



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 08:19 PM UTC

PDB ID : 4DR7 / pdb_00004dr7
Title : Crystal structure of the *Thermus thermophilus* (HB8) 30S ribosomal subunit with codon, crystallographically disordered near-cognate transfer RNA anti-codon stem-loop mismatched at the second codon position, and streptomycin bound
Authors : Demirci, H.; Murphy IV, F.; Murphy, E.; Gregory, S.T.; Dahlberg, A.E.; Jogl, G.
Deposited on : 2012-02-16
Resolution : 3.75 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)

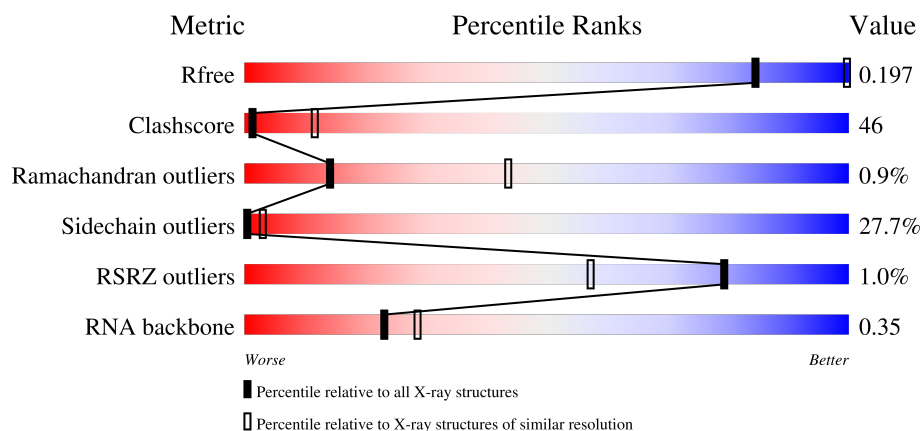
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

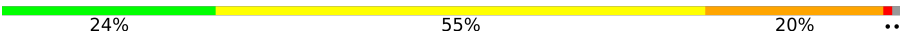
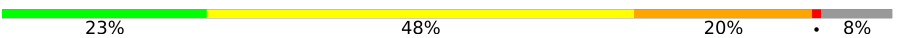
The reported resolution of this entry is 3.75 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1029 (3.90-3.62)
Clashscore	190562	1061 (3.90-3.62)
Ramachandran outliers	187476	1014 (3.90-3.62)
Sidechain outliers	187428	1009 (3.90-3.62)
RSRZ outliers	180081	1028 (3.90-3.62)
RNA backbone	3983	1001 (4.40-3.10)

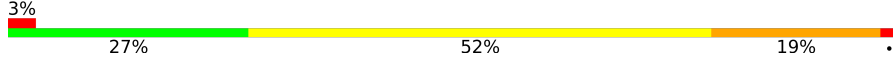
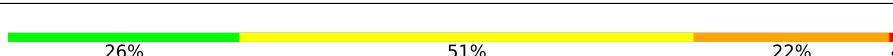
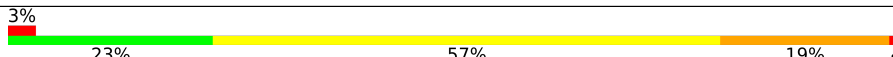
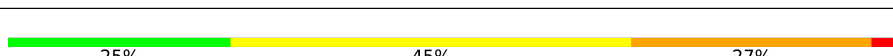
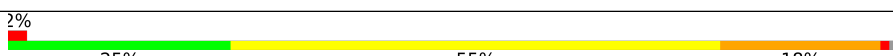
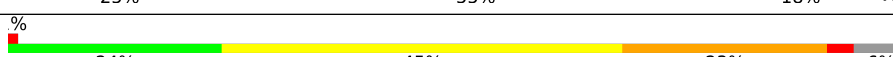
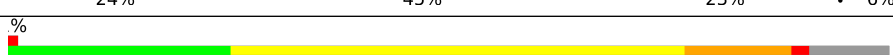
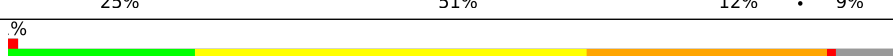
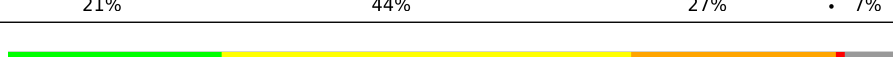
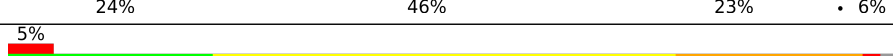
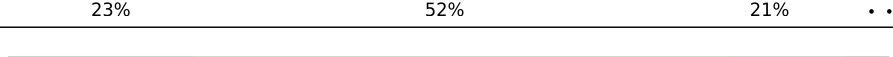
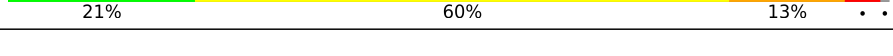
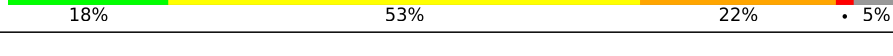
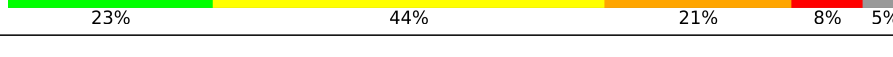
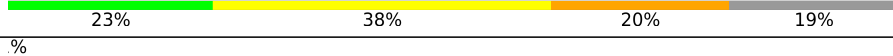
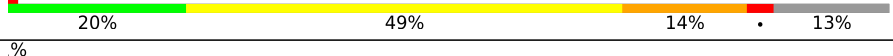
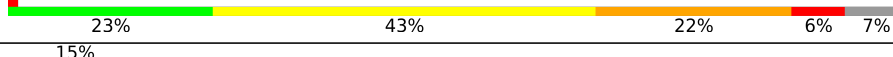
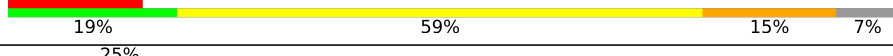
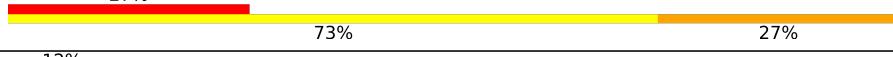
The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1522	 24% 55% 20% ..
2	B	256	 23% 48% 20% . 8%

Continued on next page...

Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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Mol	Chain	Length	Quality of chain
3	C	239	
4	D	209	
5	E	162	
6	F	101	
7	G	156	
8	H	138	
9	I	128	
10	J	105	
11	K	129	
12	L	135	
13	M	126	
14	N	61	
15	O	89	
16	P	88	
17	Q	105	
18	R	88	
19	S	93	
20	T	106	
21	U	27	
22	V	4	
23	W	11	
24	a	8	
25	b	3	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	2MG	A	1207	-	-	X	-
1	5MC	A	1407	-	-	X	-
1	UR3	A	1498	-	-	X	-
1	MA6	A	1518[A]	-	-	X	-
1	MA6	A	1518[B]	-	-	X	-
1	MA6	A	1519[A]	-	-	X	-
1	MA6	A	1519[B]	-	-	X	-
26	MG	A	1728	-	-	-	X

2 Entry composition

There are 29 unique types of molecules in this entry. The entry contains 53659 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 16S rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1513	Total	C	N	O	P	0	8	0
			32707	14570	6056	10561	1520			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1534	C	A	conflict	GB M26923.1
A	1535	A	C	conflict	GB M26923.1

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	236	Total	C	N	O	S	0	0	1
			1896	1211	337	343	5			

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	207	Total	C	N	O	S	0	0	1
			1613	1016	315	281	1			

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	208	Total	C	N	O	S	0	0	0
			1703	1066	339	291	7			

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	151	Total	C	N	O	S	0	0	1
			1147	724	218	201	4			

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	101	Total	C	N	O	S	0	0	0
			843	531	155	154	3			

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	155	Total	C	N	O	S	0	0	0
			1257	781	252	218	6			

- Molecule 8 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	138	Total	C	N	O	S	0	0	0
			1116	705	215	193	3			

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	I	127	Total	C	N	O	S	0	0	0
			1010	639	197	174				

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	99	Total	C	N	O	S	0	0	1
			793	498	157	137	1			

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	117	Total	C	N	O	S	0	0	0
			873	543	166	161	3			

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	125	Total	C	N	O	S	0	0	1
			973	612	196	163	2			

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	M	118	Total	C	N	O	S	0	0	0
			937	579	193	163	2			

- Molecule 14 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	N	60	Total	C	N	O	S	0	0	0
			492	312	104	72	4			

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	O	88	Total	C	N	O	S	0	0	0
			734	459	147	126	2			

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	P	84	Total	C	N	O	S	0	0	1
			701	443	140	117	1			

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	Q	100	Total	C	N	O	S	0	0	0
			834	534	156	142	2			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	96	GLN	GLU	conflict	UNP Q5SHP7

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	R	71	Total	C	N	O		0	0	0
			585	373	116	96				

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	S	81	Total	C	N	O	S	0	0	1
			648	414	120	112	2			

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	T	99	Total	C	N	O	S	0	0	0
			763	470	162	129	2			

- Molecule 21 is a protein called 30S ribosomal protein THX.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
21	U	25	Total	C	N	O	0	0	1
			209	128	51	30			

- Molecule 22 is a RNA chain called 5'-R(*UP*UP*UP*U)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	V	4	Total	C	N	O	P	0	0	0
			77	36	8	30	3			

- Molecule 23 is a RNA chain called 5'-R(*GP*CP*CP*UP*GP*GP*AP*AP*AP*GP*(PSU))-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	W	11	Total	C	N	O	P	0	0	0
			235	106	45	74	10			

- Molecule 24 is a RNA chain called 5'-R(P*UP*GP*GP*AP*AP*AP*GP*(PSU))-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	a	8	Total	C	N	O	P	0	0	0
			175	78	34	55	8			

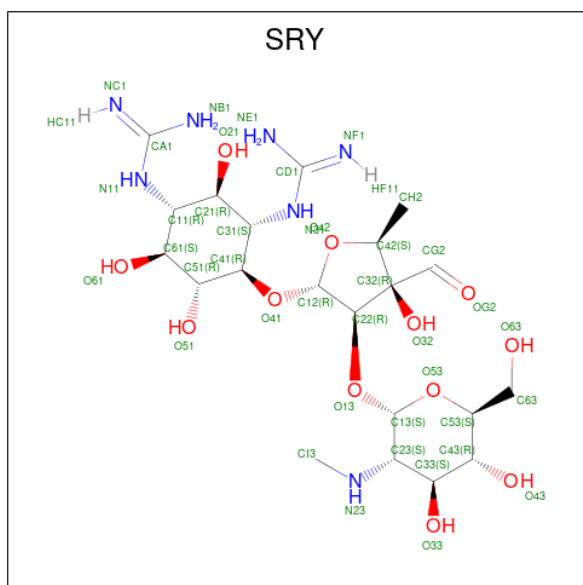
- Molecule 25 is a RNA chain called 5'-R(P*UP*UP*U)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	b	3	Total	C	N	O	P	0	0	0
			60	27	6	24	3			

- Molecule 26 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
26	A	326	Total	Mg	0	0
			326	326		
26	D	3	Total	Mg	0	0
			3	3		
26	E	4	Total	Mg	0	0
			4	4		
26	F	1	Total	Mg	0	0
			1	1		
26	G	1	Total	Mg	0	0
			1	1		
26	H	1	Total	Mg	0	0
			1	1		
26	J	1	Total	Mg	0	0
			1	1		
26	N	1	Total	Mg	0	0
			1	1		
26	P	3	Total	Mg	0	0
			3	3		
26	Q	1	Total	Mg	0	0
			1	1		
26	S	2	Total	Mg	0	0
			2	2		

- Molecule 27 is STREPTOMYCIN (CCD ID: SRY) (formula: $C_{21}H_{39}N_7O_{12}$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
27	A	1	Total	C	N	O	0	0
			40	21	7	12		

- Molecule 28 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
28	D	1	Total	Zn	0	0
			1	1		
28	N	1	Total	Zn	0	0
			1	1		

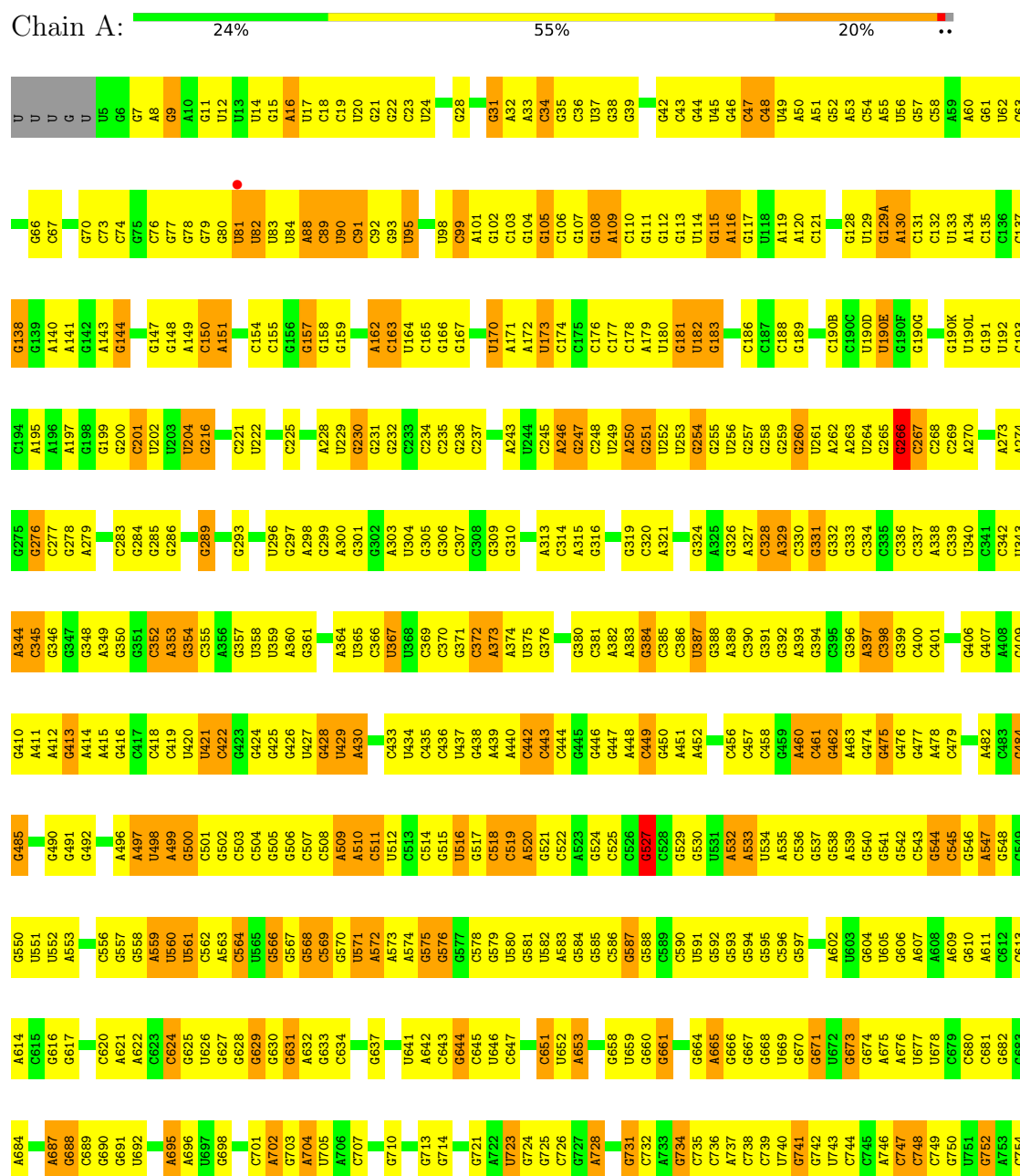
- Molecule 29 is water.

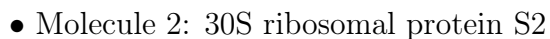
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
29	A	866	Total	O	0	0
			866	866		
29	C	1	Total	O	0	0
			1	1		
29	D	7	Total	O	0	0
			7	7		
29	E	5	Total	O	0	0
			5	5		
29	L	1	Total	O	0	0
			1	1		
29	N	1	Total	O	0	0
			1	1		
29	P	1	Total	O	0	0
			1	1		
29	Q	2	Total	O	0	0
			2	2		
29	T	3	Total	O	0	0
			3	3		
29	U	4	Total	O	0	0
			4	4		
29	W	1	Total	O	0	0
			1	1		

3 Residue-property plots

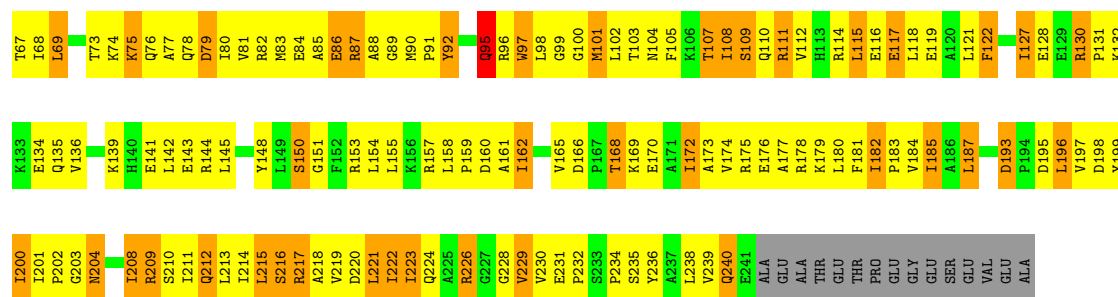
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

• Molecule 1: 16S rRNA

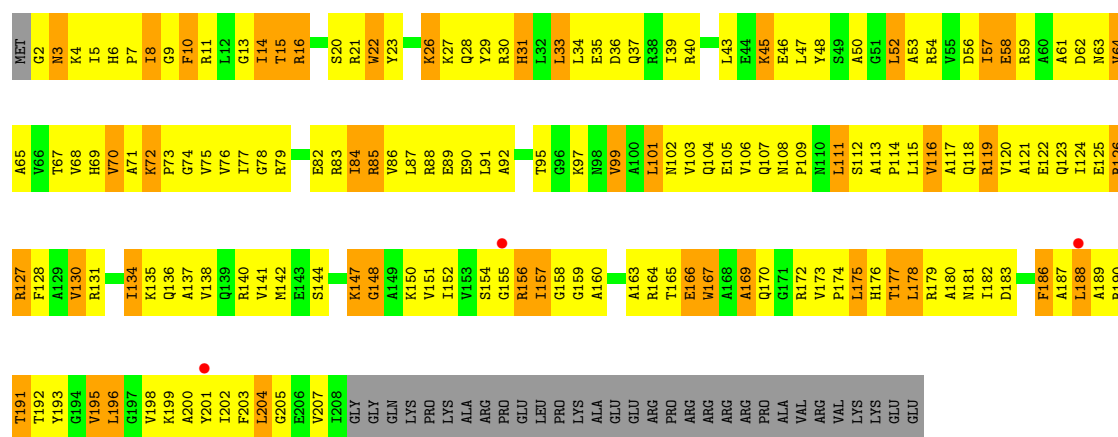




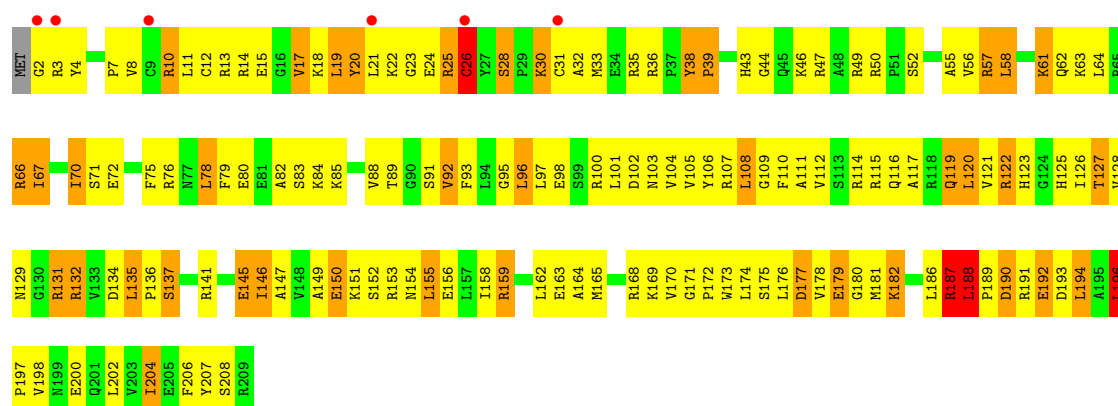
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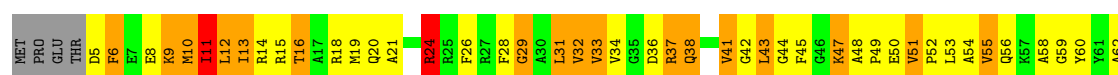
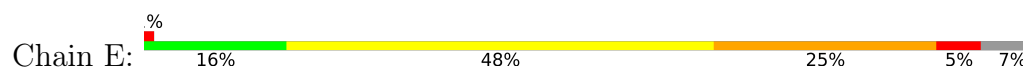
• Molecule 3: 30S ribosomal protein S3

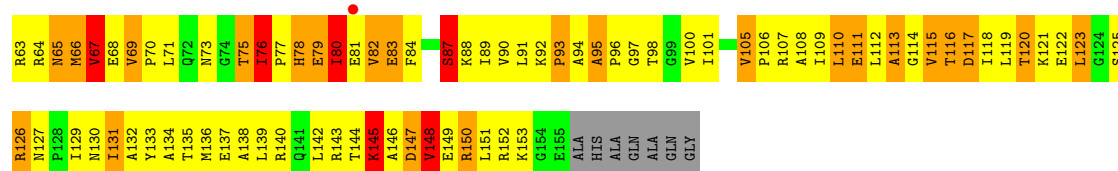


• Molecule 4: 30S ribosomal protein S4

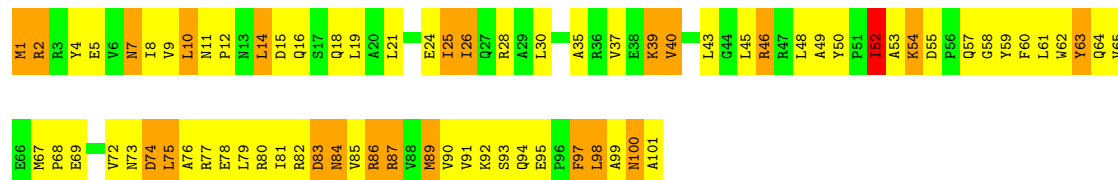


• Molecule 5: 30S ribosomal protein S5





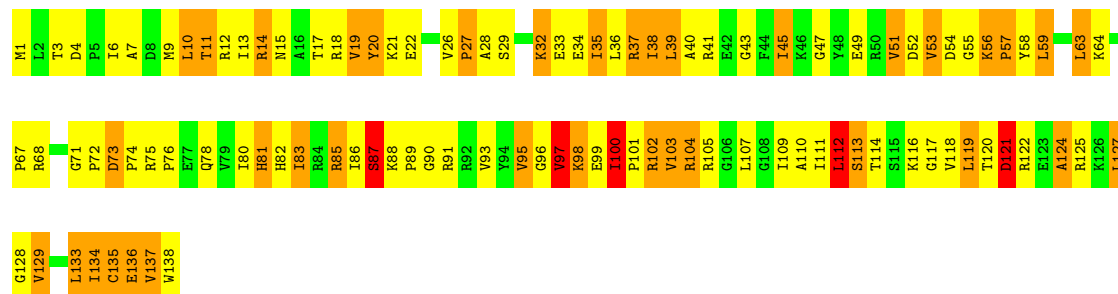
• Molecule 6: 30S ribosomal protein S6



• Molecule 7: 30S ribosomal protein S7



• Molecule 8: 30S ribosomal protein S8

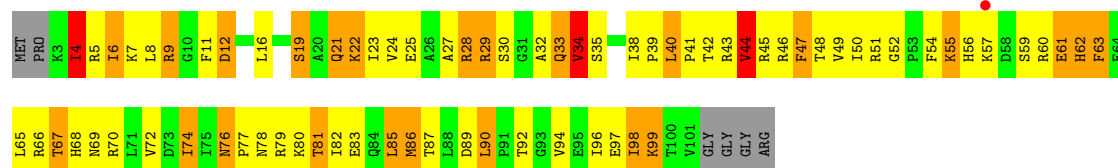


• Molecule 9: 30S ribosomal protein S9

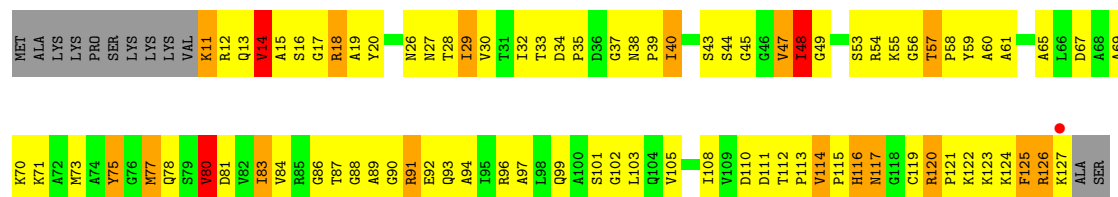




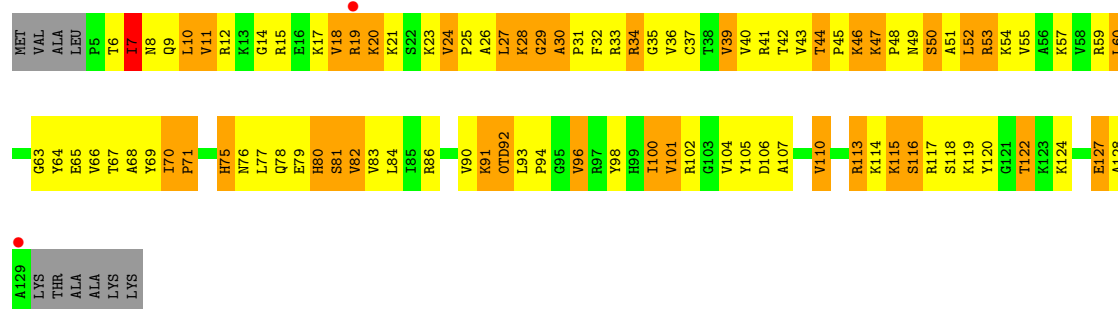
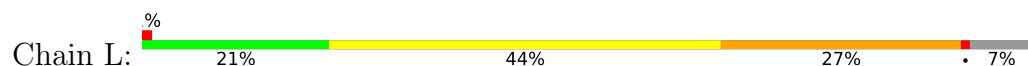
• Molecule 10: 30S ribosomal protein S10



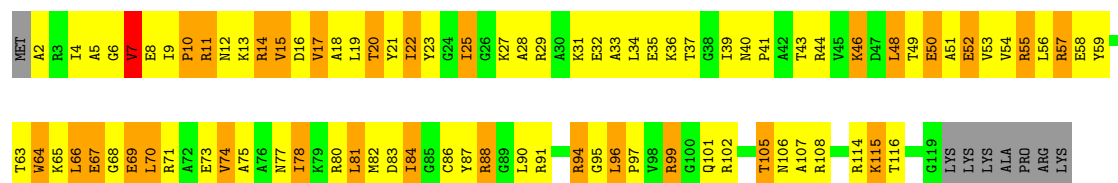
• Molecule 11: 30S ribosomal protein S11



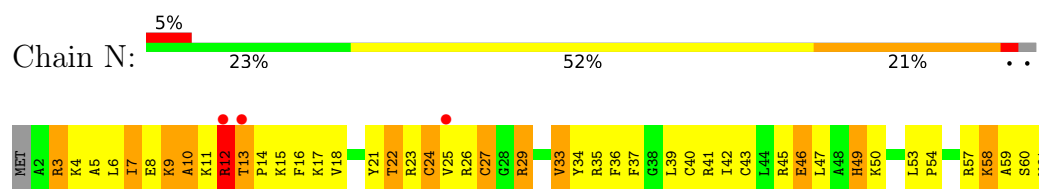
• Molecule 12: 30S ribosomal protein S12



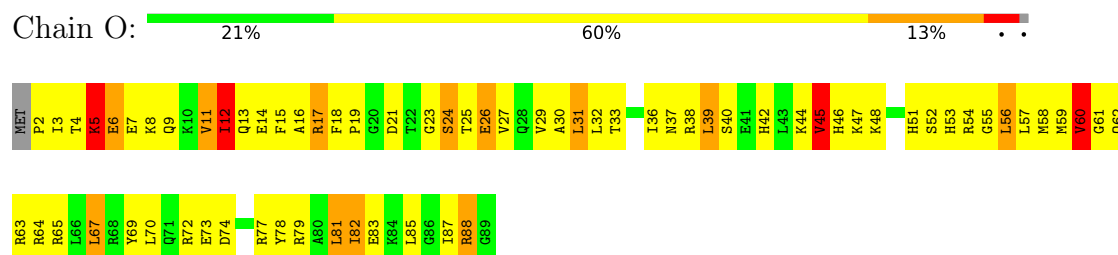
• Molecule 13: 30S ribosomal protein S13



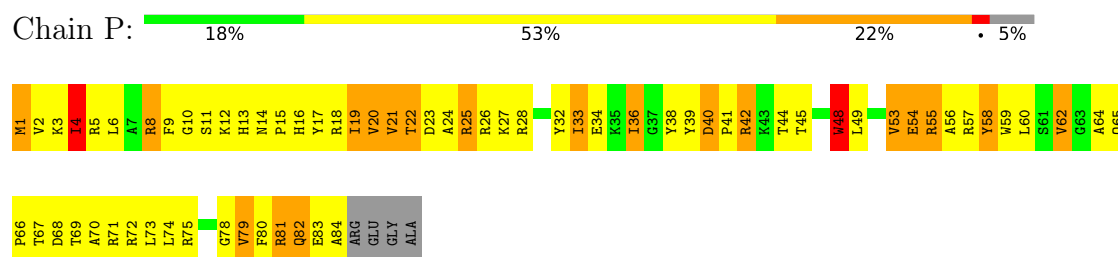
- Molecule 14: 30S ribosomal protein S14



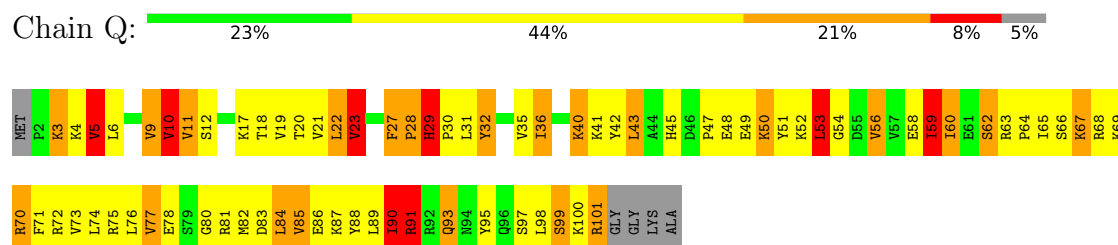
- Molecule 15: 30S ribosomal protein S15



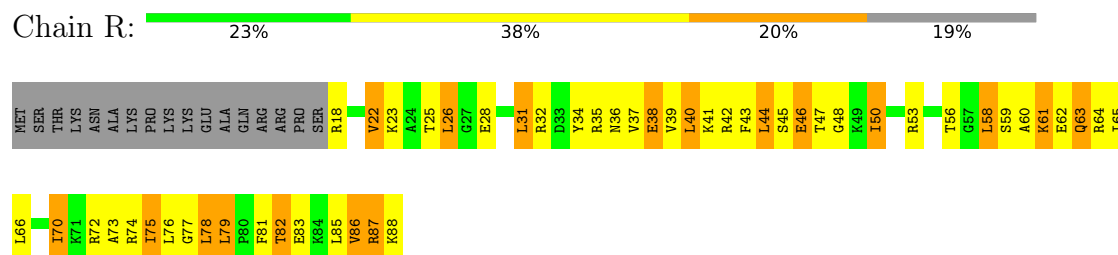
- Molecule 16: 30S ribosomal protein S16



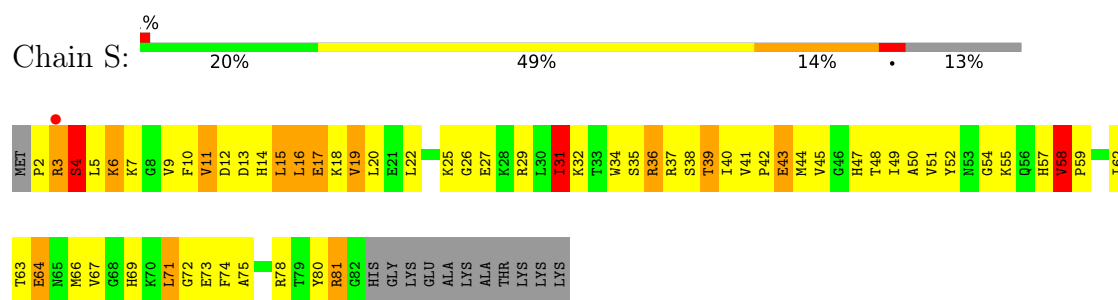
- Molecule 17: 30S ribosomal protein S17



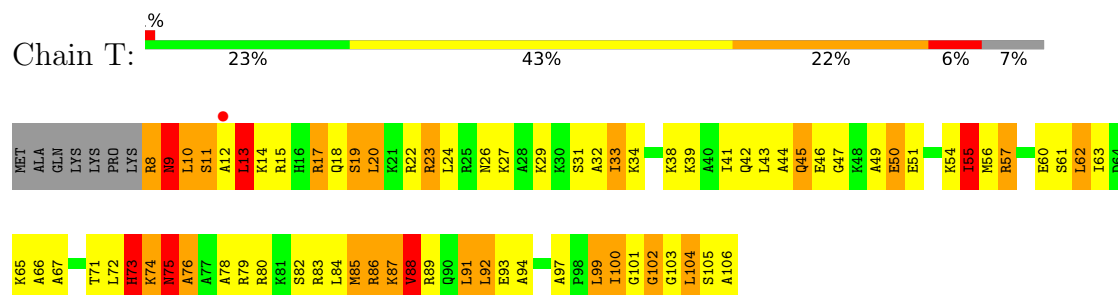
- Molecule 18: 30S ribosomal protein S18



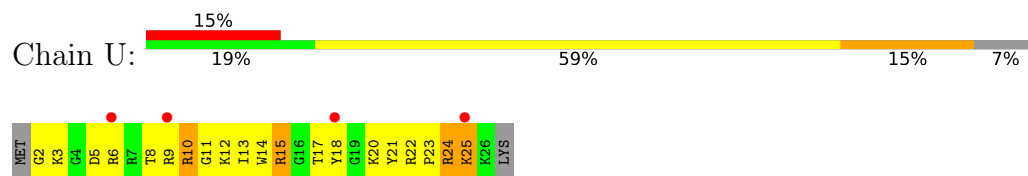
- Molecule 19: 30S ribosomal protein S19



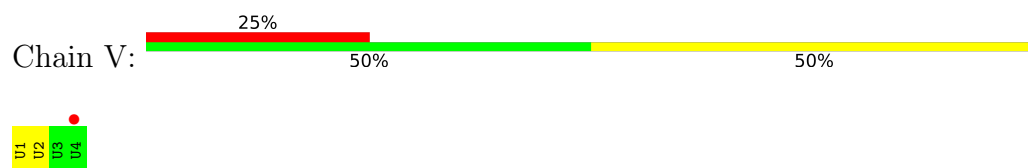
- Molecule 20: 30S ribosomal protein S20



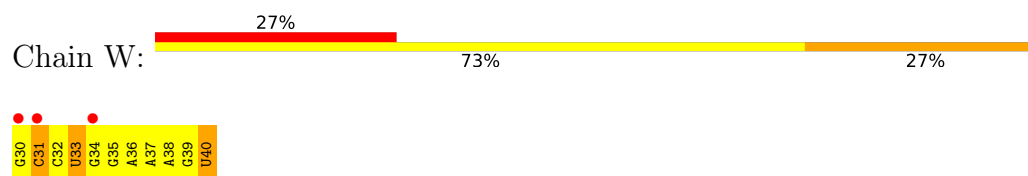
- Molecule 21: 30S ribosomal protein THX



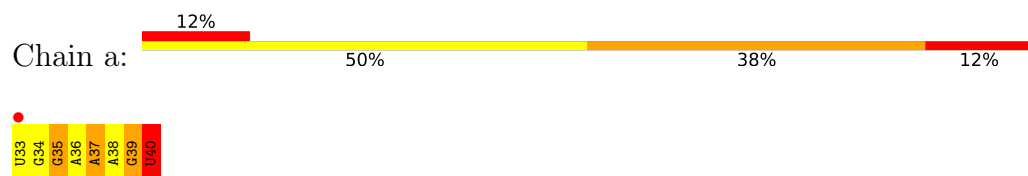
- Molecule 22: 5'-R(*UP*UP*UP*U)-3'



- Molecule 23: 5'-R(*GP*CP*CP*UP*GP*GP*AP*AP*AP*GP*(PSU))-3'



- Molecule 24: 5'-R(P*UP*GP*GP*AP*AP*AP*GP*(PSU))-3'



- Molecule 25: 5'-R(P*UP*UP*U)-3'



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	402.49Å 402.49Å 174.79Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.91 – 3.75 48.91 – 3.75	Depositor EDS
% Data completeness (in resolution range)	99.9 (48.91-3.75) 99.9 (48.91-3.75)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.41 (at 3.77Å)	Xtriage
Refinement program	PHENIX dev_978	Depositor
R, R_{free}	0.148 , 0.201 0.146 , 0.197	Depositor DCC
R_{free} test set	7304 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	130.7	Xtriage
Anisotropy	0.226	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 98.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	53659	wwPDB-VP
Average B, all atoms (Å ²)	146.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.65% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 7MG, MG, 2MG, ZN, SRY, UR3, PSU, 5MC, 4OC, M2G, 0TD, MA6

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	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.66	2/36234 (0.0%)	0.64	4/56547 (0.0%)
2	B	0.94	0/1931	1.40	17/2607 (0.7%)
3	C	0.83	0/1637	1.20	5/2207 (0.2%)
4	D	0.91	0/1733	1.31	19/2318 (0.8%)
5	E	1.37	6/1163 (0.5%)	1.66	29/1566 (1.9%)
6	F	0.79	0/856	1.27	3/1154 (0.3%)
7	G	0.80	0/1276	1.29	9/1709 (0.5%)
8	H	1.41	7/1136 (0.6%)	1.76	23/1527 (1.5%)
9	I	0.85	0/1029	1.27	7/1379 (0.5%)
10	J	0.96	0/806	1.41	13/1084 (1.2%)
11	K	1.05	0/888	1.48	14/1198 (1.2%)
12	L	1.15	1/978 (0.1%)	1.69	26/1308 (2.0%)
13	M	0.88	0/947	1.32	6/1270 (0.5%)
14	N	0.79	0/501	1.26	5/664 (0.8%)
15	O	1.12	2/745 (0.3%)	1.30	6/992 (0.6%)
16	P	1.20	3/717 (0.4%)	1.45	8/965 (0.8%)
17	Q	1.36	6/847 (0.7%)	1.69	14/1131 (1.2%)
18	R	0.98	1/590 (0.2%)	1.39	7/782 (0.9%)
19	S	0.77	0/662	1.22	5/892 (0.6%)
20	T	1.17	1/765 (0.1%)	1.55	12/1007 (1.2%)
21	U	0.85	0/213	1.18	0/279
22	V	0.37	0/84	0.46	0/128
23	W	0.31	0/241	0.40	0/375
24	a	0.47	0/174	0.54	0/270
25	b	0.46	0/65	0.52	0/98
All	All	0.80	29/56218 (0.1%)	0.95	232/83457 (0.3%)

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	3
3	C	0	2
4	D	0	1
8	H	0	2
9	I	0	1
10	J	0	2
12	L	0	2
16	P	0	1
19	S	0	1
20	T	0	2
21	U	0	1
All	All	0	18

All (29) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	Q	9	VAL	CA-CB	-9.65	1.42	1.54
12	L	7	ILE	CA-CB	-8.12	1.44	1.54
15	O	60	VAL	CA-CB	-7.94	1.44	1.54
8	H	134	ILE	CA-CB	-7.74	1.44	1.54
5	E	129	ILE	CA-CB	-7.51	1.46	1.54
5	E	148	VAL	CA-CB	-7.42	1.44	1.54
5	E	80	ILE	CA-CB	-7.12	1.45	1.54
8	H	111	ILE	CA-CB	-6.98	1.45	1.53
17	Q	5	VAL	CA-CB	-6.85	1.46	1.54
17	Q	23	VAL	CA-CB	-6.85	1.45	1.53
5	E	109	ILE	CA-CB	-6.78	1.47	1.54
16	P	20	VAL	CA-CB	-6.38	1.45	1.55
1	A	1498	UR3	O3'-P	6.38	1.62	1.56
8	H	97	VAL	CA-CB	-6.37	1.45	1.54
8	H	103	VAL	CA-CB	-6.21	1.46	1.54
8	H	124	ALA	CA-CB	-6.09	1.43	1.53
5	E	13	ILE	CA-CB	-5.93	1.45	1.54
17	Q	28	PRO	CA-C	-5.55	1.45	1.52
17	Q	56	VAL	CA-CB	-5.54	1.47	1.54
8	H	112	LEU	CA-C	-5.45	1.46	1.52
15	O	69	TYR	CA-C	-5.44	1.46	1.52
5	E	115	VAL	CA-CB	-5.44	1.47	1.54
16	P	19	ILE	CA-CB	-5.37	1.47	1.54
17	Q	10	VAL	CA-CB	-5.34	1.47	1.54
18	R	75	ILE	CA-CB	-5.22	1.48	1.54
1	A	1403	C	C1'-N1	-5.18	1.40	1.48
8	H	20	TYR	C-O	-5.12	1.17	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
20	T	88	VAL	CA-CB	-5.12	1.48	1.54
16	P	36	ILE	CA-CB	-5.06	1.48	1.54

All (232) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	H	100	ILE	CA-C-N	16.37	136.64	119.78
8	H	100	ILE	C-N-CA	16.37	136.64	119.78
9	I	39	GLY	N-CA-C	-13.78	93.41	116.01
12	L	47	LYS	CA-C-N	13.75	133.30	119.82
12	L	47	LYS	C-N-CA	13.75	133.30	119.82
2	B	208	ILE	N-CA-C	13.36	122.98	110.42
2	B	25	ASN	CA-C-N	-12.59	106.84	119.56
2	B	25	ASN	C-N-CA	-12.59	106.84	119.56
8	H	73	ASP	CA-C-N	12.49	132.85	119.87
8	H	73	ASP	C-N-CA	12.49	132.85	119.87
17	Q	29	HIS	CA-C-N	12.37	132.74	119.87
17	Q	29	HIS	C-N-CA	12.37	132.74	119.87
7	G	111	ARG	CA-C-N	11.54	131.42	119.19
7	G	111	ARG	C-N-CA	11.54	131.42	119.19
2	B	130	ARG	CA-C-N	11.09	131.21	119.90
2	B	130	ARG	C-N-CA	11.09	131.21	119.90
6	F	55	ASP	CA-C-N	10.85	130.51	119.56
6	F	55	ASP	C-N-CA	10.85	130.51	119.56
12	L	30	ALA	CA-C-N	10.67	130.50	119.19
12	L	30	ALA	C-N-CA	10.67	130.50	119.19
11	K	114	VAL	CA-C-N	-10.56	109.45	120.85
11	K	114	VAL	C-N-CA	-10.56	109.45	120.85
4	D	26	CYS	N-CA-C	-10.43	100.58	113.20
20	T	76	ALA	N-CA-C	-9.40	101.03	111.28
20	T	75	ASN	N-CA-C	-9.30	101.93	113.28
8	H	38	ILE	CB-CA-C	-9.25	99.46	112.22
20	T	9	ASN	N-CA-C	9.13	123.10	109.95
19	S	58	VAL	CA-C-N	9.01	131.10	119.84
19	S	58	VAL	C-N-CA	9.01	131.10	119.84
12	L	26	ALA	N-CA-C	-8.99	101.37	111.71
9	I	22	GLY	N-CA-C	8.85	124.78	111.42
2	B	32	ILE	N-CA-C	8.84	120.54	108.17
5	E	109	ILE	N-CA-C	8.66	119.23	110.23
5	E	95	ALA	CA-C-N	8.59	128.66	119.90
5	E	95	ALA	C-N-CA	8.59	128.66	119.90
12	L	18	VAL	N-CA-C	8.55	120.15	108.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	67	VAL	N-CA-C	8.55	120.43	108.12
12	L	17	LYS	N-CA-C	-8.55	98.45	110.50
2	B	34	ALA	N-CA-C	8.54	119.17	107.73
18	R	79	LEU	CA-C-N	8.48	129.15	119.99
18	R	79	LEU	C-N-CA	8.48	129.15	119.99
2	B	7	VAL	N-CA-C	8.46	126.93	109.34
17	Q	91	ARG	N-CA-C	-8.02	101.48	111.11
16	P	48	TRP	N-CA-C	-7.91	103.53	113.02
11	K	14	VAL	N-CA-C	7.88	117.91	110.74
17	Q	9	VAL	CB-CA-C	-7.87	98.85	110.81
20	T	71	THR	CB-CA-C	-7.74	98.67	110.90
7	G	155	ARG	N-CA-C	7.73	122.15	112.87
4	D	155	LEU	N-CA-C	7.59	119.61	110.19
2	B	86	GLU	N-CA-C	-7.57	102.97	111.07
13	M	10	PRO	CA-C-O	-7.44	112.93	121.56
8	H	80	ILE	CB-CA-C	-7.43	101.63	111.81
8	H	136	GLU	N-CA-C	-7.42	95.13	108.48
13	M	11	ARG	N-CA-C	7.42	120.64	108.99
12	L	24	VAL	CA-C-N	-7.38	110.56	120.96
12	L	24	VAL	C-N-CA	-7.38	110.56	120.96
12	L	80	HIS	N-CA-C	7.33	121.94	112.92
2	B	87	ARG	N-CA-C	-7.28	100.89	110.43
5	E	145	LYS	N-CA-C	-7.22	103.49	111.36
20	T	97	ALA	CA-C-N	7.21	128.86	119.84
20	T	97	ALA	C-N-CA	7.21	128.86	119.84
17	Q	99	SER	N-CA-C	7.16	126.06	110.80
2	B	174	VAL	CB-CA-C	-7.12	102.85	111.97
18	R	22	VAL	N-CA-C	7.09	117.61	110.23
11	K	26	ASN	N-CA-C	7.05	122.06	113.38
16	P	33	ILE	N-CA-C	7.05	117.77	110.36
19	S	36	ARG	N-CA-C	-7.05	103.34	112.23
17	Q	67	LYS	N-CA-C	-7.03	99.63	110.10
5	E	6	PHE	N-CA-C	6.95	120.50	108.76
7	G	118	VAL	CB-CA-C	-6.92	103.16	111.81
17	Q	28	PRO	N-CA-C	-6.88	99.55	111.32
8	H	81	HIS	N-CA-C	-6.85	103.60	112.23
14	N	12	ARG	N-CA-C	-6.84	104.81	113.01
16	P	58	TYR	CB-CA-C	-6.83	99.40	110.74
16	P	40	ASP	CA-C-N	6.82	126.62	119.05
16	P	40	ASP	C-N-CA	6.82	126.62	119.05
2	B	15	VAL	N-CA-C	6.76	120.50	111.44
13	M	78	ILE	CB-CA-C	-6.74	103.22	112.04

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	T	102	GLY	N-CA-C	-6.73	99.78	112.64
4	D	38	TYR	CA-C-N	6.69	127.27	120.38
4	D	38	TYR	C-N-CA	6.69	127.27	120.38
5	E	24	ARG	N-CA-C	-6.68	101.71	110.53
11	K	87	THR	CB-CA-C	-6.66	99.40	110.19
11	K	91	ARG	N-CA-C	-6.66	101.37	111.56
9	I	122	ALA	CA-C-N	6.64	127.16	119.99
9	I	122	ALA	C-N-CA	6.64	127.16	119.99
17	Q	59	ILE	N-CA-C	-6.64	98.82	108.11
12	L	41	ARG	N-CA-C	6.63	116.80	108.45
11	K	101	SER	N-CA-C	-6.61	104.45	113.30
14	N	10	ALA	N-CA-C	-6.59	96.76	110.80
19	S	3	ARG	N-CA-C	6.59	119.06	110.43
5	E	29	GLY	N-CA-C	6.58	123.26	111.62
15	O	5	LYS	N-CA-C	-6.56	104.05	111.14
10	J	55	LYS	CB-CA-C	-6.55	107.24	115.89
10	J	21	GLN	N-CA-C	-6.46	104.66	112.54
4	D	196	LEU	CA-C-N	6.43	127.88	119.84
4	D	196	LEU	C-N-CA	6.43	127.88	119.84
10	J	62	HIS	N-CA-C	6.43	119.35	110.35
2	B	187	LEU	N-CA-C	-6.41	100.34	109.96
12	L	63	GLY	N-CA-C	-6.41	107.06	114.69
15	O	13	GLN	N-CA-C	-6.22	105.41	112.87
3	C	169	ALA	N-CA-C	6.18	118.35	109.14
8	H	35	ILE	CB-CA-C	-6.18	103.97	111.88
4	D	188	LEU	CA-C-N	6.17	125.93	119.76
4	D	188	LEU	C-N-CA	6.17	125.93	119.76
7	G	45	ASP	N-CA-C	-6.14	104.59	111.28
4	D	50	ARG	CA-C-N	6.13	126.61	119.99
4	D	50	ARG	C-N-CA	6.13	126.61	119.99
8	H	51	VAL	N-CA-C	6.11	117.09	108.17
16	P	4	ILE	CB-CA-C	-6.09	103.48	110.73
7	G	80	VAL	N-CA-C	-6.08	99.50	108.99
9	I	54	ASP	N-CA-C	6.06	118.00	110.91
13	M	15	VAL	N-CA-C	6.04	116.78	110.62
8	H	67	PRO	N-CA-C	-6.03	102.41	111.57
18	R	75	ILE	CB-CA-C	-6.02	104.15	112.04
15	O	45	VAL	CB-CA-C	-6.01	101.44	111.29
12	L	124	LYS	CA-C-N	5.99	125.93	119.76
12	L	124	LYS	C-N-CA	5.99	125.93	119.76
11	K	111	ASP	N-CA-C	5.96	120.68	113.17
17	Q	90	ILE	CB-CA-C	-5.96	104.23	112.04

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	J	52	GLY	CA-C-N	5.89	125.27	118.85
10	J	52	GLY	C-N-CA	5.89	125.27	118.85
7	G	69	VAL	N-CA-C	5.89	120.46	113.22
8	H	49	GLU	N-CA-C	-5.86	100.50	109.41
5	E	109	ILE	CB-CA-C	-5.86	104.20	111.70
1	A	1528	U	P-O3'-C3'	5.85	128.97	120.20
12	L	29	GLY	N-CA-C	-5.82	108.16	115.08
11	K	102	GLY	N-CA-C	-5.80	108.18	115.08
14	N	22	THR	N-CA-C	-5.79	101.61	109.95
20	T	55	ILE	CB-CA-C	-5.79	104.46	112.04
14	N	13	THR	CA-C-N	5.79	125.16	118.85
14	N	13	THR	C-N-CA	5.79	125.16	118.85
9	I	125	TYR	N-CA-C	5.77	117.02	108.60
8	H	100	ILE	CB-CA-C	-5.75	104.68	110.89
12	L	100	ILE	CB-CA-C	-5.74	103.34	111.21
10	J	44	VAL	CB-CA-C	-5.74	103.21	111.19
1	A	1528	U	C2'-C3'-O3'	5.71	118.06	109.50
10	J	76	ASN	N-CA-C	5.71	122.42	109.81
5	E	93	PRO	CA-C-O	-5.69	114.92	121.86
20	T	13	LEU	CB-CA-C	-5.68	99.11	110.42
5	E	111	GLU	N-CA-C	-5.68	104.47	111.40
4	D	39	PRO	CA-C-N	5.68	125.87	120.31
4	D	39	PRO	C-N-CA	5.68	125.87	120.31
11	K	17	GLY	N-CA-C	5.63	119.35	111.19
4	D	39	PRO	N-CA-C	5.62	117.56	110.70
2	B	117	GLU	N-CA-C	5.61	117.47	111.36
6	F	52	ILE	CB-CA-C	-5.61	102.85	110.42
11	K	48	ILE	CB-CA-C	-5.61	102.09	111.29
19	S	4	SER	N-CA-C	5.60	118.57	108.48
1	A	266	G	C2'-C3'-O3'	5.60	117.90	109.50
5	E	64	ARG	N-CA-C	5.59	117.17	111.14
5	E	69	VAL	CB-CA-C	-5.58	101.20	111.36
5	E	82	VAL	N-CA-C	5.58	115.72	108.35
3	C	198	VAL	N-CA-C	5.56	116.07	107.78
4	D	198	VAL	CB-CA-C	-5.56	102.56	110.12
2	B	79	ASP	N-CA-C	5.55	118.51	111.69
1	A	1200	C	C2-N1-C1'	5.54	135.43	118.80
5	E	9	LYS	CA-C-N	-5.52	115.66	122.84
5	E	9	LYS	C-N-CA	-5.52	115.66	122.84
8	H	37	ARG	N-CA-C	-5.51	104.66	111.33
3	C	57	ILE	N-CA-C	5.51	115.79	107.75
12	L	49	ASN	N-CA-C	5.51	118.43	109.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	58	ILE	CB-CA-C	-5.50	104.84	111.88
17	Q	53	LEU	N-CA-C	5.50	118.20	109.96
12	L	17	LYS	CA-C-N	-5.48	116.40	123.19
12	L	17	LYS	C-N-CA	-5.48	116.40	123.19
17	Q	35	VAL	CB-CA-C	-5.46	103.42	110.84
20	T	20	LEU	CA-CB-CG	-5.43	97.30	116.30
8	H	100	ILE	N-CA-CB	5.42	115.12	110.08
5	E	69	VAL	CA-C-N	5.40	126.59	119.84
5	E	69	VAL	C-N-CA	5.40	126.59	119.84
4	D	17	VAL	CB-CA-C	-5.38	102.60	110.62
5	E	87	SER	N-CA-C	5.36	117.48	108.96
4	D	30	LYS	N-CA-C	5.35	119.92	113.17
7	G	66	VAL	N-CA-C	-5.32	104.78	110.36
8	H	56	LYS	CA-C-N	5.31	125.77	120.14
8	H	56	LYS	C-N-CA	5.31	125.77	120.14
17	Q	78	GLU	N-CA-C	5.31	117.73	108.76
12	L	70	ILE	CA-C-N	5.30	126.46	119.84
12	L	70	ILE	C-N-CA	5.30	126.46	119.84
3	C	148	GLY	N-CA-C	5.30	120.67	111.14
5	E	41	VAL	CB-CA-C	-5.29	102.50	110.55
20	T	57	ARG	N-CA-C	-5.29	105.59	111.36
11	K	80	VAL	N-CA-C	5.29	117.49	108.86
18	R	31	LEU	N-CA-C	-5.29	106.50	113.17
20	T	23	ARG	N-CA-C	-5.27	104.78	111.11
12	L	66	VAL	CB-CA-C	-5.27	101.40	110.30
8	H	51	VAL	CB-CA-C	-5.26	101.96	110.28
15	O	69	TYR	CB-CA-C	-5.26	102.59	110.90
8	H	32	LYS	N-CA-C	-5.25	105.64	111.36
5	E	113	ALA	N-CA-C	-5.25	106.71	113.01
8	H	110	ALA	N-CA-C	-5.24	100.49	109.24
5	E	76	ILE	CA-C-N	5.23	124.90	119.56
5	E	76	ILE	C-N-CA	5.23	124.90	119.56
8	H	13	ILE	N-CA-C	5.23	115.44	110.42
10	J	40	LEU	CA-C-N	5.23	125.24	119.90
10	J	40	LEU	C-N-CA	5.23	125.24	119.90
18	R	63	GLN	N-CA-C	-5.22	105.59	111.28
5	E	11	ILE	N-CA-C	5.21	115.43	110.53
5	E	66	MET	CA-C-N	-5.20	115.76	122.99
5	E	66	MET	C-N-CA	-5.20	115.76	122.99
5	E	94	ALA	N-CA-C	5.20	118.07	109.85
8	H	134	ILE	N-CA-C	5.20	120.16	109.34
11	K	77	MET	N-CA-C	5.19	118.27	109.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	Q	5	VAL	CB-CA-C	-5.19	102.95	110.63
12	L	14	GLY	CA-C-O	-5.19	117.83	121.88
3	C	158	GLY	N-CA-C	-5.19	108.74	115.59
10	J	47	PHE	CA-C-N	-5.16	116.13	122.84
10	J	47	PHE	C-N-CA	-5.16	116.13	122.84
16	P	21	VAL	CB-CA-C	-5.16	104.02	111.19
18	R	61	LYS	N-CA-C	-5.14	105.58	111.14
4	D	88	VAL	CB-CA-C	-5.13	103.68	111.69
8	H	87	SER	N-CA-C	-5.13	103.37	110.35
10	J	4	ILE	N-CA-C	5.12	116.06	108.23
17	Q	32	TYR	CA-CB-CG	-5.12	104.69	113.90
4	D	187	ARG	CA-C-N	5.12	127.61	120.65
4	D	187	ARG	C-N-CA	5.12	127.61	120.65
10	J	55	LYS	N-CA-C	5.12	117.61	109.02
16	P	33	ILE	CB-CA-C	-5.11	105.34	111.88
9	I	124	GLN	N-CA-C	5.11	117.78	109.86
13	M	25	ILE	N-CA-C	5.11	115.26	108.11
12	L	115	LYS	CA-C-N	-5.10	115.60	123.14
12	L	115	LYS	C-N-CA	-5.10	115.60	123.14
5	E	33	VAL	CB-CA-C	-5.09	102.97	110.82
15	O	12	ILE	CB-CA-C	-5.09	105.37	112.04
7	G	89	MET	N-CA-C	5.08	116.02	108.60
13	M	20	THR	N-CA-C	5.08	117.55	111.71
5	E	130	ASN	N-CA-C	5.04	118.20	111.75
11	K	84	VAL	N-CA-C	5.04	115.23	107.77
15	O	67	LEU	CA-CB-CG	-5.03	98.70	116.30
2	B	25	ASN	N-CA-C	-5.01	103.33	109.65
12	L	10	LEU	N-CA-C	-5.01	105.90	111.36

There are no chirality outliers.

