C5-C6-N1	-5.40	115.00	117.70
1	A	49	A	C5-C6-N1	-5.40	115.00	117.70
1	A	30	A	C5-C6-N1	-5.39	115.01	117.70
1	A	123	A	OP1-P-OP2	-5.39	111.52	119.60
1	A	158	A	C5-C6-N1	-5.39	115.01	117.70
1	A	13	A	C5-C6-N1	-5.38	115.01	117.70
1	A	72	A	C5-C6-N1	-5.38	115.01	117.70
1	A	124	C	OP1-P-OP2	-5.36	111.55	119.60
1	A	126	A	C6-N1-C2	5.36	121.82	118.60
1	A	28	A	C5-C6-N1	-5.36	115.02	117.70
1	A	140	C	N3-C4-C5	-5.36	119.76	121.90
1	A	164	U	OP1-P-OP2	-5.35	111.57	119.60
1	A	128	A	C5-C6-N1	-5.35	115.02	117.70
1	A	32	U	O4'-C1'-N1	5.35	112.48	108.20
1	A	100	C	OP1-P-OP2	-5.35	111.58	119.60
1	A	89	A	C5-C6-N1	-5.35	115.03	117.70
1	A	125	A	C5-C6-N1	-5.34	115.03	117.70
1	A	148	G	OP1-P-OP2	-5.34	111.58	119.60
8	H	95	PHE	CB-CG-CD2	-5.34	117.06	120.80
1	A	118	G	O4'-C1'-N9	5.34	112.47	108.20
1	A	53	C	N3-C4-C5	-5.34	119.76	121.90
1	A	122	C	N3-C4-C5	-5.34	119.76	121.90
1	A	188	C	N3-C4-C5	-5.34	119.76	121.90
1	A	45	A	C5-C6-N1	-5.34	115.03	117.70
1	A	87	U	O4'-C1'-N1	5.34	112.47	108.20
1	A	36	G	O4'-C1'-N9	5.34	112.47	108.20
1	A	159	U	OP1-P-OP2	-5.33	111.60	119.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	5	A	O4'-C1'-N9	5.33	112.47	108.20
1	A	176	C	OP1-P-OP2	-5.33	111.60	119.60
1	A	62	C	N3-C4-C5	-5.33	119.77	121.90
1	A	116	C	N3-C4-C5	-5.33	119.77	121.90
1	A	52	A	C5-C6-N1	-5.32	115.04	117.70
1	A	127	U	OP1-P-OP2	-5.32	111.61	119.60
1	A	158	A	C6-N1-C2	5.32	121.79	118.60
1	A	58	A	C6-N1-C2	5.32	121.79	118.60
1	A	4	A	O4'-C1'-N9	5.32	112.45	108.20
1	A	110	U	OP1-P-OP2	-5.32	111.63	119.60
1	A	114	G	OP1-P-OP2	-5.32	111.63	119.60
1	A	183	A	C5-C6-N1	-5.32	115.04	117.70
1	A	173	A	C5-C6-N1	-5.31	115.04	117.70
1	A	54	A	C5-C6-N1	-5.31	115.05	117.70
1	A	26	A	C5-C6-N1	-5.31	115.05	117.70
1	A	135	A	C6-N1-C2	5.31	121.78	118.60
1	A	187	A	OP1-P-OP2	-5.31	111.64	119.60
1	A	193	U	O4'-C1'-N1	5.31	112.45	108.20
1	A	60	U	OP1-P-OP2	-5.30	111.64	119.60
1	A	132	A	C5-C6-N1	-5.30	115.05	117.70
1	A	49	A	OP1-P-OP2	-5.30	111.65	119.60
1	A	6	A	O4'-C1'-N9	5.30	112.44	108.20
1	A	166	G	O4'-C1'-N9	5.30	112.44	108.20
1	A	121	C	OP1-P-OP2	-5.30	111.66	119.60
1	A	131	C	P-O3'-C3'	-5.30	113.34	119.70
1	A	135	A	OP1-P-OP2	-5.30	111.65	119.60
1	A	6	A	C5-C6-N1	-5.29	115.05	117.70
1	A	30	A	C6-N1-C2	5.29	121.78	118.60
1	A	174	A	C5-C6-N1	-5.29	115.05	117.70
1	A	120	C	N3-C4-C5	-5.29	119.78	121.90
1	A	117	A	C5-C6-N1	-5.29	115.06	117.70
1	A	24	A	C5-C6-N1	-5.29	115.06	117.70
1	A	169	G	OP1-P-OP2	-5.29	111.67	119.60
1	A	5	A	C5-C6-N1	-5.29	115.06	117.70
1	A	8	A	O4'-C1'-N9	5.29	112.43	108.20
1	A	9	U	O4'-C1'-N1	5.29	112.43	108.20
1	A	42	U	O4'-C1'-N1	5.29	112.43	108.20
1	A	130	C	OP1-P-OP2	-5.29	111.67	119.60
1	A	187	A	C5-C6-N1	-5.29	115.06	117.70
8	H	76	GLU	CB-CG-CD	-5.29	99.93	114.20
1	A	122	C	OP1-P-OP2	-5.28	111.68	119.60
1	A	167	U	O4'-C1'-N1	5.28	112.42	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	175	C	N3-C4-C5	-5.28	119.79	121.90
1	A	179	A	C5-C6-N1	-5.28	115.06	117.70
1	A	31	A	C5-C6-N1	-5.28	115.06	117.70
1	A	117	A	C6-N1-C2	5.27	121.76	118.60
1	A	119	C	N3-C4-C5	-5.27	119.79	121.90
1	A	136	A	C5-C6-N1	-5.27	115.06	117.70
1	A	172	A	C5-C6-N1	-5.27	115.07	117.70
1	A	83	C	N3-C4-C5	-5.26	119.79	121.90
1	A	25	A	OP1-P-OP2	-5.26	111.70	119.60
1	A	15	C	N3-C4-C5	-5.26	119.80	121.90
1	A	151	U	O4'-C1'-N1	5.26	112.41	108.20
1	A	168	C	N3-C4-C5	-5.26	119.80	121.90
1	A	40	G	O4'-C1'-N9	5.26	112.41	108.20
1	A	64	A	C5-C6-N1	-5.26	115.07	117.70
1	A	66	U	OP1-P-OP2	-5.26	111.71	119.60
1	A	116	C	O4'-C1'-N1	5.26	112.41	108.20
1	A	142	C	OP1-P-OP2	-5.26	111.71	119.60
1	A	144	C	O4'-C1'-N1	5.26	112.41	108.20
1	A	96	C	N3-C4-C5	-5.26	119.80	121.90
1	A	88	U	O4'-C1'-N1	5.25	112.40	108.20
1	A	37	A	C5-C6-N1	-5.25	115.07	117.70
1	A	178	A	C5-C6-N1	-5.25	115.07	117.70
1	A	140	C	O4'-C1'-N1	5.25	112.40	108.20
1	A	47	A	P-O5'-C5'	5.25	129.30	120.90
1	A	171	A	C5-C6-N1	-5.25	115.08	117.70
1	A	83	C	O4'-C1'-N1	5.25	112.40	108.20
1	A	57	U	O4'-C1'-N1	5.24	112.40	108.20
1	A	82	G	C6-N1-C2	-5.24	121.95	125.10
1	A	8	A	C6-N1-C2	5.24	121.74	118.60
1	A	86	U	O4'-C1'-N1	5.24	112.39	108.20
1	A	28	A	C6-N1-C2	5.24	121.74	118.60
1	A	43	U	O4'-C1'-N1	5.24	112.39	108.20
1	A	162	G	OP1-P-OP2	-5.24	111.74	119.60
1	A	192	C	N3-C4-C5	-5.24	119.81	121.90
1	A	39	A	C5-C6-N1	-5.23	115.08	117.70
1	A	85	A	C5-C6-N1	-5.23	115.09	117.70
1	A	119	C	OP1-P-OP2	-5.23	111.76	119.60
1	A	162	G	O4'-C1'-N9	5.23	112.38	108.20
1	A	46	U	O4'-C1'-N1	5.22	112.38	108.20
1	A	49	A	C6-N1-C2	5.22	121.73	118.60
1	A	29	C	N3-C4-C5	-5.22	119.81	121.90
1	A	44	A	C6-N1-C2	5.22	121.73	118.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	69	U	OP1-P-OP2	-5.22	111.77	119.60
1	A	178	A	C6-N1-C2	5.22	121.73	118.60
1	A	181	A	P-O3'-C3'	5.22	125.96	119.70
1	A	189	C	N3-C4-C5	-5.22	119.81	121.90
1	A	173	A	C6-N1-C2	5.22	121.73	118.60
1	A	181	A	C5-C6-N1	-5.22	115.09	117.70
1	A	115	G	OP1-P-OP2	-5.21	111.78	119.60
1	A	7	A	C5-C6-N1	-5.21	115.09	117.70
1	A	21	U	OP1-P-OP2	-5.21	111.78	119.60
1	A	166	G	P-O3'-C3'	5.21	125.96	119.70
1	A	47	A	C5-C6-N1	-5.21	115.09	117.70
1	A	141	U	OP1-P-OP2	-5.21	111.79	119.60
1	A	170	A	OP1-P-OP2	-5.20	111.80	119.60
1	A	33	U	O4'-C1'-N1	5.20	112.36	108.20
1	A	19	C	OP1-P-OP2	-5.20	111.80	119.60
1	A	25	A	C5-C6-N1	-5.20	115.10	117.70
1	A	183	A	C6-N1-C2	5.20	121.72	118.60
1	A	71	U	OP1-P-OP2	-5.19	111.81	119.60
1	A	81	A	C5-C6-N1	-5.19	115.10	117.70
1	A	14	U	OP1-P-OP2	-5.19	111.81	119.60
1	A	31	A	C6-N1-C2	5.19	121.72	118.60
1	A	63	U	OP1-P-OP2	-5.19	111.81	119.60
1	A	45	A	C6-N1-C2	5.19	121.71	118.60
8	H	78	ILE	N-CA-C	-5.19	97.00	111.00
1	A	68	U	OP1-P-OP2	-5.19	111.82	119.60
1	A	176	C	N3-C4-C5	-5.18	119.83	121.90
1	A	105	A	OP1-P-OP2	-5.18	111.83	119.60
1	A	13	A	C6-N1-C2	5.18	121.71	118.60
1	A	10	G	O4'-C1'-N9	5.18	112.34	108.20
1	A	72	A	C6-N1-C2	5.18	121.71	118.60
1	A	6	A	C6-N1-C2	5.17	121.70	118.60
1	A	189	C	O4'-C1'-N1	5.17	112.34	108.20
1	A	89	A	C6-N1-C2	5.17	121.70	118.60
1	A	13	A	OP1-P-OP2	-5.17	111.84	119.60
1	A	103	G	C6-N1-C2	-5.17	122.00	125.10
1	A	11	U	OP1-P-OP2	-5.17	111.85	119.60
1	A	117	A	OP1-P-OP2	-5.17	111.85	119.60
1	A	178	A	O4'-C1'-N9	5.17	112.33	108.20
1	A	52	A	O4'-C1'-N9	5.16	112.33	108.20
1	A	131	C	OP1-P-OP2	-5.16	111.85	119.60
1	A	48	A	OP1-P-OP2	-5.16	111.86	119.60
1	A	64	A	C6-N1-C2	5.16	121.70	118.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	136	A	OP1-P-OP2	-5.16	111.86	119.60
1	A	17	U	C5-C4-O4	-5.16	122.80	125.90
1	A	26	A	C6-N1-C2	5.16	121.70	118.60
1	A	4	A	C5-C6-N1	-5.15	115.12	117.70
1	A	61	G	OP1-P-OP2	-5.15	111.88	119.60
1	A	124	C	C2-N3-C4	5.15	122.47	119.90
1	A	53	C	OP1-P-OP2	-5.15	111.88	119.60
1	A	85	A	C6-N1-C2	5.15	121.69	118.60
1	A	55	A	C5-C6-N1	-5.15	115.13	117.70
1	A	5	A	C6-N1-C2	5.14	121.69	118.60
1	A	52	A	C6-N1-C2	5.14	121.69	118.60
1	A	95	A	C6-N1-C2	5.14	121.69	118.60
1	A	39	A	C6-N1-C2	5.13	121.68	118.60
1	A	24	A	O4'-C1'-N9	5.13	112.31	108.20
1	A	182	A	C6-N1-C2	5.13	121.68	118.60
8	H	69	THR	N-CA-C	-5.13	97.15	111.00
1	A	20	U	OP1-P-OP2	-5.13	111.91	119.60
1	A	12	G	OP1-P-OP2	-5.12	111.92	119.60
1	A	24	A	C6-N1-C2	5.12	121.67	118.60
1	A	51	U	OP1-P-OP2	-5.12	111.91	119.60
1	A	170	A	C5-C6-N1	-5.12	115.14	117.70
1	A	171	A	C6-N1-C2	5.12	121.67	118.60
1	A	185	U	OP1-P-OP2	-5.12	111.92	119.60
7	G	12	HIS	CA-CB-CG	5.12	122.31	113.60
1	A	23	U	OP1-P-OP2	-5.12	111.92	119.60
1	A	40	G	OP1-P-OP2	-5.12	111.93	119.60
1	A	136	A	C6-N1-C2	5.12	121.67	118.60
1	A	112	G	C6-N1-C2	-5.11	122.03	125.10
1	A	172	A	C6-N1-C2	5.11	121.67	118.60
1	A	15	C	O4'-C1'-N1	5.11	112.28	108.20
1	A	160	U	OP1-P-OP2	-5.11	111.94	119.60
1	A	54	A	C6-N1-C2	5.11	121.66	118.60
1	A	47	A	C6-N1-C2	5.10	121.66	118.60
1	A	174	A	C6-N1-C2	5.10	121.66	118.60
1	A	32	U	OP1-P-OP2	-5.10	111.95	119.60
1	A	125	A	C6-N1-C2	5.10	121.66	118.60
1	A	96	C	OP1-P-OP2	-5.10	111.95	119.60
1	A	111	A	C5-C6-N1	-5.10	115.15	117.70
1	A	131	C	C2-N3-C4	5.10	122.45	119.90
1	A	161	A	OP1-P-OP2	-5.10	111.96	119.60
1	A	88	U	OP1-P-OP2	-5.09	111.96	119.60
1	A	181	A	C6-N1-C2	5.09	121.66	118.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	80	U	N1-C1'-C2'	-5.09	106.40	112.00
1	A	142	C	N3-C4-C5	-5.09	119.86	121.90
1	A	175	C	O4'-C1'-N1	5.09	112.27	108.20
1	A	179	A	C6-N1-C2	5.09	121.65	118.60
1	A	184	U	O4'-C1'-N1	5.09	112.27	108.20
1	A	67	U	OP1-P-OP2	-5.08	111.98	119.60
1	A	109	C	N3-C4-C5	-5.08	119.87	121.90
1	A	60	U	N1-C1'-C2'	-5.07	106.43	112.00
1	A	134	G	OP1-P-OP2	-5.07	112.00	119.60
1	A	155	C	O4'-C1'-N1	5.07	112.25	108.20
1	A	176	C	O4'-C1'-N1	5.07	112.25	108.20
1	A	193	U	OP1-P-OP2	-5.06	112.00	119.60
1	A	101	C	OP1-P-OP2	-5.05	112.02	119.60
1	A	97	G	OP1-P-OP2	-5.05	112.03	119.60
1	A	25	A	C6-N1-C2	5.04	121.63	118.60
1	A	4	A	OP1-P-OP2	-5.04	112.04	119.60
1	A	54	A	OP1-P-OP2	-5.04	112.05	119.60
1	A	57	U	OP1-P-OP2	-5.04	112.05	119.60
1	A	79	U	P-O3'-C3'	5.03	125.74	119.70
1	A	84	U	OP1-P-OP2	-5.03	112.05	119.60
1	A	139	C	N3-C4-C5	-5.03	119.89	121.90
1	A	38	G	OP1-P-OP2	-5.03	112.06	119.60
1	A	76	A	C5-C6-N1	-5.03	115.19	117.70
1	A	138	C	OP1-P-OP2	-5.02	112.06	119.60
8	H	72	GLY	CA-C-N	5.02	131.17	117.10
1	A	48	A	O4'-C1'-N9	5.02	112.22	108.20
1	A	108	C	N3-C4-C5	-5.02	119.89	121.90
1	A	86	U	OP1-P-OP2	-5.01	112.08	119.60
1	A	91	C	OP1-P-OP2	-5.01	112.08	119.60
1	A	4	A	C6-N1-C2	5.01	121.61	118.60
1	A	37	A	C6-N1-C2	5.01	121.61	118.60
1	A	41	G	OP1-P-OP2	-5.01	112.09	119.60
1	A	152	U	OP1-P-OP2	-5.01	112.08	119.60
1	A	102	A	C6-N1-C2	5.01	121.60	118.60
1	A	147	C	OP1-P-OP2	-5.01	112.09	119.60
1	A	24	A	OP1-P-OP2	-5.00	112.09	119.60
1	A	118	G	OP1-P-OP2	-5.00	112.10	119.60
1	A	175	C	OP1-P-OP2	-5.00	112.09	119.60
1	A	108	C	OP1-P-OP2	-5.00	112.10	119.60
1	A	109	C	OP1-P-OP2	-5.00	112.10	119.60

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	528	C	Sidechain
2	B	529	G	Sidechain
5	E	2150	A	Sidechain
5	E	2162	G	Sidechain
5	E	2174	G	Sidechain
8	H	132	ARG	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	4023	0	2022	648	0
2	B	986	0	500	69	0
3	C	276	0	142	46	0
4	D	319	0	161	21	0
5	E	1142	0	573	137	0
6	F	1161	0	1230	226	0
7	G	1683	0	1750	551	0
8	H	1319	0	1347	459	0
All	All	10909	0	7725	1899	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 102.

All (1899) 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)
5:E:2154:G:H2'	7:G:160:LYS:CD	1.18	1.57
5:E:2185:C:P	7:G:163:LEU:HD12	1.46	1.52
1:A:87:U:O4	6:F:218:ARG:CG	1.65	1.43
1:A:189:C:C4	3:C:1054:C:N4	1.88	1.42
7:G:151:VAL:C	7:G:154:THR:H	1.22	1.40
5:E:2154:G:C2'	7:G:160:LYS:HD2	1.50	1.40
5:E:2154:G:C2'	7:G:160:LYS:CD	2.00	1.39
5:E:2153:G:N2	7:G:161:LYS:HE2	1.38	1.38

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:2171:G:C8	7:G:102:LYS:NZ	1.93	1.35
5:E:2171:G:OP2	7:G:102:LYS:CG	1.77	1.32
1:A:87:U:N3	6:F:218:ARG:CD	1.93	1.30
1:A:87:U:H3	6:F:218:ARG:CD	1.43	1.30
5:E:2185:C:OP1	7:G:163:LEU:CG	1.78	1.30
5:E:2154:G:O2'	7:G:160:LYS:HB3	1.31	1.29
5:E:2175:A:O2'	7:G:130:LYS:HD3	1.30	1.27
1:A:12:G:O2'	7:G:117:ILE:CB	1.74	1.26
1:A:191:G:N2	2:B:530:G:P	2.08	1.25
5:E:2157:G:OP1	7:G:108:ASN:ND2	1.66	1.25
5:E:2155:U:O2'	7:G:158:GLN:O	1.55	1.24
1:A:189:C:N3	3:C:1054:C:N4	1.80	1.23
5:E:2153:G:C2	7:G:161:LYS:HE2	1.74	1.22
1:A:87:U:N3	6:F:218:ARG:HD2	1.47	1.20
1:A:189:C:C4	3:C:1054:C:C4	2.29	1.19
7:G:59:PRO:HG2	7:G:152:ARG:O	1.38	1.19
1:A:87:U:O4	6:F:218:ARG:HG3	1.13	1.18
6:F:132:VAL:HG12	6:F:197:LEU:HD13	1.25	1.18
5:E:2175:A:O2'	7:G:130:LYS:CD	1.91	1.17
1:A:87:U:C4	6:F:218:ARG:CG	2.26	1.17
7:G:131:ALA:HB1	7:G:133:LYS:HD3	1.27	1.16
7:G:59:PRO:HG2	7:G:152:ARG:C	1.64	1.15
5:E:2175:A:C2'	7:G:130:LYS:HD3	1.75	1.15
5:E:2171:G:OP2	7:G:102:LYS:HG2	0.96	1.14
5:E:2185:C:OP1	7:G:163:LEU:HD13	1.36	1.14
1:A:63:U:H2'	1:A:64:A:H5'	1.26	1.14
8:H:15:LYS:HA	8:H:70:VAL:HG21	1.31	1.13
1:A:90:G:P	6:F:211:LYS:HZ1	1.71	1.13
5:E:2184:C:O4'	7:G:164:CYS:SG	2.07	1.12
5:E:2154:G:O2'	7:G:160:LYS:CB	1.96	1.12
7:G:120:VAL:HG13	7:G:121:PRO:HD2	1.29	1.12
7:G:151:VAL:C	7:G:154:THR:N	2.00	1.12
7:G:152:ARG:N	7:G:153:SER:N	1.96	1.11
5:E:2170:C:OP2	7:G:105:LYS:HE2	1.33	1.11
8:H:22:VAL:HA	8:H:64:ILE:HD11	1.32	1.11
7:G:205:VAL:HG11	7:G:213:ALA:HB1	1.18	1.11
1:A:60:U:H2'	1:A:61:G:H5''	1.20	1.11
1:A:193:U:O2	2:B:534:U:H5''	1.33	1.11
7:G:94:ASN:HB2	7:G:123:LEU:HB3	1.17	1.10
1:A:193:U:O2	2:B:534:U:C5'	1.98	1.10
7:G:63:MET:HG3	7:G:108:ASN:HB3	1.20	1.10