All (18) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	14	GLY	Peptide
2	B	75	LYS	Peptide
2	B	89	GLY	Peptide
3	C	166	GLU	Peptide
3	C	2	GLY	Peptide
4	D	154	ASN	Peptide
8	H	27	PRO	Peptide
8	H	90	GLY	Peptide
9	I	38	GLN	Peptide

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Mol	Chain	Res	Type	Group
10	J	61	GLU	Peptide
10	J	85	LEU	Peptide
12	L	46	LYS	Peptide
12	L	91	LYS	Peptide
16	P	82	GLN	Peptide
19	S	4	SER	Peptide
20	T	12	ALA	Peptide
20	T	8	ARG	Peptide
21	U	24	ARG	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32707	0	16542	1880	1
2	B	1896	0	1936	230	0
3	C	1613	0	1677	215	0
4	D	1703	0	1763	212	0
5	E	1147	0	1207	144	1
6	F	843	0	857	92	0
7	G	1257	0	1296	158	0
8	H	1116	0	1177	120	0
9	I	1010	0	1037	145	0
10	J	793	0	835	126	0
11	K	873	0	894	78	0
12	L	973	0	1058	109	0
13	M	937	0	995	138	0
14	N	492	0	529	88	0
15	O	734	0	771	103	0
16	P	701	0	720	79	0
17	Q	834	0	906	118	0
18	R	585	0	657	86	0
19	S	648	0	673	84	0
20	T	763	0	861	107	0
21	U	209	0	221	43	0
22	V	77	0	42	3	0
23	W	235	0	121	34	0
24	a	175	0	87	42	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
25	b	60	0	31	3	0
26	A	326	0	0	0	0
26	D	3	0	0	0	0
26	E	4	0	0	0	0
26	F	1	0	0	0	0
26	G	1	0	0	0	0
26	H	1	0	0	0	0
26	J	1	0	0	0	0
26	N	1	0	0	0	0
26	P	3	0	0	0	0
26	Q	1	0	0	0	0
26	S	2	0	0	0	0
27	A	40	0	38	15	0
28	D	1	0	0	0	0
28	N	1	0	0	0	0
29	A	866	0	0	96	0
29	C	1	0	0	0	0
29	D	7	0	0	1	0
29	E	5	0	0	0	0
29	L	1	0	0	0	0
29	N	1	0	0	0	0
29	P	1	0	0	0	0
29	Q	2	0	0	0	0
29	T	3	0	0	0	0
29	U	4	0	0	0	0
29	W	1	0	0	0	0
All	All	53659	0	36931	4112	2

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 46.

All (4112) 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)
1:A:451:A:O2'	29:A:2729:HOH:O	1.59	1.20
12:L:70:ILE:HG21	12:L:75:HIS:HD2	1.13	1.14
15:O:88:ARG:HA	15:O:88:ARG:HE	1.10	1.12
1:A:266:G:H5'	1:A:266:G:C8	1.83	1.12
21:U:10:ARG:CB	21:U:10:ARG:HH11	1.62	1.12
7:G:12:LEU:H	7:G:12:LEU:HD12	1.08	1.11
1:A:1054:C:O2	1:A:1054:C:H3'	1.48	1.11