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:2170:C:OP2	7:G:105:LYS:CE	1.82	1.10
1:A:10:G:H22	7:G:122:ARG:NH1	1.49	1.10
6:F:122:VAL:HG23	6:F:123:LEU:HD12	1.20	1.10
6:F:112:ILE:HG23	6:F:113:ILE:HD12	1.30	1.10
7:G:169:VAL:HG23	7:G:179:LEU:HD21	1.32	1.10
1:A:191:G:N2	2:B:530:G:OP2	1.82	1.10
7:G:114:GLU:HG2	7:G:137:PRO:HB2	1.32	1.10
8:H:59:ARG:HD2	8:H:62:GLU:HA	1.20	1.09
5:E:2185:C:O5'	7:G:163:LEU:HG	1.42	1.08
5:E:2155:U:H4'	7:G:158:GLN:HG2	1.33	1.08
5:E:2153:G:H22	7:G:162:VAL:CG2	1.66	1.08
8:H:20:ILE:HG21	8:H:65:ALA:HB3	1.35	1.07
8:H:87:GLU:HG2	8:H:90:LEU:HG	1.31	1.07
1:A:110:U:H2'	1:A:111:A:H5''	1.32	1.07
8:H:46:GLN:HG2	8:H:66:VAL:HB	1.37	1.07
1:A:16:U:H1'	1:A:59:G:H21	1.17	1.05
8:H:133:PRO:HG2	8:H:135:ALA:H	1.20	1.05
5:E:2185:C:OP1	7:G:163:LEU:HD11	1.54	1.05
5:E:2185:C:OP1	7:G:163:LEU:CD1	0.75	1.04
8:H:75:ALA:HA	8:H:78:ILE:HG13	1.36	1.04
5:E:2173:U:C4	7:G:101:LYS:HD3	1.91	1.04
1:A:144:C:C4	1:A:145:U:H1'	1.93	1.04
8:H:18:LEU:HG	8:H:68:VAL:HG21	1.37	1.03
6:F:105:LYS:HB3	6:F:108:LYS:HD3	1.40	1.03
1:A:27:U:H3'	1:A:28:A:H5'	1.39	1.03
7:G:150:ASP:HA	7:G:153:SER:HB2	1.41	1.03
8:H:70:VAL:HB	8:H:71:ARG:HH11	1.21	1.03
8:H:16:LEU:HD13	8:H:70:VAL:HG11	1.41	1.03
1:A:193:U:H4'	2:B:535:A:H2'	1.41	1.02
1:A:87:U:O4	6:F:218:ARG:HG2	1.57	1.01
1:A:160:U:O2	2:B:531:U:OP1	1.77	1.01
8:H:53:VAL:HB	8:H:56:PHE:HB2	1.37	1.01
6:F:202:LYS:HA	6:F:205:SER:HB3	1.39	1.01
1:A:74:U:O2'	1:A:75:U:H4'	1.59	1.01
5:E:2185:C:P	7:G:163:LEU:CD1	2.08	1.00
8:H:25:SER:HB2	8:H:65:ALA:HB2	1.39	1.00
8:H:87:GLU:HG3	8:H:122:PHE:HZ	1.25	1.00
1:A:193:U:H4'	2:B:535:A:C2'	1.92	1.00
6:F:139:THR:HG21	6:F:174:LEU:HD21	1.42	1.00
1:A:128:A:H2'	1:A:129:U:C5	1.97	1.00
1:A:192:C:O2'	2:B:528:C:O2'	1.61	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:162:G:O4'	2:B:530:G:O6	1.79	1.00
7:G:151:VAL:HA	7:G:154:THR:HG23	1.42	0.99
1:A:13:A:H5'	7:G:121:PRO:HG2	1.43	0.99
7:G:29:LEU:HD22	7:G:172:VAL:HG11	1.44	0.99
5:E:2173:U:C5	7:G:101:LYS:HD2	1.97	0.99
1:A:189:C:N4	3:C:1054:C:N4	2.10	0.98
1:A:190:U:OP2	3:C:1054:C:O2	1.81	0.98
5:E:2154:G:O2'	7:G:160:LYS:CG	2.11	0.98
7:G:151:VAL:O	7:G:154:THR:N	1.97	0.98
1:A:87:U:N3	6:F:218:ARG:CG	2.26	0.98
1:A:191:G:N2	2:B:530:G:OP1	1.95	0.98
8:H:15:LYS:CA	8:H:70:VAL:HG21	1.92	0.98
7:G:174:MET:HB3	7:G:178:VAL:HG21	1.45	0.98
7:G:26:ARG:HG3	7:G:210:MET:HG3	1.44	0.97
1:A:112:G:H2'	1:A:113:U:C6	1.99	0.97
5:E:2173:U:C5	7:G:101:LYS:CD	2.47	0.97
8:H:95:PHE:HB3	8:H:101:PHE:HB2	1.42	0.97
1:A:81:A:H1'	1:A:94:U:N1	1.80	0.97
1:A:110:U:C2'	1:A:111:A:H5''	1.93	0.97
5:E:2153:G:N2	7:G:161:LYS:CE	2.27	0.96
1:A:151:U:H2'	1:A:152:U:C6	1.99	0.96
1:A:46:U:O2'	1:A:47:A:H4'	1.66	0.96
1:A:193:U:O2	2:B:535:A:OP2	1.84	0.96
1:A:14:U:H2'	1:A:15:C:H6	1.29	0.96
8:H:165:LYS:HG2	8:H:166:TYR:CD2	2.01	0.96
7:G:45:ARG:HB2	7:G:47:LYS:HD3	1.46	0.96
1:A:87:U:H3	6:F:218:ARG:NE	1.62	0.96
7:G:9:VAL:HG21	7:G:180:VAL:HG13	1.48	0.95
1:A:87:U:O2	6:F:218:ARG:CZ	2.14	0.95
1:A:14:U:H2'	1:A:15:C:C6	2.01	0.95
1:A:87:U:H3	6:F:218:ARG:CG	1.78	0.95
7:G:60:ARG:CB	7:G:171:ASN:HB2	1.97	0.95
1:A:7:A:H2'	1:A:8:A:H8	1.31	0.95
6:F:208:TYR:CD2	6:F:212:LYS:HE3	2.01	0.95
1:A:87:U:C4	6:F:218:ARG:HG2	1.95	0.95
8:H:140:ARG:HA	8:H:140:ARG:CZ	1.97	0.95
7:G:53:LEU:HD22	7:G:189:PHE:CE1	2.02	0.94
7:G:60:ARG:HG3	7:G:61:PRO:HD3	1.49	0.94
1:A:90:G:P	6:F:211:LYS:NZ	2.39	0.94
5:E:2154:G:H2'	7:G:160:LYS:HD3	1.46	0.94
8:H:53:VAL:CB	8:H:56:PHE:HB2	1.97	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:53:LEU:HD22	7:G:189:PHE:CZ	2.02	0.94
5:E:2154:G:C2'	7:G:160:LYS:HD3	1.96	0.94
1:A:128:A:H2'	1:A:129:U:C6	2.02	0.94
8:H:162:PHE:HA	8:H:165:LYS:HD3	1.50	0.93
7:G:152:ARG:H	7:G:153:SER:N	1.56	0.93
1:A:14:U:O4'	7:G:121:PRO:O	1.85	0.93
1:A:58:A:C6	1:A:59:G:H1'	2.03	0.93
1:A:16:U:H1'	1:A:59:G:N2	1.83	0.93
7:G:190:PHE:CE2	7:G:200:ASN:HB2	2.04	0.92
8:H:17:VAL:HB	8:H:69:THR:HA	1.51	0.92
1:A:62:C:H2'	1:A:63:U:C6	2.04	0.92
1:A:78:G:O2'	1:A:79:U:H5'	1.70	0.92
1:A:41:G:O2'	1:A:43:U:H4'	1.67	0.92
8:H:141:LYS:HA	8:H:144:LYS:HE2	1.50	0.92
8:H:114:LYS:HD2	8:H:115:TYR:H	1.32	0.92
1:A:94:U:OP2	1:A:94:U:C5	2.22	0.92
7:G:151:VAL:CA	7:G:154:THR:N	2.33	0.92
7:G:32:VAL:HG13	7:G:169:VAL:HG23	1.49	0.92
7:G:131:ALA:CB	7:G:133:LYS:HD3	2.00	0.92
1:A:76:A:H2'	1:A:77:G:C8	2.05	0.92
7:G:194:LEU:HD23	7:G:200:ASN:HD21	1.33	0.92
1:A:154:U:H1'	1:A:184:U:O4	1.69	0.91
6:F:200:ALA:HA	6:F:210:ILE:HD11	1.51	0.91
1:A:103:G:H2'	1:A:104:G:C8	2.04	0.91
8:H:16:LEU:H	8:H:70:VAL:HG11	1.35	0.91
8:H:163:LYS:CE	8:H:169:ASP:HA	2.01	0.91
1:A:39:A:H2'	1:A:40:G:H5'	1.53	0.91
1:A:87:U:C4	6:F:218:ARG:HD2	2.04	0.91
1:A:88:U:H2'	1:A:89:A:H5'	1.52	0.91
7:G:205:VAL:CG1	7:G:213:ALA:HB1	2.00	0.91
7:G:94:ASN:HB2	7:G:123:LEU:CB	2.01	0.91
8:H:16:LEU:HD21	8:H:78:ILE:HD11	1.52	0.91
1:A:88:U:C2'	1:A:89:A:H5'	2.01	0.91
1:A:193:U:OP1	2:B:535:A:N7	2.02	0.91
1:A:75:U:O2'	1:A:76:A:H5'	1.70	0.90
1:A:189:C:H3'	3:C:1054:C:O2	1.70	0.90
1:A:190:U:C5	3:C:1054:C:C2	2.58	0.90
1:A:131:C:H2'	1:A:132:A:H4'	1.51	0.90
7:G:36:VAL:HG13	7:G:204:LEU:HD13	1.52	0.90
1:A:87:U:C4	6:F:218:ARG:CD	2.54	0.90
7:G:151:VAL:HA	7:G:154:THR:CG2	2.02	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:90:G:C5'	6:F:211:LYS:HZ1	1.84	0.90
1:A:95:A:H2'	1:A:96:C:H5''	1.53	0.90
1:A:76:A:H2'	1:A:77:G:H8	1.34	0.90
5:E:2153:G:C2	7:G:161:LYS:CE	2.55	0.90
7:G:63:MET:HG3	7:G:108:ASN:CB	2.02	0.90
1:A:81:A:O2'	1:A:94:U:H1'	1.72	0.90
5:E:2171:G:O5'	7:G:98:LYS:NZ	1.83	0.90
8:H:90:LEU:HD13	8:H:163:LYS:HE3	1.50	0.90
8:H:75:ALA:HA	8:H:78:ILE:CG1	2.02	0.90
5:E:2153:G:H21	7:G:161:LYS:HE2	1.30	0.89
6:F:85:GLN:HG3	6:F:93:THR:HB	1.54	0.89
8:H:26:GLY:HA3	8:H:31:ARG:H	1.33	0.89
5:E:2173:U:C4	7:G:101:LYS:CD	2.56	0.89
1:A:39:A:C2'	1:A:40:G:H5'	2.02	0.89
1:A:81:A:H1'	1:A:94:U:C1'	2.02	0.89
1:A:90:G:OP1	6:F:211:LYS:NZ	2.04	0.89
1:A:147:C:H5''	1:A:148:G:C8	2.07	0.89
8:H:141:LYS:HD3	8:H:144:LYS:HE2	1.53	0.89
5:E:2153:G:H22	7:G:162:VAL:HG23	1.36	0.89
8:H:133:PRO:HD2	8:H:135:ALA:HB3	1.55	0.89
7:G:67:ILE:HG21	7:G:77:ALA:CB	2.02	0.89
8:H:31:ARG:HB3	8:H:34:LYS:CE	2.01	0.89
8:H:162:PHE:HD1	8:H:166:TYR:HE2	1.21	0.89
8:H:46:GLN:CG	8:H:66:VAL:HB	2.03	0.89
7:G:12:HIS:CE1	7:G:206:VAL:HG13	2.08	0.89
1:A:76:A:O2'	1:A:77:G:H5'	1.73	0.89
1:A:149:G:N2	1:A:175:C:H42	1.71	0.89
5:E:2144:C:H4'	5:E:2145:G:OP1	1.73	0.88
1:A:58:A:C2	1:A:59:G:H1'	2.07	0.88
6:F:186:ILE:HG23	6:F:188:THR:H	1.37	0.88
8:H:91:ARG:HE	8:H:169:ASP:HB2	1.36	0.88
7:G:157:PHE:CE2	7:G:165:LEU:HD22	2.08	0.88
1:A:7:A:H2'	1:A:8:A:C8	2.08	0.88
1:A:102:A:H2'	1:A:103:G:O4'	1.71	0.88
6:F:161:VAL:CG2	6:F:165:ARG:HD2	2.03	0.88
1:A:181:A:H2'	1:A:182:A:C8	2.08	0.88
8:H:95:PHE:HB3	8:H:101:PHE:CB	2.02	0.88
1:A:78:G:N2	1:A:79:U:H1'	1.89	0.88
8:H:95:PHE:HA	8:H:101:PHE:CD2	2.08	0.88
8:H:75:ALA:CB	8:H:78:ILE:HD11	2.03	0.88
6:F:86:CYS:HB2	6:F:87:PRO:HD3	1.54	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:51:TYR:O	8:H:58:ILE:HA	1.73	0.88
8:H:59:ARG:CD	8:H:62:GLU:HA	2.03	0.88
5:E:2173:U:OP2	7:G:98:LYS:HB2	1.74	0.87
1:A:129:U:C2'	1:A:130:C:H5'	2.03	0.87
5:E:2154:G:C2'	7:G:160:LYS:CG	2.53	0.87
7:G:149:THR:O	7:G:153:SER:N	2.08	0.87
1:A:96:C:H4'	1:A:98:U:OP2	1.75	0.87
7:G:12:HIS:CD2	7:G:206:VAL:HG22	2.09	0.87
1:A:59:G:H3'	1:A:60:U:H6	1.38	0.86
1:A:14:U:O4'	7:G:121:PRO:C	2.10	0.86
7:G:68:PHE:CE2	7:G:116:LEU:HD13	2.10	0.86
8:H:70:VAL:HB	8:H:71:ARG:NH1	1.91	0.86
1:A:190:U:C5	3:C:1054:C:N3	2.43	0.86
8:H:18:LEU:CG	8:H:68:VAL:HG21	2.06	0.86
7:G:63:MET:CG	7:G:108:ASN:HB3	2.03	0.86
1:A:192:C:O2	2:B:529:G:H5''	1.74	0.86
8:H:136:ARG:NH1	8:H:137:VAL:HG22	1.91	0.86
7:G:29:LEU:HD22	7:G:172:VAL:CG1	2.06	0.86
7:G:169:VAL:CG2	7:G:179:LEU:HD21	2.04	0.85
8:H:87:GLU:HG3	8:H:122:PHE:CZ	2.12	0.85
1:A:87:U:O2	6:F:218:ARG:NH1	2.09	0.85
7:G:16:LEU:CD1	7:G:207:LYS:HA	2.06	0.85
8:H:20:ILE:HG13	8:H:21:SER:H	1.42	0.85
8:H:83:LEU:HD13	8:H:84:LYS:N	1.92	0.85
1:A:112:G:H2'	1:A:113:U:C5	2.10	0.85
8:H:20:ILE:HG21	8:H:65:ALA:CB	2.05	0.84
8:H:83:LEU:HD12	8:H:166:TYR:HE1	1.41	0.84
1:A:96:C:O2'	1:A:97:G:H5''	1.76	0.84
7:G:155:ILE:HG21	7:G:167:VAL:HG13	1.59	0.84
5:E:2159:A:H4'	5:E:2160:G:O5'	1.77	0.84
5:E:2160:G:C6	5:E:2161:C:N4	2.45	0.84
8:H:53:VAL:HG23	8:H:57:GLY:O	1.78	0.84
8:H:70:VAL:HG12	8:H:75:ALA:HB2	1.57	0.84
1:A:193:U:H4'	2:B:535:A:C1'	2.07	0.84
6:F:138:ASN:ND2	6:F:202:LYS:HB2	1.93	0.84
1:A:63:U:C2'	1:A:64:A:H5'	2.08	0.84
8:H:71:ARG:NH1	8:H:75:ALA:HB3	1.91	0.84
7:G:53:LEU:CD1	7:G:186:SER:HA	2.07	0.84
7:G:59:PRO:CG	7:G:152:ARG:C	2.45	0.84
5:E:2154:G:C3'	7:G:160:LYS:HD3	2.08	0.83
1:A:160:U:C2	2:B:531:U:OP1	2.22	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:173:LEU:CD1	6:F:174:LEU:HD22	2.07	0.83
6:F:173:LEU:HD12	6:F:174:LEU:HD22	1.58	0.83
1:A:84:U:C2'	1:A:85:A:H5'	2.08	0.83
1:A:58:A:N1	1:A:59:G:H1'	1.91	0.83
7:G:179:LEU:HA	7:G:182:GLN:NE2	1.94	0.83
7:G:32:VAL:CG1	7:G:169:VAL:HG23	2.08	0.83
6:F:112:ILE:O	6:F:116:THR:HG23	1.77	0.83
8:H:71:ARG:HD2	8:H:74:LYS:CB	2.08	0.83
8:H:74:LYS:HA	8:H:77:GLU:OE2	1.79	0.83
8:H:53:VAL:CG2	8:H:56:PHE:HB2	2.08	0.83
6:F:116:THR:HG22	6:F:190:ALA:O	1.79	0.83
1:A:46:U:C2'	1:A:47:A:H4'	2.09	0.83
5:E:2153:G:H21	7:G:161:LYS:CE	1.89	0.83
1:A:59:G:H3'	1:A:60:U:C6	2.14	0.83
6:F:83:LYS:HD3	6:F:83:LYS:H	1.44	0.83
1:A:154:U:O2'	1:A:155:C:H5'	1.78	0.83
7:G:32:VAL:HG11	7:G:179:LEU:CD2	2.08	0.82
6:F:139:THR:HB	6:F:173:LEU:HD11	1.60	0.82
7:G:4:ILE:HG23	7:G:5:THR:H	1.43	0.82
7:G:60:ARG:CG	7:G:61:PRO:HD3	2.08	0.82
5:E:2153:G:H22	7:G:162:VAL:HG22	1.44	0.82
6:F:185:ASN:HB2	6:F:191:GLU:CB	2.09	0.82
5:E:2173:U:O4	7:G:101:LYS:HD3	1.80	0.82
8:H:83:LEU:HD12	8:H:166:TYR:CE1	2.15	0.82
7:G:198:TRP:O	7:G:201:VAL:HG22	1.78	0.82
1:A:189:C:O5'	4:D:1196:U:H2'	1.80	0.82
1:A:12:G:O2'	7:G:117:ILE:HB	0.99	0.82
1:A:59:G:N3	1:A:59:G:H2'	1.92	0.82
8:H:155:LYS:O	8:H:158:THR:HG22	1.78	0.82
8:H:31:ARG:HB3	8:H:34:LYS:HE2	1.59	0.82
8:H:16:LEU:HD21	8:H:75:ALA:HB1	1.59	0.82
6:F:122:VAL:CG2	6:F:123:LEU:HD12	2.09	0.82
7:G:196:LYS:HG3	7:G:199:GLN:HB2	1.61	0.82
5:E:2171:G:OP2	7:G:102:LYS:CB	2.28	0.82
8:H:71:ARG:HD2	8:H:74:LYS:HB3	1.60	0.81
1:A:190:U:H5	3:C:1054:C:C2	1.95	0.81
1:A:26:A:C2	1:A:27:U:H1'	2.14	0.81
8:H:79:LEU:HD23	8:H:126:PHE:CZ	2.15	0.81
8:H:33:SER:HA	8:H:36:LEU:CD2	2.11	0.81
1:A:46:U:HO2'	1:A:47:A:H4'	1.46	0.81
6:F:112:ILE:CD1	6:F:189:ILE:HB	2.10	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:9:ARG:NH1	8:H:9:ARG:HA	1.96	0.81
1:A:173:A:H1'	1:A:181:A:N1	1.96	0.81
8:H:59:ARG:NH1	8:H:59:ARG:HB3	1.94	0.81
6:F:208:TYR:CE2	6:F:212:LYS:HE3	2.15	0.81
6:F:199:ASN:HB3	6:F:207:SER:HB2	1.61	0.81
8:H:9:ARG:CZ	8:H:9:ARG:HA	2.10	0.81
1:A:87:U:N3	6:F:218:ARG:HG2	1.91	0.81
7:G:151:VAL:HA	7:G:154:THR:CB	2.10	0.81
7:G:151:VAL:CA	7:G:154:THR:H	1.93	0.81
7:G:67:ILE:HD13	7:G:77:ALA:HB2	1.63	0.81
8:H:74:LYS:HD3	8:H:74:LYS:O	1.80	0.80
1:A:168:C:H3'	1:A:169:G:H5''	1.63	0.80
6:F:84:ALA:HB3	6:F:89:ILE:CD1	2.11	0.80
1:A:90:G:C5'	6:F:211:LYS:NZ	2.44	0.80
7:G:150:ASP:CA	7:G:153:SER:HB2	2.12	0.80
7:G:179:LEU:HA	7:G:182:GLN:HE21	1.45	0.80
1:A:192:C:O2	2:B:533:A:H1'	1.82	0.80
5:E:2172:G:H3'	7:G:98:LYS:CG	2.12	0.80
5:E:2153:G:N3	7:G:161:LYS:CE	2.45	0.80
8:H:28:ARG:C	8:H:29:LEU:HD22	2.03	0.80
8:H:165:LYS:H	8:H:165:LYS:HD2	1.46	0.80
7:G:24:LYS:HD2	7:G:25:LYS:N	1.97	0.80
8:H:59:ARG:CZ	8:H:62:GLU:HG2	2.11	0.79
7:G:90:LEU:HG	7:G:124:LEU:HD11	1.61	0.79
8:H:33:SER:HA	8:H:36:LEU:HD23	1.64	0.79
7:G:16:LEU:HD13	7:G:207:LYS:HA	1.63	0.79
6:F:139:THR:HG21	6:F:174:LEU:CD2	2.12	0.79
7:G:175:GLU:O	7:G:178:VAL:HG22	1.81	0.79
6:F:185:ASN:HB2	6:F:191:GLU:HB3	1.65	0.79
1:A:189:C:C5	3:C:1054:C:C4	2.71	0.79
7:G:59:PRO:CG	7:G:152:ARG:O	2.28	0.79
8:H:31:ARG:HE	8:H:34:LYS:HE2	1.48	0.79
8:H:18:LEU:H	8:H:68:VAL:HB	1.46	0.79
7:G:64:SER:HB3	7:G:107:TYR:CD2	2.16	0.79
7:G:60:ARG:CG	7:G:171:ASN:HB2	2.13	0.79
6:F:133:VAL:O	6:F:136:ILE:HG22	1.83	0.79
8:H:83:LEU:HD13	8:H:84:LYS:H	1.47	0.79
6:F:186:ILE:HG23	6:F:188:THR:N	1.98	0.79
6:F:161:VAL:HG22	6:F:165:ARG:HD2	1.64	0.79
2:B:501:C:H2'	2:B:502:G:H8	1.45	0.79
5:E:2175:A:C2'	7:G:130:LYS:CD	2.52	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:129:U:O2'	1:A:130:C:H5'	1.82	0.79
1:A:168:C:O5'	1:A:169:G:H5''	1.83	0.79
7:G:26:ARG:HD2	7:G:210:MET:CE	2.12	0.78
1:A:60:U:H2'	1:A:61:G:C5'	2.06	0.78
7:G:117:ILE:HD12	7:G:118:LYS:N	1.93	0.78
1:A:193:U:C4'	2:B:535:A:H2'	2.12	0.78
5:E:2154:G:H2'	7:G:160:LYS:CG	2.13	0.78
1:A:58:A:C5	1:A:59:G:H1'	2.17	0.78
1:A:189:C:C6	3:C:1054:C:N3	2.52	0.78
7:G:120:VAL:HG22	7:G:121:PRO:HD3	1.66	0.78
5:E:2171:G:P	7:G:102:LYS:HG2	2.22	0.78
7:G:124:LEU:HB3	7:G:128:LEU:HD13	1.64	0.78
8:H:68:VAL:HG12	8:H:69:THR:H	1.49	0.78
8:H:136:ARG:CZ	8:H:137:VAL:HG22	2.14	0.78
7:G:67:ILE:HD11	7:G:73:ASP:OD1	1.83	0.78
7:G:114:GLU:HG2	7:G:137:PRO:CB	2.13	0.78
1:A:71:U:H2'	1:A:72:A:O4'	1.84	0.78
7:G:150:ASP:HA	7:G:153:SER:CB	2.13	0.77
8:H:71:ARG:NE	8:H:75:ALA:H	1.81	0.77
8:H:16:LEU:CD1	8:H:70:VAL:HG11	2.14	0.77
1:A:75:U:C2'	1:A:76:A:H5'	2.14	0.77
1:A:173:A:H2'	1:A:174:A:O4'	1.83	0.77
6:F:112:ILE:CG2	6:F:113:ILE:HD12	2.14	0.77
5:E:2153:G:N3	7:G:161:LYS:HE3	2.00	0.77
1:A:190:U:C5	3:C:1054:C:C4	2.73	0.77
6:F:208:TYR:HD2	6:F:212:LYS:HE3	1.48	0.77
8:H:71:ARG:HD3	8:H:71:ARG:N	1.98	0.76
8:H:77:GLU:O	8:H:78:ILE:HG23	1.84	0.76
7:G:73:ASP:OD1	7:G:144:LEU:HD21	1.85	0.76
1:A:77:G:O2'	1:A:78:G:H5'	1.85	0.76
6:F:202:LYS:HA	6:F:205:SER:CB	2.16	0.76
7:G:26:ARG:HD2	7:G:210:MET:HE2	1.67	0.76
1:A:9:U:H2'	1:A:10:G:O4'	1.85	0.76
1:A:149:G:H21	1:A:175:C:H42	1.34	0.76
7:G:41:TYR:OH	7:G:163:LEU:HA	1.86	0.76
1:A:189:C:C3'	3:C:1054:C:O2	2.34	0.76
8:H:161:TRP:O	8:H:164:GLN:HG2	1.83	0.76
1:A:193:U:OP1	2:B:535:A:N6	2.19	0.76
1:A:74:U:HO2'	1:A:75:U:H4'	1.45	0.76
7:G:16:LEU:HD11	7:G:208:SER:H	1.50	0.76
8:H:20:ILE:CG2	8:H:65:ALA:HB3	2.14	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:85:GLN:HG3	6:F:93:THR:CB	2.15	0.76
6:F:85:GLN:HG3	6:F:93:THR:CG2	2.16	0.76
6:F:85:GLN:HB2	6:F:88:ILE:O	1.86	0.76
8:H:13:ILE:O	8:H:13:ILE:HD12	1.85	0.76
8:H:23:GLY:H	8:H:64:ILE:HD13	1.50	0.76
8:H:36:LEU:HD22	8:H:67:HIS:CD2	2.21	0.75
8:H:32:ALA:H	8:H:34:LYS:CE	1.99	0.75
8:H:70:VAL:HG12	8:H:75:ALA:CB	2.15	0.75
7:G:100:ILE:O	7:G:100:ILE:HD13	1.86	0.75
6:F:189:ILE:HG22	6:F:193:LEU:CD1	2.16	0.75
5:E:2155:U:H4'	7:G:158:GLN:CG	2.15	0.75
7:G:98:LYS:HE2	7:G:102:LYS:HZ1	1.50	0.75
7:G:90:LEU:HD21	7:G:123:LEU:HB2	1.67	0.75
8:H:14:GLU:OE2	8:H:129:VAL:HG13	1.86	0.75
1:A:45:A:H2'	1:A:46:U:C6	2.20	0.75
6:F:187:LYS:HD2	6:F:187:LYS:O	1.85	0.75
1:A:191:G:H21	2:B:530:G:P	1.92	0.75
8:H:121:ILE:HA	8:H:125:ASP:HB3	1.66	0.75
1:A:27:U:C3'	1:A:28:A:H5'	2.16	0.75
7:G:8:GLN:HB3	7:G:216:LEU:HD11	1.67	0.75
8:H:84:LYS:HB2	8:H:167:ASP:OD2	1.86	0.75
8:H:91:ARG:NE	8:H:159:VAL:HG21	2.01	0.75
7:G:56:PRO:CD	7:G:185:MET:HG3	2.16	0.75
7:G:32:VAL:HG11	7:G:179:LEU:HD21	1.67	0.75
8:H:163:LYS:CD	8:H:169:ASP:HA	2.17	0.75
8:H:31:ARG:HB3	8:H:34:LYS:HE3	1.68	0.75
7:G:151:VAL:HA	7:G:154:THR:N	2.00	0.75
7:G:77:ALA:HB1	7:G:82:VAL:CG2	2.16	0.75
8:H:157:ASP:O	8:H:160:SER:HB3	1.87	0.74
8:H:18:LEU:N	8:H:68:VAL:HB	2.02	0.74
6:F:206:THR:O	6:F:210:ILE:HD13	1.87	0.74
6:F:85:GLN:CG	6:F:93:THR:HB	2.15	0.74
8:H:98:THR:O	8:H:153:THR:HB	1.87	0.74
5:E:2155:U:O2'	7:G:158:GLN:HB3	1.86	0.74
7:G:48:ARG:HD2	7:G:160:LYS:C	2.08	0.74
7:G:149:THR:O	7:G:153:SER:OG	2.02	0.74
7:G:102:LYS:HG3	7:G:105:LYS:HE3	1.70	0.74
1:A:59:G:H5''	1:A:60:U:H5	1.53	0.74
7:G:159:LEU:HD12	7:G:164:CYS:O	1.88	0.74
7:G:48:ARG:HD2	7:G:160:LYS:O	1.87	0.74
7:G:157:PHE:CZ	7:G:165:LEU:HD22	2.22	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:102:A:H2'	1:A:103:G:C4'	2.17	0.74
1:A:10:G:H1	7:G:122:ARG:NE	1.86	0.74
7:G:161:LYS:HD3	7:G:161:LYS:H	1.53	0.73
8:H:17:VAL:HG23	8:H:68:VAL:C	2.08	0.73
6:F:164:LEU:O	6:F:167:VAL:HG22	1.87	0.73
8:H:162:PHE:HB3	8:H:166:TYR:OH	1.89	0.73
8:H:165:LYS:HG2	8:H:166:TYR:CE2	2.23	0.73
1:A:81:A:H1'	1:A:94:U:H1'	1.70	0.73
1:A:95:A:C2'	1:A:96:C:H5''	2.18	0.73
5:E:2172:G:H8	7:G:98:LYS:HG2	1.53	0.73
7:G:94:ASN:CB	7:G:123:LEU:HD12	2.18	0.73
8:H:163:LYS:HD2	8:H:169:ASP:HA	1.69	0.73
1:A:9:U:C2'	1:A:10:G:H5'	2.17	0.73
8:H:16:LEU:HD22	8:H:70:VAL:CG1	2.19	0.73
8:H:36:LEU:HD12	8:H:36:LEU:O	1.88	0.73
1:A:89:A:O2'	1:A:90:G:H5'	1.87	0.73
7:G:8:GLN:HE21	7:G:216:LEU:HD11	1.53	0.73
1:A:84:U:O2'	1:A:85:A:H5'	1.87	0.73
1:A:62:C:H2'	1:A:63:U:H6	1.54	0.73
8:H:155:LYS:O	8:H:159:VAL:HG12	1.87	0.73
6:F:112:ILE:HD12	6:F:189:ILE:HB	1.69	0.73
7:G:194:LEU:HD23	7:G:200:ASN:ND2	2.02	0.73
1:A:49:A:OP1	1:A:131:C:H5'	1.89	0.73
7:G:205:VAL:HG13	7:G:214:PHE:O	1.88	0.73
6:F:117:LEU:HG	6:F:128:PRO:HB2	1.71	0.73
6:F:173:LEU:HD12	6:F:174:LEU:N	2.03	0.73
7:G:56:PRO:HD3	7:G:185:MET:HG3	1.69	0.73
7:G:179:LEU:O	7:G:179:LEU:HD13	1.89	0.73
8:H:133:PRO:HG2	8:H:135:ALA:N	2.01	0.73
1:A:183:A:N3	1:A:183:A:H2'	2.04	0.73
8:H:163:LYS:HE2	8:H:169:ASP:HA	1.70	0.73
6:F:116:THR:HG21	6:F:193:LEU:HB2	1.70	0.73
8:H:67:HIS:HD2	8:H:68:VAL:HG23	1.53	0.72
1:A:91:C:H2'	1:A:92:U:O4'	1.89	0.72
5:E:2184:C:H6	7:G:164:CYS:SG	2.13	0.72
8:H:79:LEU:HD13	8:H:79:LEU:O	1.88	0.72
6:F:185:ASN:O	6:F:186:ILE:HG22	1.90	0.72
1:A:168:C:H3'	1:A:169:G:C5'	2.20	0.72
1:A:191:G:H22	2:B:530:G:P	1.95	0.72
8:H:15:LYS:HA	8:H:70:VAL:CG2	2.16	0.72
8:H:33:SER:O	8:H:37:GLU:HG3	1.89	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:44:PRO:HG2	8:H:68:VAL:H	1.55	0.72
5:E:2172:G:C8	7:G:98:LYS:HG2	2.24	0.72
7:G:53:LEU:HD13	7:G:186:SER:HA	1.70	0.72
1:A:48:A:H2'	1:A:49:A:O4'	1.90	0.72
6:F:175:THR:O	6:F:179:ARG:HG3	1.90	0.72
7:G:58:CYS:HA	7:G:153:SER:HB3	1.72	0.72
7:G:120:VAL:HA	7:G:124:LEU:HD13	1.72	0.72
8:H:67:HIS:CD2	8:H:68:VAL:HG23	2.24	0.72
8:H:15:LYS:O	8:H:129:VAL:HG12	1.90	0.72
1:A:27:U:H3'	1:A:28:A:C5'	2.17	0.72
8:H:22:VAL:HA	8:H:64:ILE:CD1	2.16	0.72
6:F:177:GLY:O	6:F:180:GLU:HB3	1.89	0.72
1:A:65:U:H2'	1:A:66:U:C6	2.25	0.72
8:H:33:SER:O	8:H:36:LEU:HG	1.89	0.71
7:G:152:ARG:C	7:G:153:SER:HA	2.10	0.71
8:H:32:ALA:H	8:H:34:LYS:HD2	1.55	0.71
7:G:53:LEU:HD22	7:G:189:PHE:CE2	2.26	0.71
1:A:189:C:C5	3:C:1054:C:N3	2.58	0.71
8:H:13:ILE:HG23	8:H:162:PHE:HE2	1.55	0.71
1:A:144:C:N3	1:A:145:U:H1'	2.05	0.71
2:B:524:G:H2'	2:B:525:C:C6	2.25	0.71
1:A:119:C:H2'	1:A:121:C:C5	2.25	0.71
1:A:162:G:C1'	2:B:530:G:O6	2.38	0.71
1:A:13:A:H5'	1:A:61:G:O6	1.89	0.71
8:H:25:SER:OG	8:H:32:ALA:HB3	1.90	0.71
1:A:90:G:O2'	1:A:91:C:H5'	1.90	0.71
1:A:92:U:N3	1:A:93:U:H1'	2.05	0.71
6:F:107:LEU:H	6:F:107:LEU:HD23	1.56	0.71
6:F:138:ASN:HD21	6:F:202:LYS:HB2	1.52	0.71
5:E:2166:G:C6	5:E:2167:C:C4	2.79	0.71
1:A:46:U:H2'	1:A:47:A:H4'	1.72	0.71
1:A:95:A:H2'	1:A:96:C:C5'	2.19	0.71
8:H:8:MET:HG3	8:H:9:ARG:N	2.06	0.70
7:G:102:LYS:HA	7:G:105:LYS:HE3	1.73	0.70
7:G:34:LEU:HD22	7:G:205:VAL:O	1.91	0.70
5:E:2173:U:H5	7:G:101:LYS:HD2	1.54	0.70
1:A:102:A:O2'	1:A:103:G:H4'	1.91	0.70
1:A:81:A:H2'	1:A:82:G:C8	2.26	0.70
8:H:132:ARG:H	8:H:132:ARG:NH1	1.90	0.70
8:H:16:LEU:HD13	8:H:16:LEU:H	1.56	0.70
6:F:163:PRO:O	6:F:166:ARG:HG3	1.90	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:215:ARG:H	7:G:215:ARG:HD2	1.55	0.70
5:E:2153:G:H21	7:G:161:LYS:HG2	1.55	0.70
8:H:83:LEU:HD21	8:H:90:LEU:CG	2.22	0.70
1:A:103:G:H2'	1:A:104:G:N7	2.07	0.70
6:F:84:ALA:CB	6:F:89:ILE:HG13	2.21	0.70
1:A:78:G:H2'	1:A:79:U:O4'	1.90	0.70
6:F:107:LEU:HG	6:F:108:LYS:HD2	1.72	0.70
1:A:173:A:H1'	1:A:181:A:C2	2.27	0.70
1:A:13:A:C5'	7:G:121:PRO:HG2	2.14	0.70
1:A:78:G:H21	1:A:79:U:H1'	1.55	0.70
7:G:190:PHE:CZ	7:G:200:ASN:HB2	2.26	0.70
7:G:77:ALA:O	7:G:82:VAL:HG22	1.91	0.70
6:F:213:LYS:HE2	6:F:217:GLU:OE2	1.91	0.70
1:A:73:U:OP2	1:A:74:U:H5'	1.92	0.70
8:H:18:LEU:H	8:H:68:VAL:CG1	2.05	0.70
1:A:132:A:H2'	1:A:133:G:N7	2.07	0.70
8:H:59:ARG:NE	8:H:62:GLU:HG2	2.06	0.70
8:H:91:ARG:CD	8:H:159:VAL:HG21	2.21	0.70
1:A:182:A:H2'	1:A:183:A:H8	1.57	0.70
8:H:148:GLY:HA3	8:H:151:HIS:CE1	2.27	0.70
7:G:151:VAL:C	7:G:153:SER:N	2.43	0.69
7:G:59:PRO:O	7:G:60:ARG:HG3	1.91	0.69
1:A:58:A:C4	1:A:59:G:H1'	2.26	0.69
6:F:200:ALA:CA	6:F:210:ILE:HD11	2.22	0.69
1:A:185:U:O2'	1:A:186:U:H5'	1.92	0.69
7:G:97:LYS:O	7:G:100:ILE:HG22	1.93	0.69
8:H:18:LEU:HG	8:H:68:VAL:CG2	2.16	0.69
8:H:44:PRO:HB2	8:H:67:HIS:CB	2.23	0.69
1:A:42:U:H5''	1:A:43:U:H5'	1.73	0.69
7:G:157:PHE:HE2	7:G:165:LEU:HD22	1.54	0.69
6:F:200:ALA:HA	6:F:210:ILE:CD1	2.22	0.69
5:E:2155:U:O3'	7:G:158:GLN:HB3	1.91	0.69
8:H:16:LEU:HD21	8:H:78:ILE:CD1	2.21	0.69
1:A:26:A:N6	1:A:49:A:H2	1.90	0.69
8:H:26:GLY:CA	8:H:31:ARG:H	2.05	0.69
1:A:89:A:O3'	6:F:211:LYS:NZ	2.22	0.69
1:A:109:C:H1'	1:A:126:A:H1'	1.73	0.69
7:G:60:ARG:HG2	7:G:171:ASN:HB2	1.72	0.69
7:G:53:LEU:HD22	7:G:189:PHE:CD1	2.26	0.69
1:A:78:G:C2	1:A:79:U:H1'	2.27	0.69
8:H:141:LYS:HD3	8:H:144:LYS:CE	2.22	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:190:PHE:HE2	7:G:200:ASN:HB2	1.54	0.69
1:A:96:C:H4'	1:A:98:U:P	2.32	0.69
1:A:63:U:H2'	1:A:64:A:C5'	2.14	0.69
8:H:17:VAL:HG22	8:H:18:LEU:O	1.93	0.69
8:H:32:ALA:H	8:H:34:LYS:CD	2.05	0.69
7:G:195:LYS:HD2	7:G:195:LYS:O	1.93	0.69
7:G:215:ARG:HH11	7:G:215:ARG:N	1.91	0.69
1:A:139:C:H2'	1:A:140:C:C5'	2.23	0.69
7:G:49:PHE:HD2	7:G:193:LEU:CD2	2.06	0.69
7:G:65:ILE:HD11	7:G:151:VAL:HG23	1.75	0.69
1:A:92:U:H2'	1:A:93:U:C5'	2.23	0.68
6:F:112:ILE:HG13	6:F:190:ALA:HA	1.74	0.68
1:A:87:U:C2	6:F:218:ARG:NH1	2.61	0.68
1:A:170:A:H2'	1:A:171:A:C8	2.28	0.68
8:H:77:GLU:H	8:H:80:GLU:HG3	1.58	0.68
8:H:13:ILE:CG2	8:H:162:PHE:HE2	2.06	0.68
1:A:193:U:C2	2:B:535:A:OP2	2.46	0.68
6:F:79:LYS:HE3	6:F:164:LEU:HD13	1.75	0.68
6:F:199:ASN:CB	6:F:207:SER:HB2	2.22	0.68
1:A:12:G:HO2'	7:G:117:ILE:CB	1.76	0.68
1:A:10:G:N2	7:G:122:ARG:NH1	2.34	0.68
8:H:71:ARG:CD	8:H:75:ALA:H	2.07	0.68
1:A:189:C:H5''	4:D:1196:U:H3'	1.76	0.68
7:G:96:ASN:OD1	7:G:99:LEU:HB2	1.93	0.68
8:H:19:ASN:HB3	8:H:125:ASP:OD2	1.93	0.68
8:H:71:ARG:HD2	8:H:74:LYS:CA	2.24	0.68
7:G:90:LEU:CD2	7:G:123:LEU:HB2	2.24	0.68
1:A:129:U:H2'	1:A:130:C:H5'	1.76	0.68
1:A:92:U:H2'	1:A:93:U:C4'	2.23	0.68
7:G:41:TYR:CE1	7:G:163:LEU:HD22	2.29	0.68
7:G:152:ARG:N	7:G:153:SER:CA	2.56	0.68
1:A:17:U:H2'	1:A:18:G:O4'	1.94	0.68
8:H:103:PHE:N	8:H:122:PHE:HB2	2.08	0.68
8:H:162:PHE:O	8:H:163:LYS:HG2	1.94	0.68
8:H:46:GLN:OE1	8:H:66:VAL:HB	1.93	0.68
7:G:121:PRO:HD3	7:G:134:PHE:HE1	1.57	0.68
8:H:16:LEU:HD11	8:H:75:ALA:CB	2.24	0.68
7:G:36:VAL:HG22	7:G:204:LEU:HD12	1.76	0.67
1:A:102:A:N6	1:A:132:A:H2	1.92	0.67
8:H:132:ARG:CZ	8:H:133:PRO:HD3	2.24	0.67
1:A:167:U:O2'	1:A:168:C:H5'	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:12:G:H2'	1:A:61:G:C6	2.29	0.67
8:H:75:ALA:HB1	8:H:78:ILE:HD11	1.74	0.67
6:F:84:ALA:HB3	6:F:89:ILE:HG13	1.75	0.67
6:F:109:ALA:O	6:F:112:ILE:HG22	1.95	0.67
1:A:78:G:N3	1:A:126:A:H2	1.92	0.67
6:F:107:LEU:O	6:F:110:VAL:HG22	1.93	0.67
5:E:2171:G:N7	7:G:102:LYS:NZ	2.21	0.67
6:F:112:ILE:CG1	6:F:190:ALA:HA	2.23	0.67
7:G:216:LEU:HD13	7:G:216:LEU:OXT	1.95	0.67
5:E:2153:G:H21	7:G:161:LYS:CG	2.08	0.67
7:G:32:VAL:HG13	7:G:169:VAL:CG2	2.24	0.67
6:F:173:LEU:HD13	6:F:209:ALA:HB1	1.77	0.67
8:H:18:LEU:CD1	8:H:68:VAL:HG21	2.25	0.67
8:H:87:GLU:HB3	8:H:90:LEU:HA	1.76	0.67
6:F:139:THR:OG1	6:F:170:ALA:HB1	1.94	0.67
7:G:23:THR:HG23	7:G:25:LYS:H	1.60	0.67
8:H:25:SER:CB	8:H:65:ALA:HB2	2.21	0.67
8:H:83:LEU:HD21	8:H:90:LEU:HG	1.77	0.67
8:H:141:LYS:C	8:H:142:ARG:HD2	2.15	0.67
8:H:8:MET:HE2	8:H:9:ARG:HG2	1.76	0.67
1:A:147:C:H5''	1:A:148:G:N7	2.07	0.67
1:A:12:G:HO2'	7:G:117:ILE:HB	0.80	0.67
6:F:129:ILE:HG13	6:F:130:GLN:N	2.09	0.67
8:H:36:LEU:HD11	8:H:43:THR:HG23	1.77	0.67
1:A:112:G:H2'	1:A:113:U:H6	1.57	0.67
5:E:2172:G:H3'	7:G:98:LYS:HG2	1.77	0.67
7:G:36:VAL:HB	7:G:165:LEU:HD21	1.77	0.67
6:F:112:ILE:HG13	6:F:190:ALA:CA	2.25	0.67
7:G:16:LEU:HD21	7:G:207:LYS:C	2.15	0.67
7:G:60:ARG:HD3	7:G:61:PRO:HD3	1.76	0.66
5:E:2175:A:O2'	7:G:130:LYS:CB	2.43	0.66
8:H:16:LEU:HD11	8:H:75:ALA:HB1	1.77	0.66
1:A:139:C:H2'	1:A:140:C:H5'	1.77	0.66
1:A:11:U:O2	1:A:64:A:H1'	1.95	0.66
7:G:122:ARG:HB2	7:G:123:LEU:HD22	1.78	0.66
8:H:162:PHE:HD1	8:H:166:TYR:CE2	2.09	0.66
8:H:163:LYS:HD2	8:H:169:ASP:CA	2.25	0.66
3:C:1057:G:O2'	3:C:1058:G:H5'	1.95	0.66
5:E:2153:G:N2	7:G:162:VAL:HG23	2.09	0.66
8:H:95:PHE:HA	8:H:101:PHE:HD2	1.55	0.66
1:A:138:C:O2	1:A:138:C:H2'	1.95	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:145:THR:HG21	6:F:219:VAL:HG12	1.78	0.66
1:A:192:C:H4'	2:B:528:C:H5''	1.77	0.66
5:E:2184:C:C6	7:G:164:CYS:SG	2.88	0.66
8:H:32:ALA:H	8:H:34:LYS:HE3	1.58	0.66
8:H:71:ARG:HH11	8:H:71:ARG:H	1.43	0.66
1:A:26:A:H62	1:A:49:A:H2	1.43	0.66
7:G:6:SER:O	7:G:9:VAL:HG22	1.96	0.66
8:H:87:GLU:HG2	8:H:90:LEU:CG	2.18	0.66
1:A:136:A:C2'	1:A:137:G:H5'	2.26	0.66
1:A:43:U:C2'	1:A:44:A:H5'	2.26	0.66
7:G:5:THR:HG23	7:G:8:GLN:H	1.59	0.66
8:H:19:ASN:CG	8:H:66:VAL:HG13	2.15	0.66
7:G:98:LYS:HE2	7:G:102:LYS:NZ	2.11	0.66
8:H:34:LYS:O	8:H:37:GLU:HB2	1.95	0.66
7:G:9:VAL:HG21	7:G:180:VAL:CG1	2.24	0.66
7:G:63:MET:HE3	7:G:154:THR:O	1.95	0.66
1:A:192:C:C2	2:B:533:A:H1'	2.31	0.66
6:F:119:ILE:O	6:F:123:LEU:HD13	1.95	0.66
1:A:192:C:O2	2:B:529:G:C5'	2.44	0.66
7:G:58:CYS:HA	7:G:153:SER:CB	2.25	0.66
6:F:187:LYS:C	6:F:187:LYS:HD2	2.16	0.66
7:G:60:ARG:CD	7:G:61:PRO:HD3	2.26	0.65
8:H:69:THR:O	8:H:70:VAL:HG13	1.96	0.65
1:A:92:U:H2'	1:A:93:U:O4'	1.95	0.65
6:F:186:ILE:HG21	6:F:190:ALA:HB3	1.77	0.65
7:G:7:SER:HA	7:G:10:ARG:HE	1.60	0.65
1:A:181:A:H2'	1:A:182:A:N7	2.10	0.65
7:G:67:ILE:HD12	7:G:144:LEU:CD2	2.26	0.65
8:H:41:GLY:HA3	8:H:74:LYS:HZ3	1.62	0.65
8:H:132:ARG:HG3	8:H:132:ARG:HH11	1.61	0.65
1:A:36:G:H2'	1:A:37:A:H8	1.61	0.65
7:G:60:ARG:HB2	7:G:171:ASN:HB2	1.79	0.65
6:F:83:LYS:HD3	6:F:83:LYS:N	2.11	0.65
5:E:2154:G:O2'	7:G:160:LYS:HG2	1.95	0.65
1:A:87:U:C2	6:F:218:ARG:CZ	2.79	0.65
1:A:13:A:N3	7:G:120:VAL:O	2.30	0.65
7:G:121:PRO:HG3	7:G:134:PHE:CE1	2.31	0.65
1:A:44:A:OP2	1:A:45:A:OP2	2.15	0.65
6:F:132:VAL:HG12	6:F:197:LEU:CD1	2.16	0.65
6:F:195:GLU:O	6:F:198:ILE:HG22	1.97	0.65
8:H:162:PHE:HA	8:H:165:LYS:CD	2.27	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:18:LEU:H	8:H:68:VAL:CB	2.09	0.65
1:A:97:G:N3	1:A:97:G:H2'	2.11	0.65
1:A:170:A:H2'	1:A:171:A:H8	1.61	0.65
1:A:30:A:H2'	1:A:31:A:O4'	1.96	0.65
5:E:2155:U:O3'	7:G:158:GLN:CB	2.44	0.64
5:E:2157:G:P	7:G:108:ASN:ND2	2.69	0.64
7:G:54:LYS:HZ2	7:G:153:SER:HB2	1.51	0.64
1:A:156:A:H61	1:A:185:U:H5	1.44	0.64
8:H:19:ASN:OD1	8:H:66:VAL:HG13	1.97	0.64
8:H:20:ILE:HG13	8:H:21:SER:N	2.12	0.64
1:A:182:A:HO2'	1:A:183:A:H8	1.45	0.64
8:H:162:PHE:CD1	8:H:166:TYR:HE2	2.09	0.64
8:H:48:LYS:HG2	8:H:49:ALA:H	1.61	0.64
1:A:87:U:H3	6:F:218:ARG:HG2	1.52	0.64
1:A:159:U:H5''	1:A:160:U:C5	2.33	0.64
1:A:161:A:O4'	2:B:530:G:H1'	1.97	0.64
8:H:19:ASN:OD1	8:H:66:VAL:HG22	1.98	0.64
8:H:16:LEU:HD21	8:H:75:ALA:CB	2.28	0.64
7:G:114:GLU:HG3	7:G:138:VAL:O	1.97	0.64
1:A:182:A:H2'	1:A:183:A:C8	2.32	0.64
8:H:16:LEU:N	8:H:70:VAL:HG11	2.08	0.64
7:G:26:ARG:CG	7:G:210:MET:HG3	2.22	0.64
7:G:215:ARG:HH11	7:G:215:ARG:H	1.46	0.64
1:A:87:U:C2	6:F:218:ARG:HD2	2.28	0.64
7:G:174:MET:HB3	7:G:178:VAL:CG2	2.25	0.64
8:H:6:ASN:HB3	8:H:7:PRO:HD3	1.78	0.64
8:H:36:LEU:HD22	8:H:67:HIS:CE1	2.33	0.64
8:H:59:ARG:HD2	8:H:62:GLU:CA	2.13	0.64
1:A:144:C:H2'	1:A:145:U:H5'	1.78	0.64
5:E:2171:G:H8	7:G:102:LYS:NZ	1.90	0.64
8:H:76:GLU:O	8:H:77:GLU:HG3	1.98	0.64
1:A:133:G:H2'	1:A:134:G:C8	2.33	0.63
7:G:49:PHE:HD2	7:G:193:LEU:HD22	1.63	0.63
8:H:141:LYS:HA	8:H:144:LYS:CE	2.24	0.63
7:G:8:GLN:HE21	7:G:216:LEU:CD1	2.10	0.63
8:H:31:ARG:NE	8:H:34:LYS:HE2	2.13	0.63
1:A:72:A:H2'	1:A:73:U:H5'	1.79	0.63
7:G:4:ILE:HG23	7:G:5:THR:N	2.11	0.63
3:C:1053:G:C3'	3:C:1054:C:H5'	2.27	0.63
1:A:90:G:C2'	1:A:91:C:H5'	2.29	0.63
7:G:34:LEU:CD1	7:G:36:VAL:HG23	2.28	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:192:C:N3	2:B:533:A:O4'	2.31	0.63
1:A:186:U:H2'	1:A:187:A:C8	2.34	0.63
1:A:59:G:H5''	1:A:60:U:C5	2.33	0.63
1:A:119:C:O2'	1:A:120:C:H2'	1.98	0.63
1:A:162:G:O4'	2:B:530:G:C6	2.52	0.63
1:A:60:U:C2'	1:A:61:G:H5''	2.12	0.63
1:A:102:A:N6	1:A:132:A:C2	2.66	0.63
7:G:11:GLU:O	7:G:15:GLU:HG3	1.98	0.63
7:G:57:ASN:O	7:G:174:MET:HE3	1.99	0.63
1:A:176:C:C5'	1:A:177:U:H5'	2.27	0.63
6:F:161:VAL:HG23	6:F:165:ARG:HD2	1.81	0.63
8:H:11:LEU:HD21	8:H:153:THR:HG23	1.81	0.63
1:A:189:C:O2'	4:D:1196:U:C4	2.23	0.63
1:A:55:A:H2'	1:A:56:G:H8	1.62	0.63
8:H:71:ARG:CZ	8:H:75:ALA:H	2.12	0.63
5:E:2172:G:C3'	7:G:98:LYS:CG	2.74	0.62
7:G:94:ASN:HB3	7:G:123:LEU:HD12	1.79	0.62
1:A:46:U:H2'	1:A:47:A:C4'	2.28	0.62
1:A:189:C:C5'	4:D:1196:U:H3'	2.29	0.62
7:G:5:THR:CG2	7:G:8:GLN:HG3	2.29	0.62
8:H:16:LEU:H	8:H:70:VAL:CG1	2.09	0.62
8:H:83:LEU:HD11	8:H:90:LEU:CD1	2.28	0.62
7:G:60:ARG:HG2	7:G:171:ASN:CB	2.29	0.62
7:G:179:LEU:CD1	7:G:183:ILE:HD11	2.28	0.62
7:G:183:ILE:O	7:G:187:VAL:HG23	1.99	0.62
2:B:528:C:H5'	2:B:535:A:C6	2.34	0.62
1:A:72:A:C2'	1:A:73:U:H5'	2.29	0.62
7:G:55:LEU:N	7:G:55:LEU:HD12	2.14	0.62
5:E:2172:G:H3'	7:G:98:LYS:CB	2.30	0.62
1:A:57:U:H2'	1:A:58:A:H8	1.64	0.62
1:A:59:G:C8	1:A:60:U:C5	2.88	0.62
1:A:103:G:H2'	1:A:104:G:H8	1.62	0.62
8:H:140:ARG:HA	8:H:140:ARG:NE	2.12	0.62
1:A:147:C:H2'	1:A:147:C:O2	1.99	0.62
6:F:84:ALA:HB3	6:F:89:ILE:CG1	2.28	0.62
5:E:2175:A:O2'	7:G:130:LYS:HD2	1.97	0.62
1:A:81:A:HO2'	1:A:94:U:H1'	1.64	0.62
1:A:90:G:H5'	6:F:211:LYS:HZ1	1.64	0.62
7:G:66:CYS:HA	7:G:83:ASP:OD1	2.00	0.62
8:H:83:LEU:CD1	8:H:166:TYR:HE1	2.13	0.62
6:F:112:ILE:HD11	6:F:193:LEU:HD13	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:110:U:C3'	1:A:111:A:H5''	2.29	0.62
7:G:5:THR:HG22	7:G:8:GLN:CG	2.30	0.62
7:G:60:ARG:HD3	7:G:61:PRO:CD	2.30	0.62
1:A:10:G:H1	7:G:122:ARG:CZ	2.12	0.62
7:G:195:LYS:C	7:G:195:LYS:HD2	2.20	0.62
1:A:133:G:H2'	1:A:134:G:H8	1.64	0.61
6:F:122:VAL:HG23	6:F:123:LEU:CD1	2.13	0.61
6:F:159:VAL:HG22	6:F:160:ASP:N	2.15	0.61
8:H:87:GLU:HB3	8:H:90:LEU:CA	2.30	0.61
8:H:132:ARG:N	8:H:133:PRO:HD3	2.14	0.61
1:A:143:U:H2'	1:A:144:C:H6	1.64	0.61
7:G:120:VAL:HG22	7:G:121:PRO:CD	2.31	0.61
8:H:32:ALA:N	8:H:34:LYS:HD2	2.16	0.61
1:A:80:U:N3	1:A:105:A:N7	2.49	0.61
7:G:23:THR:HG23	7:G:25:LYS:N	2.15	0.61
1:A:59:G:C8	1:A:60:U:C4	2.88	0.61
7:G:204:LEU:N	7:G:204:LEU:HD22	2.14	0.61
6:F:122:VAL:HG23	6:F:123:LEU:N	2.15	0.61
1:A:153:U:H2'	1:A:154:U:C6	2.35	0.61
1:A:15:C:OP2	7:G:122:ARG:NH2	2.33	0.61
1:A:95:A:C4	1:A:132:A:N6	2.69	0.61
1:A:92:U:C2'	1:A:93:U:H5'	2.31	0.61
1:A:10:G:H22	7:G:122:ARG:HH11	1.46	0.61
8:H:13:ILE:HD11	8:H:75:ALA:O	1.99	0.61
1:A:125:A:N6	1:A:126:A:N1	2.49	0.61
6:F:107:LEU:H	6:F:107:LEU:CD2	2.14	0.61
5:E:2166:G:C5	5:E:2167:C:C5	2.88	0.61
7:G:149:THR:C	7:G:153:SER:N	2.52	0.61
7:G:96:ASN:OD1	7:G:99:LEU:HD23	2.01	0.61
8:H:83:LEU:HD11	8:H:90:LEU:HD11	1.82	0.61
1:A:193:U:OP1	2:B:535:A:C5	2.53	0.61
1:A:190:U:C4	3:C:1054:C:C4	2.88	0.61
8:H:96:SER:HB2	8:H:101:PHE:CE2	2.35	0.61
6:F:215:GLU:O	6:F:219:VAL:HG23	2.01	0.61
1:A:192:C:C2	2:B:529:G:H5''	2.36	0.61
6:F:165:ARG:HA	6:F:168:ASN:OD1	2.00	0.61
8:H:82:GLY:O	8:H:85:VAL:HG13	2.01	0.61
1:A:161:A:N3	2:B:530:G:N7	2.49	0.60
1:A:10:G:H22	7:G:122:ARG:CZ	2.13	0.60