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:30:SER:HB2	10:J:80:LYS:HB2	1.32	1.11
10:J:55:LYS:HG2	10:J:56:HIS:H	0.99	1.11
1:A:692:U:OP1	11:K:124:LYS:NZ	1.82	1.10
9:I:50:LEU:HD11	9:I:81:ILE:HG21	1.20	1.10
6:F:14:LEU:HD13	6:F:18:GLN:HB3	1.33	1.10
1:A:1493[A]:A:H8	1:A:1493[A]:A:H3'	1.10	1.10
2:B:88:ALA:HB2	2:B:219:VAL:HG13	1.33	1.10
2:B:25:ASN:ND2	2:B:193:ASP:HB2	1.67	1.09
1:A:266:G:O2'	1:A:267:C:OP2	1.72	1.08
1:A:538:G:H5''	12:L:114:LYS:HB2	1.35	1.08
24:a:34:G:H2'	24:a:35:G:H8	1.18	1.08
1:A:1493[A]:A:H3'	1:A:1493[A]:A:C8	1.86	1.07
4:D:36:ARG:HB3	4:D:38:TYR:CE2	1.87	1.07
12:L:127:GLU:CG	12:L:128:ALA:H	1.62	1.07
14:N:27:CYS:SG	14:N:29:ARG:HB2	1.94	1.07
20:T:57:ARG:HH21	20:T:100:ILE:HD13	1.19	1.07
1:A:328:C:O2'	1:A:329:A:OP2	1.72	1.06
12:L:127:GLU:HG3	12:L:128:ALA:H	0.93	1.06
5:E:126:ARG:HG2	5:E:126:ARG:HH11	1.16	1.06
7:G:50:ILE:HG21	7:G:58:PRO:HA	1.34	1.06
1:A:328:C:O2	1:A:328:C:H2'	1.55	1.06
2:B:75:LYS:HA	2:B:78:GLN:HG3	1.37	1.06
7:G:5:ARG:HG3	7:G:7:ALA:H	1.17	1.06
10:J:82:ILE:HA	10:J:85:LEU:HB2	1.14	1.06
8:H:102:ARG:H	8:H:102:ARG:HD2	1.17	1.05
15:O:17:ARG:HG3	15:O:17:ARG:HH11	1.14	1.05
20:T:49:ALA:HB3	20:T:99:LEU:HD21	1.38	1.04
1:A:89:C:H5	1:A:90:U:N3	1.54	1.04
1:A:543:C:C2'	1:A:544:G:H5'	1.87	1.04
1:A:61:G:O2'	29:A:2002:HOH:O	1.76	1.04
4:D:32:ALA:HA	4:D:35:ARG:HB2	1.39	1.04
6:F:12:PRO:HG3	6:F:58:GLY:HA2	1.33	1.03
1:A:1443:G:H4'	1:A:1446:A:H5'	1.41	1.03
1:A:107:G:H2'	1:A:108:G:H5''	1.40	1.03
21:U:10:ARG:HH11	21:U:10:ARG:HB2	1.21	1.03
1:A:89:C:C5	1:A:90:U:N3	2.25	1.02
1:A:858:G:O2'	1:A:859:A:H5'	1.59	1.02
1:A:1402:4OC:HM22	1:A:1403:C:H5'	1.37	1.02
6:F:50:TYR:CE1	18:R:77:GLY:HA2	1.95	1.02
1:A:1026:G:H2'	1:A:1027:C:H5''	1.42	1.01
7:G:152:ALA:O	7:G:155:ARG:NH1	1.93	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:87:ARG:HH21	18:R:87:ARG:HG3	1.22	1.01
1:A:1498:UR3:H4'	1:A:1519[A]:MA6:C2	1.91	1.01
10:J:86:MET:HG3	10:J:87:THR:H	1.26	1.00
1:A:103:C:OP1	20:T:17:ARG:NH1	1.93	1.00
1:A:1148:U:H2'	1:A:1149:C:O4'	1.61	1.00
1:A:1347:G:H3'	9:I:108:VAL:O	1.59	1.00
17:Q:100:LYS:HB2	17:Q:101:ARG:HH11	1.21	1.00
18:R:37:VAL:O	18:R:40:LEU:N	1.92	1.00
4:D:150:GLU:N	4:D:150:GLU:OE2	1.92	1.00
11:K:15:ALA:HA	11:K:77:MET:HA	1.43	1.00
1:A:1497:G:C2'	1:A:1498:UR3:H5'	1.91	1.00
1:A:9:G:OP1	5:E:122:GLU:HG3	1.60	0.99
1:A:1328:C:OP1	21:U:20:LYS:NZ	1.96	0.99
1:A:1539:C:O2	24:a:34:G:N2	1.95	0.99
13:M:16:ASP:OD2	13:M:17:VAL:N	1.95	0.99
1:A:710:G:H5''	6:F:54:LYS:HE3	1.43	0.99
1:A:746:A:H2'	1:A:747:C:H5'	1.44	0.99
1:A:571:U:H5''	1:A:572:A:OP2	1.63	0.98
1:A:1049:U:H4'	1:A:1050:G:O5'	1.60	0.98
1:A:1316:G:N2	1:A:1319:A:OP2	1.96	0.98
4:D:18:LYS:HE3	4:D:20:TYR:HE2	1.29	0.98
1:A:1404:5MC:H1'	1:A:1499:A:C2	1.99	0.98
1:A:1399:C:H4'	1:A:1400:5MC:H5''	1.46	0.98
7:G:16:LEU:H	7:G:16:LEU:HD22	1.29	0.98
1:A:1026:G:O2'	1:A:1027:C:OP1	1.80	0.97
1:A:867:G:H2'	1:A:868:C:H5'	1.44	0.97
27:A:1928:SRV:HI32	27:A:1928:SRV:H22	1.46	0.97
2:B:231:GLU:HB3	2:B:232:PRO:HD2	1.45	0.97
12:L:127:GLU:HG3	12:L:128:ALA:N	1.70	0.97
1:A:1435:G:H2'	1:A:1436:U:C6	1.99	0.97
18:R:26:LEU:HD11	18:R:42:ARG:HD3	1.45	0.97
10:J:55:LYS:HG2	10:J:56:HIS:N	1.79	0.96
9:I:9:ARG:HB2	9:I:13:ALA:O	1.63	0.96
24:a:35:G:H2'	24:a:36:A:C8	2.00	0.96
7:G:120:ILE:HD13	7:G:120:ILE:N	1.78	0.96
12:L:27:LEU:HG	12:L:28:LYS:H	1.30	0.96
1:A:1532:U:H2'	1:A:1533:C:C6	2.01	0.96
12:L:70:ILE:HG21	12:L:75:HIS:CD2	2.00	0.96
1:A:644:G:H8	1:A:644:G:H5'	1.28	0.95
1:A:914:A:P	27:A:1928:SRV:HI33	2.06	0.95
1:A:1305:G:OP2	21:U:2:GLY:N	1.99	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:108:VAL:HG12	9:I:109:VAL:H	1.31	0.95
6:F:50:TYR:HE1	18:R:77:GLY:HA2	1.30	0.94
1:A:1299:A:C5	1:A:1301:U:O2	2.20	0.94
1:A:792:A:H4'	1:A:793:U:OP1	1.65	0.94
23:W:31:C:N4	23:W:39:G:H1	1.63	0.94
1:A:372:C:O2'	29:A:2721:HOH:O	1.84	0.94
1:A:1068:G:P	29:A:2218:HOH:O	2.25	0.94
1:A:1104:G:O5'	2:B:111:ARG:HD2	1.67	0.94
1:A:707:C:H4'	11:K:20:TYR:CD1	2.01	0.94
1:A:746:A:C2'	1:A:747:C:H5'	1.96	0.94
10:J:30:SER:CB	10:J:80:LYS:HB2	1.98	0.94
6:F:87:ARG:HH11	6:F:87:ARG:HG3	1.33	0.94
1:A:1064:G:H22	1:A:1190:G:H2'	1.31	0.93
10:J:44:VAL:HG13	10:J:66:ARG:HD3	1.50	0.93
13:M:49:THR:HG22	13:M:51:ALA:H	1.32	0.93
15:O:5:LYS:HA	15:O:5:LYS:NZ	1.83	0.93
3:C:188:LEU:HD11	3:C:195:VAL:HG13	1.51	0.93
13:M:49:THR:HB	13:M:52:GLU:HG3	1.50	0.93
8:H:54:ASP:OD2	8:H:55:GLY:N	2.02	0.93
9:I:8:GLY:HA3	9:I:79:LEU:HB3	1.49	0.93
17:Q:40:LYS:HD2	17:Q:42:TYR:CE1	2.04	0.93
1:A:1064:G:N2	1:A:1190:G:H2'	1.84	0.93
12:L:20:LYS:H	12:L:20:LYS:HE2	1.34	0.92
1:A:499:A:H4'	1:A:500:G:OP1	1.66	0.92
1:A:1412:C:H2'	1:A:1413:A:C8	2.05	0.92
2:B:97:TRP:HZ2	2:B:102:LEU:HD13	1.34	0.92
1:A:229:U:C2'	1:A:230:G:H5'	2.00	0.92
5:E:37:ARG:HG2	5:E:37:ARG:HH11	1.32	0.92
4:D:22:LYS:HB2	4:D:26:CYS:SG	2.10	0.92
4:D:36:ARG:HB3	4:D:38:TYR:HE2	1.30	0.92
15:O:79:ARG:HH11	15:O:79:ARG:HG3	1.35	0.92
4:D:83:SER:HA	4:D:89:THR:HG23	1.52	0.91
18:R:87:ARG:HH21	18:R:87:ARG:CG	1.82	0.91
11:K:120:ARG:HH11	11:K:120:ARG:HG2	1.34	0.91
8:H:102:ARG:HD2	8:H:102:ARG:N	1.85	0.91
1:A:279:A:OP2	17:Q:95:TYR:OH	1.86	0.91
1:A:1392:G:C2'	1:A:1393:U:H5'	1.99	0.91
1:A:867:G:C2'	1:A:868:C:H5'	2.01	0.91
13:M:34:LEU:HD13	13:M:41:PRO:HA	1.52	0.91
1:A:1035:A:H2'	1:A:1036:G:H8	1.34	0.91
1:A:1392:G:H2'	1:A:1393:U:H5'	1.49	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1381:U:C5	1:A:1382:C:C5	2.58	0.91
5:E:106:PRO:O	5:E:110:LEU:HD12	1.71	0.91
15:O:88:ARG:HA	15:O:88:ARG:NE	1.85	0.91
1:A:1497:G:H2'	1:A:1498:UR3:H5'	1.54	0.90
12:L:47:LYS:N	12:L:48:PRO:HD2	1.85	0.90
10:J:55:LYS:CG	10:J:56:HIS:H	1.78	0.90
15:O:33:THR:HG23	15:O:63:ARG:HH12	1.35	0.89
2:B:92:TYR:CD1	2:B:151:GLY:HA3	2.07	0.89
3:C:127:ARG:NE	3:C:127:ARG:HA	1.85	0.89
12:L:76:ASN:O	12:L:77:LEU:HD23	1.72	0.89
1:A:991:U:O2'	1:A:992:U:O5'	1.90	0.89
2:B:74:LYS:HE3	2:B:166:ASP:HB2	1.54	0.89
3:C:91:LEU:HD21	3:C:99:VAL:HG22	1.54	0.89
15:O:16:ALA:HB1	15:O:21:ASP:HB3	1.53	0.89
1:A:192:U:H1'	20:T:103:GLY:HA2	1.55	0.89
1:A:1538:C:H2'	1:A:1539:C:O4'	1.73	0.89
16:P:67:THR:HG22	16:P:68:ASP:H	1.36	0.89
10:J:25:GLU:HA	10:J:28:ARG:HB2	1.55	0.89
1:A:791:G:H2'	1:A:792:A:H5'	1.55	0.88
1:A:1442:G:C6	1:A:1446:A:N6	2.41	0.88
1:A:1056:U:H5'	3:C:163:ALA:HB2	1.55	0.88
1:A:484:G:O2'	1:A:485:G:OP2	1.90	0.88
1:A:500:G:C5	1:A:546:G:N2	2.42	0.88
10:J:48:THR:HA	10:J:62:HIS:HB3	1.54	0.88
1:A:1047:G:C2'	1:A:1048:G:H5'	2.04	0.88
1:A:1400:5MC:H3'	1:A:1401:G:H5'	1.55	0.88
7:G:38:LEU:O	7:G:42:ILE:HG13	1.71	0.88
1:A:604:G:H2'	1:A:605:U:H5'	1.54	0.88
15:O:88:ARG:HE	15:O:88:ARG:CA	1.83	0.88
24:a:34:G:H2'	24:a:35:G:C8	2.09	0.88
1:A:543:C:H2'	1:A:544:G:H5'	1.52	0.88
12:L:117:ARG:O	12:L:120:TYR:N	2.06	0.88
13:M:10:PRO:HB2	13:M:18:ALA:HB1	1.52	0.88
2:B:236:TYR:O	2:B:239:VAL:HG23	1.73	0.88
7:G:18:TYR:OH	7:G:58:PRO:HG2	1.74	0.87
1:A:1136:U:H5''	1:A:1137:C:OP2	1.74	0.87
1:A:353:A:OP1	29:A:2224:HOH:O	1.91	0.87
9:I:8:GLY:HA2	9:I:79:LEU:HD13	1.55	0.87
1:A:1047:G:H5''	14:N:4:LYS:HD3	1.56	0.87
16:P:1:MET:O	16:P:1:MET:HG2	1.75	0.87
1:A:1035:A:H2'	1:A:1036:G:C8	2.09	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:25:THR:O	15:O:29:VAL:HG23	1.75	0.87
16:P:74:LEU:HB3	16:P:79:VAL:HG21	1.54	0.87
1:A:839:U:O2	1:A:839:U:H2'	1.72	0.87
1:A:1256:A:H4'	1:A:1257:U:O5'	1.74	0.86
1:A:974:A:OP2	14:N:41:ARG:NH1	2.09	0.86
1:A:176:C:O2'	1:A:177:C:H5'	1.75	0.86
10:J:82:ILE:HA	10:J:85:LEU:CB	2.05	0.86
20:T:61:SER:OG	20:T:65:LYS:HD2	1.73	0.86
1:A:1381:U:H5	1:A:1382:C:C5	1.92	0.86
13:M:39:ILE:HG22	13:M:40:ASN:O	1.76	0.86
1:A:1493[A]:A:C8	1:A:1493[A]:A:C3'	2.59	0.86
5:E:51:VAL:HG23	5:E:52:PRO:HD3	1.57	0.86
6:F:98:LEU:H	6:F:98:LEU:HD13	1.41	0.85
1:A:1412:C:H2'	1:A:1413:A:H8	1.39	0.85
8:H:112:LEU:N	8:H:112:LEU:HD23	1.91	0.85
10:J:40:LEU:HB2	10:J:69:ASN:HB2	1.58	0.85
12:L:27:LEU:C	12:L:29:GLY:H	1.81	0.85
13:M:19:LEU:O	13:M:22:ILE:HG12	1.76	0.85
1:A:54:C:C4	1:A:352:C:C5	2.65	0.85
1:A:284:G:H2'	1:A:285:G:H8	1.41	0.85
1:A:1004:A:H5''	29:A:2325:HOH:O	1.75	0.85
13:M:108:ARG:NH2	13:M:114:ARG:HA	1.92	0.85
1:A:192:U:C1'	20:T:103:GLY:HA2	2.05	0.85
1:A:328:C:O2	1:A:328:C:C2'	2.22	0.85
1:A:1068:G:OP2	1:A:1068:G:H8	1.59	0.85
1:A:1225:A:H5'	1:A:1226:C:OP2	1.77	0.85
4:D:150:GLU:HA	4:D:153:ARG:HG3	1.56	0.85
1:A:981:U:H5'	14:N:21:TYR:CE1	2.12	0.85
4:D:192:GLU:N	4:D:192:GLU:OE2	2.10	0.85
1:A:393:A:C2	1:A:394:G:C8	2.64	0.85
1:A:821:G:H4'	29:A:2105:HOH:O	1.74	0.84
20:T:56:MET:HE3	20:T:85:MET:HG3	1.58	0.84
3:C:123:GLN:O	3:C:128:PHE:HB2	1.77	0.84
3:C:16:ARG:HG2	3:C:16:ARG:HH11	1.40	0.84
24:a:37:A:H2'	24:a:38:A:H8	1.41	0.84
3:C:58:GLU:H	3:C:65:ALA:HB3	1.43	0.84
18:R:43:PHE:C	18:R:44:LEU:HD23	2.02	0.84
19:S:15:LEU:O	19:S:19:VAL:HG12	1.77	0.84
20:T:57:ARG:NH2	20:T:100:ILE:HD13	1.93	0.84
1:A:54:C:C4	1:A:352:C:H5	1.96	0.84
2:B:61:LEU:HD13	2:B:66:GLY:HA3	1.60	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:33:THR:HG22	11:K:39:PRO:HA	1.58	0.84
1:A:304:U:O4	29:A:2495:HOH:O	1.94	0.84
17:Q:10:VAL:HG11	17:Q:52:LYS:O	1.77	0.84
1:A:114:U:O2'	1:A:115:G:H5'	1.78	0.83
1:A:509:A:O2'	1:A:510:A:OP1	1.93	0.83
4:D:189:PRO:HB2	4:D:194:LEU:HD21	1.59	0.83
1:A:604:G:C2'	1:A:605:U:H5'	2.07	0.83
1:A:1321:C:H4'	13:M:87:TYR:HE2	1.42	0.83
4:D:98:GLU:OE2	4:D:107:ARG:HD3	1.77	0.83
10:J:34:VAL:HG13	10:J:74:ILE:HG22	1.59	0.83
5:E:90:VAL:O	5:E:91:LEU:HD23	1.77	0.83
1:A:1212:U:H1'	1:A:1213:A:OP2	1.78	0.83
2:B:170:GLU:OE2	2:B:170:GLU:HA	1.79	0.83
16:P:67:THR:HG22	16:P:68:ASP:N	1.91	0.83
18:R:38:GLU:N	18:R:38:GLU:OE2	2.12	0.83
1:A:1281:U:H4'	1:A:1282:C:OP2	1.76	0.83
1:A:1300:G:O2'	1:A:1301:U:P	2.37	0.83
8:H:112:LEU:HD23	8:H:112:LEU:H	1.44	0.83
1:A:448:A:O2'	1:A:449:C:H5'	1.79	0.83
15:O:45:VAL:HB	15:O:46:HIS:ND1	1.92	0.83
19:S:18:LYS:HG2	19:S:31:ILE:HD11	1.59	0.83
4:D:70:ILE:HG22	4:D:71:SER:O	1.79	0.82
10:J:47:PHE:CZ	14:N:37:PHE:HE1	1.97	0.82
2:B:82:ARG:HA	2:B:92:TYR:CE2	2.14	0.82
9:I:32:ASP:OD1	9:I:33:PHE:N	2.12	0.82
1:A:1057:G:H5''	3:C:154:SER:HB2	1.61	0.82
1:A:1435:G:H2'	1:A:1436:U:H6	1.40	0.82
2:B:130:ARG:NH1	2:B:134:GLU:OE1	2.12	0.82
19:S:17:GLU:HA	19:S:20:LEU:HD12	1.60	0.82
23:W:31:C:H42	23:W:39:G:H1	0.84	0.82
3:C:120:VAL:O	3:C:124:ILE:HG13	1.80	0.82
1:A:1399:C:O2	1:A:1401:G:C5	2.32	0.82
9:I:17:VAL:HG13	9:I:63:ILE:HD11	1.62	0.82
15:O:26:GLU:OE2	15:O:77:ARG:NH1	2.12	0.82
1:A:512:U:O2	1:A:540:G:N2	2.13	0.81
5:E:144:THR:O	5:E:148:VAL:CG2	2.28	0.81
1:A:1532:U:C4	1:A:1533:C:N4	2.48	0.81
19:S:10:PHE:O	19:S:39:THR:OG1	1.98	0.81
1:A:107:G:C2'	1:A:108:G:H5''	2.09	0.81
1:A:1314:C:OP2	19:S:6:LYS:HD3	1.80	0.81
4:D:173:TRP:O	4:D:174:LEU:HD23	1.80	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:839:U:H5'	1:A:840:C:H5	1.44	0.81
1:A:1054:C:O2	1:A:1054:C:C3'	2.28	0.81
2:B:131:PRO:O	2:B:134:GLU:HB3	1.80	0.81
1:A:117:G:OP2	29:A:2018:HOH:O	1.98	0.81
1:A:138:G:H5'	1:A:138:G:H8	1.45	0.81
1:A:1152:A:OP1	10:J:68:HIS:ND1	2.14	0.81
17:Q:100:LYS:HB2	17:Q:101:ARG:NH1	1.96	0.81
17:Q:40:LYS:HG2	17:Q:41:LYS:N	1.93	0.81
21:U:10:ARG:HH11	21:U:10:ARG:CG	1.94	0.81
1:A:1532:U:H2'	1:A:1533:C:H6	1.46	0.81
1:A:1399:C:C6	1:A:1502:A:N6	2.48	0.81
7:G:5:ARG:HG3	7:G:7:ALA:N	1.96	0.81
19:S:18:LYS:O	19:S:22:LEU:HG	1.81	0.81
4:D:19:LEU:HD23	4:D:19:LEU:H	1.45	0.80
4:D:120:LEU:HD22	4:D:126:ILE:HD11	1.61	0.80
1:A:673:G:H2'	1:A:674:G:C8	2.15	0.80
1:A:392:G:H2'	1:A:393:A:H8	1.46	0.80
1:A:303:A:N6	29:A:2495:HOH:O	2.15	0.80
1:A:1057:G:H5''	3:C:154:SER:CB	2.12	0.80
1:A:1300:G:O2'	1:A:1301:U:O5'	1.99	0.80
1:A:141:A:H1'	1:A:182:U:O2	1.82	0.80
1:A:415:A:H2'	1:A:416:G:H8	1.44	0.80
1:A:539:A:H2'	1:A:540:G:C8	2.17	0.80
1:A:250:A:H4'	1:A:251:G:O5'	1.82	0.80
1:A:628:G:C2'	1:A:629:G:H5'	2.12	0.80
1:A:984:C:H42	1:A:1221:G:H1	1.28	0.80
1:A:853:G:C2'	1:A:854:G:H5'	2.12	0.80
1:A:1412:C:OP1	12:L:57:LYS:NZ	2.15	0.80
1:A:1496:C:H2'	1:A:1497:G:C8	2.16	0.80
10:J:16:LEU:HD21	10:J:70:ARG:HG3	1.63	0.80
10:J:76:ASN:C	10:J:78:ASN:H	1.88	0.80
1:A:1356:G:H2'	1:A:1357:A:C8	2.17	0.80
4:D:18:LYS:HE3	4:D:20:TYR:CE2	2.17	0.80
1:A:89:C:H5	1:A:90:U:C4	2.00	0.80
1:A:1054:C:O2	23:W:34:G:H5'	1.81	0.80
13:M:19:LEU:O	13:M:22:ILE:CG1	2.30	0.79
2:B:87:ARG:HD2	2:B:88:ALA:H	1.47	0.79
13:M:84:ILE:HD12	13:M:86:CYS:HB2	1.64	0.79
7:G:74:GLU:HG2	7:G:91:VAL:HG22	1.63	0.79
17:Q:29:HIS:CE1	17:Q:32:TYR:H	2.01	0.79
19:S:80:TYR:CE1	19:S:81:ARG:HG2	2.16	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:114:U:C2'	1:A:115:G:H5'	2.13	0.79
1:A:1101:A:H4'	1:A:1102:A:O5'	1.82	0.79
1:A:624:C:H5''	29:A:2767:HOH:O	1.82	0.79
4:D:100:ARG:NH1	4:D:137:SER:HA	1.97	0.79
15:O:5:LYS:HA	15:O:5:LYS:HZ2	1.43	0.79
7:G:120:ILE:HD13	7:G:120:ILE:H	1.48	0.79
8:H:55:GLY:HA3	8:H:56:LYS:HE3	1.63	0.79
15:O:9:GLN:OE1	15:O:9:GLN:HA	1.81	0.79
1:A:1515[B]:C:N4	1:A:1520[B]:G:O6	2.14	0.79
1:A:89:C:H5	1:A:90:U:H3	1.16	0.79
1:A:229:U:H2'	1:A:230:G:H5'	1.62	0.79
1:A:777:A:OP1	29:A:2536:HOH:O	2.00	0.79
1:A:542:G:OP1	4:D:10:ARG:NH2	2.16	0.79
9:I:50:LEU:CD1	9:I:81:ILE:HG21	2.08	0.79
20:T:50:GLU:CA	20:T:99:LEU:HD11	2.13	0.79
1:A:924:C:O2'	1:A:1399:C:H6	1.65	0.78
1:A:1272:G:N7	29:A:2695:HOH:O	2.16	0.78
1:A:527:7MG:OP2	27:A:1928:SRV:O32	2.01	0.78
1:A:1346:A:C4	7:G:10:ARG:NH1	2.51	0.78
2:B:87:ARG:HE	2:B:219:VAL:HG11	1.48	0.78
8:H:10:LEU:HD23	8:H:10:LEU:N	1.97	0.78
9:I:43:ALA:HA	9:I:74:ILE:HD12	1.63	0.78
9:I:69:GLY:O	9:I:73:GLN:HG3	1.83	0.78
9:I:90:PRO:O	9:I:93:ARG:HG3	1.82	0.78
20:T:67:ALA:O	20:T:73:HIS:ND1	2.16	0.78
3:C:86:VAL:O	3:C:89:GLU:HB3	1.82	0.78
1:A:643:C:H2'	1:A:644:G:H5''	1.65	0.78
1:A:1033:G:H2'	1:A:1034:G:H5'	1.66	0.78
4:D:61:LYS:HD2	4:D:62:GLN:N	1.97	0.78
15:O:85:LEU:HD23	15:O:85:LEU:N	1.97	0.78
1:A:352:C:O2'	1:A:354:G:OP1	2.02	0.78
1:A:1147:C:H4'	9:I:5:TYR:HE2	1.47	0.78
4:D:159:ARG:HH11	4:D:159:ARG:HG2	1.48	0.78
5:E:24:ARG:HG2	5:E:24:ARG:HH11	1.47	0.78
5:E:126:ARG:HH11	5:E:126:ARG:CG	1.97	0.78
8:H:4:ASP:OD2	8:H:85:ARG:NE	2.15	0.78
1:A:76:C:O2'	1:A:77:G:H5'	1.83	0.78
5:E:48:ALA:HB1	5:E:49:PRO:HD2	1.65	0.78
20:T:10:LEU:CD2	20:T:13:LEU:H	1.96	0.78
1:A:597:G:H1	1:A:643:C:H42	1.29	0.78
1:A:965:A:C2	1:A:969:A:C2	2.72	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1400:5MC:H3'	1:A:1401:G:C5'	2.14	0.78
1:A:1347:G:O2'	1:A:1348:U:P	2.41	0.78
5:E:144:THR:HG22	5:E:145:LYS:H	1.49	0.78
9:I:31:GLN:NE2	9:I:36:TYR:HD1	1.81	0.78
1:A:643:C:C2'	1:A:644:G:H5''	2.14	0.77
1:A:1157:A:H4'	1:A:1158:C:O5'	1.83	0.77
7:G:97:GLN:O	7:G:101:LEU:HD12	1.84	0.77
1:A:768:A:OP2	29:A:2052:HOH:O	2.02	0.77
3:C:46:GLU:HB3	3:C:47:LEU:HD12	1.66	0.77
4:D:15:GLU:HG3	4:D:63:LYS:HD3	1.65	0.77
6:F:48:LEU:CD1	6:F:52:ILE:HG13	2.14	0.77
9:I:121:ARG:HG3	9:I:121:ARG:HH11	1.48	0.77
21:U:10:ARG:CB	21:U:10:ARG:NH1	2.45	0.77
15:O:74:ASP:OD2	15:O:77:ARG:HG2	1.84	0.77
20:T:54:LYS:HG2	20:T:55:ILE:HD12	1.65	0.77
3:C:179:ARG:HD2	3:C:207:VAL:HG22	1.65	0.77
1:A:1534:C:N3	1:A:1535:A:C2	2.53	0.77
1:A:1535:A:C2	24:a:37:A:H2	2.03	0.77
2:B:36:ARG:HG3	2:B:41:ILE:HD11	1.66	0.77
4:D:208:SER:HA	29:D:404:HOH:O	1.85	0.77
9:I:108:VAL:HG12	9:I:109:VAL:N	1.99	0.77
10:J:29:ARG:N	10:J:29:ARG:HD2	2.00	0.77
19:S:80:TYR:CD1	19:S:81:ARG:N	2.53	0.77
18:R:47:THR:HG22	18:R:48:GLY:H	1.50	0.77
1:A:673:G:H5''	6:F:87:ARG:NH1	2.00	0.77
3:C:116:VAL:O	3:C:120:VAL:HG23	1.85	0.77
13:M:11:ARG:HG3	13:M:12:ASN:N	1.99	0.77
1:A:89:C:C2'	1:A:90:U:O5'	2.33	0.77
1:A:201:C:H42	1:A:216:G:H1	1.32	0.77
1:A:1026:G:H2'	1:A:1027:C:O2	1.84	0.76
12:L:53:ARG:HD2	12:L:93:LEU:HD21	1.65	0.76
1:A:1245:A:C2	1:A:1293:G:C2	2.74	0.76
27:A:1928:SRV:HI32	27:A:1928:SRV:C22	2.16	0.76
2:B:219:VAL:HA	2:B:222:ILE:HG12	1.66	0.76
3:C:195:VAL:C	3:C:196:LEU:HD23	2.11	0.76
4:D:32:ALA:O	4:D:36:ARG:N	2.17	0.76
5:E:8:GLU:HB3	5:E:34:VAL:HG12	1.65	0.76
13:M:51:ALA:O	13:M:54:VAL:HG12	1.85	0.76
1:A:512:U:OP1	4:D:46:LYS:NZ	2.15	0.76
1:A:1047:G:N7	29:A:2425:HOH:O	2.19	0.76
1:A:1498:UR3:H4'	1:A:1519[A]:MA6:H2	1.67	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:26:ARG:HD3	14:N:47:LEU:HD11	1.66	0.76
15:O:33:THR:HG23	15:O:63:ARG:NH1	1.99	0.76
1:A:137:C:C2'	1:A:138:G:H5''	2.15	0.76
1:A:247:G:OP2	17:Q:100:LYS:HG2	1.85	0.76
2:B:240:GLN:HG2	2:B:240:GLN:O	1.84	0.76
6:F:7:ASN:HD21	18:R:34:TYR:HE1	1.32	0.76
6:F:12:PRO:CG	6:F:58:GLY:HA2	2.14	0.76
3:C:151:VAL:C	3:C:152:ILE:HD12	2.10	0.76
3:C:155:GLY:O	3:C:196:LEU:HD22	1.85	0.76
11:K:48:ILE:HG22	11:K:49:GLY:H	1.48	0.76
1:A:628:G:O2'	1:A:629:G:H5'	1.86	0.76
7:G:64:GLN:O	7:G:68:ASN:ND2	2.18	0.76
1:A:284:G:H2'	1:A:285:G:C8	2.21	0.76
1:A:438:G:H4'	4:D:123:HIS:HD2	1.51	0.76
1:A:677:U:H3	1:A:713:G:H22	1.32	0.76
1:A:1268:A:OP1	29:A:2314:HOH:O	2.02	0.76
3:C:11:ARG:NH1	3:C:177:THR:O	2.19	0.76
5:E:144:THR:HG22	5:E:145:LYS:N	2.01	0.76
10:J:42:THR:HG23	10:J:67:THR:O	1.85	0.76
1:A:543:C:O2'	1:A:544:G:H5'	1.85	0.76
1:A:1314:C:C5	19:S:6:LYS:HE2	2.21	0.76
1:A:1504:G:OP1	1:A:1507:A:H4'	1.86	0.76
2:B:16:HIS:CD2	2:B:17:PHE:HD2	2.04	0.76
18:R:26:LEU:HD11	18:R:42:ARG:CD	2.16	0.76
1:A:438:G:H4'	4:D:123:HIS:CD2	2.21	0.75
3:C:180:ALA:HB1	3:C:182:ILE:HG13	1.68	0.75
1:A:1034:G:H2'	1:A:1035:A:C8	2.22	0.75
1:A:1343:G:H1'	9:I:121:ARG:HH12	1.51	0.75
1:A:461:C:OP2	29:A:2254:HOH:O	2.04	0.75
1:A:1407:5MC:C2'	1:A:1408:A:H5'	2.17	0.75
9:I:53:VAL:HG21	9:I:85:LEU:HD11	1.66	0.75
1:A:463:A:H2'	1:A:474:G:H8	1.50	0.75
1:A:731:G:OP1	1:A:766:A:H1'	1.87	0.75
1:A:827:U:H5''	1:A:828:A:OP2	1.85	0.75
1:A:1003(A):G:N2	1:A:1038:C:O2	2.19	0.75
1:A:1408:A:H2'	1:A:1409:C:H6	1.49	0.75
20:T:51:GLU:O	20:T:55:ILE:HD13	1.85	0.75
1:A:1225:A:H2'	1:A:1225:A:N3	2.00	0.75
10:J:76:ASN:O	10:J:78:ASN:N	2.19	0.75
12:L:27:LEU:C	12:L:29:GLY:N	2.45	0.75
12:L:117:ARG:O	12:L:119:LYS:N	2.20	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:8:LYS:O	15:O:11:VAL:HG13	1.86	0.75
24:a:35:G:H2'	24:a:36:A:H8	1.50	0.75
1:A:73:C:N4	1:A:74:C:N4	2.34	0.75
1:A:853:G:H2'	1:A:854:G:H5'	1.68	0.75
15:O:70:LEU:CD2	15:O:78:TYR:HB2	2.15	0.75
1:A:1006:C:H42	1:A:1023:G:H1	1.34	0.75
1:A:1256:A:N6	1:A:1277:C:C5	2.54	0.75
4:D:173:TRP:HB3	4:D:187:ARG:HH21	1.52	0.75
5:E:122:GLU:OE1	5:E:131:ILE:HG13	1.86	0.75
7:G:90:GLU:OE1	7:G:90:GLU:HA	1.87	0.75
13:M:37:THR:O	13:M:55:ARG:HD2	1.86	0.75
1:A:1005:A:N7	1:A:1026:G:N1	2.30	0.75
1:A:1010:G:N2	1:A:1020:U:H1'	2.02	0.75
7:G:103:TRP:CE2	7:G:137:LYS:HG2	2.21	0.75
8:H:118:VAL:C	8:H:119:LEU:HD23	2.12	0.75
1:A:1054:C:OP1	1:A:1197:G:OP2	2.04	0.75
2:B:97:TRP:CE3	2:B:98:LEU:O	2.40	0.75
6:F:87:ARG:HG3	6:F:87:ARG:NH1	2.01	0.75
11:K:18:ARG:NH1	11:K:35:PRO:O	2.19	0.75
5:E:13:ILE:HG22	5:E:14:ARG:N	2.02	0.74
5:E:76:ILE:HG22	5:E:93:PRO:HG3	1.67	0.74
10:J:28:ARG:HB3	10:J:29:ARG:HH11	1.52	0.74
21:U:10:ARG:HB2	21:U:10:ARG:NH1	2.00	0.74
1:A:229:U:O2'	1:A:230:G:H5'	1.87	0.74
1:A:427:U:OP1	4:D:13:ARG:NH2	2.20	0.74
15:O:15:PHE:CE2	15:O:85:LEU:HD21	2.21	0.74
15:O:17:ARG:HG3	15:O:17:ARG:NH1	1.91	0.74
20:T:44:ALA:HA	20:T:92:LEU:HD21	1.68	0.74
24:a:39:G:H2'	24:a:39:G:N3	2.02	0.74
1:A:839:U:H5'	1:A:840:C:C5	2.23	0.74
4:D:8:VAL:O	4:D:11:LEU:N	2.17	0.74
1:A:1212:U:H4'	1:A:1213:A:O5'	1.84	0.74
9:I:48:GLU:HB3	9:I:101:PHE:CZ	2.23	0.74
1:A:474:G:H4'	16:P:81:ARG:HH21	1.51	0.74
1:A:644:G:H5'	1:A:644:G:C8	2.18	0.74
20:T:82:SER:O	20:T:86:ARG:HG3	1.87	0.74
1:A:503:C:OP2	12:L:116:SER:HB3	1.87	0.74
3:C:137:ALA:O	3:C:141:VAL:HG23	1.87	0.74
23:W:39:G:N2	23:W:40:PSU:O4	2.21	0.74
1:A:297:G:N7	29:A:2519:HOH:O	2.19	0.74
1:A:348:G:N7	29:A:2636:HOH:O	2.21	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:440:A:H5'	1:A:442:C:OP2	1.88	0.74
1:A:583:A:OP2	29:A:2103:HOH:O	2.05	0.74
1:A:620:C:C2	4:D:135:LEU:HD22	2.22	0.74
1:A:1404:5MC:H1'	1:A:1499:A:H2	1.52	0.74
10:J:78:ASN:OD1	10:J:79:ARG:NH1	2.21	0.74
1:A:331:G:OP2	29:A:2266:HOH:O	2.06	0.74
1:A:413:G:O2'	1:A:428:G:N2	2.20	0.74
1:A:949:A:C2	1:A:1233:G:N3	2.56	0.74
1:A:1090:U:H2'	1:A:1091:U:H6	1.53	0.74
4:D:52:SER:O	4:D:56:VAL:HG23	1.88	0.74
20:T:10:LEU:HD21	20:T:13:LEU:H	1.53	0.74
2:B:75:LYS:HA	2:B:78:GLN:CG	2.16	0.73
2:B:212:GLN:O	2:B:216:SER:HB3	1.88	0.73
7:G:17:VAL:HG12	7:G:18:TYR:N	2.01	0.73
14:N:9:LYS:HD2	14:N:9:LYS:O	1.88	0.73
1:A:289:G:OP2	29:A:2015:HOH:O	2.04	0.73
13:M:87:TYR:CE1	13:M:91:ARG:HD3	2.23	0.73
2:B:97:TRP:CZ2	2:B:102:LEU:HD13	2.22	0.73
6:F:25:ILE:HD12	6:F:82:ARG:HH11	1.53	0.73
6:F:101:ALA:HA	18:R:28:GLU:HB2	1.71	0.73
1:A:182:U:H5	1:A:183:G:C4	2.06	0.73
1:A:1133:G:N2	1:A:1141:C:N3	2.36	0.73
10:J:63:PHE:HA	14:N:59:ALA:CB	2.18	0.73
17:Q:81:ARG:HE	17:Q:84:LEU:HD11	1.52	0.73
17:Q:23:VAL:HG21	17:Q:42:TYR:CD1	2.23	0.73
20:T:10:LEU:HD21	20:T:13:LEU:N	2.04	0.73
1:A:52:G:O6	29:A:2441:HOH:O	2.06	0.73
9:I:89:ASN:HB3	9:I:92:TYR:CD1	2.23	0.73
15:O:15:PHE:CD2	15:O:30:ALA:HB2	2.23	0.73
1:A:939:G:H5'	7:G:102:ARG:NH2	2.04	0.73
1:A:1226:C:H4'	1:A:1227:A:OP1	1.88	0.73
1:A:1286:A:H2	21:U:22:ARG:NH2	1.86	0.73
1:A:243:A:C2	1:A:246:A:C8	2.76	0.73
2:B:103:THR:N	2:B:176:GLU:OE1	2.20	0.73
1:A:1321:C:H4'	13:M:87:TYR:CE2	2.23	0.73
1:A:1518[B]:MA6:N6	1:A:1519[B]:MA6:H103	2.04	0.73
20:T:13:LEU:HD12	20:T:14:LYS:HA	1.71	0.73
1:A:9:G:OP2	5:E:121:LYS:NZ	2.20	0.72
1:A:1408:A:H2'	1:A:1409:C:C6	2.24	0.72
1:A:1510:U:H2'	1:A:1511:G:C8	2.23	0.72
2:B:44:LEU:H	2:B:44:LEU:HD22	1.53	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:15:PHE:CZ	15:O:85:LEU:HD21	2.24	0.72
1:A:444:C:H42	1:A:490:G:H1	1.37	0.72
1:A:1193:G:H2'	1:A:1194:U:H6	1.54	0.72
1:A:1407:5MC:H2'	1:A:1408:A:H5'	1.71	0.72
3:C:130:VAL:HG11	3:C:157:ILE:HG22	1.70	0.72
1:A:157:G:H5''	1:A:158:G:OP2	1.90	0.72
1:A:500:G:C6	1:A:501:C:N4	2.58	0.72
6:F:74:ASP:OD2	6:F:74:ASP:N	2.19	0.72
9:I:118:LYS:O	9:I:120:ARG:N	2.20	0.72
20:T:45:GLN:HA	20:T:91:LEU:CD2	2.19	0.72
1:A:421:U:OP2	1:A:422:C:N4	2.22	0.72
6:F:82:ARG:HB2	6:F:85:VAL:HG23	1.72	0.72
1:A:977:A:H2'	1:A:978:A:H5'	1.69	0.72
1:A:1403:C:O2'	1:A:1404:5MC:H5'	1.89	0.72
5:E:144:THR:O	5:E:148:VAL:HG23	1.89	0.72
13:M:19:LEU:O	13:M:22:ILE:HD11	1.89	0.72
1:A:345:C:OP2	1:A:345:C:H6	1.71	0.72
1:A:427:U:OP2	1:A:428:G:O2'	2.07	0.72
19:S:69:HIS:HB3	19:S:73:GLU:OE1	1.88	0.72
1:A:1329:A:OP1	13:M:29:ARG:HG3	1.89	0.72
1:A:1537:U:H2'	1:A:1538:C:C6	2.25	0.72
3:C:150:LYS:HG3	3:C:169:ALA:CB	2.18	0.72
1:A:107:G:H2'	1:A:108:G:C5'	2.20	0.72
1:A:914:A:O5'	27:A:1928:SRV:HI33	1.88	0.72
1:A:928:G:O2'	1:A:1533:C:OP1	2.08	0.72
1:A:1385:G:N7	29:A:2670:HOH:O	2.23	0.72
1:A:1536:C:H5	1:A:1537:U:C4	2.08	0.72
4:D:22:LYS:CB	4:D:26:CYS:SG	2.78	0.72
13:M:19:LEU:O	13:M:22:ILE:CD1	2.37	0.72
18:R:47:THR:HG22	18:R:48:GLY:N	2.05	0.72
1:A:616:G:H1'	1:A:625:G:N2	2.05	0.71
1:A:1347:G:O2'	1:A:1348:U:OP2	2.08	0.71
1:A:1402:4OC:CM2	1:A:1403:C:H5'	2.15	0.71
1:A:1493[A]:A:O2'	1:A:1494:G:OP1	2.04	0.71
3:C:174:PRO:O	3:C:177:THR:N	2.23	0.71
8:H:95:VAL:HG12	8:H:99:GLU:HB2	1.72	0.71
10:J:16:LEU:HD21	10:J:70:ARG:CG	2.20	0.71
16:P:22:THR:HA	16:P:33:ILE:HD12	1.71	0.71
17:Q:51:TYR:CD1	17:Q:73:VAL:HG11	2.25	0.71
1:A:179:A:H2'	1:A:180:U:H6	1.55	0.71
1:A:266:G:HO2'	1:A:267:C:P	2.12	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:273:A:H2'	1:A:274:A:H5'	1.71	0.71
1:A:791:G:C2'	1:A:792:A:H5'	2.20	0.71
1:A:1361(A):C:O2'	1:A:1362:C:O5'	2.05	0.71
2:B:97:TRP:CZ3	2:B:98:LEU:O	2.43	0.71
10:J:41:PRO:O	10:J:69:ASN:ND2	2.23	0.71
24:a:38:A:H2'	24:a:39:G:C8	2.26	0.71
1:A:1538:C:H42	24:a:34:G:H1	1.38	0.71
1:A:532:A:N6	1:A:1207:2MG:H5'	2.06	0.71
1:A:538:G:H5''	12:L:114:LYS:CB	2.17	0.71
17:Q:81:ARG:HE	17:Q:84:LEU:CD1	2.03	0.71
1:A:1366:C:H2'	1:A:1367:C:C6	2.25	0.71
1:A:89:C:O2'	1:A:90:U:P	2.49	0.71
1:A:447:G:H2'	1:A:485:G:N2	2.05	0.71
1:A:835:U:O4	29:A:2788:HOH:O	2.06	0.71
1:A:893:C:O2'	1:A:894:G:H5'	1.90	0.71
1:A:1131:G:H8	1:A:1131:G:OP2	1.72	0.71
1:A:382:A:O2'	1:A:383:A:H5'	1.90	0.71
1:A:1518[B]:MA6:H93	1:A:1519[B]:MA6:N1	2.05	0.71
15:O:70:LEU:HD23	15:O:70:LEU:C	2.16	0.71
1:A:415:A:H2'	1:A:416:G:C8	2.25	0.71
1:A:446:G:H2'	1:A:447:G:H5'	1.72	0.71
1:A:1498:UR3:H4'	1:A:1519[A]:MA6:N1	2.04	0.71
7:G:46:ALA:O	7:G:50:ILE:HG12	1.91	0.71
1:A:352:C:H3'	1:A:352:C:H6	1.55	0.71
1:A:951:G:OP2	13:M:102:ARG:NH2	2.24	0.71
2:B:6:THR:N	2:B:48:MET:HE1	2.06	0.71
11:K:40:ILE:HG23	11:K:75:TYR:CD1	2.25	0.71
2:B:102:LEU:N	2:B:102:LEU:HD12	2.06	0.71
3:C:10:PHE:CE1	3:C:178:LEU:HD11	2.26	0.71
8:H:82:HIS:ND1	8:H:138:TRP:NE1	2.38	0.71
1:A:77:G:C4	1:A:93:G:N2	2.59	0.70
6:F:12:PRO:HG3	6:F:58:GLY:CA	2.17	0.70
10:J:81:THR:HG22	10:J:82:ILE:HG13	1.73	0.70
1:A:537:G:H2'	1:A:538:G:H8	1.55	0.70
1:A:1535:A:C2	24:a:37:A:C2	2.79	0.70
15:O:14:GLU:HG3	15:O:15:PHE:HD1	1.55	0.70
1:A:204:U:H4'	1:A:216:G:O5'	1.90	0.70
4:D:63:LYS:O	4:D:67:ILE:HD12	1.91	0.70
6:F:97:PHE:HD2	6:F:97:PHE:C	1.99	0.70
8:H:27:PRO:HA	8:H:58:TYR:CD2	2.27	0.70
10:J:50:ILE:HG13	10:J:60:ARG:HG2	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:782:A:OP1	29:A:2280:HOH:O	2.09	0.70
7:G:46:ALA:HA	7:G:49:ILE:HD12	1.74	0.70
12:L:20:LYS:H	12:L:20:LYS:CE	2.05	0.70
1:A:104:G:H2'	1:A:105:G:H5''	1.72	0.70
3:C:147:LYS:CE	3:C:205:GLY:H	2.04	0.70
5:E:81:GLU:OE2	5:E:88:LYS:HD3	1.92	0.70
10:J:62:HIS:O	14:N:59:ALA:HB3	1.90	0.70
14:N:22:THR:HG23	14:N:33:VAL:HG21	1.72	0.70
1:A:1110:A:OP2	29:A:2142:HOH:O	2.09	0.70
1:A:1270:C:OP2	21:U:24:ARG:NH2	2.25	0.70
1:A:1534:C:C4	1:A:1535:A:N1	2.59	0.70
2:B:82:ARG:HA	2:B:92:TYR:CD2	2.27	0.70
17:Q:11:VAL:HG11	17:Q:88:TYR:CD2	2.26	0.70
7:G:97:GLN:HG3	7:G:98:SER:N	2.07	0.70
19:S:39:THR:O	19:S:41:VAL:HG13	1.92	0.70
1:A:689:C:C2'	1:A:690:G:H5'	2.21	0.70
2:B:238:LEU:HD23	2:B:238:LEU:O	1.91	0.70
5:E:11:ILE:HG22	5:E:31:LEU:HB3	1.73	0.70
1:A:266:G:C8	1:A:266:G:C5'	2.69	0.70
1:A:298:A:N6	29:A:2215:HOH:O	2.25	0.70
7:G:12:LEU:HD12	7:G:12:LEU:N	1.93	0.70
1:A:22:G:H2'	1:A:23:C:H6	1.57	0.70
1:A:918:A:H2'	1:A:919:A:C8	2.27	0.70
6:F:10:LEU:CD1	6:F:59:TYR:HB3	2.21	0.70
12:L:127:GLU:CG	12:L:128:ALA:N	2.40	0.70
27:A:1928:SRY:O61	12:L:46:LYS:HD2	1.92	0.69
7:G:50:ILE:CG2	7:G:58:PRO:HA	2.16	0.69
8:H:73:ASP:OD2	8:H:75:ARG:HG3	1.92	0.69
15:O:21:ASP:OD1	15:O:24:SER:HB3	1.92	0.69
16:P:15:PRO:HD2	16:P:42:ARG:HD3	1.74	0.69
1:A:1300:G:HO2'	1:A:1301:U:P	2.14	0.69
1:A:1533:C:O2'	1:A:1534:C:OP1	2.09	0.69
2:B:25:ASN:HD21	2:B:193:ASP:HB2	1.51	0.69
4:D:146:ILE:N	4:D:146:ILE:CD1	2.56	0.69
12:L:27:LEU:HG	12:L:28:LYS:N	2.06	0.69
13:M:8:GLU:OE2	13:M:22:ILE:HA	1.92	0.69
14:N:13:THR:N	14:N:14:PRO:HD3	2.06	0.69
17:Q:51:TYR:CE1	17:Q:73:VAL:HG11	2.27	0.69
1:A:88:A:N7	1:A:89:C:N4	2.39	0.69
1:A:707:C:H4'	11:K:20:TYR:CE1	2.27	0.69
1:A:21:G:H2'	1:A:22:G:C8	2.27	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:463:A:H2'	1:A:474:G:C8	2.27	0.69
1:A:606:G:N1	29:A:2550:HOH:O	2.25	0.69
1:A:1130:A:OP1	1:A:1131:G:OP2	2.11	0.69
1:A:1213:A:H4'	1:A:1214:C:OP1	1.92	0.69
1:A:1286:A:C2	21:U:22:ARG:NH2	2.60	0.69
1:A:1454:G:N7	29:A:2825:HOH:O	2.25	0.69
19:S:48:THR:C	19:S:49:ILE:HD13	2.17	0.69
1:A:1206:G:C6	1:A:1207:2MG:C5	2.81	0.69
1:A:1518[B]:MA6:H93	1:A:1519[B]:MA6:C6	2.22	0.69
1:A:1527:C:O2'	1:A:1528:U:H5'	1.92	0.69
4:D:4:TYR:O	4:D:4:TYR:CD2	2.45	0.69
5:E:142:LEU:C	5:E:143:ARG:HG2	2.16	0.69
1:A:316:G:O2'	29:A:2463:HOH:O	2.10	0.69
2:B:84:GLU:HB3	2:B:219:VAL:HG21	1.75	0.69
3:C:5:ILE:C	3:C:5:ILE:HD12	2.18	0.69
5:E:37:ARG:HG2	5:E:37:ARG:NH1	2.03	0.69
7:G:16:LEU:H	7:G:16:LEU:CD2	2.04	0.69
10:J:47:PHE:HB3	14:N:34:TYR:HE2	1.58	0.69
12:L:34:ARG:HB2	12:L:105:TYR:HE1	1.57	0.69
19:S:31:ILE:O	19:S:50:ALA:HB3	1.91	0.69
20:T:45:GLN:HA	20:T:91:LEU:HD22	1.74	0.69
1:A:1151:A:HO2'	1:A:1152:A:H8	1.40	0.69
3:C:62:ASP:O	3:C:97:LYS:HG2	1.92	0.69
1:A:620:C:H2'	1:A:621:A:O4'	1.93	0.69
1:A:924:C:O2'	1:A:1399:C:C6	2.41	0.69
1:A:1395:C:O2'	1:A:1396:A:H5'	1.91	0.69
3:C:58:GLU:HB2	10:J:92:THR:HG21	1.75	0.69
5:E:48:ALA:HB1	5:E:49:PRO:CD	2.22	0.69
6:F:7:ASN:ND2	18:R:34:TYR:HE1	1.91	0.69
18:R:44:LEU:HD23	18:R:44:LEU:N	2.04	0.69
22:V:1:U:H5''	25:b:3:U:O3'	1.93	0.69
1:A:1003:G:C2	1:A:1003(A):G:C6	2.81	0.69
1:A:1057:G:C4	1:A:1204:A:C2	2.81	0.69
6:F:97:PHE:C	6:F:97:PHE:CD2	2.70	0.69
9:I:28:VAL:O	9:I:31:GLN:N	2.25	0.69
10:J:51:ARG:HG3	10:J:59:SER:O	1.92	0.69
14:N:15:LYS:O	14:N:16:PHE:CD2	2.46	0.69
15:O:70:LEU:HD22	15:O:78:TYR:HB2	1.72	0.69
1:A:79:G:C2	1:A:80:G:C8	2.81	0.69
1:A:119:A:OP2	29:A:2559:HOH:O	2.11	0.69
1:A:814:A:H2'	1:A:816:A:C5'	2.23	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1047:G:O2'	1:A:1048:G:H5'	1.93	0.69
2:B:47:THR:HA	2:B:202:PRO:HG2	1.75	0.69
1:A:117:G:OP2	29:A:2016:HOH:O	2.11	0.68
1:A:1062:U:H2'	1:A:1063:C:C6	2.28	0.68
1:A:1249:C:O2'	9:I:73:GLN:NE2	2.27	0.68
1:A:1419:G:C6	1:A:1420:C:C4	2.81	0.68
8:H:54:ASP:CG	8:H:55:GLY:H	2.00	0.68
9:I:19:LEU:HB3	9:I:59:PHE:CE2	2.28	0.68
20:T:50:GLU:N	20:T:99:LEU:HD11	2.08	0.68
1:A:1501:C:N4	1:A:1504:G:N3	2.42	0.68
6:F:95:GLU:O	18:R:32:ARG:NH1	2.27	0.68
7:G:148:ASN:O	7:G:150:ALA:N	2.25	0.68
8:H:121:ASP:HB2	8:H:125:ARG:NH2	2.08	0.68
18:R:59:SER:H	18:R:62:GLU:HB2	1.58	0.68
23:W:37:A:N1	23:W:38:A:C2	2.61	0.68
9:I:5:TYR:HD1	9:I:6:GLY:N	1.91	0.68
1:A:1033:G:C2'	1:A:1034:G:H5'	2.23	0.68
7:G:120:ILE:HG22	7:G:124:LEU:HD11	1.74	0.68
10:J:63:PHE:HB2	14:N:57:ARG:O	1.93	0.68
1:A:392:G:H2'	1:A:393:A:C8	2.29	0.68
1:A:1066:C:H2'	1:A:1067:A:H5'	1.76	0.68
1:A:1279:A:H4'	1:A:1280:A:OP1	1.93	0.68
1:A:1369:C:H2'	1:A:1370:G:C8	2.28	0.68
1:A:357:G:N7	29:A:2433:HOH:O	2.27	0.68
6:F:100:ASN:OD1	18:R:23:LYS:HE3	1.93	0.68
16:P:58:TYR:CD1	16:P:58:TYR:C	2.72	0.68
1:A:1067:A:O3'	29:A:2218:HOH:O	2.11	0.68
5:E:24:ARG:HH11	5:E:24:ARG:CG	2.07	0.68
10:J:9:ARG:HB3	10:J:9:ARG:CZ	2.23	0.68
16:P:58:TYR:CE1	16:P:62:VAL:HG11	2.28	0.68
21:U:13:ILE:HG22	21:U:22:ARG:CZ	2.24	0.68
1:A:828:A:H4'	1:A:828:A:OP1	1.94	0.68
1:A:1311:G:N7	19:S:2:PRO:HA	2.08	0.68
1:A:1436:U:H2'	1:A:1437:C:H6	1.59	0.68
9:I:15:ALA:HB1	9:I:77:ILE:HD12	1.76	0.68
17:Q:29:HIS:CE1	17:Q:31:LEU:H	2.11	0.68
19:S:19:VAL:HG23	19:S:47:HIS:ND1	2.09	0.68
3:C:85:ARG:HG2	3:C:86:VAL:N	2.09	0.68
3:C:112:SER:O	3:C:115:LEU:HB2	1.93	0.68
9:I:55:ALA:HA	9:I:58:HIS:HB2	1.75	0.68
20:T:61:SER:O	20:T:62:LEU:C	2.37	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:704:A:H5''	1:A:705:U:OP2	1.94	0.68
1:A:865:A:C2'	1:A:866:C:H5'	2.24	0.68
3:C:155:GLY:HA2	3:C:164:ARG:O	1.93	0.68
4:D:79:PHE:O	4:D:82:ALA:N	2.27	0.68
14:N:24:CYS:HB2	14:N:29:ARG:HB3	1.76	0.68
15:O:14:GLU:CG	15:O:15:PHE:HD1	2.07	0.68
1:A:1003:G:N2	1:A:1039:C:C2	2.61	0.67
2:B:92:TYR:HD1	2:B:151:GLY:HA3	1.59	0.67
9:I:11:LYS:O	9:I:12:GLU:HB2	1.93	0.67
10:J:28:ARG:HB3	10:J:29:ARG:HD2	1.76	0.67
11:K:33:THR:HG22	11:K:39:PRO:CA	2.24	0.67
13:M:59:TYR:C	13:M:59:TYR:CD2	2.69	0.67
4:D:206:PHE:CD2	4:D:207:TYR:CE2	2.81	0.67
24:a:38:A:H5''	24:a:39:G:OP2	1.94	0.67
1:A:358:U:H2'	1:A:359:U:C6	2.29	0.67
1:A:1086:U:H3	1:A:1099:G:H22	1.42	0.67
5:E:75:THR:HG23	5:E:76:ILE:N	2.08	0.67
5:E:131:ILE:HG22	5:E:132:ALA:N	2.09	0.67
12:L:6:THR:OG1	12:L:9:GLN:HG3	1.92	0.67
17:Q:53:LEU:HD11	17:Q:85:VAL:HG11	1.76	0.67
1:A:975:A:H5'	1:A:975:A:H8	1.60	0.67
1:A:1014:A:N7	1:A:1015:A:C6	2.63	0.67
1:A:1060:C:H1'	1:A:1198:G:N2	2.10	0.67
7:G:69:VAL:HG12	7:G:69:VAL:O	1.93	0.67
7:G:129:GLU:OE2	7:G:131:LYS:HE2	1.95	0.67
1:A:556:C:H2'	1:A:557:G:O4'	1.95	0.67
1:A:1347:G:C2'	1:A:1348:U:OP2	2.41	0.67
1:A:1497:G:O2'	1:A:1498:UR3:H5'	1.94	0.67
8:H:57:PRO:HG2	8:H:57:PRO:O	1.95	0.67
13:M:87:TYR:HE1	13:M:91:ARG:HD3	1.59	0.67
17:Q:59:ILE:HG22	17:Q:71:PHE:CD1	2.29	0.67
1:A:109:A:C6	1:A:326:G:C6	2.83	0.67
1:A:785:G:C2'	1:A:786:G:H5'	2.24	0.67
1:A:814:A:H2'	1:A:816:A:H5'	1.77	0.67
1:A:975:A:H8	1:A:975:A:C5'	2.07	0.67
1:A:1342:C:H2'	1:A:1343:G:C8	2.29	0.67
2:B:219:VAL:HA	2:B:222:ILE:CG1	2.24	0.67
8:H:86:ILE:HG21	8:H:133:LEU:HD13	1.77	0.67
10:J:48:THR:CA	10:J:62:HIS:HB3	2.25	0.67
11:K:120:ARG:HG2	11:K:120:ARG:NH1	2.08	0.67
15:O:4:THR:HG22	15:O:5:LYS:N	2.09	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:12:LYS:O	16:P:13:HIS:HB2	1.95	0.67
1:A:1310:G:O6	19:S:2:PRO:HG3	1.94	0.67
2:B:61:LEU:CD1	2:B:66:GLY:HA3	2.24	0.67
1:A:170:U:O2'	1:A:171:A:H5'	1.95	0.67
1:A:606:G:O6	29:A:2549:HOH:O	2.11	0.67
1:A:804:U:H5''	1:A:805:C:OP2	1.94	0.67
1:A:966:M2G:HM22	1:A:967:5MC:C2	2.30	0.67
1:A:995:C:O2	14:N:4:LYS:NZ	2.23	0.67
3:C:85:ARG:HH11	3:C:85:ARG:HG3	1.59	0.67
8:H:20:TYR:CE1	8:H:76:PRO:HD2	2.29	0.67
10:J:29:ARG:HD2	10:J:29:ARG:H	1.60	0.67
20:T:13:LEU:HD12	20:T:13:LEU:C	2.20	0.67
1:A:182:U:OP1	29:A:2183:HOH:O	2.11	0.67
1:A:509:A:C8	1:A:509:A:H3'	2.30	0.67
1:A:1125:U:O2'	1:A:1126:U:OP2	2.13	0.67
1:A:1443:G:C4'	1:A:1446:A:H5'	2.23	0.67
20:T:55:ILE:CD1	20:T:55:ILE:H	2.08	0.67
1:A:103:C:P	20:T:17:ARG:HH12	2.17	0.67
1:A:665:A:N3	1:A:732:C:H2'	2.10	0.67
1:A:1299:A:C6	1:A:1301:U:O2	2.48	0.67
17:Q:4:LYS:CG	17:Q:6:LEU:HD21	2.25	0.67
1:A:22:G:H2'	1:A:23:C:C6	2.30	0.66
1:A:112:G:O2'	1:A:113:G:H5'	1.96	0.66
1:A:407:G:OP1	4:D:115:ARG:NH2	2.28	0.66
2:B:36:ARG:HG3	2:B:41:ILE:CD1	2.24	0.66
4:D:15:GLU:CG	4:D:63:LYS:HD3	2.25	0.66
10:J:86:MET:HG3	10:J:87:THR:N	2.05	0.66
16:P:10:GLY:HA3	16:P:14:ASN:O	1.94	0.66
17:Q:51:TYR:CE1	17:Q:73:VAL:CG1	2.78	0.66
20:T:44:ALA:O	20:T:47:GLY:N	2.28	0.66
1:A:661:G:H8	1:A:661:G:H5''	1.58	0.66
3:C:182:ILE:HG23	3:C:202:ILE:O	1.95	0.66
5:E:105:VAL:HB	5:E:106:PRO:HD3	1.75	0.66
9:I:46:ALA:HB1	9:I:77:ILE:CG2	2.25	0.66
12:L:45:PRO:HB3	12:L:93:LEU:HD23	1.77	0.66
13:M:16:ASP:O	13:M:19:LEU:N	2.28	0.66
20:T:29:LYS:O	20:T:32:ALA:HB3	1.95	0.66
1:A:643:C:H2'	1:A:644:G:C5'	2.24	0.66
2:B:193:ASP:C	2:B:193:ASP:OD1	2.38	0.66
5:E:90:VAL:C	5:E:91:LEU:HD23	2.21	0.66
15:O:4:THR:HG22	15:O:5:LYS:H	1.60	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:349:A:C2'	1:A:350:G:H5'	2.26	0.66
1:A:1015:A:N6	1:A:1016:A:C6	2.63	0.66
1:A:1078:U:H5''	1:A:1079:G:OP2	1.94	0.66
1:A:1490:C:H5''	27:A:1928:SRV:NC1	2.11	0.66
3:C:58:GLU:CB	10:J:92:THR:HG21	2.24	0.66
12:L:93:LEU:O	12:L:96:VAL:HG23	1.95	0.66
13:M:4:ILE:HG22	13:M:5:ALA:N	2.11	0.66
16:P:62:VAL:HG23	16:P:62:VAL:O	1.95	0.66
21:U:18:TYR:CE1	21:U:24:ARG:HG3	2.31	0.66
1:A:174:C:OP1	29:A:2211:HOH:O	2.14	0.66
1:A:179:A:H2'	1:A:180:U:C6	2.31	0.66
1:A:458:C:OP2	29:A:2257:HOH:O	2.13	0.66
1:A:509:A:O3'	29:A:2165:HOH:O	2.14	0.66
1:A:783:C:H42	1:A:799:G:H1	1.43	0.66
1:A:1011:G:C2'	1:A:1012:U:H5'	2.25	0.66
1:A:273:A:C2'	1:A:274:A:H5'	2.25	0.66
1:A:443:C:H42	1:A:491:G:H1	1.41	0.66
1:A:501:C:H2'	1:A:502:G:H8	1.61	0.66
1:A:946:A:H2'	1:A:947:G:C8	2.30	0.66
2:B:162:ILE:O	2:B:185:ILE:HD12	1.94	0.66
3:C:186:PHE:CD2	3:C:187:ALA:N	2.64	0.66
1:A:137:C:O2'	1:A:138:G:H5''	1.96	0.66
1:A:192:U:O4'	20:T:103:GLY:HA2	1.96	0.66
5:E:13:ILE:CG2	5:E:14:ARG:N	2.59	0.66
18:R:87:ARG:HG3	18:R:87:ARG:NH2	1.97	0.66
20:T:22:ARG:O	20:T:23:ARG:C	2.38	0.66
20:T:50:GLU:HA	20:T:99:LEU:HD11	1.77	0.66
1:A:687:A:H4'	1:A:688:G:O5'	1.95	0.66
1:A:1026:G:C2'	1:A:1027:C:H5''	2.23	0.66
1:A:1054:C:C2	23:W:34:G:H5'	2.30	0.66
1:A:1342:C:H2'	1:A:1343:G:H8	1.61	0.66
4:D:119:GLN:HG3	4:D:123:HIS:ND1	2.11	0.66
1:A:390:C:H4'	16:P:28:ARG:HH21	1.61	0.66
1:A:944:G:OP1	29:A:2285:HOH:O	2.14	0.66
1:A:1532:U:H2'	1:A:1533:C:C5	2.31	0.66
27:A:1928:SRV:OG2	12:L:91:LYS:NZ	2.27	0.66
2:B:80:ILE:HD11	2:B:208:ILE:HG23	1.77	0.66
2:B:139:LYS:O	2:B:143:GLU:HG3	1.95	0.66
4:D:135:LEU:HD12	4:D:135:LEU:O	1.96	0.66
5:E:51:VAL:HG23	5:E:52:PRO:CD	2.26	0.66
10:J:80:LYS:HA	10:J:83:GLU:HB2	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:29:HIS:C	17:Q:29:HIS:ND1	2.54	0.66
22:V:1:U:C5'	25:b:3:U:O3'	2.44	0.66
1:A:1480:G:H2'	1:A:1481:U:C6	2.31	0.65
10:J:63:PHE:HA	14:N:59:ALA:HB2	1.77	0.65
1:A:76:C:C2'	1:A:77:G:H5'	2.27	0.65
1:A:1256:A:H8	1:A:1258:G:C2	2.15	0.65
5:E:79:GLU:HA	5:E:91:LEU:O	1.95	0.65
18:R:39:VAL:HG13	18:R:40:LEU:N	2.11	0.65
1:A:1030(A):G:H2'	1:A:1030(B):C:H5''	1.77	0.65
5:E:51:VAL:CG2	5:E:52:PRO:HD3	2.27	0.65
7:G:12:LEU:H	7:G:12:LEU:CD1	1.88	0.65
11:K:117:ASN:OD1	11:K:117:ASN:N	2.26	0.65
1:A:545:C:O2	1:A:545:C:H2'	1.95	0.65
1:A:838:G:C3'	1:A:839:U:H5''	2.27	0.65
1:A:1197:G:OP1	29:A:2229:HOH:O	2.14	0.65
1:A:1480:G:H2'	1:A:1481:U:H6	1.61	0.65
3:C:131:ARG:O	3:C:134:ILE:HG12	1.97	0.65
6:F:26:ILE:O	6:F:30:LEU:HD12	1.96	0.65
7:G:22:LEU:HD21	7:G:66:VAL:HG21	1.77	0.65
9:I:6:GLY:HA3	9:I:83:ARG:HB2	1.79	0.65
14:N:21:TYR:HE2	14:N:23:ARG:HE	1.44	0.65
20:T:49:ALA:HB3	20:T:99:LEU:CD2	2.21	0.65
1:A:1065:U:H5''	1:A:1190:G:N2	2.12	0.65
1:A:1407:5MC:C4	1:A:1408:A:N7	2.64	0.65
1:A:1425:U:H2'	1:A:1426:C:H6	1.60	0.65
7:G:27:ILE:HD11	7:G:40:ALA:HA	1.77	0.65
9:I:5:TYR:CD1	9:I:6:GLY:N	2.64	0.65
17:Q:11:VAL:HG11	17:Q:88:TYR:CE2	2.32	0.65
20:T:73:HIS:O	20:T:76:ALA:HB3	1.96	0.65
1:A:474:G:H4'	16:P:81:ARG:NH2	2.11	0.65
1:A:793:U:H4'	1:A:794:A:OP2	1.97	0.65
2:B:161:ALA:HA	2:B:183:PRO:HD2	1.78	0.65
4:D:175:SER:OG	4:D:186:LEU:HD21	1.96	0.65
4:D:191:ARG:HD2	4:D:200:GLU:OE2	1.97	0.65
9:I:108:VAL:CG1	9:I:109:VAL:H	2.05	0.65
13:M:59:TYR:HD2	13:M:59:TYR:O	1.79	0.65
20:T:56:MET:CE	20:T:85:MET:HG3	2.26	0.65
1:A:179:A:O2'	1:A:180:U:H5'	1.96	0.65
1:A:977:A:C2'	1:A:978:A:H5'	2.26	0.65
3:C:16:ARG:HG2	3:C:16:ARG:NH1	2.11	0.65
3:C:67:THR:HA	3:C:102:ASN:HB2	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:204:ILE:N	4:D:204:ILE:CD1	2.60	0.65
13:M:96:LEU:N	13:M:96:LEU:HD23	2.11	0.65
1:A:91:C:H2'	1:A:92:C:C6	2.32	0.65
1:A:204:U:O2	1:A:204:U:H2'	1.97	0.65
1:A:723:U:H5''	24:a:36:A:O2'	1.97	0.65
1:A:913:A:O3'	27:A:1928:SRV:CI3	2.45	0.65
1:A:1200:C:O2	1:A:1205:U:N3	2.19	0.65
1:A:1294:G:N7	29:A:2265:HOH:O	2.30	0.65
6:F:60:PHE:CZ	18:R:78:LEU:HD21	2.31	0.65
1:A:89:C:H2'	1:A:90:U:O5'	1.97	0.65
1:A:436:C:H2'	1:A:437:U:C6	2.31	0.65
1:A:661:G:N7	29:A:2819:HOH:O	2.30	0.65
1:A:1222:G:OP2	1:A:1322:C:N4	2.30	0.65
4:D:79:PHE:C	4:D:79:PHE:CD2	2.75	0.65
1:A:838:G:H3'	1:A:839:U:H5''	1.79	0.65
2:B:87:ARG:HD2	2:B:88:ALA:N	2.12	0.65
4:D:190:ASP:HB2	4:D:193:ASP:OD2	1.97	0.65
11:K:34:ASP:HB2	11:K:35:PRO:HD2	1.79	0.65
20:T:55:ILE:CD1	20:T:55:ILE:N	2.61	0.65
1:A:411:A:C2	1:A:413:G:H1'	2.32	0.64
1:A:1047:G:H2'	1:A:1048:G:H5'	1.77	0.64
2:B:8:LYS:C	2:B:10:LEU:H	2.02	0.64
7:G:50:ILE:HG21	7:G:58:PRO:CA	2.20	0.64
1:A:393:A:O2'	1:A:394:G:H5'	1.97	0.64
7:G:71:PRO:O	7:G:96:GLN:NE2	2.24	0.64
11:K:27:ASN:OD1	11:K:28:THR:N	2.30	0.64
17:Q:29:HIS:CG	17:Q:30:PRO:HD2	2.33	0.64
24:a:35:G:C2	24:a:36:A:C5	2.85	0.64
1:A:1129:C:OP1	9:I:62:TYR:OH	2.15	0.64
2:B:84:GLU:OE1	2:B:216:SER:HA	1.97	0.64
1:A:16:A:C2'	1:A:17:U:H5'	2.27	0.64
1:A:150:C:H2'	1:A:151:A:O5'	1.97	0.64
1:A:976:G:OP2	1:A:1358:U:O2'	2.15	0.64
1:A:1536:C:H5	1:A:1537:U:N3	1.94	0.64
4:D:180:GLY:O	4:D:182:LYS:HG2	1.98	0.64
5:E:11:ILE:HG22	5:E:12:LEU:N	2.10	0.64
9:I:97:LYS:HA	9:I:102:LEU:HD11	1.78	0.64
15:O:14:GLU:CG	15:O:15:PHE:CD1	2.80	0.64
16:P:21:VAL:O	16:P:33:ILE:HB	1.96	0.64
17:Q:5:VAL:HG22	17:Q:60:ILE:HD12	1.79	0.64
20:T:13:LEU:HD12	20:T:14:LYS:CA	2.27	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:99:LEU:HD12	20:T:100:ILE:N	2.12	0.64
1:A:89:C:HO2'	1:A:90:U:P	2.21	0.64
1:A:1201:A:H4'	1:A:1202:G:O5'	1.97	0.64
2:B:201:ILE:O	2:B:203:GLY:N	2.31	0.64
1:A:514:C:O2'	1:A:515:G:H5'	1.97	0.64
3:C:131:ARG:NH1	5:E:50:GLU:OE1	2.31	0.64
4:D:189:PRO:HB2	4:D:194:LEU:CD2	2.25	0.64
18:R:61:LYS:O	18:R:65:ILE:HD12	1.97	0.64
1:A:1132:C:H2'	1:A:1133:G:H5'	1.79	0.64
5:E:36:ASP:CG	5:E:38:GLN:HB2	2.23	0.64
10:J:16:LEU:CD2	10:J:70:ARG:HG3	2.28	0.64
11:K:92:GLU:HB3	11:K:96:ARG:HH22	1.63	0.64
2:B:103:THR:HG23	2:B:176:GLU:OE1	1.98	0.64
4:D:131:ARG:HB2	4:D:131:ARG:NH1	2.13	0.64
4:D:146:ILE:N	4:D:146:ILE:HD12	2.12	0.64
6:F:1:MET:HE3	6:F:1:MET:H3	1.63	0.64
6:F:67:MET:HB2	6:F:68:PRO:HD2	1.80	0.64
6:F:99:ALA:HB1	18:R:23:LYS:HZ3	1.63	0.64
13:M:15:VAL:HG21	13:M:48:LEU:HD21	1.77	0.64
4:D:117:ALA:O	4:D:121:VAL:HG23	1.98	0.64
6:F:10:LEU:HD12	6:F:59:TYR:HB3	1.79	0.64
16:P:8:ARG:HB2	16:P:28:ARG:NH1	2.13	0.64
20:T:55:ILE:HD12	20:T:55:ILE:N	2.13	0.64
1:A:580:U:OP2	29:A:2740:HOH:O	2.15	0.64
1:A:689:C:O2'	1:A:690:G:H5'	1.98	0.64
3:C:47:LEU:CD2	3:C:68:VAL:HG11	2.28	0.64
4:D:32:ALA:HA	4:D:35:ARG:CB	2.22	0.64
1:A:1330:U:OP1	13:M:23:TYR:O	2.16	0.63
2:B:157:ARG:HG3	2:B:158:LEU:N	2.13	0.63
3:C:203:PHE:C	3:C:204:LEU:HD23	2.23	0.63
6:F:8:ILE:HD13	6:F:26:ILE:HD12	1.80	0.63
1:A:627:G:O2'	1:A:628:G:H5'	1.98	0.63
1:A:1081:G:OP1	5:E:16:THR:OG1	2.16	0.63
1:A:1303:C:O2	1:A:1303:C:H2'	1.97	0.63
1:A:1366:C:H2'	1:A:1367:C:H6	1.63	0.63
3:C:62:ASP:HA	3:C:97:LYS:NZ	2.12	0.63
4:D:61:LYS:HZ2	4:D:72:GLU:CD	2.06	0.63
10:J:25:GLU:HG2	10:J:28:ARG:HD2	1.79	0.63
17:Q:29:HIS:HB2	17:Q:36:ILE:CD1	2.29	0.63
17:Q:74:LEU:HD22	17:Q:75:ARG:HG2	1.78	0.63
1:A:15:G:H4'	5:E:24:ARG:NH2	2.12	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:539:A:H2'	1:A:540:G:H8	1.63	0.63
1:A:943:U:C2'	1:A:944:G:H5'	2.28	0.63
1:A:959:A:H3'	1:A:960:U:H5''	1.81	0.63
1:A:1020:U:H2'	1:A:1021:G:H8	1.62	0.63
1:A:1256:A:C8	1:A:1258:G:N1	2.66	0.63
1:A:1372:U:OP1	9:I:71:SER:HB3	1.99	0.63
1:A:1493[B]:A:H2'	1:A:1494:G:N7	2.13	0.63
1:A:1518[B]:MA6:C10	1:A:1519[B]:MA6:H103	2.28	0.63
2:B:119:GLU:HG3	2:B:142:LEU:HD11	1.79	0.63
8:H:97:VAL:HG12	8:H:98:LYS:N	2.13	0.63
1:A:166:G:C2'	1:A:167:G:H5'	2.29	0.63
1:A:790:A:C8	1:A:791:G:N7	2.67	0.63
3:C:119:ARG:O	3:C:122:GLU:HB2	1.97	0.63
3:C:136:GLN:O	3:C:140:ARG:HG3	1.98	0.63
9:I:17:VAL:HG13	9:I:63:ILE:CD1	2.28	0.63
10:J:77:PRO:HA	10:J:81:THR:OG1	1.98	0.63
15:O:79:ARG:HG3	15:O:79:ARG:NH1	2.07	0.63
1:A:943:U:H2'	1:A:944:G:H5'	1.80	0.63
1:A:1068:G:OP2	1:A:1068:G:C8	2.48	0.63
1:A:1305:G:N2	1:A:1331:G:H1'	2.12	0.63
2:B:69:LEU:HD23	2:B:91:PRO:O	1.99	0.63
2:B:218:ALA:O	2:B:222:ILE:HG12	1.98	0.63
9:I:55:ALA:O	9:I:56:LEU:C	2.42	0.63
19:S:19:VAL:HG23	19:S:47:HIS:CE1	2.33	0.63
19:S:34:TRP:CZ2	19:S:57:HIS:HE1	2.16	0.63
1:A:54:C:N3	1:A:352:C:C5	2.67	0.63
1:A:112:G:C2'	1:A:113:G:H5'	2.29	0.63
1:A:500:G:C6	1:A:546:G:N2	2.66	0.63
1:A:627:G:O6	29:A:2664:HOH:O	2.14	0.63
1:A:785:G:H2'	1:A:786:G:H5'	1.79	0.63
1:A:1343:G:H1'	9:I:121:ARG:NH1	2.13	0.63
3:C:14:ILE:HD13	3:C:14:ILE:N	2.13	0.63
3:C:16:ARG:NH2	3:C:183:ASP:OD2	2.32	0.63
3:C:150:LYS:HG3	3:C:169:ALA:HB2	1.80	0.63
3:C:186:PHE:CD2	3:C:186:PHE:C	2.76	0.63
4:D:164:ALA:O	4:D:168:ARG:HD2	1.99	0.63
7:G:16:LEU:HD11	9:I:45:ALA:HB2	1.80	0.63
18:R:50:ILE:HD11	18:R:70:ILE:HG21	1.78	0.63
20:T:41:ILE:N	20:T:41:ILE:HD12	2.14	0.63
1:A:266:G:H5'	1:A:266:G:H8	1.57	0.63
1:A:616:G:O2'	1:A:617:G:H5'	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1291:G:H2'	1:A:1292:U:C6	2.34	0.63
2:B:179:LYS:HA	8:H:72:PRO:HD3	1.80	0.63
3:C:10:PHE:HD1	3:C:10:PHE:O	1.82	0.63
8:H:28:ALA:HA	8:H:59:LEU:HD11	1.80	0.63
10:J:30:SER:HB2	10:J:80:LYS:CB	2.21	0.63
15:O:62:GLN:O	15:O:63:ARG:C	2.39	0.63
18:R:74:ARG:HB3	18:R:81:PHE:CE1	2.34	0.63
20:T:13:LEU:HD12	20:T:14:LYS:N	2.14	0.63
1:A:1125:U:O2'	1:A:1126:U:P	2.57	0.63
1:A:1125:U:H3'	1:A:1126:U:H5	1.62	0.63
1:A:1130:A:OP1	1:A:1131:G:P	2.56	0.63
1:A:1204:A:OP2	29:A:2248:HOH:O	2.15	0.63
1:A:1281:U:C4'	1:A:1282:C:OP2	2.47	0.63
3:C:119:ARG:HG3	3:C:119:ARG:HH11	1.63	0.63
4:D:79:PHE:HD2	4:D:80:GLU:N	1.96	0.63
8:H:103:VAL:HG21	8:H:109:ILE:C	2.24	0.63
10:J:86:MET:HA	10:J:86:MET:HE3	1.81	0.63
13:M:59:TYR:C	13:M:59:TYR:HD2	2.07	0.63
19:S:36:ARG:NH2	19:S:75:ALA:O	2.32	0.63
1:A:235:C:N4	29:A:2113:HOH:O	2.31	0.63
3:C:119:ARG:HH11	3:C:119:ARG:CG	2.11	0.63
3:C:188:LEU:HD11	3:C:195:VAL:CG1	2.28	0.63
1:A:837:G:C2	1:A:850:U:O2	2.51	0.62
1:A:1001:A:H2'	1:A:1002:G:C8	2.34	0.62
1:A:1003:G:N1	1:A:1003(A):G:O6	2.31	0.62
1:A:1314:C:OP2	19:S:6:LYS:CD	2.46	0.62
9:I:121:ARG:HH11	9:I:121:ARG:CG	2.10	0.62
12:L:84:LEU:O	12:L:101:VAL:HG23	1.99	0.62
15:O:14:GLU:HG2	15:O:15:PHE:CE1	2.34	0.62
1:A:1126:U:OP2	1:A:1281:U:H1'	1.99	0.62
3:C:191:THR:OG1	3:C:193:TYR:CE1	2.49	0.62
20:T:67:ALA:HA	20:T:73:HIS:H	1.65	0.62
1:A:1026:G:C8	1:A:1027:C:N3	2.68	0.62
1:A:1057:G:C5	1:A:1204:A:C2	2.87	0.62
6:F:62:TRP:CH2	6:F:64:GLN:HB2	2.35	0.62
7:G:120:ILE:HG22	7:G:124:LEU:CD1	2.29	0.62
19:S:15:LEU:HD13	19:S:16:LEU:N	2.15	0.62
1:A:352:C:H3'	1:A:352:C:C6	2.35	0.62
1:A:750:G:N3	15:O:23:GLY:HA3	2.14	0.62
1:A:1160:G:O6	1:A:1181:G:O6	2.16	0.62
1:A:1328:C:OP1	21:U:21:TYR:OH	2.13	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:180:LEU:O	2:B:181:PHE:HB2	1.98	0.62
8:H:127:LEU:HD23	8:H:127:LEU:O	1.99	0.62
23:W:37:A:N6	23:W:38:A:N1	2.47	0.62
1:A:1124:G:N7	1:A:1145:C:O2'	2.28	0.62
1:A:1316:G:H2'	1:A:1317:C:H5''	1.81	0.62
1:A:1425:U:H2'	1:A:1426:C:C6	2.34	0.62
16:P:26:ARG:HG3	16:P:27:LYS:N	2.13	0.62
1:A:99:C:H2'	1:A:101:A:C8	2.35	0.62
1:A:330:C:H2'	1:A:331:G:H5'	1.81	0.62
1:A:506:G:C5	1:A:507:C:C5	2.87	0.62
1:A:1519[A]:MA6:H3'	1:A:1520[A]:G:C5'	2.29	0.62
2:B:87:ARG:HE	2:B:219:VAL:CG1	2.11	0.62
3:C:10:PHE:HD1	3:C:10:PHE:C	2.07	0.62
7:G:120:ILE:N	7:G:120:ILE:CD1	2.52	0.62
8:H:28:ALA:HA	8:H:59:LEU:CD1	2.29	0.62
9:I:112:LYS:HA	9:I:119:ALA:HB2	1.80	0.62
13:M:16:ASP:O	13:M:19:LEU:HB2	1.99	0.62
1:A:35:G:C6	1:A:36:C:N4	2.68	0.62
3:C:33:LEU:HD21	14:N:53:LEU:HD22	1.82	0.62
4:D:31:CYS:O	4:D:31:CYS:SG	2.57	0.62
4:D:150:GLU:N	4:D:150:GLU:CD	2.57	0.62
6:F:14:LEU:CD1	6:F:18:GLN:HB3	2.22	0.62
16:P:8:ARG:HB2	16:P:28:ARG:HH11	1.64	0.62
16:P:74:LEU:O	16:P:79:VAL:HG23	1.99	0.62
17:Q:54:GLY:O	17:Q:80:GLY:HA2	1.99	0.62
18:R:26:LEU:HD13	18:R:26:LEU:N	2.13	0.62
20:T:83:ARG:O	20:T:87:LYS:HD2	2.00	0.62
1:A:544:G:C5	1:A:545:C:C5	2.88	0.62
1:A:975:A:H4'	1:A:976:G:H5''	1.81	0.62
4:D:150:GLU:OE1	4:D:151:LYS:HG3	2.00	0.62
8:H:113:SER:HB3	8:H:134:ILE:HD11	1.80	0.62
15:O:14:GLU:HG2	15:O:15:PHE:CD1	2.35	0.62
20:T:104:LEU:N	20:T:104:LEU:HD23	2.15	0.62
1:A:1052:U:H2'	1:A:1055:A:OP1	2.00	0.62
1:A:414:A:C2	1:A:415:A:N9	2.68	0.62
1:A:415:A:C4	1:A:416:G:C8	2.88	0.62
1:A:551:U:H2'	1:A:552:U:C6	2.35	0.62
1:A:592:G:O2'	1:A:593:G:H5'	2.00	0.62
1:A:922:G:H5''	1:A:922:G:H8	1.64	0.62
1:A:1368:G:H2'	1:A:1369:C:H5'	1.82	0.62
9:I:11:LYS:O	9:I:11:LYS:HG3	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:125:TYR:CD2	9:I:125:TYR:N	2.67	0.62
20:T:44:ALA:HB1	20:T:91:LEU:HB3	1.82	0.62
1:A:88:A:C5	1:A:89:C:N3	2.68	0.61
1:A:349:A:O2'	1:A:350:G:H5'	2.00	0.61
1:A:501:C:H2'	1:A:502:G:C8	2.34	0.61
1:A:1493[A]:A:H2	23:W:36:A:O2'	1.83	0.61
2:B:74:LYS:HE3	2:B:166:ASP:CB	2.28	0.61
3:C:10:PHE:C	3:C:10:PHE:CD1	2.77	0.61
3:C:204:LEU:HD23	3:C:204:LEU:N	2.15	0.61
4:D:14:ARG:O	4:D:14:ARG:HD3	2.00	0.61
11:K:125:PHE:N	11:K:125:PHE:CD2	2.68	0.61
1:A:986:A:C2	1:A:1220:G:C2	2.88	0.61
1:A:1338:G:H2'	1:A:1339:A:C8	2.35	0.61
13:M:87:TYR:C	13:M:87:TYR:CD1	2.77	0.61
17:Q:74:LEU:HD23	17:Q:74:LEU:C	2.25	0.61
20:T:41:ILE:HD12	20:T:41:ILE:H	1.64	0.61
1:A:130:A:H5'	17:Q:63:ARG:HE	1.66	0.61
1:A:200:G:H2'	1:A:201:C:O4'	2.00	0.61
1:A:1385:G:C5	29:A:2670:HOH:O	2.52	0.61
1:A:1536:C:C5	1:A:1537:U:C2	2.87	0.61
3:C:156:ARG:H	3:C:163:ALA:HA	1.65	0.61
4:D:24:GLU:O	4:D:25:ARG:HB3	1.98	0.61
4:D:38:TYR:H	4:D:38:TYR:HD2	1.48	0.61
5:E:126:ARG:HG2	5:E:126:ARG:NH1	1.97	0.61
6:F:83:ASP:OD1	6:F:83:ASP:N	2.32	0.61
7:G:135:VAL:O	7:G:139:GLU:HG3	2.00	0.61
8:H:104:ARG:CZ	8:H:138:TRP:CZ2	2.82	0.61
11:K:29:ILE:HG22	11:K:43:SER:O	2.00	0.61
1:A:16:A:H2'	1:A:17:U:H5'	1.81	0.61
1:A:188:C:C2'	1:A:189:G:H5'	2.30	0.61
1:A:353:A:C5'	1:A:353:A:H8	2.12	0.61
1:A:358:U:H2'	1:A:359:U:H6	1.66	0.61
1:A:544:G:C6	1:A:545:C:C5	2.89	0.61
1:A:642:A:H2'	1:A:643:C:C6	2.35	0.61
1:A:831:U:H2'	1:A:832:C:H6	1.65	0.61
1:A:892:A:C2	1:A:907:A:C4	2.89	0.61
1:A:983:A:H3'	1:A:983:A:N3	2.15	0.61
1:A:1194:U:O2	1:A:1194:U:H2'	2.00	0.61
2:B:178:ARG:HD2	2:B:196:LEU:O	2.00	0.61
5:E:110:LEU:O	5:E:115:VAL:HB	2.01	0.61
11:K:16:SER:O	11:K:35:PRO:HD3	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:30:ALA:HB1	12:L:31:PRO:HD2	1.82	0.61
12:L:86:ARG:HH11	12:L:86:ARG:HG3	1.66	0.61
17:Q:53:LEU:HD12	17:Q:54:GLY:N	2.14	0.61
1:A:442:C:H2'	1:A:443:C:H5'	1.81	0.61
1:A:865:A:O2'	1:A:866:C:H5'	1.99	0.61
1:A:914:A:P	27:A:1928:SRV:CI3	2.87	0.61
2:B:160:ASP:O	2:B:161:ALA:HB2	2.00	0.61
7:G:51:GLN:O	7:G:52:GLU:HG2	2.00	0.61
13:M:37:THR:CG2	13:M:39:ILE:HD13	2.31	0.61
18:R:36:ASN:OD1	18:R:39:VAL:HG12	2.00	0.61
1:A:137:C:H2'	1:A:138:G:C5'	2.30	0.61
1:A:190(D):U:O2'	1:A:190(E):U:H5'	2.01	0.61
1:A:191:G:N3	20:T:103:GLY:O	2.34	0.61
1:A:248:C:C2'	1:A:249:U:H5'	2.31	0.61
1:A:304:U:C4	29:A:2495:HOH:O	2.48	0.61
1:A:414:A:H2'	1:A:414:A:N3	2.15	0.61
1:A:544:G:C4	1:A:545:C:C6	2.89	0.61
1:A:767:A:H2'	1:A:768:A:O4'	2.01	0.61
1:A:829:G:O2'	1:A:830:G:H5'	2.00	0.61
1:A:890:G:O2'	1:A:906:G:O6	2.16	0.61
1:A:923:A:H8	1:A:923:A:O5'	1.82	0.61
1:A:1348:U:H4'	9:I:120:ARG:HD2	1.81	0.61
1:A:1482:G:N1	29:A:2362:HOH:O	2.16	0.61
2:B:172:ILE:HD13	2:B:172:ILE:H	1.64	0.61
4:D:23:GLY:HA2	4:D:112:VAL:O	2.00	0.61
7:G:21:VAL:HG23	7:G:22:LEU:H	1.65	0.61
1:A:778:G:H8	1:A:778:G:O5'	1.83	0.61
2:B:178:ARG:NH1	2:B:198:ASP:OD1	2.33	0.61
11:K:124:LYS:C	11:K:125:PHE:HD2	2.09	0.61
1:A:53:A:C6	1:A:54:C:C5	2.89	0.61
1:A:289:G:P	29:A:2015:HOH:O	2.57	0.61
1:A:448:A:C2'	1:A:449:C:H5'	2.30	0.61
1:A:1103:C:H5'	2:B:98:LEU:HD12	1.82	0.61
14:N:15:LYS:O	14:N:16:PHE:CG	2.53	0.61
23:W:32:C:O2'	23:W:33:U:O4'	2.17	0.61
1:A:109:A:H3'	1:A:110:C:H5'	1.83	0.61
1:A:114:U:H2'	1:A:115:G:H5'	1.82	0.61
1:A:1399:C:O2	1:A:1401:G:C4	2.54	0.61
2:B:88:ALA:HB2	2:B:219:VAL:CG1	2.21	0.61
2:B:157:ARG:HG3	2:B:158:LEU:O	2.01	0.61
4:D:159:ARG:HH11	4:D:159:ARG:CG	2.14	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:89:ASN:HB3	9:I:92:TYR:CE1	2.35	0.61
9:I:118:LYS:C	9:I:120:ARG:H	2.08	0.61
10:J:76:ASN:C	10:J:78:ASN:N	2.59	0.61
12:L:7:ILE:HG22	12:L:8:ASN:N	2.16	0.61
1:A:182:U:C5	1:A:183:G:N9	2.69	0.61
1:A:1035:A:N6	1:A:1036:G:O6	2.33	0.61
8:H:112:LEU:N	8:H:112:LEU:CD2	2.64	0.61
9:I:37:PHE:CD2	9:I:74:ILE:HD11	2.36	0.61
10:J:27:ALA:CB	10:J:74:ILE:HD12	2.31	0.61
16:P:57:ARG:O	16:P:58:TYR:C	2.40	0.61
2:B:15:VAL:O	2:B:42:ILE:HD12	2.01	0.60
4:D:131:ARG:HB2	4:D:131:ARG:HH11	1.66	0.60
7:G:17:VAL:CG1	7:G:18:TYR:N	2.62	0.60
7:G:54:THR:HG22	7:G:56:GLN:HB2	1.83	0.60
8:H:97:VAL:O	8:H:100:ILE:HG12	2.01	0.60
9:I:31:GLN:NE2	9:I:36:TYR:CD1	2.66	0.60
17:Q:83:ASP:OD1	17:Q:84:LEU:N	2.34	0.60
1:A:259:G:O2'	1:A:260:G:H5'	2.01	0.60
1:A:1015:A:C6	1:A:1016:A:C6	2.89	0.60
4:D:170:VAL:HG22	4:D:171:GLY:N	2.16	0.60
8:H:118:VAL:O	8:H:119:LEU:HD23	2.01	0.60
17:Q:40:LYS:CD	17:Q:42:TYR:CE1	2.83	0.60
1:A:109:A:H2'	1:A:326:G:N2	2.16	0.60
1:A:386:C:O2'	29:A:2002:HOH:O	2.15	0.60
1:A:633:G:H2'	1:A:634:C:C6	2.35	0.60
1:A:644:G:C5	1:A:645:C:C5	2.89	0.60
1:A:783:C:O2'	1:A:784:C:H5'	2.01	0.60
1:A:1279:A:C4'	1:A:1280:A:OP1	2.50	0.60
1:A:1454:G:O6	29:A:2826:HOH:O	2.16	0.60
3:C:91:LEU:HD23	3:C:92:ALA:N	2.16	0.60
7:G:37:ASN:ND2	7:G:41:ARG:HH21	1.98	0.60
15:O:7:GLU:O	15:O:11:VAL:HG12	2.01	0.60
1:A:1027:C:C5	1:A:1035:A:N1	2.69	0.60
1:A:1535:A:N1	24:a:37:A:N1	2.49	0.60
2:B:19:HIS:O	2:B:39:ILE:HG13	2.01	0.60
7:G:153:HIS:NE2	11:K:57:THR:HG22	2.16	0.60
9:I:46:ALA:HB1	9:I:77:ILE:HG22	1.83	0.60
1:A:14:U:O2	1:A:16:A:C8	2.54	0.60
1:A:130:A:H1'	1:A:263:A:O2'	2.01	0.60
1:A:182:U:C5	1:A:183:G:H1'	2.35	0.60
1:A:446:G:H2'	1:A:447:G:C5'	2.32	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1251:A:H2'	1:A:1252:A:O4'	2.02	0.60
5:E:41:VAL:HG13	5:E:113:ALA:HA	1.83	0.60
14:N:12:ARG:HH11	14:N:12:ARG:H	1.48	0.60
15:O:12:ILE:C	15:O:14:GLU:N	2.57	0.60
1:A:44:G:N2	1:A:399:G:C4	2.70	0.60
1:A:875:C:O2'	8:H:14:ARG:NH1	2.35	0.60
1:A:972:C:OP1	10:J:57:LYS:HD2	2.02	0.60
1:A:1500:A:OP2	1:A:1505:G:OP1	2.19	0.60
2:B:185:ILE:HD12	2:B:185:ILE:H	1.66	0.60
2:B:231:GLU:HB3	2:B:232:PRO:CD	2.28	0.60
3:C:148:GLY:HA3	3:C:172:ARG:O	2.01	0.60
5:E:50:GLU:HG3	5:E:52:PRO:HD2	1.83	0.60
8:H:36:LEU:O	8:H:37:ARG:C	2.44	0.60
9:I:9:ARG:HA	9:I:76:ALA:CB	2.31	0.60
1:A:740:U:O2'	1:A:741:G:H5'	2.01	0.60
1:A:1126:U:C4	1:A:1127:G:C2	2.89	0.60
2:B:240:GLN:O	2:B:240:GLN:CG	2.50	0.60
7:G:38:LEU:HD12	7:G:42:ILE:HD11	1.83	0.60
8:H:38:ILE:O	8:H:38:ILE:HG22	2.02	0.60
14:N:29:ARG:HG2	14:N:40:CYS:CB	2.31	0.60
1:A:1066:C:C2'	1:A:1067:A:H5'	2.31	0.60
3:C:14:ILE:O	3:C:16:ARG:N	2.35	0.60
7:G:26:PHE:HD1	7:G:101:LEU:HD23	1.66	0.60
13:M:99:ARG:HB2	13:M:101:GLN:HE22	1.66	0.60
1:A:276:G:OP1	17:Q:12:SER:OG	2.14	0.60
1:A:476:G:H2'	1:A:477:G:H8	1.66	0.60
1:A:1004:A:N7	1:A:1037:C:N3	2.49	0.60
1:A:1234:C:H1'	1:A:1364:U:O2	2.00	0.60
1:A:1518[A]:MA6:H93	1:A:1519[A]:MA6:H103	1.82	0.60
2:B:8:LYS:C	2:B:10:LEU:N	2.58	0.60
2:B:20:GLU:HA	2:B:39:ILE:CD1	2.31	0.60
2:B:100:GLY:HA2	2:B:176:GLU:OE2	2.01	0.60
10:J:63:PHE:CD1	10:J:63:PHE:N	2.68	0.60
17:Q:23:VAL:HG21	17:Q:42:TYR:HD1	1.64	0.60
18:R:87:ARG:HH21	18:R:87:ARG:CB	2.13	0.60
23:W:37:A:C6	23:W:38:A:C2	2.89	0.60
1:A:254:G:OP1	17:Q:67:LYS:O	2.20	0.60
1:A:543:C:H2'	1:A:544:G:C5'	2.30	0.60
1:A:710:G:H5''	6:F:54:LYS:CE	2.27	0.60
1:A:868:C:H2'	1:A:869:G:C5'	2.31	0.60
3:C:8:ILE:HG22	3:C:9:GLY:N	2.16	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:5:ARG:NH2	7:G:8:GLU:HG2	2.17	0.60
7:G:65:ALA:HB2	7:G:128:ALA:HB2	1.83	0.60
11:K:48:ILE:HD13	11:K:48:ILE:N	2.15	0.60
11:K:73:MET:HG3	11:K:103:LEU:HD21	1.83	0.60
1:A:524:G:H2'	1:A:525:C:C6	2.37	0.59
1:A:1060:C:O2	1:A:1198:G:C2	2.55	0.59
1:A:1118:C:H1'	1:A:1179:A:C4	2.37	0.59
1:A:1494:G:O2'	1:A:1495:U:H5'	2.02	0.59
1:A:1503:A:C4	1:A:1531:A:C2	2.90	0.59
4:D:13:ARG:HD2	4:D:38:TYR:O	2.02	0.59
12:L:90:VAL:O	12:L:90:VAL:HG12	2.02	0.59
13:M:78:ILE:O	13:M:81:LEU:N	2.34	0.59
15:O:60:VAL:HG12	15:O:61:GLY:N	2.17	0.59
19:S:34:TRP:CZ2	19:S:57:HIS:CE1	2.90	0.59
19:S:80:TYR:CZ	19:S:81:ARG:HG2	2.36	0.59
1:A:182:U:C5	1:A:183:G:C1'	2.85	0.59
1:A:1027:C:O2	1:A:1027:C:O4'	2.17	0.59
1:A:1060:C:C2	1:A:1198:G:N1	2.70	0.59
6:F:98:LEU:HD13	6:F:98:LEU:N	2.15	0.59
8:H:26:VAL:HG22	8:H:27:PRO:HD2	1.84	0.59
13:M:73:GLU:O	13:M:77:ASN:HB2	2.02	0.59
19:S:51:VAL:CG2	19:S:58:VAL:HG23	2.33	0.59
19:S:64:GLU:O	19:S:67:VAL:HG23	2.02	0.59
1:A:89:C:O2'	1:A:90:U:O5'	2.19	0.59
1:A:149:A:O2'	1:A:150:C:H5'	2.03	0.59
1:A:667:G:H4'	15:O:51:HIS:CE1	2.38	0.59
3:C:84:ILE:HG23	3:C:88:ARG:HH12	1.67	0.59
4:D:206:PHE:CE2	4:D:207:TYR:HE2	2.20	0.59
7:G:52:GLU:OE1	7:G:52:GLU:N	2.35	0.59
7:G:74:GLU:HG2	7:G:91:VAL:CG2	2.32	0.59
17:Q:29:HIS:ND1	17:Q:30:PRO:HD2	2.17	0.59
18:R:58:LEU:HD12	18:R:62:GLU:HB3	1.85	0.59
20:T:99:LEU:HD12	20:T:100:ILE:H	1.65	0.59
1:A:17:U:H2'	1:A:18:C:C6	2.37	0.59
1:A:399:G:OP1	29:A:2086:HOH:O	2.17	0.59
1:A:939:G:H5'	7:G:102:ARG:HH22	1.67	0.59
1:A:1026:G:N7	1:A:1027:C:N3	2.50	0.59
1:A:1130:A:P	1:A:1131:G:OP2	2.60	0.59
4:D:18:LYS:HB3	4:D:33:MET:HG3	1.84	0.59
1:A:380:G:N7	29:A:2680:HOH:O	2.35	0.59
1:A:848:C:H6	1:A:848:C:O5'	1.86	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1124:G:O4'	10:J:38:ILE:HD11	2.02	0.59
1:A:1399:C:O2	1:A:1401:G:C8	2.55	0.59
4:D:127:THR:HG23	4:D:147:ALA:O	2.03	0.59
5:E:80:ILE:HG23	5:E:80:ILE:O	2.03	0.59
5:E:121:LYS:HG2	5:E:123:LEU:HD21	1.84	0.59
6:F:12:PRO:HG2	6:F:57:GLN:O	2.01	0.59
6:F:74:ASP:O	6:F:77:ARG:HB3	2.02	0.59
12:L:76:ASN:O	12:L:76:ASN:CG	2.45	0.59
16:P:82:GLN:O	16:P:84:ALA:N	2.35	0.59
1:A:504:C:OP1	29:A:2163:HOH:O	2.17	0.59
1:A:868:C:H2'	1:A:869:G:O5'	2.02	0.59
1:A:1124:G:H2'	1:A:1145:C:H5	1.68	0.59
4:D:128:VAL:HG12	4:D:129:ASN:ND2	2.18	0.59
4:D:172:PRO:HD2	4:D:173:TRP:CZ3	2.37	0.59
5:E:33:VAL:HG12	5:E:34:VAL:N	2.16	0.59
13:M:70:LEU:O	13:M:74:VAL:HG22	2.03	0.59
1:A:138:G:H5'	1:A:138:G:C8	2.34	0.59
3:C:6:HIS:CD2	3:C:7:PRO:HD2	2.38	0.59
9:I:2:GLU:O	9:I:20:ARG:HG2	2.02	0.59
11:K:47:VAL:HG12	11:K:48:ILE:HD13	1.84	0.59
17:Q:29:HIS:HB2	17:Q:36:ILE:HD12	1.84	0.59
1:A:747:C:H2'	1:A:748:C:O5'	2.03	0.59
1:A:960:U:H4'	1:A:961:U:C5'	2.32	0.59
1:A:1291:G:H4'	9:I:39:GLY:CA	2.32	0.59
1:A:1527:C:C2'	1:A:1528:U:H5'	2.32	0.59
6:F:5:GLU:OE1	18:R:34:TYR:OH	2.15	0.59
19:S:22:LEU:O	19:S:26:GLY:O	2.21	0.59
1:A:180:U:H2'	1:A:181:G:H5'	1.85	0.59
1:A:500:G:C6	1:A:501:C:C4	2.91	0.59
1:A:644:G:H8	1:A:644:G:C5'	2.09	0.59
1:A:994:A:C2	1:A:995:C:C6	2.90	0.59
1:A:1190:G:C5'	1:A:1190:G:H8	2.16	0.59
2:B:74:LYS:C	2:B:76:GLN:H	2.10	0.59
2:B:105:PHE:O	2:B:109:SER:OG	2.20	0.59
6:F:53:ALA:C	6:F:54:LYS:HG2	2.28	0.59
10:J:24:VAL:HG22	10:J:28:ARG:HH12	1.68	0.59
19:S:25:LYS:HG3	19:S:26:GLY:H	1.67	0.59
1:A:433:C:C2	1:A:434:U:H5	2.21	0.59
1:A:510:A:H5''	1:A:511:C:P	2.43	0.59
1:A:1010:G:H22	1:A:1020:U:H1'	1.67	0.59
1:A:1126:U:O4	1:A:1127:G:N2	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1256:A:N6	1:A:1277:C:C6	2.71	0.59
1:A:1499:A:H5'	1:A:1519[A]:MA6:N1	2.18	0.59
1:A:1538:C:N4	24:a:34:G:H1	2.01	0.59
8:H:87:SER:HA	8:H:93:VAL:HG23	1.84	0.59
10:J:44:VAL:HG13	10:J:66:ARG:CD	2.29	0.59
11:K:45:GLY:HA3	11:K:55:LYS:HB3	1.84	0.59
11:K:119:CYS:O	11:K:121:PRO:HD3	2.02	0.59
1:A:923:A:O4'	1:A:1398:A:C2	2.56	0.58
5:E:15:ARG:NH1	5:E:26:PHE:CE2	2.71	0.58
9:I:102:LEU:H	9:I:102:LEU:HD12	1.68	0.58
17:Q:45:HIS:HE2	17:Q:47:PRO:HB3	1.67	0.58
17:Q:90:ILE:O	17:Q:91:ARG:C	2.46	0.58
19:S:12:ASP:O	19:S:15:LEU:CD1	2.51	0.58
20:T:82:SER:O	20:T:83:ARG:C	2.44	0.58
1:A:128:G:H4'	17:Q:3:LYS:HG3	1.84	0.58
1:A:529:G:H3'	1:A:529:G:C8	2.37	0.58
1:A:790:A:H2'	1:A:791:G:C8	2.38	0.58
1:A:893:C:C2'	1:A:894:G:H5'	2.32	0.58
1:A:1332:A:C2	1:A:1333:A:C4	2.91	0.58
5:E:107:ARG:O	5:E:108:ALA:C	2.46	0.58
9:I:39:GLY:O	9:I:40:LEU:HD22	2.03	0.58
11:K:125:PHE:N	11:K:125:PHE:HD2	2.02	0.58
18:R:82:THR:HG23	18:R:83:GLU:N	2.17	0.58
1:A:364:A:H2'	1:A:365:U:O2	2.03	0.58
1:A:1018:C:O5'	1:A:1018:C:H6	1.86	0.58
5:E:152:ARG:HB3	8:H:43:GLY:HA3	1.83	0.58
9:I:14:VAL:HG23	9:I:66:ARG:O	2.03	0.58
14:N:37:PHE:HB3	14:N:39:LEU:HD12	1.85	0.58
19:S:51:VAL:HG23	19:S:51:VAL:O	2.04	0.58
1:A:11:G:O6	29:A:2647:HOH:O	2.16	0.58
1:A:345:C:OP2	1:A:345:C:C6	2.56	0.58
1:A:625:G:H4'	16:P:16:HIS:CD2	2.37	0.58
1:A:737:A:H2'	1:A:738:C:C6	2.37	0.58
1:A:864:A:H2'	1:A:865:A:C8	2.37	0.58
8:H:53:VAL:HG12	8:H:58:TYR:CE1	2.38	0.58
12:L:113:ARG:NH1	12:L:116:SER:H	2.00	0.58
13:M:37:THR:HG23	13:M:39:ILE:CD1	2.33	0.58
24:a:37:A:H8	24:a:37:A:O5'	1.86	0.58
1:A:101:A:H2'	1:A:102:G:H8	1.68	0.58
1:A:1147:C:O2	9:I:16:ARG:NH2	2.37	0.58
1:A:1329:A:C2'	1:A:1330:U:H5'	2.34	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1371:G:C5	1:A:1372:U:C5	2.90	0.58
4:D:100:ARG:HH12	4:D:137:SER:HA	1.68	0.58
4:D:152:SER:O	4:D:155:LEU:HB2	2.04	0.58
6:F:62:TRP:C	6:F:63:TYR:HD2	2.11	0.58
18:R:44:LEU:HD13	18:R:48:GLY:O	2.03	0.58
1:A:820:U:H4'	1:A:821:G:OP2	2.03	0.58
1:A:1003:G:N1	1:A:1003(A):G:C6	2.71	0.58
1:A:1035:A:C6	1:A:1036:G:O6	2.57	0.58
1:A:1405:G:C2'	1:A:1406:U:H5'	2.33	0.58
1:A:1424:C:C4	1:A:1425:U:C5	2.91	0.58
4:D:58:LEU:HD23	4:D:58:LEU:C	2.27	0.58
13:M:86:CYS:SG	13:M:87:TYR:N	2.77	0.58
1:A:358:U:O2'	1:A:359:U:H5'	2.04	0.58
1:A:741:G:H5''	15:O:39:LEU:CD1	2.33	0.58
1:A:1329:A:O2'	1:A:1330:U:H5'	2.03	0.58
5:E:19:MET:HE1	5:E:24:ARG:NH1	2.19	0.58
11:K:56:GLY:O	11:K:57:THR:C	2.45	0.58
12:L:70:ILE:CG2	12:L:75:HIS:HD2	2.02	0.58
19:S:44:MET:HB2	19:S:62:ILE:HD13	1.86	0.58
20:T:84:LEU:HD23	20:T:84:LEU:C	2.29	0.58
1:A:162:A:H5''	1:A:163:C:OP2	2.03	0.58
1:A:409:G:OP1	4:D:24:GLU:O	2.21	0.58
1:A:1054:C:O2'	1:A:1055:A:O5'	2.22	0.58
1:A:1124:G:O2'	1:A:1145:C:N4	2.36	0.58
1:A:1347:G:N2	1:A:1373:G:H2'	2.18	0.58
2:B:25:ASN:ND2	2:B:193:ASP:CB	2.55	0.58
4:D:106:TYR:O	4:D:109:GLY:N	2.29	0.58
11:K:11:LYS:N	11:K:75:TYR:HE2	2.01	0.58
17:Q:4:LYS:HG2	17:Q:6:LEU:HD21	1.85	0.58
18:R:38:GLU:H	18:R:38:GLU:CD	2.11	0.58
21:U:10:ARG:CG	21:U:10:ARG:NH1	2.59	0.58
1:A:386:C:C2'	1:A:387:U:H5'	2.34	0.58
1:A:1501:C:C4	1:A:1504:G:C4	2.92	0.58
1:A:1502:A:H2'	1:A:1504:G:N7	2.19	0.58
3:C:151:VAL:O	3:C:167:TRP:O	2.20	0.58
4:D:25:ARG:NH2	4:D:30:LYS:HD3	2.19	0.58
5:E:24:ARG:HG2	5:E:24:ARG:NH1	2.18	0.58
6:F:87:ARG:HH11	6:F:87:ARG:CG	2.14	0.58
10:J:24:VAL:HG22	10:J:28:ARG:NH1	2.19	0.58
13:M:4:ILE:HD13	13:M:57:ARG:HB2	1.85	0.58
16:P:23:ASP:OD1	16:P:25:ARG:HG3	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:150:C:C2'	1:A:151:A:O5'	2.51	0.58
1:A:984:C:N4	1:A:1221:G:H1	2.01	0.58
1:A:1095:U:H2'	1:A:1096:C:O4'	2.03	0.58
1:A:1206:G:H2'	1:A:1207:2MG:O4'	2.04	0.58
1:A:1250:A:C2	1:A:1287:A:C2	2.91	0.58
1:A:1418:A:H2'	1:A:1419:G:O4'	2.04	0.58
2:B:165:VAL:HG12	2:B:166:ASP:N	2.18	0.58
3:C:82:GLU:HG3	3:C:83:ARG:H	1.69	0.58
10:J:49:VAL:HA	10:J:50:ILE:HD12	1.84	0.58
17:Q:40:LYS:HD2	17:Q:42:TYR:CZ	2.38	0.58
24:a:38:A:C2	24:a:39:G:N7	2.72	0.58
1:A:419:C:C2'	1:A:420:U:H5'	2.34	0.57
1:A:966:M2G:HM22	1:A:967:5MC:O2	2.04	0.57
2:B:97:TRP:CE2	2:B:101:MET:HG3	2.39	0.57
2:B:107:THR:O	2:B:110:GLN:HB2	2.04	0.57
1:A:137:C:H2'	1:A:138:G:H5''	1.84	0.57
1:A:409:G:N2	1:A:434:U:C5	2.72	0.57
1:A:540:G:C6	1:A:541:G:C5	2.92	0.57
1:A:633:G:H2'	1:A:634:C:H6	1.68	0.57
1:A:909:A:C8	1:A:910:C:C6	2.91	0.57
1:A:1501:C:N4	1:A:1504:G:C2	2.72	0.57
7:G:62:PHE:C	7:G:62:PHE:CD1	2.79	0.57
9:I:55:ALA:HB1	9:I:59:PHE:HB2	1.85	0.57
1:A:581:G:O2'	1:A:582:U:H5'	2.04	0.57
1:A:734:G:H8	1:A:734:G:O5'	1.87	0.57
1:A:993:G:H2'	1:A:993:G:N3	2.19	0.57
1:A:1004:A:H2'	1:A:1005:A:H5'	1.86	0.57
3:C:118:GLN:O	3:C:122:GLU:HG3	2.04	0.57
5:E:116:THR:HB	5:E:117:ASP:OD2	2.04	0.57
7:G:16:LEU:CD1	9:I:45:ALA:HB2	2.34	0.57
10:J:50:ILE:HD12	10:J:50:ILE:N	2.19	0.57
24:a:34:G:O2'	24:a:35:G:H5'	2.04	0.57
1:A:53:A:N6	1:A:54:C:C4	2.73	0.57
1:A:691:G:H2'	1:A:692:U:C6	2.40	0.57
1:A:1193:G:C2	1:A:1194:U:C5	2.92	0.57
21:U:8:THR:HG22	21:U:9:ARG:H	1.68	0.57
1:A:134:A:N6	16:P:25:ARG:HH21	2.02	0.57
1:A:1063:C:H2'	1:A:1064:G:C8	2.39	0.57
1:A:1189:C:H5''	1:A:1190:G:OP2	2.04	0.57
1:A:1402:4OC:HM41	25:b:3:U:OP2	2.05	0.57
1:A:1419:G:O6	1:A:1420:C:N4	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:187:ARG:CG	4:D:188:LEU:HD12	2.35	0.57
5:E:9:LYS:NZ	5:E:111:GLU:OE1	2.38	0.57
13:M:74:VAL:HG23	13:M:75:ALA:H	1.69	0.57
14:N:4:LYS:O	14:N:7:ILE:HG12	2.05	0.57
20:T:39:LYS:O	20:T:43:LEU:HG	2.04	0.57
1:A:293:G:C4	1:A:305:G:N2	2.72	0.57
1:A:510:A:H5''	1:A:511:C:OP2	2.04	0.57
1:A:1277:C:H1'	1:A:1282:C:H1'	1.86	0.57
9:I:26:VAL:HG12	9:I:61:ALA:HB3	1.85	0.57
12:L:92:OTD:OD1	12:L:92:OTD:N	2.36	0.57
17:Q:58:GLU:O	17:Q:59:ILE:HD13	2.02	0.57
17:Q:81:ARG:HG3	17:Q:84:LEU:HD12	1.87	0.57
1:A:54:C:O2'	1:A:55:A:H5'	2.03	0.57
1:A:1055:A:C2	1:A:1056:U:H1'	2.40	0.57
2:B:97:TRP:HH2	2:B:176:GLU:CD	2.13	0.57
9:I:31:GLN:HE22	9:I:36:TYR:HD1	1.50	0.57
19:S:15:LEU:HD12	19:S:15:LEU:H	1.70	0.57
1:A:54:C:N3	1:A:352:C:H5	2.02	0.57
1:A:315:A:OP1	29:A:2576:HOH:O	2.17	0.57
1:A:1241:G:H2'	1:A:1242:C:H6	1.70	0.57
2:B:204:ASN:C	2:B:204:ASN:OD1	2.47	0.57
3:C:33:LEU:O	3:C:37:GLN:HG2	2.04	0.57
5:E:11:ILE:HD11	5:E:105:VAL:HA	1.87	0.57
13:M:87:TYR:HE1	13:M:91:ARG:CD	2.18	0.57
17:Q:18:THR:CG2	17:Q:69:LYS:HD3	2.35	0.57
18:R:43:PHE:CD2	18:R:66:LEU:HD21	2.40	0.57
1:A:174:C:O5'	1:A:174:C:H6	1.86	0.57
1:A:540:G:C4	1:A:541:G:C8	2.92	0.57
1:A:954:G:H21	1:A:1227:A:H62	1.51	0.57
1:A:975:A:C5'	1:A:975:A:C8	2.87	0.57
1:A:1494:G:N3	1:A:1495:U:C6	2.73	0.57
1:A:1533:C:O2'	1:A:1534:C:P	2.63	0.57
2:B:88:ALA:CB	2:B:219:VAL:HG13	2.22	0.57
2:B:170:GLU:O	2:B:173:ALA:N	2.38	0.57
4:D:79:PHE:CD2	4:D:80:GLU:N	2.73	0.57
5:E:65:ASN:ND2	5:E:65:ASN:O	2.38	0.57
12:L:28:LYS:HE3	12:L:33:ARG:NH2	2.19	0.57
13:M:40:ASN:OD1	13:M:41:PRO:HD2	2.04	0.57
20:T:63:ILE:O	20:T:66:ALA:HB3	2.04	0.57
1:A:264:U:H2'	1:A:265:G:H5'	1.87	0.57
1:A:1279:A:H5''	1:A:1280:A:OP1	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:17:THR:O	8:H:78:GLN:NE2	2.38	0.57
9:I:125:TYR:N	9:I:125:TYR:HD2	2.03	0.57
11:K:80:VAL:HG13	11:K:81:ASP:N	2.20	0.57
12:L:53:ARG:NH1	12:L:92:0TD:OD2	2.38	0.57
16:P:18:ARG:O	16:P:20:VAL:HG23	2.05	0.57
3:C:50:ALA:O	3:C:71:ALA:HB3	2.04	0.56
4:D:114:ARG:HH11	4:D:114:ARG:HG3	1.70	0.56
5:E:79:GLU:HB3	5:E:92:LYS:HG2	1.87	0.56
10:J:49:VAL:HG23	14:N:41:ARG:HB2	1.86	0.56
13:M:4:ILE:CG2	13:M:5:ALA:N	2.68	0.56
13:M:87:TYR:O	13:M:90:LEU:N	2.38	0.56
16:P:23:ASP:OD1	16:P:24:ALA:N	2.39	0.56
1:A:502:G:H2'	1:A:503:C:O4'	2.05	0.56
1:A:994:A:C2	1:A:995:C:C5	2.92	0.56
1:A:1054:C:N3	23:W:34:G:C5'	2.68	0.56
1:A:1126:U:O4	1:A:1127:G:C2	2.58	0.56
1:A:1507:A:C8	1:A:1530:G:N2	2.73	0.56
1:A:1535:A:N1	24:a:37:A:C2	2.73	0.56
3:C:174:PRO:O	3:C:176:HIS:N	2.38	0.56
5:E:96:PRO:HA	5:E:117:ASP:OD1	2.05	0.56
7:G:136:LYS:HD2	7:G:140:ASP:OD1	2.04	0.56
8:H:114:THR:HG21	8:H:129:VAL:CG2	2.35	0.56
9:I:105:ASP:OD2	9:I:107:ARG:HG3	2.04	0.56
10:J:48:THR:HA	10:J:62:HIS:CB	2.31	0.56
20:T:41:ILE:O	20:T:44:ALA:HB3	2.04	0.56
1:A:537:G:H2'	1:A:538:G:C8	2.37	0.56
1:A:667:G:H4'	15:O:51:HIS:ND1	2.19	0.56
1:A:695:A:H2'	1:A:696:A:C8	2.41	0.56
1:A:854:G:N2	1:A:855:G:C4	2.74	0.56
1:A:910:C:OP2	12:L:21:LYS:NZ	2.38	0.56
1:A:1004:A:N6	1:A:1037:C:H42	2.04	0.56
1:A:1124:G:O2'	1:A:1145:C:C5	2.58	0.56
1:A:1126:U:H2'	1:A:1127:G:O5'	2.06	0.56
3:C:134:ILE:O	3:C:138:VAL:HG23	2.05	0.56
4:D:173:TRP:C	4:D:174:LEU:HD23	2.30	0.56
4:D:206:PHE:HD2	4:D:207:TYR:CE2	2.22	0.56
7:G:27:ILE:CD1	7:G:40:ALA:HA	2.36	0.56
8:H:29:SER:OG	8:H:32:LYS:HG3	2.06	0.56
13:M:44:ARG:HB3	13:M:46:LYS:HG3	1.86	0.56
13:M:87:TYR:CE1	13:M:91:ARG:CD	2.88	0.56
13:M:87:TYR:O	13:M:90:LEU:HB2	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:101:ARG:HD3	17:Q:101:ARG:H	1.70	0.56
19:S:62:ILE:HA	19:S:66:MET:CE	2.35	0.56
21:U:8:THR:HG22	21:U:9:ARG:N	2.20	0.56
1:A:106:C:C2'	1:A:107:G:H5'	2.34	0.56
1:A:344:A:H5''	1:A:345:C:H5	1.70	0.56
1:A:830:G:O3'	2:B:22:LYS:HB3	2.05	0.56
1:A:945:G:N1	1:A:1337:G:C2	2.73	0.56
1:A:1092:A:C5'	1:A:1092:A:H8	2.18	0.56
1:A:1124:G:H5'	10:J:35:SER:O	2.05	0.56
1:A:1534:C:C2	1:A:1535:A:C2	2.93	0.56
2:B:36:ARG:CG	2:B:41:ILE:HD11	2.35	0.56
5:E:55:VAL:O	5:E:56:GLN:C	2.47	0.56
10:J:69:ASN:O	10:J:70:ARG:HD3	2.04	0.56
12:L:11:VAL:HG22	17:Q:29:HIS:CD2	2.40	0.56
21:U:18:TYR:HD1	21:U:24:ARG:CZ	2.18	0.56
1:A:83:U:H5	1:A:84:U:C5	2.24	0.56
1:A:564:C:H5'	17:Q:32:TYR:CE2	2.41	0.56
1:A:1125:U:H3'	1:A:1126:U:C5	2.40	0.56
1:A:1499:A:OP1	1:A:1519[A]:MA6:N1	2.38	0.56
2:B:97:TRP:CH2	2:B:176:GLU:OE2	2.58	0.56
6:F:4:TYR:CZ	6:F:72:VAL:HG21	2.41	0.56
19:S:41:VAL:HB	19:S:42:PRO:HD2	1.86	0.56
1:A:337:C:H2'	1:A:338:A:C8	2.41	0.56
1:A:831:U:H2'	1:A:832:C:C6	2.41	0.56
1:A:1250:A:C2	1:A:1287:A:N1	2.74	0.56
1:A:1360:A:H2'	1:A:1361:G:O5'	2.06	0.56
4:D:196:LEU:N	4:D:196:LEU:HD23	2.21	0.56
1:A:28:G:O2'	1:A:296:U:OP1	2.20	0.56
1:A:427:U:C4	1:A:428:G:C6	2.94	0.56
1:A:827:U:O2	1:A:827:U:H2'	2.05	0.56
1:A:1014:A:N7	1:A:1015:A:N6	2.54	0.56
1:A:1065:U:O2'	1:A:1066:C:OP2	2.19	0.56
1:A:1395:C:C2'	1:A:1396:A:H5'	2.35	0.56
1:A:1536:C:H3'	1:A:1536:C:H6	1.69	0.56
3:C:8:ILE:HG12	3:C:16:ARG:HG3	1.88	0.56
4:D:173:TRP:CD1	4:D:189:PRO:HD3	2.41	0.56
11:K:122:LYS:O	11:K:123:LYS:C	2.47	0.56
11:K:122:LYS:O	11:K:124:LYS:N	2.39	0.56
1:A:476:G:H2'	1:A:477:G:C8	2.40	0.56
1:A:908:A:C2	1:A:909:A:C4	2.94	0.56
1:A:1128:C:O2'	1:A:1130:A:C8	2.58	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:105:GLU:HG2	3:C:106:VAL:N	2.21	0.56
4:D:19:LEU:HD12	4:D:67:ILE:HG13	1.86	0.56
4:D:32:ALA:C	4:D:35:ARG:H	2.13	0.56
8:H:36:LEU:HA	8:H:39:LEU:HD23	1.88	0.56
8:H:102:ARG:H	8:H:102:ARG:CD	2.01	0.56
12:L:27:LEU:CG	12:L:28:LYS:H	2.05	0.56
16:P:21:VAL:O	16:P:21:VAL:HG12	2.05	0.56
17:Q:86:GLU:O	17:Q:90:ILE:HG12	2.05	0.56
1:A:559:A:OP1	5:E:126:ARG:NH2	2.39	0.56
1:A:1082:G:C2'	1:A:1083:U:H5'	2.35	0.56
1:A:1316:G:H4'	14:N:18:VAL:HG11	1.86	0.56
1:A:1407:5MC:C2	1:A:1408:A:C8	2.94	0.56
2:B:170:GLU:O	2:B:173:ALA:HB3	2.06	0.56
3:C:59:ARG:HG2	3:C:64:VAL:HG13	1.88	0.56
4:D:145:GLU:C	4:D:146:ILE:HD12	2.31	0.56
9:I:5:TYR:HD1	9:I:6:GLY:H	1.54	0.56
10:J:82:ILE:HG22	10:J:82:ILE:O	2.05	0.56
1:A:188:C:O2'	1:A:189:G:H5'	2.06	0.56
1:A:273:A:N6	1:A:274:A:C6	2.73	0.56
1:A:1096:C:H2'	1:A:1097:C:H6	1.71	0.56
3:C:147:LYS:HE3	3:C:205:GLY:H	1.69	0.56
4:D:18:LYS:CE	4:D:20:TYR:HE2	2.11	0.56
5:E:76:ILE:HG12	5:E:118:ILE:CD1	2.36	0.56
5:E:137:GLU:HG2	5:E:140:ARG:HH11	1.71	0.56
12:L:127:GLU:HG3	12:L:128:ALA:O	2.05	0.56
18:R:37:VAL:O	18:R:39:VAL:N	2.39	0.56
23:W:32:C:HO2'	23:W:33:U:H6	1.54	0.56
1:A:137:C:C2'	1:A:138:G:C5'	2.84	0.55
1:A:190(E):U:C5	17:Q:72:ARG:NH2	2.74	0.55
1:A:353:A:H8	1:A:353:A:H5'	1.70	0.55
1:A:500:G:O6	1:A:501:C:N4	2.39	0.55
2:B:141:GLU:O	2:B:144:ARG:HG3	2.06	0.55
4:D:172:PRO:HG2	4:D:173:TRP:HE3	1.71	0.55
8:H:124:ALA:O	8:H:128:GLY:N	2.38	0.55
9:I:27:THR:OG1	9:I:28:VAL:N	2.39	0.55
10:J:61:GLU:HG2	10:J:61:GLU:O	2.06	0.55
12:L:24:VAL:HG13	12:L:98:TYR:HE2	1.71	0.55
12:L:34:ARG:HB2	12:L:105:TYR:CE1	2.41	0.55
1:A:21:G:P	29:A:2044:HOH:O	2.65	0.55
1:A:264:U:C2'	1:A:265:G:H5'	2.37	0.55
1:A:446:G:C2'	1:A:447:G:H5'	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:462:G:H5'	1:A:463:A:OP2	2.07	0.55
1:A:939:G:H5'	7:G:102:ARG:CZ	2.36	0.55
1:A:1126:U:OP1	1:A:1126:U:H6	1.89	0.55
1:A:1248:A:H2'	1:A:1249:C:H5'	1.87	0.55
1:A:1399:C:O2	1:A:1401:G:N7	2.38	0.55
1:A:1436:U:C2	1:A:1437:C:C6	2.93	0.55
3:C:8:ILE:CG2	3:C:9:GLY:N	2.70	0.55
5:E:11:ILE:CG2	5:E:12:LEU:N	2.68	0.55
5:E:117:ASP:OD2	5:E:117:ASP:N	2.37	0.55
9:I:10:ARG:HG3	9:I:11:LYS:HG2	1.89	0.55
13:M:99:ARG:NH2	19:S:2:PRO:CG	2.70	0.55
14:N:12:ARG:HH11	14:N:12:ARG:N	2.04	0.55
19:S:13:ASP:O	19:S:16:LEU:HB3	2.06	0.55
1:A:89:C:C5	1:A:90:U:C4	2.84	0.55
1:A:414:A:C2	1:A:415:A:C4	2.93	0.55
1:A:506:G:C2'	1:A:507:C:H5'	2.36	0.55
1:A:569:C:H5''	1:A:570:G:OP1	2.07	0.55
1:A:1360:A:C2'	1:A:1361:G:O5'	2.54	0.55
1:A:1408:A:O2'	1:A:1409:C:H5'	2.07	0.55
1:A:1536:C:C5	1:A:1537:U:N3	2.74	0.55
4:D:61:LYS:C	4:D:61:LYS:CD	2.79	0.55
9:I:27:THR:CG2	9:I:62:TYR:HA	2.37	0.55
10:J:48:THR:CB	10:J:62:HIS:HB3	2.36	0.55
20:T:10:LEU:CD2	20:T:13:LEU:N	2.64	0.55
1:A:547:A:OP2	4:D:2:GLY:CA	2.55	0.55
1:A:829:G:C2'	1:A:830:G:H5'	2.35	0.55
1:A:1027:C:O2'	1:A:1034:G:N2	2.40	0.55
1:A:1029:C:C2'	1:A:1030:C:H5'	2.37	0.55
1:A:1195:C:H5''	1:A:1196:U:O5'	2.06	0.55
4:D:92:VAL:O	4:D:93:PHE:C	2.47	0.55
5:E:69:VAL:HG12	5:E:70:PRO:N	2.20	0.55
7:G:75:VAL:O	7:G:75:VAL:HG22	2.06	0.55
8:H:28:ALA:HB2	8:H:58:TYR:CA	2.36	0.55
12:L:83:VAL:HG12	12:L:107:ALA:HB2	1.88	0.55
13:M:23:TYR:CE2	13:M:70:LEU:HD13	2.42	0.55
20:T:84:LEU:HD23	20:T:84:LEU:O	2.07	0.55
1:A:255:G:O6	1:A:266:G:O6	2.25	0.55
1:A:337:C:H2'	1:A:338:A:H8	1.71	0.55
1:A:922:G:N3	1:A:1398:A:H2	2.05	0.55
1:A:1006:C:N4	1:A:1023:G:H1	2.02	0.55
1:A:1015:A:H2'	1:A:1016:A:O4'	2.05	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1124:G:HO2'	1:A:1145:C:N4	2.03	0.55
2:B:100:GLY:O	2:B:101:MET:C	2.49	0.55
4:D:196:LEU:HD23	4:D:196:LEU:H	1.72	0.55
5:E:76:ILE:HG12	5:E:118:ILE:HD12	1.88	0.55
7:G:121:ALA:O	7:G:125:MET:HG3	2.07	0.55
9:I:63:ILE:O	9:I:63:ILE:HG22	2.06	0.55
1:A:261:U:O2	1:A:263:A:C8	2.60	0.55
1:A:668:G:O2'	1:A:669:U:H5'	2.07	0.55
1:A:838:G:N2	1:A:849:C:C2	2.75	0.55
1:A:933:G:OP2	7:G:3:ARG:HB3	2.07	0.55
1:A:1114:C:H1'	14:N:60:SER:OG	2.05	0.55
1:A:1139:G:N2	1:A:1143:G:N2	2.54	0.55
1:A:1417:G:O2'	1:A:1418:A:H5'	2.06	0.55
1:A:1448:C:H2'	1:A:1449:C:H6	1.71	0.55
2:B:7:VAL:O	2:B:10:LEU:HB2	2.06	0.55
8:H:57:PRO:O	8:H:57:PRO:CG	2.53	0.55
12:L:60:LEU:HB2	12:L:64:TYR:O	2.06	0.55
17:Q:5:VAL:C	17:Q:6:LEU:HD23	2.32	0.55
23:W:35:G:H2'	23:W:36:A:H8	1.70	0.55
1:A:36:C:C2'	1:A:37:U:H5'	2.37	0.55
1:A:822:C:C2'	1:A:823:G:H5'	2.37	0.55
1:A:1028:C:N3	1:A:1034:G:C2	2.75	0.55
3:C:54:ARG:NH1	3:C:56:ASP:OD1	2.27	0.55
4:D:170:VAL:HG22	4:D:171:GLY:H	1.71	0.55
7:G:108:ALA:O	7:G:119:ARG:HB3	2.07	0.55
8:H:20:TYR:CZ	8:H:76:PRO:HD2	2.41	0.55
10:J:4:ILE:HG22	10:J:77:PRO:HD3	1.87	0.55
23:W:39:G:C2	23:W:40:PSU:N3	2.74	0.55
1:A:961:U:C2'	1:A:962:C:H5'	2.36	0.55
1:A:998:G:H2'	1:A:999:C:C6	2.41	0.55
1:A:1415:G:C2'	1:A:1416:G:H5'	2.36	0.55
5:E:67:VAL:HG21	5:E:140:ARG:HB3	1.89	0.55
13:M:27:LYS:CE	21:U:21:TYR:HE2	2.20	0.55
13:M:37:THR:HG23	13:M:39:ILE:HD13	1.88	0.55
18:R:37:VAL:O	18:R:38:GLU:C	2.49	0.55
19:S:63:THR:OG1	19:S:66:MET:HG3	2.07	0.55
1:A:278:G:C6	17:Q:95:TYR:HD2	2.25	0.55
1:A:545:C:O2	1:A:546:G:O4'	2.25	0.55
1:A:1005:A:C8	1:A:1026:G:N1	2.73	0.55
1:A:1027:C:C5	1:A:1035:A:C2	2.95	0.55
1:A:1206:G:C6	1:A:1207:2MG:C6	2.94	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:56:ARG:NH1	2:B:56:ARG:HB2	2.22	0.55
2:B:101:MET:HB2	2:B:102:LEU:HD12	1.89	0.55
3:C:5:ILE:CD1	3:C:10:PHE:HB2	2.37	0.55
3:C:59:ARG:NH1	3:C:97:LYS:HE2	2.22	0.55
8:H:4:ASP:HB3	8:H:7:ALA:HB3	1.88	0.55
10:J:78:ASN:CG	10:J:79:ARG:HH11	2.14	0.55
1:A:107:G:C3'	1:A:108:G:H5''	2.36	0.55
1:A:357:G:C2	1:A:358:U:C5	2.95	0.55
1:A:597:G:N2	1:A:643:C:N3	2.40	0.55
1:A:1011:G:H2'	1:A:1012:U:H5'	1.87	0.55
1:A:1117:G:H5''	9:I:104:ARG:NH2	2.22	0.55
4:D:204:ILE:HD13	4:D:204:ILE:H	1.73	0.55
16:P:19:ILE:HG22	16:P:36:ILE:HG13	1.87	0.55
1:A:192:U:H1'	20:T:103:GLY:CA	2.34	0.54
1:A:421:U:O2	1:A:421:U:O4'	2.25	0.54
1:A:1160:G:O6	1:A:1181:G:C6	2.60	0.54
1:A:1190:G:C8	1:A:1190:G:H5''	2.42	0.54
2:B:101:MET:C	2:B:102:LEU:HD12	2.31	0.54
3:C:76:VAL:HG23	3:C:77:ILE:N	2.22	0.54
7:G:66:VAL:HG12	7:G:67:GLU:N	2.21	0.54
7:G:113:GLU:HB2	7:G:119:ARG:HG2	1.89	0.54
9:I:16:ARG:HD3	9:I:64:THR:HG22	1.89	0.54
9:I:64:THR:HG22	9:I:64:THR:O	2.07	0.54
10:J:38:ILE:HG23	10:J:39:PRO:HD2	1.88	0.54
14:N:39:LEU:HD22	14:N:43:CYS:HB3	1.89	0.54
18:R:45:SER:OG	18:R:46:GLU:N	2.38	0.54
19:S:11:VAL:CG1	19:S:16:LEU:HD22	2.37	0.54
1:A:132:C:O2'	1:A:133:U:H5'	2.08	0.54
1:A:389:A:C5	1:A:390:C:H1'	2.42	0.54
1:A:860:A:OP2	29:A:2124:HOH:O	2.18	0.54
1:A:1030(A):G:C4	1:A:1030(C):G:OP2	2.60	0.54
1:A:1319:A:OP1	19:S:5:LEU:HD22	2.08	0.54
1:A:1346:A:C5	7:G:10:ARG:NH1	2.75	0.54
1:A:1500:A:P	1:A:1505:G:OP1	2.65	0.54
2:B:212:GLN:HE21	2:B:235:SER:HB3	1.72	0.54
3:C:20:SER:HA	3:C:57:ILE:O	2.07	0.54
3:C:130:VAL:O	3:C:134:ILE:CD1	2.56	0.54
4:D:72:GLU:O	4:D:75:PHE:HB3	2.07	0.54
6:F:98:LEU:H	6:F:98:LEU:CD1	2.17	0.54
12:L:78:GLN:N	12:L:81:SER:OG	2.29	0.54
15:O:56:LEU:CD1	15:O:56:LEU:C	2.80	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:23:PRO:C	21:U:25:LYS:H	2.15	0.54
24:a:38:A:N3	24:a:39:G:N7	2.56	0.54
1:A:178:C:C2'	1:A:179:A:H5'	2.38	0.54
1:A:529:G:C8	1:A:529:G:C3'	2.89	0.54
1:A:568:G:N2	1:A:883:C:C2	2.75	0.54
1:A:676:A:O2'	1:A:677:U:H5'	2.06	0.54
1:A:839:U:C5'	1:A:840:C:H5	2.18	0.54
1:A:1122:U:H2'	1:A:1123:A:H5'	1.89	0.54
1:A:1381:U:C6	1:A:1382:C:C5	2.96	0.54
3:C:36:ASP:O	3:C:39:ILE:HB	2.07	0.54
3:C:157:ILE:C	3:C:159:GLY:H	2.15	0.54
9:I:23:ASN:OD1	9:I:25:LYS:HE3	2.07	0.54
9:I:46:ALA:HB2	9:I:74:ILE:HG23	1.89	0.54
9:I:128:ARG:HG2	9:I:128:ARG:OXT	2.06	0.54
11:K:91:ARG:O	11:K:94:ALA:N	2.35	0.54
2:B:172:ILE:HG12	2:B:173:ALA:N	2.22	0.54
8:H:10:LEU:HD22	8:H:83:ILE:HD11	1.90	0.54
9:I:99:LEU:HD22	9:I:99:LEU:N	2.22	0.54
17:Q:23:VAL:CG2	17:Q:42:TYR:HD1	2.21	0.54
17:Q:58:GLU:C	17:Q:59:ILE:HD13	2.33	0.54
1:A:22:G:C6	1:A:23:C:C4	2.96	0.54
1:A:22:G:C5	1:A:23:C:C5	2.96	0.54
1:A:448:A:H2'	1:A:449:C:H6	1.73	0.54
1:A:998:G:H2'	1:A:999:C:H6	1.73	0.54
1:A:1108:G:O6	29:A:2136:HOH:O	2.16	0.54
1:A:1122:U:C2'	1:A:1123:A:H5'	2.38	0.54
4:D:63:LYS:NZ	4:D:197:PRO:O	2.40	0.54
7:G:51:GLN:HA	7:G:54:THR:O	2.07	0.54
8:H:86:ILE:HG22	8:H:87:SER:N	2.22	0.54
19:S:42:PRO:O	19:S:45:VAL:HG23	2.06	0.54
21:U:6:ARG:HG3	21:U:15:ARG:NH1	2.22	0.54
1:A:53:A:C6	1:A:54:C:C4	2.96	0.54
1:A:380:G:C8	29:A:2680:HOH:O	2.54	0.54
1:A:1197:G:H2'	1:A:1198:G:H5''	1.90	0.54
1:A:1533:C:H2'	1:A:1534:C:C6	2.42	0.54
1:A:1539:C:O2	24:a:34:G:C2	2.59	0.54
3:C:13:GLY:HA2	14:N:57:ARG:HH12	1.72	0.54
4:D:21:LEU:HD21	4:D:66:ARG:O	2.07	0.54
15:O:15:PHE:HE2	15:O:85:LEU:HD21	1.72	0.54
19:S:80:TYR:HD1	19:S:81:ARG:H	1.51	0.54
20:T:10:LEU:HD23	20:T:13:LEU:H	1.68	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:88:VAL:HG12	20:T:89:ARG:N	2.21	0.54
1:A:98:U:C2'	1:A:99:C:H5'	2.37	0.54
1:A:991:U:O2'	1:A:992:U:P	2.66	0.54
1:A:1005:A:H2'	1:A:1005:A:N3	2.23	0.54
1:A:1256:A:C8	1:A:1258:G:C2	2.94	0.54
1:A:1498:UR3:C4'	1:A:1519[A]:MA6:H2	2.37	0.54
1:A:1532:U:H3	24:a:39:G:H1	1.55	0.54
2:B:97:TRP:CZ2	2:B:101:MET:HB2	2.43	0.54
6:F:48:LEU:HG	6:F:57:GLN:HA	1.88	0.54
6:F:48:LEU:HD13	6:F:52:ILE:HG13	1.89	0.54
8:H:4:ASP:OD1	8:H:6:ILE:N	2.40	0.54
9:I:33:PHE:CE2	9:I:47:LEU:HD11	2.41	0.54
17:Q:12:SER:HB3	17:Q:20:THR:OG1	2.07	0.54
19:S:19:VAL:HG23	19:S:47:HIS:HD1	1.71	0.54
1:A:89:C:C6	1:A:90:U:N3	2.75	0.54
1:A:119:A:P	29:A:2559:HOH:O	2.64	0.54
1:A:257:G:C2	1:A:270:A:C2	2.94	0.54
1:A:259:G:H2'	1:A:260:G:O5'	2.08	0.54
1:A:895:G:H2'	1:A:896:C:H6	1.73	0.54
1:A:1279:A:C5'	1:A:1280:A:OP1	2.56	0.54
2:B:92:TYR:CE1	2:B:151:GLY:HA3	2.42	0.54
3:C:3:ASN:N	3:C:3:ASN:OD1	2.40	0.54
12:L:59:ARG:HG3	12:L:65:GLU:OE2	2.08	0.54
17:Q:45:HIS:NE2	17:Q:47:PRO:HB3	2.22	0.54
17:Q:81:ARG:NE	17:Q:84:LEU:CD1	2.71	0.54
1:A:500:G:C6	1:A:546:G:C2	2.96	0.54
1:A:1055:A:C8	1:A:1206:G:N2	2.76	0.54
3:C:6:HIS:HD2	3:C:7:PRO:HD2	1.70	0.54
3:C:156:ARG:NH1	3:C:193:TYR:HB2	2.23	0.54
3:C:178:LEU:C	3:C:180:ALA:H	2.14	0.54
7:G:54:THR:CG2	7:G:56:GLN:HB2	2.38	0.54
10:J:79:ARG:H	10:J:79:ARG:HD2	1.73	0.54
14:N:9:LYS:O	14:N:11:LYS:N	2.40	0.54
19:S:41:VAL:HG22	19:S:44:MET:HG3	1.89	0.54
1:A:91:C:H2'	1:A:92:C:H6	1.70	0.54
1:A:610:G:H2'	1:A:611:A:H5'	1.89	0.54
1:A:1018:C:H2'	1:A:1019:C:C6	2.43	0.54
4:D:57:ARG:HG3	4:D:202:LEU:HD22	1.89	0.54
5:E:11:ILE:CG2	5:E:31:LEU:HB3	2.37	0.54
10:J:79:ARG:H	10:J:79:ARG:CD	2.21	0.54
13:M:37:THR:OG1	13:M:55:ARG:HG2	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:384:G:H2'	1:A:385:C:C6	2.42	0.53
1:A:579:G:H5'	1:A:728:A:H1'	1.90	0.53
1:A:671:G:H5'	6:F:77:ARG:NH2	2.23	0.53
1:A:725:G:C2'	1:A:726:C:H5'	2.38	0.53
1:A:769:G:C2'	1:A:770:C:H5'	2.38	0.53
1:A:1004:A:C5'	29:A:2327:HOH:O	2.55	0.53
1:A:1054:C:N3	23:W:34:G:H5'	2.21	0.53
1:A:1190:G:C5'	1:A:1190:G:C8	2.91	0.53
1:A:1206:G:C4	1:A:1207:2MG:C8	2.96	0.53
1:A:1505:G:H5'	1:A:1506:U:OP1	2.08	0.53
2:B:114:ARG:O	2:B:117:GLU:HB3	2.08	0.53
3:C:46:GLU:HG3	3:C:83:ARG:HH21	1.71	0.53
6:F:98:LEU:N	6:F:98:LEU:CD1	2.71	0.53
14:N:46:GLU:O	14:N:49:HIS:HB2	2.08	0.53
18:R:50:ILE:HG12	18:R:70:ILE:HD13	1.89	0.53
19:S:31:ILE:O	19:S:50:ALA:CB	2.56	0.53
20:T:44:ALA:O	20:T:45:GLN:C	2.50	0.53
20:T:45:GLN:HA	20:T:91:LEU:HD21	1.90	0.53
1:A:602:A:C2	1:A:637:G:C2	2.96	0.53
1:A:689:C:H2'	1:A:690:G:H5'	1.89	0.53
1:A:691:G:H2'	1:A:692:U:H6	1.73	0.53
1:A:865:A:O5'	1:A:865:A:H8	1.91	0.53
1:A:947:G:H2'	1:A:948:C:O4'	2.08	0.53
1:A:1006:C:O2'	1:A:1007:C:H5'	2.08	0.53
1:A:1236:A:H4'	1:A:1304:G:H4'	1.91	0.53
1:A:1278:U:H2'	1:A:1278:U:O2	2.07	0.53
1:A:1502:A:C2'	1:A:1502:A:N3	2.70	0.53
3:C:150:LYS:HA	3:C:169:ALA:HB2	1.90	0.53
4:D:83:SER:CA	4:D:89:THR:HG23	2.32	0.53
7:G:69:VAL:HA	7:G:138:LYS:HD3	1.89	0.53
9:I:15:ALA:CB	9:I:77:ILE:HD12	2.37	0.53
17:Q:59:ILE:CG2	17:Q:71:PHE:CD1	2.90	0.53
19:S:41:VAL:HG23	19:S:43:GLU:OE2	2.07	0.53
20:T:13:LEU:C	20:T:13:LEU:CD1	2.80	0.53
1:A:34:C:H1'	12:L:32:PHE:CZ	2.43	0.53
1:A:154:C:C2'	1:A:155:C:H5'	2.38	0.53
1:A:256:U:O2'	1:A:257:G:H5'	2.07	0.53
1:A:778:G:H2'	1:A:779:C:O4'	2.08	0.53
1:A:784:C:H2'	1:A:785:G:O5'	2.08	0.53
1:A:858:G:O2'	1:A:859:A:C5'	2.44	0.53
1:A:1054:C:N4	23:W:34:G:C8	2.76	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:43:HIS:HA	4:D:46:LYS:HG3	1.90	0.53
5:E:8:GLU:CB	5:E:34:VAL:HG12	2.38	0.53
7:G:27:ILE:HG22	7:G:28:ASN:N	2.24	0.53
12:L:55:VAL:N	12:L:70:ILE:HD12	2.23	0.53
24:a:34:G:C2'	24:a:35:G:H8	2.07	0.53
1:A:594:G:H2'	1:A:595:G:H5'	1.90	0.53
1:A:664:G:OP1	18:R:64:ARG:HD2	2.09	0.53
1:A:688:G:H2'	1:A:689:C:C6	2.43	0.53
1:A:1371:G:O3'	9:I:69:GLY:HA3	2.09	0.53
2:B:168:THR:O	2:B:169:LYS:C	2.51	0.53
3:C:35:GLU:O	3:C:36:ASP:C	2.51	0.53
3:C:113:ALA:N	3:C:114:PRO:HD2	2.24	0.53
3:C:142:MET:O	3:C:142:MET:HE3	2.08	0.53
4:D:105:VAL:HG13	4:D:110:PHE:HB2	1.91	0.53
7:G:115:ARG:HG3	7:G:118:VAL:HG23	1.90	0.53
8:H:9:MET:SD	8:H:36:LEU:HD21	2.48	0.53
8:H:97:VAL:HG23	8:H:129:VAL:C	2.33	0.53
12:L:19:ARG:HA	12:L:20:LYS:NZ	2.23	0.53
17:Q:81:ARG:HG3	17:Q:81:ARG:O	2.08	0.53
21:U:18:TYR:CD1	21:U:24:ARG:HG3	2.44	0.53
1:A:229:U:O2'	16:P:23:ASP:HB2	2.09	0.53
1:A:1055:A:C8	1:A:1206:G:C2	2.96	0.53
1:A:1413:A:C2	1:A:1414:U:C2	2.97	0.53
2:B:30:ARG:HD2	2:B:31:TYR:CE1	2.43	0.53
7:G:59:LEU:HD23	7:G:60:LYS:HE3	1.91	0.53
7:G:78:ARG:HD2	7:G:156:TRP:CB	2.38	0.53
9:I:48:GLU:HB3	9:I:101:PHE:CE1	2.43	0.53
17:Q:48:GLU:O	17:Q:49:GLU:HB2	2.08	0.53
18:R:22:VAL:HG23	18:R:56:THR:HA	1.91	0.53
1:A:98:U:O2'	1:A:99:C:H5'	2.09	0.53
1:A:144:G:H1	1:A:178:C:H42	1.57	0.53
1:A:182:U:C5	1:A:183:G:C4	2.94	0.53
1:A:392:G:N3	1:A:393:A:C8	2.77	0.53
1:A:1026:G:C8	1:A:1027:C:C2	2.96	0.53
1:A:1321:C:C4'	13:M:87:TYR:HE2	2.18	0.53
1:A:1472:U:H2'	1:A:1473:A:O5'	2.09	0.53
2:B:212:GLN:O	2:B:213:LEU:C	2.51	0.53
4:D:147:ALA:CB	4:D:182:LYS:HB3	2.39	0.53
5:E:51:VAL:O	5:E:54:ALA:HB3	2.09	0.53
6:F:99:ALA:HB1	18:R:23:LYS:NZ	2.23	0.53
10:J:29:ARG:H	10:J:29:ARG:CD	2.16	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:26:ARG:HD3	14:N:47:LEU:CD1	2.39	0.53
17:Q:11:VAL:HG13	17:Q:85:VAL:HG12	1.91	0.53
20:T:18:GLN:O	20:T:19:SER:C	2.52	0.53
23:W:35:G:N3	23:W:36:A:C8	2.76	0.53
1:A:89:C:O2'	1:A:90:U:OP1	2.23	0.53
1:A:443:C:N4	1:A:491:G:H1	2.06	0.53
1:A:1212:U:C1'	1:A:1213:A:OP2	2.52	0.53
1:A:1369:C:H2'	1:A:1370:G:H8	1.73	0.53
2:B:122:PHE:CE1	2:B:127:ILE:HD12	2.44	0.53
7:G:5:ARG:CZ	7:G:8:GLU:HG2	2.37	0.53
12:L:117:ARG:O	12:L:118:SER:C	2.52	0.53
13:M:15:VAL:O	13:M:19:LEU:HG	2.08	0.53
1:A:532:A:H61	1:A:1207:2MG:H5'	1.74	0.53
1:A:560:U:H5'	1:A:566:G:N2	2.24	0.53
1:A:922:G:C6	1:A:923:A:C6	2.97	0.53
1:A:1026:G:C8	1:A:1027:C:O2	2.62	0.53
1:A:1303:C:N4	1:A:1304:G:C6	2.77	0.53
1:A:1407:5MC:N3	1:A:1408:A:C8	2.77	0.53
2:B:100:GLY:CA	2:B:176:GLU:OE2	2.55	0.53
6:F:49:ALA:HB3	6:F:50:TYR:HD1	1.74	0.53
10:J:49:VAL:O	10:J:61:GLU:N	2.36	0.53
11:K:48:ILE:HG22	11:K:49:GLY:N	2.22	0.53
12:L:50:SER:O	12:L:51:ALA:HB2	2.09	0.53
12:L:79:GLU:HG2	12:L:80:HIS:NE2	2.23	0.53
20:T:74:LYS:HB2	20:T:76:ALA:H	1.74	0.53
1:A:456:C:H2'	1:A:457:C:C6	2.43	0.53
1:A:984:C:N3	1:A:1221:G:N2	2.47	0.53
1:A:1035:A:C4	1:A:1036:G:N7	2.76	0.53
1:A:1077:G:N2	1:A:1081:G:C4	2.77	0.53
1:A:1090:U:H2'	1:A:1091:U:C6	2.38	0.53
1:A:1131:G:OP2	1:A:1131:G:C8	2.59	0.53
4:D:98:GLU:CD	4:D:103:ASN:HD21	2.17	0.53
4:D:150:GLU:O	4:D:153:ARG:N	2.34	0.53
6:F:2:ARG:HE	6:F:69:GLU:HG2	1.74	0.53
7:G:37:ASN:HD22	7:G:41:ARG:HH21	1.57	0.53
8:H:28:ALA:HB2	8:H:58:TYR:HA	1.90	0.53
9:I:53:VAL:HG21	9:I:85:LEU:CD1	2.35	0.53
10:J:47:PHE:HD2	14:N:34:TYR:CD2	2.27	0.53
10:J:65:LEU:HD12	10:J:66:ARG:N	2.24	0.53
13:M:65:LYS:C	13:M:66:LEU:HD23	2.33	0.53
16:P:15:PRO:HB2	16:P:41:PRO:HG2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:a:36:A:H2'	24:a:36:A:N3	2.22	0.53
1:A:781:A:C5	1:A:802:A:C2	2.97	0.53
1:A:1130:A:H5''	9:I:62:TYR:CE2	2.43	0.53
1:A:1314:C:O2'	1:A:1315:U:H5'	2.08	0.53
1:A:1349:A:OP1	9:I:118:LYS:HG3	2.08	0.53
5:E:95:ALA:O	5:E:98:THR:OG1	2.17	0.53
6:F:67:MET:HB2	6:F:68:PRO:CD	2.38	0.53
7:G:139:GLU:HB3	7:G:143:ARG:HH22	1.73	0.53
9:I:8:GLY:CA	9:I:79:LEU:HB3	2.30	0.53
10:J:61:GLU:O	10:J:61:GLU:CG	2.57	0.53
11:K:14:VAL:O	11:K:15:ALA:HB3	2.08	0.53
11:K:92:GLU:HB3	11:K:96:ARG:NH2	2.24	0.53
15:O:14:GLU:HG3	15:O:15:PHE:CD1	2.38	0.53
17:Q:40:LYS:HG2	17:Q:41:LYS:H	1.73	0.53
18:R:50:ILE:HD11	18:R:70:ILE:CG2	2.38	0.53
20:T:105:SER:O	20:T:106:ALA:OXT	2.27	0.53
1:A:178:C:H2'	1:A:179:A:H5'	1.92	0.52
1:A:375:U:C4	1:A:376:G:N7	2.77	0.52
1:A:437:U:OP2	29:A:2795:HOH:O	2.19	0.52
1:A:783:C:C2'	1:A:784:C:H5'	2.39	0.52
1:A:1058:G:H2'	1:A:1059:C:C6	2.43	0.52
5:E:11:ILE:HG21	5:E:31:LEU:HD13	1.90	0.52
6:F:89:MET:HE2	18:R:76:LEU:HG	1.91	0.52
8:H:19:VAL:HG23	8:H:19:VAL:O	2.09	0.52
8:H:40:ALA:O	8:H:41:ARG:C	2.52	0.52
11:K:40:ILE:CG2	11:K:75:TYR:CD1	2.92	0.52
14:N:26:ARG:CD	14:N:47:LEU:HD11	2.36	0.52
15:O:12:ILE:C	15:O:14:GLU:H	2.17	0.52
1:A:56:U:H2'	1:A:57:G:C8	2.43	0.52
1:A:164:U:H2'	1:A:165:C:C6	2.43	0.52
1:A:514:C:H2'	1:A:515:G:H8	1.73	0.52
1:A:1003(A):G:N1	1:A:1038:C:N3	2.46	0.52
1:A:1054:C:N4	23:W:34:G:OP1	2.41	0.52
1:A:1057:G:H5''	3:C:154:SER:OG	2.08	0.52
1:A:1130:A:H5''	9:I:62:TYR:HE2	1.74	0.52
1:A:1320:C:C2'	1:A:1321:C:H5'	2.40	0.52
2:B:26:PRO:O	2:B:29:ALA:HB2	2.09	0.52
2:B:212:GLN:NE2	2:B:235:SER:HB2	2.23	0.52
5:E:152:ARG:O	8:H:64:LYS:NZ	2.42	0.52
6:F:10:LEU:HD12	6:F:10:LEU:H	1.73	0.52
6:F:78:GLU:O	6:F:81:ILE:HG12	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:11:THR:O	8:H:12:ARG:C	2.53	0.52
11:K:120:ARG:NH1	11:K:120:ARG:CG	2.72	0.52
12:L:75:HIS:C	12:L:75:HIS:ND1	2.67	0.52
18:R:47:THR:HA	18:R:83:GLU:HB2	1.90	0.52
19:S:38:SER:HB3	19:S:71:LEU:HD12	1.91	0.52
1:A:35:G:C5	1:A:36:C:C5	2.97	0.52
1:A:509:A:H3'	1:A:509:A:H8	1.70	0.52
1:A:520:A:H61	1:A:529:G:H1'	1.74	0.52
1:A:661:G:H5''	1:A:661:G:C8	2.42	0.52
1:A:1005:A:OP2	1:A:1006:C:C5	2.62	0.52
1:A:1054:C:C4	23:W:34:G:OP1	2.63	0.52
1:A:1517[B]:G:O6	1:A:1518[B]:MA6:H103	2.09	0.52
4:D:155:LEU:CD2	4:D:156:GLU:H	2.22	0.52
7:G:46:ALA:HB1	7:G:121:ALA:HB2	1.90	0.52
12:L:54:LYS:N	12:L:54:LYS:HD3	2.25	0.52
12:L:75:HIS:HB3	12:L:102:ARG:NH1	2.24	0.52
13:M:23:TYR:CD2	13:M:70:LEU:HD13	2.44	0.52
1:A:93:G:C2'	1:A:95:U:H5'	2.40	0.52
1:A:509:A:HO2'	1:A:510:A:P	2.24	0.52
1:A:1056:U:H5'	3:C:163:ALA:CB	2.34	0.52
1:A:1186:G:N2	1:A:1187:G:H1'	2.25	0.52
1:A:1350:A:C5	1:A:1351:U:C5	2.97	0.52
1:A:1391:U:H2'	1:A:1392:G:H8	1.74	0.52
1:A:1519[A]:MA6:H2'	1:A:1520[A]:G:H5'	1.90	0.52
1:A:1537:U:H6	1:A:1537:U:O5'	1.93	0.52
2:B:92:TYR:HD1	2:B:92:TYR:O	1.92	0.52
4:D:2:GLY:O	4:D:3:ARG:HB3	2.08	0.52
5:E:5:ASP:CG	5:E:6:PHE:H	2.16	0.52
10:J:44:VAL:CG1	10:J:66:ARG:HD3	2.32	0.52
10:J:54:PHE:C	10:J:54:PHE:CD2	2.87	0.52
14:N:36:PHE:C	14:N:36:PHE:CD1	2.87	0.52
16:P:67:THR:CG2	16:P:68:ASP:N	2.63	0.52
17:Q:50:LYS:HE3	17:Q:51:TYR:CE2	2.44	0.52
19:S:11:VAL:HG11	19:S:16:LEU:HD22	1.91	0.52
1:A:259:G:C2'	1:A:260:G:O5'	2.58	0.52
1:A:442:C:C2'	1:A:443:C:H5'	2.39	0.52
1:A:461:C:H4'	1:A:462:G:OP2	2.09	0.52
1:A:735:C:H1'	18:R:75:ILE:HD11	1.92	0.52
1:A:746:A:O2'	1:A:747:C:H5'	2.09	0.52
1:A:837:G:N2	1:A:850:U:O2	2.42	0.52
1:A:995:C:H1'	14:N:4:LYS:HE2	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1069:C:O2'	1:A:1192:C:H1'	2.10	0.52
1:A:1085:U:C6	1:A:1094:G:N1	2.78	0.52
1:A:1439:C:OP1	20:T:38:LYS:HE2	2.10	0.52
2:B:121:LEU:HD23	2:B:121:LEU:C	2.35	0.52
2:B:184:VAL:HG12	2:B:197:VAL:HG13	1.90	0.52
2:B:212:GLN:NE2	2:B:235:SER:CB	2.72	0.52
3:C:77:ILE:HG13	3:C:103:VAL:HG21	1.92	0.52
5:E:92:LYS:O	5:E:118:ILE:HG13	2.09	0.52
6:F:48:LEU:HD11	6:F:52:ILE:HG13	1.87	0.52
7:G:75:VAL:HG21	7:G:86:GLN:HB3	1.90	0.52
9:I:27:THR:OG1	9:I:31:GLN:O	2.19	0.52
11:K:33:THR:HG21	11:K:37:GLY:O	2.10	0.52
19:S:49:ILE:HD13	19:S:49:ILE:N	2.24	0.52
1:A:171:A:P	29:A:2844:HOH:O	2.68	0.52
1:A:182:U:H5	1:A:183:G:N9	2.05	0.52
1:A:191:G:O2'	20:T:101:GLY:O	2.28	0.52
1:A:506:G:H2'	1:A:507:C:H5'	1.92	0.52
1:A:969:A:H2'	1:A:970:C:H5'	1.90	0.52
1:A:1392:G:N2	1:A:1502:A:H8	2.08	0.52
2:B:47:THR:HG23	2:B:202:PRO:O	2.09	0.52
3:C:62:ASP:HA	3:C:97:LYS:HZ1	1.74	0.52
13:M:71:ARG:HA	13:M:74:VAL:CG2	2.40	0.52
13:M:95:GLY:C	13:M:96:LEU:HD23	2.34	0.52
16:P:8:ARG:C	16:P:9:PHE:HD2	2.17	0.52
16:P:9:PHE:HB2	16:P:16:HIS:O	2.10	0.52
19:S:51:VAL:HG23	19:S:58:VAL:HG23	1.91	0.52
21:U:18:TYR:HD2	21:U:22:ARG:HD3	1.73	0.52
1:A:532:A:N1	1:A:1207:2MG:H4'	2.25	0.52
1:A:740:U:H4'	15:O:42:HIS:CD2	2.45	0.52
1:A:1054:C:H2'	1:A:1055:A:H5''	1.92	0.52
1:A:1190:G:O2'	1:A:1191:A:O5'	2.27	0.52
1:A:1241:G:H2'	1:A:1242:C:C6	2.45	0.52
4:D:111:ALA:HB1	4:D:116:GLN:HG2	1.91	0.52
5:E:88:LYS:HB3	5:E:123:LEU:HB2	1.92	0.52
7:G:89:MET:SD	7:G:156:TRP:CZ3	3.03	0.52
9:I:118:LYS:O	9:I:118:LYS:HG3	2.09	0.52
18:R:87:ARG:NH2	18:R:87:ARG:HB2	2.25	0.52
1:A:35:G:C4	1:A:36:C:C5	2.98	0.52
1:A:1067:A:O2'	1:A:1093:A:O2'	2.07	0.52
1:A:1396:A:H4'	1:A:1397:C:H5''	1.90	0.52
1:A:1494:G:C2	1:A:1495:U:C6	2.98	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:10:LEU:HD11	8:H:135:CYS:HB3	1.90	0.52
13:M:99:ARG:C	13:M:101:GLN:HE22	2.17	0.52
19:S:15:LEU:HD12	19:S:15:LEU:N	2.25	0.52
1:A:92:C:H2'	1:A:93:G:C8	2.44	0.52
1:A:414:A:C2	1:A:415:A:C8	2.98	0.52
1:A:512:U:O2	1:A:540:G:C2	2.62	0.52
1:A:909:A:C8	1:A:910:C:C5	2.98	0.52
1:A:1147:C:H4'	9:I:5:TYR:CE2	2.38	0.52
1:A:1288:A:N6	1:A:1289:A:N6	2.57	0.52
6:F:14:LEU:HD12	6:F:19:LEU:HA	1.91	0.52
12:L:19:ARG:HA	12:L:20:LYS:HZ3	1.75	0.52
12:L:79:GLU:HG2	12:L:80:HIS:CE1	2.45	0.52
18:R:36:ASN:CG	18:R:39:VAL:HG11	2.35	0.52
1:A:132:C:C2'	1:A:133:U:H5'	2.40	0.52
1:A:504:C:C2	1:A:542:G:N2	2.78	0.52
1:A:568:G:H5''	1:A:568:G:H8	1.75	0.52
1:A:1110:A:H8	1:A:1110:A:O5'	1.92	0.52
1:A:1124:G:C8	1:A:1145:C:C6	2.98	0.52
9:I:17:VAL:HG22	9:I:63:ILE:HD11	1.92	0.52
10:J:6:ILE:CD1	10:J:98:ILE:HG23	2.40	0.52
10:J:48:THR:HG23	10:J:62:HIS:HB3	1.91	0.52
18:R:22:VAL:CG2	18:R:56:THR:HA	2.39	0.52
20:T:75:ASN:O	20:T:76:ALA:C	2.53	0.52
24:a:36:A:C2	24:a:37:A:C4	2.98	0.52
1:A:630:G:H8	1:A:630:G:OP2	1.92	0.51
1:A:1003:G:H2'	1:A:1003(A):G:C8	2.45	0.51
1:A:1009:G:N2	1:A:1010:G:C4	2.78	0.51
3:C:34:LEU:O	3:C:34:LEU:HD12	2.10	0.51
7:G:22:LEU:CD2	7:G:66:VAL:HG21	2.38	0.51
7:G:123:GLU:O	7:G:124:LEU:C	2.53	0.51
9:I:27:THR:HG22	9:I:62:TYR:HA	1.92	0.51
10:J:7:LYS:HE2	10:J:9:ARG:HH21	1.73	0.51
12:L:10:LEU:HD11	12:L:15:ARG:HE	1.75	0.51
13:M:22:ILE:HG13	13:M:25:ILE:HD12	1.91	0.51
1:A:428:G:H1'	1:A:429:U:OP2	2.10	0.51
1:A:1031:G:N2	1:A:1032:G:C4	2.78	0.51
1:A:1103:C:OP1	2:B:96:ARG:NH1	2.43	0.51
1:A:1206:G:C5	1:A:1207:2MG:N7	2.78	0.51
3:C:78:GLY:HA3	3:C:83:ARG:HB3	1.92	0.51
7:G:54:THR:HG22	7:G:56:GLN:CB	2.40	0.51
10:J:32:ALA:HB2	10:J:76:ASN:OD1	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:75:HIS:HB3	12:L:102:ARG:HH12	1.75	0.51
13:M:99:ARG:NH2	19:S:2:PRO:HG2	2.24	0.51
15:O:46:HIS:C	15:O:48:LYS:H	2.17	0.51
16:P:67:THR:CG2	16:P:68:ASP:H	2.15	0.51
1:A:36:C:H2'	1:A:37:U:H5'	1.93	0.51
1:A:328:C:C2'	1:A:329:A:OP2	2.58	0.51
1:A:747:C:C2'	1:A:748:C:O5'	2.58	0.51
1:A:770:C:O2'	1:A:771:G:H5'	2.10	0.51
1:A:840:C:H5'	1:A:848:C:O2	2.11	0.51
1:A:924:C:H5'	1:A:1399:C:OP2	2.09	0.51
1:A:975:A:H5'	1:A:975:A:C8	2.43	0.51
1:A:988:G:C2	1:A:1218:C:O2	2.64	0.51
1:A:1009:G:N3	1:A:1009:G:H2'	2.25	0.51
1:A:1103:C:C5'	2:B:98:LEU:HD12	2.40	0.51
3:C:13:GLY:HA2	14:N:57:ARG:NH1	2.25	0.51
10:J:47:PHE:CD2	14:N:34:TYR:CD2	2.99	0.51
13:M:22:ILE:HD13	13:M:22:ILE:N	2.25	0.51
13:M:36:LYS:HB2	13:M:59:TYR:HE1	1.75	0.51
16:P:58:TYR:O	16:P:62:VAL:HG13	2.11	0.51
1:A:688:G:H2'	1:A:689:C:H6	1.75	0.51
1:A:1061:G:C6	1:A:1062:U:N3	2.78	0.51
1:A:1407:5MC:N3	1:A:1408:A:N7	2.58	0.51
1:A:1519[B]:MA6:H93	1:A:1520[B]:G:H21	1.75	0.51
2:B:219:VAL:CA	2:B:222:ILE:HG12	2.39	0.51
2:B:239:VAL:O	2:B:239:VAL:HG12	2.09	0.51
4:D:78:LEU:HD21	4:D:96:LEU:HB3	1.92	0.51
4:D:82:ALA:HB2	4:D:96:LEU:HD22	1.92	0.51
6:F:14:LEU:HD21	6:F:84:ASN:OD1	2.10	0.51
7:G:21:VAL:HG23	7:G:22:LEU:N	2.26	0.51
7:G:26:PHE:CE2	7:G:30:ILE:HD11	2.46	0.51
13:M:23:TYR:CE2	13:M:71:ARG:HG3	2.45	0.51
15:O:56:LEU:C	15:O:56:LEU:HD12	2.35	0.51
18:R:39:VAL:HG13	18:R:40:LEU:H	1.75	0.51
19:S:41:VAL:O	19:S:42:PRO:C	2.52	0.51
1:A:1162:C:O2'	1:A:1163:C:H5'	2.10	0.51
1:A:1168:A:H2'	1:A:1169:A:C8	2.45	0.51
1:A:1441:G:H5''	1:A:1442:G:O5'	2.10	0.51
1:A:1482:G:H8	1:A:1482:G:O5'	1.94	0.51
3:C:84:ILE:HG12	3:C:88:ARG:HH22	1.75	0.51
24:a:33:U:O2	24:a:34:G:C2	2.63	0.51
1:A:658:G:C2	1:A:749:C:N3	2.79	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1152:A:OP1	10:J:68:HIS:CE1	2.63	0.51
1:A:1267:C:O2'	21:U:20:LYS:HG3	2.11	0.51
1:A:1368:G:C2'	1:A:1369:C:H5'	2.41	0.51
1:A:1408:A:C4	1:A:1409:C:C5	2.99	0.51
7:G:111:ARG:HD3	7:G:113:GLU:HG3	1.93	0.51
15:O:39:LEU:HD23	15:O:39:LEU:O	2.11	0.51
23:W:35:G:C4	23:W:36:A:N7	2.79	0.51
24:a:38:A:C2	24:a:39:G:C5	2.99	0.51
1:A:509:A:C8	1:A:509:A:C3'	2.92	0.51
1:A:849:C:H2'	1:A:850:U:H5'	1.92	0.51
1:A:865:A:H2'	1:A:866:C:C6	2.45	0.51
1:A:1060:C:OP1	14:N:45:ARG:NH2	2.44	0.51
1:A:1203:C:H2'	1:A:1204:A:O4'	2.11	0.51
8:H:96:GLY:H	8:H:99:GLU:CD	2.18	0.51
13:M:48:LEU:HB3	13:M:53:VAL:HG23	1.91	0.51
14:N:9:LYS:HD2	14:N:9:LYS:C	2.36	0.51
15:O:11:VAL:HG22	15:O:12:ILE:HD13	1.92	0.51
24:a:38:A:C2	24:a:39:G:C6	2.99	0.51
1:A:278:G:OP2	17:Q:41:LYS:NZ	2.44	0.51
1:A:429:U:O2	1:A:430:A:C8	2.64	0.51
1:A:1055:A:N7	1:A:1206:G:C2	2.79	0.51
1:A:1148:U:C4	1:A:1149:C:C2	2.99	0.51
1:A:1163:C:C2	1:A:1174:G:N2	2.79	0.51
1:A:1351:U:H5'	7:G:33:ASP:OD1	2.10	0.51
4:D:18:LYS:CB	4:D:33:MET:HG3	2.40	0.51
5:E:150:ARG:HG2	5:E:151:LEU:HD23	1.92	0.51
7:G:38:LEU:O	7:G:42:ILE:CG1	2.52	0.51
8:H:83:ILE:HB	8:H:137:VAL:HG22	1.93	0.51
12:L:90:VAL:O	12:L:91:LYS:C	2.53	0.51
1:A:22:G:C4	1:A:23:C:C5	2.99	0.51
1:A:31:G:N2	1:A:48:C:OP1	2.34	0.51
1:A:191:G:N2	20:T:103:GLY:O	2.43	0.51
1:A:433:C:H2'	1:A:434:U:H6	1.75	0.51
1:A:676:A:O5'	1:A:676:A:H8	1.94	0.51
1:A:814:A:H2'	1:A:816:A:H5''	1.93	0.51
1:A:983:A:H2	1:A:984:C:C6	2.29	0.51
1:A:1020:U:H2'	1:A:1021:G:C8	2.42	0.51
1:A:1098:C:H2'	1:A:1099:G:O4'	2.10	0.51
1:A:1126:U:O4	1:A:1127:G:N1	2.44	0.51
1:A:1518[A]:MA6:C9	1:A:1519[A]:MA6:H103	2.41	0.51
1:A:1534:C:C4	1:A:1535:A:C2	2.99	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:8:LYS:O	2:B:11:LEU:HD13	2.11	0.51
2:B:83:MET:SD	2:B:234:PRO:O	2.69	0.51
8:H:54:ASP:CG	8:H:55:GLY:N	2.61	0.51
10:J:50:ILE:HA	10:J:60:ARG:HA	1.92	0.51
14:N:22:THR:O	14:N:23:ARG:HG3	2.10	0.51
23:W:39:G:C2	23:W:40:PSU:O4	2.64	0.51
24:a:37:A:C4	24:a:38:A:C8	2.99	0.51
1:A:134:A:N6	16:P:25:ARG:NH2	2.59	0.51
1:A:266:G:H5''	1:A:268:C:H41	1.76	0.51
1:A:352:C:C6	1:A:352:C:C3'	2.94	0.51
1:A:922:G:C2	1:A:1396:A:C6	2.98	0.51
1:A:1048:G:C6	1:A:1210:C:N4	2.79	0.51
1:A:1088:G:C2'	1:A:1089:G:H5'	2.41	0.51
1:A:1173:G:H2'	1:A:1174:G:C8	2.45	0.51
1:A:1243:C:H5''	21:U:8:THR:HG23	1.91	0.51
1:A:1328:C:H2'	1:A:1329:A:H8	1.76	0.51
1:A:1494:G:C2'	1:A:1495:U:H5'	2.41	0.51
3:C:29:TYR:OH	14:N:54:PRO:O	2.29	0.51
9:I:121:ARG:NH1	9:I:121:ARG:CG	2.69	0.51
10:J:21:GLN:HA	10:J:24:VAL:HG12	1.93	0.51
10:J:63:PHE:HB3	14:N:58:LYS:HA	1.93	0.51
12:L:90:VAL:CG1	12:L:93:LEU:HG	2.41	0.51
17:Q:63:ARG:HG2	17:Q:64:PRO:HD2	1.93	0.51
1:A:162:A:H3'	1:A:163:C:O4'	2.11	0.50
1:A:297:G:N2	1:A:300:A:OP2	2.37	0.50
1:A:475:G:O6	29:A:2600:HOH:O	2.20	0.50
1:A:581:G:O3'	15:O:64:ARG:NH2	2.39	0.50
1:A:658:G:H2'	1:A:659:U:C6	2.46	0.50
1:A:797:C:O2'	1:A:798:G:H5'	2.10	0.50
1:A:981:U:H5'	14:N:21:TYR:CZ	2.45	0.50
1:A:1081:G:P	5:E:16:THR:HG1	2.34	0.50
1:A:1172:C:O2'	1:A:1173:G:H5'	2.11	0.50
1:A:1499:A:H5'	1:A:1519[A]:MA6:C2	2.42	0.50
10:J:47:PHE:CZ	14:N:37:PHE:CE1	2.88	0.50
19:S:47:HIS:O	19:S:62:ILE:HG22	2.10	0.50
1:A:928:G:C2	1:A:1390:U:O2	2.65	0.50
1:A:1297:C:O2'	1:A:1298:C:OP2	2.29	0.50
1:A:1375:A:C5	1:A:1376:U:C5	2.99	0.50
1:A:1470:G:O2'	1:A:1471:G:H5'	2.11	0.50
9:I:95:LYS:H	9:I:95:LYS:HD2	1.76	0.50
17:Q:40:LYS:CD	17:Q:42:TYR:CZ	2.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:50:GLU:HA	20:T:99:LEU:CD1	2.39	0.50
1:A:973:G:H2'	1:A:974:A:OP1	2.11	0.50
1:A:976:G:C8	1:A:1358:U:C2	2.99	0.50
1:A:1110:A:N7	29:A:2140:HOH:O	2.35	0.50
1:A:1305:G:OP1	21:U:2:GLY:HA3	2.11	0.50
9:I:77:ILE:O	9:I:78:LYS:C	2.54	0.50
10:J:63:PHE:HA	14:N:59:ALA:H	1.76	0.50
16:P:48:TRP:CD1	16:P:48:TRP:H	2.23	0.50
1:A:849:C:C2'	1:A:850:U:H5'	2.41	0.50
1:A:1052:U:C2'	1:A:1055:A:OP1	2.59	0.50
1:A:1179:A:H2'	1:A:1180:A:O4'	2.11	0.50
1:A:1349:A:C2	1:A:1374:A:C4	3.00	0.50
1:A:1493[B]:A:H2'	1:A:1494:G:C8	2.46	0.50
1:A:1530:G:C6	24:a:40:PSU:C4	2.99	0.50
2:B:57:PHE:CG	2:B:199:TYR:CE1	2.99	0.50
2:B:80:ILE:HD12	2:B:208:ILE:HD12	1.94	0.50
3:C:33:LEU:HD21	14:N:53:LEU:CD2	2.41	0.50
3:C:58:GLU:O	3:C:65:ALA:HB2	2.11	0.50
5:E:147:ASP:O	5:E:150:ARG:HB3	2.12	0.50
7:G:143:ARG:HB2	7:G:143:ARG:NH2	2.27	0.50
8:H:18:ARG:NH2	8:H:81:HIS:O	2.45	0.50
10:J:24:VAL:HG23	10:J:34:VAL:HG11	1.94	0.50
12:L:46:LYS:C	12:L:48:PRO:HD2	2.36	0.50
12:L:90:VAL:HG11	12:L:93:LEU:HD12	1.93	0.50
13:M:4:ILE:HG22	13:M:5:ALA:HB2	1.93	0.50
21:U:13:ILE:HA	21:U:22:ARG:NH1	2.26	0.50
1:A:411:A:H8	1:A:411:A:H3'	1.77	0.50
1:A:1438:G:C6	1:A:1439:C:C4	2.99	0.50
1:A:1517[A]:G:C6	1:A:1518[A]:MA6:C5	2.95	0.50
5:E:10:MET:HA	5:E:32:VAL:HG23	1.93	0.50
9:I:48:GLU:HB3	9:I:101:PHE:HZ	1.74	0.50
12:L:52:LEU:O	12:L:54:LYS:NZ	2.41	0.50
12:L:55:VAL:CG1	12:L:67:THR:OG1	2.59	0.50
17:Q:59:ILE:HG23	17:Q:71:PHE:HB3	1.94	0.50
1:A:83:U:C5	1:A:84:U:C6	3.00	0.50
1:A:193:C:O3'	20:T:61:SER:HB2	2.11	0.50
1:A:228:A:H2'	1:A:229:U:C6	2.46	0.50
1:A:324:G:OP1	20:T:22:ARG:HD3	2.11	0.50
1:A:725:G:O2'	1:A:726:C:H5'	2.12	0.50
1:A:736:C:H2'	1:A:737:A:C8	2.47	0.50
1:A:738:C:OP1	6:F:92:LYS:HD3	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:768:A:C5	1:A:769:G:C8	2.99	0.50
1:A:1123:A:C2	10:J:39:PRO:HG3	2.47	0.50
1:A:1251:A:H4'	9:I:12:GLU:OE2	2.12	0.50
1:A:1515[A]:C:H42	1:A:1520[A]:G:H1	1.59	0.50
2:B:102:LEU:O	2:B:105:PHE:HB2	2.11	0.50
2:B:213:LEU:HB3	2:B:214:ILE:HD12	1.94	0.50
3:C:39:ILE:HG21	3:C:57:ILE:HD11	1.94	0.50
4:D:31:CYS:C	4:D:33:MET:H	2.19	0.50
9:I:19:LEU:HB3	9:I:59:PHE:CD2	2.47	0.50
12:L:35:GLY:HA3	12:L:60:LEU:HD13	1.94	0.50
12:L:39:VAL:HG12	12:L:40:VAL:N	2.27	0.50
19:S:10:PHE:C	19:S:10:PHE:CD2	2.89	0.50
1:A:53:A:OP2	29:A:2222:HOH:O	2.19	0.50
1:A:201:C:N4	1:A:216:G:H1	2.04	0.50
1:A:491:G:C4	1:A:492:G:C8	3.00	0.50
1:A:802:A:C2'	1:A:803:G:H5'	2.42	0.50
1:A:939:G:H2'	1:A:940:C:C6	2.46	0.50
2:B:97:TRP:CZ3	2:B:176:GLU:OE2	2.65	0.50
2:B:211:ILE:O	2:B:215:LEU:HB2	2.11	0.50
7:G:148:ASN:O	7:G:149:ARG:C	2.55	0.50
8:H:4:ASP:CG	8:H:7:ALA:H	2.20	0.50
8:H:59:LEU:HD12	8:H:59:LEU:N	2.26	0.50
12:L:7:ILE:O	12:L:8:ASN:C	2.55	0.50
14:N:13:THR:N	14:N:14:PRO:CD	2.75	0.50
15:O:46:HIS:C	15:O:48:LYS:N	2.70	0.50
15:O:88:ARG:NE	15:O:88:ARG:CA	2.57	0.50
23:W:35:G:C4	23:W:36:A:C8	2.99	0.50
1:A:478:A:O2'	1:A:479:C:H5'	2.12	0.50
1:A:690:G:H2'	1:A:691:G:O4'	2.12	0.50
1:A:740:U:H4'	15:O:42:HIS:HD2	1.77	0.50
1:A:834:C:O2'	1:A:835:U:H5'	2.12	0.50
1:A:1248:A:C2'	1:A:1249:C:H5'	2.42	0.50
1:A:1492[B]:A:H2'	1:A:1492[B]:A:N3	2.27	0.50
2:B:158:LEU:HB3	2:B:159:PRO:HD2	1.94	0.50
4:D:177:ASP:OD1	4:D:177:ASP:C	2.54	0.50
5:E:77:PRO:O	5:E:78:HIS:HB3	2.11	0.50
8:H:20:TYR:CE1	8:H:76:PRO:HG2	2.46	0.50
9:I:32:ASP:CG	9:I:33:PHE:N	2.69	0.50
11:K:20:TYR:CD2	11:K:83:ILE:HB	2.47	0.50
11:K:116:HIS:C	11:K:117:ASN:OD1	2.54	0.50
13:M:63:THR:HG23	13:M:64:TRP:N	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:31:SER:O	20:T:32:ALA:C	2.55	0.50
21:U:5:ASP:HB3	21:U:8:THR:OG1	2.12	0.50
1:A:264:U:H2'	1:A:265:G:C5'	2.42	0.50
1:A:1115:C:H6	1:A:1115:C:O5'	1.95	0.50
7:G:48:LYS:O	7:G:52:GLU:OE2	2.30	0.50
7:G:148:ASN:C	7:G:150:ALA:N	2.66	0.50
9:I:36:TYR:HE2	9:I:73:GLN:OE1	1.93	0.50
13:M:4:ILE:O	13:M:6:GLY:O	2.30	0.50
17:Q:53:LEU:CD1	17:Q:54:GLY:N	2.74	0.50
1:A:172:A:O2'	1:A:173:U:H5'	2.12	0.49
1:A:586:C:C2'	1:A:587:G:H5'	2.41	0.49
1:A:664:G:H22	1:A:741:G:H1	1.60	0.49
1:A:1057:G:C5'	3:C:154:SER:OG	2.60	0.49
1:A:1072:G:H2'	1:A:1073:U:C6	2.46	0.49
1:A:1123:A:H2	10:J:39:PRO:HG3	1.77	0.49
1:A:1126:U:C2'	1:A:1127:G:O5'	2.59	0.49
1:A:1352:C:H2'	1:A:1353:G:O4'	2.12	0.49
1:A:1368:G:OP2	9:I:114:TYR:N	2.45	0.49
1:A:1434:A:H2'	1:A:1435:G:O4'	2.11	0.49
2:B:195:ASP:O	8:H:68:ARG:NH2	2.45	0.49
4:D:127:THR:HA	4:D:132:ARG:HA	1.94	0.49
4:D:180:GLY:O	4:D:182:LYS:CG	2.60	0.49
7:G:101:LEU:O	7:G:105:VAL:HG23	2.11	0.49
9:I:126:SER:C	9:I:128:ARG:H	2.18	0.49
11:K:12:ARG:HG2	11:K:12:ARG:O	2.10	0.49
15:O:39:LEU:O	15:O:42:HIS:HB3	2.12	0.49
18:R:73:ALA:HB3	18:R:79:LEU:HD12	1.94	0.49
1:A:440:A:C5'	1:A:442:C:OP2	2.58	0.49
1:A:540:G:C5	1:A:541:G:N7	2.80	0.49
1:A:866:C:H2'	1:A:867:G:O4'	2.13	0.49
1:A:990:C:H42	1:A:1215:G:H1	1.61	0.49
1:A:1031:G:C2	1:A:1032:G:C5	3.00	0.49
1:A:1518[B]:MA6:H93	1:A:1519[B]:MA6:N6	2.27	0.49
13:M:33:ALA:O	13:M:37:THR:HG22	2.12	0.49
23:W:30:G:H2'	23:W:30:G:N3	2.27	0.49
1:A:37:U:H2'	1:A:38:G:O4'	2.12	0.49
1:A:91:C:H2'	1:A:92:C:C5	2.47	0.49
1:A:250:A:H1'	1:A:251:G:OP2	2.12	0.49
1:A:357:G:O2'	1:A:358:U:H5'	2.12	0.49
1:A:426:G:O2'	1:A:427:U:H5'	2.12	0.49
1:A:676:A:H5''	11:K:113:PRO:HB3	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1090:U:C2	1:A:1091:U:C6	3.00	0.49
1:A:1326:C:OP2	21:U:6:ARG:HD3	2.12	0.49
3:C:76:VAL:HG21	3:C:103:VAL:HG13	1.94	0.49
3:C:130:VAL:O	3:C:134:ILE:HD11	2.12	0.49
4:D:19:LEU:H	4:D:19:LEU:CD2	2.21	0.49
4:D:64:LEU:HA	4:D:67:ILE:HD12	1.92	0.49
7:G:72:ARG:NH1	7:G:142:GLU:OE2	2.46	0.49
8:H:9:MET:O	8:H:10:LEU:C	2.54	0.49
8:H:85:ARG:HD2	8:H:87:SER:O	2.12	0.49
11:K:43:SER:OG	11:K:44:SER:N	2.45	0.49
12:L:82:VAL:HG23	12:L:106:ASP:OD1	2.13	0.49
15:O:36:ILE:HG22	15:O:37:ASN:N	2.26	0.49
1:A:19:C:O2'	1:A:20:U:H5'	2.12	0.49
1:A:45:U:H2'	1:A:46:G:C8	2.47	0.49
1:A:106:C:H2'	1:A:107:G:H5'	1.93	0.49
1:A:166:G:H2'	1:A:167:G:H5'	1.94	0.49
1:A:491:G:N3	1:A:492:G:C8	2.80	0.49
1:A:854:G:N1	1:A:855:G:C5	2.80	0.49
1:A:922:G:O2'	1:A:1398:A:N1	2.37	0.49
1:A:1026:G:C2'	1:A:1027:C:OP1	2.60	0.49
1:A:1300:G:C6	1:A:1335:C:C5	3.01	0.49
1:A:1425:U:C2	1:A:1426:C:C5	3.00	0.49
1:A:1441:G:O2'	1:A:1442:G:N2	2.45	0.49
1:A:1539:C:C2	24:a:34:G:N2	2.77	0.49
12:L:42:THR:HA	12:L:53:ARG:O	2.13	0.49
16:P:40:ASP:HB3	16:P:48:TRP:CB	2.42	0.49
17:Q:6:LEU:HB3	17:Q:23:VAL:HG11	1.94	0.49
20:T:44:ALA:HB3	20:T:91:LEU:HD13	1.95	0.49
20:T:55:ILE:HD13	20:T:55:ILE:H	1.77	0.49
1:A:116:A:H3'	29:A:2018:HOH:O	2.12	0.49
1:A:186:C:O2'	20:T:85:MET:SD	2.63	0.49
1:A:811:C:O2'	1:A:901:A:N1	2.45	0.49
1:A:1112:C:O2	3:C:179:ARG:HG3	2.12	0.49
1:A:1305:G:P	21:U:2:GLY:HA3	2.52	0.49
1:A:1321:C:C5'	13:M:87:TYR:HE2	2.25	0.49
2:B:28:PHE:O	2:B:28:PHE:CD2	2.66	0.49
4:D:177:ASP:CG	4:D:180:GLY:H	2.18	0.49
13:M:52:GLU:O	13:M:53:VAL:C	2.54	0.49
17:Q:62:SER:CB	17:Q:72:ARG:HD3	2.42	0.49
17:Q:82:MET:O	17:Q:85:VAL:HG23	2.12	0.49
19:S:35:SER:OG	19:S:38:SER:HB2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:10:LEU:HG	20:T:11:SER:N	2.27	0.49
1:A:544:G:C2	1:A:545:C:C6	3.00	0.49
1:A:653:A:OP1	8:H:56:LYS:HE2	2.13	0.49
1:A:836:G:C6	1:A:851:G:C5	3.00	0.49
1:A:1166:G:C2	1:A:1171:G:C6	3.01	0.49
1:A:1193:G:N3	1:A:1194:U:C6	2.80	0.49
1:A:1197:G:C2'	1:A:1198:G:H5''	2.42	0.49
1:A:1501:C:C5	1:A:1504:G:C4	3.00	0.49
1:A:1532:U:C6	1:A:1533:C:H5	2.30	0.49
3:C:5:ILE:C	3:C:5:ILE:CD1	2.85	0.49
3:C:22:TRP:CG	3:C:59:ARG:HD2	2.48	0.49
3:C:92:ALA:O	3:C:95:THR:O	2.30	0.49
4:D:8:VAL:C	4:D:10:ARG:N	2.69	0.49
5:E:42:GLY:HA2	5:E:136:MET:CE	2.43	0.49
6:F:1:MET:HE3	6:F:1:MET:N	2.28	0.49
13:M:22:ILE:HG13	13:M:25:ILE:CD1	2.43	0.49
1:A:47:C:C6	1:A:365:U:H2'	2.48	0.49
1:A:89:C:O2'	1:A:90:U:C5'	2.61	0.49
1:A:741:G:H5''	15:O:39:LEU:HD12	1.95	0.49
1:A:741:G:H2'	1:A:742:G:O4'	2.13	0.49
1:A:1090:U:C2	1:A:1091:U:C5	3.00	0.49
1:A:1507:A:C5	1:A:1530:G:C2	3.00	0.49
3:C:47:LEU:HD12	3:C:47:LEU:N	2.26	0.49
3:C:131:ARG:C	3:C:134:ILE:HG12	2.36	0.49
4:D:43:HIS:ND1	4:D:46:LYS:HE2	2.28	0.49
4:D:194:LEU:HB3	4:D:196:LEU:HD21	1.94	0.49
5:E:10:MET:SD	5:E:13:ILE:HG13	2.53	0.49
7:G:40:ALA:O	7:G:41:ARG:C	2.53	0.49
8:H:86:ILE:HG21	8:H:133:LEU:HB3	1.95	0.49
9:I:113:LYS:H	9:I:119:ALA:HA	1.77	0.49
17:Q:53:LEU:CD1	17:Q:85:VAL:HG11	2.43	0.49
1:A:110:C:H2'	1:A:111:G:O4'	2.13	0.49
1:A:137:C:H2'	1:A:138:G:H5'	1.94	0.49
1:A:355:C:H5'	1:A:389:A:OP2	2.13	0.49
1:A:443:C:C4	1:A:444:C:C5	3.01	0.49
1:A:490:G:C6	1:A:491:G:N7	2.81	0.49
1:A:630:G:H5'	1:A:631:G:OP2	2.13	0.49
1:A:949:A:C2	1:A:1233:G:C4	3.01	0.49
1:A:1047:G:C5	29:A:2425:HOH:O	2.63	0.49
1:A:1057:G:C4	1:A:1204:A:H2	2.28	0.49
1:A:1067:A:H1'	1:A:1068:G:OP2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1082:G:H2'	1:A:1083:U:H5'	1.93	0.49
1:A:1233:G:N2	1:A:1234:C:C2	2.81	0.49
1:A:1361(A):C:C2'	1:A:1362:C:O5'	2.60	0.49
1:A:1419:G:C6	1:A:1420:C:N4	2.81	0.49
2:B:97:TRP:CH2	2:B:176:GLU:CD	2.90	0.49
2:B:144:ARG:NH1	2:B:148:TYR:HE1	2.10	0.49
11:K:88:GLY:O	11:K:89:ALA:C	2.56	0.49
16:P:2:VAL:O	16:P:64:ALA:HA	2.13	0.49
17:Q:68:ARG:H	17:Q:70:ARG:NH1	2.10	0.49
19:S:62:ILE:HA	19:S:66:MET:SD	2.52	0.49
20:T:10:LEU:HD23	20:T:13:LEU:HB3	1.95	0.49
1:A:1128:C:H5'	9:I:16:ARG:NH2	2.28	0.49
2:B:238:LEU:O	2:B:238:LEU:CD2	2.60	0.49
3:C:88:ARG:HB2	3:C:101:LEU:HD22	1.95	0.49
4:D:39:PRO:O	4:D:44:GLY:HA3	2.12	0.49
5:E:84:PHE:C	5:E:84:PHE:CD2	2.90	0.49
6:F:25:ILE:HD12	6:F:82:ARG:NH1	2.26	0.49
7:G:20:ASP:OD2	7:G:63:LYS:NZ	2.46	0.49
7:G:123:GLU:O	7:G:126:ASP:N	2.46	0.49
10:J:33:GLN:C	10:J:34:VAL:HG23	2.38	0.49
1:A:19:C:P	5:E:127:ASN:HD22	2.35	0.49
1:A:349:A:H2'	1:A:350:G:H5'	1.95	0.49
1:A:507:C:OP2	1:A:508:C:O2'	2.25	0.49
1:A:945:G:H2'	1:A:945:G:N3	2.28	0.49
1:A:1055:A:O2'	3:C:156:ARG:NH2	2.46	0.49
1:A:1202:G:H2'	1:A:1203:C:H5'	1.94	0.49
1:A:1352:C:H2'	1:A:1353:G:C8	2.48	0.49
4:D:187:ARG:HG2	4:D:188:LEU:N	2.27	0.49
5:E:32:VAL:HG12	5:E:58:ALA:HB1	1.93	0.49
5:E:84:PHE:HB3	5:E:134:ALA:HB2	1.95	0.49
5:E:135:THR:O	5:E:136:MET:C	2.52	0.49
13:M:11:ARG:HG3	13:M:12:ASN:H	1.74	0.49
14:N:15:LYS:O	14:N:15:LYS:HG2	2.11	0.49
15:O:70:LEU:HD23	15:O:78:TYR:HB2	1.95	0.49
17:Q:65:ILE:CG2	17:Q:69:LYS:HE3	2.43	0.49
1:A:77:G:O2'	1:A:78:G:H5'	2.13	0.48
1:A:79:G:N3	1:A:80:G:C8	2.81	0.48
1:A:154:C:O2'	1:A:155:C:H5'	2.13	0.48
1:A:610:G:C2'	1:A:611:A:H5'	2.43	0.48
1:A:954:G:N2	1:A:1227:A:H62	2.11	0.48
1:A:1071:C:O2'	1:A:1072:G:H5'	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1330:U:H2'	1:A:1331:G:H5'	1.93	0.48
1:A:1357:A:H5''	1:A:1358:U:OP2	2.13	0.48
1:A:1385:G:H2'	1:A:1386:G:O4'	2.12	0.48
2:B:220:ASP:O	2:B:223:ILE:HG13	2.13	0.48
3:C:121:ALA:HA	3:C:124:ILE:HD12	1.94	0.48
4:D:206:PHE:CE2	4:D:207:TYR:CE2	3.01	0.48
5:E:34:VAL:HG22	5:E:62:ALA:HB1	1.95	0.48
7:G:47:CYS:HA	7:G:50:ILE:HG12	1.95	0.48
17:Q:60:ILE:O	17:Q:60:ILE:HG23	2.12	0.48
1:A:56:U:H2'	1:A:57:G:H8	1.78	0.48
1:A:83:U:C5	1:A:84:U:C5	3.01	0.48
1:A:570:G:C6	1:A:873:A:C2	3.01	0.48
1:A:807:A:H2'	1:A:808:C:C6	2.49	0.48
1:A:834:C:N4	29:A:2788:HOH:O	2.45	0.48
1:A:1124:G:H2'	1:A:1145:C:C5	2.46	0.48
1:A:1248:A:C6	1:A:1249:C:C4	3.01	0.48
1:A:1350:A:OP1	9:I:121:ARG:HD2	2.12	0.48
1:A:1520[A]:G:H2'	1:A:1521:G:H8	1.78	0.48
2:B:16:HIS:HD2	2:B:17:PHE:N	2.11	0.48
2:B:224:GLN:HG3	2:B:229:VAL:HG22	1.94	0.48
3:C:45:LYS:HA	3:C:45:LYS:HE3	1.95	0.48
3:C:64:VAL:CG2	3:C:99:VAL:HB	2.43	0.48
6:F:62:TRP:CE2	18:R:35:ARG:NH2	2.81	0.48
8:H:87:SER:C	8:H:88:LYS:HG3	2.38	0.48
12:L:117:ARG:C	12:L:119:LYS:N	2.70	0.48
14:N:11:LYS:HE3	14:N:13:THR:OG1	2.12	0.48
15:O:4:THR:CG2	15:O:5:LYS:H	2.26	0.48
21:U:5:ASP:O	21:U:11:GLY:HA3	2.12	0.48
1:A:254:G:C2	1:A:273:A:C2	3.01	0.48
1:A:429:U:H1'	1:A:430:A:H5''	1.95	0.48
1:A:777:A:H2'	1:A:777:A:N3	2.28	0.48
1:A:994:A:H2'	1:A:994:A:N3	2.28	0.48
3:C:82:GLU:HG3	3:C:83:ARG:N	2.28	0.48
7:G:43:PHE:O	7:G:46:ALA:HB3	2.13	0.48
9:I:36:TYR:HD2	9:I:37:PHE:CE1	2.31	0.48
14:N:23:ARG:HG2	14:N:29:ARG:O	2.13	0.48
18:R:61:LYS:O	18:R:62:GLU:C	2.54	0.48
19:S:52:TYR:CE1	19:S:55:LYS:C	2.91	0.48
1:A:418:C:H2'	1:A:419:C:C6	2.48	0.48
1:A:421:U:H4'	1:A:422:C:OP2	2.14	0.48
1:A:923:A:C1'	1:A:1398:A:C2	2.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1060:C:O2'	1:A:1061:G:H5'	2.13	0.48
1:A:1229:A:C2	1:A:1230:C:C4	3.02	0.48
1:A:1347:G:H1'	1:A:1348:U:H5	1.78	0.48
1:A:1399:C:C2	1:A:1401:G:C4	3.02	0.48
3:C:50:ALA:HA	3:C:72:LYS:HG3	1.94	0.48
3:C:86:VAL:O	3:C:89:GLU:CB	2.57	0.48
3:C:152:ILE:HD12	3:C:152:ILE:N	2.27	0.48
3:C:175:LEU:HD21	3:C:201:TYR:CE2	2.49	0.48
8:H:38:ILE:HD13	8:H:41:ARG:NH2	2.27	0.48
11:K:90:GLY:HA2	11:K:93:GLN:HB2	1.95	0.48
12:L:75:HIS:CB	12:L:102:ARG:HH12	2.26	0.48
13:M:27:LYS:C	13:M:27:LYS:HD2	2.38	0.48
16:P:8:ARG:CB	16:P:28:ARG:NH1	2.75	0.48
16:P:65:GLN:OE1	16:P:65:GLN:HA	2.13	0.48
17:Q:9:VAL:O	17:Q:11:VAL:HG23	2.14	0.48
17:Q:21:VAL:HG12	17:Q:22:LEU:N	2.28	0.48
17:Q:48:GLU:OE1	17:Q:50:LYS:HG3	2.13	0.48
20:T:43:LEU:N	20:T:43:LEU:HD23	2.27	0.48
1:A:180:U:C2'	1:A:181:G:H5'	2.44	0.48
1:A:426:G:OP1	4:D:38:TYR:OH	2.29	0.48
1:A:547:A:OP2	4:D:2:GLY:HA3	2.12	0.48
1:A:802:A:H2'	1:A:803:G:H5'	1.96	0.48
1:A:1248:A:N6	1:A:1249:C:N4	2.62	0.48
1:A:1392:G:H21	1:A:1502:A:H8	1.61	0.48
1:A:1397:C:H4'	1:A:1398:A:OP2	2.14	0.48
7:G:16:LEU:HD22	7:G:16:LEU:N	2.13	0.48
7:G:31:MET:HG3	7:G:32:ARG:N	2.28	0.48
15:O:31:LEU:HD13	15:O:31:LEU:N	2.28	0.48
16:P:9:PHE:N	16:P:16:HIS:O	2.46	0.48
18:R:38:GLU:N	18:R:38:GLU:CD	2.71	0.48
24:a:39:G:N3	24:a:39:G:C2'	2.74	0.48
1:A:926:G:C6	1:A:1505:G:C6	3.01	0.48
1:A:1238:A:H5'	1:A:1336:C:H41	1.78	0.48
1:A:1330:U:OP1	13:M:25:ILE:O	2.31	0.48
2:B:83:MET:SD	2:B:238:LEU:HD12	2.53	0.48
2:B:102:LEU:N	2:B:102:LEU:CD1	2.75	0.48
2:B:212:GLN:HE22	2:B:235:SER:HB2	1.79	0.48
3:C:126:ARG:NE	3:C:128:PHE:HD1	2.11	0.48
4:D:61:LYS:HD2	4:D:61:LYS:C	2.38	0.48
4:D:165:MET:HE2	4:D:176:LEU:CD2	2.44	0.48
4:D:172:PRO:HD2	4:D:173:TRP:HZ3	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:26:PHE:CD1	7:G:101:LEU:HD23	2.48	0.48
12:L:24:VAL:HG13	12:L:98:TYR:CE2	2.48	0.48
16:P:74:LEU:HB3	16:P:79:VAL:CG2	2.35	0.48
18:R:40:LEU:HB3	18:R:79:LEU:HD11	1.96	0.48
18:R:86:VAL:O	18:R:87:ARG:NH2	2.46	0.48
1:A:154:C:O5'	1:A:154:C:H6	1.97	0.48
1:A:228:A:H2'	1:A:229:U:H6	1.78	0.48
1:A:668:G:H1	1:A:738:C:H42	1.62	0.48
1:A:967:5MC:O2	1:A:967:5MC:H2'	2.13	0.48
1:A:1143:G:H2'	1:A:1144:G:C8	2.47	0.48
1:A:1290:G:H2'	1:A:1291:G:C8	2.48	0.48
27:A:1928:SRV:H12	27:A:1928:SRV:O53	2.13	0.48
2:B:24:TRP:CZ3	2:B:26:PRO:HA	2.49	0.48
2:B:122:PHE:HE2	2:B:139:LYS:HD2	1.78	0.48
5:E:84:PHE:C	5:E:84:PHE:HD2	2.22	0.48
6:F:76:ALA:HA	6:F:79:LEU:HD12	1.95	0.48
10:J:28:ARG:HB3	10:J:29:ARG:NH1	2.25	0.48
12:L:33:ARG:C	12:L:84:LEU:HD12	2.38	0.48
13:M:68:GLY:C	13:M:70:LEU:N	2.70	0.48
15:O:15:PHE:HZ	15:O:85:LEU:HD21	1.77	0.48
19:S:31:ILE:HG23	19:S:32:LYS:N	2.29	0.48
20:T:60:GLU:HA	20:T:63:ILE:HD12	1.96	0.48
1:A:109:A:C4	1:A:327:A:C2	3.01	0.48
1:A:333:G:O2'	1:A:334:C:H5'	2.13	0.48
1:A:840:C:OP2	1:A:840:C:H3'	2.13	0.48
1:A:945:G:O6	1:A:1236:A:N1	2.47	0.48
1:A:1228:C:OP1	13:M:115:LYS:HE2	2.13	0.48
1:A:1392:G:O2'	1:A:1393:U:H5'	2.14	0.48
2:B:118:LEU:HB2	2:B:142:LEU:CD1	2.44	0.48
5:E:105:VAL:HB	5:E:106:PRO:CD	2.43	0.48
7:G:116:ALA:O	7:G:119:ARG:N	2.47	0.48
8:H:14:ARG:CB	8:H:14:ARG:CZ	2.91	0.48
9:I:10:ARG:HD3	9:I:105:ASP:HB3	1.95	0.48
9:I:127:LYS:O	9:I:127:LYS:HG3	2.14	0.48
13:M:81:LEU:HD11	13:M:88:ARG:HH22	1.77	0.48
15:O:8:LYS:O	15:O:12:ILE:HG12	2.14	0.48
15:O:78:TYR:CE1	15:O:82:ILE:HD12	2.49	0.48
19:S:40:ILE:HG22	19:S:67:VAL:HG13	1.96	0.48
1:A:754:C:P	15:O:72:ARG:HH12	2.37	0.48
1:A:1133:G:N2	1:A:1141:C:C2	2.77	0.48
1:A:1391:U:H2'	1:A:1392:G:C8	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:58:LEU:C	4:D:58:LEU:CD2	2.86	0.48
9:I:17:VAL:CG2	9:I:80:GLY:HA3	2.44	0.48
9:I:46:ALA:HB1	9:I:77:ILE:HG21	1.96	0.48
10:J:79:ARG:HD2	10:J:79:ARG:N	2.29	0.48
12:L:57:LYS:HA	12:L:67:THR:HA	1.96	0.48
13:M:99:ARG:NH2	19:S:2:PRO:CD	2.77	0.48
1:A:782:A:P	29:A:2280:HOH:O	2.71	0.48
1:A:961:U:O2'	1:A:962:C:H5'	2.13	0.48
1:A:1004:A:H5''	29:A:2327:HOH:O	2.13	0.48
1:A:1054:C:N3	23:W:34:G:O4'	2.47	0.48
1:A:1084:G:H5'	1:A:1102:A:OP2	2.14	0.48
1:A:1371:G:C6	1:A:1372:U:C4	3.01	0.48
1:A:1441:G:H4'	1:A:1442:G:C2	2.48	0.48
4:D:187:ARG:HG3	4:D:188:LEU:HD12	1.94	0.48
5:E:97:GLY:N	5:E:117:ASP:OD1	2.47	0.48
5:E:112:LEU:C	5:E:114:GLY:N	2.70	0.48
7:G:111:ARG:CB	7:G:112:PRO:HD2	2.43	0.48
1:A:794:A:C8	1:A:794:A:H3'	2.48	0.47
1:A:1006:C:N3	1:A:1023:G:N2	2.56	0.47
1:A:1263:C:N4	1:A:1264:C:N4	2.62	0.47
2:B:73:THR:HG23	2:B:95:GLN:O	2.14	0.47
2:B:162:ILE:HD13	2:B:177:ALA:HB2	1.95	0.47
5:E:87:SER:HB3	5:E:131:ILE:HD13	1.96	0.47
6:F:7:ASN:N	6:F:7:ASN:OD1	2.47	0.47
6:F:39:LYS:HB2	6:F:39:LYS:HE3	1.66	0.47
8:H:19:VAL:CG2	8:H:21:LYS:HD3	2.44	0.47
13:M:4:ILE:HG22	13:M:5:ALA:CB	2.44	0.47
15:O:18:PHE:HD1	15:O:19:PRO:O	1.97	0.47
15:O:70:LEU:HD22	15:O:78:TYR:CB	2.41	0.47
17:Q:4:LYS:HG3	17:Q:6:LEU:CD2	2.44	0.47
1:A:257:G:H8	1:A:257:G:O5'	1.97	0.47
1:A:277:C:C2'	1:A:278:G:H5'	2.44	0.47
1:A:373:A:H2'	1:A:374:A:H8	1.79	0.47
1:A:390:C:O3'	16:P:28:ARG:NH2	2.47	0.47
1:A:500:G:N7	1:A:546:G:N2	2.60	0.47
1:A:584:G:OP2	17:Q:87:LYS:NZ	2.31	0.47
1:A:877:C:O2'	1:A:878:G:H5'	2.13	0.47
1:A:924:C:C4'	1:A:1399:C:OP2	2.62	0.47
1:A:1015:A:N6	1:A:1016:A:N6	2.61	0.47
1:A:1048:G:O6	1:A:1210:C:N4	2.47	0.47
1:A:1204:A:N7	1:A:1205:U:C5	2.82	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:76:VAL:HG21	3:C:103:VAL:CG1	2.44	0.47
5:E:38:GLN:HA	5:E:38:GLN:OE1	2.14	0.47
5:E:142:LEU:O	5:E:143:ARG:HG2	2.13	0.47
8:H:27:PRO:CA	8:H:58:TYR:CD2	2.96	0.47
10:J:47:PHE:HB3	14:N:34:TYR:CE2	2.44	0.47
12:L:110:VAL:O	12:L:122:THR:HG21	2.13	0.47
13:M:35:GLU:HG2	13:M:36:LYS:N	2.29	0.47
14:N:12:ARG:C	14:N:14:PRO:HD3	2.39	0.47
15:O:70:LEU:HD22	15:O:78:TYR:CA	2.44	0.47
18:R:87:ARG:CG	18:R:87:ARG:NH2	2.53	0.47
1:A:190(K):G:H2'	1:A:190(L):U:C6	2.48	0.47
1:A:1162:C:N3	1:A:1175:G:C2	2.83	0.47
1:A:1329:A:H5'	13:M:29:ARG:HD2	1.97	0.47
12:L:93:LEU:O	12:L:94:PRO:C	2.56	0.47
14:N:24:CYS:HB2	14:N:29:ARG:CB	2.43	0.47
16:P:53:VAL:O	16:P:54:GLU:C	2.53	0.47
1:A:60:A:H4'	1:A:61:G:O5'	2.14	0.47
1:A:116:A:H61	1:A:313:A:H1'	1.80	0.47
1:A:609:A:N6	29:A:2320:HOH:O	2.39	0.47
1:A:1202:G:C2'	1:A:1203:C:H5'	2.44	0.47
1:A:1329:A:P	13:M:29:ARG:HG3	2.55	0.47
2:B:27:LYS:C	2:B:29:ALA:H	2.23	0.47
3:C:52:LEU:HA	3:C:70:VAL:HA	1.97	0.47
3:C:112:SER:O	3:C:116:VAL:HG23	2.15	0.47
5:E:69:VAL:CG1	5:E:71:LEU:HD23	2.44	0.47
8:H:101:PRO:HA	8:H:102:ARG:HH11	1.78	0.47
9:I:66:ARG:HE	9:I:66:ARG:HB3	1.38	0.47
10:J:25:GLU:HG2	10:J:28:ARG:CD	2.43	0.47
17:Q:11:VAL:CG1	17:Q:88:TYR:CD2	2.94	0.47
17:Q:29:HIS:ND1	17:Q:30:PRO:CD	2.76	0.47
18:R:66:LEU:HD12	18:R:66:LEU:O	2.13	0.47
19:S:40:ILE:HG23	19:S:62:ILE:CD1	2.44	0.47
1:A:147:G:C2	1:A:148:G:C8	3.03	0.47
1:A:645:C:C2	1:A:646:U:C6	3.02	0.47
1:A:838:G:H3'	1:A:839:U:C5'	2.42	0.47
1:A:892:A:C2	1:A:907:A:C5	3.02	0.47
1:A:956:U:O2'	1:A:957:U:H5'	2.14	0.47
1:A:969:A:C2'	1:A:970:C:H5'	2.45	0.47
1:A:1381:U:C6	1:A:1382:C:C6	3.02	0.47
1:A:1402:4OC:HM22	1:A:1402:4OC:O3'	2.15	0.47
1:A:1498:UR3:C4'	1:A:1519[A]:MA6:C2	2.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:50:ILE:HB	7:G:58:PRO:HB3	1.97	0.47
12:L:113:ARG:HH11	12:L:116:SER:H	1.62	0.47
1:A:70:G:C2	1:A:99:C:O2	2.67	0.47
1:A:437:U:H5'	4:D:155:LEU:HD21	1.96	0.47
1:A:506:G:C6	1:A:507:C:C4	3.02	0.47
1:A:836:G:C6	1:A:851:G:C6	3.03	0.47
1:A:1520[A]:G:H2'	1:A:1521:G:C8	2.49	0.47
2:B:6:THR:HB	2:B:48:MET:HE3	1.96	0.47
2:B:101:MET:HA	2:B:108:ILE:HD12	1.96	0.47
3:C:22:TRP:CD1	3:C:59:ARG:HD2	2.50	0.47
3:C:130:VAL:O	3:C:134:ILE:HG12	2.15	0.47
3:C:173:VAL:N	3:C:174:PRO:HD3	2.29	0.47
7:G:78:ARG:HD2	7:G:156:TRP:HB3	1.95	0.47
10:J:63:PHE:HA	14:N:59:ALA:HB3	1.95	0.47
16:P:40:ASP:OD1	16:P:44:THR:OG1	2.31	0.47
17:Q:47:PRO:HD2	17:Q:48:GLU:H	1.79	0.47
20:T:41:ILE:H	20:T:41:ILE:CD1	2.27	0.47
20:T:102:GLY:O	20:T:104:LEU:N	2.47	0.47
1:A:19:C:H2'	1:A:20:U:H6	1.80	0.47
1:A:77:G:C6	1:A:93:G:N1	2.83	0.47
1:A:78:G:C6	1:A:79:G:N7	2.83	0.47
1:A:232:G:H1'	1:A:262:A:N1	2.29	0.47
1:A:284:G:N3	1:A:285:G:C8	2.82	0.47
1:A:514:C:H2'	1:A:515:G:C8	2.48	0.47
1:A:811:C:H4'	1:A:900:A:N6	2.30	0.47
1:A:976:G:H5'	1:A:1358:U:O2'	2.15	0.47
1:A:1027:C:H5''	1:A:1027:C:O2	2.13	0.47
1:A:1060:C:C2	1:A:1198:G:C2	3.03	0.47
1:A:1092:A:H8	1:A:1092:A:O5'	1.98	0.47
1:A:1148:U:C5	1:A:1149:C:C4	3.03	0.47
1:A:1286:A:H3'	1:A:1287:A:H5''	1.96	0.47
1:A:1351:U:O2'	1:A:1352:C:H5'	2.14	0.47
1:A:1435:G:C4	1:A:1436:U:C5	3.03	0.47
1:A:1503:A:C5	1:A:1531:A:C2	3.02	0.47
3:C:26:LYS:HB2	3:C:26:LYS:NZ	2.29	0.47
3:C:117:ALA:HB2	3:C:200:ALA:HB2	1.96	0.47
4:D:12:CYS:HA	4:D:19:LEU:CD2	2.44	0.47
4:D:70:ILE:HD11	4:D:100:ARG:NE	2.30	0.47
4:D:177:ASP:OD1	4:D:179:GLU:N	2.47	0.47
8:H:133:LEU:C	8:H:133:LEU:CD2	2.85	0.47
9:I:48:GLU:N	9:I:49:PRO:CD	2.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:95:LYS:HD2	9:I:95:LYS:N	2.29	0.47
10:J:21:GLN:O	10:J:24:VAL:HG12	2.15	0.47
10:J:85:LEU:O	10:J:86:MET:HB3	2.15	0.47
13:M:27:LYS:HD2	13:M:28:ALA:N	2.30	0.47
13:M:90:LEU:HD23	13:M:90:LEU:HA	1.81	0.47
14:N:45:ARG:CG	14:N:45:ARG:HH11	2.28	0.47
15:O:8:LYS:O	15:O:9:GLN:C	2.55	0.47
16:P:1:MET:O	16:P:2:VAL:C	2.56	0.47
16:P:8:ARG:O	16:P:9:PHE:CD2	2.68	0.47
17:Q:66:SER:OG	17:Q:69:LYS:HG3	2.14	0.47
20:T:54:LYS:HG2	20:T:55:ILE:N	2.28	0.47
1:A:35:G:O2'	12:L:118:SER:O	2.20	0.47
1:A:644:G:C6	1:A:645:C:C5	3.01	0.47
1:A:868:C:H2'	1:A:869:G:H5'	1.97	0.47
1:A:1035:A:C6	1:A:1036:G:C6	3.02	0.47
1:A:1073:U:O2	2:B:104:ASN:ND2	2.45	0.47
1:A:1163:C:H3'	1:A:1163:C:C6	2.49	0.47
1:A:1228:C:H4'	13:M:116:THR:HA	1.96	0.47
1:A:1405:G:H2'	1:A:1406:U:H5'	1.95	0.47
2:B:92:TYR:HE1	2:B:150:SER:HG	1.61	0.47
4:D:31:CYS:O	4:D:32:ALA:HB3	2.14	0.47
4:D:188:LEU:CD1	4:D:188:LEU:H	2.24	0.47
7:G:103:TRP:NE1	7:G:137:LYS:HE2	2.30	0.47
7:G:153:HIS:CE1	7:G:154:TYR:CE2	3.03	0.47
11:K:57:THR:HG22	11:K:58:PRO:HD2	1.95	0.47
13:M:39:ILE:HD12	13:M:39:ILE:N	2.30	0.47