8:H:16:LEU:HD13	8:H:16:LEU:N	2.15	0.60
6:F:138:ASN:CG	6:F:202:LYS:HB2	2.21	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:85:GLN:O	6:F:89:ILE:HA	2.00	0.60
1:A:87:U:N3	6:F:218:ARG:NE	2.36	0.60
7:G:124:LEU:HD12	7:G:124:LEU:N	2.16	0.60
1:A:103:G:C2'	1:A:104:G:C8	2.82	0.60
1:A:144:C:H2'	1:A:145:U:C5'	2.31	0.60
7:G:85:MET:SD	7:G:93:LEU:HD12	2.41	0.60
8:H:166:TYR:CE1	8:H:167:ASP:HB2	2.36	0.60
7:G:56:PRO:CG	7:G:185:MET:HG3	2.32	0.60
7:G:36:VAL:CG1	7:G:204:LEU:HD13	2.29	0.60
1:A:48:A:O3'	1:A:131:C:H4'	2.02	0.60
1:A:192:C:H4'	2:B:528:C:C5'	2.31	0.60
6:F:113:ILE:O	6:F:117:LEU:HD13	2.01	0.60
7:G:67:ILE:HG21	7:G:77:ALA:HB1	1.83	0.60
8:H:53:VAL:HB	8:H:56:PHE:CB	2.22	0.60
1:A:70:G:H21	1:A:73:U:H6	1.48	0.60
1:A:135:A:H2'	1:A:136:A:H8	1.67	0.60
7:G:12:HIS:ND1	7:G:206:VAL:HG13	2.16	0.60
8:H:89:GLN:O	8:H:89:GLN:HG2	2.02	0.60
7:G:70:ASP:C	7:G:74:VAL:HG23	2.21	0.60
1:A:188:C:C2'	1:A:189:C:H5'	2.32	0.60
1:A:188:C:H2'	1:A:189:C:O4'	2.02	0.60
1:A:189:C:C2	3:C:1054:C:N3	2.70	0.60
1:A:55:A:H2'	1:A:56:G:C8	2.35	0.60
1:A:12:G:C5	1:A:61:G:N2	2.70	0.60
6:F:109:ALA:O	6:F:113:ILE:HD13	2.01	0.60
1:A:128:A:H2'	1:A:129:U:H5	1.64	0.60
1:A:45:A:C5	1:A:46:U:C4	2.90	0.60
1:A:75:U:N3	1:A:111:A:N6	2.50	0.60
8:H:132:ARG:HB2	8:H:133:PRO:CB	2.32	0.60
8:H:132:ARG:HB2	8:H:133:PRO:HB3	1.84	0.60
6:F:83:LYS:H	6:F:83:LYS:CD	2.14	0.60
2:B:501:C:H2'	2:B:502:G:C8	2.33	0.60
1:A:62:C:C2	1:A:63:U:C5	2.89	0.59
1:A:15:C:OP2	7:G:122:ARG:CZ	2.50	0.59
8:H:165:LYS:HG2	8:H:166:TYR:HD2	1.62	0.59
1:A:164:U:H2'	1:A:165:A:O4'	2.01	0.59
7:G:100:ILE:HG21	7:G:127:GLN:HG3	1.83	0.59
1:A:62:C:H2'	1:A:63:U:C5	2.37	0.59
1:A:75:U:H3	1:A:111:A:N6	1.99	0.59
8:H:82:GLY:O	8:H:85:VAL:HG22	2.02	0.59
6:F:91:ARG:HG3	6:F:92:LEU:HD12	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:46:GLN:CD	8:H:66:VAL:HB	2.22	0.59
8:H:16:LEU:CD2	8:H:75:ALA:HB1	2.32	0.59
1:A:172:A:H1'	1:A:182:A:N1	2.18	0.59
7:G:151:VAL:CA	7:G:154:THR:HG23	2.24	0.59
7:G:179:LEU:HD13	7:G:183:ILE:HG13	1.84	0.59
7:G:120:VAL:CG1	7:G:121:PRO:HD2	2.18	0.59
1:A:90:G:H5''	6:F:211:LYS:NZ	2.16	0.59
7:G:36:VAL:HG22	7:G:204:LEU:CD1	2.32	0.59
1:A:72:A:O2'	1:A:73:U:H5'	2.02	0.59
7:G:77:ALA:HB1	7:G:82:VAL:HG23	1.83	0.59
8:H:84:LYS:O	8:H:84:LYS:HG3	2.01	0.59
8:H:152:LYS:H	8:H:152:LYS:HD3	1.67	0.59
8:H:69:THR:HG23	8:H:70:VAL:N	2.17	0.59
8:H:41:GLY:HA3	8:H:74:LYS:NZ	2.16	0.59
1:A:128:A:C2'	1:A:129:U:C6	2.84	0.59
1:A:40:G:C2'	1:A:41:G:H5'	2.33	0.59
1:A:8:A:N3	1:A:8:A:H2'	2.18	0.59
8:H:146:THR:HG22	8:H:147:VAL:N	2.18	0.59
6:F:132:VAL:HG23	6:F:133:VAL:N	2.17	0.59
8:H:36:LEU:HD22	8:H:67:HIS:NE2	2.17	0.59
7:G:165:LEU:HD12	7:G:165:LEU:O	2.01	0.59
6:F:202:LYS:CA	6:F:205:SER:HB3	2.24	0.59
6:F:170:ALA:O	6:F:174:LEU:HD23	2.03	0.59
5:E:2172:G:H3'	7:G:98:LYS:HB2	1.85	0.59
1:A:64:A:H2'	1:A:64:A:N3	2.17	0.59
8:H:59:ARG:HB3	8:H:59:ARG:CZ	2.32	0.59
6:F:83:LYS:HE2	6:F:94:ASN:OD1	2.03	0.59
7:G:24:LYS:HD2	7:G:25:LYS:CB	2.33	0.59
1:A:85:A:H2'	1:A:87:U:OP2	2.03	0.59
3:C:1054:C:OP1	4:D:1197:G:OP1	2.21	0.59
1:A:76:A:C6	1:A:77:G:C6	2.91	0.59
8:H:8:MET:HG3	8:H:9:ARG:NE	2.18	0.59
7:G:155:ILE:HG21	7:G:167:VAL:CG1	2.30	0.59
6:F:91:ARG:CG	6:F:92:LEU:HD12	2.32	0.59
3:C:1053:G:C4'	3:C:1054:C:H5'	2.33	0.59
1:A:9:U:O2'	1:A:10:G:H5'	2.01	0.59
1:A:61:G:C2	1:A:62:C:N4	2.71	0.59
1:A:10:G:C2'	7:G:118:LYS:HD3	2.33	0.59
1:A:81:A:C1'	1:A:94:U:H1'	2.32	0.59
1:A:70:G:N2	1:A:72:A:H3'	2.18	0.59
1:A:76:A:C5	1:A:77:G:N7	2.71	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:11:LEU:CD2	8:H:153:THR:HG23	2.33	0.59
1:A:189:C:N4	3:C:1054:C:H41	1.98	0.58
8:H:68:VAL:HG12	8:H:69:THR:N	2.15	0.58
4:D:1195:C:H3'	4:D:1196:U:C5'	2.33	0.58
1:A:15:C:H1'	1:A:60:U:H4'	1.85	0.58
1:A:172:A:H2'	1:A:173:A:C8	2.38	0.58
1:A:182:A:C2'	1:A:183:A:H8	2.16	0.58
8:H:15:LYS:HB2	8:H:15:LYS:NZ	2.17	0.58
8:H:75:ALA:HB2	8:H:78:ILE:HD11	1.84	0.58
1:A:130:C:N4	1:A:131:C:N4	2.51	0.58
8:H:140:ARG:O	8:H:144:LYS:HD3	2.03	0.58
8:H:114:LYS:HD2	8:H:115:TYR:N	2.11	0.58
8:H:51:TYR:CE1	8:H:58:ILE:HB	2.38	0.58
8:H:109:ILE:HG22	8:H:110:ASP:N	2.18	0.58
8:H:163:LYS:HD2	8:H:169:ASP:N	2.18	0.58
8:H:61:ASN:H	8:H:61:ASN:HD22	1.52	0.58
7:G:97:LYS:HA	7:G:100:ILE:HG22	1.85	0.58
7:G:68:PHE:HE2	7:G:116:LEU:HB3	1.68	0.58
6:F:129:ILE:O	6:F:132:VAL:HG22	2.02	0.58
1:A:112:G:C4	1:A:113:U:C5	2.92	0.58
6:F:210:ILE:N	6:F:210:ILE:HD12	2.18	0.58
7:G:32:VAL:HG11	7:G:179:LEU:HD23	1.85	0.58
7:G:121:PRO:CD	7:G:134:PHE:HE1	2.17	0.58
7:G:68:PHE:CZ	7:G:90:LEU:HD12	2.38	0.58
7:G:6:SER:O	7:G:10:ARG:HG3	2.03	0.58
8:H:140:ARG:C	8:H:142:ARG:HD2	2.24	0.58
1:A:71:U:C4	1:A:72:A:C4	2.92	0.58
6:F:107:LEU:HD23	6:F:107:LEU:N	2.19	0.58
7:G:123:LEU:HD22	7:G:123:LEU:N	2.18	0.58
8:H:91:ARG:HD3	8:H:159:VAL:HG21	1.85	0.58
1:A:107:G:O2'	1:A:108:C:H5'	2.03	0.58
1:A:95:A:C8	1:A:132:A:N6	2.71	0.58
1:A:43:U:C4	1:A:44:A:C5	2.92	0.58
1:A:81:A:C2	1:A:82:G:C5	2.92	0.58
7:G:29:LEU:HB3	7:G:172:VAL:HG12	1.85	0.58
6:F:89:ILE:O	6:F:89:ILE:HG23	2.04	0.58
7:G:67:ILE:CD1	7:G:77:ALA:HB2	2.33	0.58
7:G:16:LEU:HD11	7:G:207:LYS:HA	1.85	0.58
1:A:41:G:HO2'	1:A:43:U:H4'	1.68	0.58
1:A:192:C:O3'	2:B:528:C:H4'	2.04	0.58
8:H:136:ARG:CZ	8:H:137:VAL:HA	2.33	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:84:U:H2'	1:A:85:A:H5'	1.85	0.58
1:A:12:G:C5	1:A:61:G:C2	2.92	0.58
1:A:106:U:C4	1:A:107:G:C5	2.92	0.58
1:A:45:A:C8	1:A:46:U:C5	2.92	0.58
1:A:112:G:C2'	1:A:113:U:C6	2.82	0.58
7:G:67:ILE:CD1	7:G:144:LEU:HD21	2.34	0.58
1:A:36:G:H2'	1:A:37:A:C8	2.38	0.58
1:A:189:C:C4	3:C:1054:C:N3	2.67	0.57
7:G:151:VAL:HA	7:G:154:THR:OG1	2.04	0.57
7:G:34:LEU:HD11	7:G:36:VAL:CG2	2.34	0.57
1:A:181:A:C2'	1:A:182:A:C8	2.86	0.57
6:F:157:GLN:HA	6:F:157:GLN:HE21	1.68	0.57
8:H:39:LEU:HD23	8:H:40:SER:N	2.18	0.57
8:H:44:PRO:HB2	8:H:67:HIS:HB2	1.86	0.57
6:F:112:ILE:HD11	6:F:189:ILE:HB	1.86	0.57
1:A:125:A:C8	1:A:126:A:N7	2.72	0.57
8:H:28:ARG:HG3	8:H:29:LEU:N	2.18	0.57
7:G:48:ARG:HA	7:G:159:LEU:HD23	1.85	0.57
7:G:36:VAL:HG13	7:G:204:LEU:CD1	2.32	0.57
1:A:144:C:H2'	1:A:145:U:C4'	2.34	0.57
7:G:67:ILE:HG21	7:G:77:ALA:HB2	1.84	0.57
8:H:119:ILE:C	8:H:119:ILE:HD13	2.25	0.57
1:A:94:U:O5'	1:A:94:U:C6	2.57	0.57
8:H:48:LYS:HG2	8:H:49:ALA:N	2.19	0.57
8:H:166:TYR:CD1	8:H:167:ASP:HB2	2.39	0.57
8:H:59:ARG:HD2	8:H:61:ASN:O	2.04	0.57
1:A:30:A:C4	1:A:31:A:C8	2.92	0.57
8:H:113:ILE:O	8:H:113:ILE:HG13	2.02	0.57
1:A:103:G:N3	1:A:104:G:N7	2.53	0.57
8:H:132:ARG:HH21	8:H:133:PRO:HG3	1.70	0.57
7:G:106:LYS:HG2	7:G:107:TYR:CE1	2.40	0.57
7:G:60:ARG:HB3	7:G:171:ASN:HB2	1.81	0.57
8:H:91:ARG:HG2	8:H:163:LYS:HE2	1.87	0.57
7:G:32:VAL:CG1	7:G:179:LEU:HD21	2.33	0.57
1:A:61:G:H2'	1:A:62:C:C5	2.40	0.57
1:A:15:C:N4	1:A:64:A:N6	2.52	0.57
1:A:125:A:C5	1:A:126:A:C5	2.93	0.57
1:A:144:C:C2'	1:A:145:U:H5'	2.35	0.57
1:A:143:U:H2'	1:A:144:C:C6	2.39	0.57
7:G:99:LEU:N	7:G:99:LEU:HD22	2.20	0.57
7:G:116:LEU:O	7:G:120:VAL:HG12	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:14:GLU:HG2	8:H:129:VAL:HG13	1.87	0.57
8:H:16:LEU:O	8:H:70:VAL:HG13	2.05	0.57
1:A:48:A:N6	1:A:49:A:C2	2.73	0.57
7:G:9:VAL:CG2	7:G:180:VAL:HG13	2.31	0.57
2:B:538:G:H2'	2:B:539:A:C8	2.40	0.57
8:H:84:LYS:HD3	8:H:167:ASP:OD1	2.05	0.57
1:A:81:A:C2'	1:A:94:U:H1'	2.35	0.57
1:A:139:C:C2'	1:A:140:C:H5'	2.35	0.57
1:A:107:G:N2	1:A:128:A:N6	2.53	0.56
1:A:190:U:OP2	3:C:1054:C:H1'	2.04	0.56
8:H:31:ARG:HE	8:H:34:LYS:CE	2.16	0.56
8:H:44:PRO:C	8:H:67:HIS:HB3	2.26	0.56
1:A:81:A:C2	1:A:93:U:O2'	2.52	0.56
6:F:112:ILE:HG23	6:F:113:ILE:N	2.20	0.56
6:F:202:LYS:H	6:F:204:SER:C	2.09	0.56
2:B:538:G:H2'	2:B:539:A:H8	1.70	0.56
5:E:2155:U:C5'	7:G:158:GLN:OE1	2.53	0.56
7:G:159:LEU:O	7:G:160:LYS:HB2	2.06	0.56
8:H:68:VAL:CG1	8:H:69:THR:H	2.17	0.56
1:A:103:G:C2'	1:A:104:G:H8	2.18	0.56
7:G:49:PHE:CE1	7:G:51:GLY:HA3	2.41	0.56
7:G:114:GLU:HG3	7:G:138:VAL:C	2.25	0.56
1:A:72:A:H2'	1:A:73:U:C5'	2.35	0.56
1:A:125:A:N7	1:A:126:A:C5	2.74	0.56
6:F:167:VAL:HG23	6:F:168:ASN:N	2.20	0.56
7:G:16:LEU:HD11	7:G:208:SER:N	2.17	0.56
7:G:24:LYS:NZ	7:G:25:LYS:HB3	2.21	0.56
1:A:65:U:H2'	1:A:66:U:H6	1.68	0.56
7:G:215:ARG:NH1	7:G:215:ARG:HB3	2.21	0.56
8:H:30:THR:HG23	8:H:30:THR:O	2.05	0.56
8:H:54:ARG:HG3	8:H:55:THR:N	2.20	0.56
1:A:95:A:N9	1:A:132:A:N6	2.53	0.56
1:A:125:A:C5	1:A:126:A:C6	2.94	0.56
1:A:158:A:H2'	1:A:158:A:N3	2.19	0.56
8:H:44:PRO:HG2	8:H:68:VAL:N	2.19	0.56
1:A:69:U:H2'	1:A:70:G:C8	2.40	0.56
8:H:133:PRO:HD2	8:H:135:ALA:CB	2.33	0.56
7:G:194:LEU:HG	7:G:196:LYS:H	1.71	0.56
7:G:97:LYS:O	7:G:101:LYS:HG3	2.06	0.56
8:H:71:ARG:NH1	8:H:71:ARG:H	2.03	0.56
8:H:91:ARG:HD2	8:H:91:ARG:C	2.26	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:23:GLY:H	8:H:64:ILE:CD1	2.19	0.56
1:A:182:A:C2	1:A:183:A:N7	2.72	0.56
7:G:123:LEU:HB2	7:G:124:LEU:HD12	1.87	0.56
8:H:14:GLU:HG2	8:H:129:VAL:CG1	2.35	0.56
7:G:205:VAL:HG13	7:G:214:PHE:C	2.25	0.56
7:G:7:SER:HA	7:G:10:ARG:NE	2.20	0.56
7:G:201:VAL:HG23	7:G:201:VAL:O	2.06	0.56
1:A:58:A:N7	1:A:59:G:C8	2.73	0.56
1:A:70:G:N2	1:A:73:U:C5	2.73	0.56
8:H:20:ILE:HG23	8:H:21:SER:O	2.04	0.56
1:A:26:A:N6	1:A:49:A:C2	2.72	0.56
7:G:52:SER:O	7:G:53:LEU:HD23	2.06	0.56
7:G:159:LEU:HG	7:G:162:VAL:O	2.06	0.56
7:G:54:LYS:CE	7:G:153:SER:HB2	2.36	0.56
8:H:67:HIS:C	8:H:68:VAL:HG23	2.25	0.56
1:A:43:U:C4	1:A:44:A:C6	2.94	0.56
8:H:48:LYS:HG2	8:H:49:ALA:O	2.06	0.56
7:G:67:ILE:HG22	7:G:83:ASP:O	2.06	0.56
1:A:35:U:H2'	1:A:35:U:O2	2.06	0.56
8:H:33:SER:HA	8:H:36:LEU:HD21	1.85	0.55
7:G:205:VAL:HG12	7:G:206:VAL:N	2.20	0.55
1:A:119:C:H2'	1:A:121:C:C6	2.41	0.55
8:H:121:ILE:O	8:H:121:ILE:HG23	2.06	0.55
7:G:49:PHE:CD1	7:G:157:PHE:CD1	2.94	0.55
1:A:177:U:O2'	1:A:178:A:C8	2.60	0.55
1:A:183:A:C5	1:A:184:U:C5	2.94	0.55
7:G:75:ASP:HA	7:G:78:LYS:HE3	1.88	0.55
7:G:98:LYS:O	7:G:102:LYS:HD3	2.06	0.55
7:G:90:LEU:HG	7:G:124:LEU:CD1	2.33	0.55
1:A:89:A:O3'	6:F:211:LYS:HE3	2.06	0.55
1:A:77:G:C2'	1:A:78:G:H5'	2.36	0.55
8:H:44:PRO:CG	8:H:68:VAL:H	2.19	0.55
6:F:122:VAL:HG23	6:F:123:LEU:H	1.72	0.55
8:H:140:ARG:NH1	8:H:140:ARG:HA	2.21	0.55
1:A:181:A:C2'	1:A:182:A:H8	2.19	0.55
7:G:151:VAL:O	7:G:154:THR:O	2.24	0.55
6:F:186:ILE:HG22	6:F:188:THR:O	2.06	0.55
5:E:2153:G:H21	7:G:161:LYS:CD	2.19	0.55
5:E:2156:G:H5'	7:G:158:GLN:HB3	1.89	0.55
7:G:85:MET:HG2	7:G:89:ASP:OD1	2.07	0.55
1:A:89:A:O3'	6:F:211:LYS:CE	2.54	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:77:G:N2	1:A:125:A:C2	2.75	0.55
8:H:91:ARG:CZ	8:H:159:VAL:HG21	2.36	0.55
7:G:165:LEU:C	7:G:165:LEU:HD12	2.27	0.55
7:G:49:PHE:CZ	7:G:51:GLY:HA3	2.41	0.55
1:A:74:U:C2'	1:A:75:U:H4'	2.37	0.55
5:E:2143:G:O2'	5:E:2153:G:H5'	2.06	0.55
8:H:59:ARG:HB3	8:H:59:ARG:HH11	1.69	0.55
7:G:34:LEU:HD13	7:G:35:GLN:N	2.21	0.55
5:E:2149:G:H4'	5:E:2150:A:OP1	2.05	0.55
5:E:2154:G:C2'	7:G:160:LYS:HB3	2.34	0.55
5:E:2173:U:C5	7:G:101:LYS:CE	2.90	0.55
8:H:103:PHE:H	8:H:122:PHE:HB2	1.72	0.55
7:G:167:VAL:HG12	7:G:168:ALA:N	2.21	0.55
8:H:159:VAL:O	8:H:159:VAL:HG13	2.07	0.55
8:H:44:PRO:HG2	8:H:68:VAL:CA	2.37	0.55
1:A:136:A:C2	1:A:137:G:H1'	2.42	0.55
1:A:43:U:H2'	1:A:44:A:H5'	1.88	0.55
8:H:57:GLY:HA3	8:H:59:ARG:HH12	1.72	0.55
8:H:64:ILE:HG23	8:H:64:ILE:O	2.06	0.55
1:A:109:C:O2	1:A:125:A:C2	2.60	0.55
6:F:198:ILE:HG23	6:F:199:ASN:N	2.22	0.55
4:D:1202:G:O2'	4:D:1203:C:H5'	2.07	0.55
1:A:58:A:C5	1:A:59:G:C8	2.94	0.54
1:A:58:A:C6	1:A:59:G:C1'	2.85	0.54
1:A:90:G:H5''	6:F:211:LYS:HZ3	1.73	0.54
7:G:49:PHE:HE2	7:G:193:LEU:HD11	1.72	0.54
6:F:116:THR:HG21	6:F:193:LEU:CB	2.37	0.54
5:E:2143:G:H4'	5:E:2144:C:OP2	2.07	0.54
8:H:130:MET:CE	8:H:162:PHE:HD2	2.20	0.54
1:A:48:A:O2'	1:A:131:C:H1'	2.07	0.54
5:E:2155:U:O2'	7:G:158:GLN:C	2.42	0.54
7:G:10:ARG:O	7:G:14:LYS:HG3	2.07	0.54
8:H:11:LEU:N	8:H:11:LEU:HD12	2.22	0.54
8:H:91:ARG:HB2	8:H:95:PHE:CZ	2.42	0.54
1:A:176:C:O5'	1:A:177:U:H5'	2.06	0.54
1:A:112:G:HO2'	1:A:113:U:H6	1.55	0.54
7:G:187:VAL:O	7:G:191:VAL:HG23	2.07	0.54
7:G:60:ARG:HG2	7:G:171:ASN:CA	2.37	0.54
8:H:159:VAL:HG22	8:H:159:VAL:O	2.07	0.54
8:H:95:PHE:HB3	8:H:101:PHE:N	2.23	0.54
1:A:192:C:H4'	2:B:528:C:C3'	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:148:G:H2'	1:A:149:G:O4'	2.07	0.54
6:F:159:VAL:HG22	6:F:160:ASP:H	1.73	0.54
5:E:2154:G:H2'	7:G:160:LYS:HD2	0.54	0.54
8:H:79:LEU:HD23	8:H:126:PHE:CE1	2.41	0.54
8:H:165:LYS:HD2	8:H:165:LYS:N	2.19	0.54
1:A:106:U:C4	1:A:107:G:C4	2.96	0.54
8:H:6:ASN:HB3	8:H:7:PRO:CD	2.37	0.54
7:G:130:LYS:HG3	7:G:131:ALA:N	2.23	0.54
1:A:59:G:N9	1:A:60:U:C5	2.76	0.54
8:H:18:LEU:HD12	8:H:19:ASN:N	2.23	0.54
8:H:75:ALA:HA	8:H:78:ILE:CD1	2.37	0.54
1:A:48:A:H1'	1:A:133:G:H4'	1.90	0.54
8:H:48:LYS:HB3	8:H:48:LYS:NZ	2.23	0.54
8:H:140:ARG:NH1	8:H:141:LYS:H	2.05	0.54
5:E:2165:A:H2'	5:E:2166:G:O4'	2.07	0.54
8:H:67:HIS:HD2	8:H:68:VAL:CG2	2.21	0.54
8:H:80:GLU:O	8:H:81:ARG:HB2	2.08	0.54
1:A:81:A:C2	1:A:82:G:C6	2.96	0.54
7:G:180:VAL:O	7:G:184:LEU:HG	2.07	0.54
1:A:125:A:N7	1:A:126:A:C6	2.75	0.54
8:H:8:MET:HG3	8:H:9:ARG:HE	1.73	0.54
2:B:502:G:H2'	2:B:503:C:H6	1.72	0.54
1:A:156:A:N6	1:A:185:U:H5	2.06	0.54
2:B:513:C:H2'	2:B:514:C:C6	2.43	0.54
1:A:62:C:C4	1:A:63:U:O4	2.60	0.54
1:A:43:U:O4	1:A:44:A:C6	2.61	0.54
5:E:2172:G:OP1	7:G:99:LEU:HD21	2.08	0.54
1:A:58:A:C5	1:A:59:G:C1'	2.90	0.54
1:A:9:U:H2'	1:A:10:G:H5'	1.87	0.54
8:H:78:ILE:HD12	8:H:78:ILE:C	2.27	0.54
1:A:136:A:H2'	1:A:137:G:O4'	2.07	0.54
1:A:75:U:C4	1:A:111:A:N6	2.75	0.54
6:F:107:LEU:HD21	6:F:108:LYS:NZ	2.23	0.54
6:F:139:THR:O	6:F:141:PRO:HD3	2.08	0.54
5:E:2155:U:H5''	7:G:158:GLN:OE1	2.08	0.53
5:E:2153:G:N2	7:G:162:VAL:CG2	2.52	0.53
6:F:169:GLN:O	6:F:173:LEU:HG	2.07	0.53
1:A:183:A:C2	1:A:184:U:C1'	2.91	0.53
7:G:216:LEU:HD13	7:G:216:LEU:C	2.28	0.53
1:A:49:A:H2'	1:A:50:U:C6	2.43	0.53
6:F:215:GLU:OE1	6:F:215:GLU:HA	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:110:VAL:HG23	6:F:111:ARG:N	2.23	0.53
6:F:124:THR:HG22	6:F:126:GLN:H	1.72	0.53
7:G:57:ASN:O	7:G:58:CYS:HB3	2.08	0.53
6:F:212:LYS:O	6:F:216:LEU:HD13	2.08	0.53
1:A:183:A:C4	1:A:184:U:C6	2.96	0.53
1:A:19:C:H2'	1:A:20:U:C6	2.44	0.53
7:G:117:ILE:HA	7:G:120:VAL:CG1	2.39	0.53
1:A:92:U:C2'	1:A:93:U:C5'	2.85	0.53
7:G:34:LEU:HD13	7:G:34:LEU:C	2.29	0.53
8:H:29:LEU:HD22	8:H:29:LEU:N	2.22	0.53
7:G:161:LYS:CD	7:G:161:LYS:H	2.22	0.53
1:A:63:U:O2	1:A:63:U:H2'	2.08	0.53
1:A:81:A:H1'	1:A:94:U:C6	2.42	0.53
7:G:157:PHE:CZ	7:G:165:LEU:HB3	2.44	0.53
6:F:186:ILE:HG21	6:F:190:ALA:CB	2.38	0.53
8:H:136:ARG:NE	8:H:137:VAL:HA	2.24	0.53
8:H:8:MET:CE	8:H:9:ARG:HE	2.22	0.53
1:A:119:C:C4	1:A:121:C:C2	2.97	0.53
7:G:54:LYS:HZ2	7:G:153:SER:CB	2.09	0.53
8:H:13:ILE:HD13	8:H:16:LEU:HD12	1.90	0.53
8:H:16:LEU:C	8:H:70:VAL:HG13	2.29	0.53
1:A:92:U:C2	1:A:93:U:O4'	2.62	0.53
1:A:144:C:C5	1:A:145:U:H1'	2.44	0.53
1:A:112:G:C2	1:A:113:U:C4	2.97	0.53
6:F:138:ASN:HD21	6:F:202:LYS:HD2	1.74	0.53
8:H:28:ARG:HG3	8:H:29:LEU:CD2	2.38	0.53
1:A:121:C:O2	1:A:121:C:H2'	2.09	0.53
1:A:18:G:C6	1:A:58:A:N6	2.77	0.53
8:H:95:PHE:HB3	8:H:101:PHE:CA	2.38	0.53
1:A:172:A:H1'	1:A:182:A:C2	2.44	0.53
2:B:539:A:H2'	2:B:540:G:C8	2.43	0.53
1:A:115:G:H2'	1:A:116:C:O4'	2.09	0.53
5:E:2154:G:H1'	7:G:161:LYS:HD3	1.88	0.53
7:G:45:ARG:C	7:G:47:LYS:H	2.11	0.53
7:G:90:LEU:HD11	7:G:120:VAL:N	2.24	0.53
1:A:27:U:H5''	1:A:28:A:O4'	2.08	0.53
1:A:189:C:N1	3:C:1054:C:N3	2.57	0.53
7:G:59:PRO:CD	7:G:152:ARG:C	2.78	0.53
5:E:2175:A:O2'	7:G:130:LYS:CG	2.57	0.53
7:G:90:LEU:C	7:G:90:LEU:HD23	2.29	0.53
8:H:14:GLU:CG	8:H:129:VAL:HG13	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:39:LEU:O	8:H:40:SER:HB2	2.09	0.53
1:A:151:U:H1'	1:A:179:A:O2'	2.09	0.53