15:O:17:ARG:HA	15:O:17:ARG:HD2	1.78	0.47
1:A:90:U:O2'	1:A:91:C:O5'	2.33	0.47
1:A:129(A):G:N3	1:A:190(E):U:H5''	2.29	0.47
1:A:262:A:C6	1:A:263:A:C6	3.03	0.47
1:A:826:C:C2	1:A:827:U:C5	3.02	0.47
1:A:875:C:H1'	8:H:15:ASN:HD21	1.80	0.47
1:A:1061:G:C2	1:A:1062:U:O2	2.67	0.47
1:A:1131:G:H2'	1:A:1132:C:C6	2.50	0.47
1:A:1288:A:H2'	1:A:1289:A:C8	2.50	0.47
1:A:1360:A:O2'	1:A:1361:G:H5'	2.15	0.47
1:A:1533:C:HO2'	1:A:1534:C:P	2.30	0.47
2:B:231:GLU:O	2:B:232:PRO:C	2.55	0.47
3:C:175:LEU:H	3:C:175:LEU:HD12	1.80	0.47
4:D:111:ALA:HB2	4:D:120:LEU:HD12	1.95	0.47
12:L:19:ARG:HH12	12:L:21:LYS:HB3	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:11:VAL:O	15:O:14:GLU:HB3	2.15	0.47
18:R:45:SER:HB3	18:R:47:THR:O	2.15	0.47
1:A:248:C:H2'	1:A:249:U:H5'	1.95	0.47
1:A:401:C:H1'	1:A:622:A:H1'	1.97	0.47
1:A:913:A:O3'	27:A:1928:SRV:HI33	2.10	0.47
1:A:1054:C:N3	23:W:34:G:OP1	2.48	0.47
1:A:1182:G:H4'	1:A:1183:A:O5'	2.14	0.47
1:A:1206:G:O6	1:A:1207:2MG:C6	2.68	0.47
1:A:1286:A:H3'	1:A:1286:A:C8	2.50	0.47
3:C:121:ALA:HB1	3:C:189:ALA:HB2	1.95	0.47
4:D:145:GLU:O	4:D:145:GLU:HG3	2.13	0.47
7:G:47:CYS:HA	7:G:50:ILE:CG1	2.45	0.47
7:G:69:VAL:HG22	7:G:135:VAL:HG22	1.96	0.47
8:H:100:ILE:HG12	8:H:100:ILE:H	1.52	0.47
9:I:8:GLY:HA2	9:I:79:LEU:CD1	2.38	0.47
10:J:86:MET:CG	10:J:87:THR:H	2.09	0.47
10:J:99:LYS:HD2	10:J:99:LYS:N	2.30	0.47
13:M:16:ASP:O	13:M:17:VAL:C	2.58	0.47
17:Q:17:LYS:HG2	17:Q:47:PRO:HA	1.97	0.47
24:a:38:A:C2	24:a:39:G:O6	2.68	0.47
1:A:22:G:C6	1:A:23:C:N4	2.83	0.46
1:A:77:G:N2	1:A:92:C:O2	2.48	0.46
1:A:339:C:H2'	1:A:340:U:C6	2.51	0.46
1:A:353:A:C5'	1:A:353:A:C8	2.96	0.46
1:A:385:C:H2'	1:A:386:C:H6	1.81	0.46
1:A:819:A:H4'	1:A:820:U:OP2	2.15	0.46
1:A:925:G:H1'	1:A:1502:A:N9	2.30	0.46
1:A:1181:G:C2	1:A:1182:G:N2	2.83	0.46
2:B:97:TRP:HH2	2:B:176:GLU:OE2	1.98	0.46
2:B:208:ILE:HD13	2:B:211:ILE:HD12	1.96	0.46
4:D:107:ARG:HH11	4:D:114:ARG:NH2	2.13	0.46
4:D:196:LEU:HA	4:D:197:PRO:HD3	1.52	0.46
6:F:14:LEU:HD13	6:F:18:GLN:CB	2.24	0.46
9:I:64:THR:HG23	9:I:66:ARG:NH2	2.30	0.46
11:K:120:ARG:CZ	11:K:126:ARG:HE	2.28	0.46
13:M:17:VAL:HG12	13:M:18:ALA:N	2.30	0.46
15:O:55:GLY:O	15:O:59:MET:HG3	2.16	0.46
21:U:10:ARG:NH1	21:U:10:ARG:HG3	2.30	0.46
1:A:264:U:O2'	17:Q:63:ARG:HD3	2.15	0.46
1:A:743:U:H2'	1:A:744:C:H6	1.81	0.46
1:A:822:C:H2'	1:A:823:G:H5'	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:983:A:OP1	14:N:3:ARG:NH2	2.41	0.46
1:A:983:A:H5'	1:A:984:C:OP2	2.16	0.46
1:A:1258:G:O2'	1:A:1259:C:H5'	2.15	0.46
2:B:132:LYS:O	2:B:136:VAL:HG23	2.15	0.46
3:C:15:THR:HB	3:C:181:ASN:HA	1.97	0.46
3:C:157:ILE:CD1	3:C:166:GLU:HG2	2.45	0.46
7:G:126:ASP:OD2	7:G:131:LYS:HE3	2.15	0.46
10:J:4:ILE:HG23	10:J:74:ILE:O	2.15	0.46
14:N:11:LYS:C	14:N:13:THR:H	2.22	0.46
15:O:52:SER:O	15:O:53:HIS:C	2.58	0.46
16:P:48:TRP:CD1	16:P:48:TRP:N	2.81	0.46
1:A:44:G:C2	1:A:399:G:C4	3.04	0.46
1:A:81:U:C6	1:A:81:U:H3'	2.49	0.46
1:A:116:A:H5''	29:A:2018:HOH:O	2.15	0.46
1:A:162:A:H1'	1:A:348:G:O2'	2.16	0.46
1:A:419:C:O2'	1:A:420:U:H5'	2.16	0.46
1:A:570:G:H2'	1:A:571:U:C6	2.50	0.46
1:A:653:A:OP1	8:H:56:LYS:NZ	2.45	0.46
1:A:669:U:H2'	1:A:670:G:C8	2.51	0.46
1:A:853:G:C2	1:A:854:G:C8	3.02	0.46
1:A:861:G:H8	1:A:861:G:O5'	1.98	0.46
1:A:918:A:OP2	29:A:2624:HOH:O	2.21	0.46
1:A:1054:C:C3'	1:A:1054:C:C2	2.98	0.46
1:A:1064:G:H1'	1:A:1190:G:H21	1.81	0.46
1:A:1290:G:H2'	1:A:1291:G:H8	1.81	0.46
1:A:1367:C:N3	1:A:1368:G:C8	2.84	0.46
1:A:1368:G:H5''	9:I:112:LYS:HB3	1.97	0.46
3:C:20:SER:HB3	3:C:57:ILE:HB	1.97	0.46
3:C:64:VAL:HG23	3:C:99:VAL:HB	1.95	0.46
6:F:15:ASP:OD2	6:F:18:GLN:HB2	2.15	0.46
8:H:4:ASP:HB3	8:H:7:ALA:CB	2.45	0.46
10:J:28:ARG:CB	10:J:29:ARG:HH11	2.25	0.46
11:K:20:TYR:O	11:K:30:VAL:HA	2.16	0.46
12:L:54:LYS:HB2	12:L:70:ILE:HB	1.97	0.46
12:L:90:VAL:HG11	12:L:93:LEU:CD1	2.46	0.46
13:M:49:THR:C	13:M:51:ALA:N	2.73	0.46
1:A:11:G:H2'	1:A:12:U:O4'	2.15	0.46
1:A:285:G:C2	1:A:286:G:C8	3.03	0.46
1:A:382:A:H2'	1:A:383:A:C8	2.50	0.46
1:A:391:G:C6	1:A:392:G:C5	3.04	0.46
1:A:433:C:H2'	1:A:434:U:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:544:G:H2'	1:A:545:C:O5'	2.14	0.46
1:A:547:A:OP2	4:D:2:GLY:HA2	2.15	0.46
1:A:553:A:O2'	12:L:29:GLY:O	2.31	0.46
1:A:575:G:C8	1:A:881:G:N2	2.83	0.46
1:A:1519[A]:MA6:H3'	1:A:1520[A]:G:H5'	1.98	0.46
1:A:1519[B]:MA6:C9	1:A:1520[B]:G:H21	2.29	0.46
2:B:121:LEU:HD23	2:B:121:LEU:O	2.15	0.46
3:C:119:ARG:CG	3:C:119:ARG:NH1	2.76	0.46
5:E:142:LEU:HD23	5:E:142:LEU:HA	1.62	0.46
7:G:51:GLN:C	7:G:53:LYS:H	2.23	0.46
8:H:137:VAL:O	8:H:138:TRP:HB3	2.14	0.46
12:L:30:ALA:CB	12:L:31:PRO:HD2	2.43	0.46
13:M:25:ILE:HG23	13:M:29:ARG:HB2	1.97	0.46
13:M:54:VAL:HG13	13:M:55:ARG:N	2.30	0.46
15:O:5:LYS:O	15:O:6:GLU:C	2.57	0.46
15:O:55:GLY:HA2	15:O:58:MET:HE2	1.97	0.46
15:O:70:LEU:HD23	15:O:70:LEU:O	2.14	0.46
16:P:19:ILE:HG22	16:P:36:ILE:CG1	2.45	0.46
1:A:92:C:H2'	1:A:93:G:H8	1.81	0.46
1:A:438:G:O6	29:A:2233:HOH:O	2.17	0.46
1:A:491:G:C2	1:A:492:G:C4	3.04	0.46
1:A:516:PSU:O2'	1:A:519:C:N3	2.46	0.46
1:A:1109:C:OP2	3:C:176:HIS:ND1	2.48	0.46
1:A:1148:U:C5	1:A:1149:C:C5	3.03	0.46
1:A:1233:G:H2'	1:A:1234:C:C6	2.51	0.46
1:A:1393:U:C3'	1:A:1393:U:C6	2.99	0.46
2:B:16:HIS:NE2	2:B:17:PHE:HD2	2.12	0.46
2:B:107:THR:HG23	2:B:110:GLN:OE1	2.16	0.46
4:D:100:ARG:HH12	4:D:137:SER:HB3	1.81	0.46
7:G:74:GLU:HA	7:G:141:VAL:HG12	1.97	0.46
8:H:105:ARG:HD3	8:H:105:ARG:HA	1.73	0.46
10:J:12:ASP:O	10:J:12:ASP:OD2	2.33	0.46
11:K:89:ALA:O	11:K:90:GLY:C	2.56	0.46
13:M:2:ALA:O	13:M:10:PRO:HD2	2.15	0.46
20:T:105:SER:O	20:T:106:ALA:C	2.58	0.46
1:A:448:A:HO2'	1:A:449:C:H5'	1.74	0.46
1:A:610:G:H5'	29:A:2771:HOH:O	2.14	0.46
1:A:1300:G:O2'	1:A:1301:U:OP2	2.34	0.46
2:B:97:TRP:HZ2	2:B:102:LEU:CD1	2.18	0.46
2:B:185:ILE:HD12	2:B:185:ILE:N	2.29	0.46
4:D:122:ARG:HA	4:D:134:ASP:O	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:127:ALA:C	7:G:129:GLU:N	2.71	0.46
7:G:150:ALA:HA	11:K:59:TYR:CD2	2.51	0.46
10:J:9:ARG:HB3	10:J:9:ARG:NH1	2.31	0.46
1:A:89:C:C6	1:A:90:U:C2	3.03	0.46
1:A:164:U:H2'	1:A:165:C:H6	1.81	0.46
1:A:643:C:C2'	1:A:644:G:C5'	2.87	0.46
1:A:666:G:H5'	1:A:726:C:H1'	1.98	0.46
1:A:668:G:C2'	1:A:669:U:H5'	2.46	0.46
1:A:961:U:H2'	1:A:962:C:C5'	2.45	0.46
1:A:1148:U:C6	1:A:1149:C:C6	3.04	0.46
1:A:1314:C:OP2	19:S:6:LYS:HG2	2.15	0.46
1:A:1370:G:C2	1:A:1371:G:C8	3.04	0.46
1:A:1407:5MC:H2'	1:A:1408:A:C5'	2.43	0.46
4:D:150:GLU:C	4:D:152:SER:N	2.72	0.46
7:G:64:GLN:OE1	7:G:64:GLN:HA	2.15	0.46
7:G:111:ARG:HD3	7:G:113:GLU:CG	2.45	0.46
11:K:11:LYS:N	11:K:75:TYR:CE2	2.82	0.46
13:M:59:TYR:CE2	13:M:63:THR:HG21	2.50	0.46
18:R:39:VAL:CG1	18:R:40:LEU:N	2.79	0.46
21:U:23:PRO:C	21:U:25:LYS:N	2.74	0.46
1:A:344:A:C5'	1:A:345:C:H5	2.27	0.46
1:A:460:A:C6	1:A:462:G:C6	3.04	0.46
1:A:499:A:C4'	1:A:500:G:OP1	2.49	0.46
1:A:538:G:C2	1:A:539:A:C4	3.04	0.46
1:A:923:A:H1'	1:A:1398:A:N3	2.30	0.46
1:A:1502:A:C2	1:A:1504:G:C2	3.04	0.46
1:A:1519[B]:MA6:C9	1:A:1520[B]:G:N2	2.79	0.46
2:B:115:LEU:HD21	2:B:153:ARG:NH1	2.31	0.46
4:D:107:ARG:NH1	4:D:114:ARG:NH2	2.64	0.46
5:E:84:PHE:CB	5:E:134:ALA:HB2	2.46	0.46
5:E:84:PHE:CE1	5:E:133:TYR:HB3	2.50	0.46
6:F:45:LEU:HB3	6:F:59:TYR:HD1	1.81	0.46
11:K:30:VAL:HG21	11:K:65:ALA:HA	1.97	0.46
16:P:21:VAL:HG21	16:P:59:TRP:CD1	2.51	0.46
1:A:66:G:C2	1:A:67:C:C6	3.03	0.46
1:A:411:A:H3'	1:A:411:A:C8	2.51	0.46
1:A:630:G:C5'	1:A:631:G:OP2	2.64	0.46
1:A:920:U:H2'	1:A:921:U:C6	2.51	0.46
1:A:923:A:C2'	1:A:924:C:H5'	2.45	0.46
1:A:1015:A:C5	1:A:1016:A:C5	3.04	0.46
1:A:1413:A:H2'	1:A:1414:U:O4'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1511:G:H2'	1:A:1512:U:O4'	2.16	0.46
1:A:1518[B]:MA6:H102	1:A:1519[B]:MA6:H103	1.98	0.46
4:D:127:THR:HG22	4:D:149:ALA:HB2	1.97	0.46
5:E:45:PHE:CE2	5:E:47:LYS:HE3	2.51	0.46
9:I:103:THR:HG22	9:I:104:ARG:O	2.15	0.46
10:J:46:ARG:HH11	10:J:46:ARG:HG3	1.80	0.46
15:O:53:HIS:O	15:O:54:ARG:C	2.54	0.46
16:P:6:LEU:HD23	16:P:17:TYR:CG	2.51	0.46
19:S:51:VAL:CG2	19:S:51:VAL:O	2.64	0.46
1:A:166:G:O2'	1:A:167:G:H5'	2.15	0.46
1:A:336:C:N4	29:A:2573:HOH:O	2.49	0.46
1:A:342:C:H2'	1:A:343:U:H5'	1.98	0.46
1:A:407:G:C5'	4:D:3:ARG:HH12	2.29	0.46
1:A:510:A:P	29:A:2165:HOH:O	2.74	0.46
1:A:511:C:O2'	1:A:534:U:H1'	2.16	0.46
1:A:803:G:C6	1:A:804:U:C4	3.04	0.46
1:A:978:A:O2'	1:A:1322:C:O2	2.27	0.46
1:A:1454:G:C5	29:A:2825:HOH:O	2.65	0.46
3:C:39:ILE:HG22	3:C:40:ARG:N	2.31	0.46
3:C:113:ALA:O	3:C:116:VAL:N	2.50	0.46
3:C:178:LEU:HA	3:C:178:LEU:HD13	1.78	0.46
4:D:52:SER:O	4:D:55:ALA:HB3	2.16	0.46
9:I:17:VAL:CG1	9:I:63:ILE:HD11	2.40	0.46
9:I:17:VAL:HG21	9:I:80:GLY:HA3	1.98	0.46
11:K:116:HIS:N	11:K:116:HIS:ND1	2.62	0.46
12:L:25:PRO:C	12:L:27:LEU:N	2.73	0.46
13:M:65:LYS:HB2	13:M:65:LYS:HE3	1.68	0.46
16:P:78:GLY:C	16:P:80:PHE:N	2.69	0.46
18:R:36:ASN:OD1	18:R:39:VAL:CG1	2.64	0.46
24:a:37:A:C5	24:a:38:A:N7	2.83	0.46
1:A:76:C:H2'	1:A:77:G:H8	1.82	0.45
1:A:182:U:P	29:A:2183:HOH:O	2.73	0.45
1:A:515:G:C6	1:A:516:PSU:C2	3.04	0.45
1:A:642:A:C4	8:H:114:THR:O	2.70	0.45
1:A:1032:G:H2'	1:A:1033:G:H8	1.82	0.45
1:A:1125:U:C3'	1:A:1126:U:H5	2.28	0.45
1:A:1304:G:C6	1:A:1305:G:N1	2.83	0.45
1:A:1379:G:C6	1:A:1380:U:C5	3.04	0.45
2:B:74:LYS:C	2:B:76:GLN:N	2.72	0.45
3:C:5:ILE:HD11	3:C:10:PHE:CD2	2.51	0.45
3:C:6:HIS:CD2	3:C:6:HIS:C	2.94	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:120:LEU:HD23	4:D:125:HIS:HB2	1.98	0.45
4:D:172:PRO:HG2	4:D:173:TRP:CE3	2.51	0.45
4:D:196:LEU:H	4:D:196:LEU:CD2	2.29	0.45
9:I:15:ALA:HA	9:I:65:VAL:HG13	1.98	0.45
12:L:44:THR:HA	12:L:45:PRO:HD3	1.76	0.45
13:M:40:ASN:HD22	13:M:43:THR:HG23	1.81	0.45
16:P:34:GLU:OE2	16:P:55:ARG:HD2	2.15	0.45
20:T:57:ARG:HD3	20:T:102:GLY:CA	2.45	0.45
24:a:33:U:O2	24:a:34:G:N3	2.49	0.45
1:A:89:C:C5	1:A:90:U:C2	3.03	0.45
1:A:109:A:C3'	1:A:110:C:H5'	2.46	0.45
1:A:179:A:C2'	1:A:180:U:H5'	2.46	0.45
1:A:373:A:C2	1:A:482:A:C6	3.04	0.45
1:A:386:C:H2'	1:A:387:U:H5'	1.97	0.45
1:A:642:A:H2'	1:A:643:C:H6	1.76	0.45
1:A:792:A:C4'	1:A:793:U:OP1	2.48	0.45
1:A:1068:G:OP2	1:A:1068:G:O4'	2.33	0.45
1:A:1151:A:O2'	1:A:1152:A:H8	1.99	0.45
1:A:1178:G:N2	1:A:1180:A:H3'	2.31	0.45
1:A:1190:G:HO2'	1:A:1191:A:P	2.39	0.45
1:A:1290:G:C6	1:A:1291:G:C6	3.04	0.45
1:A:1315:U:H2'	1:A:1316:G:O4'	2.16	0.45
1:A:1368:G:H2'	1:A:1369:C:C5'	2.46	0.45
1:A:1425:U:H3	1:A:1475:G:H1	1.64	0.45
3:C:85:ARG:O	3:C:86:VAL:C	2.60	0.45
4:D:155:LEU:HD22	4:D:156:GLU:H	1.80	0.45
4:D:159:ARG:CG	4:D:159:ARG:NH1	2.77	0.45
11:K:69:ALA:O	11:K:70:LYS:C	2.58	0.45
15:O:5:LYS:HA	15:O:5:LYS:HZ3	1.72	0.45
1:A:437:U:C5'	4:D:155:LEU:HD21	2.46	0.45
1:A:566:G:H4'	1:A:567:G:OP1	2.16	0.45
1:A:575:G:H4'	1:A:576:G:OP1	2.16	0.45
1:A:631:G:H2'	1:A:632:A:C8	2.51	0.45
1:A:853:G:O2'	1:A:854:G:H5'	2.17	0.45
1:A:1502:A:H2'	1:A:1504:G:C8	2.51	0.45
1:A:1503:A:C4	1:A:1531:A:N3	2.85	0.45
2:B:200:ILE:HG23	2:B:201:ILE:N	2.29	0.45
3:C:27:LYS:HA	3:C:30:ARG:HH12	1.81	0.45
3:C:152:ILE:HB	3:C:199:LYS:HB2	1.98	0.45
4:D:188:LEU:HD12	4:D:188:LEU:H	1.81	0.45
8:H:20:TYR:HE1	8:H:76:PRO:HG2	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:47:PHE:HD2	14:N:34:TYR:CE2	2.34	0.45
11:K:58:PRO:O	11:K:61:ALA:HB3	2.16	0.45
12:L:11:VAL:HG12	12:L:12:ARG:N	2.31	0.45
13:M:66:LEU:O	13:M:69:GLU:HG2	2.16	0.45
15:O:4:THR:CG2	15:O:5:LYS:N	2.76	0.45
15:O:61:GLY:O	15:O:65:ARG:HD2	2.17	0.45
15:O:78:TYR:CZ	15:O:82:ILE:HD12	2.51	0.45
17:Q:18:THR:HG23	17:Q:69:LYS:HD3	1.99	0.45
17:Q:59:ILE:HD12	17:Q:59:ILE:HA	1.59	0.45
17:Q:86:GLU:O	17:Q:87:LYS:C	2.60	0.45
18:R:53:ARG:HG3	18:R:63:GLN:NE2	2.31	0.45
1:A:101:A:N3	1:A:102:G:C8	2.85	0.45
1:A:411:A:N3	1:A:413:G:H1'	2.32	0.45
1:A:557:G:H5''	1:A:558:G:OP2	2.16	0.45
1:A:626:U:H2'	1:A:627:G:C8	2.51	0.45
1:A:933:G:OP1	7:G:4:ARG:HG3	2.17	0.45
1:A:1084:G:N2	29:A:2128:HOH:O	2.50	0.45
1:A:1319:A:H4'	1:A:1320:C:OP1	2.16	0.45
1:A:1400:5MC:O5'	1:A:1400:5MC:H6	2.00	0.45
1:A:1415:G:C6	1:A:1486:G:C6	3.04	0.45
1:A:1518[A]:MA6:H2'	1:A:1519[A]:MA6:H8	1.98	0.45
1:A:1519[A]:MA6:C3'	1:A:1520[A]:G:H5'	2.47	0.45
2:B:77:ALA:O	2:B:81:VAL:HG23	2.16	0.45
3:C:199:LYS:HB3	3:C:201:TYR:HE1	1.80	0.45
4:D:38:TYR:CD2	4:D:38:TYR:N	2.84	0.45
4:D:149:ALA:O	4:D:152:SER:HB2	2.15	0.45
5:E:144:THR:HB	5:E:146:ALA:HB3	1.98	0.45
9:I:37:PHE:HB3	9:I:43:ALA:HB2	1.99	0.45
13:M:6:GLY:O	13:M:7:VAL:C	2.59	0.45
13:M:74:VAL:HG23	13:M:75:ALA:N	2.31	0.45
14:N:27:CYS:SG	14:N:29:ARG:CB	2.86	0.45
16:P:67:THR:HB	16:P:70:ALA:H	1.80	0.45
17:Q:81:ARG:O	17:Q:81:ARG:CG	2.65	0.45
1:A:77:G:C2	1:A:93:G:C2	3.05	0.45
1:A:590:C:O2'	1:A:591:U:H5'	2.16	0.45
1:A:1003(A):G:N1	1:A:1004:A:H1'	2.32	0.45
1:A:1005:A:C8	1:A:1026:G:O6	2.70	0.45
1:A:1112:C:C2	3:C:178:LEU:HB2	2.51	0.45
1:A:1233:G:C2	1:A:1234:C:C4	3.05	0.45
1:A:1286:A:H3'	1:A:1286:A:H8	1.81	0.45
1:A:1288:A:C6	1:A:1289:A:C6	3.04	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:223:ILE:HD13	2:B:230:VAL:HG23	1.99	0.45
4:D:70:ILE:CG2	4:D:71:SER:O	2.59	0.45
4:D:119:GLN:HG3	4:D:123:HIS:CE1	2.51	0.45
6:F:97:PHE:HD2	6:F:98:LEU:N	2.14	0.45
7:G:150:ALA:HA	11:K:59:TYR:HD2	1.82	0.45
13:M:77:ASN:O	13:M:80:ARG:HB3	2.16	0.45
13:M:91:ARG:HH21	13:M:96:LEU:CB	2.30	0.45
14:N:12:ARG:H	14:N:12:ARG:NH1	2.13	0.45
14:N:14:PRO:O	14:N:15:LYS:CB	2.64	0.45
15:O:17:ARG:HD3	15:O:26:GLU:OE2	2.16	0.45
18:R:56:THR:HB	18:R:58:LEU:HD23	1.97	0.45
20:T:73:HIS:HB3	20:T:74:LYS:HG2	1.99	0.45
1:A:147:G:O2'	1:A:148:G:H5'	2.17	0.45
1:A:434:U:O2	1:A:434:U:H2'	2.14	0.45
1:A:646:U:H2'	1:A:647:C:C6	2.51	0.45
1:A:769:G:H2'	1:A:770:C:H5'	1.98	0.45
1:A:770:C:C2'	1:A:771:G:H5'	2.47	0.45
1:A:1003(A):G:C6	1:A:1004:A:H1'	2.51	0.45
1:A:1250:A:C6	1:A:1251:A:N1	2.84	0.45
1:A:1393:U:C6	1:A:1393:U:H3'	2.52	0.45
1:A:1494:G:C2	1:A:1495:U:C5	3.05	0.45
3:C:131:ARG:HH21	3:C:166:GLU:CD	2.25	0.45
4:D:92:VAL:O	4:D:95:GLY:N	2.49	0.45
4:D:102:ASP:OD1	4:D:102:ASP:N	2.48	0.45
14:N:27:CYS:HB3	14:N:43:CYS:SG	2.57	0.45
14:N:41:ARG:HG3	14:N:42:ILE:N	2.32	0.45
17:Q:47:PRO:CD	17:Q:48:GLU:H	2.30	0.45
18:R:25:THR:OG1	18:R:26:LEU:HD13	2.16	0.45
1:A:129:U:O3'	1:A:129(A):G:H3'	2.16	0.45
1:A:507:C:H3'	1:A:508:C:H2'	1.98	0.45
1:A:651:C:O2'	1:A:652:U:H5'	2.17	0.45
1:A:1112:C:H1'	3:C:179:ARG:HH11	1.82	0.45
1:A:1514:C:N4	1:A:1515[B]:C:H41	2.15	0.45
2:B:231:GLU:CB	2:B:232:PRO:HD2	2.30	0.45
6:F:61:LEU:HB3	6:F:63:TYR:HE2	1.81	0.45
10:J:63:PHE:H	10:J:63:PHE:HD1	1.60	0.45
11:K:20:TYR:HD2	11:K:83:ILE:HB	1.80	0.45
13:M:97:PRO:HB3	13:M:101:GLN:OE1	2.16	0.45
17:Q:43:LEU:HA	17:Q:43:LEU:HD23	1.27	0.45
20:T:8:ARG:HG3	20:T:9:ASN:HB3	1.99	0.45
20:T:78:ALA:O	20:T:79:ARG:C	2.59	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:79:ARG:HD2	20:T:83:ARG:HH12	1.82	0.45
1:A:401:C:O2'	1:A:621:A:N3	2.47	0.45
1:A:613:C:O2'	1:A:614:A:H5'	2.15	0.45
1:A:946:A:H2'	1:A:947:G:H8	1.79	0.45
1:A:1054:C:O2'	1:A:1056:U:OP2	2.32	0.45
1:A:1157:A:C4	1:A:1181:G:C2	3.05	0.45
1:A:1162:C:C2	1:A:1175:G:C2	3.05	0.45
1:A:1166:G:N2	1:A:1171:G:C6	2.85	0.45
1:A:1194:U:H5''	1:A:1195:C:OP2	2.17	0.45
1:A:1277:C:C1'	1:A:1282:C:H1'	2.46	0.45
1:A:1345:U:P	29:A:2503:HOH:O	2.74	0.45
1:A:1451:A:H8	1:A:1451:A:O5'	2.00	0.45
2:B:226:ARG:H	2:B:226:ARG:HG2	1.43	0.45
5:E:105:VAL:O	5:E:106:PRO:C	2.56	0.45
6:F:73:ASN:O	6:F:74:ASP:C	2.59	0.45
7:G:8:GLU:HG3	7:G:8:GLU:O	2.17	0.45
9:I:89:ASN:O	9:I:92:TYR:HB2	2.16	0.45
11:K:124:LYS:HE3	11:K:125:PHE:HE2	1.82	0.45
12:L:68:ALA:HB1	12:L:100:ILE:HD12	1.99	0.45
13:M:7:VAL:O	13:M:9:ILE:CD1	2.65	0.45
14:N:9:LYS:C	14:N:9:LYS:CD	2.89	0.45
19:S:52:TYR:CE2	19:S:54:GLY:CA	3.00	0.45
1:A:186:C:H5'	20:T:78:ALA:HB1	1.98	0.45
1:A:283:C:C2	1:A:284:G:C8	3.04	0.45
1:A:438:G:N2	1:A:496:A:C8	2.85	0.45
1:A:533:A:OP1	29:A:2170:HOH:O	2.21	0.45
1:A:582:U:H5''	15:O:64:ARG:HH21	1.82	0.45
1:A:1059:C:N3	1:A:1198:G:O6	2.50	0.45
1:A:1090:U:N3	1:A:1091:U:C5	2.84	0.45
1:A:1420:C:H2'	1:A:1421:G:H8	1.81	0.45
1:A:1442:G:N1	1:A:1446:A:N6	2.63	0.45
2:B:53:ARG:HA	2:B:56:ARG:HH12	1.80	0.45
2:B:197:VAL:HG11	2:B:200:ILE:HG13	1.99	0.45
3:C:46:GLU:HB3	3:C:47:LEU:CD1	2.42	0.45
3:C:84:ILE:CG2	3:C:85:ARG:N	2.80	0.45
3:C:90:GLU:H	3:C:90:GLU:HG3	1.57	0.45
4:D:204:ILE:N	4:D:204:ILE:HD12	2.32	0.45
7:G:69:VAL:O	7:G:69:VAL:CG1	2.63	0.45
7:G:120:ILE:H	7:G:120:ILE:CD1	2.16	0.45
11:K:14:VAL:HG12	11:K:15:ALA:N	2.32	0.45
13:M:49:THR:O	13:M:50:GLU:C	2.60	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:82:MET:HE3	13:M:82:MET:HB2	1.61	0.45
17:Q:10:VAL:CG2	17:Q:19:VAL:HB	2.47	0.45
17:Q:27:PHE:CZ	17:Q:36:ILE:HD11	2.52	0.45
18:R:56:THR:HB	18:R:58:LEU:CD2	2.47	0.45
1:A:503:C:OP2	12:L:116:SER:CB	2.63	0.45
1:A:677:U:C2'	1:A:678:U:H5'	2.47	0.45
1:A:713:G:N2	1:A:714:G:C2	2.85	0.45
1:A:741:G:H5''	15:O:39:LEU:HD11	1.98	0.45
1:A:895:G:C5	1:A:896:C:C5	3.05	0.45
1:A:1015:A:N3	1:A:1218:C:O2'	2.50	0.45
1:A:1029:C:H2'	1:A:1030:C:H5'	1.98	0.45
1:A:1110:A:C8	29:A:2140:HOH:O	2.69	0.45
1:A:1248:A:C6	1:A:1249:C:N4	2.85	0.45
2:B:68:ILE:O	2:B:90:MET:HB3	2.16	0.45
2:B:196:LEU:H	2:B:196:LEU:HG	1.28	0.45
4:D:63:LYS:O	4:D:67:ILE:CD1	2.63	0.45
5:E:122:GLU:C	5:E:123:LEU:HD23	2.41	0.45
11:K:34:ASP:HB2	11:K:35:PRO:CD	2.45	0.45
11:K:114:VAL:HG22	11:K:115:PRO:O	2.17	0.45
1:A:44:G:H2'	1:A:45:U:O4'	2.17	0.44
1:A:306:G:H2'	1:A:307:C:H6	1.82	0.44
1:A:355:C:C5'	1:A:389:A:OP2	2.65	0.44
1:A:1003(A):G:N1	1:A:1038:C:C2	2.77	0.44
1:A:1130:A:H3'	1:A:1130:A:OP2	2.17	0.44
1:A:1201:A:H4'	1:A:1202:G:C5'	2.46	0.44
1:A:1303:C:O2	1:A:1303:C:C2'	2.56	0.44
1:A:1313:U:H5	19:S:4:SER:HB2	1.81	0.44
1:A:1314:C:OP2	19:S:6:LYS:CG	2.65	0.44
2:B:46:LYS:O	2:B:47:THR:C	2.59	0.44
2:B:57:PHE:CD1	2:B:199:TYR:CE1	3.05	0.44
2:B:224:GLN:OE1	2:B:229:VAL:HG22	2.16	0.44
3:C:53:ALA:C	3:C:54:ARG:HG3	2.42	0.44
5:E:20:GLN:O	5:E:21:ALA:C	2.59	0.44
5:E:37:ARG:HA	5:E:114:GLY:CA	2.47	0.44
7:G:103:TRP:HE1	7:G:137:LYS:HE2	1.82	0.44
8:H:56:LYS:HB3	8:H:57:PRO:HD2	2.00	0.44
8:H:88:LYS:O	8:H:89:PRO:C	2.55	0.44
8:H:121:ASP:O	8:H:122:ARG:C	2.60	0.44
9:I:10:ARG:O	9:I:11:LYS:C	2.60	0.44
13:M:10:PRO:HB3	13:M:18:ALA:O	2.17	0.44
17:Q:10:VAL:O	17:Q:10:VAL:CG1	2.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:62:ILE:HA	19:S:66:MET:HE1	1.98	0.44
24:a:38:A:H2'	24:a:38:A:N3	2.33	0.44
1:A:42:G:C2	1:A:43:C:C2	3.05	0.44
1:A:55:A:C2	1:A:56:U:H1'	2.51	0.44
1:A:400:C:N4	1:A:401:C:N4	2.65	0.44
1:A:427:U:O2'	1:A:541:G:OP1	2.31	0.44
1:A:784:C:C2'	1:A:785:G:O5'	2.65	0.44
1:A:1052:U:O4	1:A:1200:C:C2	2.70	0.44
1:A:1053:G:C4'	1:A:1054:C:H5'	2.47	0.44
1:A:1054:C:N3	23:W:34:G:P	2.91	0.44
1:A:1507:A:C4	1:A:1530:G:C2	3.05	0.44
4:D:11:LEU:O	4:D:12:CYS:C	2.60	0.44
5:E:98:THR:HB	5:E:117:ASP:HB3	1.98	0.44
8:H:104:ARG:HD2	8:H:138:TRP:CD2	2.53	0.44
9:I:28:VAL:HA	9:I:63:ILE:HG22	1.99	0.44
11:K:86:GLY:H	11:K:112:THR:HG23	1.81	0.44
13:M:22:ILE:HD13	13:M:22:ILE:H	1.82	0.44
16:P:4:ILE:HG12	16:P:21:VAL:HG22	1.99	0.44
16:P:20:VAL:HG13	16:P:32:TYR:HD2	1.82	0.44
19:S:41:VAL:CG2	19:S:43:GLU:OE2	2.65	0.44
23:W:36:A:H2'	23:W:36:A:N3	2.33	0.44
23:W:39:G:N2	23:W:40:PSU:C4	2.86	0.44
1:A:1004:A:O2'	1:A:1005:A:OP1	2.27	0.44
1:A:1055:A:N1	1:A:1056:U:H1'	2.32	0.44
1:A:1291:G:H8	1:A:1291:G:O5'	2.00	0.44
7:G:59:LEU:O	7:G:62:PHE:HB3	2.17	0.44
7:G:113:GLU:O	7:G:119:ARG:HD3	2.17	0.44
13:M:19:LEU:HD23	13:M:19:LEU:HA	1.48	0.44
13:M:115:LYS:HE2	13:M:115:LYS:HB2	1.72	0.44
14:N:24:CYS:SG	14:N:40:CYS:N	2.83	0.44
17:Q:56:VAL:O	17:Q:76:LEU:HD12	2.17	0.44
20:T:42:GLN:OE1	20:T:42:GLN:HA	2.17	0.44
1:A:229:U:H2'	1:A:230:G:C5'	2.41	0.44
1:A:256:U:C2'	1:A:257:G:H5'	2.48	0.44
1:A:514:C:C2'	1:A:515:G:H5'	2.47	0.44
1:A:616:G:C2'	1:A:617:G:H5'	2.47	0.44
1:A:629:G:H2'	1:A:630:G:O4'	2.17	0.44
1:A:681:C:C2	1:A:682:G:C8	3.06	0.44
1:A:925:G:C1'	1:A:1502:A:C8	3.01	0.44
1:A:1014:A:C5	1:A:1015:A:C6	3.06	0.44
1:A:1347:G:H2'	1:A:1348:U:OP2	2.15	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1403:C:O2'	1:A:1404:5MC:C5'	2.61	0.44
1:A:1488:G:H2'	1:A:1489:G:H8	1.83	0.44
1:A:1493[A]:A:H2	23:W:36:A:HO2'	1.64	0.44
2:B:76:GLN:O	2:B:208:ILE:HD11	2.16	0.44
2:B:139:LYS:HD2	2:B:139:LYS:HA	1.72	0.44
3:C:69:HIS:HA	3:C:104:GLN:O	2.17	0.44
5:E:148:VAL:O	5:E:152:ARG:HG3	2.18	0.44
8:H:4:ASP:OD2	8:H:85:ARG:CZ	2.64	0.44
10:J:19:SER:HA	10:J:22:LYS:HB3	1.99	0.44
11:K:54:ARG:O	11:K:57:THR:OG1	2.35	0.44
16:P:6:LEU:HD23	16:P:17:TYR:CB	2.47	0.44
16:P:57:ARG:HD3	16:P:79:VAL:O	2.18	0.44
18:R:47:THR:CG2	18:R:48:GLY:N	2.76	0.44
1:A:176:C:C2'	1:A:177:C:H5'	2.46	0.44
1:A:440:A:C8	1:A:442:C:C6	3.05	0.44
1:A:444:C:N4	1:A:490:G:H1	2.12	0.44
1:A:448:A:C4	1:A:449:C:C5	3.05	0.44
1:A:778:G:H2'	1:A:779:C:C5'	2.48	0.44
1:A:815:A:O2'	1:A:1527:C:H1'	2.18	0.44
1:A:862:C:H5''	29:A:2609:HOH:O	2.16	0.44
1:A:868:C:C2'	1:A:869:G:O5'	2.63	0.44
1:A:942:G:N3	1:A:942:G:H2'	2.31	0.44
1:A:1126:U:P	1:A:1126:U:H6	2.40	0.44
1:A:1126:U:H3	1:A:1127:G:N2	2.15	0.44
1:A:1227:A:H2'	1:A:1228:C:O5'	2.18	0.44
1:A:1347:G:C6	9:I:107:ARG:NH1	2.85	0.44
1:A:1394:A:C6	1:A:1501:C:H4'	2.53	0.44
1:A:1518[A]:MA6:N6	1:A:1519[A]:MA6:H103	2.33	0.44
1:A:1519[B]:MA6:H93	1:A:1520[B]:G:N2	2.32	0.44
4:D:190:ASP:O	4:D:194:LEU:HD23	2.17	0.44
5:E:36:ASP:OD2	5:E:38:GLN:HB2	2.18	0.44
8:H:10:LEU:HD22	8:H:10:LEU:HA	1.52	0.44
9:I:64:THR:HG23	9:I:66:ARG:CZ	2.47	0.44
9:I:97:LYS:HD2	9:I:97:LYS:O	2.18	0.44
13:M:67:GLU:HB3	13:M:68:GLY:H	1.20	0.44
1:A:73:C:N4	1:A:74:C:H41	2.15	0.44
1:A:108:G:N3	1:A:108:G:H5'	2.33	0.44
1:A:155:C:C2	1:A:167:G:C2	3.06	0.44
1:A:532:A:H61	1:A:1207:2MG:C5'	2.30	0.44
1:A:540:G:H2'	1:A:541:G:O4'	2.18	0.44
1:A:630:G:H3'	1:A:631:G:H5''	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1027:C:H5	1:A:1035:A:C2	2.36	0.44
1:A:1088:G:H2'	1:A:1089:G:H5'	2.00	0.44
1:A:1245:A:C2	1:A:1293:G:N3	2.86	0.44
1:A:1346:A:N3	7:G:10:ARG:NH1	2.66	0.44
1:A:1350:A:C4	1:A:1351:U:C6	3.06	0.44
1:A:1437:C:O2	1:A:1437:C:H2'	2.17	0.44
3:C:7:PRO:CB	3:C:11:ARG:HH21	2.30	0.44
3:C:28:GLN:O	3:C:29:TYR:C	2.61	0.44
3:C:157:ILE:C	3:C:159:GLY:N	2.75	0.44
4:D:158:ILE:HD13	4:D:158:ILE:HA	1.88	0.44
4:D:190:ASP:O	4:D:191:ARG:C	2.61	0.44
6:F:91:VAL:HG12	6:F:92:LYS:O	2.17	0.44
8:H:102:ARG:N	8:H:102:ARG:CD	2.64	0.44
9:I:40:LEU:HD13	9:I:40:LEU:HA	1.56	0.44
10:J:50:ILE:N	10:J:50:ILE:CD1	2.80	0.44
10:J:85:LEU:HB3	10:J:86:MET:H	1.61	0.44
18:R:76:LEU:HD23	18:R:76:LEU:HA	1.38	0.44
1:A:54:C:C2	1:A:352:C:H5	2.36	0.44
1:A:77:G:H2'	1:A:78:G:O5'	2.18	0.44
1:A:154:C:H2'	1:A:155:C:H5'	1.99	0.44
1:A:428:G:C1'	1:A:429:U:OP2	2.65	0.44
1:A:433:C:C2	1:A:434:U:C5	3.02	0.44
1:A:521:G:O2'	1:A:522:C:H5'	2.17	0.44
1:A:595:G:C2	1:A:641:U:C2	3.05	0.44
1:A:1113:C:O5'	1:A:1113:C:H6	2.01	0.44
1:A:1347:G:O2'	1:A:1348:U:O5'	2.36	0.44
2:B:178:ARG:O	8:H:71:GLY:HA2	2.18	0.44
2:B:228:GLY:O	2:B:229:VAL:C	2.61	0.44
3:C:48:TYR:CD2	3:C:48:TYR:C	2.96	0.44
3:C:125:GLU:C	3:C:127:ARG:H	2.24	0.44
4:D:62:GLN:HB3	4:D:66:ARG:NH1	2.32	0.44
4:D:114:ARG:HG3	4:D:114:ARG:NH1	2.33	0.44
5:E:90:VAL:O	5:E:120:THR:HA	2.17	0.44
5:E:112:LEU:C	5:E:114:GLY:H	2.25	0.44
7:G:15:ASP:OD2	7:G:44:TYR:OH	2.35	0.44
9:I:49:PRO:HG3	9:I:101:PHE:HD1	1.82	0.44
20:T:26:ASN:O	20:T:27:LYS:C	2.61	0.44
20:T:84:LEU:C	20:T:84:LEU:CD2	2.90	0.44
1:A:21:G:H2'	1:A:22:G:H8	1.78	0.44
1:A:277:C:O2'	1:A:278:G:H5'	2.18	0.44
1:A:510:A:H1'	1:A:543:C:O4'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:653:A:OP1	8:H:56:LYS:CE	2.66	0.44
1:A:710:G:N7	29:A:2472:HOH:O	2.36	0.44
1:A:960:U:H1'	1:A:1223:C:H5'	1.99	0.44
1:A:1112:C:N3	3:C:178:LEU:HB2	2.32	0.44
1:A:1516[A]:G:H2'	1:A:1518[A]:MA6:OP2	2.17	0.44
1:A:1527:C:H2'	1:A:1528:U:H5'	1.98	0.44
2:B:30:ARG:HD2	2:B:31:TYR:CZ	2.53	0.44
8:H:120:THR:O	8:H:121:ASP:C	2.59	0.44
13:M:108:ARG:HH21	13:M:114:ARG:HA	1.81	0.44
16:P:60:LEU:HA	16:P:60:LEU:HD23	1.34	0.44
1:A:89:C:O2'	1:A:90:U:H5'	2.17	0.44
1:A:236:G:H2'	1:A:237:C:O4'	2.18	0.44
1:A:594:G:C2'	1:A:595:G:H5'	2.47	0.44
1:A:886:G:H1	1:A:911:U:H3	1.66	0.44
1:A:1003(A):G:C2	1:A:1004:A:H1'	2.53	0.44
1:A:1271:G:H2'	1:A:1272:G:H8	1.83	0.44
2:B:77:ALA:O	2:B:78:GLN:C	2.59	0.44
2:B:92:TYR:CE1	2:B:151:GLY:CA	3.00	0.44
2:B:168:THR:HG22	2:B:169:LYS:N	2.33	0.44
3:C:73:PRO:HD3	3:C:105:GLU:HB2	1.99	0.44
5:E:43:LEU:HD12	5:E:43:LEU:O	2.18	0.44
5:E:51:VAL:CB	5:E:52:PRO:HD3	2.48	0.44
6:F:76:ALA:O	6:F:77:ARG:C	2.60	0.44
8:H:116:LYS:HD2	8:H:129:VAL:HG11	2.00	0.44
9:I:9:ARG:HA	9:I:76:ALA:HB1	2.00	0.44
14:N:5:ALA:O	14:N:8:GLU:HG3	2.18	0.44
16:P:4:ILE:HB	16:P:66:PRO:HA	1.99	0.44
20:T:92:LEU:N	20:T:92:LEU:HD23	2.33	0.44
1:A:102:G:O2'	1:A:151:A:N3	2.39	0.43
1:A:285:G:O6	29:A:2039:HOH:O	2.20	0.43
1:A:956:U:C2	1:A:1225:A:C2	3.06	0.43
1:A:1111:A:N1	3:C:177:THR:OG1	2.49	0.43
1:A:1124:G:C2'	1:A:1145:C:C5	3.01	0.43
1:A:1250:A:H4'	9:I:68:GLY:N	2.33	0.43
1:A:1401:G:C5	1:A:1402:4OC:C5	3.01	0.43
1:A:1436:U:H2'	1:A:1437:C:C6	2.47	0.43
3:C:34:LEU:HD13	14:N:25:VAL:CG2	2.48	0.43
4:D:70:ILE:HD13	4:D:70:ILE:HA	1.79	0.43
4:D:101:LEU:O	4:D:101:LEU:HG	2.17	0.43
5:E:33:VAL:CG1	5:E:34:VAL:N	2.80	0.43
8:H:36:LEU:H	8:H:36:LEU:HG	1.65	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:47:PHE:CD2	14:N:34:TYR:HD2	2.36	0.43
10:J:99:LYS:HD2	10:J:99:LYS:H	1.83	0.43
11:K:122:LYS:C	11:K:124:LYS:N	2.74	0.43
15:O:26:GLU:CD	15:O:77:ARG:HH11	2.22	0.43
16:P:78:GLY:O	16:P:79:VAL:C	2.60	0.43
18:R:36:ASN:O	18:R:40:LEU:HG	2.18	0.43
21:U:21:TYR:N	21:U:21:TYR:CD1	2.86	0.43
24:a:35:G:C2'	24:a:36:A:H8	2.27	0.43
1:A:81:U:C5'	1:A:82:U:OP2	2.66	0.43
1:A:1004:A:N6	1:A:1037:C:N4	2.66	0.43
1:A:1071:C:H42	1:A:1104:G:H1	1.66	0.43
1:A:1255:G:C2	1:A:1283:G:C2	3.06	0.43
1:A:1465:C:C5	1:A:1466:C:C5	3.06	0.43
1:A:1537:U:H2'	1:A:1538:C:N1	2.33	0.43
2:B:114:ARG:NE	2:B:118:LEU:HD21	2.33	0.43
3:C:114:PRO:O	3:C:118:GLN:HG3	2.18	0.43
5:E:89:ILE:HD12	5:E:90:VAL:H	1.82	0.43
8:H:20:TYR:CE1	8:H:76:PRO:CD	3.00	0.43
8:H:63:LEU:HD13	8:H:63:LEU:HA	1.53	0.43
9:I:37:PHE:CE2	9:I:74:ILE:HD11	2.52	0.43
10:J:12:ASP:OD2	10:J:12:ASP:C	2.61	0.43
12:L:39:VAL:HG23	12:L:57:LYS:HB3	1.99	0.43
13:M:87:TYR:C	13:M:87:TYR:HD1	2.26	0.43
14:N:29:ARG:HG2	14:N:40:CYS:HB3	2.00	0.43
16:P:4:ILE:O	16:P:66:PRO:HA	2.18	0.43
20:T:10:LEU:HD23	20:T:10:LEU:O	2.18	0.43
1:A:134:A:H2'	1:A:135:C:O4'	2.18	0.43
1:A:1242:C:H4'	1:A:1304:G:OP1	2.17	0.43
1:A:1342:C:O2'	1:A:1343:G:H5'	2.18	0.43
1:A:1502:A:H2	1:A:1505:G:H1	1.66	0.43
2:B:98:LEU:HB2	2:B:101:MET:SD	2.59	0.43
3:C:62:ASP:HA	3:C:97:LYS:HZ2	1.82	0.43
6:F:90:VAL:HG12	6:F:91:VAL:N	2.33	0.43
13:M:99:ARG:CB	13:M:101:GLN:HE22	2.31	0.43
18:R:40:LEU:O	18:R:41:LYS:C	2.59	0.43
18:R:59:SER:O	18:R:60:ALA:C	2.60	0.43
19:S:44:MET:HB2	19:S:62:ILE:CD1	2.48	0.43
1:A:537:G:C2	1:A:538:G:C5	3.06	0.43
1:A:644:G:C8	1:A:644:G:C4'	3.02	0.43
1:A:707:C:H4'	11:K:20:TYR:HD1	1.74	0.43
1:A:949:A:N1	1:A:1233:G:C4	2.86	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:986:A:O2'	19:S:55:LYS:O	2.35	0.43
1:A:1148:U:O3'	9:I:14:VAL:HG11	2.19	0.43
1:A:1163:C:C6	1:A:1163:C:C3'	3.02	0.43
1:A:1225:A:C5'	1:A:1226:C:OP2	2.58	0.43
1:A:1332:A:C2	1:A:1333:A:N9	2.86	0.43
1:A:1407:5MC:O2'	1:A:1408:A:H5'	2.18	0.43
3:C:37:GLN:OE1	14:N:47:LEU:CD2	2.66	0.43
4:D:104:VAL:O	4:D:105:VAL:C	2.59	0.43
7:G:51:GLN:HB2	7:G:52:GLU:OE1	2.18	0.43
8:H:45:ILE:HG13	8:H:47:GLY:N	2.34	0.43
8:H:127:LEU:O	8:H:127:LEU:CD2	2.65	0.43
10:J:4:ILE:HD12	10:J:5:ARG:N	2.32	0.43
11:K:19:ALA:HA	11:K:32:ILE:HD13	2.00	0.43
11:K:110:ASP:N	18:R:85:LEU:O	2.39	0.43
12:L:48:PRO:CG	12:L:92:0TD:H3	2.49	0.43
13:M:63:THR:HG23	13:M:64:TRP:H	1.84	0.43
13:M:78:ILE:O	13:M:81:LEU:HB2	2.19	0.43
13:M:99:ARG:HB2	13:M:101:GLN:NE2	2.32	0.43
15:O:82:ILE:HG22	15:O:83:GLU:N	2.34	0.43
18:R:43:PHE:HE2	18:R:58:LEU:HD21	1.83	0.43
20:T:33:ILE:O	20:T:34:LYS:C	2.60	0.43
20:T:44:ALA:O	20:T:46:GLU:N	2.51	0.43
1:A:231:G:C2	1:A:232:G:C8	3.06	0.43
1:A:353:A:H5'	1:A:353:A:C8	2.50	0.43
1:A:778:G:C6	1:A:779:C:N3	2.87	0.43
1:A:1082:G:H2'	1:A:1083:U:C5'	2.49	0.43
1:A:1166:G:N2	1:A:1171:G:C5	2.86	0.43
1:A:1168:A:C6	1:A:1169:A:C6	3.07	0.43
1:A:1221:G:C4	1:A:1222:G:C8	3.06	0.43
1:A:1515[B]:C:C4	1:A:1520[B]:G:O6	2.69	0.43
1:A:1526:G:C2'	1:A:1527:C:H5'	2.48	0.43
2:B:44:LEU:H	2:B:44:LEU:CD2	2.25	0.43
2:B:79:ASP:O	2:B:80:ILE:C	2.61	0.43
3:C:78:GLY:HA3	3:C:83:ARG:CB	2.48	0.43
3:C:111:LEU:N	3:C:111:LEU:HD23	2.33	0.43
4:D:79:PHE:O	4:D:80:GLU:C	2.62	0.43
6:F:35:ALA:CB	6:F:67:MET:HB3	2.49	0.43
7:G:65:ALA:O	7:G:66:VAL:C	2.60	0.43
8:H:9:MET:HG3	8:H:26:VAL:HG21	2.01	0.43
9:I:47:LEU:HA	9:I:47:LEU:HD23	1.59	0.43
10:J:97:GLU:HG2	10:J:99:LYS:HE2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:36:ILE:HA	15:O:59:MET:CE	2.49	0.43
17:Q:4:LYS:HG3	17:Q:6:LEU:HD21	1.98	0.43
20:T:44:ALA:HA	20:T:92:LEU:CD2	2.43	0.43
1:A:90:U:C2'	1:A:91:C:O5'	2.66	0.43
1:A:132:C:H2'	1:A:133:U:H5'	2.01	0.43
1:A:360:A:C6	1:A:361:G:C6	3.06	0.43
1:A:448:A:C2	1:A:449:C:C5	3.06	0.43
1:A:484:G:C2'	1:A:485:G:OP2	2.66	0.43
1:A:925:G:C2	1:A:927:G:C8	3.07	0.43
1:A:1039:C:N3	1:A:1040:U:C4	2.86	0.43
1:A:1054:C:OP1	1:A:1197:G:P	2.76	0.43
1:A:1132:C:C6	1:A:1132:C:H3'	2.52	0.43
1:A:1351:U:C2'	1:A:1352:C:H5'	2.48	0.43
2:B:145:LEU:HD23	2:B:145:LEU:HA	1.85	0.43
2:B:155:LEU:HD22	2:B:157:ARG:O	2.19	0.43
3:C:135:LYS:NZ	5:E:50:GLU:HG2	2.34	0.43
4:D:173:TRP:HE3	4:D:173:TRP:H	1.64	0.43
5:E:13:ILE:HA	5:E:29:GLY:O	2.19	0.43
7:G:54:THR:HG22	7:G:56:GLN:H	1.84	0.43
9:I:126:SER:O	9:I:128:ARG:N	2.52	0.43
10:J:40:LEU:CB	10:J:69:ASN:HB2	2.39	0.43
20:T:41:ILE:N	20:T:41:ILE:CD1	2.82	0.43
20:T:99:LEU:CD1	20:T:100:ILE:H	2.32	0.43
1:A:77:G:N2	1:A:78:G:C4	2.86	0.43
1:A:236:G:C6	1:A:237:C:C2	3.06	0.43
1:A:397:A:C6	1:A:548:G:C8	3.07	0.43
1:A:443:C:N3	1:A:491:G:N2	2.58	0.43
1:A:652:U:O4	1:A:752:G:O2'	2.29	0.43
1:A:909:A:H2'	1:A:910:C:O4'	2.18	0.43
1:A:1360:A:HO2'	1:A:1361:G:P	2.42	0.43
1:A:1501:C:C4	1:A:1504:G:C2	3.07	0.43
1:A:1517[B]:G:H2'	1:A:1518[B]:MA6:H8	2.00	0.43
1:A:1521:G:C2	1:A:1522:U:C2	3.07	0.43
2:B:223:ILE:HD13	2:B:230:VAL:CG2	2.49	0.43
3:C:142:MET:HE3	3:C:142:MET:CA	2.49	0.43
4:D:24:GLU:O	4:D:25:ARG:CB	2.67	0.43
4:D:78:LEU:HA	4:D:78:LEU:HD23	1.81	0.43
4:D:96:LEU:O	4:D:97:LEU:C	2.60	0.43
5:E:76:ILE:HA	5:E:77:PRO:HD3	1.89	0.43
5:E:121:LYS:CG	5:E:123:LEU:CD2	2.96	0.43
5:E:139:LEU:HA	5:E:139:LEU:HD23	1.62	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:66:PRO:C	16:P:67:THR:O	2.59	0.43
1:A:78:G:C6	1:A:79:G:C8	3.06	0.43
1:A:234:C:H2'	1:A:235:C:H6	1.83	0.43
1:A:702:A:OP2	29:A:2798:HOH:O	2.21	0.43
1:A:848:C:C6	1:A:848:C:H3'	2.53	0.43
1:A:1032:G:C4	1:A:1033:G:C8	3.06	0.43
1:A:1048:G:H5''	14:N:3:ARG:HG3	2.01	0.43
1:A:1053:G:O3'	1:A:1054:C:H4'	2.18	0.43
1:A:1056:U:H2'	1:A:1057:G:H8	1.84	0.43
1:A:1126:U:C4	1:A:1127:G:N2	2.87	0.43
1:A:1480:G:C4	1:A:1481:U:C5	3.07	0.43
2:B:56:ARG:HB2	2:B:56:ARG:HH11	1.82	0.43
2:B:83:MET:O	2:B:84:GLU:C	2.60	0.43
2:B:208:ILE:O	2:B:209:ARG:C	2.61	0.43
3:C:72:LYS:C	3:C:74:GLY:H	2.27	0.43
3:C:136:GLN:O	3:C:137:ALA:C	2.61	0.43
3:C:156:ARG:NE	3:C:160:ALA:O	2.51	0.43
4:D:7:PRO:HG2	4:D:10:ARG:HD2	2.00	0.43
4:D:28:SER:O	4:D:30:LYS:N	2.41	0.43
6:F:46:ARG:HE	6:F:46:ARG:HB3	1.59	0.43
7:G:65:ALA:HB2	7:G:128:ALA:CA	2.49	0.43
7:G:125:MET:HE2	7:G:125:MET:HB3	1.83	0.43
7:G:148:ASN:C	7:G:150:ALA:H	2.26	0.43
10:J:45:ARG:HH11	14:N:36:PHE:HE2	1.65	0.43
12:L:90:VAL:HG11	12:L:93:LEU:HG	1.99	0.43
1:A:46:G:C2	1:A:396:G:C2	3.06	0.43
1:A:93:G:O2'	1:A:95:U:H5'	2.19	0.43
1:A:680:C:H2'	1:A:681:C:H6	1.82	0.43
1:A:988:G:N2	1:A:1218:C:O2	2.51	0.43
1:A:1287:A:C6	1:A:1288:A:C6	3.07	0.43
1:A:1298:C:OP2	7:G:114:ARG:NH2	2.51	0.43
1:A:1478:C:H2'	1:A:1479:C:H6	1.84	0.43
1:A:1519[A]:MA6:C2'	1:A:1520[A]:G:H5'	2.49	0.43
2:B:43:ASP:OD2	2:B:46:LYS:HB2	2.19	0.43
3:C:33:LEU:HD11	14:N:53:LEU:HA	2.01	0.43
7:G:62:PHE:C	7:G:62:PHE:HD1	2.24	0.43
8:H:20:TYR:CE1	8:H:76:PRO:CG	3.02	0.43
12:L:104:VAL:O	12:L:105:TYR:HB2	2.19	0.43
14:N:11:LYS:HG3	14:N:13:THR:OG1	2.19	0.43
17:Q:74:LEU:C	17:Q:74:LEU:CD2	2.92	0.43
20:T:41:ILE:O	20:T:42:GLN:C	2.59	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:57:G:C2	1:A:58:C:C2	3.07	0.43
1:A:77:G:C2'	1:A:78:G:O5'	2.67	0.43
1:A:110:C:N4	1:A:111:G:C6	2.87	0.43
1:A:266:G:C8	1:A:266:G:C4'	3.01	0.43
1:A:284:G:C4	1:A:285:G:C8	3.07	0.43
1:A:702:A:H3'	1:A:703:G:C5'	2.49	0.43
1:A:1135:U:N3	1:A:1137:C:O2	2.52	0.43
1:A:1326:C:P	21:U:6:ARG:HD3	2.59	0.43
1:A:1472:U:C2'	1:A:1473:A:O5'	2.67	0.43
2:B:11:LEU:CD1	2:B:11:LEU:H	2.31	0.43
3:C:6:HIS:HE1	14:N:50:LYS:HE2	1.83	0.43
3:C:21:ARG:HG2	3:C:21:ARG:O	2.18	0.43
3:C:178:LEU:C	3:C:180:ALA:N	2.73	0.43
5:E:69:VAL:HG21	5:E:113:ALA:HB1	2.01	0.43
5:E:135:THR:O	5:E:138:ALA:HB3	2.18	0.43
6:F:97:PHE:HE1	18:R:61:LYS:HE2	1.84	0.43
8:H:36:LEU:HA	8:H:39:LEU:CD2	2.49	0.43
9:I:16:ARG:CD	9:I:64:THR:HG22	2.49	0.43
11:K:53:SER:O	11:K:55:LYS:N	2.51	0.43
13:M:94:ARG:H	13:M:94:ARG:HG2	1.54	0.43
15:O:26:GLU:OE1	15:O:77:ARG:HB2	2.18	0.43
15:O:78:TYR:CZ	15:O:82:ILE:CD1	3.01	0.43
18:R:78:LEU:N	18:R:78:LEU:CD2	2.79	0.43
18:R:78:LEU:N	18:R:78:LEU:HD23	2.34	0.43
19:S:15:LEU:HD13	19:S:16:LEU:H	1.82	0.43
20:T:60:GLU:O	20:T:63:ILE:HB	2.18	0.43
24:a:36:A:C6	24:a:37:A:C6	3.07	0.43
1:A:54:C:C5	1:A:352:C:H5	2.35	0.42
1:A:81:U:C6	1:A:81:U:C3'	3.02	0.42
1:A:248:C:O2'	1:A:249:U:H5'	2.19	0.42
1:A:497:A:H4'	1:A:498:U:OP2	2.19	0.42
1:A:942:G:C2	1:A:943:U:C6	3.07	0.42
1:A:976:G:N7	1:A:1358:U:N3	2.67	0.42
1:A:995:C:C2'	1:A:996:A:H5'	2.49	0.42
1:A:1126:U:OP1	1:A:1126:U:C6	2.71	0.42
1:A:1501:C:C4	1:A:1504:G:N3	2.87	0.42
2:B:61:LEU:HD13	2:B:66:GLY:CA	2.41	0.42
3:C:84:ILE:HG12	3:C:88:ARG:NH2	2.32	0.42
3:C:156:ARG:HB3	3:C:196:LEU:HD21	2.01	0.42
4:D:62:GLN:OE1	4:D:62:GLN:HA	2.19	0.42
5:E:148:VAL:HG23	5:E:148:VAL:H	1.31	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:113:GLU:H	7:G:113:GLU:HG2	1.32	0.42
10:J:6:ILE:O	10:J:72:VAL:HG23	2.19	0.42
10:J:90:LEU:HD22	10:J:90:LEU:N	2.34	0.42
11:K:57:THR:O	11:K:60:ALA:HB3	2.18	0.42
11:K:124:LYS:HG2	11:K:125:PHE:CE2	2.55	0.42
13:M:37:THR:HG23	13:M:39:ILE:HD12	2.01	0.42
1:A:106:C:O2'	1:A:107:G:H5'	2.19	0.42
1:A:134:A:H62	16:P:25:ARG:HH21	1.67	0.42
1:A:397:A:H5'	1:A:398:C:OP1	2.19	0.42
1:A:826:C:H2'	1:A:827:U:H6	1.84	0.42
1:A:1053:G:C3'	1:A:1054:C:H5'	2.48	0.42
1:A:1126:U:N3	1:A:1127:G:C2	2.87	0.42
1:A:1190:G:O3'	3:C:3:ASN:HB2	2.19	0.42
1:A:1508:G:C5	1:A:1509:C:C5	3.07	0.42
3:C:87:LEU:C	3:C:89:GLU:N	2.77	0.42
3:C:109:PRO:HA	3:C:115:LEU:HD12	2.01	0.42
5:E:43:LEU:O	5:E:65:ASN:ND2	2.52	0.42
6:F:14:LEU:HD22	6:F:14:LEU:HA	1.70	0.42
7:G:39:ALA:O	7:G:40:ALA:C	2.63	0.42
7:G:47:CYS:O	7:G:48:LYS:C	2.62	0.42
8:H:33:GLU:O	8:H:34:GLU:C	2.60	0.42
8:H:100:ILE:HA	8:H:101:PRO:HD2	1.57	0.42
11:K:58:PRO:HB2	11:K:93:GLN:HG3	2.01	0.42
12:L:100:ILE:HD12	12:L:100:ILE:N	2.34	0.42
20:T:8:ARG:CG	20:T:9:ASN:HB3	2.50	0.42
23:W:37:A:C6	23:W:38:A:N1	2.87	0.42
1:A:245:C:C6	1:A:284:G:N2	2.87	0.42
1:A:731:G:O2'	1:A:732:C:H5'	2.19	0.42
1:A:792:A:C6	1:A:794:A:C2	3.07	0.42
1:A:1052:U:O2'	1:A:1055:A:OP1	2.38	0.42
1:A:1092:A:C4'	1:A:1092:A:C8	3.02	0.42
1:A:1193:G:C4	1:A:1194:U:C5	3.08	0.42
1:A:1321:C:C5'	13:M:87:TYR:CE2	3.02	0.42
1:A:1341:U:O2'	1:A:1342:C:H5'	2.19	0.42
1:A:1437:C:C2	1:A:1438:G:C8	3.07	0.42
1:A:1480:G:C5	1:A:1481:U:C5	3.07	0.42
2:B:172:ILE:H	2:B:172:ILE:CD1	2.32	0.42
3:C:16:ARG:NH1	3:C:16:ARG:CG	2.78	0.42
3:C:203:PHE:C	3:C:203:PHE:CD1	2.96	0.42
8:H:27:PRO:HB3	8:H:58:TYR:CE2	2.54	0.42
11:K:96:ARG:O	11:K:97:ALA:C	2.62	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:15:PHE:CD1	15:O:15:PHE:N	2.86	0.42
16:P:39:TYR:CG	16:P:73:LEU:HD11	2.54	0.42
17:Q:31:LEU:HD12	17:Q:31:LEU:HA	1.44	0.42
20:T:75:ASN:OD1	20:T:75:ASN:N	2.52	0.42
23:W:39:G:C2	23:W:40:PSU:C4	3.07	0.42
1:A:518:C:O3'	12:L:50:SER:HB3	2.19	0.42
1:A:833:U:H2'	1:A:834:C:C6	2.53	0.42
1:A:903:G:H2'	1:A:904:C:H6	1.85	0.42
1:A:925:G:O4'	1:A:1502:A:C5	2.72	0.42
1:A:961:U:H2'	1:A:962:C:H5'	2.01	0.42
1:A:1026:G:HO2'	1:A:1027:C:P	2.23	0.42
1:A:1104:G:P	2:B:111:ARG:HD2	2.60	0.42
1:A:1221:G:C6	1:A:1222:G:N7	2.87	0.42
1:A:1263:C:N4	1:A:1264:C:H41	2.17	0.42
1:A:1367:C:C2	1:A:1368:G:C8	3.08	0.42
1:A:1503:A:H5'	1:A:1531:A:H1'	2.01	0.42
2:B:36:ARG:CB	2:B:41:ILE:HD11	2.48	0.42
3:C:88:ARG:HB2	3:C:101:LEU:CD2	2.49	0.42
4:D:173:TRP:O	4:D:186:LEU:HG	2.19	0.42
4:D:192:GLU:OE2	4:D:192:GLU:CA	2.68	0.42
7:G:51:GLN:C	7:G:52:GLU:CD	2.87	0.42
7:G:65:ALA:HB2	7:G:128:ALA:N	2.33	0.42
14:N:8:GLU:OE2	14:N:11:LYS:HD3	2.20	0.42
15:O:56:LEU:HA	15:O:56:LEU:HD13	1.83	0.42
17:Q:11:VAL:CG1	17:Q:88:TYR:CE2	3.01	0.42
20:T:101:GLY:C	20:T:102:GLY:O	2.60	0.42
24:a:37:A:C4	24:a:38:A:N7	2.87	0.42
1:A:157:G:H2'	1:A:157:G:N3	2.35	0.42
1:A:320:C:O2'	1:A:1435:G:H1'	2.20	0.42
1:A:366:C:H1'	1:A:394:G:H22	1.84	0.42
1:A:596:C:C2	1:A:644:G:N2	2.88	0.42
1:A:914:A:OP1	27:A:1928:SRV:HI33	2.19	0.42
1:A:1072:G:C5	1:A:1073:U:C4	3.07	0.42
1:A:1077:G:N2	1:A:1081:G:C5	2.88	0.42
1:A:1115:C:C4	1:A:1116:C:C5	3.08	0.42
1:A:1225:A:H1'	19:S:78:ARG:HH11	1.83	0.42
1:A:1241:G:C4	1:A:1242:C:C5	3.07	0.42
1:A:1358:U:H5''	14:N:35:ARG:HG3	2.01	0.42
1:A:1379:G:OP2	7:G:6:ARG:HG2	2.20	0.42
1:A:1518[B]:MA6:C9	1:A:1519[B]:MA6:H103	2.49	0.42
2:B:97:TRP:CZ2	2:B:101:MET:HG3	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:100:GLY:N	2:B:176:GLU:OE2	2.52	0.42
2:B:221:LEU:O	2:B:222:ILE:C	2.62	0.42
3:C:157:ILE:HD12	3:C:164:ARG:NH1	2.34	0.42
4:D:76:ARG:O	4:D:80:GLU:HG2	2.19	0.42
6:F:82:ARG:CB	6:F:85:VAL:HG23	2.46	0.42
8:H:114:THR:OG1	8:H:117:GLY:O	2.34	0.42
8:H:121:ASP:O	8:H:124:ALA:N	2.49	0.42
14:N:60:SER:O	14:N:61:TRP:HB3	2.19	0.42
14:N:61:TRP:O	14:N:61:TRP:CD1	2.73	0.42
15:O:2:PRO:O	15:O:3:ILE:HG13	2.20	0.42
15:O:31:LEU:HD12	15:O:31:LEU:HA	1.56	0.42
15:O:79:ARG:NH1	15:O:79:ARG:CG	2.76	0.42
17:Q:48:GLU:CD	17:Q:50:LYS:HG3	2.44	0.42
17:Q:90:ILE:HA	17:Q:93:GLN:HB3	2.00	0.42
18:R:58:LEU:CD2	18:R:58:LEU:N	2.82	0.42
20:T:99:LEU:O	20:T:101:GLY:N	2.52	0.42
21:U:10:ARG:HH11	21:U:10:ARG:HG3	1.79	0.42
1:A:376:G:H5''	16:P:5:ARG:HD2	2.01	0.42
1:A:448:A:N3	1:A:449:C:C6	2.87	0.42
1:A:665:A:H3'	1:A:725:G:H21	1.84	0.42
1:A:891:U:C2'	1:A:892:A:H5'	2.49	0.42
1:A:922:G:H8	1:A:922:G:C5'	2.32	0.42
1:A:1401:G:C5	1:A:1402:4OC:C6	3.03	0.42
3:C:72:LYS:C	3:C:74:GLY:N	2.76	0.42
4:D:64:LEU:CA	4:D:67:ILE:HD12	2.50	0.42
4:D:66:ARG:O	4:D:67:ILE:C	2.62	0.42
4:D:100:ARG:NH2	4:D:136:PRO:HB2	2.35	0.42
4:D:147:ALA:HB2	4:D:182:LYS:HB3	2.00	0.42
4:D:191:ARG:HB3	4:D:192:GLU:OE2	2.20	0.42
5:E:59:GLY:O	5:E:60:TYR:C	2.62	0.42
7:G:137:LYS:O	7:G:138:LYS:C	2.63	0.42
8:H:19:VAL:HG21	8:H:21:LYS:HD3	2.02	0.42
12:L:69:TYR:HE2	12:L:71:PRO:HA	1.83	0.42
15:O:31:LEU:O	15:O:32:LEU:C	2.61	0.42
16:P:8:ARG:C	16:P:9:PHE:CD2	2.97	0.42
16:P:17:TYR:HB2	16:P:39:TYR:HB3	2.02	0.42
19:S:44:MET:O	19:S:62:ILE:HG21	2.19	0.42
1:A:53:A:C5	1:A:54:C:C5	3.08	0.42
1:A:114:U:C2'	1:A:115:G:C5'	2.92	0.42
1:A:415:A:C5	1:A:416:G:C5	3.08	0.42
1:A:429:U:H4'	1:A:430:A:O5'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:885:G:O2'	1:A:886:G:H5'	2.20	0.42
1:A:934:C:H5''	29:A:2502:HOH:O	2.20	0.42
1:A:1255:G:O2'	1:A:1258:G:H1'	2.19	0.42
1:A:1493[B]:A:O2'	1:A:1494:G:C8	2.66	0.42
1:A:1505:G:C5'	1:A:1506:U:OP1	2.67	0.42
2:B:115:LEU:HD21	2:B:153:ARG:HH12	1.85	0.42
2:B:154:LEU:HA	2:B:154:LEU:HD23	1.74	0.42
3:C:23:TYR:CD2	3:C:23:TYR:C	2.96	0.42
3:C:82:GLU:CG	3:C:83:ARG:H	2.31	0.42
3:C:112:SER:HB3	3:C:115:LEU:HD12	2.01	0.42
4:D:17:VAL:O	4:D:17:VAL:HG13	2.19	0.42
4:D:21:LEU:HD12	4:D:21:LEU:N	2.34	0.42
5:E:5:ASP:CG	5:E:6:PHE:N	2.77	0.42
8:H:39:LEU:HB3	8:H:45:ILE:HG23	2.01	0.42
10:J:19:SER:O	10:J:22:LYS:HB3	2.20	0.42
11:K:59:TYR:O	11:K:60:ALA:C	2.63	0.42
12:L:105:TYR:N	12:L:105:TYR:CD2	2.83	0.42
13:M:37:THR:HG21	13:M:39:ILE:HD13	2.00	0.42
1:A:49:U:O2'	1:A:50:A:H2'	2.20	0.42
1:A:425:G:C2'	1:A:426:G:H5'	2.48	0.42
1:A:1053:G:H4'	1:A:1054:C:H5'	2.02	0.42
1:A:1130:A:C2	1:A:1146:A:H1'	2.54	0.42
1:A:1149:C:O2'	1:A:1280:A:N1	2.51	0.42
3:C:173:VAL:O	3:C:175:LEU:HD12	2.19	0.42
4:D:8:VAL:O	4:D:10:ARG:N	2.53	0.42
4:D:188:LEU:HA	4:D:189:PRO:HD2	1.79	0.42
5:E:126:ARG:CG	5:E:126:ARG:NH1	2.65	0.42
9:I:22:GLY:O	9:I:57:GLY:O	2.38	0.42
13:M:21:TYR:N	13:M:21:TYR:CD1	2.87	0.42
13:M:54:VAL:CG1	13:M:55:ARG:N	2.83	0.42
14:N:8:GLU:OE2	14:N:8:GLU:C	2.63	0.42
15:O:15:PHE:HD1	15:O:15:PHE:N	2.17	0.42
19:S:58:VAL:HA	19:S:59:PRO:HD3	1.52	0.42
19:S:72:GLY:O	19:S:74:PHE:N	2.53	0.42
1:A:24:U:OP1	12:L:23:LYS:HE2	2.20	0.42
1:A:309:G:O2'	1:A:310:G:H5'	2.20	0.42
1:A:327:A:O2'	1:A:328:C:H6	2.02	0.42
1:A:397:A:C6	1:A:548:G:N7	2.88	0.42
1:A:407:G:H5''	4:D:3:ARG:NH1	2.35	0.42
1:A:442:C:H42	1:A:492:G:H1	1.68	0.42
1:A:496:A:H4'	1:A:497:A:OP1	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:505:G:C5	1:A:535:A:C2	3.08	0.42
1:A:605:U:H3'	1:A:605:U:C6	2.55	0.42
1:A:877:C:OP1	8:H:88:LYS:HE3	2.19	0.42
1:A:1040:U:O2'	1:A:1041:A:H5'	2.20	0.42
1:A:1051:C:H2'	1:A:1052:U:O5'	2.19	0.42
1:A:1086:U:O5'	1:A:1086:U:H6	2.02	0.42
1:A:1182:G:H8	1:A:1182:G:H2'	1.78	0.42
1:A:1199:U:H4'	10:J:54:PHE:CD1	2.55	0.42
1:A:1250:A:N1	1:A:1287:A:C2	2.88	0.42
1:A:1368:G:H5'	9:I:112:LYS:O	2.19	0.42
1:A:1379:G:C6	1:A:1380:U:C4	3.07	0.42
1:A:1493[B]:A:C2'	1:A:1494:G:C8	3.03	0.42
2:B:101:MET:HB2	2:B:102:LEU:CD1	2.49	0.42
3:C:8:ILE:HG22	3:C:9:GLY:H	1.84	0.42
3:C:115:LEU:HA	3:C:115:LEU:HD23	1.59	0.42
5:E:5:ASP:OD1	5:E:6:PHE:N	2.49	0.42
5:E:62:ALA:O	5:E:63:ARG:C	2.63	0.42
7:G:70:LYS:HB3	7:G:96:GLN:HG2	2.02	0.42
9:I:99:LEU:HD22	9:I:99:LEU:H	1.85	0.42
12:L:71:PRO:HG2	12:L:102:ARG:HG3	2.01	0.42
13:M:22:ILE:CD1	13:M:22:ILE:H	2.33	0.42
19:S:34:TRP:CD1	19:S:52:TYR:HB3	2.54	0.42
21:U:12:LYS:HD3	21:U:17:THR:OG1	2.20	0.42
1:A:154:C:C6	1:A:154:C:C3'	3.03	0.42
1:A:415:A:C5	1:A:416:G:N7	2.88	0.42
1:A:491:G:H2'	1:A:492:G:H8	1.85	0.42
1:A:924:C:C6	1:A:924:C:C3'	3.03	0.42
1:A:1172:C:H6	1:A:1172:C:O5'	2.03	0.42
1:A:1204:A:C5	1:A:1205:U:C6	3.08	0.42
1:A:1381:U:C5	1:A:1382:C:C6	3.08	0.42
2:B:10:LEU:CD1	2:B:15:VAL:HG21	2.50	0.42
2:B:85:ALA:C	2:B:87:ARG:O	2.63	0.42
5:E:80:ILE:HA	8:H:104:ARG:NH2	2.35	0.42
6:F:10:LEU:HD12	6:F:10:LEU:N	2.35	0.42
6:F:35:ALA:HA	6:F:67:MET:HB3	2.02	0.42
7:G:5:ARG:NH1	7:G:8:GLU:HG2	2.34	0.42
8:H:52:ASP:HA	8:H:57:PRO:HA	2.02	0.42
17:Q:18:THR:HG21	17:Q:69:LYS:HD3	2.01	0.42
17:Q:20:THR:HA	17:Q:43:LEU:CD2	2.50	0.42
17:Q:54:GLY:HA3	17:Q:82:MET:HG2	2.02	0.42
1:A:114:U:H1'	1:A:353:A:H1'	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:316:G:C5	29:A:2572:HOH:O	2.72	0.41
1:A:560:U:H4'	1:A:561:U:H5''	2.01	0.41
1:A:1032:G:H2'	1:A:1033:G:O4'	2.20	0.41
1:A:1111:A:O2'	1:A:1112:C:H5'	2.20	0.41
1:A:1190:G:H5'	3:C:4:LYS:H	1.85	0.41
1:A:1222:G:N2	1:A:1223:C:C2	2.88	0.41
1:A:1310:G:H2'	1:A:1311:G:O4'	2.20	0.41
1:A:1410:G:C4	1:A:1411:C:C5	3.08	0.41
1:A:1536:C:C3'	1:A:1536:C:C6	3.03	0.41
2:B:47:THR:HA	2:B:202:PRO:CG	2.46	0.41
2:B:107:THR:O	2:B:108:ILE:C	2.62	0.41
2:B:115:LEU:O	2:B:116:GLU:C	2.60	0.41
2:B:135:GLN:O	2:B:139:LYS:HB2	2.20	0.41
2:B:175:ARG:O	2:B:176:GLU:C	2.63	0.41
3:C:120:VAL:HG12	3:C:124:ILE:HD11	2.02	0.41
4:D:83:SER:HA	4:D:89:THR:CG2	2.37	0.41
6:F:45:LEU:HA	6:F:59:TYR:HA	2.02	0.41
7:G:54:THR:C	7:G:56:GLN:H	2.27	0.41
7:G:58:PRO:O	7:G:59:LEU:C	2.63	0.41
12:L:60:LEU:HD13	12:L:60:LEU:HA	1.33	0.41
13:M:13:LYS:O	13:M:14:ARG:C	2.60	0.41
13:M:63:THR:CG2	13:M:64:TRP:H	2.32	0.41
14:N:7:ILE:HD13	14:N:7:ILE:N	2.35	0.41
16:P:38:TYR:O	16:P:49:LEU:HD12	2.19	0.41
16:P:66:PRO:HG2	16:P:71:ARG:NH1	2.35	0.41
18:R:78:LEU:HD22	18:R:78:LEU:HA	1.73	0.41
19:S:40:ILE:HG23	19:S:62:ILE:HD12	2.02	0.41
1:A:78:G:C2	1:A:79:G:C8	3.08	0.41
1:A:79:G:N3	1:A:91:C:O2	2.54	0.41
1:A:574:A:H5''	1:A:575:G:OP2	2.20	0.41
1:A:665:A:H3'	1:A:725:G:N2	2.36	0.41
1:A:973:G:C2'	1:A:974:A:OP1	2.68	0.41
1:A:1030(A):G:N2	1:A:1030(D):A:OP2	2.53	0.41
1:A:1137:C:H4'	1:A:1138:G:O5'	2.19	0.41
1:A:1190:G:C8	1:A:1190:G:C4'	3.02	0.41
1:A:1241:G:OP1	7:G:35:LYS:NZ	2.53	0.41
1:A:1288:A:H2'	1:A:1289:A:H8	1.85	0.41
1:A:1376:U:OP1	7:G:98:SER:OG	2.25	0.41
1:A:1502:A:C2	1:A:1504:G:N3	2.88	0.41
1:A:1536:C:H3'	1:A:1536:C:C6	2.52	0.41
3:C:78:GLY:CA	3:C:83:ARG:HB3	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:19:LEU:CD1	4:D:67:ILE:HG13	2.50	0.41
4:D:162:LEU:O	4:D:165:MET:HB2	2.20	0.41
5:E:69:VAL:HA	5:E:70:PRO:HD3	1.82	0.41
6:F:97:PHE:CE1	18:R:61:LYS:HE2	2.55	0.41
7:G:79:ARG:CB	7:G:83:ALA:O	2.68	0.41
8:H:100:ILE:HG21	8:H:112:LEU:HD11	2.02	0.41
9:I:9:ARG:HA	9:I:76:ALA:HB2	2.00	0.41
9:I:33:PHE:HD1	9:I:33:PHE:HA	1.66	0.41
13:M:70:LEU:HD23	13:M:70:LEU:HA	1.75	0.41
16:P:4:ILE:O	16:P:4:ILE:HG22	2.18	0.41
19:S:51:VAL:HG11	19:S:71:LEU:HD22	2.01	0.41
1:A:101:A:C2	1:A:102:G:C8	3.08	0.41
1:A:140:A:O2'	1:A:141:A:H5'	2.20	0.41
1:A:243:A:C2	1:A:246:A:N7	2.88	0.41
1:A:268:C:H2'	1:A:269:C:H6	1.85	0.41
1:A:922:G:N3	1:A:1398:A:C2	2.86	0.41
1:A:937:A:N6	1:A:1345:U:O4	2.53	0.41
1:A:1052:U:O2	1:A:1207:2MG:N2	2.54	0.41
1:A:1128:C:O2'	1:A:1130:A:H8	2.02	0.41
2:B:16:HIS:CD2	2:B:16:HIS:C	2.98	0.41
3:C:174:PRO:HB2	3:C:177:THR:HB	2.02	0.41
4:D:19:LEU:HD23	4:D:19:LEU:N	2.22	0.41
6:F:63:TYR:N	6:F:63:TYR:CD2	2.89	0.41
6:F:89:MET:HE1	18:R:72:ARG:O	2.21	0.41
17:Q:32:TYR:HD2	17:Q:32:TYR:HA	1.62	0.41
17:Q:76:LEU:HD12	17:Q:77:VAL:N	2.35	0.41
22:V:1:U:N3	23:W:37:A:C2	2.88	0.41
1:A:89:C:H5	1:A:90:U:O4	2.02	0.41
1:A:370:C:C2	1:A:371:G:C8	3.09	0.41
1:A:504:C:C2	1:A:542:G:C2	3.09	0.41
1:A:505:G:C6	1:A:535:A:C2	3.07	0.41
1:A:684:A:N3	11:K:39:PRO:HD2	2.36	0.41
1:A:850:U:H6	1:A:850:U:H3'	1.86	0.41
1:A:892:A:C6	1:A:907:A:C8	3.09	0.41
1:A:986:A:H1'	19:S:52:TYR:OH	2.19	0.41
1:A:1091:U:O2	1:A:1093:A:C8	2.74	0.41
1:A:1329:A:C5'	13:M:29:ARG:HD2	2.50	0.41
2:B:158:LEU:HB3	2:B:159:PRO:CD	2.50	0.41
2:B:180:LEU:C	2:B:181:PHE:HD1	2.29	0.41
2:B:208:ILE:HD13	2:B:208:ILE:HA	1.85	0.41
2:B:230:VAL:HG12	2:B:231:GLU:N	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:17:VAL:HG11	4:D:63:LYS:HD2	2.02	0.41
5:E:95:ALA:HB1	5:E:96:PRO:HD2	2.03	0.41
5:E:105:VAL:CB	5:E:106:PRO:HD3	2.49	0.41
5:E:131:ILE:HD13	5:E:131:ILE:HA	1.50	0.41
9:I:50:LEU:HD23	9:I:55:ALA:HB3	2.01	0.41
13:M:36:LYS:HD2	13:M:59:TYR:OH	2.20	0.41
15:O:12:ILE:O	15:O:14:GLU:N	2.53	0.41
15:O:21:ASP:OD1	15:O:24:SER:CB	2.66	0.41
17:Q:27:PHE:CE2	17:Q:36:ILE:HD11	2.55	0.41
17:Q:95:TYR:O	17:Q:97:SER:N	2.53	0.41
1:A:62:U:H2'	1:A:63:C:C6	2.56	0.41
1:A:88:A:N7	1:A:89:C:N3	2.68	0.41
1:A:188:C:H2'	1:A:189:G:H5'	2.02	0.41
1:A:247:G:OP2	17:Q:99:SER:HB2	2.20	0.41
1:A:313:A:H2'	1:A:314:C:O4'	2.21	0.41
1:A:739:C:N4	1:A:740:U:C4	2.89	0.41
1:A:777:A:N6	1:A:778:G:C2	2.89	0.41
1:A:794:A:N6	1:A:795:C:N4	2.68	0.41
1:A:1195:C:H5''	1:A:1196:U:P	2.61	0.41
1:A:1492[B]:A:C6	1:A:1493[B]:A:H1'	2.56	0.41
27:A:1928:SRY:C61	12:L:46:LYS:HD2	2.51	0.41
2:B:16:HIS:HB3	2:B:44:LEU:HD11	2.02	0.41
4:D:22:LYS:HB3	4:D:26:CYS:SG	2.59	0.41
4:D:141:ARG:HE	4:D:141:ARG:HB2	1.48	0.41
5:E:42:GLY:HA2	5:E:136:MET:HE1	2.02	0.41
9:I:17:VAL:HG11	9:I:81:ILE:HA	2.01	0.41
9:I:126:SER:C	9:I:128:ARG:N	2.78	0.41
10:J:8:LEU:HD21	10:J:96:ILE:HG23	2.02	0.41
13:M:27:LYS:HE2	21:U:21:TYR:HE2	1.84	0.41
13:M:82:MET:O	13:M:83:ASP:C	2.63	0.41
16:P:20:VAL:CG1	16:P:21:VAL:N	2.78	0.41
17:Q:22:LEU:HD12	17:Q:23:VAL:N	2.36	0.41
18:R:59:SER:OG	18:R:62:GLU:HG3	2.21	0.41
1:A:21:G:C2	1:A:22:G:C6	3.09	0.41
1:A:22:G:C5	1:A:23:C:C4	3.09	0.41
1:A:328:C:OP1	1:A:328:C:H4'	2.19	0.41
1:A:536:C:OP2	29:A:2174:HOH:O	2.22	0.41
1:A:544:G:N3	1:A:545:C:C6	2.88	0.41
1:A:584:G:C2'	1:A:585:G:H5'	2.50	0.41
1:A:924:C:C6	1:A:924:C:H3'	2.55	0.41
1:A:1022:G:C2	1:A:1023:G:C8	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1029:C:C4	1:A:1030:C:H5	2.39	0.41
1:A:1068:G:OP1	29:A:2218:HOH:O	2.20	0.41
2:B:215:LEU:O	2:B:219:VAL:HG23	2.21	0.41
4:D:165:MET:HE2	4:D:176:LEU:HD21	2.03	0.41
5:E:31:LEU:HD23	5:E:44:GLY:O	2.21	0.41
7:G:23:VAL:HA	7:G:62:PHE:HE2	1.85	0.41
11:K:67:ASP:CG	11:K:71:LYS:HD2	2.46	0.41
16:P:1:MET:HE2	16:P:1:MET:HB3	1.93	0.41
16:P:19:ILE:CG2	16:P:36:ILE:HG13	2.51	0.41
17:Q:101:ARG:HD3	17:Q:101:ARG:N	2.34	0.41
19:S:15:LEU:CD1	19:S:15:LEU:N	2.83	0.41
21:U:13:ILE:HG13	21:U:14:TRP:N	2.35	0.41
1:A:106:C:H2'	1:A:107:G:C5'	2.50	0.41
1:A:357:G:C2	1:A:358:U:C6	3.09	0.41
1:A:491:G:C2	1:A:492:G:C8	3.08	0.41
1:A:552:U:H2'	1:A:553:A:C8	2.56	0.41
1:A:756:C:H2'	1:A:757:U:O4'	2.20	0.41
1:A:922:G:N3	1:A:1396:A:C2	2.89	0.41
1:A:1042:G:C6	1:A:1043:C:C4	3.08	0.41
1:A:1121:U:O2'	1:A:1122:U:H5'	2.21	0.41
1:A:1124:G:C4'	10:J:38:ILE:HD11	2.50	0.41
1:A:1350:A:OP2	9:I:118:LYS:HD2	2.21	0.41
1:A:1377:A:O2'	7:G:2:ALA:HB3	2.21	0.41
1:A:1497:G:O2'	1:A:1518[A]:MA6:N1	2.53	0.41
27:A:1928:SRV:O42	27:A:1928:SRV:O51	2.30	0.41
2:B:20:GLU:HG2	2:B:39:ILE:HD11	2.02	0.41
2:B:102:LEU:HB2	2:B:176:GLU:OE1	2.20	0.41
4:D:4:TYR:CD2	4:D:4:TYR:C	2.98	0.41
4:D:150:GLU:O	4:D:152:SER:N	2.54	0.41
5:E:101:ILE:N	5:E:101:ILE:HD13	2.36	0.41
6:F:11:ASN:HD22	6:F:86:ARG:NH1	2.19	0.41
6:F:39:LYS:HG2	6:F:40:VAL:N	2.36	0.41
7:G:78:ARG:HD2	7:G:156:TRP:HB2	2.02	0.41
15:O:15:PHE:CE2	15:O:30:ALA:HB2	2.55	0.41
16:P:32:TYR:N	16:P:32:TYR:CD1	2.88	0.41
17:Q:89:LEU:O	17:Q:93:GLN:HB3	2.20	0.41
18:R:22:VAL:HG21	18:R:56:THR:HG22	2.02	0.41
18:R:36:ASN:CG	18:R:39:VAL:CG1	2.94	0.41
21:U:10:ARG:HA	21:U:13:ILE:HG12	2.02	0.41
1:A:112:G:H2'	1:A:113:G:H5'	2.02	0.41
1:A:133:U:H6	1:A:133:U:O5'	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:148:G:N2	1:A:149:A:C4	2.89	0.41
1:A:740:U:C4'	15:O:42:HIS:CD2	3.03	0.41
1:A:1006:C:H2'	1:A:1007:C:H6	1.85	0.41
1:A:1010:G:C2	1:A:1020:U:O2	2.74	0.41
1:A:1202:G:H1'	14:N:42:ILE:HD12	2.02	0.41
2:B:16:HIS:NE2	2:B:17:PHE:CD2	2.89	0.41
2:B:24:TRP:CZ2	2:B:26:PRO:HB3	2.56	0.41
2:B:86:GLU:O	2:B:88:ALA:O	2.38	0.41
3:C:112:SER:OG	3:C:115:LEU:HB2	2.20	0.41
3:C:175:LEU:CD2	3:C:201:TYR:HE2	2.34	0.41
3:C:182:ILE:O	3:C:183:ASP:C	2.63	0.41
4:D:204:ILE:N	4:D:204:ILE:HD13	2.31	0.41
5:E:76:ILE:HA	5:E:76:ILE:HD12	1.46	0.41
5:E:118:ILE:C	5:E:119:LEU:HD23	2.45	0.41
5:E:119:LEU:HD23	5:E:119:LEU:HA	1.56	0.41
5:E:145:LYS:O	5:E:146:ALA:C	2.64	0.41
6:F:52:ILE:O	6:F:53:ALA:HB3	2.21	0.41
7:G:50:ILE:CB	7:G:58:PRO:HB3	2.50	0.41
8:H:11:THR:OG1	8:H:14:ARG:NH2	2.50	0.41
9:I:49:PRO:HD3	9:I:101:PHE:HE1	1.85	0.41
11:K:58:PRO:O	11:K:61:ALA:N	2.54	0.41
14:N:9:LYS:O	14:N:11:LYS:HB2	2.20	0.41
14:N:29:ARG:HG2	14:N:40:CYS:HB2	2.02	0.41
18:R:47:THR:CG2	18:R:48:GLY:H	2.27	0.41
18:R:87:ARG:NH2	18:R:87:ARG:CB	2.79	0.41
1:A:262:A:H5'	20:T:74:LYS:HD3	2.03	0.41
1:A:392:G:C2	1:A:393:A:C8	3.09	0.41
1:A:500:G:C5	1:A:501:C:C4	3.09	0.41
1:A:575:G:C6	1:A:821:G:N7	2.89	0.41
1:A:652:U:O2'	1:A:752:G:N1	2.54	0.41
1:A:674:G:H5'	6:F:50:TYR:CE2	2.56	0.41
1:A:791:G:N2	1:A:1518[A]:MA6:C9	2.84	0.41
1:A:1038:C:O2'	1:A:1039:C:H5'	2.21	0.41
1:A:1063:C:H2'	1:A:1064:G:H8	1.83	0.41
1:A:1343:G:H2'	1:A:1344:C:C6	2.56	0.41
2:B:20:GLU:HA	2:B:39:ILE:HD11	2.01	0.41
2:B:216:SER:OG	2:B:217:ARG:N	2.53	0.41
3:C:56:ASP:HB3	3:C:67:THR:HB	2.03	0.41
3:C:85:ARG:HH11	3:C:85:ARG:CG	2.29	0.41
3:C:113:ALA:C	3:C:115:LEU:N	2.78	0.41
4:D:64:LEU:HA	4:D:67:ILE:CD1	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:100:ARG:HH12	4:D:137:SER:CA	2.34	0.41
4:D:107:ARG:HH11	4:D:114:ARG:HH21	1.68	0.41
4:D:108:LEU:HD23	4:D:108:LEU:HA	1.73	0.41
5:E:28:PHE:O	5:E:47:LYS:HA	2.21	0.41
5:E:41:VAL:HG13	5:E:113:ALA:CA	2.49	0.41
6:F:50:TYR:CD1	6:F:50:TYR:N	2.88	0.41
6:F:101:ALA:HA	18:R:28:GLU:CB	2.46	0.41
8:H:35:ILE:O	8:H:39:LEU:HD22	2.21	0.41
9:I:5:TYR:O	9:I:84:ALA:HA	2.21	0.41
12:L:10:LEU:HD11	12:L:15:ARG:NE	2.35	0.41
12:L:68:ALA:HB3	12:L:100:ILE:HD11	2.03	0.41
13:M:49:THR:HB	13:M:52:GLU:CG	2.35	0.41
13:M:105:THR:O	13:M:106:ASN:C	2.63	0.41
14:N:36:PHE:CD1	14:N:36:PHE:O	2.73	0.41
15:O:26:GLU:HG3	15:O:81:LEU:HG	2.03	0.41
16:P:19:ILE:C	16:P:20:VAL:HG23	2.45	0.41
17:Q:81:ARG:NE	17:Q:84:LEU:HD12	2.34	0.41
19:S:52:TYR:CE2	19:S:54:GLY:HA2	2.56	0.41
20:T:13:LEU:C	20:T:15:ARG:N	2.77	0.41
20:T:73:HIS:C	20:T:74:LYS:HG2	2.45	0.41
23:W:33:U:O2	23:W:33:U:H2'	2.21	0.41
1:A:16:A:C2	1:A:920:U:O2	2.74	0.41
1:A:143:A:C2	1:A:221:C:O2	2.74	0.41
1:A:179:A:C4	1:A:180:U:C5	3.09	0.41
1:A:442:C:N4	1:A:492:G:H1	2.19	0.41
1:A:447:G:H2'	1:A:485:G:C2	2.54	0.41
1:A:474:G:C2	1:A:475:G:C8	3.09	0.41
1:A:1022:G:N3	1:A:1022:G:H2'	2.35	0.41
1:A:1038:C:C2	1:A:1039:C:C6	3.09	0.41
1:A:1104:G:H4'	2:B:111:ARG:NE	2.36	0.41
1:A:1190:G:O2'	1:A:1191:A:P	2.79	0.41
1:A:1318:A:H5'	19:S:10:PHE:CD1	2.56	0.41
1:A:1330:U:C2'	1:A:1331:G:H5'	2.50	0.41
3:C:182:ILE:HA	3:C:202:ILE:O	2.20	0.41
8:H:73:ASP:HA	8:H:74:PRO:HD2	1.73	0.41
8:H:82:HIS:ND1	8:H:138:TRP:CE2	2.89	0.41
8:H:86:ILE:N	8:H:134:ILE:O	2.54	0.41
11:K:120:ARG:NH2	11:K:126:ARG:NE	2.69	0.41
16:P:67:THR:N	16:P:70:ALA:HB3	2.35	0.41
17:Q:53:LEU:HA	17:Q:53:LEU:HD13	1.79	0.41
17:Q:95:TYR:C	17:Q:97:SER:N	2.77	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:411:A:C8	1:A:411:A:C3'	3.05	0.40
1:A:865:A:H1'	1:A:918:A:O2'	2.21	0.40
1:A:891:U:O2'	1:A:892:A:H5'	2.21	0.40
1:A:1005:A:C8	1:A:1026:G:C6	3.10	0.40
1:A:1102:A:O2'	2:B:99:GLY:N	2.54	0.40
1:A:1404:5MC:C2	1:A:1499:A:N1	2.89	0.40
1:A:1415:G:H2'	1:A:1416:G:H5'	2.02	0.40
1:A:1418:A:H61	1:A:1482:G:H1'	1.86	0.40
2:B:60:ASP:O	2:B:64:ARG:HB2	2.20	0.40
2:B:183:PRO:HA	2:B:198:ASP:OD2	2.21	0.40
3:C:107:GLN:HG3	3:C:108:ASN:N	2.34	0.40
4:D:19:LEU:CD2	4:D:19:LEU:N	2.83	0.40
5:E:52:PRO:C	5:E:54:ALA:N	2.79	0.40
5:E:121:LYS:HG3	5:E:123:LEU:CD2	2.50	0.40
6:F:25:ILE:HD12	6:F:82:ARG:HD3	2.02	0.40
7:G:51:GLN:CB	7:G:52:GLU:OE1	2.69	0.40
7:G:75:VAL:CG2	7:G:86:GLN:HB3	2.51	0.40
9:I:118:LYS:HB3	9:I:118:LYS:HE2	1.90	0.40
10:J:7:LYS:HE2	10:J:9:ARG:NH2	2.35	0.40
12:L:113:ARG:NH2	12:L:120:TYR:CE1	2.89	0.40
13:M:106:ASN:HB3	13:M:107:ALA:H	1.50	0.40
18:R:37:VAL:C	18:R:39:VAL:N	2.78	0.40
20:T:93:GLU:O	20:T:94:ALA:C	2.64	0.40
24:a:34:G:H8	24:a:34:G:O5'	2.03	0.40
1:A:47:C:H6	1:A:365:U:H2'	1.86	0.40
1:A:108:G:H2'	1:A:109:A:OP1	2.21	0.40
1:A:149:A:H2'	1:A:150:C:C6	2.56	0.40
1:A:367:U:O2	1:A:369:C:C6	2.73	0.40
1:A:427:U:O4	1:A:428:G:C6	2.74	0.40
1:A:919:A:H8	1:A:919:A:O5'	2.04	0.40
1:A:972:C:OP1	10:J:57:LYS:NZ	2.50	0.40
1:A:1124:G:N2	1:A:1127:G:H21	2.19	0.40
1:A:1305:G:P	21:U:2:GLY:N	2.94	0.40
1:A:1390:U:H2'	1:A:1391:U:C6	2.57	0.40
1:A:1517[A]:G:H2'	1:A:1518[A]:MA6:H8	2.04	0.40
1:A:1518[A]:MA6:C2	1:A:1519[A]:MA6:C5	2.99	0.40
2:B:15:VAL:O	2:B:15:VAL:HG12	2.21	0.40
2:B:98:LEU:HB2	2:B:101:MET:HE3	2.02	0.40
3:C:88:ARG:NH2	3:C:101:LEU:HD23	2.36	0.40
4:D:180:GLY:O	4:D:181:MET:C	2.63	0.40
7:G:65:ALA:HB2	7:G:128:ALA:CB	2.50	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:65:ALA:HA	7:G:128:ALA:HA	2.03	0.40
11:K:38:ASN:HA	11:K:39:PRO:HD3	1.85	0.40
13:M:20:THR:O	13:M:20:THR:CG2	2.62	0.40
17:Q:9:VAL:H	17:Q:9:VAL:HG23	1.70	0.40
17:Q:63:ARG:HA	17:Q:64:PRO:HD3	1.90	0.40
19:S:3:ARG:HA	19:S:3:ARG:HD3	1.76	0.40
19:S:31:ILE:HG21	19:S:49:ILE:HD12	2.02	0.40
19:S:80:TYR:CD1	19:S:80:TYR:C	2.91	0.40
24:a:37:A:H2'	24:a:38:A:C8	2.33	0.40
1:A:79:G:N1	1:A:80:G:C5	2.89	0.40
1:A:166:G:C6	1:A:167:G:N7	2.89	0.40
1:A:246:A:C4	1:A:279:A:N6	2.90	0.40
1:A:393:A:N3	1:A:394:G:C8	2.89	0.40
1:A:643:C:C3'	1:A:644:G:H5''	2.52	0.40
1:A:660:G:C2	1:A:746:A:C2	3.10	0.40
1:A:777:A:N3	1:A:777:A:C2'	2.85	0.40
1:A:838:G:C2	1:A:849:C:C2	3.10	0.40
1:A:848:C:C6	1:A:848:C:C3'	3.05	0.40
1:A:1027:C:C6	1:A:1035:A:C2	3.10	0.40
1:A:1236:A:OP1	21:U:3:LYS:HG3	2.21	0.40
1:A:1440:C:H2'	1:A:1441:G:O4'	2.22	0.40
2:B:16:HIS:CD2	2:B:17:PHE:CD2	2.96	0.40
2:B:177:ALA:O	2:B:178:ARG:C	2.64	0.40
2:B:214:ILE:HD12	2:B:214:ILE:N	2.36	0.40
3:C:61:ALA:C	3:C:63:ASN:H	2.29	0.40
4:D:30:LYS:C	4:D:32:ALA:H	2.29	0.40
5:E:83:GLU:O	5:E:83:GLU:CG	2.65	0.40
6:F:75:LEU:HD22	6:F:75:LEU:C	2.47	0.40
7:G:111:ARG:HG2	7:G:112:PRO:HD2	2.03	0.40
7:G:145:ALA:C	7:G:147:ALA:H	2.30	0.40
12:L:86:ARG:HG3	12:L:86:ARG:NH1	2.33	0.40
17:Q:27:PHE:HA	17:Q:28:PRO:HD3	1.84	0.40
23:W:32:C:O2'	23:W:33:U:H6	2.03	0.40
1:A:36:C:C2	1:A:37:U:C6	3.10	0.40
1:A:115:G:O2'	1:A:116:A:OP2	2.22	0.40
1:A:392:G:C4	1:A:393:A:C8	3.09	0.40
1:A:543:C:C2'	1:A:544:G:C5'	2.79	0.40
1:A:632:A:H5''	1:A:633:G:OP2	2.21	0.40
1:A:735:C:H1'	18:R:75:ILE:CD1	2.52	0.40
1:A:747:C:C3'	1:A:747:C:C6	3.04	0.40
1:A:977:A:C2'	1:A:978:A:C5'	2.98	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1027:C:H5	1:A:1035:A:N1	2.16	0.40
1:A:1032:G:H2'	1:A:1033:G:C8	2.57	0.40
1:A:1133:G:H1	1:A:1141:C:N4	2.20	0.40
1:A:1158:C:C5	1:A:1160:G:C8	3.09	0.40
1:A:1244:C:C2	1:A:1294:G:N2	2.90	0.40
1:A:1425:U:O2	1:A:1426:C:C6	2.75	0.40
2:B:109:SER:O	2:B:112:VAL:HB	2.21	0.40
2:B:130:ARG:HA	2:B:131:PRO:HD2	1.88	0.40
2:B:180:LEU:HB2	2:B:182:ILE:HG13	2.04	0.40
3:C:126:ARG:HE	3:C:128:PHE:HD1	1.68	0.40
5:E:12:LEU:HG	5:E:13:ILE:N	2.36	0.40
7:G:5:ARG:HE	7:G:7:ALA:HA	1.86	0.40
7:G:51:GLN:O	7:G:52:GLU:CG	2.69	0.40
7:G:51:GLN:C	7:G:53:LYS:N	2.80	0.40
12:L:45:PRO:HB3	12:L:93:LEU:CD2	2.49	0.40
13:M:23:TYR:CZ	13:M:71:ARG:HG3	2.57	0.40
13:M:91:ARG:HH21	13:M:96:LEU:HB2	1.86	0.40
15:O:16:ALA:CB	15:O:21:ASP:HB3	2.38	0.40
15:O:70:LEU:HD22	15:O:78:TYR:HA	2.02	0.40
21:U:18:TYR:CD2	21:U:22:ARG:HD3	2.56	0.40
1:A:35:G:H2'	1:A:36:C:H6	1.87	0.40
1:A:328:C:O2'	1:A:329:A:P	2.74	0.40
1:A:442:C:C3'	1:A:443:C:H5'	2.51	0.40
1:A:490:G:C4	1:A:491:G:C8	3.10	0.40
1:A:503:C:H2'	1:A:504:C:C6	2.55	0.40
1:A:765:G:C6	1:A:812:C:C2	3.09	0.40
1:A:961:U:H2'	1:A:962:C:O4'	2.22	0.40
1:A:1234:C:C2'	1:A:1235:U:H5'	2.52	0.40
1:A:1327:C:P	21:U:12:LYS:HZ1	2.42	0.40
1:A:1372:U:H2'	1:A:1373:G:O4'	2.22	0.40
1:A:1378:C:O2	7:G:76:ARG:NH1	2.55	0.40
1:A:1502:A:H2	1:A:1505:G:N1	2.20	0.40
2:B:75:LYS:HG2	2:B:78:GLN:HG3	2.04	0.40
2:B:172:ILE:HD13	2:B:172:ILE:N	2.33	0.40
3:C:31:HIS:HA	3:C:34:LEU:HB3	2.04	0.40
3:C:47:LEU:O	3:C:50:ALA:N	2.49	0.40
8:H:14:ARG:CZ	8:H:14:ARG:HB2	2.50	0.40
9:I:70:LYS:O	9:I:74:ILE:HG12	2.21	0.40
10:J:9:ARG:NH1	10:J:9:ARG:CB	2.85	0.40
10:J:11:PHE:HD2	10:J:11:PHE:HA	1.63	0.40
10:J:79:ARG:HB3	10:J:80:LYS:HE2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:113:ARG:CZ	12:L:120:TYR:HD1	2.35	0.40
13:M:63:THR:CG2	13:M:64:TRP:N	2.84	0.40
14:N:9:LYS:O	14:N:10:ALA:C	2.62	0.40
15:O:42:HIS:HE1	15:O:46:HIS:CD2	2.39	0.40
16:P:55:ARG:O	16:P:56:ALA:C	2.63	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:82:U:O2	1:A:1400:5MC:N4[3_545]	2.15	0.05
5:E:73:ASN:N	5:E:149:GLU:OE1[7_555]	2.18	0.02

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 X-ray entries followed by that with respect to entries of similar resolution.

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	
2	B	234/256 (91%)	197 (84%)	34 (14%)	3 (1%)	9	37
3	C	205/239 (86%)	169 (82%)	35 (17%)	1 (0%)	24	56
4	D	206/209 (99%)	180 (87%)	25 (12%)	1 (0%)	24	56
5	E	149/162 (92%)	137 (92%)	11 (7%)	1 (1%)	18	50
6	F	99/101 (98%)	93 (94%)	6 (6%)	0	100	100
7	G	153/156 (98%)	132 (86%)	21 (14%)	0	100	100
8	H	136/138 (99%)	128 (94%)	7 (5%)	1 (1%)	18	50
9	I	125/128 (98%)	107 (86%)	17 (14%)	1 (1%)	16	47
10	J	97/105 (92%)	77 (79%)	17 (18%)	3 (3%)	3	24
11	K	115/129 (89%)	98 (85%)	17 (15%)	0	100	100
12	L	122/135 (90%)	110 (90%)	8 (7%)	4 (3%)	3	23

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	M	116/126 (92%)	99 (85%)	16 (14%)	1 (1%)	14	43
14	N	58/61 (95%)	50 (86%)	8 (14%)	0	100	100
15	O	86/89 (97%)	72 (84%)	14 (16%)	0	100	100
16	P	82/88 (93%)	74 (90%)	7 (8%)	1 (1%)	10	39
17	Q	98/105 (93%)	93 (95%)	5 (5%)	0	100	100
18	R	69/88 (78%)	60 (87%)	9 (13%)	0	100	100
19	S	79/93 (85%)	68 (86%)	9 (11%)	2 (2%)	4	27
20	T	97/106 (92%)	80 (82%)	16 (16%)	1 (1%)	12	42
21	U	23/27 (85%)	22 (96%)	1 (4%)	0	100	100
All	All	2349/2541 (92%)	2046 (87%)	283 (12%)	20 (1%)	14	43