1:A:31:A:H2'	1:A:31:A:N3	2.24	0.53
2:B:513:C:H2'	2:B:514:C:H6	1.72	0.53
7:G:42:ASP:OD2	7:G:45:ARG:HG2	2.09	0.52
1:A:130:C:C4	1:A:131:C:N4	2.77	0.52
1:A:7:A:C4	1:A:8:A:C8	2.97	0.52
1:A:63:U:C2	1:A:64:A:O4'	2.62	0.52
1:A:14:U:C4'	7:G:121:PRO:O	2.57	0.52
8:H:160:SER:O	8:H:161:TRP:HB2	2.09	0.52
8:H:44:PRO:O	8:H:67:HIS:HB3	2.09	0.52
8:H:70:VAL:C	8:H:71:ARG:HD3	2.28	0.52
8:H:70:VAL:O	8:H:71:ARG:HB3	2.09	0.52
2:B:528:C:H5'	2:B:535:A:N6	2.23	0.52
8:H:8:MET:CG	8:H:9:ARG:HE	2.23	0.52
7:G:67:ILE:HG23	7:G:67:ILE:O	2.09	0.52
7:G:102:LYS:HG3	7:G:105:LYS:CE	2.37	0.52
8:H:13:ILE:HD13	8:H:16:LEU:CD1	2.39	0.52
8:H:91:ARG:HD2	8:H:92:ASP:N	2.25	0.52
1:A:102:A:C2'	1:A:103:G:C4'	2.85	0.52
1:A:95:A:C5	1:A:132:A:C6	2.97	0.52
1:A:192:C:N3	2:B:533:A:C1'	2.72	0.52
7:G:24:LYS:HD2	7:G:25:LYS:HB3	1.91	0.52
7:G:24:LYS:NZ	7:G:25:LYS:HE2	2.24	0.52
8:H:153:THR:HG22	8:H:154:THR:N	2.24	0.52
8:H:97:ALA:O	8:H:98:THR:HB	2.09	0.52
1:A:159:U:H5''	1:A:160:U:C6	2.44	0.52
7:G:58:CYS:HA	7:G:153:SER:OG	2.09	0.52
8:H:166:TYR:HD1	8:H:167:ASP:OD2	1.92	0.52
8:H:71:ARG:NH2	8:H:72:GLY:HA2	2.25	0.52
1:A:150:U:O2	1:A:179:A:C2	2.62	0.52
3:C:1059:C:O2'	3:C:1060:C:H5'	2.09	0.52
7:G:179:LEU:HD13	7:G:179:LEU:C	2.29	0.52
7:G:68:PHE:CD1	7:G:85:MET:HE3	2.45	0.52
8:H:15:LYS:CB	8:H:70:VAL:HG21	2.40	0.52
1:A:44:A:C8	1:A:44:A:H3'	2.45	0.52
1:A:156:A:N1	1:A:185:U:H5	2.07	0.52
8:H:162:PHE:CD1	8:H:165:LYS:HD3	2.44	0.52
1:A:104:G:O2'	1:A:105:A:H5'	2.09	0.52
1:A:43:U:O2'	1:A:44:A:H5'	2.09	0.52
1:A:45:A:OP2	1:A:45:A:C8	2.63	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:76:A:C6	1:A:111:A:N6	2.77	0.52
1:A:59:G:C5'	1:A:60:U:H5	2.22	0.52
6:F:116:THR:HA	6:F:119:ILE:HD12	1.91	0.52
6:F:121:ASN:OD1	6:F:128:PRO:HD3	2.09	0.52
7:G:48:ARG:HD3	7:G:161:LYS:HA	1.91	0.52
3:C:1053:G:H4'	3:C:1054:C:H5'	1.92	0.52
1:A:190:U:P	3:C:1054:C:O2	2.68	0.52
1:A:44:A:H2'	1:A:45:A:O5'	2.10	0.52
1:A:12:G:O2'	7:G:117:ILE:C	2.48	0.52
8:H:155:LYS:N	8:H:155:LYS:HD2	2.24	0.52
1:A:92:U:O2'	1:A:93:U:H5'	2.09	0.52
7:G:36:VAL:CG2	7:G:204:LEU:HD12	2.38	0.52
1:A:70:G:N3	1:A:73:U:H5	2.08	0.52
1:A:162:G:H1'	2:B:530:G:O6	2.07	0.52
1:A:10:G:H2'	7:G:118:LYS:HD3	1.91	0.52
8:H:156:GLU:HG3	8:H:157:ASP:N	2.25	0.52
8:H:67:HIS:O	8:H:68:VAL:HG23	2.10	0.52
1:A:94:U:O2	1:A:94:U:H2'	2.10	0.52
1:A:76:A:HO2'	1:A:77:G:H5'	1.70	0.52
2:B:521:G:O2'	2:B:522:C:H5'	2.09	0.52
5:E:2153:G:N2	7:G:162:VAL:HG22	2.21	0.51
1:A:14:U:C2	1:A:15:C:C5	2.98	0.51
8:H:78:ILE:O	8:H:79:LEU:HB3	2.09	0.51
1:A:145:U:C5	1:A:177:U:OP2	2.63	0.51
8:H:162:PHE:HB3	8:H:166:TYR:HH	1.74	0.51
1:A:76:A:C5	1:A:77:G:C5	2.99	0.51
5:E:2155:U:C4'	7:G:158:GLN:HG2	2.23	0.51
8:H:96:SER:CB	8:H:101:PHE:CE2	2.93	0.51
1:A:46:U:O2	1:A:47:A:H1'	2.10	0.51
7:G:155:ILE:HG22	7:G:156:LYS:N	2.24	0.51
1:A:66:U:H2'	1:A:67:U:C6	2.46	0.51
7:G:117:ILE:HD12	7:G:117:ILE:C	2.31	0.51
2:B:538:G:O2'	2:B:539:A:H5'	2.10	0.51
8:H:34:LYS:CD	8:H:35:VAL:H	2.24	0.51
7:G:49:PHE:HD1	7:G:157:PHE:CD1	2.28	0.51
1:A:70:G:N2	1:A:73:U:C6	2.72	0.51
1:A:78:G:C2	1:A:79:U:C1'	2.93	0.51
1:A:176:C:H5''	1:A:177:U:H5'	1.91	0.51
6:F:79:LYS:HE3	6:F:164:LEU:CD1	2.41	0.51
5:E:2156:G:H5'	7:G:158:GLN:CB	2.40	0.51
8:H:16:LEU:O	8:H:70:VAL:HG22	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:94:ASN:O	8:H:101:PHE:HD2	1.93	0.51
1:A:103:G:C4	1:A:104:G:N7	2.79	0.51
1:A:88:U:H3	6:F:215:GLU:CD	2.14	0.51
1:A:90:G:H5'	6:F:211:LYS:NZ	2.21	0.51
7:G:8:GLN:NE2	7:G:216:LEU:HD11	2.24	0.51
1:A:189:C:N3	3:C:1054:C:C4	2.57	0.51
5:E:2172:G:OP1	7:G:99:LEU:CD2	2.58	0.51
1:A:12:G:O2'	7:G:117:ILE:CA	2.52	0.51
1:A:26:A:C2	1:A:27:U:C1'	2.90	0.51
6:F:185:ASN:HB2	6:F:191:GLU:HB2	1.92	0.51
8:H:107:GLU:HG2	8:H:108:HIS:N	2.25	0.51
1:A:13:A:N3	7:G:124:LEU:N	2.59	0.51
8:H:37:GLU:O	8:H:38:GLN:HB2	2.11	0.51
8:H:71:ARG:HH11	8:H:71:ARG:N	2.07	0.51
1:A:29:C:OP2	1:A:135:A:H5'	2.10	0.51
1:A:45:A:P	1:A:45:A:H8	2.34	0.51
1:A:72:A:C2'	1:A:73:U:C5'	2.89	0.51
8:H:132:ARG:HB2	8:H:133:PRO:CD	2.40	0.51
6:F:139:THR:CG2	6:F:174:LEU:HD21	2.28	0.51
8:H:150:SER:O	8:H:152:LYS:HD3	2.11	0.51
1:A:188:C:O2'	1:A:189:C:H5'	2.11	0.51
1:A:190:U:O2'	1:A:191:G:H5'	2.11	0.51
8:H:140:ARG:HB3	8:H:142:ARG:NE	2.26	0.51
7:G:196:LYS:O	7:G:197:ASN:HB2	2.10	0.51
7:G:21:ASN:O	7:G:22:GLU:HB2	2.11	0.51
7:G:119:GLN:O	7:G:123:LEU:HD23	2.10	0.50
8:H:48:LYS:HZ2	8:H:48:LYS:HB3	1.76	0.50
5:E:2159:A:HO2'	5:E:2160:G:P	2.34	0.50
5:E:2160:G:N1	5:E:2161:C:C4	2.79	0.50
8:H:28:ARG:HG3	8:H:29:LEU:HD23	1.93	0.50
1:A:16:U:H2'	1:A:16:U:O2	2.11	0.50
8:H:91:ARG:HG2	8:H:159:VAL:HG23	1.93	0.50
8:H:36:LEU:C	8:H:36:LEU:HD12	2.31	0.50
8:H:71:ARG:HH21	8:H:72:GLY:HA2	1.75	0.50
1:A:136:A:H2'	1:A:137:G:H5'	1.93	0.50
6:F:201:ALA:O	6:F:202:LYS:HB3	2.11	0.50
1:A:181:A:H2'	1:A:182:A:H8	1.65	0.50
6:F:84:ALA:HB3	6:F:89:ILE:HD11	1.89	0.50
8:H:95:PHE:CB	8:H:101:PHE:HB2	2.30	0.50
8:H:71:ARG:HD2	8:H:75:ALA:N	2.27	0.50
7:G:53:LEU:CD2	7:G:189:PHE:CD2	2.95	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:67:ILE:HD12	7:G:144:LEU:HD21	1.92	0.50
7:G:41:TYR:CE1	7:G:163:LEU:CD2	2.94	0.50
1:A:17:U:H2'	1:A:18:G:O5'	2.11	0.50
7:G:120:VAL:HG23	7:G:124:LEU:HB2	1.94	0.50
8:H:16:LEU:C	8:H:17:VAL:HG12	2.32	0.50
8:H:17:VAL:HB	8:H:69:THR:CA	2.31	0.50
8:H:132:ARG:NH2	8:H:133:PRO:HG3	2.26	0.50
7:G:91:LYS:HD3	7:G:91:LYS:N	2.26	0.50
1:A:13:A:N6	7:G:125:GLY:O	2.35	0.50
1:A:56:G:C6	1:A:57:U:C4	2.99	0.50
1:A:63:U:C5	1:A:64:A:C8	3.00	0.50
8:H:15:LYS:HB2	8:H:15:LYS:HZ2	1.76	0.50
1:A:125:A:N6	1:A:126:A:C6	2.80	0.50
8:H:137:VAL:HG12	8:H:144:LYS:O	2.11	0.50
7:G:67:ILE:HD11	7:G:73:ASP:CG	2.32	0.50
7:G:91:LYS:H	7:G:91:LYS:HD3	1.76	0.50
1:A:161:A:O4'	2:B:530:G:C1'	2.54	0.50
7:G:100:ILE:HG23	7:G:101:LYS:N	2.26	0.50
8:H:9:ARG:HH22	8:H:133:PRO:CB	2.25	0.50
1:A:180:G:H3'	1:A:181:A:H8	1.77	0.50
7:G:16:LEU:HD21	7:G:208:SER:N	2.27	0.50
1:A:156:A:C2'	1:A:157:G:O5'	2.59	0.50
5:E:2172:G:OP2	7:G:99:LEU:HD13	2.12	0.50
6:F:213:LYS:HD3	6:F:213:LYS:C	2.32	0.50
7:G:134:PHE:CD1	7:G:135:PRO:HD2	2.46	0.50
8:H:14:GLU:CD	8:H:129:VAL:HG13	2.32	0.50
8:H:17:VAL:HG23	8:H:68:VAL:O	2.11	0.50
1:A:81:A:N3	1:A:94:U:O4'	2.45	0.50
7:G:157:PHE:CZ	7:G:165:LEU:CB	2.94	0.50
1:A:141:U:H2'	1:A:142:C:C6	2.46	0.50
1:A:183:A:C2	1:A:184:U:O4'	2.65	0.50
6:F:99:ASN:OD1	6:F:171:ILE:HG22	2.11	0.50
5:E:2173:U:O4	7:G:101:LYS:CD	2.55	0.50
7:G:53:LEU:CD2	7:G:189:PHE:CE2	2.95	0.50
7:G:150:ASP:CA	7:G:153:SER:CB	2.74	0.49
7:G:100:ILE:CG2	7:G:127:GLN:HG3	2.42	0.49
8:H:96:SER:HB3	8:H:101:PHE:CZ	2.47	0.49
8:H:48:LYS:HZ2	8:H:62:GLU:HG3	1.77	0.49
6:F:189:ILE:HG22	6:F:193:LEU:HD13	1.91	0.49
7:G:53:LEU:CD2	7:G:189:PHE:CG	2.95	0.49
3:C:1056:U:O2'	3:C:1057:G:H5'	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:70:ASP:O	7:G:74:VAL:HG23	2.11	0.49
4:D:1194:U:H2'	4:D:1195:C:C6	2.47	0.49
1:A:12:G:H2'	1:A:61:G:N1	2.27	0.49
8:H:165:LYS:HB3	8:H:165:LYS:HZ2	1.76	0.49
8:H:36:LEU:HD22	8:H:67:HIS:CG	2.46	0.49
8:H:76:GLU:C	8:H:77:GLU:HG3	2.33	0.49
1:A:95:A:N3	1:A:95:A:H2'	2.26	0.49
1:A:12:G:N7	1:A:61:G:N2	2.60	0.49
7:G:70:ASP:OD1	7:G:87:VAL:HB	2.12	0.49
7:G:161:LYS:HD3	7:G:161:LYS:N	2.26	0.49
7:G:147:LYS:O	7:G:151:VAL:HG22	2.12	0.49
8:H:130:MET:CE	8:H:162:PHE:CD2	2.95	0.49
2:B:522:C:O2'	2:B:523:A:H5'	2.12	0.49
1:A:189:C:H5''	4:D:1196:U:C3'	2.41	0.49
7:G:151:VAL:HA	7:G:154:THR:CA	2.41	0.49
8:H:17:VAL:HA	8:H:69:THR:O	2.12	0.49
2:B:518:C:O2'	2:B:519:C:OP2	2.24	0.49
7:G:85:MET:HG3	7:G:89:ASP:OD2	2.12	0.49
1:A:49:A:H2'	1:A:50:U:C5	2.47	0.49
1:A:88:U:H2'	1:A:89:A:C5'	2.33	0.49
6:F:219:VAL:O	6:F:222:SER:HB2	2.13	0.49
1:A:70:G:H2'	1:A:72:A:N7	2.28	0.49
5:E:2177:A:H4'	5:E:2178:U:OP1	2.12	0.49
7:G:68:PHE:CD1	7:G:85:MET:CE	2.95	0.49
1:A:40:G:O2'	1:A:41:G:H5'	2.12	0.49
1:A:125:A:C6	1:A:126:A:C6	3.00	0.49
1:A:173:A:O2'	1:A:181:A:C2	2.60	0.49
1:A:189:C:N4	3:C:1054:C:C4	2.72	0.49
7:G:41:TYR:OH	7:G:159:LEU:HD21	2.13	0.49
1:A:190:U:O4	3:C:1054:C:C4	2.65	0.49
7:G:59:PRO:HD2	7:G:152:ARG:C	2.33	0.49
8:H:10:ASP:HB3	8:H:161:TRP:CH2	2.48	0.49
1:A:132:A:C2'	1:A:133:G:C8	2.96	0.49
1:A:136:A:N6	1:A:137:G:C2	2.81	0.49
1:A:29:C:OP1	1:A:135:A:H5'	2.13	0.49
1:A:44:A:P	1:A:45:A:OP2	2.71	0.49
8:H:23:GLY:O	8:H:64:ILE:HD12	2.13	0.49
1:A:72:A:O2'	1:A:73:U:C5'	2.61	0.49
8:H:132:ARG:HG3	8:H:132:ARG:NH1	2.27	0.49
1:A:147:C:OP2	1:A:148:G:C4	2.65	0.49
7:G:53:LEU:HD22	7:G:189:PHE:CD2	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:1202:G:H2'	4:D:1203:C:O4'	2.12	0.49
6:F:136:ILE:HG23	6:F:137:THR:N	2.28	0.49
1:A:81:A:C6	1:A:93:U:O2	2.65	0.49
6:F:88:ILE:O	6:F:88:ILE:HG23	2.13	0.49
7:G:5:THR:HG22	7:G:8:GLN:HG3	1.94	0.49
1:A:189:C:C2'	3:C:1054:C:O2	2.61	0.48
8:H:62:GLU:HB3	8:H:64:ILE:HG22	1.94	0.48
7:G:87:VAL:HG13	7:G:88:ASP:N	2.27	0.48
1:A:12:G:C4	1:A:61:G:C2	3.01	0.48
8:H:44:PRO:HB2	8:H:67:HIS:CA	2.42	0.48
8:H:74:LYS:O	8:H:78:ILE:HG13	2.13	0.48
1:A:42:U:H4'	1:A:138:C:C5	2.47	0.48
1:A:88:U:N3	6:F:215:GLU:OE1	2.29	0.48
3:C:1051:C:H2'	3:C:1052:U:H6	1.79	0.48
6:F:102:ASN:N	6:F:102:ASN:HD22	2.10	0.48
8:H:121:ILE:HG13	8:H:125:ASP:H	1.78	0.48
6:F:166:ARG:HD2	6:F:167:VAL:HG13	1.94	0.48
7:G:194:LEU:HG	7:G:195:LYS:N	2.28	0.48
1:A:10:G:C6	1:A:14:U:OP1	2.67	0.48
1:A:136:A:O2'	1:A:137:G:H5'	2.12	0.48
1:A:193:U:OP1	2:B:535:A:C6	2.66	0.48
7:G:29:LEU:CD2	7:G:172:VAL:HG11	2.29	0.48
5:E:2186:U:H2'	5:E:2187:U:C6	2.47	0.48
4:D:1194:U:O2'	4:D:1195:C:H5'	2.13	0.48
1:A:15:C:O2	1:A:60:U:H4'	2.13	0.48
7:G:69:GLY:HA2	7:G:116:LEU:CD1	2.44	0.48
8:H:16:LEU:N	8:H:70:VAL:HG21	2.28	0.48
1:A:28:A:H2'	1:A:29:C:O4'	2.14	0.48
1:A:76:A:C2'	1:A:77:G:H5'	2.43	0.48
2:B:501:C:O2'	2:B:502:G:H5'	2.14	0.48
7:G:60:ARG:HD3	7:G:61:PRO:HG3	1.95	0.48
8:H:91:ARG:NE	8:H:169:ASP:HB2	2.17	0.48
8:H:16:LEU:HD11	8:H:75:ALA:HB3	1.95	0.48
8:H:31:ARG:C	8:H:33:SER:H	2.16	0.48
1:A:103:G:C6	1:A:104:G:O6	2.66	0.48
1:A:107:G:C2	1:A:128:A:N6	2.81	0.48
1:A:125:A:H2'	1:A:126:A:C8	2.49	0.48
7:G:190:PHE:CZ	7:G:200:ASN:CB	2.95	0.48
1:A:182:A:N3	1:A:183:A:N7	2.61	0.48
6:F:210:ILE:H	6:F:210:ILE:HD12	1.78	0.48
3:C:1051:C:O2'	3:C:1052:U:H5'	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:81:A:H1'	1:A:94:U:C2	2.48	0.48
1:A:94:U:O2'	1:A:95:A:C8	2.61	0.48
8:H:114:LYS:CD	8:H:115:TYR:H	2.16	0.48
7:G:66:CYS:SG	7:G:107:TYR:CG	3.06	0.48
2:B:502:G:H2'	2:B:503:C:C6	2.49	0.48
1:A:115:G:O2'	1:A:116:C:H5'	2.13	0.48
1:A:189:C:C6	3:C:1054:C:C2	3.02	0.48
7:G:151:VAL:CA	7:G:154:THR:OG1	2.61	0.48
1:A:59:G:C4	1:A:60:U:C6	3.02	0.48
8:H:95:PHE:CA	8:H:101:PHE:CD2	2.91	0.48
8:H:83:LEU:O	8:H:84:LYS:HB3	2.14	0.48
7:G:53:LEU:HD22	7:G:189:PHE:CG	2.48	0.48
1:A:168:C:C5	1:A:170:A:OP1	2.66	0.48
1:A:157:G:H2'	1:A:157:G:N3	2.27	0.48
8:H:85:VAL:HG23	8:H:86:LYS:N	2.27	0.48
1:A:17:U:C2'	1:A:18:G:O5'	2.61	0.48
1:A:63:U:C4	1:A:64:A:C8	3.02	0.48
1:A:45:A:H2'	1:A:46:U:O4'	2.13	0.48
1:A:78:G:N3	1:A:126:A:C2	2.78	0.48
6:F:166:ARG:HD3	6:F:167:VAL:N	2.29	0.48
6:F:157:GLN:HA	6:F:157:GLN:NE2	2.29	0.48
5:E:2182:A:H2'	5:E:2183:C:C6	2.48	0.48
1:A:13:A:H4'	7:G:120:VAL:N	2.28	0.48
8:H:130:MET:HE3	8:H:162:PHE:HD2	1.78	0.48
1:A:142:C:H2'	1:A:143:U:C6	2.49	0.48
1:A:139:C:H3'	1:A:139:C:H6	1.79	0.48
7:G:48:ARG:CD	7:G:161:LYS:HA	2.44	0.47
1:A:9:U:H2'	1:A:10:G:C5'	2.43	0.47
8:H:16:LEU:HD22	8:H:70:VAL:HG12	1.96	0.47
8:H:90:LEU:HD23	8:H:90:LEU:O	2.13	0.47
1:A:109:C:O2	1:A:125:A:H2	1.97	0.47
1:A:73:U:P	1:A:74:U:H5'	2.54	0.47
8:H:140:ARG:O	8:H:142:ARG:HD2	2.13	0.47
7:G:53:LEU:CD2	7:G:189:PHE:CD1	2.95	0.47
6:F:86:CYS:CB	6:F:87:PRO:HD3	2.32	0.47
6:F:213:LYS:HD2	6:F:214:ASP:OD1	2.13	0.47
5:E:2163:C:H2'	5:E:2164:A:O4'	2.14	0.47
5:E:2171:G:OP2	7:G:102:LYS:HB3	2.11	0.47
7:G:41:TYR:CZ	7:G:163:LEU:HD23	2.50	0.47
7:G:65:ILE:CD1	7:G:151:VAL:HG23	2.43	0.47
8:H:36:LEU:HB2	8:H:67:HIS:CD2	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:83:LEU:HD21	8:H:90:LEU:CD1	2.45	0.47
8:H:19:ASN:ND2	8:H:66:VAL:HG13	2.30	0.47
8:H:83:LEU:HD21	8:H:90:LEU:CD2	2.44	0.47
1:A:39:A:C6	1:A:40:G:N7	2.82	0.47
1:A:78:G:C2	1:A:79:U:C2	3.03	0.47
1:A:78:G:C2'	1:A:79:U:H5'	2.44	0.47
3:C:1057:G:C2'	3:C:1058:G:H5'	2.44	0.47
1:A:36:G:O2'	1:A:37:A:H5'	2.15	0.47
5:E:2173:U:OP2	7:G:98:LYS:CB	2.56	0.47
6:F:138:ASN:OD1	6:F:202:LYS:HB2	2.15	0.47
6:F:208:TYR:CE2	6:F:212:LYS:CE	2.94	0.47
6:F:114:LYS:O	6:F:114:LYS:HD3	2.15	0.47
7:G:45:ARG:CB	7:G:47:LYS:HD3	2.32	0.47
7:G:59:PRO:HD3	7:G:153:SER:HB3	1.96	0.47
1:A:16:U:O2'	1:A:17:U:C4	2.56	0.47
8:H:169:ASP:O	8:H:170:VAL:HB	2.15	0.47
8:H:16:LEU:CD1	8:H:75:ALA:CB	2.93	0.47
8:H:32:ALA:O	8:H:35:VAL:HG12	2.15	0.47
1:A:46:U:H2'	1:A:47:A:O5'	2.14	0.47
8:H:62:GLU:CD	8:H:64:ILE:H	2.17	0.47
7:G:12:HIS:NE2	7:G:205:VAL:HA	2.30	0.47
6:F:97:MET:HG3	6:F:110:VAL:HG12	1.95	0.47
1:A:149:G:HO2'	1:A:150:U:H6	1.61	0.47
1:A:151:U:H1'	1:A:179:A:C2'	2.45	0.47
2:B:539:A:H2'	2:B:540:G:H8	1.80	0.47
3:C:1051:C:H2'	3:C:1052:U:C6	2.50	0.47
1:A:40:G:H2'	1:A:41:G:H5'	1.96	0.47
1:A:151:U:H2'	1:A:152:U:C5	2.45	0.47
6:F:78:ASN:HD22	6:F:78:ASN:H	1.63	0.47
5:E:2155:U:P	7:G:160:LYS:HD3	2.54	0.47
1:A:159:U:H3'	1:A:160:U:C5	2.50	0.47
4:D:1196:U:H4'	4:D:1197:G:OP2	2.14	0.47
8:H:37:GLU:HB3	8:H:38:GLN:NE2	2.30	0.47
8:H:71:ARG:CG	8:H:72:GLY:N	2.78	0.47
7:G:49:PHE:CE1	7:G:51:GLY:CA	2.98	0.47
7:G:179:LEU:O	7:G:183:ILE:HG13	2.14	0.47
8:H:59:ARG:HD3	8:H:62:GLU:OE1	2.14	0.47
1:A:116:C:C2	1:A:118:G:OP2	2.68	0.47
1:A:32:U:H2'	1:A:33:U:O4'	2.15	0.47
7:G:45:ARG:HB2	7:G:47:LYS:CD	2.33	0.46
8:H:95:PHE:CB	8:H:101:PHE:N	2.78	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:193:U:O3'	2:B:535:A:C5'	2.63	0.46
1:A:180:G:C8	1:A:181:A:C8	3.03	0.46
3:C:1060:C:O2'	3:C:1061:G:H5'	2.15	0.46
5:E:2155:U:O5'	7:G:160:LYS:HD3	2.15	0.46
1:A:29:C:P	1:A:135:A:H5'	2.55	0.46
1:A:137:G:O2'	1:A:138:C:H5'	2.15	0.46
8:H:141:LYS:O	8:H:142:ARG:HB3	2.15	0.46
7:G:30:GLU:HB3	7:G:209:SER:H	1.79	0.46
7:G:179:LEU:HD12	7:G:183:ILE:HD11	1.97	0.46
7:G:97:LYS:CA	7:G:100:ILE:HG22	2.45	0.46
8:H:83:LEU:HD21	8:H:90:LEU:HD21	1.97	0.46
6:F:189:ILE:HG22	6:F:189:ILE:O	2.15	0.46
5:E:2166:G:C6	5:E:2167:C:N3	2.84	0.46
1:A:189:C:P	4:D:1196:U:H2'	2.56	0.46
7:G:90:LEU:CG	7:G:124:LEU:HD11	2.39	0.46
1:A:135:A:C4	1:A:136:A:C8	3.04	0.46
7:G:157:PHE:CZ	7:G:165:LEU:CD2	2.94	0.46
7:G:176:GLU:O	7:G:180:VAL:HG23	2.16	0.46
7:G:49:PHE:CE2	7:G:193:LEU:HD11	2.51	0.46
7:G:49:PHE:CE1	7:G:51:GLY:N	2.83	0.46
7:G:52:SER:C	7:G:53:LEU:HD23	2.35	0.46
7:G:190:PHE:HE2	7:G:197:ASN:O	1.98	0.46
1:A:185:U:O2'	1:A:186:U:C5'	2.63	0.46
5:E:2177:A:O2'	5:E:2178:U:H6	1.98	0.46
8:H:70:VAL:CG1	8:H:75:ALA:CB	2.92	0.46
1:A:103:G:C2	1:A:104:G:C5	3.03	0.46
1:A:70:G:C2	1:A:73:U:H5	2.33	0.46
1:A:76:A:C4	1:A:77:G:C8	3.03	0.46
1:A:149:G:N2	1:A:175:C:N4	2.54	0.46
4:D:1202:G:C2'	4:D:1203:C:H5'	2.46	0.46
5:E:2154:G:C2'	7:G:160:LYS:CB	2.83	0.46
6:F:133:VAL:O	6:F:137:THR:HG23	2.15	0.46
1:A:45:A:C8	1:A:45:A:P	3.09	0.46
8:H:109:ILE:O	8:H:111:LEU:HD12	2.16	0.46
8:H:16:LEU:CD2	8:H:70:VAL:CG1	2.93	0.46
8:H:71:ARG:CD	8:H:74:LYS:N	2.79	0.46
1:A:132:A:H2'	1:A:133:G:C8	2.49	0.46
1:A:148:G:O2'	1:A:149:G:H5'	2.15	0.46
7:G:97:LYS:C	7:G:100:ILE:HG22	2.36	0.46
1:A:78:G:N3	1:A:79:U:C1'	2.78	0.46
6:F:108:LYS:H	6:F:108:LYS:HD2	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:65:ILE:HD13	7:G:151:VAL:HG21	1.98	0.46
1:A:13:A:H4'	7:G:119:GLN:C	2.36	0.46
6:F:123:LEU:HD12	6:F:123:LEU:N	2.31	0.46
1:A:76:A:N6	1:A:77:G:O6	2.49	0.46
7:G:144:LEU:N	7:G:144:LEU:HD12	2.31	0.46
7:G:63:MET:SD	7:G:109:ALA:HB2	2.56	0.46
6:F:123:LEU:HD12	6:F:123:LEU:H	1.81	0.46
6:F:135:ALA:HB1	6:F:200:ALA:HB3	1.98	0.46
5:E:2177:A:O2'	5:E:2178:U:C6	2.70	0.46
8:H:83:LEU:HD12	8:H:167:ASP:OD2	2.15	0.45
1:A:82:G:N2	1:A:92:U:O2	2.49	0.45
6:F:116:THR:CG2	6:F:193:LEU:HB2	2.44	0.45
6:F:201:ALA:C	6:F:203:GLY:H	2.18	0.45
1:A:112:G:C2'	1:A:113:U:H6	2.22	0.45
6:F:99:ASN:HB3	6:F:175:THR:HG21	1.98	0.45
6:F:102:ASN:O	6:F:103:ASN:HB2	2.15	0.45
8:H:46:GLN:HG2	8:H:66:VAL:CB	2.26	0.45
1:A:89:A:H2'	1:A:90:G:H8	1.82	0.45
6:F:220:ALA:C	6:F:222:SER:H	2.18	0.45
8:H:48:LYS:HB2	8:H:64:ILE:HG21	1.97	0.45
6:F:213:LYS:HE2	6:F:217:GLU:CD	2.36	0.45
1:A:34:U:C6	1:A:36:G:OP1	2.69	0.45
5:E:2155:U:O2'	7:G:158:GLN:CB	2.61	0.45
7:G:65:ILE:CD1	7:G:151:VAL:CG2	2.94	0.45
1:A:171:A:O2'	1:A:172:A:H5'	2.17	0.45
7:G:41:TYR:O	7:G:43:PRO:HD3	2.16	0.45
7:G:98:LYS:C	7:G:98:LYS:HD3	2.36	0.45
7:G:98:LYS:HD2	7:G:99:LEU:HD22	1.99	0.45
7:G:203:SER:C	7:G:204:LEU:HD22	2.36	0.45
7:G:26:ARG:HD2	7:G:210:MET:HE1	1.94	0.45
1:A:190:U:H5	3:C:1054:C:N1	2.12	0.45
7:G:100:ILE:C	7:G:100:ILE:HD13	2.35	0.45
5:E:2175:A:C3'	7:G:130:LYS:HD3	2.02	0.45
7:G:117:ILE:O	7:G:121:PRO:HG2	2.16	0.45
8:H:69:THR:C	8:H:70:VAL:HG22	2.23	0.45
8:H:68:VAL:CG1	8:H:69:THR:N	2.79	0.45
6:F:200:ALA:CB	6:F:210:ILE:HD11	2.46	0.45
7:G:64:SER:CB	7:G:107:TYR:CD2	2.95	0.45
5:E:2159:A:O2'	5:E:2160:G:OP2	2.34	0.45
1:A:139:C:H2'	1:A:140:C:O4'	2.17	0.45
8:H:12:LYS:C	8:H:12:LYS:HD2	2.37	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:2157:G:P	7:G:108:ASN:HD21	2.34	0.45
7:G:151:VAL:C	7:G:153:SER:CA	2.85	0.45
1:A:92:U:H3	1:A:93:U:H1'	1.79	0.45
1:A:71:U:O4	1:A:72:A:C2	2.69	0.45
1:A:182:A:N3	1:A:183:A:C8	2.84	0.45
7:G:106:LYS:CG	7:G:107:TYR:CE1	3.00	0.45
7:G:97:LYS:HA	7:G:100:ILE:CG2	2.46	0.45
1:A:57:U:H2'	1:A:58:A:C8	2.48	0.45
8:H:18:LEU:CD1	8:H:68:VAL:CG2	2.95	0.45
8:H:32:ALA:N	8:H:34:LYS:HE3	2.29	0.45
5:E:2172:G:C3'	7:G:98:LYS:HG2	2.44	0.45
1:A:59:G:C3'	1:A:60:U:C6	2.94	0.45
1:A:127:U:O5'	1:A:127:U:H6	2.00	0.45
1:A:92:U:C2	1:A:93:U:H1'	2.52	0.45
1:A:147:C:C2'	1:A:147:C:O2	2.64	0.45
1:A:147:C:OP2	1:A:148:G:C5	2.70	0.45
8:H:83:LEU:HD11	8:H:90:LEU:HD12	1.99	0.45
8:H:96:SER:HB2	8:H:101:PHE:HE2	1.78	0.45
1:A:107:G:H2'	1:A:108:C:H6	1.82	0.45
8:H:54:ARG:HG3	8:H:55:THR:H	1.82	0.45
7:G:58:CYS:SG	7:G:59:PRO:HD2	2.56	0.45
8:H:44:PRO:CB	8:H:67:HIS:HB2	2.46	0.45
8:H:83:LEU:HD21	8:H:90:LEU:HD11	1.99	0.45
7:G:49:PHE:CE1	7:G:157:PHE:HB3	2.52	0.45
1:A:70:G:C2'	1:A:72:A:N7	2.80	0.45
7:G:30:GLU:HG2	7:G:210:MET:H	1.82	0.45
6:F:86:CYS:HB2	6:F:87:PRO:CD	2.38	0.45
7:G:120:VAL:HG13	7:G:121:PRO:CD	2.21	0.44
1:A:48:A:C6	1:A:49:A:C2	3.05	0.44
1:A:95:A:C2'	1:A:96:C:C5'	2.88	0.44
6:F:112:ILE:HD11	6:F:189:ILE:CB	2.47	0.44
8:H:134:GLY:O	8:H:136:ARG:HD3	2.18	0.44
7:G:64:SER:HB3	7:G:107:TYR:CE2	2.52	0.44
7:G:67:ILE:CG2	7:G:84:ALA:HA	2.47	0.44
1:A:156:A:H2	1:A:185:U:OP1	1.99	0.44
2:B:514:C:O2'	2:B:515:G:H5'	2.17	0.44
7:G:60:ARG:HE	7:G:60:ARG:HB2	1.58	0.44
1:A:48:A:H4'	1:A:131:C:O2'	2.17	0.44
6:F:185:ASN:HB2	6:F:191:GLU:CD	2.38	0.44
1:A:159:U:C5'	1:A:160:U:C5	2.99	0.44
4:D:1195:C:H3'	4:D:1196:U:H5''	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:59:ARG:CB	8:H:59:ARG:CZ	2.95	0.44
1:A:70:G:O2'	1:A:72:A:N7	2.48	0.44
1:A:168:C:H5	1:A:170:A:OP1	1.99	0.44
7:G:60:ARG:HD3	7:G:61:PRO:CG	2.48	0.44
7:G:90:LEU:HD11	7:G:120:VAL:CA	2.48	0.44
8:H:79:LEU:HD23	8:H:126:PHE:HZ	1.78	0.44
1:A:29:C:OP2	1:A:135:A:C4'	2.66	0.44
7:G:205:VAL:HG11	7:G:213:ALA:CB	2.13	0.44
7:G:34:LEU:HD11	7:G:36:VAL:HG23	1.95	0.44
8:H:136:ARG:NH2	8:H:137:VAL:HA	2.32	0.44
4:D:1206:G:C6	4:D:1207:G:C5	3.04	0.44
7:G:19:TYR:CD2	7:G:214:PHE:CE1	3.06	0.44
5:E:2160:G:N1	5:E:2161:C:N4	2.64	0.44
7:G:70:ASP:CA	7:G:74:VAL:HG23	2.47	0.44
8:H:16:LEU:CG	8:H:70:VAL:HG11	2.48	0.44
1:A:104:G:N3	1:A:104:G:H2'	2.31	0.44
1:A:135:A:H2'	1:A:136:A:C8	2.50	0.44
1:A:44:A:C3'	1:A:44:A:C8	3.01	0.44
6:F:161:VAL:HG21	6:F:169:GLN:OE1	2.17	0.44
7:G:58:CYS:SG	7:G:59:PRO:N	2.91	0.44
1:A:11:U:H3'	7:G:118:LYS:HE3	1.93	0.44
8:H:40:SER:O	8:H:74:LYS:HD2	2.18	0.44
7:G:49:PHE:HD1	7:G:157:PHE:HD1	1.65	0.44
1:A:144:C:C2	1:A:145:U:O4'	2.71	0.44
8:H:36:LEU:HB3	8:H:67:HIS:NE2	2.32	0.44
1:A:102:A:C2'	1:A:103:G:H4'	2.46	0.44
1:A:131:C:H6	1:A:131:C:H3'	1.83	0.44
1:A:45:A:H2'	1:A:46:U:H6	1.77	0.44
7:G:49:PHE:CD2	7:G:193:LEU:CD2	2.94	0.44
7:G:36:VAL:CG2	7:G:204:LEU:CD1	2.95	0.44
1:A:78:G:C2	1:A:79:U:N1	2.85	0.44
1:A:156:A:C6	1:A:185:U:H5	2.36	0.44
7:G:120:VAL:HG23	7:G:124:LEU:HD22	1.99	0.44
8:H:71:ARG:CD	8:H:71:ARG:N	2.74	0.44
8:H:16:LEU:CD2	8:H:75:ALA:CB	2.94	0.44
1:A:46:U:C2'	1:A:47:A:O5'	2.66	0.44
7:G:49:PHE:CD2	7:G:193:LEU:HD21	2.52	0.44
1:A:139:C:H2'	1:A:140:C:C4'	2.48	0.44
7:G:102:LYS:O	7:G:105:LYS:HG2	2.18	0.43
8:H:126:PHE:CD1	8:H:128:VAL:HG23	2.53	0.43
8:H:66:VAL:CG1	8:H:67:HIS:N	2.81	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:48:LYS:CG	8:H:49:ALA:H	2.28	0.43
2:B:533:A:C2	2:B:536:C:C5	3.06	0.43
8:H:8:MET:HB2	8:H:9:ARG:HH21	1.83	0.43
8:H:42:GLN:HA	8:H:42:GLN:NE2	2.33	0.43
7:G:67:ILE:HD11	7:G:144:LEU:HD21	1.98	0.43
8:H:98:THR:HG23	8:H:99:GLY:N	2.33	0.43
1:A:21:U:H2'	1:A:22:G:H8	1.83	0.43
7:G:152:ARG:N	7:G:153:SER:HA	2.33	0.43
7:G:90:LEU:CD2	7:G:123:LEU:CB	2.94	0.43
8:H:155:LYS:H	8:H:155:LYS:HD2	1.82	0.43
6:F:107:LEU:HD21	6:F:108:LYS:HZ2	1.82	0.43
6:F:98:MET:O	6:F:101:ARG:HG2	2.18	0.43
7:G:196:LYS:HD2	7:G:199:GLN:OE1	2.19	0.43
8:H:51:TYR:CD1	8:H:58:ILE:O	2.71	0.43
8:H:98:THR:CG2	8:H:99:GLY:N	2.81	0.43
7:G:169:VAL:HG21	7:G:179:LEU:HD11	2.00	0.43
8:H:166:TYR:CD1	8:H:167:ASP:CB	3.01	0.43
1:A:127:U:C4	1:A:128:A:C5	3.06	0.43
7:G:36:VAL:CG1	7:G:204:LEU:CD1	2.95	0.43
7:G:49:PHE:HD2	7:G:193:LEU:HD21	1.82	0.43
8:H:136:ARG:HD3	8:H:137:VAL:N	2.34	0.43
7:G:24:LYS:HZ3	7:G:25:LYS:HE2	1.83	0.43
6:F:96:LEU:HD12	6:F:171:ILE:HG23	1.99	0.43
2:B:540:G:H2'	2:B:541:G:O4'	2.18	0.43
1:A:115:G:C2'	1:A:116:C:H5'	2.48	0.43
6:F:148:VAL:HG22	6:F:149:GLY:N	2.33	0.43
8:H:101:PHE:HB3	8:H:102:GLY:H	1.53	0.43
8:H:165:LYS:O	8:H:166:TYR:CD2	2.72	0.43
8:H:31:ARG:CB	8:H:34:LYS:HE2	2.40	0.43
1:A:158:A:N1	1:A:163:G:O6	2.52	0.43
7:G:148:VAL:O	7:G:151:VAL:HG22	2.18	0.43
8:H:34:LYS:CG	8:H:35:VAL:N	2.82	0.43
8:H:92:ASP:HB3	8:H:93:ARG:H	1.29	0.43
1:A:81:A:N6	1:A:93:U:O2	2.52	0.43
1:A:76:A:C6	1:A:77:G:C5	3.07	0.43
6:F:84:ALA:HB1	6:F:89:ILE:C	2.39	0.43
5:E:2152:A:O2'	5:E:2154:G:OP2	2.35	0.43
5:E:2154:G:C2	7:G:160:LYS:NZ	2.87	0.43
7:G:59:PRO:CD	7:G:153:SER:HA	2.48	0.43
8:H:18:LEU:CD1	8:H:19:ASN:N	2.82	0.43
8:H:91:ARG:CD	8:H:159:VAL:CG2	2.94	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:8:MET:HG3	8:H:9:ARG:H	1.82	0.43
5:E:2166:G:O6	5:E:2167:C:C4	2.72	0.43
1:A:4:A:H2'	1:A:5:A:H8	1.84	0.43
7:G:100:ILE:CG2	7:G:101:LYS:N	2.82	0.43
1:A:92:U:H2'	1:A:93:U:H5'	1.95	0.43
8:H:56:PHE:HB3	8:H:57:GLY:H	1.44	0.43
6:F:210:ILE:CD1	6:F:210:ILE:H	2.30	0.43
3:C:1057:G:H2'	3:C:1058:G:O4'	2.19	0.43
7:G:68:PHE:CZ	7:G:90:LEU:HB2	2.53	0.43
1:A:107:G:N3	1:A:127:U:O4	2.52	0.43
1:A:193:U:O3'	2:B:535:A:O5'	2.33	0.43
6:F:195:GLU:HG2	6:F:199:ASN:ND2	2.34	0.43
8:H:148:GLY:O	8:H:149:ASN:HB3	2.19	0.43
5:E:2155:U:H5'	7:G:160:LYS:HG2	1.19	0.43
1:A:190:U:OP2	3:C:1054:C:C1'	2.66	0.43
7:G:128:LEU:HD23	7:G:135:PRO:HD3	1.99	0.43
8:H:155:LYS:HD2	8:H:156:GLU:H	1.84	0.43
2:B:533:A:H2'	2:B:535:A:OP2	2.19	0.43
6:F:91:ARG:HG2	6:F:92:LEU:HD12	2.00	0.43
7:G:71:ALA:O	7:G:72:PHE:HB3	2.19	0.43
5:E:2143:G:C4'	5:E:2144:C:OP2	2.67	0.42
4:D:1195:C:H2'	4:D:1197:G:H5'	2.02	0.42
7:G:178:VAL:HG23	7:G:179:LEU:N	2.34	0.42
1:A:48:A:O3'	1:A:131:C:C4'	2.68	0.42
1:A:148:G:C2'	1:A:149:G:O5'	2.67	0.42
7:G:24:LYS:C	7:G:24:LYS:HD2	2.38	0.42
6:F:92:LEU:N	6:F:92:LEU:HD12	2.34	0.42
8:H:109:ILE:CG2	8:H:110:ASP:N	2.82	0.42
7:G:58:CYS:SG	7:G:152:ARG:HD2	2.59	0.42
1:A:16:U:C1'	1:A:59:G:N2	2.70	0.42
8:H:36:LEU:CB	8:H:67:HIS:NE2	2.83	0.42
1:A:82:G:H2'	1:A:83:C:C6	2.55	0.42
8:H:132:ARG:HB2	8:H:133:PRO:CA	2.49	0.42
1:A:144:C:H2'	1:A:145:U:O4'	2.19	0.42
8:H:6:ASN:N	8:H:7:PRO:HD2	2.34	0.42
5:E:2149:G:O3'	5:E:2150:A:O4'	2.37	0.42
2:B:519:C:H2'	2:B:520:A:O4'	2.19	0.42
3:C:1053:G:O2'	4:D:1199:U:H5	2.02	0.42
7:G:57:ASN:ND2	7:G:178:VAL:HB	2.34	0.42
1:A:58:A:C4	1:A:59:G:C1'	2.99	0.42
8:H:31:ARG:O	8:H:32:ALA:HB3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:9:VAL:O	7:G:12:HIS:HB3	2.19	0.42
8:H:136:ARG:HD3	8:H:136:ARG:N	2.34	0.42
6:F:101:ARG:HD2	6:F:106:LYS:HD2	2.00	0.42
1:A:30:A:C5	1:A:31:A:C8	3.06	0.42
1:A:190:U:C6	3:C:1054:C:C2	3.05	0.42
7:G:179:LEU:CD1	7:G:183:ILE:CD1	2.94	0.42
5:E:2176:A:OP1	7:G:127:GLN:HA	2.19	0.42
1:A:15:C:C4	1:A:64:A:N6	2.88	0.42
1:A:9:U:C2'	1:A:10:G:C5'	2.95	0.42
7:G:205:VAL:CG1	7:G:206:VAL:N	2.83	0.42
1:A:73:U:OP2	1:A:74:U:C5'	2.64	0.42
6:F:138:ASN:HD21	6:F:202:LYS:CD	2.32	0.42
6:F:139:THR:CB	6:F:173:LEU:HD11	2.39	0.42
6:F:88:ILE:HG13	6:F:90:GLU:HG2	2.00	0.42
8:H:28:ARG:HG3	8:H:29:LEU:H	1.83	0.42
8:H:146:THR:CG2	8:H:147:VAL:N	2.83	0.42
8:H:47:SER:HA	8:H:64:ILE:HG22	2.02	0.42
1:A:13:A:H5'	7:G:121:PRO:CG	2.30	0.42
1:A:17:U:H6	1:A:17:U:H3'	1.83	0.42
1:A:60:U:H2'	1:A:60:U:O2	2.17	0.42
1:A:14:U:H6	7:G:122:ARG:HD2	1.83	0.42
8:H:166:TYR:C	8:H:166:TYR:CD1	2.92	0.42
6:F:173:LEU:HD11	6:F:174:LEU:HD22	1.93	0.42
7:G:149:THR:O	7:G:153:SER:CA	2.67	0.42
1:A:58:A:C2	1:A:59:G:C1'	2.93	0.42
8:H:66:VAL:O	8:H:67:HIS:HB3	2.18	0.42
8:H:36:LEU:CD2	8:H:67:HIS:NE2	2.82	0.42
1:A:127:U:O4	1:A:128:A:C6	2.73	0.42
7:G:15:GLU:O	7:G:19:TYR:HD2	2.02	0.42
6:F:118:ASP:HA	6:F:121:ASN:HD22	1.83	0.42
1:A:70:G:N2	1:A:73:U:H6	2.15	0.42
5:E:2160:G:C6	5:E:2161:C:C4	3.07	0.42
3:C:1053:G:C3'	3:C:1054:C:C5'	2.98	0.42
1:A:102:A:HO2'	1:A:103:G:H4'	1.79	0.42
1:A:78:G:N3	1:A:79:U:H1'	2.35	0.42
1:A:112:G:N2	1:A:113:U:C2	2.88	0.42
1:A:156:A:H2'	1:A:157:G:O5'	2.20	0.42
7:G:68:PHE:CD2	7:G:116:LEU:HD13	2.54	0.42
1:A:13:A:C4	7:G:120:VAL:O	2.73	0.42
1:A:95:A:C5	1:A:132:A:N6	2.88	0.42
1:A:45:A:N7	1:A:46:U:C5	2.87	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:133:PRO:HB2	8:H:134:GLY:H	1.52	0.42
7:G:4:ILE:CG2	7:G:5:THR:N	2.81	0.42
8:H:22:VAL:CA	8:H:64:ILE:HD11	2.24	0.42
8:H:8:MET:HE3	8:H:9:ARG:CD	2.49	0.42
2:B:513:C:O2'	2:B:514:C:H5'	2.19	0.42
2:B:543:C:O2'	2:B:544:G:H5'	2.20	0.42
5:E:2155:U:C4'	7:G:158:GLN:CG	2.90	0.41
1:A:161:A:N3	2:B:530:G:C5	2.88	0.41
7:G:124:LEU:CD1	7:G:124:LEU:N	2.83	0.41
8:H:162:PHE:CD1	8:H:166:TYR:CE2	2.96	0.41
1:A:81:A:C2	1:A:82:G:C4	3.08	0.41
1:A:89:A:H2'	1:A:90:G:O4'	2.20	0.41
7:G:30:GLU:CG	7:G:209:SER:HB2	2.49	0.41
6:F:210:ILE:CD1	6:F:210:ILE:N	2.82	0.41
6:F:198:ILE:CG2	6:F:199:ASN:N	2.82	0.41
7:G:59:PRO:HD2	7:G:153:SER:HA	2.02	0.41
8:H:18:LEU:HG	8:H:68:VAL:CB	2.50	0.41
8:H:71:ARG:C	8:H:71:ARG:CZ	2.89	0.41
1:A:26:A:N1	1:A:27:U:C2	2.88	0.41
1:A:92:U:C2	1:A:93:U:C1'	3.03	0.41
1:A:193:U:H2'	2:B:534:U:H3'	1.10	0.41
7:G:185:MET:O	7:G:189:PHE:HD1	2.02	0.41
6:F:85:GLN:HG2	6:F:93:THR:HB	1.99	0.41
1:A:165:A:H2	1:A:186:U:O2	2.03	0.41
5:E:2185:C:O5'	7:G:163:LEU:CG	2.26	0.41
1:A:27:U:C5'	1:A:28:A:H5'	2.50	0.41
7:G:9:VAL:CG2	7:G:180:VAL:CG1	2.95	0.41
1:A:109:C:C1'	1:A:126:A:H1'	2.45	0.41
6:F:82:ARG:NH1	6:F:95:SER:HB2	2.34	0.41
5:E:2178:U:O2'	5:E:2179:A:OP1	2.29	0.41
1:A:189:C:H2'	3:C:1054:C:O2	2.20	0.41
7:G:85:MET:SD	7:G:93:LEU:CD1	3.07	0.41
1:A:128:A:C2'	1:A:129:U:H6	2.31	0.41
6:F:95:SER:HA	6:F:98:MET:HE2	2.02	0.41
7:G:30:GLU:HG2	7:G:209:SER:HB2	2.03	0.41
1:A:151:U:H2'	1:A:152:U:H6	1.70	0.41
1:A:149:G:H22	1:A:175:C:H42	1.63	0.41
7:G:55:LEU:H	7:G:55:LEU:HD12	1.84	0.41
8:H:163:LYS:HA	8:H:167:ASP:O	2.21	0.41
1:A:136:A:C6	1:A:137:G:N3	2.87	0.41
8:H:23:GLY:N	8:H:64:ILE:CD1	2.82	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:167:VAL:CG2	6:F:168:ASN:N	2.82	0.41
6:F:157:GLN:CA	6:F:157:GLN:HE21	2.29	0.41
7:G:90:LEU:HD11	7:G:120:VAL:HA	2.02	0.41
6:F:136:ILE:CG2	6:F:137:THR:N	2.83	0.41
8:H:158:THR:CG2	8:H:159:VAL:N	2.82	0.41
8:H:166:TYR:HD1	8:H:167:ASP:CG	2.23	0.41
8:H:68:VAL:HG12	8:H:69:THR:O	2.21	0.41
1:A:143:U:C2	1:A:144:C:C5	3.09	0.41
7:G:38:LEU:CD1	7:G:190:PHE:CE1	3.04	0.41
5:E:2154:G:O3'	7:G:160:LYS:HD3	2.21	0.41
7:G:121:PRO:CG	7:G:134:PHE:CE1	3.03	0.41
6:F:129:ILE:CG1	6:F:130:GLN:N	2.82	0.41
8:H:70:VAL:HG23	8:H:71:ARG:N	2.35	0.41
1:A:106:U:C5	1:A:107:G:C5	3.08	0.41
1:A:72:A:C2'	1:A:73:U:O5'	2.69	0.41
8:H:136:ARG:HA	8:H:139:ARG:NH2	2.35	0.41
8:H:52:THR:HA	8:H:58:ILE:HG22	2.01	0.41
6:F:159:VAL:CG2	6:F:160:ASP:N	2.83	0.41
5:E:2154:G:H1'	7:G:161:LYS:CD	2.01	0.41
8:H:16:LEU:N	8:H:16:LEU:CD1	2.83	0.41
1:A:138:C:C2'	1:A:138:C:O2	2.61	0.41
8:H:49:ALA:O	8:H:50:ARG:HB3	2.20	0.41
5:E:2155:U:H5''	7:G:158:GLN:CD	2.41	0.41
7:G:42:ASP:HA	7:G:43:PRO:HD2	1.80	0.41
1:A:189:C:P	4:D:1196:U:C2'	3.08	0.41
1:A:159:U:OP1	1:A:161:A:N7	2.52	0.41
7:G:99:LEU:N	7:G:99:LEU:CD2	2.84	0.41
8:H:155:LYS:HA	8:H:158:THR:CG2	2.51	0.41
8:H:130:MET:HE3	8:H:162:PHE:CD2	2.55	0.41
1:A:128:A:H2'	1:A:129:U:H6	1.72	0.41
1:A:96:C:H2'	1:A:96:C:O2	2.19	0.41
1:A:82:G:H2'	1:A:83:C:H6	1.86	0.41
1:A:94:U:HO2'	1:A:132:A:H61	1.69	0.41
7:G:157:PHE:C	7:G:157:PHE:CD1	2.94	0.41
3:C:1061:G:C2'	3:C:1062:U:H5'	2.50	0.41
7:G:123:LEU:CD2	7:G:123:LEU:N	2.83	0.41
8:H:155:LYS:C	8:H:158:THR:HG22	2.40	0.41
8:H:71:ARG:NE	8:H:72:GLY:CA	2.84	0.41
8:H:90:LEU:HD13	8:H:163:LYS:CE	2.37	0.41
1:A:42:U:O2	1:A:137:G:N7	2.54	0.41
1:A:92:U:N3	1:A:93:U:C1'	2.82	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:9:VAL:O	7:G:13:VAL:HG23	2.21	0.41
6:F:189:ILE:CG2	6:F:193:LEU:CD1	2.94	0.41
7:G:155:ILE:CG2	7:G:156:LYS:N	2.83	0.41
7:G:155:ILE:CG2	7:G:167:VAL:HG13	2.39	0.41
4:D:1207:G:H2'	4:D:1208:C:H6	1.86	0.41
8:H:155:LYS:HA	8:H:158:THR:HG22	2.02	0.40
8:H:16:LEU:HB3	8:H:128:VAL:HA	2.03	0.40
8:H:35:VAL:C	8:H:37:GLU:H	2.22	0.40
1:A:70:G:C5	1:A:72:A:OP2	2.75	0.40
8:H:28:ARG:CG	8:H:29:LEU:N	2.82	0.40
6:F:99:ASN:HD22	6:F:99:ASN:N	2.20	0.40
2:B:517:G:H5'	2:B:519:C:C2	2.56	0.40
7:G:151:VAL:O	7:G:154:THR:CA	2.68	0.40
1:A:59:G:H3'	1:A:60:U:C5	2.55	0.40
7:G:90:LEU:HD23	7:G:90:LEU:O	2.21	0.40
1:A:192:C:N4	2:B:533:A:H4'	2.37	0.40
6:F:110:VAL:CG2	6:F:111:ARG:N	2.84	0.40
1:A:112:G:N3	1:A:113:U:C5	2.89	0.40
1:A:189:C:O5'	4:D:1196:U:C2'	2.58	0.40
1:A:63:U:N3	1:A:64:A:O4'	2.54	0.40
6:F:132:VAL:CG2	6:F:133:VAL:N	2.82	0.40
8:H:37:GLU:HB3	8:H:38:GLN:HE22	1.87	0.40
8:H:71:ARG:NE	8:H:74:LYS:N	2.69	0.40
1:A:81:A:N3	1:A:94:U:C6	2.90	0.40
7:G:15:GLU:O	7:G:19:TYR:CD2	2.74	0.40
6:F:185:ASN:CB	6:F:191:GLU:HB2	2.51	0.40
8:H:133:PRO:CG	8:H:135:ALA:H	2.10	0.40
6:F:208:TYR:HE2	6:F:212:LYS:CE	2.34	0.40
7:G:185:MET:O	7:G:189:PHE:CD1	2.75	0.40
1:A:154:U:O2'	1:A:155:C:C5'	2.61	0.40
5:E:2173:U:P	7:G:98:LYS:HB2	2.61	0.40
7:G:134:PHE:CD2	7:G:135:PRO:O	2.74	0.40
8:H:73:PRO:HA	8:H:76:GLU:OE1	2.20	0.40
1:A:26:A:H2'	1:A:27:U:O4'	2.21	0.40
8:H:8:MET:CG	8:H:9:ARG:N	2.81	0.40
6:F:106:LYS:O	6:F:110:VAL:HG13	2.21	0.40
1:A:173:A:C2'	1:A:174:A:O4'	2.63	0.40
5:E:2160:G:C2	5:E:2161:C:C4	3.10	0.40
1:A:61:G:H2'	1:A:62:C:C6	2.56	0.40
7:G:90:LEU:CD2	7:G:124:LEU:CD1	3.00	0.40
8:H:17:VAL:HG13	8:H:17:VAL:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:35:VAL:O	8:H:36:LEU:HG	2.21	0.40
8:H:66:VAL:HG12	8:H:67:HIS:N	2.36	0.40
8:H:16:LEU:CD1	8:H:75:ALA:HB1	2.46	0.40
7:G:190:PHE:CE2	7:G:197:ASN:O	2.75	0.40
7:G:55:LEU:N	7:G:55:LEU:CD1	2.83	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	F	148/150 (99%)	136 (92%)	10 (7%)	2 (1%)	14	58
7	G	207/213 (97%)	195 (94%)	8 (4%)	4 (2%)	10	52
8	H	163/165 (99%)	113 (69%)	32 (20%)	18 (11%)	0	11
All	All	518/528 (98%)	444 (86%)	50 (10%)	24 (5%)	5	32