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	15	THR
9	I	119	ALA
12	L	28	LYS
16	P	83	GLU
19	S	31	ILE
10	J	81	THR
10	J	86	MET
19	S	6	LYS
12	L	115	LYS
20	T	73	HIS
2	B	21	ARG
2	B	95	GLN
2	B	229	VAL
5	E	153	LYS
8	H	121	ASP
12	L	27	LEU
10	J	34	VAL
12	L	71	PRO
13	M	7	VAL
4	D	67	ILE

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	
2	B	201/220 (91%)	149 (74%)	52 (26%)	0	4
3	C	160/188 (85%)	113 (71%)	47 (29%)	0	2
4	D	180/181 (99%)	135 (75%)	45 (25%)	0	4
5	E	115/123 (94%)	74 (64%)	41 (36%)	0	1
6	F	90/90 (100%)	56 (62%)	34 (38%)	0	0
7	G	126/127 (99%)	96 (76%)	30 (24%)	1	5
8	H	119/119 (100%)	84 (71%)	35 (29%)	0	2
9	I	98/99 (99%)	74 (76%)	24 (24%)	1	4
10	J	87/92 (95%)	66 (76%)	21 (24%)	1	5
11	K	89/99 (90%)	67 (75%)	22 (25%)	1	4
12	L	103/110 (94%)	78 (76%)	25 (24%)	1	4
13	M	94/101 (93%)	66 (70%)	28 (30%)	0	2
14	N	49/50 (98%)	36 (74%)	13 (26%)	0	3
15	O	79/80 (99%)	55 (70%)	24 (30%)	0	1
16	P	72/74 (97%)	53 (74%)	19 (26%)	0	3
17	Q	95/97 (98%)	70 (74%)	25 (26%)	0	3
18	R	62/77 (80%)	47 (76%)	15 (24%)	1	5
19	S	71/80 (89%)	52 (73%)	19 (27%)	0	3
20	T	76/82 (93%)	49 (64%)	27 (36%)	0	1
21	U	19/22 (86%)	16 (84%)	3 (16%)	2	15
All	All	1985/2111 (94%)	1436 (72%)	549 (28%)	0	3

All (549) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	7	VAL
2	B	8	LYS
2	B	10	LEU

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Mol	Chain	Res	Type
2	B	11	LEU
2	B	15	VAL
2	B	20	GLU
2	B	30	ARG
2	B	33	TYR
2	B	35	GLU
2	B	39	ILE
2	B	42	ILE
2	B	44	LEU
2	B	53	ARG
2	B	61	LEU
2	B	63	MET
2	B	64	ARG
2	B	67	THR
2	B	69	LEU
2	B	92	TYR
2	B	95	GLN
2	B	97	TRP
2	B	101	MET
2	B	107	THR
2	B	108	ILE
2	B	109	SER
2	B	111	ARG
2	B	115	LEU
2	B	122	PHE
2	B	127	ILE
2	B	128	GLU
2	B	150	SER
2	B	162	ILE
2	B	168	THR
2	B	172	ILE
2	B	182	ILE
2	B	185	ILE
2	B	187	LEU
2	B	193	ASP
2	B	196	LEU
2	B	200	ILE
2	B	204	ASN
2	B	209	ARG
2	B	210	SER
2	B	212	GLN
2	B	215	LEU

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Mol	Chain	Res	Type
2	B	216	SER
2	B	217	ARG
2	B	221	LEU
2	B	222	ILE
2	B	223	ILE
2	B	226	ARG
2	B	240	GLN
3	C	3	ASN
3	C	8	ILE
3	C	10	PHE
3	C	14	ILE
3	C	16	ARG
3	C	22	TRP
3	C	26	LYS
3	C	31	HIS
3	C	33	LEU
3	C	43	LEU
3	C	45	LYS
3	C	52	LEU
3	C	58	GLU
3	C	64	VAL
3	C	70	VAL
3	C	72	LYS
3	C	75	VAL
3	C	79	ARG
3	C	84	ILE
3	C	85	ARG
3	C	99	VAL
3	C	101	LEU
3	C	111	LEU
3	C	116	VAL
3	C	119	ARG
3	C	126	ARG
3	C	127	ARG
3	C	130	VAL
3	C	134	ILE
3	C	144	SER
3	C	147	LYS
3	C	156	ARG
3	C	157	ILE
3	C	165	THR
3	C	167	TRP

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Mol	Chain	Res	Type
3	C	170	GLN
3	C	175	LEU
3	C	177	THR
3	C	178	LEU
3	C	186	PHE
3	C	188	LEU
3	C	190	ARG
3	C	191	THR
3	C	192	THR
3	C	195	VAL
3	C	196	LEU
3	C	204	LEU
4	D	10	ARG
4	D	19	LEU
4	D	20	TYR
4	D	25	ARG
4	D	26	CYS
4	D	28	SER
4	D	47	ARG
4	D	49	ARG
4	D	57	ARG
4	D	58	LEU
4	D	61	LYS
4	D	66	ARG
4	D	70	ILE
4	D	78	LEU
4	D	84	LYS
4	D	85	LYS
4	D	91	SER
4	D	92	VAL
4	D	96	LEU
4	D	108	LEU
4	D	119	GLN
4	D	120	LEU
4	D	122	ARG
4	D	127	THR
4	D	131	ARG
4	D	132	ARG
4	D	135	LEU
4	D	137	SER
4	D	145	GLU
4	D	146	ILE

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Mol	Chain	Res	Type
4	D	150	GLU
4	D	159	ARG
4	D	163	GLU
4	D	169	LYS
4	D	177	ASP
4	D	178	VAL
4	D	179	GLU
4	D	182	LYS
4	D	187	ARG
4	D	188	LEU
4	D	190	ASP
4	D	192	GLU
4	D	194	LEU
4	D	196	LEU
4	D	204	ILE
5	E	10	MET
5	E	11	ILE
5	E	12	LEU
5	E	16	THR
5	E	18	ARG
5	E	24	ARG
5	E	31	LEU
5	E	32	VAL
5	E	37	ARG
5	E	38	GLN
5	E	43	LEU
5	E	47	LYS
5	E	51	VAL
5	E	53	LEU
5	E	55	VAL
5	E	65	ASN
5	E	66	MET
5	E	67	VAL
5	E	68	GLU
5	E	75	THR
5	E	76	ILE
5	E	78	HIS
5	E	79	GLU
5	E	80	ILE
5	E	82	VAL
5	E	83	GLU
5	E	87	SER

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Mol	Chain	Res	Type
5	E	100	VAL
5	E	105	VAL
5	E	110	LEU
5	E	116	THR
5	E	117	ASP
5	E	120	THR
5	E	123	LEU
5	E	125	SER
5	E	126	ARG
5	E	131	ILE
5	E	145	LYS
5	E	147	ASP
5	E	148	VAL
5	E	150	ARG
6	F	1	MET
6	F	2	ARG
6	F	7	ASN
6	F	9	VAL
6	F	10	LEU
6	F	14	LEU
6	F	16	GLN
6	F	21	LEU
6	F	24	GLU
6	F	25	ILE
6	F	26	ILE
6	F	28	ARG
6	F	37	VAL
6	F	39	LYS
6	F	40	VAL
6	F	43	LEU
6	F	46	ARG
6	F	52	ILE
6	F	54	LYS
6	F	63	TYR
6	F	65	VAL
6	F	74	ASP
6	F	75	LEU
6	F	80	ARG
6	F	83	ASP
6	F	84	ASN
6	F	86	ARG
6	F	87	ARG

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Mol	Chain	Res	Type
6	F	89	MET
6	F	93	SER
6	F	94	GLN
6	F	97	PHE
6	F	98	LEU
6	F	100	ASN
7	G	9	VAL
7	G	10	ARG
7	G	12	LEU
7	G	16	LEU
7	G	17	VAL
7	G	22	LEU
7	G	27	ILE
7	G	29	LYS
7	G	38	LEU
7	G	41	ARG
7	G	49	ILE
7	G	52	GLU
7	G	60	LYS
7	G	66	VAL
7	G	72	ARG
7	G	75	VAL
7	G	78	ARG
7	G	87	VAL
7	G	97	GLN
7	G	101	LEU
7	G	113	GLU
7	G	114	ARG
7	G	120	ILE
7	G	122	HIS
7	G	126	ASP
7	G	129	GLU
7	G	135	VAL
7	G	141	VAL
7	G	146	GLU
7	G	156	TRP
8	H	1	MET
8	H	3	THR
8	H	10	LEU
8	H	11	THR
8	H	14	ARG
8	H	19	VAL

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Mol	Chain	Res	Type
8	H	22	GLU
8	H	39	LEU
8	H	45	ILE
8	H	51	VAL
8	H	53	VAL
8	H	57	PRO
8	H	59	LEU
8	H	63	LEU
8	H	83	ILE
8	H	85	ARG
8	H	87	SER
8	H	91	ARG
8	H	95	VAL
8	H	97	VAL
8	H	98	LYS
8	H	100	ILE
8	H	102	ARG
8	H	104	ARG
8	H	107	LEU
8	H	112	LEU
8	H	113	SER
8	H	119	LEU
8	H	121	ASP
8	H	127	LEU
8	H	129	VAL
8	H	133	LEU
8	H	135	CYS
8	H	136	GLU
8	H	137	VAL
9	I	14	VAL
9	I	16	ARG
9	I	19	LEU
9	I	23	ASN
9	I	29	ASN
9	I	33	PHE
9	I	34	ASN
9	I	40	LEU
9	I	42	ARG
9	I	48	GLU
9	I	53	VAL
9	I	63	ILE
9	I	64	THR

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Mol	Chain	Res	Type
9	I	65	VAL
9	I	66	ARG
9	I	79	LEU
9	I	85	LEU
9	I	99	LEU
9	I	102	LEU
9	I	109	VAL
9	I	112	LYS
9	I	121	ARG
9	I	125	TYR
9	I	127	LYS
10	J	4	ILE
10	J	6	ILE
10	J	9	ARG
10	J	12	ASP
10	J	19	SER
10	J	22	LYS
10	J	23	ILE
10	J	28	ARG
10	J	29	ARG
10	J	33	GLN
10	J	34	VAL
10	J	43	ARG
10	J	44	VAL
10	J	63	PHE
10	J	67	THR
10	J	74	ILE
10	J	89	ASP
10	J	90	LEU
10	J	94	VAL
10	J	98	ILE
10	J	99	LYS
11	K	11	LYS
11	K	13	GLN
11	K	14	VAL
11	K	18	ARG
11	K	29	ILE
11	K	40	ILE
11	K	47	VAL
11	K	48	ILE
11	K	57	THR
11	K	75	TYR

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Mol	Chain	Res	Type
11	K	78	GLN
11	K	80	VAL
11	K	83	ILE
11	K	99	GLN
11	K	105	VAL
11	K	108	ILE
11	K	116	HIS
11	K	117	ASN
11	K	120	ARG
11	K	125	PHE
11	K	126	ARG
11	K	127	LYS
12	L	7	ILE
12	L	11	VAL
12	L	18	VAL
12	L	19	ARG
12	L	20	LYS
12	L	34	ARG
12	L	36	VAL
12	L	37	CYS
12	L	39	VAL
12	L	43	VAL
12	L	44	THR
12	L	50	SER
12	L	52	LEU
12	L	53	ARG
12	L	60	LEU
12	L	75	HIS
12	L	81	SER
12	L	82	VAL
12	L	96	VAL
12	L	101	VAL
12	L	110	VAL
12	L	113	ARG
12	L	116	SER
12	L	122	THR
12	L	127	GLU
13	M	7	VAL
13	M	14	ARG
13	M	17	VAL
13	M	22	ILE
13	M	31	LYS

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Mol	Chain	Res	Type
13	M	32	GLU
13	M	46	LYS
13	M	48	LEU
13	M	50	GLU
13	M	52	GLU
13	M	55	ARG
13	M	56	LEU
13	M	57	ARG
13	M	58	GLU
13	M	64	TRP
13	M	66	LEU
13	M	67	GLU
13	M	69	GLU
13	M	70	LEU
13	M	74	VAL
13	M	81	LEU
13	M	84	ILE
13	M	88	ARG
13	M	94	ARG
13	M	96	LEU
13	M	99	ARG
13	M	105	THR
13	M	115	LYS
14	N	3	ARG
14	N	6	LEU
14	N	7	ILE
14	N	9	LYS
14	N	12	ARG
14	N	17	LYS
14	N	24	CYS
14	N	27	CYS
14	N	29	ARG
14	N	33	VAL
14	N	46	GLU
14	N	49	HIS
14	N	58	LYS
15	O	5	LYS
15	O	6	GLU
15	O	11	VAL
15	O	12	ILE
15	O	17	ARG
15	O	24	SER

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Mol	Chain	Res	Type
15	O	26	GLU
15	O	27	VAL
15	O	31	LEU
15	O	38	ARG
15	O	39	LEU
15	O	40	SER
15	O	44	LYS
15	O	45	VAL
15	O	47	LYS
15	O	56	LEU
15	O	57	LEU
15	O	60	VAL
15	O	67	LEU
15	O	73	GLU
15	O	81	LEU
15	O	82	ILE
15	O	87	ILE
15	O	88	ARG
16	P	1	MET
16	P	3	LYS
16	P	4	ILE
16	P	8	ARG
16	P	11	SER
16	P	22	THR
16	P	25	ARG
16	P	42	ARG
16	P	45	THR
16	P	48	TRP
16	P	53	VAL
16	P	54	GLU
16	P	55	ARG
16	P	62	VAL
16	P	69	THR
16	P	72	ARG
16	P	75	ARG
16	P	79	VAL
16	P	81	ARG
17	Q	3	LYS
17	Q	5	VAL
17	Q	10	VAL
17	Q	11	VAL
17	Q	22	LEU

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Mol	Chain	Res	Type
17	Q	23	VAL
17	Q	27	PHE
17	Q	29	HIS
17	Q	36	ILE
17	Q	40	LYS
17	Q	43	LEU
17	Q	50	LYS
17	Q	53	LEU
17	Q	59	ILE
17	Q	60	ILE
17	Q	62	SER
17	Q	70	ARG
17	Q	77	VAL
17	Q	84	LEU
17	Q	85	VAL
17	Q	90	ILE
17	Q	91	ARG
17	Q	93	GLN
17	Q	98	LEU
17	Q	101	ARG
18	R	18	ARG
18	R	26	LEU
18	R	31	LEU
18	R	38	GLU
18	R	40	LEU
18	R	44	LEU
18	R	46	GLU
18	R	50	ILE
18	R	58	LEU
18	R	70	ILE
18	R	78	LEU
18	R	82	THR
18	R	86	VAL
18	R	87	ARG
18	R	88	LYS
19	S	4	SER
19	S	7	LYS
19	S	9	VAL
19	S	11	VAL
19	S	14	HIS
19	S	15	LEU
19	S	16	LEU

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Mol	Chain	Res	Type
19	S	17	GLU
19	S	19	VAL
19	S	27	GLU
19	S	29	ARG
19	S	31	ILE
19	S	37	ARG
19	S	39	THR
19	S	43	GLU
19	S	58	VAL
19	S	64	GLU
19	S	71	LEU
19	S	81	ARG
20	T	9	ASN
20	T	10	LEU
20	T	11	SER
20	T	13	LEU
20	T	17	ARG
20	T	19	SER
20	T	20	LEU
20	T	24	LEU
20	T	33	ILE
20	T	45	GLN
20	T	50	GLU
20	T	55	ILE
20	T	62	LEU
20	T	72	LEU
20	T	73	HIS
20	T	74	LYS
20	T	75	ASN
20	T	80	ARG
20	T	85	MET
20	T	86	ARG
20	T	87	LYS
20	T	88	VAL
20	T	91	LEU
20	T	92	LEU
20	T	99	LEU
20	T	100	ILE
20	T	104	LEU
21	U	10	ARG
21	U	15	ARG
21	U	25	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	212	GLN
3	C	6	HIS
3	C	98	ASN
4	D	42	GLN
4	D	125	HIS
5	E	65	ASN
6	F	57	GLN
7	G	37	ASN
9	I	73	GLN
10	J	56	HIS
11	K	99	GLN
12	L	75	HIS
13	M	101	GLN
15	O	42	HIS
16	P	14	ASN
16	P	16	HIS
17	Q	96	GLN
19	S	23	ASN
19	S	57	HIS
20	T	18	GLN
20	T	90	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1504/1522 (98%)	378 (25%)	48 (3%)
22	V	3/4 (75%)	1 (33%)	0
23	W	10/11 (90%)	2 (20%)	0
24	a	7/8 (87%)	4 (57%)	0
25	b	2/3 (66%)	0	0
All	All	1526/1548 (98%)	385 (25%)	48 (3%)

All (385) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	7	G
1	A	8	A
1	A	9	G
1	A	16	A
1	A	31	G

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Mol	Chain	Res	Type
1	A	32	A
1	A	33	A
1	A	34	C
1	A	39	G
1	A	47	C
1	A	48	C
1	A	51	A
1	A	81	U
1	A	82	U
1	A	88	A
1	A	89	C
1	A	90	U
1	A	91	C
1	A	95	U
1	A	99	C
1	A	105	G
1	A	108	G
1	A	109	A
1	A	115	G
1	A	116	A
1	A	120	A
1	A	121	C
1	A	129(A)	G
1	A	130	A
1	A	131	C
1	A	138	G
1	A	144	G
1	A	151	A
1	A	157	G
1	A	159	G
1	A	162	A
1	A	163	C
1	A	170	U
1	A	173	U
1	A	181	G
1	A	182	U
1	A	183	G
1	A	190(B)	C
1	A	190(E)	U
1	A	190(G)	G
1	A	195	A
1	A	197	A

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Mol	Chain	Res	Type
1	A	199	G
1	A	201	C
1	A	202	U
1	A	216	G
1	A	222	U
1	A	225	C
1	A	230	G
1	A	246	A
1	A	247	G
1	A	250	A
1	A	251	G
1	A	252	U
1	A	253	U
1	A	254	G
1	A	258	G
1	A	260	G
1	A	266	G
1	A	267	C
1	A	276	G
1	A	289	G
1	A	299	G
1	A	301	G
1	A	319	G
1	A	321	A
1	A	328	C
1	A	329	A
1	A	331	G
1	A	332	G
1	A	345	C
1	A	346	G
1	A	352	C
1	A	353	A
1	A	354	G
1	A	367	U
1	A	372	C
1	A	373	A
1	A	381	C
1	A	384	G
1	A	387	U
1	A	388	G
1	A	397	A
1	A	398	C

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Mol	Chain	Res	Type
1	A	406	G
1	A	410	G
1	A	412	A
1	A	413	G
1	A	421	U
1	A	422	C
1	A	424	G
1	A	429	U
1	A	430	A
1	A	435	C
1	A	439	A
1	A	442	C
1	A	443	C
1	A	449	C
1	A	450	G
1	A	452	A
1	A	460	A
1	A	461	C
1	A	462	G
1	A	475	G
1	A	485	G
1	A	497	A
1	A	498	U
1	A	500	G
1	A	509	A
1	A	510	A
1	A	511	C
1	A	517	G
1	A	518	C
1	A	519	C
1	A	520	A
1	A	527	7MG
1	A	530	G
1	A	532	A
1	A	533	A
1	A	544	G
1	A	545	C
1	A	547	A
1	A	550	G
1	A	559	A
1	A	560	U
1	A	561	U

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Mol	Chain	Res	Type
1	A	562	C
1	A	563	A
1	A	564	C
1	A	566	G
1	A	568	G
1	A	569	C
1	A	571	U
1	A	572	A
1	A	573	A
1	A	575	G
1	A	576	G
1	A	578	C
1	A	587	G
1	A	588	G
1	A	607	A
1	A	624	C
1	A	629	G
1	A	631	G
1	A	644	G
1	A	651	C
1	A	653	A
1	A	661	G
1	A	665	A
1	A	671	G
1	A	673	G
1	A	675	A
1	A	687	A
1	A	688	G
1	A	695	A
1	A	698	G
1	A	701	C
1	A	702	A
1	A	704	A
1	A	721	G
1	A	723	U
1	A	724	G
1	A	728	A
1	A	731	G
1	A	734	G
1	A	741	G
1	A	747	C
1	A	748	C

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Mol	Chain	Res	Type
1	A	752	G
1	A	755	G
1	A	777	A
1	A	785	G
1	A	786	G
1	A	788	U
1	A	789	U
1	A	792	A
1	A	793	U
1	A	794	A
1	A	795	C
1	A	804	U
1	A	812	C
1	A	813	U
1	A	815	A
1	A	816	A
1	A	817	C
1	A	827	U
1	A	828	A
1	A	829	G
1	A	839	U
1	A	840	C
1	A	841	U
1	A	848	C
1	A	851	G
1	A	866	C
1	A	867	G
1	A	868	C
1	A	869	G
1	A	873	A
1	A	889	A
1	A	902	G
1	A	905	U
1	A	914	A
1	A	922	G
1	A	926	G
1	A	927	G
1	A	933	G
1	A	934	C
1	A	935	A
1	A	944	G
1	A	950	U

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Mol	Chain	Res	Type
1	A	954	G
1	A	961	U
1	A	966	M2G
1	A	967	5MC
1	A	968	A
1	A	969	A
1	A	971	G
1	A	974	A
1	A	975	A
1	A	976	G
1	A	977	A
1	A	978	A
1	A	984	C
1	A	985	C
1	A	992	U
1	A	993	G
1	A	1003(A)	G
1	A	1004	A
1	A	1005	A
1	A	1006	C
1	A	1021	G
1	A	1025	U
1	A	1026	G
1	A	1027	C
1	A	1028	C
1	A	1030(B)	C
1	A	1030(C)	G
1	A	1045	C
1	A	1048	G
1	A	1050	G
1	A	1052	U
1	A	1053	G
1	A	1054	C
1	A	1055	A
1	A	1064	G
1	A	1065	U
1	A	1066	C
1	A	1068	G
1	A	1078	U
1	A	1079	G
1	A	1094	G
1	A	1095	U

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Mol	Chain	Res	Type
1	A	1101	A
1	A	1104	G
1	A	1111	A
1	A	1122	U
1	A	1124	G
1	A	1125	U
1	A	1126	U
1	A	1127	G
1	A	1129	C
1	A	1130	A
1	A	1131	G
1	A	1137	C
1	A	1138	G
1	A	1139	G
1	A	1141	C
1	A	1142	G
1	A	1143	G
1	A	1159	U
1	A	1162	C
1	A	1164	G
1	A	1171	G
1	A	1178	G
1	A	1181	G
1	A	1182	G
1	A	1183	A
1	A	1184	G
1	A	1190	G
1	A	1191	A
1	A	1193	G
1	A	1196	U
1	A	1198	G
1	A	1200	C
1	A	1201	A
1	A	1202	G
1	A	1206	G
1	A	1211	U
1	A	1212	U
1	A	1213	A
1	A	1214	C
1	A	1215	G
1	A	1225	A
1	A	1226	C

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Mol	Chain	Res	Type
1	A	1227	A
1	A	1235	U
1	A	1238	A
1	A	1245	A
1	A	1249	C
1	A	1250	A
1	A	1251	A
1	A	1253	G
1	A	1256	A
1	A	1257	U
1	A	1258	G
1	A	1270	C
1	A	1273	G
1	A	1279	A
1	A	1280	A
1	A	1281	U
1	A	1282	C
1	A	1286	A
1	A	1287	A
1	A	1288	A
1	A	1300	G
1	A	1301	U
1	A	1302	U
1	A	1303	C
1	A	1304	G
1	A	1305	G
1	A	1312	G
1	A	1313	U
1	A	1317	C
1	A	1318	A
1	A	1319	A
1	A	1320	C
1	A	1322	C
1	A	1328	C
1	A	1338	G
1	A	1348	U
1	A	1353	G
1	A	1356	G
1	A	1359	C
1	A	1360	A
1	A	1361	G
1	A	1362	C

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Mol	Chain	Res	Type
1	A	1363	A
1	A	1370	G
1	A	1379	G
1	A	1381	U
1	A	1382	C
1	A	1393	U
1	A	1394	A
1	A	1397	C
1	A	1398	A
1	A	1399	C
1	A	1400	5MC
1	A	1401	G
1	A	1402	4OC
1	A	1406	U
1	A	1407	5MC
1	A	1414	U
1	A	1418	A
1	A	1419	G
1	A	1420	C
1	A	1442	G
1	A	1443	G
1	A	1447	G
1	A	1451	A
1	A	1455	G
1	A	1478	C
1	A	1487	G
1	A	1497	G
1	A	1502	A
1	A	1504	G
1	A	1505	G
1	A	1506	U
1	A	1507	A
1	A	1526	G
1	A	1529	G
1	A	1530	G
1	A	1534	C
1	A	1538	C
22	V	2	U
23	W	31	C
23	W	33	U
24	a	35	G
24	a	37	A

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Mol	Chain	Res	Type
24	a	39	G
24	a	40	PSU

All (48) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	7	G
1	A	89	C
1	A	115	G
1	A	129(A)	G
1	A	150	C
1	A	181	G
1	A	204	U
1	A	246	A
1	A	250	A
1	A	251	G
1	A	266	G
1	A	328	C
1	A	344	A
1	A	428	G
1	A	429	U
1	A	484	G
1	A	499	A
1	A	509	A
1	A	544	G
1	A	559	A
1	A	560	U
1	A	587	G
1	A	687	A
1	A	701	C
1	A	812	C
1	A	913	A
1	A	960	U
1	A	991	U
1	A	1026	G
1	A	1049	U
1	A	1065	U
1	A	1067	A
1	A	1137	C
1	A	1182	G
1	A	1190	G
1	A	1201	A

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Mol	Chain	Res	Type
1	A	1212	U
1	A	1256	A
1	A	1279	A
1	A	1281	U
1	A	1300	G
1	A	1319	A
1	A	1347	G
1	A	1360	A
1	A	1361(A)	C
1	A	1397	C
1	A	1528	U
1	A	1533	C

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

18 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	5MC	A	1404	1	19,22,23	1.09	2 (10%)	26,32,35	1.26	5 (19%)
1	UR3	A	1498	1	19,22,23	0.89	1 (5%)	26,32,35	1.09	1 (3%)
1	4OC	A	1402	1	20,23,24	1.73	4 (20%)	25,32,35	1.11	2 (8%)
1	MA6	A	1518[B]	1	23,26,27	1.40	3 (13%)	33,38,41	0.86	1 (3%)
1	MA6	A	1518[A]	1	23,26,27	1.82	6 (26%)	33,38,41	1.01	2 (6%)
1	5MC	A	1407	1	19,22,23	2.47	3 (15%)	26,32,35	1.33	2 (7%)
23	PSU	W	40	23	18,21,22	1.12	1 (5%)	21,30,33	1.84	5 (23%)
24	PSU	a	40	1,24	18,21,22	1.39	3 (16%)	21,30,33	1.99	6 (28%)
1	MA6	A	1519[A]	1	23,26,27	1.35	3 (13%)	33,38,41	1.09	3 (9%)
1	2MG	A	1207	1	23,26,27	2.03	7 (30%)	33,38,41	1.14	4 (12%)
1	MA6	A	1519[B]	1	23,26,27	2.02	9 (39%)	33,38,41	1.02	3 (9%)
1	7MG	A	527	1	23,26,27	4.96	7 (30%)	27,39,42	2.65	9 (33%)
1	PSU	A	1540	1	18,21,22	1.22	1 (5%)	21,30,33	1.69	3 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	M2G	A	966	1	24,27,28	0.86	1 (4%)	33,40,43	0.91	2 (6%)
1	5MC	A	967	1	19,22,23	1.35	3 (15%)	26,32,35	0.73	1 (3%)
1	5MC	A	1400	1	19,22,23	2.10	7 (36%)	26,32,35	1.13	3 (11%)
12	0TD	L	92	12	8,9,10	1.39	1 (12%)	6,11,13	3.62	3 (50%)
1	PSU	A	516	1	18,21,22	1.52	2 (11%)	21,30,33	1.71	6 (28%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	5MC	A	1404	1	-	0/7/25/26	0/2/2/2
1	UR3	A	1498	1	-	1/7/25/26	0/2/2/2
1	4OC	A	1402	1	-	4/9/29/30	0/2/2/2
1	MA6	A	1518[B]	1	-	0/11/29/30	0/3/3/3
1	MA6	A	1518[A]	1	-	5/11/29/30	0/3/3/3
1	5MC	A	1407	1	-	2/7/25/26	0/2/2/2
23	PSU	W	40	23	-	3/7/25/26	0/2/2/2
24	PSU	a	40	1,24	-	3/7/25/26	0/2/2/2
1	MA6	A	1519[A]	1	-	5/11/29/30	0/3/3/3
1	2MG	A	1207	1	-	0/9/27/28	0/3/3/3
1	MA6	A	1519[B]	1	-	5/11/29/30	0/3/3/3
1	7MG	A	527	1	-	2/7/37/38	0/3/3/3
1	PSU	A	1540	1	-	2/7/25/26	0/2/2/2
1	M2G	A	966	1	-	4/11/29/30	0/3/3/3
1	5MC	A	967	1	-	3/7/25/26	0/2/2/2
1	5MC	A	1400	1	-	2/7/25/26	0/2/2/2
12	0TD	L	92	12	-	3/7/12/14	-
1	PSU	A	516	1	-	0/7/25/26	0/2/2/2

All (64) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	527	7MG	C8-N9	-20.99	1.32	1.45
1	A	1407	5MC	C5-C4	8.60	1.50	1.44
1	A	527	7MG	C5-N7	8.43	1.46	1.35
1	A	1400	5MC	C2-N1	5.62	1.51	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1207	2MG	C2-N1	5.53	1.45	1.36
1	A	516	PSU	C6-C5	5.26	1.41	1.35
1	A	1402	4OC	C2-N3	5.19	1.46	1.36
1	A	1519[B]	MA6	C5-C4	4.76	1.47	1.39
1	A	1518[A]	MA6	C5-C4	4.49	1.47	1.39
1	A	1519[B]	MA6	C2-N1	4.45	1.41	1.33
1	A	1540	PSU	C6-C5	4.41	1.40	1.35
1	A	1400	5MC	C2-N3	4.13	1.44	1.36
24	a	40	PSU	C6-C5	4.13	1.39	1.35
1	A	527	7MG	C2-N2	3.89	1.43	1.34
1	A	1407	5MC	C2-N1	3.81	1.48	1.40
1	A	1518[A]	MA6	C8-N9	3.79	1.44	1.37
23	W	40	PSU	C6-C5	3.77	1.39	1.35
1	A	1207	2MG	C2-N2	3.66	1.41	1.33
1	A	1207	2MG	C6-N1	3.55	1.45	1.38
1	A	1407	5MC	C2-N3	3.48	1.43	1.36
1	A	1404	5MC	C2-N1	3.41	1.47	1.40
1	A	1518[A]	MA6	C4-N9	3.37	1.44	1.37
1	A	1519[A]	MA6	C5-C4	3.34	1.45	1.39
1	A	1518[B]	MA6	C5-C4	3.32	1.45	1.39
1	A	1519[B]	MA6	C6-N1	3.09	1.40	1.34
1	A	1519[A]	MA6	C8-N7	2.98	1.37	1.31
1	A	1518[B]	MA6	C8-N9	2.98	1.42	1.37
1	A	1518[A]	MA6	C2-N1	2.97	1.39	1.33
1	A	1207	2MG	O6-C6	2.94	1.29	1.23
1	A	1400	5MC	C4-N4	2.93	1.41	1.34
24	a	40	PSU	C1'-C5	2.88	1.56	1.50
1	A	1518[B]	MA6	C2-N1	2.88	1.39	1.33
1	A	1518[A]	MA6	C8-N7	2.84	1.37	1.31
1	A	527	7MG	C5-C6	2.82	1.50	1.43
1	A	1519[B]	MA6	C4-N3	2.78	1.39	1.34
1	A	1519[B]	MA6	C6-N6	2.61	1.44	1.36
1	A	1400	5MC	C5-C4	2.61	1.46	1.44
1	A	967	5MC	O2-C2	-2.61	1.18	1.23
1	A	1207	2MG	C5-C4	2.60	1.45	1.38
1	A	1518[A]	MA6	C4-N3	2.55	1.39	1.34
1	A	1402	4OC	CM4-N4	2.55	1.50	1.45
1	A	1519[A]	MA6	C2-N1	2.54	1.38	1.33
1	A	967	5MC	C6-C5	2.52	1.38	1.34
1	A	527	7MG	C4-N3	2.46	1.39	1.34
1	A	1207	2MG	C8-N9	2.46	1.43	1.37
12	L	92	0TD	CB-CA	-2.41	1.54	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1400	5MC	C1'-N1	2.36	1.54	1.47
1	A	1400	5MC	C4-N3	2.35	1.37	1.34
1	A	1519[B]	MA6	C2-N3	2.34	1.38	1.33
1	A	1519[B]	MA6	C8-N9	2.30	1.41	1.37
1	A	516	PSU	C2-N1	2.26	1.39	1.36
1	A	1498	UR3	C6-N1	-2.25	1.32	1.38
1	A	966	M2G	C4-N3	2.23	1.39	1.34
1	A	967	5MC	C2-N3	2.21	1.40	1.36
1	A	1402	4OC	C4-N4	-2.20	1.31	1.36
1	A	1400	5MC	C6-C5	2.11	1.38	1.34
1	A	1519[B]	MA6	C8-N7	2.09	1.35	1.31
1	A	1404	5MC	C2-N3	2.07	1.40	1.36
1	A	1402	4OC	O2-C2	2.07	1.27	1.23
24	a	40	PSU	C2-N1	2.07	1.39	1.36
1	A	527	7MG	C8-N7	-2.06	1.32	1.42
1	A	1207	2MG	C4-N3	2.04	1.38	1.34
1	A	527	7MG	C2-N1	-2.03	1.32	1.37
1	A	1519[B]	MA6	C5-C6	2.01	1.46	1.41

All (61) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	L	92	0TD	CB-CA-N	-6.30	96.33	109.10
1	A	527	7MG	C6-C5-N7	6.25	141.62	131.93
1	A	527	7MG	C5-C6-N1	5.77	121.09	110.94
1	A	527	7MG	C2-N3-C4	5.49	121.76	112.30
12	L	92	0TD	CSB-SB-CB	-4.90	93.56	102.36
23	W	40	PSU	N1-C2-N3	4.76	120.19	115.17
24	a	40	PSU	C4-N3-C2	-4.73	119.85	126.37
1	A	527	7MG	C6-C5-C4	-4.54	114.42	122.40
1	A	1540	PSU	C4-N3-C2	-4.47	120.22	126.37
23	W	40	PSU	C4-N3-C2	-4.45	120.25	126.37
1	A	516	PSU	C4-N3-C2	-4.03	120.82	126.37
1	A	1540	PSU	N1-C2-N3	3.97	119.36	115.17
24	a	40	PSU	O4-C4-N3	-3.82	112.93	120.11
1	A	516	PSU	N1-C2-N3	3.82	119.19	115.17
1	A	527	7MG	C5-C4-N3	-3.63	121.31	128.13
24	a	40	PSU	C6-C5-C4	-3.56	115.77	118.17
1	A	527	7MG	C2-N1-C6	-3.38	118.98	125.11
1	A	1498	UR3	C6-N1-C2	-3.33	119.07	121.80
1	A	1407	5MC	N4-C4-N3	-3.30	112.52	118.51
1	A	527	7MG	N9-C4-N3	3.22	130.18	125.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	a	40	PSU	N1-C2-N3	3.18	118.52	115.17
1	A	527	7MG	O6-C6-N1	-3.02	114.44	120.11
1	A	1404	5MC	C5-C4-N3	2.96	124.79	121.75
1	A	1400	5MC	C1'-N1-C6	-2.80	116.54	121.15
12	L	92	0TD	OD1-CG-CB	-2.80	116.58	122.44
1	A	527	7MG	N9-C8-N7	2.79	107.33	103.37
1	A	1519[B]	MA6	C4-C5-C6	2.77	118.78	115.91
1	A	1402	4OC	C5-C4-N4	-2.71	116.44	122.40
24	a	40	PSU	O2-C2-N3	-2.70	117.06	121.86
24	a	40	PSU	C5-C4-N3	2.66	122.40	116.55
1	A	1207	2MG	C5-C4-N3	-2.56	124.32	128.39
23	W	40	PSU	C6-N1-C2	-2.54	120.33	122.69
23	W	40	PSU	C6-C5-C4	2.53	119.88	118.17
23	W	40	PSU	O2-C2-N1	-2.49	120.22	122.79
1	A	1400	5MC	C1'-N1-C2	2.48	123.92	118.44
1	A	1540	PSU	O2-C2-N1	-2.47	120.24	122.79
1	A	966	M2G	C5-C4-N3	-2.42	124.53	128.39
1	A	1404	5MC	N4-C4-N3	-2.42	114.13	118.51
1	A	1518[A]	MA6	C5-C4-N3	-2.39	123.42	126.72
1	A	516	PSU	O4-C4-N3	-2.37	115.66	120.11
1	A	1207	2MG	O6-C6-C5	2.37	132.78	126.53
1	A	1207	2MG	C6-C5-C4	2.33	122.33	118.83
1	A	1404	5MC	C5-C6-N1	-2.32	120.79	123.31
1	A	1400	5MC	O2-C2-N1	2.31	123.43	118.90
1	A	1518[B]	MA6	C2-N1-C6	2.31	117.48	111.83
1	A	1402	4OC	C1'-N1-C2	2.29	123.50	118.44
1	A	1519[B]	MA6	C4-C5-N7	-2.28	107.98	110.58
1	A	1518[A]	MA6	C2-N1-C6	2.24	117.30	111.83
1	A	1519[A]	MA6	C4-C5-N7	-2.24	108.03	110.58
1	A	1407	5MC	CM5-C5-C6	-2.23	119.84	122.85
1	A	1519[A]	MA6	C2-N1-C6	2.18	117.16	111.83
1	A	967	5MC	N4-C4-N3	-2.18	114.56	118.51
1	A	516	PSU	O4'-C1'-C2'	2.17	108.16	105.15
1	A	1404	5MC	C1'-N1-C6	-2.17	117.58	121.15
1	A	516	PSU	C6-N1-C2	-2.17	120.68	122.69
1	A	1404	5MC	C4-N3-C2	-2.17	117.80	120.81
1	A	1519[B]	MA6	C2-N1-C6	2.15	117.08	111.83
1	A	966	M2G	O6-C6-N1	-2.11	116.15	120.11
1	A	1519[A]	MA6	C5-C4-N3	-2.07	123.86	126.72
1	A	1207	2MG	N2-C2-N3	-2.05	117.90	120.51
1	A	516	PSU	C6-C5-C4	-2.01	116.82	118.17

There are no chirality outliers.

All (44) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	966	M2G	N1-C2-N2-CM1
1	A	966	M2G	N3-C2-N2-CM1
1	A	966	M2G	N3-C2-N2-CM2
1	A	967	5MC	O4'-C4'-C5'-O5'
1	A	1400	5MC	O4'-C4'-C5'-O5'
1	A	1402	4OC	O4'-C4'-C5'-O5'
1	A	1407	5MC	O4'-C4'-C5'-O5'
1	A	1518[A]	MA6	C5-C6-N6-C9
1	A	1519[A]	MA6	C5-C6-N6-C9
1	A	1519[B]	MA6	O4'-C4'-C5'-O5'
1	A	1519[B]	MA6	C3'-C4'-C5'-O5'
1	A	1519[B]	MA6	C5-C6-N6-C9
1	A	1519[B]	MA6	N1-C6-N6-C9
24	a	40	PSU	O4'-C1'-C5-C4
24	a	40	PSU	O4'-C1'-C5-C6
1	A	527	7MG	C3'-C4'-C5'-O5'
1	A	967	5MC	C3'-C4'-C5'-O5'
1	A	1400	5MC	C3'-C4'-C5'-O5'
1	A	1402	4OC	C3'-C4'-C5'-O5'
1	A	1519[A]	MA6	O4'-C4'-C5'-O5'
1	A	527	7MG	O4'-C4'-C5'-O5'
1	A	1518[A]	MA6	N1-C6-N6-C9
1	A	1519[A]	MA6	N1-C6-N6-C9
1	A	1407	5MC	C3'-C4'-C5'-O5'
1	A	1519[A]	MA6	C3'-C4'-C5'-O5'
1	A	1519[A]	MA6	C5-C6-N6-C10
1	A	966	M2G	N1-C2-N2-CM2
1	A	1519[B]	MA6	C5-C6-N6-C10
23	W	40	PSU	C3'-C4'-C5'-O5'
12	L	92	0TD	CG-CB-SB-CSB
23	W	40	PSU	O4'-C4'-C5'-O5'
12	L	92	0TD	SB-CB-CG-OD1
1	A	1540	PSU	O4'-C1'-C5-C4
1	A	1518[A]	MA6	C5-C6-N6-C10
1	A	1518[A]	MA6	C3'-C4'-C5'-O5'
12	L	92	0TD	CA-CB-SB-CSB
1	A	1540	PSU	O4'-C1'-C5-C6
1	A	1402	4OC	C2'-C1'-N1-C6
23	W	40	PSU	C2'-C1'-C5-C6
24	a	40	PSU	C2'-C1'-C5-C6
1	A	1518[A]	MA6	O4'-C4'-C5'-O5'
1	A	1402	4OC	C2'-C1'-N1-C2

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Mol	Chain	Res	Type	Atoms
1	A	1498	UR3	O4'-C4'-C5'-O5'
1	A	967	5MC	C2'-C1'-N1-C6

There are no ring outliers.

17 monomers are involved in 89 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1404	5MC	5	0
1	A	1498	UR3	8	0
1	A	1402	4OC	6	0
1	A	1518[B]	MA6	9	0
1	A	1518[A]	MA6	10	0
1	A	1407	5MC	8	0
23	W	40	PSU	5	0
24	a	40	PSU	1	0
1	A	1519[A]	MA6	18	0
1	A	1207	2MG	11	0
1	A	1519[B]	MA6	11	0
1	A	527	7MG	1	0
1	A	966	M2G	2	0
1	A	967	5MC	3	0
1	A	1400	5MC	4	1
12	L	92	0TD	3	0
1	A	516	PSU	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 347 ligands modelled in this entry, 346 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
27	SRY	A	1928	-	40,42,42	2.36	11 (27%)	49,63,63	2.54	16 (32%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
27	SRY	A	1928	-	-	6/20/87/87	0/3/3/3

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
27	A	1928	SRY	CD1-N31	9.40	1.49	1.33
27	A	1928	SRY	CA1-N11	5.81	1.43	1.33
27	A	1928	SRY	O53-C53	-3.58	1.35	1.44
27	A	1928	SRY	C23-N23	-3.11	1.42	1.47
27	A	1928	SRY	C32-CG2	-3.04	1.47	1.52
27	A	1928	SRY	CD1-NE1	2.97	1.45	1.34
27	A	1928	SRY	CA1-NB1	2.79	1.44	1.34
27	A	1928	SRY	C11-N11	-2.67	1.41	1.45
27	A	1928	SRY	C21-C11	-2.52	1.48	1.53
27	A	1928	SRY	C21-C31	-2.14	1.49	1.53
27	A	1928	SRY	O32-C32	-2.02	1.41	1.44

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
27	A	1928	SRY	C43-C33-C23	-7.61	99.32	110.40
27	A	1928	SRY	C61-C11-N11	-6.57	98.51	110.62
27	A	1928	SRY	C12-O42-C42	-6.05	98.71	108.48
27	A	1928	SRY	C13-O13-C22	-5.57	106.79	116.26
27	A	1928	SRY	O53-C13-C23	4.53	119.15	110.59
27	A	1928	SRY	O53-C53-C43	3.97	116.86	109.70
27	A	1928	SRY	O41-C41-C51	3.84	116.99	107.23
27	A	1928	SRY	C51-C61-C11	3.19	115.05	110.40
27	A	1928	SRY	O21-C21-C31	3.08	115.72	109.58
27	A	1928	SRY	O51-C51-C61	-2.91	103.52	110.38
27	A	1928	SRY	OG2-CG2-C32	-2.81	117.71	124.17
27	A	1928	SRY	O53-C53-C63	-2.50	100.26	106.44
27	A	1928	SRY	O43-C43-C33	2.23	115.64	110.38
27	A	1928	SRY	CI3-N23-C23	-2.16	111.44	114.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
27	A	1928	SRY	O63-C63-C53	-2.08	104.24	111.33
27	A	1928	SRY	C63-C53-C43	-2.08	107.92	113.02

There are no chirality outliers.

All (6) torsion outliers are listed below:

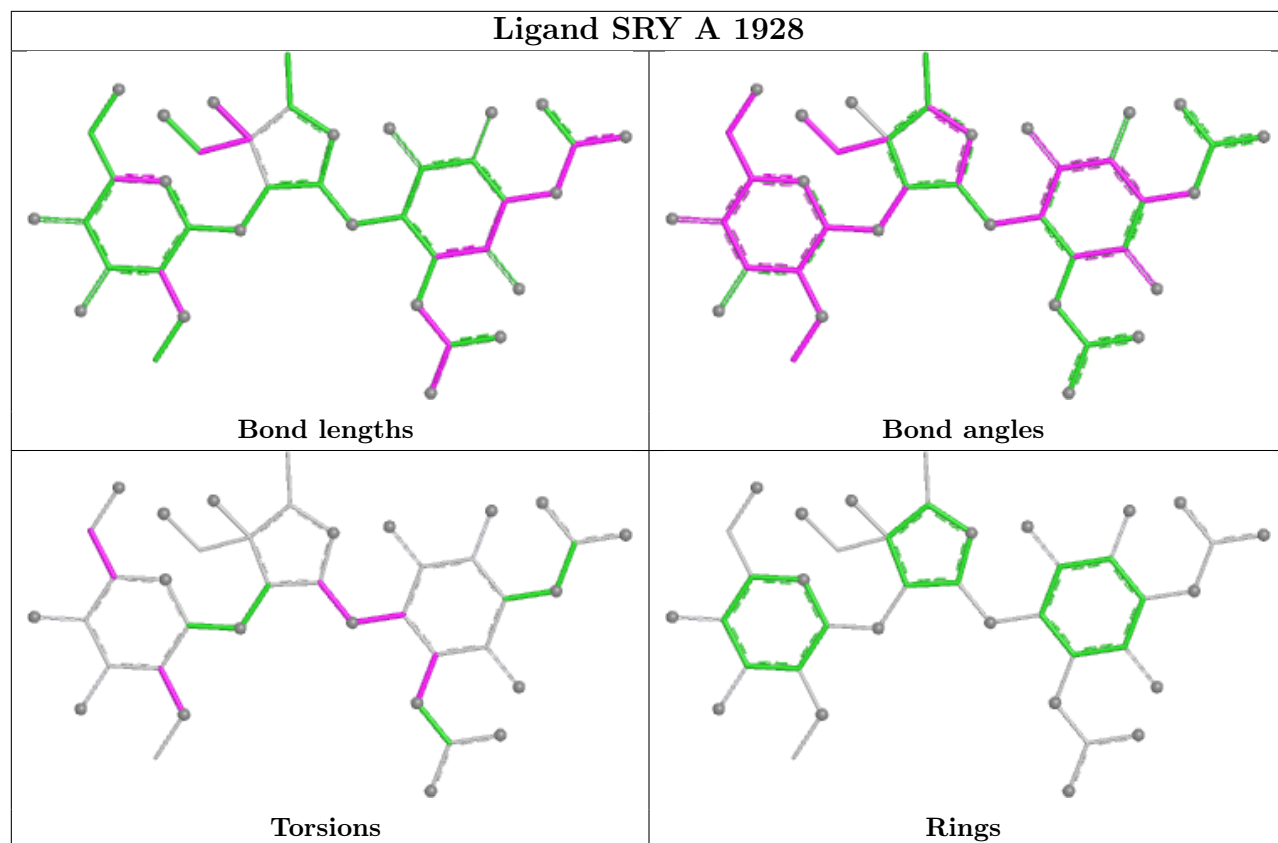
Mol	Chain	Res	Type	Atoms
27	A	1928	SRY	O53-C53-C63-O63
27	A	1928	SRY	C43-C53-C63-O63
27	A	1928	SRY	O42-C12-O41-C41
27	A	1928	SRY	C51-C41-O41-C12
27	A	1928	SRY	C13-C23-N23-CI3
27	A	1928	SRY	C21-C31-N31-CD1

There are no ring outliers.

1 monomer is involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
27	A	1928	SRY	15	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	1500/1522 (98%)	-0.68	6 (0%) 88 73	55, 129, 232, 327	6 (0%)
2	B	236/256 (92%)	-0.33	0 100 100	62, 153, 220, 247	0
3	C	207/239 (86%)	-0.35	3 (1%) 73 50	94, 191, 226, 244	0
4	D	208/209 (99%)	-0.22	6 (2%) 53 36	105, 149, 198, 214	0
5	E	151/162 (93%)	-0.55	1 (0%) 84 65	80, 114, 166, 193	0
6	F	101/101 (100%)	-0.62	0 100 100	110, 150, 182, 226	0
7	G	155/156 (99%)	-0.40	4 (2%) 57 38	121, 160, 223, 238	0
8	H	138/138 (100%)	-0.49	0 100 100	75, 104, 138, 155	0
9	I	127/128 (99%)	-0.17	2 (1%) 70 47	125, 184, 217, 240	0
10	J	99/105 (94%)	-0.09	1 (1%) 79 57	81, 203, 272, 295	0
11	K	117/129 (90%)	-0.42	1 (0%) 81 59	88, 130, 160, 167	0
12	L	124/135 (91%)	-0.19	2 (1%) 70 47	97, 136, 168, 247	0
13	M	118/126 (93%)	-0.34	0 100 100	127, 158, 192, 211	0
14	N	60/61 (98%)	0.07	3 (5%) 34 25	144, 169, 210, 246	0
15	O	88/89 (98%)	-0.47	0 100 100	94, 127, 182, 225	0
16	P	84/88 (95%)	-0.11	0 100 100	96, 126, 164, 239	0
17	Q	100/105 (95%)	-0.41	0 100 100	83, 111, 150, 189	0
18	R	71/88 (80%)	-0.60	0 100 100	95, 132, 178, 229	0
19	S	81/93 (87%)	-0.30	1 (1%) 76 54	84, 184, 228, 234	0
20	T	99/106 (93%)	-0.17	1 (1%) 79 57	95, 126, 167, 212	0
21	U	25/27 (92%)	0.70	4 (16%) 5 7	77, 163, 192, 220	0
22	V	4/4 (100%)	2.02	1 (25%) 2 3	252, 267, 272, 275	0
23	W	10/11 (90%)	1.52	3 (30%) 1 2	173, 279, 296, 387	5 (50%)
24	a	7/8 (87%)	1.00	1 (14%) 6 9	200, 217, 282, 330	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
25	b	3/3 (100%)	0.76	0	100 100	160, 160, 206, 218	0
All	All	3913/4089 (95%)	-0.45	40 (1%)	79 57	55, 140, 221, 387	11 (0%)

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1517[A]	G	7.4
11	K	127	LYS	4.9
12	L	129	ALA	4.8
21	U	25	LYS	4.8
1	A	1516[A]	G	4.6
22	V	4	U	4.1
9	I	9	ARG	4.0
23	W	30	G	4.0
20	T	12	ALA	3.8
4	D	9	CYS	3.7
12	L	19	ARG	3.7
23	W	31	C	3.5
24	a	33	U	3.5
14	N	12	ARG	3.4
19	S	3	ARG	3.3
1	A	1129	C	2.9
3	C	188	LEU	2.9
7	G	84	ASN	2.9
5	E	81	GLU	2.9
3	C	155	GLY	2.8
21	U	6	ARG	2.8
4	D	21	LEU	2.8
7	G	5	ARG	2.6
4	D	2	GLY	2.6
1	A	1493[A]	A	2.5
4	D	31	CYS	2.4
21	U	18	TYR	2.4
4	D	26	CYS	2.4
21	U	9	ARG	2.4
1	A	81	U	2.4
3	C	201	TYR	2.3
4	D	3	ARG	2.3
23	W	34	G	2.3
9	I	105	ASP	2.3
10	J	57	LYS	2.3
14	N	25	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	1492[A]	A	2.1
14	N	13	THR	2.1
7	G	8	GLU	2.1
7	G	80	VAL	2.1

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
23	PSU	W	40	20/21	0.36	0.12	291,301,325,326	0
1	PSU	A	1540	20/21	0.71	0.18	253,269,289,293	0
24	PSU	a	40	20/21	0.86	0.24	208,236,258,262	0
1	2MG	A	1207	24/25	0.93	0.09	154,167,200,202	0
1	UR3	A	1498	21/22	0.94	0.12	111,124,183,193	0
1	5MC	A	1407	21/22	0.94	0.07	127,152,158,162	0
1	PSU	A	516	20/21	0.95	0.05	123,147,168,168	0
1	MA6	A	1518[A]	24/25	0.95	0.28	110,122,127,131	24
1	MA6	A	1518[B]	24/25	0.95	0.28	107,122,137,148	24
1	5MC	A	1400	21/22	0.97	0.08	103,130,148,159	0
1	4OC	A	1402	22/23	0.97	0.08	104,119,127,142	0
1	M2G	A	966	25/26	0.97	0.09	122,137,142,145	0
1	MA6	A	1519[A]	24/25	0.98	0.17	100,115,125,126	24
1	MA6	A	1519[B]	24/25	0.98	0.17	101,116,129,130	24
1	7MG	A	527	24/25	0.98	0.07	91,114,123,126	0
1	5MC	A	1404	21/22	0.98	0.09	102,129,148,149	0
1	5MC	A	967	21/22	0.98	0.06	117,131,145,146	0
12	0TD	L	92	10/11	0.99	0.06	113,121,127,289	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
26	MG	A	1814	1/1	0.35	0.14	440,440,440,440	0
26	MG	A	1797	1/1	0.38	0.08	502,502,502,502	0
26	MG	A	1808	1/1	0.42	0.13	498,498,498,498	0
26	MG	A	1926	1/1	0.46	0.38	116,116,116,116	0
26	MG	A	1801	1/1	0.49	0.08	464,464,464,464	0
26	MG	A	1839	1/1	0.50	0.10	467,467,467,467	0
26	MG	A	1863	1/1	0.53	0.07	409,409,409,409	0
26	MG	A	1683	1/1	0.56	0.18	154,154,154,154	0
26	MG	A	1675	1/1	0.57	0.33	122,122,122,122	0
26	MG	A	1728	1/1	0.57	0.42	114,114,114,114	0
26	MG	A	1819	1/1	0.57	0.14	493,493,493,493	0
26	MG	A	1884	1/1	0.60	0.23	119,119,119,119	0
26	MG	A	1845	1/1	0.60	0.11	410,410,410,410	0
26	MG	A	1826	1/1	0.61	0.10	395,395,395,395	0
26	MG	A	1925	1/1	0.63	0.14	114,114,114,114	0
26	MG	A	1917	1/1	0.63	0.12	128,128,128,128	0
26	MG	A	1837	1/1	0.64	0.07	469,469,469,469	0
26	MG	A	1700	1/1	0.65	0.10	302,302,302,302	0
26	MG	A	1724	1/1	0.65	0.20	117,117,117,117	0
26	MG	A	1820	1/1	0.65	0.08	373,373,373,373	0
26	MG	A	1618	1/1	0.65	0.09	130,130,130,130	0
26	MG	A	1717	1/1	0.66	0.17	152,152,152,152	0
26	MG	A	1841	1/1	0.67	0.07	496,496,496,496	0
26	MG	A	1910	1/1	0.67	0.19	120,120,120,120	0
26	MG	A	1719	1/1	0.67	0.14	262,262,262,262	0
26	MG	A	1614	1/1	0.67	0.19	285,285,285,285	0
26	MG	A	1875	1/1	0.67	0.07	460,460,460,460	0
26	MG	A	1916	1/1	0.68	0.13	119,119,119,119	0
26	MG	A	1766	1/1	0.69	0.19	105,105,105,105	0
26	MG	A	1830	1/1	0.69	0.08	480,480,480,480	0
26	MG	S	101	1/1	0.69	0.21	115,115,115,115	0
26	MG	A	1871	1/1	0.70	0.13	392,392,392,392	0
26	MG	A	1792	1/1	0.71	0.08	415,415,415,415	0
26	MG	A	1898	1/1	0.71	0.26	89,89,89,89	0
26	MG	A	1729	1/1	0.72	0.18	101,101,101,101	0
26	MG	A	1853	1/1	0.72	0.13	502,502,502,502	0
26	MG	A	1897	1/1	0.72	0.14	114,114,114,114	0
26	MG	A	1674	1/1	0.72	0.09	260,260,260,260	0
26	MG	A	1844	1/1	0.72	0.09	420,420,420,420	0
26	MG	G	201	1/1	0.73	0.17	117,117,117,117	0
26	MG	A	1699	1/1	0.74	0.11	414,414,414,414	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
26	MG	A	1768	1/1	0.74	0.28	107,107,107,107	0
26	MG	A	1865	1/1	0.74	0.08	457,457,457,457	0
26	MG	A	1877	1/1	0.75	0.12	456,456,456,456	1
26	MG	A	1756	1/1	0.75	0.12	126,126,126,126	0
26	MG	A	1799	1/1	0.75	0.06	426,426,426,426	0
26	MG	A	1846	1/1	0.75	0.10	449,449,449,449	0
26	MG	A	1901	1/1	0.75	0.08	101,101,101,101	0
26	MG	A	1665	1/1	0.75	0.21	117,117,117,117	0
26	MG	A	1794	1/1	0.76	0.09	518,518,518,518	0
26	MG	A	1805	1/1	0.77	0.06	331,331,331,331	0
26	MG	A	1678	1/1	0.77	0.09	217,217,217,217	0
26	MG	A	1886	1/1	0.77	0.12	121,121,121,121	0
26	MG	A	1915	1/1	0.77	0.23	117,117,117,117	0
26	MG	A	1740	1/1	0.77	0.13	93,93,93,93	0
26	MG	A	1912	1/1	0.78	0.20	104,104,104,104	0
26	MG	A	1873	1/1	0.78	0.13	361,361,361,361	0
26	MG	F	601	1/1	0.78	0.12	102,102,102,102	0
26	MG	A	1777	1/1	0.78	0.08	94,94,94,94	0
26	MG	A	1790	1/1	0.78	0.08	444,444,444,444	0
26	MG	A	1913	1/1	0.79	0.23	108,108,108,108	0
26	MG	A	1878	1/1	0.79	0.10	346,346,346,346	0
26	MG	A	1787	1/1	0.79	0.19	496,496,496,496	0
26	MG	A	1650	1/1	0.80	0.13	151,151,151,151	0
26	MG	A	1679	1/1	0.80	0.09	369,369,369,369	0
26	MG	E	204	1/1	0.80	0.09	128,128,128,128	0
26	MG	A	1696	1/1	0.81	0.09	263,263,263,263	0
26	MG	A	1706	1/1	0.81	0.09	190,190,190,190	0
26	MG	A	1784	1/1	0.81	0.08	122,122,122,122	0
26	MG	A	1800	1/1	0.82	0.12	415,415,415,415	1
26	MG	A	1730	1/1	0.83	0.21	97,97,97,97	0
26	MG	A	1904	1/1	0.83	0.22	97,97,97,97	0
26	MG	A	1684	1/1	0.83	0.20	109,109,109,109	0
26	MG	A	1870	1/1	0.83	0.16	406,406,406,406	0
26	MG	A	1813	1/1	0.83	0.13	471,471,471,471	0
26	MG	A	1755	1/1	0.83	0.27	74,74,74,74	0
26	MG	A	1629	1/1	0.83	0.28	223,223,223,223	0
26	MG	A	1681	1/1	0.84	0.07	256,256,256,256	0
26	MG	A	1860	1/1	0.84	0.08	460,460,460,460	0
26	MG	A	1682	1/1	0.84	0.08	242,242,242,242	0
26	MG	A	1812	1/1	0.84	0.26	444,444,444,444	0
26	MG	A	1908	1/1	0.84	0.22	81,81,81,81	0
26	MG	A	1779	1/1	0.84	0.17	102,102,102,102	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
26	MG	A	1628	1/1	0.84	0.20	152,152,152,152	0
26	MG	A	1895	1/1	0.84	0.06	106,106,106,106	0
26	MG	A	1914	1/1	0.84	0.23	99,99,99,99	0
26	MG	A	1739	1/1	0.85	0.08	78,78,78,78	0
26	MG	A	1680	1/1	0.85	0.30	214,214,214,214	0
26	MG	A	1671	1/1	0.85	0.15	96,96,96,96	0
26	MG	A	1802	1/1	0.85	0.20	355,355,355,355	0
26	MG	A	1804	1/1	0.85	0.14	447,447,447,447	0
26	MG	A	1673	1/1	0.85	0.23	91,91,91,91	0
26	MG	A	1909	1/1	0.85	0.06	93,93,93,93	0
26	MG	A	1796	1/1	0.85	0.08	416,416,416,416	0
26	MG	A	1757	1/1	0.85	0.37	88,88,88,88	0
26	MG	A	1894	1/1	0.85	0.17	94,94,94,94	0
26	MG	A	1660	1/1	0.86	0.08	224,224,224,224	0
26	MG	A	1823	1/1	0.86	0.10	422,422,422,422	0
26	MG	A	1907	1/1	0.86	0.23	120,120,120,120	0
26	MG	A	1767	1/1	0.86	0.24	111,111,111,111	0
26	MG	A	1891	1/1	0.86	0.14	127,127,127,127	0
26	MG	A	1742	1/1	0.86	0.14	97,97,97,97	0
26	MG	A	1849	1/1	0.86	0.20	471,471,471,471	0
26	MG	A	1744	1/1	0.86	0.19	82,82,82,82	0
26	MG	A	1791	1/1	0.86	0.12	283,283,283,283	0
26	MG	A	1788	1/1	0.87	0.06	285,285,285,285	0
26	MG	A	1789	1/1	0.87	0.13	378,378,378,378	0
26	MG	A	1923	1/1	0.87	0.39	86,86,86,86	0
26	MG	A	1856	1/1	0.87	0.26	478,478,478,478	0
26	MG	A	1743	1/1	0.87	0.26	105,105,105,105	0
26	MG	D	302	1/1	0.87	0.09	104,104,104,104	0
26	MG	A	1758	1/1	0.87	0.32	101,101,101,101	0
26	MG	A	1741	1/1	0.87	0.06	105,105,105,105	0
26	MG	A	1902	1/1	0.87	0.11	119,119,119,119	0
26	MG	A	1793	1/1	0.87	0.12	483,483,483,483	0
26	MG	A	1711	1/1	0.88	0.13	133,133,133,133	0
26	MG	A	1769	1/1	0.88	0.18	127,127,127,127	0
26	MG	A	1848	1/1	0.88	0.25	407,407,407,407	0
26	MG	A	1722	1/1	0.88	0.30	95,95,95,95	0
26	MG	A	1670	1/1	0.88	0.17	234,234,234,234	0
26	MG	A	1921	1/1	0.88	0.10	84,84,84,84	0
26	MG	P	102	1/1	0.88	0.06	101,101,101,101	0
26	MG	Q	201	1/1	0.88	0.16	145,145,145,145	0
26	MG	A	1781	1/1	0.88	0.07	104,104,104,104	0
26	MG	S	102	1/1	0.88	0.08	106,106,106,106	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
26	MG	A	1798	1/1	0.89	0.07	464,464,464,464	0
26	MG	A	1734	1/1	0.89	0.60	124,124,124,124	0
26	MG	A	1887	1/1	0.89	0.23	102,102,102,102	0
26	MG	A	1855	1/1	0.89	0.10	401,401,401,401	0
26	MG	A	1892	1/1	0.89	0.27	92,92,92,92	0
26	MG	A	1872	1/1	0.89	0.14	359,359,359,359	0
26	MG	A	1809	1/1	0.89	0.10	494,494,494,494	0
26	MG	A	1874	1/1	0.89	0.24	467,467,467,467	0
26	MG	A	1859	1/1	0.89	0.17	427,427,427,427	0
26	MG	A	1838	1/1	0.89	0.27	538,538,538,538	0
26	MG	A	1824	1/1	0.89	0.18	503,503,503,503	0
26	MG	A	1918	1/1	0.89	0.11	75,75,75,75	0
26	MG	A	1666	1/1	0.90	0.09	149,149,149,149	0
26	MG	A	1880	1/1	0.90	0.11	508,508,508,508	0
26	MG	A	1726	1/1	0.90	0.30	98,98,98,98	0
26	MG	A	1835	1/1	0.90	0.21	309,309,309,309	0
26	MG	A	1817	1/1	0.90	0.19	419,419,419,419	0
26	MG	A	1890	1/1	0.90	0.09	112,112,112,112	0
26	MG	D	304	1/1	0.90	0.17	455,455,455,455	0
26	MG	A	1644	1/1	0.90	0.25	127,127,127,127	0
26	MG	A	1712	1/1	0.90	0.10	170,170,170,170	0
26	MG	A	1811	1/1	0.90	0.35	468,468,468,468	0
26	MG	A	1857	1/1	0.90	0.28	308,308,308,308	0
26	MG	A	1858	1/1	0.90	0.23	355,355,355,355	0
26	MG	A	1785	1/1	0.90	0.04	108,108,108,108	0
26	MG	A	1900	1/1	0.90	0.11	93,93,93,93	0
26	MG	A	1759	1/1	0.91	0.23	86,86,86,86	0
26	MG	A	1861	1/1	0.91	0.24	443,443,443,443	0
26	MG	A	1851	1/1	0.91	0.12	328,328,328,328	0
26	MG	A	1654	1/1	0.91	0.10	161,161,161,161	0
26	MG	A	1881	1/1	0.91	0.11	414,414,414,414	0
26	MG	A	1753	1/1	0.91	0.17	109,109,109,109	0
26	MG	A	1718	1/1	0.91	0.10	326,326,326,326	0
26	MG	N	102	1/1	0.91	0.19	107,107,107,107	0
26	MG	A	1668	1/1	0.91	0.21	173,173,173,173	0
26	MG	P	103	1/1	0.91	0.17	96,96,96,96	0
26	MG	A	1889	1/1	0.91	0.08	95,95,95,95	0
26	MG	A	1646	1/1	0.91	0.09	136,136,136,136	0
26	MG	A	1609	1/1	0.91	0.06	157,157,157,157	0
26	MG	A	1639	1/1	0.92	0.17	87,87,87,87	0
26	MG	A	1746	1/1	0.92	0.18	104,104,104,104	0
26	MG	A	1664	1/1	0.92	0.19	154,154,154,154	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
26	MG	A	1825	1/1	0.92	0.15	436,436,436,436	0
26	MG	A	1879	1/1	0.92	0.16	438,438,438,438	0
26	MG	A	1727	1/1	0.92	0.26	84,84,84,84	0
26	MG	A	1829	1/1	0.92	0.23	489,489,489,489	0
26	MG	P	101	1/1	0.92	0.20	58,58,58,58	0
26	MG	A	1677	1/1	0.92	0.19	235,235,235,235	0
26	MG	A	1832	1/1	0.92	0.09	278,278,278,278	0
26	MG	A	1815	1/1	0.92	0.24	506,506,506,506	0
26	MG	A	1642	1/1	0.92	0.08	78,78,78,78	0
26	MG	A	1617	1/1	0.92	0.19	85,85,85,85	0
26	MG	A	1816	1/1	0.93	0.13	454,454,454,454	0
26	MG	A	1655	1/1	0.93	0.13	125,125,125,125	0
26	MG	A	1772	1/1	0.93	0.05	93,93,93,93	0
26	MG	A	1669	1/1	0.93	0.06	123,123,123,123	0
26	MG	A	1659	1/1	0.93	0.19	90,90,90,90	0
26	MG	A	1748	1/1	0.93	0.10	110,110,110,110	0
26	MG	A	1782	1/1	0.93	0.22	87,87,87,87	0
26	MG	A	1709	1/1	0.93	0.17	245,245,245,245	0
26	MG	A	1828	1/1	0.93	0.15	432,432,432,432	0
26	MG	A	1613	1/1	0.93	0.07	202,202,202,202	0
26	MG	A	1663	1/1	0.93	0.16	160,160,160,160	0
26	MG	A	1807	1/1	0.93	0.48	517,517,517,517	1
26	MG	A	1604	1/1	0.93	0.10	91,91,91,91	0
26	MG	A	1737	1/1	0.93	0.17	89,89,89,89	0
26	MG	A	1899	1/1	0.93	0.15	68,68,68,68	0
26	MG	A	1810	1/1	0.93	0.13	474,474,474,474	0
26	MG	A	1622	1/1	0.93	0.08	81,81,81,81	0
26	MG	J	201	1/1	0.93	0.16	109,109,109,109	0
26	MG	A	1761	1/1	0.93	0.09	105,105,105,105	0
26	MG	A	1688	1/1	0.93	0.20	186,186,186,186	0
26	MG	A	1905	1/1	0.93	0.07	105,105,105,105	0
26	MG	A	1906	1/1	0.93	0.08	64,64,64,64	0
26	MG	A	1721	1/1	0.93	0.17	92,92,92,92	0
26	MG	A	1624	1/1	0.93	0.34	147,147,147,147	0
26	MG	A	1847	1/1	0.93	0.21	441,441,441,441	0
26	MG	A	1920	1/1	0.94	0.07	138,138,138,138	0
26	MG	A	1840	1/1	0.94	0.20	467,467,467,467	1
26	MG	A	1636	1/1	0.94	0.15	88,88,88,88	0
26	MG	A	1842	1/1	0.94	0.10	488,488,488,488	0
26	MG	A	1735	1/1	0.94	0.07	106,106,106,106	0
26	MG	A	1927	1/1	0.94	0.26	112,112,112,112	0
26	MG	A	1774	1/1	0.94	0.32	109,109,109,109	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
26	MG	A	1827	1/1	0.94	0.09	251,251,251,251	0
26	MG	A	1716	1/1	0.94	0.08	132,132,132,132	0
26	MG	A	1760	1/1	0.94	0.11	88,88,88,88	0
26	MG	A	1780	1/1	0.94	0.26	119,119,119,119	0
26	MG	A	1621	1/1	0.94	0.06	131,131,131,131	0
26	MG	A	1852	1/1	0.94	0.27	450,450,450,450	0
26	MG	A	1896	1/1	0.94	0.08	114,114,114,114	0
26	MG	A	1806	1/1	0.94	0.43	505,505,505,505	0
26	MG	A	1723	1/1	0.94	0.13	117,117,117,117	0
26	MG	A	1626	1/1	0.94	0.19	245,245,245,245	0
26	MG	A	1732	1/1	0.94	0.11	100,100,100,100	0
26	MG	A	1919	1/1	0.94	0.20	78,78,78,78	0
26	MG	A	1637	1/1	0.95	0.11	228,228,228,228	0
26	MG	A	1854	1/1	0.95	0.18	418,418,418,418	0
26	MG	A	1691	1/1	0.95	0.15	186,186,186,186	0
26	MG	A	1783	1/1	0.95	0.04	110,110,110,110	0
26	MG	A	1692	1/1	0.95	0.07	182,182,182,182	0
26	MG	A	1633	1/1	0.95	0.06	118,118,118,118	0
26	MG	A	1831	1/1	0.95	0.36	395,395,395,395	0
26	MG	A	1649	1/1	0.95	0.14	84,84,84,84	0
26	MG	A	1834	1/1	0.95	0.35	412,412,412,412	1
26	MG	A	1720	1/1	0.95	0.11	74,74,74,74	0
26	MG	A	1610	1/1	0.95	0.11	81,81,81,81	0
26	MG	A	1702	1/1	0.95	0.06	279,279,279,279	0
26	MG	A	1667	1/1	0.95	0.07	119,119,119,119	0
26	MG	A	1707	1/1	0.95	0.06	135,135,135,135	0
26	MG	A	1708	1/1	0.95	0.29	152,152,152,152	0
26	MG	A	1770	1/1	0.95	0.71	106,106,106,106	0
26	MG	A	1795	1/1	0.95	0.31	359,359,359,359	0
26	MG	A	1685	1/1	0.95	0.21	126,126,126,126	0
26	MG	A	1747	1/1	0.95	0.27	115,115,115,115	0
26	MG	A	1776	1/1	0.95	0.18	96,96,96,96	0
26	MG	A	1822	1/1	0.95	0.14	293,293,293,293	0
26	MG	A	1710	1/1	0.95	0.11	253,253,253,253	0
26	MG	A	1686	1/1	0.95	0.14	184,184,184,184	0
26	MG	A	1754	1/1	0.95	0.11	85,85,85,85	0
26	MG	A	1705	1/1	0.96	0.12	74,74,74,74	0
26	MG	A	1773	1/1	0.96	0.07	103,103,103,103	0
26	MG	A	1620	1/1	0.96	0.09	166,166,166,166	0
26	MG	A	1885	1/1	0.96	0.10	84,84,84,84	0
26	MG	A	1687	1/1	0.96	0.07	106,106,106,106	0
26	MG	A	1615	1/1	0.96	0.06	147,147,147,147	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
26	MG	A	1661	1/1	0.96	0.23	244,244,244,244	0
26	MG	A	1836	1/1	0.96	0.26	416,416,416,416	1
26	MG	A	1605	1/1	0.96	0.08	254,254,254,254	0
26	MG	A	1694	1/1	0.96	0.13	87,87,87,87	0
26	MG	A	1922	1/1	0.96	0.13	110,110,110,110	0
26	MG	A	1818	1/1	0.96	0.05	189,189,189,189	0
26	MG	A	1924	1/1	0.96	0.17	131,131,131,131	0
26	MG	A	1632	1/1	0.96	0.28	248,248,248,248	0
26	MG	A	1864	1/1	0.96	0.15	393,393,393,393	0
26	MG	A	1762	1/1	0.96	0.14	82,82,82,82	0
26	MG	A	1866	1/1	0.96	0.16	434,434,434,434	0
26	MG	A	1868	1/1	0.96	0.37	380,380,380,380	0
26	MG	E	201	1/1	0.96	0.11	95,95,95,95	0
26	MG	A	1821	1/1	0.96	0.25	428,428,428,428	0
26	MG	A	1765	1/1	0.96	0.07	104,104,104,104	0
26	MG	A	1697	1/1	0.96	0.05	135,135,135,135	0
26	MG	A	1612	1/1	0.96	0.25	281,281,281,281	0
26	MG	A	1656	1/1	0.96	0.10	236,236,236,236	0
26	MG	A	1752	1/1	0.96	0.11	91,91,91,91	0
26	MG	A	1876	1/1	0.96	0.29	463,463,463,463	1
26	MG	A	1657	1/1	0.96	0.17	220,220,220,220	0
26	MG	A	1850	1/1	0.96	0.07	236,236,236,236	0
26	MG	A	1771	1/1	0.96	0.10	102,102,102,102	0
26	MG	A	1911	1/1	0.96	0.08	100,100,100,100	0
26	MG	A	1695	1/1	0.97	0.06	176,176,176,176	0
26	MG	A	1803	1/1	0.97	0.09	345,345,345,345	0
26	MG	A	1867	1/1	0.97	0.16	413,413,413,413	1
26	MG	A	1882	1/1	0.97	0.21	315,315,315,315	0
26	MG	E	202	1/1	0.97	0.04	124,124,124,124	0
26	MG	A	1608	1/1	0.97	0.10	73,73,73,73	0
26	MG	A	1751	1/1	0.97	0.20	76,76,76,76	0
26	MG	A	1714	1/1	0.97	0.05	108,108,108,108	0
26	MG	A	1672	1/1	0.97	0.10	166,166,166,166	0
26	MG	A	1606	1/1	0.97	0.11	87,87,87,87	0
26	MG	A	1786	1/1	0.97	0.05	109,109,109,109	0
26	MG	A	1693	1/1	0.97	0.05	108,108,108,108	0
26	MG	A	1745	1/1	0.97	0.17	92,92,92,92	0
26	MG	A	1893	1/1	0.97	0.31	114,114,114,114	0
26	MG	A	1778	1/1	0.97	0.04	119,119,119,119	1
26	MG	A	1652	1/1	0.97	0.05	72,72,72,72	0
26	MG	A	1775	1/1	0.98	0.10	79,79,79,79	0
26	MG	A	1627	1/1	0.98	0.06	141,141,141,141	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
26	MG	A	1738	1/1	0.98	0.04	68,68,68,68	0
26	MG	A	1701	1/1	0.98	0.07	108,108,108,108	0
26	MG	A	1843	1/1	0.98	0.28	357,357,357,357	0
26	MG	A	1713	1/1	0.98	0.07	211,211,211,211	0
26	MG	A	1869	1/1	0.98	0.14	431,431,431,431	0
26	MG	A	1725	1/1	0.98	0.06	92,92,92,92	0
26	MG	A	1640	1/1	0.98	0.25	172,172,172,172	0
26	MG	A	1715	1/1	0.98	0.13	229,229,229,229	0
26	MG	A	1653	1/1	0.98	0.15	96,96,96,96	0
26	MG	A	1763	1/1	0.98	0.04	120,120,120,120	0
26	MG	A	1764	1/1	0.98	0.05	78,78,78,78	0
26	MG	A	1647	1/1	0.98	0.10	104,104,104,104	0
26	MG	A	1648	1/1	0.98	0.08	93,93,93,93	0
26	MG	E	203	1/1	0.98	0.05	101,101,101,101	0
26	MG	A	1731	1/1	0.98	0.09	68,68,68,68	0
26	MG	A	1689	1/1	0.98	0.06	126,126,126,126	0
26	MG	A	1749	1/1	0.98	0.06	84,84,84,84	0
26	MG	H	201	1/1	0.98	0.21	67,67,67,67	0
26	MG	A	1833	1/1	0.98	0.28	335,335,335,335	0
26	MG	A	1750	1/1	0.98	0.07	74,74,74,74	0
26	MG	A	1883	1/1	0.98	0.22	443,443,443,443	0
26	MG	A	1733	1/1	0.98	0.11	70,70,70,70	0
26	MG	A	1698	1/1	0.98	0.08	124,124,124,124	0
26	MG	A	1630	1/1	0.98	0.08	158,158,158,158	0
26	MG	A	1736	1/1	0.98	0.07	123,123,123,123	0
26	MG	A	1862	1/1	0.98	0.09	268,268,268,268	0
28	ZN	D	301	1/1	0.98	0.20	138,138,138,138	0
26	MG	A	1611	1/1	0.99	0.05	113,113,113,113	0
26	MG	A	1903	1/1	0.99	0.06	78,78,78,78	0
26	MG	A	1651	1/1	0.99	0.04	110,110,110,110	0
26	MG	A	1703	1/1	0.99	0.04	97,97,97,97	0
26	MG	A	1704	1/1	0.99	0.06	104,104,104,104	0
26	MG	D	303	1/1	0.99	0.09	104,104,104,104	0
26	MG	A	1638	1/1	0.99	0.03	86,86,86,86	0
26	MG	A	1603	1/1	0.99	0.10	277,277,277,277	0
26	MG	A	1602	1/1	0.99	0.14	66,66,66,66	1
26	MG	A	1888	1/1	0.99	0.05	89,89,89,89	0
26	MG	A	1641	1/1	0.99	0.04	102,102,102,102	0
26	MG	A	1631	1/1	0.99	0.12	158,158,158,158	0
26	MG	A	1690	1/1	0.99	0.04	114,114,114,114	0
26	MG	A	1643	1/1	0.99	0.02	71,71,71,71	0
26	MG	A	1658	1/1	0.99	0.03	115,115,115,115	0

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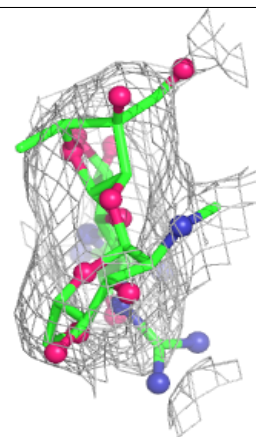
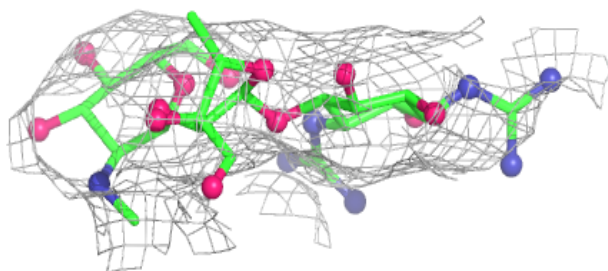
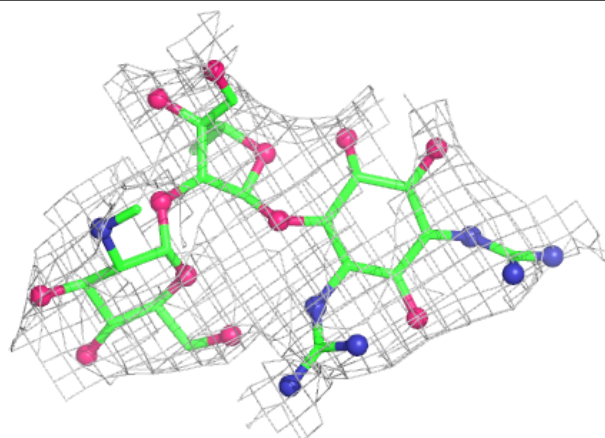
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
26	MG	A	1625	1/1	0.99	0.03	113,113,113,113	0
26	MG	A	1676	1/1	0.99	0.08	158,158,158,158	0
26	MG	A	1645	1/1	0.99	0.12	227,227,227,227	0
26	MG	A	1619	1/1	0.99	0.03	64,64,64,64	0
26	MG	A	1662	1/1	0.99	0.04	123,123,123,123	0
26	MG	A	1634	1/1	0.99	0.04	107,107,107,107	0
26	MG	A	1635	1/1	0.99	0.05	74,74,74,74	0
27	SRY	A	1928	40/40	0.99	0.05	70,100,124,130	0
26	MG	A	1607	1/1	0.99	0.04	154,154,154,154	0
28	ZN	N	101	1/1	0.99	0.03	164,164,164,164	0
26	MG	A	1623	1/1	1.00	0.03	67,67,67,67	0
26	MG	A	1616	1/1	1.00	0.05	63,63,63,63	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around SRY A 1928:

2mF_o-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.