All (24) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	F	186	ILE
7	G	60	ARG
8	H	64	ILE
8	H	66	VAL
8	H	68	VAL
8	H	70	VAL
8	H	71	ARG
8	H	78	ILE
8	H	92	ASP
8	H	133	PRO
8	H	142	ARG
6	F	207	SER

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Mol	Chain	Res	Type
7	G	22	GLU
7	G	72	PHE
7	G	197	ASN
8	H	69	THR
8	H	98	THR
8	H	120	GLY
8	H	125	ASP
8	H	136	ARG
8	H	163	LYS
8	H	135	ALA
8	H	17	VAL
8	H	85	VAL

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	F	123/123 (100%)	115 (94%)	8 (6%)	21	58
7	G	194/194 (100%)	184 (95%)	10 (5%)	29	65
8	H	143/143 (100%)	119 (83%)	24 (17%)	2	19
All	All	460/460 (100%)	418 (91%)	42 (9%)	16	43

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	F	83	LYS
6	F	94	ASN
6	F	102	ASN
6	F	106	LYS
6	F	107	LEU
6	F	166	ARG
6	F	187	LYS
6	F	202	LYS
7	G	24	LYS
7	G	60	ARG

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Mol	Chain	Res	Type
7	G	62	ASN
7	G	91	LYS
7	G	100	ILE
7	G	120	VAL
7	G	161	LYS
7	G	195	LYS
7	G	204	LEU
7	G	215	ARG
8	H	12	LYS
8	H	15	LYS
8	H	16	LEU
8	H	17	VAL
8	H	34	LYS
8	H	36	LEU
8	H	53	VAL
8	H	59	ARG
8	H	61	ASN
8	H	62	GLU
8	H	70	VAL
8	H	71	ARG
8	H	89	GLN
8	H	103	PHE
8	H	114	LYS
8	H	119	ILE
8	H	127	TYR
8	H	136	ARG
8	H	140	ARG
8	H	142	ARG
8	H	152	LYS
8	H	155	LYS
8	H	158	THR
8	H	165	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
6	F	78	ASN
6	F	102	ASN
6	F	115	HIS
6	F	138	ASN
6	F	157	GLN
7	G	8	GLN

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Mol	Chain	Res	Type
7	G	57	ASN
7	G	182	GLN
7	G	197	ASN
7	G	200	ASN
8	H	42	GLN
8	H	46	GLN
8	H	61	ASN
8	H	89	GLN
8	H	100	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	189/190 (99%)	65 (34%)	16 (8%)
2	B	45/46 (97%)	8 (17%)	3 (6%)
3	C	12/13 (92%)	2 (16%)	0
4	D	14/15 (93%)	4 (28%)	2 (14%)
5	E	52/53 (98%)	9 (17%)	7 (13%)
All	All	312/317 (98%)	88 (28%)	28 (8%)

All (88) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	12	G
1	A	13	A
1	A	17	U
1	A	18	G
1	A	30	A
1	A	33	U
1	A	35	U
1	A	36	G
1	A	40	G
1	A	41	G
1	A	42	U
1	A	44	A
1	A	45	A
1	A	47	A
1	A	48	A
1	A	60	U
1	A	64	A
1	A	73	U

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Mol	Chain	Res	Type
1	A	74	U
1	A	75	U
1	A	77	G
1	A	78	G
1	A	80	U
1	A	81	A
1	A	85	A
1	A	89	A
1	A	91	C
1	A	93	U
1	A	94	U
1	A	96	C
1	A	97	G
1	A	98	U
1	A	99	U
1	A	101	C
1	A	102	A
1	A	103	G
1	A	104	G
1	A	107	G
1	A	111	A
1	A	112	G
1	A	120	C
1	A	122	C
1	A	125	A
1	A	128	A
1	A	130	C
1	A	132	A
1	A	137	G
1	A	139	C
1	A	140	C
1	A	147	C
1	A	148	G
1	A	149	G
1	A	151	U
1	A	157	G
1	A	158	A
1	A	159	U
1	A	160	U
1	A	162	G
1	A	163	G
1	A	167	U

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Mol	Chain	Res	Type
1	A	177	U
1	A	178	A
1	A	183	A
1	A	185	U
1	A	191	G
2	B	509	A
2	B	510	A
2	B	511	C
2	B	518	C
2	B	519	C
2	B	527	G
2	B	533	A
2	B	534	U
3	C	1053	G
3	C	1054	C
4	D	1196	U
4	D	1197	G
4	D	1201	A
4	D	1202	G
5	E	2144	C
5	E	2145	G
5	E	2149	G
5	E	2150	A
5	E	2151	U
5	E	2152	A
5	E	2160	G
5	E	2178	U
5	E	2179	A

All (28) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	32	U
1	A	34	U
1	A	72	A
1	A	93	U
1	A	96	C
1	A	101	C
1	A	106	U
1	A	111	A
1	A	124	C
1	A	138	C

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Mol	Chain	Res	Type
1	A	139	C
1	A	148	G
1	A	150	U
1	A	156	A
1	A	177	U
1	A	182	A
2	B	509	A
2	B	518	C
2	B	533	A
4	D	1196	U
4	D	1201	A
5	E	2143	G
5	E	2144	C
5	E	2149	G
5	E	2151	U
5	E	2159	A
5	E	2177	A
5	E	2178	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.